Advances in Experimental Medicine and Biology 1161

### Kenneth V. Honn Darryl C. Zeldin *Editors*

# The Role of Bioactive Lipids in Cancer, Inflammation and Related Diseases



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Kenneth V. Honn • Darryl C. Zeldin Editors

## The Role of Bioactive Lipids in Cancer, Inflammation and Related Diseases



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#### **About the Editors**



Kenneth Honn, Ph.D., Distinguished V. Professor and Director, Bioactive Lipids Research Program, Wayne State University Kenneth Honn, Ph.D., is a distinguished professor and an adjunct professor in the Wayne State University School of Medicine Departments of Pathology and Oncology and Department of Chemistry, respectively. He is director of the Bioactive Lipids Research Program and serves as a member of the Cancer Biology Graduate Program and of the Barbara Ann Karmanos Cancer Institute. He is the founding member and president of the Eicosanoid Research Foundation and chairman of the International Conference on Bioactive Lipids in Cancer, Inflammation and Related Diseases, a biennial international conference he initiated in 1989. He received his Ph.D. in Endocrinology from Wayne State University in 1977. With more than 30 years of experience in the fields of cancer, inflammation, and bioactive lipids, his laboratory focuses on bioactive lipids and integrin receptors and the role they play in various aspects of tumor progression, namely, cell growth and apoptosis, angiogenesis, and tumor cell matrix interactions. His lab concentrates on lipoxygenases, in particular 12-lipoxygenase and its metabolic product 12(S)-HETE. In addition to his research on bioactive lipids in tumor progression, he has collaborated with scientists at the Perinatology Research Branch of the National Institutes of Health for the past 4 years, studying the role of lipids in human parturition, in particular their role in preterm labor and term labor. Research efforts in his laboratory have directly led to six

clinical trials, and he holds 17 US patents, 7 of which are based on the generation of novel chemotherapeutic/radiation sensitizing compounds. He is the author of more than 300 published works. He has had continuous external funding with more than 50 grants totaling in excess of \$25 million. He also has and continues to serve on numerous study sections, reviewing grants for the National Cancer Institute and the Department of Defense, and provides consultation to pharmaceutical companies. In addition, he is a member of the editorial boards of 12 scientific journals and is coeditor in chief of *Cancer and Metastasis Reviews*.



Darryl C. Zeldin, M.D., Scientific Director, National Institute of Environmental Health Sciences (NIEHS) National Institutes of Health Darryl C. Zeldin, M.D., is the scientific director at the National Institute of Environmental Health Sciences (NIEHS), National Institutes of Health (NIH). He is an internationally recognized expert on eicosanoids (lipid mediators) and their role in regulating respiratory and cardiovascular function. He received his medical degree from Indiana University in 1986 and completed his Internal Medicine Residency at Duke University Medical Center in 1989 and a Fellowship in Pulmonary/Critical Care Medicine at Vanderbilt University in 1993. He was recruited to the NIH in 1994 and promoted to senior investigator with tenure in 2001. He served as the NIEHS clinical director from 2007 to 2011 prior to becoming scientific director in 2011. He is board certified in Internal Medicine and Pulmonary Medicine, is a fellow in the American College of Chest Physicians and in the American Heart Association, and is an elected member of the American Society for Clinical Investigation and Association of American Physicians. He has coauthored over 340 primary peer-reviewed manuscripts, and his work has been cited over 25,000 times (h-index 86). He has mentored over 75 postbaccalaureate fellows, graduate students, medical students, postdoctoral research fellows,

and clinical research fellows. As the NIEHS scientific director, he is responsible for one of the largest intramural research programs at the NIH with over 1000 scientists in 10 departments and 15 core facilities and an annual budget of over \$130M. His own research has also been featured on NPR, Good Morning America, *USA Today*, US News & World Report, PBS, and on other internationally recognized media venues.

K. V. Honn (🖂)

D. C. Zeldin  $(\boxtimes)$ 

#### Introduction

#### Kenneth V. Honn and Darryl C. Zeldin

In addition to this introduction, this book contains 18 outstanding chapters based on comprehensive and detailed reviews of timely topics presented at the 15th International Conference on Bioactive Lipids in Cancer, Inflammation and Related Diseases held in Puerto Vallarta, Mexico on October 22–25, 2017.

Held biennially since 1989, this ongoing conference series provides a scientific program that is comprehensive and structured to highlight research at the cutting edge of science on the role of lipid mediators in various physiological and pathological processes in a wide range of therapeutic areas. Over 315 basic researchers and clinicians representing 32 countries attended this most recent meeting. Dr. Jeffrey M. Drazen, Editor-in-Chief of the *New England Journal of Medicine*, received the Exceptional Contributions to Human Physiology and Translational Medicine Award and presented an opening lecture on "Data Sharing in Clinical Trials." Dr. Charles N. Serhan received the Lifetime Achievement Award and

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presented a lecture on "Decoding New Lipid Mediators and Mechanisms of Resolution of Inflammation. Infections and Tissue Regeneration." Drs. Bruce D. Hammock, Jorge H. Capdevila and Darryl C. Zeldin shared the Outstanding Achievement Award for their work on the P450 epoxygenase pathway of arachidonic acid metabolism and delivered lectures on the role of fatty acids in neuropathic pain, cardiovascular disease and lung inflammation. There were three Eicosanoid Research Foundation Young Investigator awards presented to Drs. Karin Larsson (cancer), Jesmond Dalli (inflammation) and Scott Hansen (structure-function). Dr. Shu Xu from the University of Toledo was presented with the Santosh Nigam Memorial Outstanding Young Scientist award for his presentation on "The Structure of the Catalytic Domain of 12-Lipoxygenase." There were 50 lectures organized into 3 Plenary Sessions, 14 scientific sessions and 140 poster presentations.

The specialized pro-resolving lipid mediators or SPMs (e.g., resolvins, lipoxins, maresins) have received wide-spread attention as to their role in inflammatory processes. Reviews presented in this book detail recent advances in understanding the role of SPMs in inflammatory conditions of the eye, brain and cardiovascular system. Dr. Elizabeth Berger (Chap. 2) summarized recent literature on infectious keratitis (bacterial, viral, fungal) and endophthalmitis with an emphasis on





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the host response and the role of SPMs in resolution of the eye inflammation. Drs. Darlene Dartt, Robin R. Hodges, and Charles N. Serhan (Chap. 3) provided a comprehensive summary of the role of resolvin D1 (RvD1), its cognate receptor (ALX/FPR2 or GPR32) and downstream signaling pathways (PLC, PLD, PLA2, EGFR, and ERK) in preserving ocular surface homeostasis and regulating conjunctival goblet cell mucin secretion. Dr. Niccolo Terrando (Chap. 4) reported on the role of SPMs in the brain with an emphasis on postoperative neuroinflammation and cognitive function. Dr. Rafael Bojalil (Chap. 5) reviewed the role of pro-resolving mediators in cardiovascular diseases, notably in regulating inflammation. Dr. Ganesh Halade (Chap. 6) summarized recent literature on the role of SPMs in resolution of cardiac inflammation, tissue repair and remodeling in heart failure models. Dr. Jesmond Dalli (Chap. 7) reported on the biological actions of resolvins in the cardiovascular system and their role in mediating the actions of statins.

The book contains two chapters that overview recent advances in cyclooxygenase-derived eicosanoids in the brain. Dr. Philip Kingsley (Chap. 8) reported on the identification and role of prostaglandin glycerol esters (PG-Gs) in the brain, detailing their production, metabolism and bioactivity. Dr. Karin Larsson (Chap. 9) summarized recent data on the role of prostaglandin E2 (PGE2) in neuroblastoma, in particular its actions in regulating angiogenesis, immunosuppression in the tumor microenvironment, and tumor growth. There are three chapters that provide an overview on the biological relevance of cytochrome P450 (CYP) and lipoxygenase-derived eicosanoids. Dr. Pei-an Shih (Chap. 10) reported that CYP-derived eicosanoids are prognostic biomarkers for certain neuropsychiatric disorders such as depression. Dr. Guodong Zhang and coworkers (Chap. 11) discussed recent studies on the roles of CYP-derived eicosanoids and soluble epoxide hydrolase in the pathogenesis of colonic inflammation and colorectal cancer. Dr. Klaus Van Leyen and co-workers (Chap. 12) summarized the biological relevance of lipoxygenasederived eicosanoids in ischemic stroke and neuronal cell death in the brain.

Sphingolipids are a unique class of bioactive lipids with significant chemical diversity. Recent advances in the field of sphingolipids and their role in the eye, brain, intestine and immune system are discussed in this book. Dr. Yasuyuki Kihara (Chap. 13) provided a review of eicosanoid and other bioactive lipid signaling involvement in the neuroinflammatory mechanisms underlying multiple sclerosis. Drs. Koushik Mondal and Nawajes Mandal (Chap. 14) reported on the role of bioactive sphingolipids including ceramide and sphingosine in ocular inflammation and eye diseases such as uveitis, diabetic retinopathy and glaucoma. Drs. Sabrin Albeituni and Johnny Stiban (Chap. 15) reported on the role of ceramides and other sphingolipids in immune cell function and inflammation in cancer, multiple sclerosis and inflammatory bowel disease.

The endocannabinoids and their receptors affect both central nervous system and peripheral processes. There are two chapters on recent advances in endocannabinoids in the brain. Dr. Heather Bradshaw and colleagues (Chap. 16) reported on the role of endogenous cannabinoids and their receptors in the pathogenesis of traumatic brain injury. Dr. Aditi Das (Chap. 17) sumrecent information marized on the anti-inflammatory and vasoactive role of omega-3 endocannabinoid epoxide metabolites in the brain. In addition, there is a chapter by Dr. Andres Trostchansky (Chap. 18) on the relationship of lipid metabolism and lipid derived metabolites with the onset and progression of amylotrophic latereral sclerosis in humans. This book is capped off with a concise, scholarly review by Drs. Carlo Barnaba and Ilce G. Medina-Meza on the role of flavonoids in the reduction of inflammation and lipid oxidation in the pathogenesis of cardiovascular disease (Chap. 19).



2

#### Understanding the Role of Pro-resolving Lipid Mediators in Infectious Keratitis

Elizabeth A. Berger

#### 2.1 Infectious Keratitis

Keratitis is a sight-threatening inflammatory condition of the cornea that can be caused by both infectious and non-infectious agents. Physical or chemical trauma are typically related to noninfectious keratitis, which may then become secondarily infected or remain non-infected. Etiology of infectious keratitis is most often associated with bacteria; but viruses, fungi, and parasites are common causative pathogens as well. As a global concern, common risk factors include: systemic immunosuppression (secondary to malnutrition, alcoholism, diabetes, steroid use), previous corneal surgery (refractive corneal surgery, penetrating keratoplasty), extended wear contact lens use, pre-existing ocular surface diseases (dry eye, epithelial defect) and ocular trauma (agriculture- or farm-related) [1-8]. Annual rates of incidence include nearly one million clinical visits due to keratitis in the United States, while it has been reported that roughly two million people develop corneal ulcers in India. Clinically, patients may show signs of eye pain (ranging from mild to severe), blurred vision, photophobia, chemosis and redness. Pathogenesis is gener-

ally characterized by rapid progression, focal white infiltrates with underlying stromal inflammation, corneal thinning, stromal edema, mucopurulent discharge and hypopyon, which can lead to corneal scarring, endophthalmitis, and perforation. In fact, corneal opacity is not only a complication of keratitis, but among the leading causes of legal blindness worldwide. Despite that empirical treatment effectively controls most of the pathogens implicated in infectious keratitis, improved clinical outcomes are not guaranteed. Further, if treatment is not initiated in a timely manner, good visual outcome is reduced to approximately 50% of keratitis patients [9]. Moreover, resultant structural alterations, loss of tissue and an unresolved host response remain unaddressed through current clinical management of this condition.

#### 2.2 Host Response to Infectious Keratitis

A large body of work has been carried out therefore elucidating the keratitis-induced host innate immune response. During infection, corneal ulceration progresses due to inflammatory mediators released by the pathogen, as well as from corneal epithelial and stromal cells and infiltrated inflammatory cells [10]. Though infiltrating leukocytes are a requisite feature of an effective

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inflammatory response, persistence and chronic activation of macrophages, neutrophils/PMN and T cells contribute to disease pathogenesis through sustained production of inflammatory mediators, proteolytic enzymes and resultant tissue necrosis. Similarly, cytokines and chemokines such as IL-1 $\alpha/\beta$ , TNF- $\alpha$ , IFN- $\gamma$  and MIP-2 promote antimicrobial effector mechanisms, activate phagocytic killing and recruit additional inflammatory cells. However, the continued production of such pro-inflammatory cytokines/chemokines contributes to the destruction of the corneal microenvironment. In addition to an upregulation of cytokines, lipid mediators are also released, including prostaglandins, thromboxanes and platelet-activating factor. It is well-known that these arachidonic acid-derived mediators play key roles in the initiation of inflammation, including the recruitment of leukocytes (particularly neutrophils). Although necessary, it is imperative that this biological cascade is both inhibited and dissolved. These initial proinflammatory pathways are balanced by proresolving lipid signals known as specialized pro-resolving lipid mediators (SPMs). In fact, it has been shown that prostaglandins (PGE<sub>2</sub> and

PGD<sub>2</sub>) initiate lipid mediator class switching [11]. Biosynthesized during the active phase of resolution, SPMs play a pivotal role as endogenous agonists stimulating the resolution of inflammation – a key feature of a healthy, inflammatory productive response [12]. Proresolving actions include limiting PMN infiltration, regulating the cytokine profile [13, 14], reducing pain [15], and efferocytosis [16, 17]. SPMs best associated with the eye are derived from two major polyunsaturated fatty acids; arachidonic acid (AA) and docosahexaenoic acid (DHA) and are targeted by lipoxygenase (LOX) enzymes, which comprise the main pathways for SPM biosynthesis (Fig. 2.1). Studies have demonstrated LOX activity in the cornea with 15-LOX appearing to be largely protective as a key enzyme for the generation of SPMs [12, 18–20]. Alox15 is the most abundant lipoxygenase in the healthy murine cornea [21-23]. Gronert et al. have established the presence of functional 5-LOX and 12/15-LOX in mouse corneal epithelium and corneas [19]. Furthermore, both healthy and inflamed corneas express 12/15-LOX as detected from epithelial cells and infiltrated neutrophils [19]. AA-derived lipoxin A4 (LXA4) can



Fig. 2.1 Schematic of major SPM pathways involved in the cornea

be transcellularly biosynthesized during leukocyte interactions with mucosal cells, such as PMN interactions with epithelial cells [24]. Studies have revealed a protective role for LXA4, whereby it has been shown to accelerate corneal re-epithelization and limit neovascularization using a thermal injury model [25]. In addition to AA-derived lipoxins, DHA is targeted by phospholipase A2 and subsequently LOX and COX-2 produce di- and trihydroxylated DHA derivatives including D series resolvins, protectins and maresins [26]. These SPMs are particularly relevant to the eye as studies have shown that RvD1 reduces the inflammatory response during endotoxin-induced uveitis [25], allergic eye disease [27], and dry eye [28].

#### 2.3 Current Treatments for Infectious Keratitis

This collective work illuminates host factors that exacerbate the progression of keratitis, indicating that the pathogenicity of disease is a combination of microbe-induced damage and an unresolved host response - the latter of which may be due to ocular immune privilege. Regardless, a number of adjunctive treatments have been considered, including cross-linking, anti-collagenases, antiinflammatories, and corticosteroids. Collagen cross-linking was found to improve corneal re-epithelization and resistance to enzymatic degradation, reduce corneal melting, and exert effects bactericidal [29–31]. However, complications include endothelial cell loss and reactivation of HSV infections, thus warranting further investigation. Non-steroidal antiinflammatory treatments have been investigated in an attempt to prevent excessive inflammation; but shown to exacerbate the disease response in the absence of concomitant antibiotic therapy or exhibit toxicity issues complicated by corneal melting [32–34]. Indecision continues to exist regarding the benefits and risks associated with use of corticosteroids. The Steroids for Corneal Ulcers Trial (SCUT) provides evidence for improved visual acuity in bacterial keratitis patients with no reported increase in adverse

events. Yet, other studies have indicated delayed epithelial healing and worsened disease outcome [35–37]. Additionally, a comprehensive review evaluating the effects of corticosteroids from 1950 to 2000 concluded that the role of corticosteroids in the adjunctive treatment of infectious keratitis remains unsubstantiated [38]. Further, a review by McGhee et al. states that corticosteroid-induced ocular morbidity includes: ocular hypertension, glaucoma, cataract formation, tear film instability, and crystalline keratopathy [39]. To this end, this review will highlight the compelling evidence for the development of pro-resolving molecules as an adjuvant therapy for the treatment of infectious keratitis - with focus on bacterial, viral and fungal infections.

#### 2.4 Bacterial Keratitis

Bacteria remain the most common cause of infectious keratitis with studies indicating that bacterial keratitis comprises approximately 90% of infectious keratitis cases. Epidemiological studies have revealed that between 54-94% of all corneal infections are due to bacteria. Pseudomonas aeruginosa and Staphylococcus aureus have been reported as the more prevalent bacteria associated with infectious keratitis [40–42]. Staphylococcus aureus as the most common ocular isolate [43]; while Pseudomonas aeruginosa is the most frequently isolated of Gram negative ocular infections [22]. Moreover, Pseudomonas aeruginosa ulcers have been shown to result in a more progressive disease with large infiltrate and scarring [43, 56] and not benefit from the addition of corticosteroids [36]. Current treatment of microbial keratitis consists primarily of fourth generation ophthalmic fluoroquinolones (moxifloxcin and gatifloxacin), which are effective against both Gram-positive and Gram-negative bacteria. This class of antibiotics also exhibits better mutant prevention characteristics and penetrates well into ocular tissues. However, antibiotic-resistance is of major concern; in the U.S., roughly 80% of methicillin-resistant S. aureus ocular isolates have been reported as resistant to

fluoroquinolones [44–46]. Multi-drug resistance rates for *Pseudomonas* are on the rise, as well [47, 48].

Work using a mouse model of Pseudomonasinduced keratitis has revealed the importance of SPM circuits in the resolution of inflammation [23]. Lipid mediator profiles were characterized in susceptible (corneal thinning, perforation) and resistant (resolution) phenotypes and indicated that activation of SPM pathways are requisite for a balanced inflammatory response characterized by the resolution of disease. Furthermore, this study indicated a critical role for 15-LOX in influencing inflammatory cell function. Without 15-LOX enzymatic activity, essential innate inflammatory functions (phagocytosis, efferocytosis) were impaired, leading to an exacerbated disease response. This supports previous work that showed 15-LOX<sup>-/-</sup> mice resulted in impaired wound healing and amplified inflammatory angiogenesis [19, 49, 50]. In addition, potential experimental treatments that have been shown to improve disease response to Pseudomonas-induced keratitis appear to have a common theme - the activation of SPM circuitry. Vasoactive intestinal peptide or VIP has been demonstrated to exert its immunoregulatory effects, in part, through upregulation of lipoxygenase enzymes in corneas of Pseudomonas-infected mice [51, 52]. Additional work in the mouse model has revealed that VIP increases RvD1 and modulates the ALX/FPR2 receptor axis toward inflammation resolution [52]. Ligands for this receptor include both LXA4 and RvD1 [53]; the latter of which has been shown to reduce corneal neovascularization [54]. Evidence also indicates that thymosin beta-4 (T $\beta$ 4), another therapeutic molecule, may carry out its profound effects through activation of SPM circuits [55]. Adjunct T $\beta$ 4 treatment with antibiotic resulted in increased 12- and 12/15-LOX mRNA levels, while COX-2 and 5-LOX were decreased after infection [55]. This is further supported by increased RvD1 and its receptor, ALX/FPR2. In contrast, proinflammatory lipid mediator pathways were affected, as evidenced by lower levels of LTB4 and its receptor, BLT1. This work underscores

the importance of SPM circuit activation in the resolution of inflammation following corneal infection. Further, it highlights the significant potential of combination treatments - where antibiotics alone cannot activate the resolution arm of inflammation; yet without the antibiotic, T $\beta$ 4 (and other activators of SPM pathways) may not be able to overcome the bacterial burden and subsequently move toward active resolution. Work carried out by the Pearlman group investigated the role of RvE1 in the corneal inflammatory response induced by LPS and antibiotic-killed Pseudomonas aeruginosa and Staphylococcus aureus [56]. Cytokine production was significantly reduced in human corneal epithelial cells and neutrophils, as well as mouse cornea and macrophages. In addition, a decrease in neutrophil infiltrate and reduced corneal haze was observed after RvE1 treatment following bacteria- and LPS-induced corneal inflammation.

#### 2.5 Viral Keratitis

Herpes simplex virus (HSV) keratitis affects an estimated 500,000 people in the US and an estimated 1.5 million globally per annum [57, 58]. Though it begins as a subclinical infection of the cornea, HSV establishes latency within the trigeminal ganglia and when reactivated, it causes recurrent infections that result in decreased corneal sensation, neurotrophic keratitis, stromal opacity, scarring, and blindness. In fact, HSV keratitis is the predominant cause of unilateral infectious corneal blindness in most developed nations [59]. Though rare, bilateral infection does occur in approximately 1.3-12% of patients [60]. Primary HSV infections are typically overlooked in clinic as adenoviral the conjunctivitis. Epithelial infection is typically caused by actively replicating virus and presents itself as the classic herpetic corneal lesion - a dendritic ulcer - with minimal stromal inflammation [61]. Once resolved, a dendritic scar or ghost dendrite may persist in the superficial stroma. A more progressive geographic ulcer (also caused by live replicating virus) can occur in immunocompromised patients and

results in a larger epithelial defect. Unfortunately, insufficient corneal wound healing secondary to antiviral toxicity, loss of innervation, and chronic stromal inflammation can result in trophic ulcers. The greatest morbidity is associated with recurrent stromal keratitis and HSV endothelitis due to excessive corneal scarring and neovascularization commonly in response to non-replicating viral particles. Herpes stromal keratitis or HSK can range from focal, multifocal, or diffuse stromal opacities. Disciform keratitis results from endothelial dysfunction in response to viral antigens. Necrotizing keratitis is most commonly observed in patients with multiple recurrent HSV infections and can result in corneal melting and perforation. Less common viral pathogens include varicella-zoster virus (VZV) and cytomegalovirus (CMV). Though treatment varies based on the severity of disease, trifluridine is the most commonly prescribed topical antiviral medication for HSV keratitis in the US [62]. However, due to low bioavailability and ocular surface toxicity, its use is more limited. While in the rest of the world, acyclovir is the preferred treatment as it is equally effective and has lower toxicity issues. Topical corticosteroids, under antiviral cover, are used for the treatment of HSK. Ganciclovir has been found to be just as effective as acyclovir with less toxicity, less likely to promote resistance, and effective against HSV, VZV and CMV. Despite prompt treatment however, scarring is a major complication associated with viral keratitis. Furthermore, since all of the available antivirals for HSV keratitis are nucleoside analogues that inhibit viral replication, there remains the toxicity issue due to host DNA synthesis interference.

Similar to bacterial keratitis, the therapeutic potential of SPMs regarding viral keratitis has been investigated. Work by *Rajasagi* et al. revealed that topical application of aspirintriggered (AT)-RvD1 reduced lesion severity, corneal neovascularization, pro-inflammatory mediators, and infiltration of effector CD4+ T cells and neutrophils using a mouse model of HSK [63]. Further, they found that AT-RvD1 was equally efficacious regardless of whether treatment was started before or after the induction

of infection. The effect on infiltrating inflammatory leukocytes is particularly relevant given that HSK-induced lesions are primarily driven by neutrophils and CD4+ T cells [63]. Work in a corneal transplant model suggests that the observed effect on T cells may be due to an inhibition of dendritic cell maturation and activation [64]. While in vitro studies revealed that AT-RvD1 decreased IFN-y and IL-12 - the latter of which is a requisite signal for Th1 polarization [63]. Another study by the Rouse group found that RvE1 similarly improved HSVinduced keratitis through reduced neovascularization, reduced corneal infiltrate of neutrophils and Т cells (Th1/Th17), downregulation of pro-inflammatory cytokines and chemokines, along with less severe lesions [65]. Neuroprotectin D1(NPD1), another DHAderived pro-resolving mediator [66], was shown to modulate corneal inflammation through similar mechanisms following HSV-induced stromal keratitis in the mouse, as well [67]. These results are in line with a number of studies that have reported NPD1 pro-resolving bioactivities, including reduced T cell migration [68] and neutrophil influx [69], enhanced efferocytosis of apoptotic neutrophils [13], and decreased production of proinflammatory mediators (cytokines, chemokines, ROS) [70, 71]. Taken together, this body of work indicates promise for DHA-derived pro-resolving mediators in the treatment of viral keratitis.

#### 2.6 Fungal Keratitis

Fungal keratitis tends to be more prevalent in tropical and subtropical climates, where it has been reported that up to 50% of infectious ulcers are caused by fungi – predominately *Fusarium* and *Aspergillus* [72–74]. However, fungal keratitis can occur in more temperate regions as demonstrated by the *Fusarium* outbreak related to contact lens solution contamination [75–77]. The prognosis of fungal keratitis is worse than that of bacterial keratitis. Surprisingly, no new treatments have been introduced since natamycin in the 1960s [36]. This topical polyene remains the

first choice of treatment; though amphotericin B is preferred for Aspergillus and Candida keratitis. Limitations exist for both however; natamycin exhibits poor penetration into the corneal stroma and topical amphotericin B has toxicity issues [78]. Although voriconazole, a newer-generation triazole, demonstrates excellent ocular penetration [79] and high susceptibility among common fungal isolates [80], natamycin remains superior to voriconazole in the topical treatment of fungal keratitis [36, 81]. However, there are no reports examining the effects of SPMs in the treatment of this disease either as a monotherapy or as an adjunct to available antifungals. In vitro antifungal susceptibility testing and in vivo fungal keratitis models could provide valuable insight into the potential use of SPMs for fungal keratitis given the diversity of fungal aetiology and emergence of drug resistance.

#### 2.7 Endophthalmitis

In rare cases, infectious keratitis can extend from the cornea into the vitreous and/or aqueous humor and is termed endophthalmitis. Though uncommon, it is among the most devastating eye infections that bears the worst possible outcome irreversible blindness that can occur within even hours of symptom onset [82]. Incidence of disease ranges from 0.03-1.3% with cataract surgery to as high as 30-40% following open globe injuries [83]. The most prevalent pathogens related to endogenous endophthalmitis are bacteria (Staphylococcus sp., Streptococcus sp.) or fungi (Candida, Aspergillus). With more than 50% of keratitis-related endophthalmitis cases due to mold, Fusarium and Aspergillus are the most common etiologies [84]. Moreover, fungal endophthalmitis is particularly difficult to treat due to delayed diagnosis and poor ocular penetration of antifungals compounded by toxicity issues. Despite this, treatment typically consists of intravitreal antibiotics. In addition, vitrectomy is often carried out due to the rapidity and severity of disease progression.

Initial studies in a *S. aureus*-induced model of endophthalmitis show promise for pro-resolving mediators in the treatment of this disease. Intravitreal injections of RvD1 was shown to attenuate the progression of disease while preserving retinal function [85]. This was indicated by reduced levels of proinflammatory mediators, reduced bacterial burden, fewer infiltrated PMN, and induction of antimicrobial molecules. Further, it was suggested that this effect may involve TLR signaling pathways as TLR2 deficient mice were not protected by RvD1 treatment. Similar to fungal keratitis though, therapeutic potential of pro-resolving mediators have yet to be examined in fungal endopthalmitis.

#### 2.8 Conclusion

Although currently available antibiotics, antivirals, and antifungals are efficacious in successfully controlling most of the pathogens implicated in infectious keratitis, clinical outcomes remain poor. A common limitation among these therapies is evident - a sustained host response that compromises corneal integrity. The cornea demonstrates a deficiency in switching from active inflammation to active resolution - perhaps due to ocular immune privilege - resulting in structural alterations and loss of tissue. There exists a clear need for treatments that modify the immune response toward resolution and activate tissue restoration. In fact, a review on the clinical management of infectious keratitis suggested that the development of future adjuvant therapies with the greatest potential are likely to be multidimensional that are aimed at modifying the immune response to infection [36]. The current review provides evidentiary support for using proresolving molecules to treat infectious keratitis.

SPMs are being targeted as a beneficial monotherapy and adjuvant for infectious keratitis. The concept of combining SPMs with other drugs has been demonstrated to be highly effective in resolving inflammation [86]. This class of proresolving lipid mediators holds promise in the treatment of drug-resistant infections while avoiding ocular surface toxicity issues that currently impede proper treatment of infectious keratitis. As reviewed, SPMs function to dissolve inflammation through the regulation of leukocyte infiltration, activation and function. Further, chemical mediators (cytokines, chemo-kine's, ROS) that would otherwise contribute to chronic inflammation are influenced by SPMs – all of which enables the host response to return to homeostasis and is critical to restoration of corneal function and visual acuity.

One aspect of SPM-induced corneal restoration that has yet to be properly examined in the infectious keratitis model is corneal nerve regeneration. As the most innervated tissue in the body, the cornea contains predominately sensory nerves along with sympathetic and parasympathetic. Extensive work has been carried out investigating the role of corneal nerves in maintaining a healthy ocular surface, during wound healing and following infection [22, 87–90]. Clinically, damaged corneal nerves lead to decreased sensitivity, blink reflexes, tear secretion, dry eye, and neurotropic keratitis. The Bazan group has revealed a combination of DHA and pigment epithelial-derived factor (PEDF) increases NPD1 levels and corneal nerve regeneration using a lamellar keratectomy injury model in the rabbit [91–93]. Further, they found that epithelial wound healing was accelerated after nerve damage, as well. Though these results indicate that pro-resolving mediators will also influence corneal nerves following infection, a more comprehensive assessment is required. Overall, it is anticipated that SPMs will provide a promising avenue of therapy that contributes to the significant advancement in the treatment of infectious keratitis.

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Immunoresolvent Resolvin D1 Maintains the Health of the Ocular Surface 3

#### Darlene A. Dartt, Robin R. Hodges, and Charles N. Serhan

#### Abstract

The present review focuses on the role of one of the D-series resolvins (Rv) RvD1 in the regulation of conjunctival goblet cell secretion and its role in ocular surface health. RvD1 is the most thoroughly studied of the specialized proresolution mediators in the goblet cells. The anterior surface of the eye consists of the cornea (the transparent central area) and the conjunctiva (opaque tissue that surrounds the cornea and lines the eyelids). The secretory mucin MUC5AC produced by the conjunctival goblet cells is protective of the ocular surface and especially helps to maintain clear vision through the cornea. In health, a complex neural reflex stimulates goblet cell secretion to maintain an optimum amount of mucin in the tear film. The specialized pro-resolution mediator, D-series resolvin (RvD1) is present

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in human tears and induces goblet cell mucin secretion. RvD1 interacts with its receptors ALX/FPR2 and GPR32, activates phospholipases C, D, and A<sub>2</sub>, as well as the EGFR. This stimulation increases the intracellular [Ca<sup>2+</sup>] and activates extracellular regulated kinase (ERK) 1/2 to cause mucin secretion into the tear film. This mucin secretion protects the ocular surface from the challenges in the external milieu thus maintaining a healthy interface between the eye and the environment. RvD1 forms a second important mechanism along with activation of a neural reflex pathway to regulate goblet cell mucin secretion and protect the ocular surface in health.

#### Keywords

Conjunctiva · Goblet cells · Allergic eye disease · Dry eye disease · Ocular surface · Mucins · Tear film · Signaling pathways · Resolvin D1 · Inflammation · Secretion

#### 3.1 Tear Film, Cornea, and Conjunctiva

#### 3.1.1 Introduction

The present review focuses on the role of one of the D-series resolvins (Rv) RvD1 in the regulation

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of conjunctival goblet cell secretion. RvD1 is the most thoroughly studied of the specialized proresolution mediators in the goblet cells. This review is also focused on the role of RvD1 in maintenance of ocular surface health, but not its role in disease.

#### 3.1.2 Function of Tear Film and Ocular Surface

The eye is a unique, specialized organ whose function is to provide a clear optical path for image presentation on the retina and its analysis by the brain (Fig. 3.1). The first optical surface in the eye is the tear film that overspreads the cornea, a transparent avascular tissue. Together the tear film and cornea provide most of the refractive power of the eye [1]. The tear film and the cornea are among the first components of the anterior eye aided by the conjunctiva to interact with the external environment. The conjunctiva is a vascular, optically dense tissue that surrounds the cornea and lines the eyelids. Together the tear film and ocular surface tissues (cornea and conjunctiva) form the outermost protective layer that functions to maintain a transparent, healthy and impermeable cornea [1]. These components each have unique properties that contribute to the protection of the eye from mechanical, thermal, and chemical injury; desiccation; allergens and pollutants; and pathogens from the external environment.

At the basal aspect, the cornea consists of a single layered endothelium, overlaid by stroma containing keratocytes, and on the apical side a multi-layered epithelium. One of the major protective properties of the cornea is that it is a very tight epithelium with limited permeability [1]. It is difficult to permeate the corneal epithelium because of the extensive tight junctions and other types of junctions between the topmost layers of cells. For example, bacteria cannot penetrate the corneal epithelium unless it is damaged [2]. Furthermore, the cornea is an immune privileged site and maintains an immunosuppressive and environment anti-inflammatory preventing immune cells from migrating into the cornea or



Fig. 3.1 Scehmatic diagram of the eye and ocular surface

aqueous humor in response to an immune or inflammatory challenge [3]. When injured, the cornea normally heals rapidly with minimal scarring and no blood vessel ingrowth. The number of mechanisms that the cornea can use to respond to the external environment is limited and often constrained, as this tissue needs to preserve transparency and remain avascular to ensure clear vision.

The conjunctiva, the focus of this review, surrounds the cornea and lines the lids. One of its major functions is to secrete electrolytes, water, and multiple types of mucins that together form the glycocalyx and the inner layer of the tear film [4]. The conjunctiva is a stratified squamous epithelium that overlies a loose, disorganized stroma containing plentiful blood vessels and nerves. This epithelium consists of two major cell types, stratified squamous cells and goblet cells (Fig. 3.2) [4]. Stratified squamous cells are multilayered, have complex interdigitated lateral membranes, and contain a plethora of small clear vesicles. The second cell type is the goblet cells [5]. These cells occur singly or in clusters and span the entire epithelium in rodents, but only occupy the mid portion of the epithelium reaching to the surface in humans [5]. The goblet cells are polarized with a basal nucleus, substantial Golgi apparatus, and a plethora of secretory granules that occupy most of the cell volume and reach to the apical membrane and the tear film. The stratified squamous cells and the goblet cells both produce the mucous layer of the tear film but release different types of mucins. Both cells secrete electrolytes and water.

Secretion of mucins is one of the major protective mechanisms of the conjunctiva. The mucins produce an extensive glycocalyx and the soluble mucous layer that overspreads both the cornea and conjunctiva. Stratified squamous cells produce the membrane spanning mucins MUC1, MUC4, MUC16, and MUC20 (for a review see [6]). These mucins help form the glycocalyx, a thick coat of carbohydrates that emerges from the apical membranes of epithelial cells and protects the corneal and conjunctival surface. The glycocalyx interfaces with the tear film. The glycocalyx is critical to maintaining the barrier function of the cornea, preventing access of microbes to the plasma membrane, and preventing apical adhesion [7]. In contrast, the goblet cells secrete the large soluble, gel-forming mucin MUC5AC [8]. This mucin is the major component of the inner mucous layer of the tear film and is essential for ocular surface health. MUC5AC upon secretion by the goblet cells overspreads the entire ocular surface including the cornea. It protects the underlying epithelia as a mucus gel by preventing attachment of bacteria and keeping them suspended in the gel. The water and electrolytes in the gel keep the ocular surface hydrated. The movement of the mucus gel across the ocular

**Fig. 3.2** An electron micrograph of rat conjunctival goblet cells (CG). Numerous secretory vesicles can be seen in the apical portion of the cells, while nuclei can be seen in the basal portion. *SCC* stratified squamous cells. Magnification ×6000. Reprinted from Dartt [4]



surface into the lacrimal drainage ducts removes particles, pollutants, and other environmental components from the ocular surface. Goblet cells and their secretion of MUC5AC are regulated by nerves. Afferent sensory nerves and efferent parasympathetic and sympathetic nerves extend into the conjunctival epithelium interdigitating between the stratified squamous cells. Efferent parasympathetic and sympathetic nerves surround the goblet cells. The localization of the nerves in the epithelium provides the basis for these epithelial cells to respond quickly to changes in the external environment by secretion of MUC5AC into the tears.

The conjunctiva has multiple protective mechanisms in addition to the secretion of MUC5AC. As the conjunctival epithelium is opaque, well vascularized, and very permeable, unlike the cornea, it is not constrained in its responses to the environment. The conjunctiva in fact can respond very robustly. The conjunctiva contains conjunctival associated lymphoid tissue that is part of the mucosal immune system [9]. In addition the conjunctival stroma contains numerous different cells for innate defense (macrophages, neutrophils, and mast cells) and for immune protection (lymphocytes, plasma cells, and dendritic cells). In addition for the innate defense system the conjunctiva has most of the Toll-like receptors [10], multiple NOD-like receptors, and a constitutively assembled NLRP3 inflammasome poised for activation [11, 12]. The conjunctiva also has goblet cell associated passages (GAPs) that are openings between goblet cells that allow the stroma to sample antigens and other immune activating material in the external environment [13]. These GAPs are under parasympathetic muscarinic control.

#### 3.1.3 Role Goblet Cells in Ocular Surface Health

As goblet cells and their secretion of MUC5AC are critical for ocular surface health, both a decrease and an increase in goblet cell mucin secretion leads to ocular surface disease. Loss of goblet cells from the conjunctival epithelium and depletion of MUC5AC in the tear film lead to serious damaging, painful ocular surface diseases such as dry eye and vitamin A deficiency [14]. Increase in goblet cell mucin in the tear film is also characteristic of specific diseases, such as ocular allergy, that upset ocular surface homeostasis and can be damaging to the ocular surface. The finding that both a decrease and an increase in goblet cell mucin secretion leads to disease suggests that goblet cell mucin secretion must be tightly regulated to maintain an optimal amount of mucin in the tear film [6, 8, 15].

In health neural regulation of goblet cell mucin secretion provides this regulation [16, 17]. Using a complex neural reflex, goblet cell mucin secretion can be exquisitely regulated to respond to changes in the external environment to secrete mucins as needed to protect the occur surface [18]. Corneal and conjunctival afferent sensory nerves are activated by changes in temperature, acid or bases, or mechanical stimuli (including trauma and particulates that occur in pollution), for examples. The stimulated afferent nerves then activate the trigeminal ganglion that by a complex neural reflex within the brain activates efferent parasympathetic nerves In the conjunctiva parasympathetic nerve endings surround the goblet cells and stimulate them to secrete mucins into the tear film [17]. The goblet cells also likely secrete electrolytes and water, but the evidence for this is indirect [19, 20].

Parasympathetic nerves are the major stimulus of goblet cell mucin secretion in health [16, 21, 22] (Fig. 3.3). There is no published evidence for the role of sympathetic nerves in this secretion. Parasympathetic nerves release the neurotransmitters acetylcholine that activate muscarinic receptors (MAchR) type 1, 2, and 3 and vasoactive intestinal peptide (VIP) that uses the VPAC1 and 2 receptors [21]. Both acetylcholine (carbachol is used experimentally) and VIP stimulate secretion by increasing intracellular  $[Ca^{2+}]$  $([Ca^{2+}]_i)$  and activating extracellular regulated kinase (ERK)1/2 also known as p44/p42 mitogen activated protein kinase (MAPK) [13, 23]. In addition VIP activates adenylyl cyclase to increase the cellular cAMP level (For a review see [24]). Acetylcholine (carbachol), but not VIP,



**Fig. 3.3** Schematic representation of cholinergic pathway leading to goblet cell mucin secretion. Muscarinic receptors activate phospholipase C (PLC) to generate the production of inositol trisphosphate (IP<sub>3</sub>), which releases intracellular Ca<sup>2+</sup> and diacylglycerol (DAG), which activates protein kinase C (PKC). The EGF receptor (EGFR) is transactivated leading to the activation of Ras, Raf,

also works by activating a matrix metalloproteinase to cause ectodomain shedding of EGF to stimulate the EGFR that in turn increases  $[Ca^{2+}]_i$ and activates ERK1/2 to stimulate goblet cell secretion [22].

Thus under normal conditions, the parasympathetic neurotransmitters use a common intracellular signaling pathway, an increase in  $[Ca^{2+}]_i$ and activation of ERK1/2 to stimulate mucin secretion by inducing exocytosis and release of all the secretory granules within a given goblet cell [25]. The molecular mechanism by which the exocytosis occurs is unstudied in the goblet cell. This pathway is tightly regulated in response to neural activation of the cornea and conjunctiva to maintain an optimal mucin layer that is critical for a healthy ocular surface.

As there is far less research on the conjunctiva than the cornea, the mechanisms used by the conjunctiva to respond to the environment are only beginning to be described. The role of the specialized pro-resolving mediator (SPM) resolvin D1 (RvD1) is one of these mechanisms and is the topic of the present review.

mitogen activated kinase kinase (MEK), and ERK 1/2. Vasoactive intestinal peptide (VIP) binds to its receptors VPAC1 or 2 to activate adenylyl cyclase (AC) to generate cAMP from ATP. cAMP then activates protein kinase A (PKA) to stimulate secretion. Reprinted from Hodges et al. Encyclopedia of the Eye, Dartt D, Dana R, Besharse J eds. Elsevier, 2010

#### 3.2 Specialized Pro-resolving Mediators

The SPMs comprise four families, lipoxins, resolvins, protectins, and maresins. The SPMs function in the resolution phase of acute inflammatory diseases and each family possess unique bioactions to resolve inflammation [26]. Each family of mediators has very potent actions as well as being structurally distinct, displaying stereospecific actions, and utilizing different biosynthetic pathways. Lipoxins are biosynthesized from the omega 6 fatty acid arachidonic acid after class switching from production of proinflammatory mediators. The omega 3 fatty acid docosahexaenoic acid (DHA) is precursor for the biosynthesis the D-series resolvins, the protectins, and the maresins. The omega 3 fatty acid, eicosapentaenoic acid (EPA) is precursor for the biosynthesis of the potent E-series resolvins. Each member of the RvD (RvD1-6) and RvE (RvE1 and 2) families possesses unique structures and has distinct functions in the treatment of disease in animal models and in cells.

The enzymes responsible for this biosynthesis are the lipoxygenases (LOX) 5-LOX and 12/15 LOX. The location and specificity of the LOXs are cell and tissue specific. This determines the type and amount of SPM produced. In general 15-LOX and 5-LOX are needed to produce lipoxins from arachidonic acid. 5-LOX is required to biosynthesize E-series resolvins. 15-LOX and 5-LOX biosynthesize D-series resolvins and protectin (Fig. 3.4). 12-LOX biosynthesizes maresins. There is little published information on LOX enzymes in the conjunctiva and especially the goblet cells. Several articles from the 1980s found that the normal, uninflamed conjunctiva from various species of animals has the capacity to synthesize both cyclooxygenases and lipoxygenases [27, 28]. The cycloxygenase was higher than the lipoxygenase activity. The major lipoxygenases produced by the conjunctiva were 12-HETE, 5-HETE, and 5,12-diHETE suggesting production of hepoxilin and LTA<sub>4</sub>. Subsequently conjunctiva and eyelids were demonstrated to possess EPA lipoxygenase products of the 5-series suggesting the capability of producing E-series resolvins [29].



**Fig. 3.4** Synthetic Pathways of the D-series specialized pro-resolving mediators. Each is derived from DHA. 5-LO: 5 lipoxygenase Modified from Sun Y, Oh SF et al. J Biol Chem 282:9323–9234, 2007

There is substantial work on the LOX enzymes in the cornea and the draining lymph nodes of the eye that contribute to ocular surface disease especially [30–32], 5- and 15-LOX are the rate limiting enzymes responsible for the generating SPMs [33]. The corneal epithelium has high expression of 15-LOX and functions as part of a LXA<sub>4</sub>-ALX/ FPR2 circuit that controls wound healing and immune response in the cornea. In particular there is a population of tissue specific polymorphonuclear leukocytes (PMNs) that contain especially high amounts of 15-LOX and that in a sex-specific manner play a role in exacerbating autoimmune dry eye disease in females. These PMNs were detected in the lacrimal gland, draining lymph nodes, and limbus of the cornea. As the cornea and its limbus is adjacent to the conjunctiva, it is possible that conjunctival epithelial cells also have elevated levels of 15-LOX. Furthermore, conjunctival goblet cells are a target of disease in autoimmune dry eye. Study of ocular surface disease has shown the presence of high levels of the biosynthetic enzymes for the SPMs and the circuits for their regulation. These enzymes could also function in health especially as during eye closure in sleep, PMNs migrate into the tear film and could interact with the conjunctival epithelial cells to set up a transient, low level activation of a LXA<sub>4</sub>-ALX/FPR2 like circuit or other circuits potentially in the conjunctiva. The same enzymes produce RvD1 and could be critical for regulating RvD1 biosynthesis in conjunctival goblet cells.

In addition to the production of SPMs in disease, SPMs are also endogenously produced in human tissues rich in omega 3 fatty acids in the absence of disease [34]. Thus SPMs are produced in human milk [35, 36], blood [37, 38], brain [39], and retina [40]. SPMs are major players in the regulation of ocular surface health as SPMs are detected in the tear film and stimulate conjunctival goblet cell mucin secretion under physiologic conditions. They function to maintain an optimum mucin layer of the tear film in response to the normal changes in the cornea and conjunctiva and to the extracellular environment. Multiple SPM family members are present within emotional human tears and stimulate goblet cell secretion to maintain the healthy tear film [41]. Herein

we will review the evidence for the role of the D-series resolvin RvD1 in conjunctival health.

#### 3.3 RvD1 Is Present in Tears from Healthy Individuals

A number of eicosanoids as well as SPMs are found in human tears. Human emotional tears were collected from six male and six female subjects and the lipid profile analyzed using an LC-MS-MS based metabololipidomics along with deuterium-labeled SPM as internal standards for quantitation [41]. We documented the presence of pro-inflammatory prostaglandins and the leukotriene B<sub>4</sub>. For the SPMs, the D-series resolvins (RvD1, RvD2, RvD5), protectin D1, and lipoxin A4, but neither the maresins nor E-series resolvins, were identified in these samples from healthy human subjects. The SPM biopathway markers synthesis 17-HDHA, 14-HDHA, and 18-HEPE were also identified. These compounds could be bioactive themselves [42] or could suggest that both D- and E-series resolvins may be present in higher amounts locally than measured in the present study. The presence of pathway markers would also be consistent with the further metabolism of these bioactive resolvins to their oxo- and dehydro-resolvin products that were not profiled in the present study and are usually less or devoid of bioactivity. Thus, RvD1 was present in human tears and available to regulate the function of the conjunctival goblet cells. There are two other studies on SPMs in tears that are in agreement with that of English et al. [41]. Walter et al. [43] found DHA, the  $\omega$  3 fatty acid from which RvD1 is biosynthesized, in tears. RvD1 was not measured directly in this study. Masoudi S et al. [44] found RvD1 in tears, but this was the only SPM analyzed.

Surprisingly the lipid profile of male and female tears differed substantially [41]. Use of a principal component analysis demonstrated a gender difference in the SPMs in tears (Fig. 3.5). The loading plot calculated from LC-MS-MS identified RvD1, RvD2, RvD5 and protectin D1 in male tears. In contrast LXA<sub>4</sub> and aspirin-triggered LXA<sub>4</sub> were detected in female tears. When the ratio of SPMs,

Human Emotional Tears 2D Score Plot





**Fig. 3.5** PCA and quantitative ratio by gender for LM-SPMs identified in human emotional tears. (a) 2-dimensional score plot of human emotional tear donors; blue circles (n = 6) are representative of males, while green circles (n = 6) are representative of females. Gray ellipse denotes 95% confidence interval. (b) 2-dimensional loading plot of LM-SPMs identified in human emotional tears; blue circles are those mediators associated with

17-HDHA, and 18-HEPE versus the pro-inflammatory compounds PGE2 and PGF2a was compared between males and females, the ratio of SPMs to prostaglandins was much higher in males.

#### 3.4 Exogenous RvD1 Stimulates Conjunctival Goblet Cell Mucin Secretion Using Multiple Intracellular Signaling Pathways

#### 3.4.1 RvD1 Stimulates Goblet Cell Mucin Secretion

As the major function of goblet cells is to secrete mucins, the action of RvD1 on mucin secretion

male donors & green circles are associated with female donors. (c) Bar graph depicting the ratio of total SPMs including RvD1, RvD2, RvD5, PD1, LXA<sub>4</sub>, AT-LXA<sub>4</sub>, 17-HDHA, and 18-HEPE compared to PGE<sub>2</sub> and PGF<sub>2α</sub> (pg/100 µl), in males compared females (n = 6 for each gender; \*P < 0.05 for male donors vs. female donors; \*P < 0.05, females vs. males). Reprinted from English et al. [41]

was our focus. RvD1 stimulated human and rat conjunctival goblet cell high molecular weight glycoconjugate secretion (that includes mucin) [45, 46]. Secretion peaked at 1 h and then declined over time for the next 3 h. RvD1 stimulated secretion by increasing the [Ca<sup>2+</sup>]<sub>i</sub> and activating ERK1/2 [45], similarly to the effect of cholinergic agonists and VIP [21] (Fig. 3.6). RvD1 was effective in the range of  $10^{-10}$ – $10^{-8}$  M, a much lower concentration range than for carbachol  $(10^{-6}-10^{-4} \text{ M})$ , but similar to VIP  $(10^{-11}-10^{-7} \text{ M})$ [21, 23]. The RvD1 stimulation of secretion was blocked by chelating the intracellular Ca<sup>2+</sup> with BAPTA and by inhibiting ERK1/2 activation with U0126 [47] substantiating the role of these signaling molecules in RvD1 stimulation of goblet cell secretion.

а





To induce goblet cell function the appropriate receptors must be present on conjunctival goblet cells. RvD1 uses the ALX/FPR2 receptor in rat and the GPR32/DRV1 receptor in human goblet cells. PCR, western blot and immunofluorescence microscopy demonstrated that the ALX/FPR2 receptor was present on rat conjunctival goblet cells in vivo and in culture [48, 49]. There is as yet no published report of GPR32/DRV1 on human goblet cells. There is also functional evidence for the presence of ALX/FPR2 receptor in rat conjunctival goblet cells. To address whether RvD1 uses the ALX/FPR2 receptor in the rat, both the ALX/FPR2 inhibitor N-Boc<sup>-</sup>Phe-Leu-Phe-Leu-Phe (BOC-2) and siRNA for ALX/FPR2

blocked RvD1 stimulated increase in [Ca<sup>2+</sup>]<sub>i</sub> [45, 47]. Functional evidence also demonstrates that RvD1 uses the GPR32/DRV1 receptor in human goblet cells. In human cells inhibition of ALX/FPR2 with its inhibitor BOC-2 does not block RvD1 stimulated increase in  $[Ca^{2+}]_i$  [49]. Furthermore, in desensitization experiments in human cells in which LXA<sub>4</sub> and RvD1 were used sequentially, RvD1 does not desensitize  $LXA_4$  response [49]. This suggests use of separate receptors in human goblet cells. Thus RvD1 activates ALX/ FPR2 in rat goblet cells and GPR32/DRV1 in human goblet cells. Further experiments using GPR32 siRNA in human goblet cells is warranted.

#### 3.4.2 Cellular Signaling Pathways Activated by RvD1

#### 3.4.2.1 Phospholipase C Pathway

RvD1 activates a several specific intracellular signaling pathways to stimulate mucin secretion from rat goblet cells. One pathway is activation of phospholipase (PL) C that produces water soluble 1,4,5-inositol trisphosphate (IP3) and lipid soluble (membrane-bound) diacylglycerol (DAG) (Fig. 3.6). IP3 binds to its receptors (IP3R) on the endoplasmic reticulum that releases Ca2+ from this intracellular store to increase the cytosolic [Ca2+] that stimulates exocytosis and mucin secretion. The DAG produced activates protein kinase (PK)C that phosphorylates as yet unidentified substrates to stimulate secretion. We used multiple techniques and inhibitors to determine if a PLC-dependent pathway plays a role in RvD1 stimulated goblet cell secretion [47]. First the active PLC inhibitor U73122 blocked RvD1 stimulated increase in  $[Ca^{2+}]_i$  and secretion as well as the increase caused by the positive control the cholinergic agonist carbachol. As expected, the inactive inhibitor U73343 did not block either the RvD1 or cholinergic agonist stimulation of secretion nor the cholinergic agonist induced increase in [Ca<sup>2+</sup>]<sub>i</sub>. Unfortunately the inactive inhibitor blocked the RvD1 induced increase in  $[Ca^{2+}]_i$  but was not as effective as the active analog. As the inactive inhibitor did not block three out of four responses, we concluded that RvD1 activates PLC in conjunctival goblet cells. To investigate IP3 interaction with its receptor to release Ca<sup>2+</sup> from intracellular stores, an inhibitor of the IP3 receptor 2-aminoethyl diphenylborate (2-APB) was used. 2-APB blocked both the RvD1 stimulated increase in  $[Ca^{2+}]_i$  and secretion. A second method of determining the role of intracellular Ca<sup>2+</sup> stores is the use of thapsigargin that blocks the re-uptake of Ca<sup>2+</sup> into the stores, thereby depleting them of Ca<sup>2+</sup>. If RvD1 used intracellular Ca<sup>2+</sup> stores, the addition of thapsigargin before RvD1 should prevent the increase in [Ca<sup>2+</sup>]<sub>i</sub> by RvD1. In goblet cells this did not occur [45]. However, that depletion of extracellular Ca<sup>2+</sup> blocked the RvD1 stimulated elevation in

 $[Ca^{2+}]_i$  supported the activation of  $Ca^{2+}$  influx by RvD1 [45].

The DAG arm of the PLC pathway was investigated by determining the role of PKC using the PKC inhibitor Ro 31-8220. The PKC inhibitor blocked the RvD1-stimulated increase in  $[Ca^{2+}]_{i}$ , but not in secretion. Activation of PKC may be important for the increase in  $[Ca^{2+}]_{i}$ , but not for secretion. There are multiple isoforms of PKC that are differentially activated by  $Ca^{2+}$  and diacylglycerol and can have opposing effects on a given process [50]. Thus investigation of the types of PKC isoforms present in goblet cells and inhibition of single isoforms would demonstrate more accurately whether PKC isoforms are involved in goblet cell secretion.

We concluded that RvD1 uses a PLC pathway to increase IP3 that releases  $Ca^{2+}$  from intracellular stores and causes an increase in the influx of extracellular  $Ca^{2+}$  (Fig. 3.6). The resultant increase in the cytosolic  $[Ca^{2+}]_i$  stimulates secretion. The second arm of the PLC pathway production of DAG and activation of PKC is used to increase the  $[Ca^{2+}]_i$ , but whether PKC plays a role in secretion awaits investigation of the different PKC isoforms.

PLCγ is activated by EGF as PLCγ is an adapter molecule attached to the EGFR. PLCγ can be phosphorylated and activated upon stimulation and dimerization of the EGFR. We recently found that RvD1 uses a matrix metalloproteinase ADAM17 to release EGF by ectodomain shedding and activate the EGFR to increase [Ca<sup>2+</sup>]<sub>i</sub> and activate ERK1/2 to stimulate secretion [51]. Thus RvD1 could also activate PLCγ in addition to PLCβ to increase [Ca<sup>2+</sup>]<sub>i</sub> and stimulate secretion. Thus two different types of PLC are used by RvD1 to stimulate goblet cell mucin secretion.

#### 3.4.2.2 Phospholipase D and A2 Pathways

The next two pathways investigated were activation of PLD and PLA2 [47] (Fig. 3.6). These pathways were not investigated in as much detail as PLC. The role of PLD in RVD1 stimulated increase in  $[Ca^{2+}]_i$  and secretion was investigated using 1-butanol the active inhibitor of PLD and tert-butanol, its inactive control. The RvD1-induced increase in  $[Ca^{2+}]_i$  and stimulation of secretion was almost completely blocked by 1-butanol. The inactive control only partially blocked the increase in  $[Ca^{2+}]_i$  and did not block the stimulation of secretion. To study PLA2 aristolochic acid was used. Aristolochic acid blocked both the RvD1 caused increase in  $[Ca^{2+}]_i$  and stimulation of secretion. These results are consistent with RvD1 using both PLD and PLA2 to stimulate goblet cell secretion. Additional experiments should identify the components of these pathways.

#### 3.4.2.3 Extracellular Regulated Kinase 1/2 Pathway

RvD1 activates ERK1/2 to increase  $[Ca^{2+}]_i$  and stimulate secretion as shown by inhibition of both functions by the MEK inhibitor U0126 [45] (Fig. 3.6). ERK1/2 could function as a component in several of the pathways studied. ERK1/2 could be activated by induction of the EGFR using the adapter proteins Ras, Raf, and MEK. ERK1/2 could also be downstream of PLD or PLA2.

#### 3.4.3 Summary of Pathways Activated by RvD1

RvD1 stimulates mucin secretion from conjunctival goblet cells by a receptor specific mechanism using ALX/FPR2 in rats and GPR32 in humans. RvD1 uses multiple signaling pathways including PLC, PLD, and PLA2 that each use specific signaling components to increase  $[Ca^{2+}]_i$  and could also activate ERK1/2 to stimulate secretion. In addition RvD1 transactivates the EGFR to increase  $[Ca^{2+}]_i$ , activate ERK1/2 and stimulate secretion. Endogenously produced RvD1 has multiple pathways available to stimulate conjunctival goblet cell mucin secretion to help maintain a normal mucous layer of tears.

#### 3.5 Conclusion

The SPM RvD1, along neural regulation, is available to protect the ocular surface from dessicating stress, chemicals, temperature, aller-

gens, particulate matter, and pathogens in the external environment. RvD1 is present in the tear film where it can access its receptors on the basolateral membranes of the goblet cells. RvD1 uses the ALX/FPR2 receptor in rat goblet cells and the GPR32 in human goblet cells. Activation of these receptors employs multiple intracellular pathways including PLC, PLD, PLA2 and the EGFR to increase  $[Ca^{2+}]_i$  and activate ERK1/2 to stimulate secretion. The main secretory product of the goblet cells is the large, gel-forming mucin MU5AC, which is released into the innermost layer of the tear film where it is protective of the ocular surface. This mucin can trap bacteria and particulate matter and remove them from the ocular surface via the nasal lacrimal drainage. RvD1 thus preserves ocular surface homeostasis and maintains this surface in a non-inflamed, normal physiologic state of an optimum amount of mucin secretion. RvD1 forms a second important mechanism along with activation of a neural reflex pathway to regulate goblet cell mucin secretion and protect the ocular surface in health.

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4

#### The Evolving Role of Specialized Pro-resolving Mediators in Modulating Neuroinflammation in Perioperative Neurocognitive Disorders

#### Ting Yang and Niccolò Terrando

#### Abstract

Surgery can be a life-saving procedure; however, significant complications may occur after routine procedures especially in older and more frail patients. Perioperative neurocognitive disorders (PNDs), including delirium and postoperative cognitive dysfunction, are the most common complications in older adults following common procedures such as orthopedic or cardiac surgery. The consequences of PNDs can be devastating, with longer in-hospital stay, poorer prognosis, and higher mortality rates. Inflammation is gaining considerable interest as a critical driver of cognitive deficits. In this regard, resolution of inflammation, once thought to be a passive process, may provide novel approaches to treat neuroinflammation and PNDs. Herein we review the role for impaired resolution after surgery and the growing role of specialized pro-resolving mediators (SPMs) in regulating

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Center for Translational Pain Medicine, Department of Anesthesiology, Duke University Medical Center, Durham, NC, USA e-mail: niccolo.terrando@duke.edu postoperative neuroinflammation and neurological complications after surgery.

#### Keywords

Astrocytes · Blood-brain barrier · Bone · Brain · Cytokines · Delirium · Healing · Macrophages · Maresins · Memory · Microglia · Neuroinflammation · Resolvins · Surgery

Perioperative neurocognitive disorders (PNDs), previously referred to as postoperative cognitive dysfunction (POCD), include acute changes in cognitive function (i.e. delirium) and longerlasting memory impairments [1]. PNDs have become the most common complications in older adults after common surgical procedures such as cardiac and orthopedic surgery, and negatively affect post-operative outcomes and recovery in at-risk subjects [2]. Indeed, patients who suffer from PNDs require intensive nursing care, report higher mortality rates, and become at greater risk for further complications, including permanent dementia [3, 4]. Although advanced age has been recognized as a prominent risk factor for PNDs, the pathophysiology of these complications is still poorly understood. Recent studies showed pro-inflammatory signaling molecules can be identified in the central nervous system (CNS) of

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both PND patients and animal models, implicating surgery-induced neuroinflammation as a key contributor in the pathophysiology of PNDs. The aim of this review is to discuss the role of dysregulated immunity after surgery and the therapeutic potential for specialized pro-resolving lipid mediators (SPMs) in the perioperative neurocognitive arena.

We and others have been interested in clarifying the pathogenesis of PNDs and developed preclinical translational models to study the impact of anesthesia and surgery on the CNS. During surgery, aside from direct effects of anesthetic agents on the CNS (reviewed in [5]), acute inflammation triggered by trauma and sterile injury can negatively affect brain function, contributing to sickness behavior and PND-like pathology [6]. If poorly controlled, dysregulated inflammation leads to more extensive organ dysfunction and tissue injury. Release of proinflammatory cytokines, alarmins, and leukotrienes appear to associate with distant long-term effects on the brain, contributing to neuroinflammation, neurotoxicity, and subsequent memory impairments. The mechanisms whereby systemic inflammation affects CNS function remain partly defined and are object of active investigations. Systemic cytokines have been shown to enter the brain through different immune-to-brain signaling pathways, which include humoral, neuronal, and cellular routes [7]. Using a well-established PND model of orthopedic surgery, which frequently leads to cognitive dysfunctions in humans, we first reported a key role for systemic pro-inflammatory cytokines, including interleukin (IL)-1ß and tumor necrosis factor alpha (TNF $\alpha$ ), in mediating surgery-induced neuroinflammation and cognitive decline following surgery [6, 8]. These initial results as well as work from other models of surgery-induced cognitive dysfunction, prompt for a prominent role of the systemic and humoral response in PND pathogenesis. However, peripheral cytokines in response to non-CNS surgery were also shown to disrupt the blood-brain barrier (BBB), thus facilitating the migration of peripheral cells, including macrophages, into the brain parenchyma through activation of  $TNF\alpha/$ 

nuclear factor (NF)-kB signaling pathway [9] [10]. BBB homeostasis plays fundamental role in the communication between peripheral inflammation and neuroinflammation [11]. Using fibringen as a classical marker of BBB disruption, we reported a significant deposition of this blood-derived molecule in the hippocampal parenchyma [12]. Similar results were reported in other surgical models, with evident BBB opening and disruption of tight junctions after anesthesia and surgery [13]. More recently we described a role for neuronal processing, including pain signaling at the level of the spinal cord, in disrupting acute neurogenesis after orthopedic surgery [14]. These factors, together with the overall activation of innate immune pathways, have been highlighted as pathogenic mechanisms underlying cognitive decline in preclinical models and in early clinical studies. Preclinical models have evaluated multiple therapeutic strategies to modulate neuroinflammation and PND-like behavior. Selective targeting of key proinflammatory cytokines (such as anti-TNF $\alpha$  and IL-1 receptor agonist) prevent neuroinflammation and improve cognitive decline in animal models [6, 15]. Macrophage-specific deletion of IKK $\beta$ , a central coordinator of TNF $\alpha$  activation of NF-kB, prevents BBB disruption and macrophage infiltration in the hippocampus following surgery. Moreover, harnessing the cholinergic reflex by stimulating the  $\alpha$ 7 subtype of nicotinic acetylcholine receptors (a7 nAChR) in macrophages inhibited NF-kB activity and BBB disruption, thus preventing neuroinflammation and cognitive decline following surgery [12]. Although these and several other therapies may successfully reduce postoperative neuroinflammation and limit PNDs, they often contribute to side effects by over suppressing the immune system, increasing the risk of infection and delaying wound healing, which are all crucial in the context of postoperative recovery. Thus, it is pivotal to identify safer therapeutic strategies to prevent neuroinflammation without suppressing systemic immune functions.

Is now well appreciated that resolution of inflammation is an active process [16–18]. Synthesis and release of anti-inflammatory

molecules is required to balance and orchestrate the overall immune response [19]. The acute inflammatory response can be divided into two stages: initiation and resolution. Resolution launches shortly after the initiation of inflammatory response [20]. Seminal work pioneered by Dr. Serhan and colleagues has demonstrated how different mediators actively participate in resolving acute inflammation in a highly regulated manner (recently reviewed in [21]). Fundamental to the resolution process are SPMs, endogenous mediators generated by polyunsaturated fatty acids (PUFA) with signaling abilities to limit inflammation [22]. Omega-3 PUFAs are important catalysts for the synthesis of potent lipid mediators that can exert pro-resolving and antiinflammatory actions. Oxygenated metabolites derived from eicosapentaenoic acid (20:5(n-3) or EPA) and docosahexaenoic acid (22:6(n-3) or DHA), enriched in fish oils, lead to structurally distinct families of "resolution phase interaction products" [23], which include resolvins, maresins, protectins (as well as sulfide-conjugates in tissue regeneration), and lipoxins (from arachidonic acid). All SPMs display potent anti-inflammatory actions and immunoregulatory properties now tested in several pre-clinical models of acute and chronic inflammation. Indeed, SPMs inhibit the excessive swarming of neutrophils infiltration and enhance the microbial clearance function of innate immune cells [24]. SPMs also operate as "resolution agonists" to regulate the acute inflammation and limit the development of chronic inflammation; importantly they do not show immunosuppressive effects [23, 25]. The exaggerated inflammation and non-resolution of proinflammatory processes are characteristic of several neurological conditions and disease states like stroke, neurodegeneration, and chronic pain. Evidence from clinical studies using dietary fish oil supplementation suggest promising effects of omega 3 fatty acid in modulating inflammation both in acute and chronic conditions [26, 27]. Yet the role of SPMs in resolution of neuroinflammation and neuroprotection is just emerging. In Alzheimer's disease (AD), circulating SPMs and receptor expression are diminished in the brain [28]. A comprehensive review on the role of SPMs in AD is provided in [29]. Here we will review the growing role of SPMs in the perioperative space, focusing on neuroinflammation in PNDs.

Microglia are the primary active immune defense in the CNS responsible to maintain brain homeostasis. However, activated microglia can cause overproduction of pro-inflammatory cytokines and reactive oxidative species that can lead to persistent inflammation and exacerbate pathological changes in CNS [30, 31]. In PND microglia respond to surgical trauma following BBB opening and monocytes infiltration. Modulation of microglial activity is an attractive therapeutic targeted for multiple conditions ranging from neurodegeneration to chronic pain [32]. In vitro studies using immortalised murine microglial cell line BV-2 showed pre-incubation with resolvin D1 (RvD1) and E1 (RvE1) inhibit lipopolysaccharide (LPS)-induced TNF- $\alpha$ , IL-6 and IL-1 $\beta$ gene expression via regulating of miRNAs expression and NF- $\kappa$ B signaling pathway [33]. Similar effects of RvD1 were demonstrated in separate studies using human glioma cells or isolated primary rat microglia [34, 35]. RvD1 and maresin-1 (MaR1) also down-regulate β-amyloid  $(A\beta)_{42}$ -induced CD11b and CD40 expression in human microglial cells. Moreover, MaR1 and aspirin triggered lipoxin A<sub>4</sub> (ATL) both exert stimulatory effect on microglial cells to uptake A $\beta_{42}$  [36, 37]. In addition to reducing the expression of M1-like markers activation of microglia, RvD1 also promotes the expression of Arg1 and Ym1 in IL-4 activated BV2 cells [38]. These in vitro findings demonstrate that SPMs are directly involved in regulating both classical and alternative microglia activation, thus may display potent therapeutic effects in inflammatory diseases of the CNS. The regulatory effects of SPMs on microglial cells have also been also verified in vivo. A study using Tg2576 mice, which overexpresses a mutant form of amyloid precursor protein (APP) and develops early AD onset, showed neuroprotective effects of ATL by shifting microglial phenotype to a more anti-inflammatory state [37]. In models of surgery-induced microglial activation, both lipoxins and resolvins have been shown to improve neuroinflammation by attenuating release of pro-inflammatory cytokines [39-41]. Importantly, other classes of inflammatory-stop signals can modulate neuroinflammation in PND-models. Using a rat model of cardiopulmonary bypass with deep hypothermic circulatory arrest treatment with annexin A1 (ANXA1) was able to improve cognitive outcomes and modulate microglial activation by inhibiting NF-kB p65 transcriptional activity and subsequent cytokine production [42]. Recently, we demonstrated that prophylaxis with MaR1 can rescue microglial activation after orthopedic surgery, as detected by morphological changessuch as shifting to a more ramified homeostatic morphology [43]. Thus, resolution agonists including SPMs may diminish neuroinflammation in part by regulating microglial phenotype, leading to improved cognitive outcomes. To date many of the SPMs have not been evaluated in models of PND and surgical recovery, which warrants future investigations.

Aside from microglia, astrocytes also contribute a key role in maintaining CNS homeostasis, including regulating brain blood flow [44, 45], synapse function [46], extracellular ion concentration [47], and interacting with endothelial cells to support the BBB [48]. Notably, a role for immune-regulation has emerged from these cells [49]. As an active immune regulator in CNS, astrocytes also sense stimulation and danger signals, responding by releasing glia-transmitters and communicating to neurons [50]. Together with microglia they also contribute to further activating adaptive immune defense [51] [49]. Following brain injury or in neurodegenerative diseases, astrocytes undergo pronounced transformation called "astrogliosis". Astrogliosis changes the cellular expression and morphology of astrocytes and contribute to the repair and scarring process in CNS [52]. However, this reactive phenotype has also been suggested to become detrimental by upregulating the expression of IL-17 receptor and sphingosine 1-phosphate (S1P) [53, 54]. This further triggers the production of pro-inflammatory cytokines and chemokines, which can lead to exacerbated neuroinflammation and neurodegeneration [55, 56]. During neuroinflammation, the status of astrocytes actions may be determined by the danger signals in the local environment and regulated in time-specific manner [56]. The controversial roles of astrocytes indicate that these cells may play key roles in cognitive function, both in health and diseases. The specific SPMs actions on astrocytes have not been thoroughly investigated. In pain models, Lipoxin A1 exerts antinociceptive effect by modulation of astrocytic activation [57]. Similarly, AT-RvD1 was shown to attenuate TNF- $\alpha$  release from spinal astrocytes and improve mechanical hypersensitivity in a rat model of carrageenan-induced peripheral inflammation [58]. In PND models we described changes in astrocytes morphology at 24 h after orthopedic surgery [41, 43]. The astrogliosis is associated with increased basal glutamatergic synaptic transmission, reduced short term plasticity and long-term potentiation in hippocampus [41]. These pathological changes in astrocytes can be eliminated by prophylaxis with aspirin triggered resolvin-D1 (AT-RvD1) as low as ~0.1  $\mu$ g/kg [41] or MaR1 at ~4  $\mu$ g/kg [43]. The precise mechanisms underlying the effects of AT-RvD1 and MaR1 on postoperative astrogliosis further still require exploration. Accumulated evidences suggest the pro-inflammatory activity of astrocytes may be regulated by microglia [59] via cytokines, chemokine, complement activation [60], growth factors, and other signaling molecules [61]. After surgery the CCL2/CCR2 axis has been implicated in the neuroinflammatory response; Xu et al. showed that increased CCL2 expression in astrocytes is sufficient to activate microglia and cause learning impairments [62]. Therefore, regulation of astrogliosis may indirectly regulate microglia activity and targeting cell-specific interactions may result into effective therapies for different neurological conditions, including **PNDs** (Figs. 4.1 and 4.2).

Intrinsic to the postoperative neuroinflammation is the activation of the peripheral innate immune system. Sterile injury, as during surgery, rapidly triggers the release of TNF $\alpha$  and alarmins into the circulation. TNF $\alpha$  can initiate a proinflammatory cytokine cascade that eventually impairs the BBB homeostasis. The BBB dysfunction in turn facilitates the migration of macrophages into the hippocampus [6, 12, 41, 43]. Inhibition of the TNF $\alpha$  signaling by anti-TNFα antibody or genetic abrogation of macrophage-specific IKKβ prevent postoperative BBB disruption and macrophage infiltration in the hippocampus [6, 12]. This work demonstrated the primary impact of innate immune system and systemic inflammation on the development of neuroinflammation and cognitive decline. During resolution of inflammation, SPMs stimulate the cessation of PMN influx [22, 34] and macrophage clearance of cellular and toxic debris [16, 20, 63]. The regulation of macrophage phagocytosis function by SPMs may be mediated by the switch of macrophage phenotype [16]. For example, Dalli et al. demonstrated that 10 nM of MaR1 or RvD1 lead to significant reductions in CD54 and CD80 expression and a concomitant up-regulation of CD163 and CD206 in human macrophage [64]. Moreover, M2-like macrophages are more efficient in converting DHA into MaR1 [64]. Similarly, our in vitro work indicated 10 nM MaR1 can inhibit LPS-induced TNF $\alpha$  release, NF- $\kappa$ B nuclear translocation, superoxide generation and M1-like phenotype surface markers expression in primary bone marrow derived macrophages [43]. These modulatory effects on macrophage function/phenotype may be a key mechanism for SPMs to prevent surgery induced BBB disruption, ensuing neuroinflammation, and cognitive decline [43]. Importantly, because SPMs exert both antiinflammatory and pro-resolving effects, they are crucial to terminate inflammation but also stimulate tissue repair [65], which is fundamental in the context of perioperative recovery. In fact, RvD1 and maresins have shown to accelerate wound healing in diabetic patients [66, 67]. AT-RvD1 delivered through nanoparticles also enhance wound healing in a mice model of peritonitis [68]. We recently demonstrated that MaR1 pretreatment boosts systemic levels of IL-10 with a long-lasting trend up to 14 days after surgery [43]. Further, we found no difference in callus formation in mice treated with MaR1 compared to vehicle, suggesting MaR1 may be a safe option to be tested in future clinical trials.



**Fig. 4.1** Putative mechanisms of surgery-induced neuroinflammation and cognitive dysfunction. Surgery triggers systemic pro-inflammatory cytokines that can impair the blood-brain barrier, thus allowing peripheral cells into the brain parenchyma. Macrophage infiltration activates glia, including resident microglia and astrocytes, that acutely affect processes of synaptic plasticity and hippocampaldependent memory function. Treatment with SPMs, such as resolvins and maresins, actively promote resolution of inflammation after surgical trauma and prevent central nervous system dysfunction through the modulation of systemic and central cell types, such as monocytes, microglia, and neurons



**Fig. 4.2** Proposed mechanisms for neuroinflammation and surgery-induced cognitive dysfunction. Surgery has been shown to engage the innate immune system and activate a cascade of pro-inflammatory mediators, including alarmins, cytokines and eicosanoids. These molecules exert effects on the humoral and neuronal signaling overall contributing to the neuroinflammatory response. These processes are mediated not only by activation of resident

Overall, we are starting to uncover the potential for resolution agonists in the context of perioperative disorders and surgical recovery. Further research is needed to evaluate the exact mechanisms of action of different SPMs on different CNS cell types, and whether specific mediators may better target the immune response triggered by surgical trauma. SPMs have been detected in human cerebrospinal fluid, establishing proofof-principle that may serve as biomarkers for disease progression in neurological conditions like multiple sclerosis [69] and clinical PND [43]. These mediators can also be modified by dietary interventions, for example omega-3 PUFA [70], thus providing attractive strategies to

microglia but also by infiltration of peripheral cells into the brain parenchyma via a disrupted blood-brain barrier. This pro-inflammatory milieu and glia dysfunction impair neuronal activity and synaptic plasticity, impinging on processes of long-term potentiation, neurotransmission, and receptor function at the synapse. In combination, these pathological hallmarks contribute to learning and memory impairments following surgical trauma

intervene before an elective surgical procedure. SPMs biomarkers may take us a step closer to personalized approaches and targeted interventions to treat common complications, like postoperative pain and PNDs. As coined by Serhan and Savill 'alpha' programs 'omega' (i.e. the beginning programs the end) [20] could not better define the importance of the temporal events that orchestrate the acute inflammatory response in the perioperative space. Further characterizing these complex molecular events may provide novel and urgently needed approaches to safely treat PND and overall improve brain health for the millions of patients that undergo surgery every year.

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5

# Relationship Between Specialized Pro-resolving Mediators and Inflammatory Markers in Chronic Cardiac Disorders

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## Keywords

Pro-resolving mediators · Inflammation · Cardiac disorders

# 5.1 Introduction

The term cardiovascular diseases (CVD) refers to disorders of heart and blood vessels, and include coronary heart disease, cerebrovascular disease, peripheral vascular disease, and heart failure, among others. Atherosclerosis is a common background of these diseases. It is not infrequent that some acute diseases, such as coronary syndromes, appear superimposed on a chronic arterial disease. Acute coronary syndromes (ACS), found worldwide among the leading causes of death, can be the origin of disabling chronic CVD such as heart failure [46]. Clinical and experimental evidence associates this group of alterations with an inflammatory process that takes part in its pathophysiology. In fact, inflammation is one of the most important factors for its initiation, progression, and consolidation [6].

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We can consider acute inflammation as an extreme cellular response to stress that occurs when a stimulus perceived as harmful triggers mechanisms of the innate immune system [58]. Plasmatic and cellular molecules, leukocytes, and endothelial cells take part in the inflammatory process which induces an increase of vascular permeability, cell-cell interactions, and the massive recruitment of leukocytes and molecules to the tissues [8]. Since cellular dysfunction can be an inflammatory trigger, and inflammation itself can induce dysfunction or damage, a lack of control of the process can set up a perpetuating cycle [58]. Thus, if the homeostatic mechanisms are incapable of returning to the earlier limits, chronic inflammation takes place, eventually leading to systemic diseases. Various cardiovascular and metabolic diseases are examples of this phenomenon. Indeed, current knowledge permits association of metabolic disorders which show chronic inflammation, such as obesity and its comorbidities (accumulation of visceral fat, hypertension, dyslipidemia, and glucose resistance) with CVD [42]. Hence, evidence points to inflammation as an important player in CVD. The alterations in the concentrations of inflammatory markers reflect such a response. Their serum levels predict cardiovascular risk [43], and the outcome and mortality due to acute complications of ACS or to heart failure [10, 25].

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# 5.2 Cells and Mediators in CVD

As with other inflammatory-related conditions, cells of the immune and inflammatory responses crucially take part in the progression of CVD. The active and coordinated inflammatory resolution process, involves changes in subpopulations of inflammatory cells and their proportions, and changes in pro- and anti-inflammatory cytokines and lipid mediators, among other factors [51]. Macrophages are key cells that take part in multiple roles in the immune response, inflammation, and in different pathologies. They respond to various stimuli and express and secrete a wide range of soluble molecules and receptors which include lipid mediators, scavenger receptors, proand anti-inflammatory cytokines and chemokines; macrophages also present autophagic and anti-apoptotic properties [37]. We find these cells of the innate immune system in varying proportions in healthy and inflamed tissues or tissues being repaired [41]. For example, in a healthy murine heart, they represent approximately 8% of all cardiac cells [28] whilst after a myocardial infarction, the proportion of macrophages increases significantly [17].

We can distinguish two main types of macrophages: the inflammatory phenotype M1 (also known as activated by the classical route), and the anti-inflammatory phenotype M2 or activated by the alternative route; stimuli such as gamma interferon (IFNy) or interleukin-4 (IL-4), and the lymphocyte subpopulation responsible for those stimuli, differentially regulate their activation pathways [22, 54]. For example, some authors have observed that regulatory T cells induce the differentiation of macrophages to M2 in myocardial repair. Both subtypes of macrophages have different functions and capacities, partly related to the different profiles of inflammatory and pro-resolving molecules they synthesize. The pathogen-associated molecular patterns (PAMPs) activate the M1 macrophages, a fact that induces the release of pro-inflammatory cytokines [21]. These macrophages synthesize a pro-inflammatory lipid profile mainly derived from the omega-6 (n-6) arachidonic acid (AA) such as prostaglandin E2 (PGE2), PGF2,

Thromboxane B2 (TXB2) and leukotriene B4 (LTB4) [12].

Tissue repair seems to need the lipid profile of the M2 subtype. The involved mediators include derivatives of the omega-3 (n-3) polyunsaturated fatty acids (PUFAs) eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA). We call their derivates specialized pro-resolving lipid mediators (SPMs): resolvins (Rv), protectins (PD) and maresins (MaR). Lipoxins (LX) are also SPMs but their precursor is AA [32]. Serhan and his group have identified two classes of resolvins: that of the E series correspond to the EPA derivatives; and the class of the D series corresponds to the DHA derivatives; the latter being also the precursor of protectins and maresins. M2 produce more SPMs than the M1 macrophages, such as RvD5, MaR1, PD1, LXA4, LXB4, LXB5, and RvE2, [12]. Apoptotic neutrophils stimulate M2 macrophages: they produce lipid mediators that activate the SPM profile characteristic of M2 [12]. One of the main features of M2 macrophages is clearing apoptotic cells, a process known as epherocytosis, essential for restoring damaged tissue.

## 5.3 SPMs and Other Mediators

SPMs play important roles in resolving inflammation, and thus in a physiologic repair of tissues [4]. The membrane's phospholipids of activated cells are the precursors of SPMs and other lipid mediators of the inflammatory process [50]. Inflammatory stimuli such as lesions, microorganisms, and IL-8 activate phospholipase (FLP) A2 that produces free AA [8, 49]. When metabolized, this fatty acid forms a family of oxygenated products called eicosanoids, because of their 20-carbon structure [34]. Eicosanoids include prostaglandins, prostacyclins, thromboxanes, leukotrienes, lipoxins, and hydroxy and hydroperoxy fatty acids. While the enzymatic activity cyclooxygenase of (COX) synthesizes prostaglandins and thromboxanes, that of lipoxygenase (LOX) synthesizes leukotrienes and lipoxins. In a later stage of inflammation, and depending on the composition of the cell membrane, EPA and DHA substitute AA as the substrates of lipid mediators. The SPMs derived from those n-3 fatty acids, exert powerful antiinflammatory and pro-resolving actions mainly by decreasing the influx of neutrophils to tissues, by enhancing non-phlogistic recruitment of monocytes into tissues, and by decreasing the production of pro-inflammatory mediators [11]. Cell membrane surface receptors mediate their signaling [29, 33]. Annexin A1, a stress response endogenous protein, also mediates inflammatory resolution and can decrease the production of leukotrienes and prostaglandins by an inhibitory action on FLPA2 [15].

erosclerotic plaques represents a risk to develop myocardial infarction and cerebrovascular events [57]. In atherosclerosis, vascular smooth muscle cells have increased proliferative and chemotactic features, reduced expression of contractile proteins and increased production of proinflammatory cytokines [4]; they show increased inflammation and oxidative stress, and extensive areas of necrosis composed of non-clarified apoptotic cells [19]. Some authors suggest that poor resolution of inflammation merges the above [19], hence various researchers have tested diverse experimental approaches to prove this hypothesis. SPMs delay the progression of atherosclerosis



# 5.4 Resolution and CVD

Atherosclerosis is a disease that is a convincing example of the consequences of an inefficient inflammatory resolution. In humans, having athand promote greater plaque stability [18]. A notable observation is that mouse atherosclerotic plaque treated with SPMs increases its thickness and the synthesis of collagen in the fibrous layer, thus gaining stability [18, 19]. Today there is a great interest in studying resolvins in cardiac alterations because they seem to be crucial players in restoring lesions since they reduce the response of vascular smooth muscle cells and decrease the damage through the local activation of resolution mechanisms [8]. There are reports that resolvins can reduce the risk of developing atherosclerosis and its complications by preventing platelet aggregation, inducing vasodilation [13], inducing neutrophil apoptosis and limiting the size of the infarct [8]. In humans, however, there is still a long way to fully assess their therapeutic efficiency and possible toxic doses.

Resolvin E1 was the first metabolite of EPA identified, its biosynthesis depends on the interaction between endothelial cells and leukocytes in the inflammatory process [48]. Several studies suggest that RvE1 plays an important role in the restoration and repair of tissue damage, favoring resolution by decreasing the production of proinflammatory proteins and platelet aggregation. Administering RvE1 reduces the size of the lesion and decreases aortic expression of tumor necrosis factor (TNF) and IFNy in a murine model of atherosclerosis [47]. In a model of periodontitis and atherogenesis in mice, it decreases the levels of C-reactive protein (CRP) and the infiltration of macrophages to the intima [27]. RvE1 takes part in reducing platelet aggregation induced by thromboxane [20] and, in a model of ischemia-reperfusion of the myocardium in rats, its intravenous administration reduces the size of the infarct in a dose-dependent manner [31].

The mechanisms of action of resolvins of the D series in the inflammatory resolution of cardiac alterations seem to be different. In a model of arterial damage in rats, treatment with RvD1 attenuates both the levels of oxidative stress and the activation of the NF $\kappa$ B signaling pathway [9]. Intact human arteries incubated with DHA ex vivo, produce precursors of resolvins of the D series, which inhibit the adhesion of monocytes induced by stimulation of endothelial cells with TNF [9], suggesting that the local production of SPMs is necessary to promote inflammatory resolution. The in vitro treatment with RvD1 and RvD2 of vascular smooth muscle cells decreases

the proliferation, migration, and production of superoxide anion, and the expression of proinflammatory genes [3, 59]. The phosphoinositide 3-kinase (PI3K)/serine/threonine kinase Akt (PI3K/Akt) signaling interactive pathway mediates the protective effects of RvD1 (and of lipoxins), as treating with its inhibitor can block the cardioprotective effect of RvD1 [23]. In a model of damage caused by hepatic ischemia, RvD1 inhibits inflammatory pathways, decreasing the levels of IL-6, TNF, and myeloperoxidase, and increases phosphorylation of Akt, which favors its protective effect. In addition, RvD1 reduces the expression of pro-fibrotic genes and the deposition of collagen, which reduces post-infarction fibrosis [30]. In ischemic lesions, neutrophils infiltrate and release reactive oxygen species (ROS) and other mediators that damage tissue integrity [56]. Exogenous administration of RvD1 after myocardial infarction in mice reduces both the accumulation of neutrophils and fibrosis, which induces an improvement in cardiac function [30].

RvD2 has effects on cellular recruitment and proliferation. In an animal model, RvD2 limits the recruitment of neutrophils to the left ventricle and reduces the density of macrophages in the infarcted area [8]. This lipid reduces cell proliferation and lymphocyte recruitment in a model of arterial angioplasty in rabbits [38]. Similarly, in an intimal arterial neoformation model in mice induced by carotid ligation, RvD2 reduced the proliferation of smooth muscle cells and the recruitment of neutrophils and macrophages. It also induced lower levels of TNF and of granulocyte and macrophage colony-stimulating factor (GM-CSF) [3]. Acting in a similar way of RvD2, the administration of LXA4 in rats with myocarditis reduces the infiltration of inflammatory cells [53].

Not being an SPM, but because of its role in inhibiting FLPA2, annexin A1 has been studied in atherosclerosis. Asymptomatic plaques of the carotid artery have elevated levels of the protein, and its plasmatic concentrations correlate negatively with the total areas of the plaques in atherosclerosis models, which suggests an important role of annexin in resolving cardiac inflammation [15]. Its action on regulating the production of leukotrienes and prostaglandins may account for its capacity to inhibit the migration of leukocytes into the plaques and its early protective effects [19].

## 5.5 Diet PUFAs as Precursors of SPMs and CVD

Independent of the use of pure SPMs in the current approaches, there is a long history of use of their precursors n-6 and n-3 PUFAs derived from the diet, specifically by consuming seafoods or their purified compounds. Being essential in the development and function of the organism [8], the human body can synthesize only small amounts of EPA and DHA [60]. Some studies observe that consuming fatty acids changes the profile of the membrane phospholipids, and the composition of the fatty acids of different cells and tissues, affecting their availability [32]. Other studies have shown beneficial effects of n-3 on various pathological conditions [52]. The quality of life of people with chronic inflammatory diseases such as arthritis and asthma [35], the severity of chronic inflammation [7] and the risk for cardiovascular diseases [26] improve with a diet with n-3 PUFAs. The incidence of heart failure in older adults associates negatively with the total plasma concentration of n-3 [40]. Coincidently, a meta-analysis shows that supplementing with EPA and DHA has positive effects on risk factors for cardiovascular diseases because they have hypolipemic, hypotensive, antiarrhythmic and anti-inflammatory actions [1].

Until today it is not fully clear the role of diets that include DHA and EPA to protect against cardiovascular diseases. There is not a consensus despite a wide range of studies that show their beneficial effects, in part because many factors are involved and influence the outcome. For example, a diet enriched with n-6 and n-3 in a 4:1 ratio (as opposed to the 15:1 obtained with a typical occidental diet) decreases the mortality rate for cardiovascular diseases [55]. Other factors to consider include the different EPA/DHA ratios used (0.5:1–1.4:1), different lengths of consumption (few months to more than 6 years), the great variability in doses (<1-4 g/d), the diseases studied, comorbidities (diabetes, hypertension and stroke), and the interaction with drugs. [1, 2].

To reach effective blood levels to reduce the risk of CVD or prevent secondary complications, various studies have concluded that the daily consumption of EPA plus DHA must be of at least 1 g [5, 36, 44]. Consistently, in studies with lower doses of PUFAs, no protection against a possible cardiovascular event is achieved [14]. Some authors suggest higher doses to prevent complications in patients with cardiac disease, for example, consuming 3.36 g of EPA plus DHA in patients with stable coronary disease, helps to restore the levels of SPMs and promotes the phagocytosis of clots. [16]. Administering high doses of n-3 PUFAs in patients with atherosclerosis and type 2 diabetes, accompanied by adequate medical therapy, increases the serum concentrations of EPA and DHA, although it does not induce changes in the concentrations of RvD1 [45]. In rats, a diet enriched with DHA decreases pro-inflammatory proteins such as CRP, IL-6, TNF, and IL-1 $\beta$ , and favors an increase in the concentrations of RvD2 and RvD3 [39]. Fish oil treatment favors protection against thrombosis and damage induced by vascular remodeling in mice, reducing local inflammation and increasing resolution by increasing RvE1 [24].

## 5.6 Conclusions

Many studies suggest that uncontrolled inflammation and failure in the resolution response are the basis of a myriad of human diseases. SPMs seem to play a crucial role in restoring damaged tissue and in the recovery of function. In fact, it is possible that the success of the inflammatory resolution largely depends on the capacity of producing SPMs and how these mediators can contain chronic inflammation. The study of inflammatory resolution in cardiovascular diseases still represents a challenge. It is still necessary to find out if administering SPMs or their precursors will have the beneficial therapeutic use they promise. Indeed, finding successful

ways of resolving inflammation can provide important advances in preventing cardiometabolic diseases.

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6

# Specialized Pro-resolving Mediators Directs Cardiac Healing and Repair with Activation of Inflammation and Resolution Program in Heart Failure

Ganesh V. Halade and Bochra Tourki

# Abstract

After myocardial infarction, splenic leukocytes direct biosynthesis of specialized pro-resolving mediators (SPMs) that are essential for the resolution of inflammation and tissue repair. In a laboratory environment, after coronary ligation of healthy risk free rodents (young adult mice) leukocytes biosynthesize SPMs with induced activity of lipoxygenases and cyclooxygenases, which facilitate cardiac repair. Activated monocytes/macrophages drive the biosynthesis of SPMs following experimental myocardial infarction in mice during the acute heart failure. In the presented review, we provided the recent updates on SPMs (resolvins, lipoxins and maresins) in cardiac repair that may serve as novel therapeutics for future heart failure therapy/management. We incorporated the underlying causes of non-resolving inflammation following cardiac injury if superimposed with obesity, hypertension, diabetes, disrupted circadian rhythm, co-medication (painkillers or oncological therapeutics), and/or aging that may delay or impair the biosynthesis of SPMs, intensifying pathological remodeling in heart failure.

#### **Keywords**

Cardiac repair · Heart failure · Leukocytes · Myocardial infarction · Resolution of inflammation · Specialized pro-resolving mediators

# Abbreviations

AA	Arachidonic acid
AT-LXA <sub>4</sub>	Aspirin-triggered LXA <sub>4</sub>
DHA	docosahexaenoic acid
EPA	eicosapentaenoic acid
H and E	hematoxylin and eosin
HF	heart failure
LV	left ventricle
$LX_4$	lipoxin A4
$L_XB_4$	lipoxin B4
MaR1	maresin 1
MaR2	maresin 2
MI	myocardial infarction
RvD1	resolvin D1
RvD4	resolvin D4

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#### 6.1 Introduction

Heart failure (HF) is the chronic, end stage, and irreversible pathology secondary to ischemic coronary artery disease, predominantly superimposed on aging. HF is also common with non-ischemic cardiovascular diseases with preserved ejection fraction (HFpEF) [1, 2]. After myocardial infarction (MI; heart attack), inflammatory HF is categorized by maladaptive changes in size, shape, and function of the left ventricle, advancing to cardiac remodeling (Fig. 6.1) [3]. In a clinical setting, the size/area of a patient's infarct does not determine the likelihood of adverse remodeling, with or without reperfusion [4]. Therefore, the high rate of hospital admission or re-admission, as well as cardiovascular morbidity and mortality, is primarily due to HF associated with aging [5].

Currently, 5.7 million people are diagnosed with HF in the US, but the projections of this disease are expected to increase to 46% [6], with more than 8 million affected by 2030. As of today, a total of 26 million people are suffering from advanced HF worldwide [7]. During recent years, the discovery of advanced surgery tools, novel medical device technology, therapeutics, team-based symptom management and approaches have advanced in order to minimize patient discomfort. The combination of medical devices and therapeutic procedures have either helped or interfered with the majority of initial inflammatory and reparative responses to MI, but have not slowed the trajectory for disease progression to HF. Every year there are still 915,000 new cases of HF, accounting for an incidence approaching 10 in 1000 individuals over 65 years of age [7]. The continuous growth of HF patients reveals a major gap in our knowledge in how to



Fig. 6.1 Heart attack induced left ventricle (LV) structural and fibrotic remodeling from acute (day 1 and 5) to chronic (day 28–56) heart failure in mice model of permanent coronary ligation. From the top to the bottom: difference in ECG from normal mice to MI-induced heart after coronary ligation; Periodic acid–Schiff (PAS; 1.25X) staining of the LV after MI from day

1 to day 56 compared to day 0 naïve control. Hematoxylin and Eosin (H and E; 40X) staining of LV showing the organized myocardium structure before MI compared to necrotic and apoptotic disorganized myocardium from day 5 to day 56; Picrosirius red (PSR) staining confirmed the deposition of collagen and compact fibrotic remodeling in the infarcted area initiated at day 5 and progressive to day 56 properly treat and identify novel target signaling pathways to resolve inflammation without the adverse effects of medication or therapies, which frequently occurs with current anti-inflammatory treatments [8, 9]. Aspirin, often considered the safest anti-inflammatory treatment, has failed to limit the event of coronary heart disease and stroke in elderly individuals and is often associated with high incidences of intracranial and extracranial bleeding within the same risk group [10].

In this review, we summarized the leukocytedirected biosynthesis of SPMs in myocardial healing and the beginning of future applications of novel SPMs to limit chronic inflammation in the setting of HF with potential enhancement to the reparative program [11]. SPMs are biosynthesized by leukocytes triggering endogenous cardiac healing as part of the acute innate response involved in the inflammation-resolution process. The successful biosynthesis of SPMs terminates inflammation and facilitates repair by stimulating distinct resolution processes necessary for tissue repair and regeneration from MI to advanced HF [12–14].

# 6.2 Immune-Responsive Systems in Myocardium Wound Healing

Pathological inflammation and physiological inflammation are two distinct and primary challenges in identifying and treating injury, infection, or stress (physical or neuro-hormonal mental exhaustion). Physiological inflammation, although necessary, needs to be both activated and inactivated within a specified time in order to avoid damage caused by sustained pathological inflammation. Distinct differences include the phenotype and/or biomarker of injured cells and tissues and the nature and timing of immune signals. Successful physiological inflammation depends on the infiltration of neutrophils and monocytes ('get-in signal'), phagocytic activity of leukocytes ('eat-me signal'), and the on time departure, or efferocytosis, of neutrophils ('get out signal'). The synchronicity of leukocyte entry, coordinated phagocyte activity and an on time exit prevents undesirable consequences of an excessive inflammatory process through the resolution process, which enhances the healing and tissue repair mechanism [15].

Although HF is a multifactorial and heterogeneous end stage disease, the mechanisms of initial inflammation and subsequent initiation of tissue repair are relatively undefined in the acute setting of MI and the role of these critical pathways in the chronic setting remains largely unexplored [16]. HF is predominantly superimposed on other risk factors, like aging and renal failure; however, it is not only risk factors that amplify the complexity of this disease. There is an inter-organ crosstalk between the heart and peripheral organs in HF that delays the cardiac healing program (Fig. 6.1). We defined a clear interaction between the spleen and heart, as 'the splenocardiac axis' as well as the cardio-renal axis [17]. In this context, the spleen is not acting as a leukocyte reservoir but instead as a site for the continuous activation of SPMs in cardiac injury. The spleen is considered an integrative organ in cardiac healing through the production of multiple families of SPMs to activate the cardiac resolution program because splenic leukocytes define the resolution of inflammation in HF [18, 19]. In order to prevent the progression of HF pathology from acute to chronic inflammation, the inflammatory response must be actively resolved (Fig. 6.2). In this review, we highlighted the role of leukocytes, particularly macrophages, that biosynthesize SPMs in cardiac repair and remodeling after injury.

# 6.3 Immune-Responsive and Leukocytes Directed Cardiac Repair

Cardiac repair is based on the timely activation of cellular and molecular pathways that delay reactive fibrosis signaling, resulting in the formation of scar tissue [20]. Both innate and adaptive



**Fig. 6.2** SPMs balance or imbalance defines the inflammation and resolution outcome. Resolution of post-MI inflammation is an active process that requires a balance between proresolving mediators (SPMs) and clearance of leukocytes after acute inflammatory response. In case of heart failure associated to co-medication, this balance is impaired. For example doxorubicin, an oncological drug induced a spleen atrophy with a decrease of splenic macrophages that impairs SPMs biosynthesizing

immune mechanisms are involved in this process [21]. Recently, the belief that activated splenic leukocytes play a critical role in both repair and remodeling has been validated. Specialists in adaptive immune responses demonstrated that the depletion of mature B lymphocytes impeded monocyte mobilization, limited myocardial injury, and improved heart function post-MI and Treg function in cardiac repair [22, 23]. However, cardiac repair alone is insufficient due to various additional risk factors, such as obesity, insulin resistance, diabetes, dyslipidemia, and hypertension. These risk factors can hinder healing, promoting defective tissue repair or unresolved inflammation that can progress to adverse ventricular remodeling thereby leading to end stage

enzymes (Jadapalli JK et al., AJP-HC 2018). Likewise, pain-killer caprofen, when administrated before MI for 2 weeks to mice, impairs the splenocardiac axis, dysregulated resolving mediators, over activates neutrophils, and decrease the reparative macrophages at the site of the injury therefore non-resolving inflammation (Halade GV et al., J Leukoc Biol 2018). LV Left Ventricle, MI Myocardial Infarction, MØ macrophages, Neu neutrophils

of HF [24]. Following cardiac or other tissue injury, the resolution of inflammation is a prime indicator and precursor of tissue repair [25]. In a clinical setting, the hematological profile of a HF patient shows elevated levels of leukocytes, particularly neutrophils and inflammation of the arterial wall in addition to the infarcted myocardium [26, 27]. In mice, the density of leukocytes (neutrophils/monocytes) increase in the infarcted LV in response to myocardial injury [28]. This spike is due to the depletion of splenic leukocytes that occurs while a steady flow of leukocytes are provided to the infarcted LV after MI [18]. In fact, splenic leukocytes mobilize to injured myocardium enriched with fatty acids, such as arachidonic acid (AA), docosahexaenoic acid (DHA), eicosapentaenoic acid (EPA), and activated lipoxygenases (LOXs). These activated cells, primarily monocytes, then further differentiate into macrophages and biosynthesize SPMs during the acute inflammatory response, suggesting that the acute inflammatory response coincides with the resolving response in cardiac healing [18, 29].

The spleen, as the immune reservoir, coordinates the time-dependent healing of an infarcted LV and determines resolving and non-resolving inflammation. First, immune cells are recruited to stimulate the repair of damaged myocardium [30]. The fatty acid composition in the spleen and the enrichment of the immune system may indirectly affect the cellular events of both of these processes. The depletion of leukocytes (macrophages/neutrophils) is correlated with the lower levels of pro-resolving mediators. Macrophages and the interaction of macrophages with innate leukocyte players are essential for the biosynthesis of bioactive mediators and cardiac healing [31]. The magnitude of cardiac injury, the activation, and initiation of the inflammatory response, and its counter regulation triggers the recruitment of reparative cells that protect against adverse remodeling [32, 33]. Physiological importance of spleen is recorded in humans, since asplenic patients develop ischemic heart disease and excess risk of infection [34].

Recently, the technological advancements in molecular and cellular biology have yielded progress in biomarker discovery and functional characterization that improve our understanding of LV remodeling mechanisms. In the context of cardiac healing, the resolution process has become a frontline focus of inflammationresolution research and SPMs have become a new strategy for chronic diseases. Many preclinical studies and some clinical reports have shown benefits of SPMs, such as limiting the second wave of tissue infiltration of neutrophils, reducing collateral tissue damage, shortening the resolution interval, enhancing macrophage phagocytosis, amplifying efferocytosis, and counter regulating pro-inflammatory chemical mediators [35, 36].

# 6.3.1 Neutrophils – Digest Deceased Cardiomyocyte

After cardiac injury, the clearance of deceased myocytes is the primary objective of the leukocytes-based phagocytic system. Neutrophils are important effector cells to activate resolution and cardiac healing post-MI and neutrophil depletion in early healing can lead to early remodeling and HF [15]. Neutrophils dismantle the extracellular matrix and enter the site of injury in order to access the deceased and the necrotic tissue, accelerating pro-inflammatory cytokine production [37]. Neutrophils are highly phagocytic cells containing granules filled with various defensins, elastases, and proteases (matrix matelloproteinase, MMP2, cathepsins, cathelicidins, phosphatases, oxidases, and collagenases) and their primary function is to dissolve matrix and phagocytose; however, this can amplify the inflammatory response [38]. Neutrophils are classically known as immuneresponsive inflammatory cells (termed as N1 neutrophils) but recent reports indicated that, like macrophages, neutrophils undergo polarization and show anti-inflammatory properties (termed as N2). These N2 neutrophils account for 20% of the neutrophils present 7 days post-MI [39]. The phenotypes of N2 neutrophils are distinguishable by the high expression of the macrophage mannose receptor CD206 and interlukin-10 (IL-10). Neutrophils orchestrate post-MI healing by polarizing macrophages towards a reparative phenotype but can also play an active role in the resolution of inflammation by depleting the chemoattractants that initially drew them to the site of injury [40, 41]. Therefore, these cells contribute directly to the inflammation-resolution process and indirectly to cardiac repair after MI.

# 6.3.2 Macrophage – Programs Neutrophils Clearance and SPMs Biosynthesis

Recent findings imply a potential role of the mononuclear phagocytic system includes macrophage cells in the repair of infarcted myocardium [42, 43]. According to macrophage biology research, many studies are devoted to the description of mouse cardiac monocyte and macrophage subsets and the refinement of macrophage classifications are ongoing [44]. With respect to recent data, the composition of macrophage subsets in the myocardium undergo dynamic changes throughout the course of a lifetime [45]. Fate mapping studies confirmed that the monocyte/ macrophage systems placed in the heart prior to birth maintain self-renewal properties independently of a circulation feedback system [46]. Unfortunately, this discovery has limited translational potential since it is still unclear whether generation and differentiation of macrophages from precursors are impaired with age. However, it is well proven that macrophages become either partially or totally dysfunctional in wound healing within the context of obesity and diabetes superimposed on aging in both humans and rodents [47].

We know that macrophages have polarization profiles similar to neutrophils; within 1 day post-MI, macrophage exhibit a pro-inflammatory M1 profile [48–50]. At the post-MI "healing stage" (up to 7 days post-MI), there is a transition from predominately M1 macrophages to primarily anti-inflammatory macrophages, and then to reparative M2 cells [51, 52]. Cardiac reparative M2-like macrophages are a complicated mixture of heterogeneous subsets that have strengthened their tissue-repairing abilities by upregulating various anti-inflammatory and repair-associated genes after MI [42, 53]. These two types of cells (M1 and M2) are derived from Ly6C<sup>hi</sup> monocytes and Ly6C<sup>low</sup> monocytes, respectively. Reparative M2 macrophages are recruited simultaneously with inflammatory leukocytes in the post-infarct LV to mediate myocardial healing through the secretion of anti-inflammatory cytokines and growth factors, such as VEGF and TGF-B, that contribute to myofibroblast activation and neoangiogenesis [54]. Deceased cardiac fibroblasts emit signals causing the activation of monocytes via MCP-1-mediated chemotaxis and adhesion to ICAM-1/VCAM-1, and induce their differentiation to M1 or M2 macrophages [44]. Some researches include a third macrophage subtype

found in resolving exudates referred to as 'resolution phase macrophages'. These macrophages possess characteristics of both M1 and M2 cells and we believe that they represent cardiac reparative macrophages, especially with the recent clinical strategies focused on improving macrophage function to improve healing outcomes [55–57]. Macrophage biology and phagocytic systems likely vary with the magnitude of injury and therefore the monocyte and macrophage responses to injury can differ depending on the experimental model. For example, in a model of neonatal mice, the depletion of macrophages after MI impaired cardiac function and angiogenesis. The heart can fully regenerate without scarring following MI in neonatal mice; however, the regenerative capacity of macrophages is lost 7 days after birth [28]. Under other conditions, like in a model of adult mice, after MI, Ly6C<sup>hi</sup> macrophages (M1 macrophages), and Ly6Clow (M2 macrophages) are the main effectors of cardiac remodeling.

The kinetic and detailed macrophage and neutrophil profiling studies demonstrated that after cardiac injury, splenic monocyte-enriched leukocytes mobilized to the infarct area and biosynthesized SPMs. Macrophages are a major contributor in SPMs biosynthesis [58]. In addition, lipid mediator profiling of the spleen indicates that the spleen also receives feedback signal for biosynthesis of lipid mediators, which promote selfresolution of inflammation at the left ventricular site [59]. In cardiac injury, SPMs are biosynthesized immediately by primarily activated macrophages with the initiation of inflammation [60]. In response to cardiac injury or stress, the resolution-phase activated macrophages also express ALOX-15, indicating that they may also contribute to SPMs production during resolution [61, 62]. M2 macrophages produce more proresolving lipid mediators than M1 macrophages [63]. SPMs initiate the switch from inflammation to resolution by reducing neutrophil recruitment and T cell cytokine production and increasing recruitment of phagocytic monocytes [64]. Resident macrophages express TGF-B1 and IL-10, presumably because of phagocytizing apoptotic neutrophils; these cells also expressed ALOX-15 and TIMD4 (T-cell immunoglobulin domain and mucin domain 4) to facilitate the recognition and uptake of apoptotic cells [65, 66]. Recent results indicate that treatment with DHA derived pro-resolving mediators, like exogenous RvD1, stimulate a switch in macrophage phenotype from pro-inflammatory to pro-resolving, a M2-like phenotype [67, 68]. Studies found that human M2 macrophages are associated with increased MaR1 levels [61]. This increase is due to the ability of this macrophage subtype to convert the 13S, 14S epoxide intermediate to MaR1 [60]. As critical regulators of the resolution program, targeting the actions of macrophages could be an effective strategy to control inflammation and cardiac remodeling.

# 6.3.3 Knowledge Gap of Inflammation and Resolution as Part of Cardiac Reparative Program

After cardiac injury, the resolution phase is an active biosynthetic process that overlaps or coincides with the first response of the innate immune system. This was confirmed using structural elucidation of the SPMs in a variety of wound healing models [19]. Inflammation-resolution process-derived bioactive metabolites implicate an array of receptors that transduce pro-resolving action. Among them, the most studied receptors are GPCRs as effectors of resolution shown indirectly through use of the receptor knockout cells and mice. These GPCR receptors (ChemR23, GPR32, and FPR2) activate signals and transduce the pro-resolving signals of chemerin peptides, resolvin E1 (RvE1) and resolvin D1 (RvD1) and lipoxins [69–71].

Recent, emerging data added confirmation to previous thoughts that resolution is a primarily, active stage of the immune response to cardiac injury and not an inactive, secondary stage. This stage acts as an overlap with the innate response, adding a third phase after the initiation of inflammation and resolution, creating a post-resolution response dominated by macrophages and lymphocytes [72]. Although data on SPMs primarily focuses on innate immune cells involved in the resolution of acute inflammation, resolution creates a microenvironment conducive for the optimal development, tissue repair, and modulation of the adaptive immunity [19, 58, 73]. We conclude that a better understanding of SPMs biosynthesis and the pharmacology of SPMs receptors, especially in chronic inflammatory settings like HF, could minimize the gap between the initiation of inflammation and initiation of resolution, capitalizing the fundamental actions of these effectors of resolution.

# 6.4 SPMs Biosynthesis and Resolution of Inflammation in Cardiac Repair

Splenic leukocytes mobilize to the site of infarcted injury and biosynthesize SPMs to limit the excessive inflammation that can be detrimental to healthy tissues, particularly in sterile inflammation. In addition to the stop signal in acute inflammatory response, SPMs also stimulate distinct processes necessary for tissue repair and regeneration [74]. SPMs have been associated with positive feedback loops, where one pro-resolving mediator induces the biosynthesis of another [15]. The administration of RvD1 3 h after MI in mice induces lipoxin A4 and MaR1 to facilitate the resolution of inflammation and cardiac regeneration [75]. SPMs are produced mainly by the inter-organ interactions of monocyte-derived macrophages and neutrophils via distinct enzymatic pathways from essential fatty acids, such as omega-3 and omega 6, polyunsaturated fatty acids (PUFAs), eicosapentaenoic acid (EPA), and docosahexaenoic acid (DHA) [76]. Several endogenous SPMs have been discovered, including lipoxins, resolvins, protectins, and maresins [36], which are directly and indirectly involved in driving the initiation of inflammation-resolution and successfully terminating inflammation. Healthy and risk free animals, such as young or adult mice, effectively mobilize circulating neutrophils, platelets,

and monocytes/macrophages from the spleen after cardiac injury to promote left ventricle healing, which is essential to delay HF [59]. After cardiac injury, monocytes/macrophages serve as a major contributor for the biosynthesis of SPMs that have multiple cellular targets in the inflammatory response, including immune cells, platelets, and vascular cells [74]. Leukocytedirected SPMs actively counter-regulate and control the production of pro-inflammatory mediators, including cytokines, leukotrienes, and eicosanoids, and regulate leukocyte trafficking and phenotype after both sterile and infectious challenges [77].

#### 6.4.1 Resolvins

These are novel bioactive autacoids termed "resolvins" because they are endogenously generated by resolution phase interaction products classified as either E-series resolvins, if leukocyte directed biosynthesis is initiated from EPA, or D-series resolvins, when resolvins are biosynthesized from DHA [78, 79]. Subcutaneous administration of RvD1 limits the activation of neutrophils in the spleen and promotes the clearance of macrophages and neutrophils from the infarcted site to facilitate cardiac healing. After ischemic injury, treatment of RvD1 primarily activates the ALX/FPR2 receptor in both the spleen and left ventricle to promote effective resolution of inflammation and limit residual time of neutrophils at the site of infarction ('get-out' signal) [30, 80].

A reperfusion study in rats confirmed that intraventricular administration of RvD1 reduces myocardium infarct size; however, presence of excess linoleic acid attenuates the myocardial protection offered by RvD1 [81, 82]. In another experimental study, after cardiac injury using permanent coronary ligation model, RvD1 administration in mice not only resolves the inflammatory response, but also reduced the expression of fibrotic genes, such as *colla1*, *coll2a1* and *tnc*, in the early phase of cardiac healing. Thus, RvD1 limits fibrotic signaling and facilitate organ homeostasis [75, 83]. These changes of ECM in acute HF suggest that RvD1 orchestrates mature scar formation and stabilizes the ECM by resolving inflammation. An experimental model of hind limb ischemia (HLI) in mice, RvD2 stimulated arteriogenic revascularization suggesting that resolvins may be a novel class of mediators that both resolve inflammation and promote arteriogenesis [84] (Table 6.1). Presented experimental studies in rodent models strongly indicate that SPMs offer pharmacological action in the range of ng or pg doses suggestive of outstanding potency [85], in contrast to nonsteroidal anti-inflammatory drugs (NSAID) which effective in a range of mg/kg doses that are immune suppressive and impact the cardiovascular physiology and pathobiology [86].

SPMs are produced by the coordinated activity of lipoxygenases (LOXs) in the heart and cyclooxygenases (COXs) in the spleen; these are the key enzymes for generating potent bioactive lipid mediators, which primarily synchronizes the resolution of inflammation in pathophysiological settings [87]. Fredman et al. reported that RvD1 favors synthesis of the pro-resolving lipid mediator, LXA<sub>4</sub>, via limiting nuclear translocation of 5-LOX in atherosclerotic inflammation [88]. RvD1 critically balanced LOX enzymes by stimulating 5-LOX expression, which is essential for wound healing post-MI [89]. RvD1 has the potential to delay HF by limiting cytoplasmic to nucleus translocation to delay atherosclerotic inflammation and facilitate neutrophil clearance. Future long-term studies focused on RvD1 are warranted in order to prove its utilization in chronic HF management in patients with heterogeneous cardiovascular pathology [75]. Another compound of the D-series resolvins family, RvD3, was used as a model of selfresolving peritonitis in aging mice. The study, performed by Arnardottir and colleagues, reported that increased levels of RvD1 and RvD3 treatment stimulated increases in monocyte-accelerated resolution of acute inflammation via efferocytosis [90]. RvD3 has been argued to be one of the most potent of the D-series resolvins [91].

Regarding the E-series resolvins, Arita et al. reported leukocyte-directed actions of RvE1 as

Molecules		Experimental Model	Mechanisms	Effect	References
Resolvins	RvD1	<i>In vivo</i> , mice model of heart failure	ALX/FPR2 receptor	↑ clearance of neutrophils from the spleen	[75]
				↑ clearance of macrophages from healing site	
				↓ expression of fibrotic genes	
RvE1	RvE1	<i>In vivo</i> , mice model of acute heart failure	ChemR23 receptor	Protected cardiomyocytes against apoptosis	[107]
			BLT1 receptor	↓ protected cardiomyocytes against apoptosis.	
				↓infiltration of dominant Ly6C <sup>hi</sup> Mos/Mps	
Lipoxins 15-ep LXA	15-epi- LXA <sub>4</sub>	<i>In vivo</i> , mice model of heart failure	ALX/FPR2 receptor	↑ clearance of neutrophils	[103]
				Improve ventricular function	
				Activate GPR120 receptor	
				Inhibit GPR40 receptor	
Maresins	MaR1	<i>In vitro</i> , human macrophages <i>In vivo</i> , model of atherosclerosis	GPR32	↑ Efferocytosis and phagocytosis	[60, 108]
			BLT1 receptor	↓PMN infiltration	
				↑reparative macrophages	

Table 6.1 Role of SPMs in cardiac repair in different experimental models

one of the local mediators of tissue homeostasis during inflammation-resolution [92, 93]. The physiological functions of RvE1, and RvE2, both biosynthesized by neutrophils via the 5LOX pathway and RvE3 biosynthesized by 12/15-LOXs in eosinophils, have been studied in the last few years [94, 95]. The myocardial protective action of RvE1 action is quite different from other resolvins and protectins. RvE1 specifically binds to ChemR23 and BLT1 to offer proresolving responses in human polymorphonuclear (PMN) cells [96]. This binding enhances macrophage phagocytosis via phosphoproteinmediated signaling [97]. It blocks LTB<sub>4</sub> binding and signals via BLT1 to promote apoptosis of PMN for their clearance by macrophages, while LTB<sub>4</sub>-BLT1 signals PMN survival.

#### 6.4.2 Lipoxins

Lipoxins  $A_4$  and  $B_4$  are lipoxygenase-interaction products of arachidonic acid and are biosynthesized at the site of injury to facilitate resolution of inflammation. Lipoxins are endogenous that offers anti-inflammation and pro-resolution at nanomolar concentrations, inhibiting chemokinedriven recruitment of both granulocytes and monocytes [98, 99]. At the site of inflammation, lipoxins also stimulate macrophages to ingest and clear apoptotic neutrophils, exerting proresolving actions through the activation of ALX/ FPR2 [100, 101]. In correlation with lipoxins generation, LTB<sub>4</sub> was proved higher in the spleen at a naïve state and increases along with lipoxins in the LV at day 1 post-MI [18]. Recent studies demonstrated that 15-epi-LXA<sub>4</sub> coordinates the upregulation of IL-6 and IL-1ß at day 1 post-MI to facilitate an unaltered, active inflammatory phase post-MI without altering the acute inflammatory response. Liposomal delivery of 15-epi-LXA<sub>4</sub> showed a similar protective function as free 15-epi-LXA<sub>4</sub>, improving ventricular function through the activation of neutrophil clearance in the LV during the resolving phase with an increase of ALX/FPR2 and Ccl2 during the acute inflammatory phase in a murine model of HF [102]. Additionally, 15-epi-LXA<sub>4</sub> promotes the resolution of inflammation by activating GPR120 and inhibiting GPR40 in a translational HF model (Table 6.1) [3, 102, 103].

#### 6.4.3 Maresins

Maresins (macrophage mediators in resolving inflammation) are derived from the marine omega-3 fatty DHA acid [104]. Leukocyte-directed maresins (MaR) are produced by macrophages via initial lipoxygenation at the carbon-14 position created by the insertion of a molecular oxygen, producing a 13S,14Sepoxide-maresin intermediate that is enzymatically converted to maresin family members (MaR 1, MaR2, and MaR conjugate in tissue regeneration (MCTR) that regulate phagocytosis, and the repair and regeneration of damaged tissue [36, 102]. An recent study by Halade et al. showed that the quantification of MaR1 at day 1 post-MI in mice is significantly higher in LV than spleen. However, at the naïve state without any induced injury, MaR1 is higher in the spleen than in the LV. These findings confirmed that splenic monocyte-enriched leukocytes mobilize to the infarct area and biosynthesize SPMs [18]. In an in vivo study, MaR1 reduced neutrophil and macrophage recruitment and increased polarization of M2 macrophages in the arterial wall [105]. MaR1 have the ability to skew macrophage phenotypes toward resolution-like, with increased TGF- $\beta$  production and secretion [106]. After an infection, activated macrophages biosynthesize MaRs that increases phagocytosis and efferocytosis, resulting in the clearance of microbes (Table 6.1) [80].

## 6.5 SPMs Regulation and Dysregulation

Fatty acids-derived drug (FADD) discovery exemplified the generation of SPMs from essential fatty acids [59]. This discovery is unique and novel for endogenous, bioactive pro-resolving mediators, represents a paradigm shift in our understanding of the dynamic regulation of acute inflammation, and has led to a new era of resolution physiology and resolution pharmacology. Within a single cell type, lipid mediator class switching can occur and pro-resolving lipid mediators can regulate each other. SPMs have dual roles as counter-regulators of inflammation, as anti-inflammatory without being immunosuppressive, and activators of resolution [109]. For example, RvD1 reduces nuclear localization of 5-LOX in macrophages and diverts arachidonic acid metabolism from pro-inflammatory lipid mediator LTB<sub>4</sub>, to SPM LXA<sub>4</sub> [62]. RvD1, activated through ALX/FPR2, protects macrophages from oxidative stress-induced apoptosis during efferocytosis, in part, by regulating nicotinamide adenine dinucleotide phosphate oxidase activation and expression of apoptotic proteins, Bcl-XL, and Bcl-2 [110]. In the other hand, the downregulation of NF- $\kappa\beta$  and TNF- $\alpha$  by RvD5 could be beneficial in the HF model, as both of these factors are increased in the heart postcardiac injury [111]. Therefore, SPM emerge both as potent regulators of macrophage responses of interest during the resolution phase of acute inflammatory responses and effectors in macrophage mediated responses [112]. Of interest, receptors of SPMs, including ALX/FPR2 and ChemR23, are expressed in the human saphenous vein SMC, and administration of RvE1 and 15-epi-LXA<sub>4</sub> counter-regulate platelet-derived growth factor-stimulated VSMC migration in a dose-dependent manner [113]. These results build on previous studies showing that lipoxins counter-regulate leukocyte-mediated microvascular permeability in vivo during acute inflammation, stimulated by pro-inflammatory lipid mediators [114]. The actions of SPMs were recently reported in human settings where an RvE1 analog entered human clinical trials for dry eye inflammation [115]. In light of the role of SPMs in the resolution, these compounds display potent actions in the adaptive immune system including the regulation of T-cell phenotypes and responses [58, 116]. Because Treg cells are an important cell subset involved in modulating and maintaining self-regulation of the immune system, SPMs potentially induced Treg (iTreg) differentiation, with the lipids significantly enhancing Foxp3 expression compared to control iTreg cells. They affect not only Treg induction, but also specific functional properties, like TH cell polarization [58]. The actions of SPMs on T cells are mediated by GPR32 and ALX/FPR2

receptors. It has been proven that RvD1, RvD2, and MaR1 exert a non-cytotoxic regulatory role on cells; it represents a promising beginning for a new avenue of resolution physiology research.

Biosynthesized maresins counter-regulate the pro-inflammatory cytokines, such as *IL-1\beta*, *IL-6*, and *TNF-\alpha*. They also regulate nuclear factor kappa B (NF- $\kappa$  B) gene products, increase the regulation of T cell de novo synthesis and intracellular levels of cyclic adenosine monophosphate, regenerate tissue, and play a role in anti-nociceptive action [36, 117]. SPMs might possibly act on the balance between pathogenic TH1/TH17 and tolerogenic Treg cells, which are typically altered during chronic inflammation [58]. However, these endogenous pathways of resolution could be disrupted or dysregulated with co-medication. In fact, treatment with painkiller caprofen or oncologic drug doxorubicin facilitate splenocardiac resolution deficiency in mice with cardiac injury, creating non-resolving inflammation (Fig. 6.2) [118, 119]. Other factors, like metabolic dysfunction, are major contributors of SPMs dysregulation. For example, obesity, hypertension, diabetes, and aging are associated with HF and could give an extra rise to unresolved chronic inflammation [120]. Next, we discussed the impact of SPMs dysregulation in cardiometabolic disorder thereby impact on resolution physiology.

## 6.5.1 Obesity

The unprecedented, continuous rise in the prevalence of obesity and obesity-related disorders is causally linked to a chronic state of low-grade inflammation in adipose tissue and many other organs [120, 121]. In the case of obesity, the molecules and signaling pathways have dual roles as inflammatory mediators as well as regulators of energy storage and metabolism [109]. The on time resolution of inflammation and the return of this tissue to homeostasis are key components to reducing obesity-induced metabolic dysfunctions. Results indicate that in inflammatory adipose tissue, RvD1, and RvD2 are potent pro-resolving mediators that counteract both local adipokine production and monocyte accumulation in obesity-induced adipose inflammation [90]. However, it has been demonstrated, that the formation of SPMs is severely dysregulated in inflamed, obese adipose tissue [120]. A deficiency in pro-resolving mediators in obese adipose tissue within the setting of obesity could be the consequence of a structural deficiency in the tissue content of omega-3-PUFAs, which are established substrates for SPM biosynthesis [122]. Alternatively, the loss of SPMs in obesity may reflect accelerated tissue SPMs conversion and clearance to inactive further metabolites because 15-PG-dehydrogenase/eicosanoid oxidoreductase, the key enzyme in SPM inactivation, is markedly up-regulated in obese adipose tissue [123]. Moreover, not only is activated lipoxygenase essential for SPM biosynthesis, but also the substrate product of these enzymes is essential for precise immune responses. A study involving mice found lipidomic analysis showed levels of arachidonic acid higher and 12(S)-hydroxyeicosatetraenoic acid (12-HETE) at day 1 post-MI an obese group compared with the non-obese group (Fig. 6.3) [124]. However, studies involving the obesity paradox recently provided evidence that both mouse and human adipose tissue have the capacity to generate  $LXA_{4}$  [111].

#### 6.5.2 Diabetes

Uncontrolled inflammation plays an essential role in the pathogenesis of diabetes and its associated pathologies, like HF [125]. Also, the key sequela of adipose tissue inflammation is insulin resistance leading to type 2 diabetes (T2D) [126–128]. In this setting, a known complication of T2D is impaired wound healing; the administration of RvD1 to diabetic mice enhances wound healing, compared with control or vehicle treatment [129]. Therefore, SPMs may limit factors associated with T2D via its ability to quell inflammation and promote adipose and liver tissue homeostasis. RvD1 improved insulin sensitivity, reduced adipose inflammation, and reduced steatosis in mouse models of T2D [130, 131]. In



**Fig. 6.3** Physiological and pathological healing in mice delineates the effective and defective resolution in heart failure. Physiological or pathological healing depends on resolution of inflammation process. Physiological cardiac remodeling is a consequence of an effective resolution, with the production of necessary SPMs at the right time by reparative macrophages. However, many factors can lead to a defective resolution

addition to resolvins, lipoxins also showed prominent results in both mice and human and may have therapeutic potential in the context of diabetes associated vascular complications [132]. However, it is unknown if T2D affects the resolution of inflammation and whether treatment with pro-resolving mediators would stimulate resolution and ameliorate clinical complications of T2D such as impaired wound healing.

#### 6.5.3 Hypertension

Hypertension remains a significant risk factor for the development of HF with various mechanisms contributing to both systolic and diastolic dysfunctions [133]. Much less is known about the role of anti-inflammatory molecules in the regulation of blood pressure in general or in the development of hypertension [134]. In contrast, higher

like obesity and aging that induce a low-grade chronic state of inflammation with a high levels of COXs and LOXs-derived pro-inflammatory mediators with low levels of SPMs and reparative macrophages along with the increase of VCAM-1 (vascular cell adhesion molecule 1), MPO (myeloperoxidase), CD40 (cluster of differentiation 40), PGs (prostaglandins), LTs (leukotrienes), and  $TxA_2$  (thromboxane  $A_2$ )

levels of pro-inflammatory mediators, 5-HETE, 12-HETE and 15-HETE, were observed in preeclamptic placentae, a disorder of a multifactorial etiology that compromise maternal and fetal well-being as well as cardiovascular health later in life [135]. Endothelial and vascular inflammation also contribute in sustaining "low-grade inflammation" and have shown to be more associated with pulmonary hypertension (PH) [136]. Recent data demonstrated that in vitro RvD1 prevents arterial wall over-activity in human (HPH). This effect appears to be related to a decrease in Ca<sup>2+</sup> sensitivity in HPA smooth muscle cells. RvD1 also decreases the expression of transmembrane protein member 16A (TMEM16A), a specific marker of PH [137]. In the same context, Jannaway et al. demonstrated that low nanomolar concentrations of RvE1, RvD1, and RvD2 can prevent constriction in rat and human arteries induced by a thromboxane mimetic [138].

#### 6.5.4 Disruption of Circadian Clock

Many physiological functions, including leukocyte and platelet responses, are responsive to day and light schedules in order to regulate cell and organ specific circadian clocks. Results from several recent studies demonstrate that many metabolic functions are controlled by circadian rhythm genes, enzymes, and proteins [139]. Disturbances to various aspects of these fundamental mechanisms are thought to be responsible for many of the diseases that affect modern societies, including cardiovascular and metabolic disorders [140, 141]. In context to cardiac biology, the direct influence of circadian rhythms on SPMs and endogenous mechanisms in the resolution of inflammation remains largely unexplored. A study demonstrated that cardiomyocte-specific deletion of the circadian clock component, Bmal1, leads to age-dependent dilated cardiomyopathy and decreased lifespan in mice [142, 143]. Additionally, the circadian release of glucocorticoids and their link to downstream antiinflammatory and pro-resolution mediator annexin A1 facilitates the return to homeostasis [140]. A recent study suggests that patients with risk of coronary vascular disease (CVD) have defective diurnal regulation of vascular n-3 docosapentaenoic acid (DPA) derived resolvins. RvDn-3 DPA is involved in regulating peripheral blood cell responses and tissue protection. The marked reductions in plasma RvDn-3 DPA during the early morning hours indicate that alterations in biosynthesis due to dysregulation of lipoxygenase and may contribute to CVD onset and propagation. This finding can be explained by the increase of adenosine, a regulator of 5-LOX activity in plasma from patients with CVD [144].

## 6.5.5 Exercise

Exercise limitation is one of the hallmarks of heart failure, and an increasing degree of intolerance is associated with a poor prognosis [145]. One study measured SPMs in human blood during post-exercise recovery. It was demonstrated that lipoxins (LXA<sub>4</sub> and LXB<sub>4</sub>), resolvins (RvE1 and RvD1), and the protectin D1 isomer increased in human serum during the early hours of postexercise recovery (0–3 h post-exercise). However, ibuprofen treatment with exercise reduced the response of pro-resolving lipid mediators to exercise [146]. These results are consistent with those reported earlier by Gangemi et al. in which LXA<sub>4</sub> in human urine was found to increase with treadmill exercise [147]. In contrast to the former belief, exercise training in HF patients has proven to be safe and has no adverse effect on left ventricular remodeling [148]. However, an exercise paradox exists, and recently a study showed that exercise alters  $\beta$ -alanine, augments histidyl dipeptide levels, and scavenges lipid peroxidation products in human skeletal muscle [149].

#### 6.5.6 Aging and Microbiome

Aging and age-associated chronic and unresolved low-grade inflammation, "inflammaging," are progressive and all-time predominant factors for CVD [150, 151]. The underlying mechanisms of inflammaging remain of interest, but a plausible hypothesis for the non-resolving inflammation in the elderly is a defect in the inflammation-resolution process. The baseline pre- and post-MI environments are also altered with age [94, 152, 153]. A recent study in a context of muscle generation showed a correlation between aging and CCR2. The data explained that in young WT CCR2<sup>-/-</sup>, both dysfunctional macrophages and a pro-inflammatory environment were observed. Moreover, this study concludes that CCR2<sup>-/-</sup> in mice have a positive feedback loop that promotes inflammaging in young mice when compared to aging WT mice [154]. In humans, urinary lipoxins (LXs) were decreased in the elderly, resulting in a profound imbalance between pro-resolving LXs and LTs [147]. In line with these results, a study demonstrated that aging mice dysregulate the formation of pro-inflammatory and pro-resolving molecules with a decrease in LOXs expression, depending on the influx or availability of substrates that temper acute inflammatory-resolving phases, leading to the promotion or repression of inflammation post-MI (Fig. 6.3) [155]. Aged mice have increased inflammation, LTs, and decreased SPMs compared to young mice [91]. A recent, aging, metabolome human study described that RvD6 levels were decreased in an aging individuals, indicating the role of lipid metabolism in progressive aging [156]. Thus, there is evidence of defective SPMs in aging but the mechanisms remain of interest. Compared to evidence related to aging and inflammation, less is known regarding associations between aging and the microbiome; however, along with age related HF, current evidence has found links between HF in general and specifically HF in elderly women with alterations in microbial composition and function [157]. Since HF has been associated with impaired intestinal barrier function and bacterial translocation, leading to inflammatory and immune responses [158]. Studies have shown that significant alterations of the intestinal bacterial microbiome, like a significant decrease of Coriobacteriaceae, Erysipelotrichaceae and Ruminococcaceae in the familiar level and *Blautia*, *Collinsella*, *uncl*. Erysipelotrichaceae and uncl. Ruminococcaceae at the genus level [159]. Recently, a study showed biosynthesizing that resolvins substrates improved gut microbiome in elderly women [160].

# 6.6 Conclusion

After cardiac injury, leukocyte-directed biosynthesis of SPMs is necessary for cardiac healing in order to return to a hemostatic state. Leukocytederived SPM actions successfully operate the transition from inflammation to resolution. However, the dysregulation due to physical inactivity, co-medication, aging or cardiometabolic disorders like obesity, hypertension, and diabetes, or even disruption of sleep/wake up cycles impact the resolution process and the production of pro-resolving mediators and therefore nonresolving inflammation in cardiovascular diseases. Future studies are warranted to determine the mechanism of action, additional receptors for SPMs, and interactions with lifestyles or medications in the cardiac repair program.

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# Novel n-3 Docosapentaneoic Acid-Derived Pro-resolving Mediators Are Vasculoprotective and Mediate the Actions of Statins in Controlling Inflammation

Jesmond Dalli, Kimberly Pistorius, and Mary E. Walker

#### Abstract

Inflammation is a fundamentally protective process that guards the host from invading pathogens and is central in the repair and regeneration of damaged tissue. However, when uncontrolled, the overzealous response leads to tissue damage and malaise. Indeed, this process is now appreciated to be at the center of many chronic inflammatory diseases including vascular disease and arthritis. Studies investigating the mechanisms through which acute inflammation is actively turned off allowing tissues to regain function demonstrated that the essential fatty acids, arachidonic acid (AA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are enzymatically converted to bioactive mediators. These autacoids carry distinct structures and

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biological actions, actively reprogramming the inflammatory reaction to promote its termination by counter-regulating the production of pro-inflammatory mediators and regulate leukocyte trafficking as well as phenotype. Recently we found that n-3 docosapentaenoic acid (DPA), which was until then only regarded as a biosynthetic intermediate in the formation of DHA from EPA, is also converted to structurally distinct bioactive mediators that reprogram the host immune response. In the present review we will discuss the evidence underpinning the biological actions of these novel n-3 DPA-derived autacoids in particular as they pertain to the vascular system.

#### Keywords

n-3 docosapentaenoic acid · Resolution · Inflammation · Lipid mediators · Vascular inflammation · Leukocytes · Statins · Biomarkers

## 7.1 Introduction

Success in the evolution of multicellular organisms was, at least in part, reliant on the development of a system to repair and regenerate

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damaged tissues as well as to defend the organism from invading microbial pathogens [1]. This defense system is embodied in the inflammatory process which when self-limited is fundamentally protective and coordinates both the killing and disposal of invading pathogens as well as the repair and regeneration of damaged tissues [2]. However, when this process becomes dysregulated it leads to disease [3–7]. Pioneering studies investigating mechanisms that regulate the termination of inflammation uncovered a new genus of mediators produced via the stereoselective conversion of essential fatty acids, termed as specialized pro-resolving mediators (SPM) [8]. This superfamily includes the arachidonic acid (AA)derived lipoxins, the eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) resolvins [9], and the DHA-derived protectins [10] and maresins [11]. These mediators share select biological actions that include i) limiting neutrophil recruitment to the site of inflammation, ii) they counterregulate the production of pro-inflammatory mediators including prostaglandins, leukotrienes, cytokines and chemokines (e.g. Tumor necrosis factor alpha), iii) promote the uptake and killing of bacteria and iv) increase the uptake and clearance of apoptotic cells [3-6, 8]. In addition, each of the mediators exerts unique biological actions for example, the EPA-derived resolvin E1 regulates platelet activation [12], the DHA-derived protectins regulate viral replication [13] and the DHA-derived maresins promote tissue regeneration [3, 14].

SPM exert their potent biological actions via the activation of specific G-protein coupled receptors which include the Lipoxin A4 receptor (ALX/FPR2), GPR32/DRV1, GPR18/DRV2 and the chemerin receptor ChemR23/ERV1 [15]. In addition to activating cognate receptors, these protective mediators also regulate the onset and propagation of inflammatory responses by acting as partial agonists or antagonists to receptors of inflammatory mediators including BLT-1, the Leukotriene  $(LT)B_4$  (5S,12Rdihydroxy- 6Z,8E,10E,14Z- eicosatetraenoic acid) receptor [16], and cysLT1 the receptor  $LTC_4$ (5S-hydroxy-6R-(S-glutathionyl)for 7E,9E,11Z,14Z-eicosatetraenoic acid) and LTD<sub>4</sub>

(5S-hydroxy-6R-(S-cysteinylglycinyl)-7E,9E, 11Z,14Z-eicosatetraenoic acid) [16]. Studies investigating mechanisms involved in the onset and propagation of inflammatory disorders indicate defects in the production of the pro-resolving mediators, their enhanced further metabolism or an impairment in their ability to activate downstream signaling via their cognate receptors are linked with disease onset and/or progression [3– 6, 8].

In mammals, the essential fatty acid alphalinolenic acid (9Z, 12Z, 15Z-octadecatrienoic acid; ALA) is enzymatically elongated and desaturated to produce EPA and subsequently to DHA with n-3 docosapentaenoic acid (7Z,10Z,13Z,16Z,19Z-docosapentaenoic acid; n-3 DPA) being the biosynthetic intermediate in this process [17–19]. n-3 DPA contains a 22-carbon chain with 5 double bonds and differs from DHA as it lacks a cis-double bond at carbon 4, which, although a small change, provides its own specific biologically relevant actions [19, 20]. These actions have been identified in a variety of mammalian tissues, including plasma, brain, retina and heart. Genome-wide association studies in humans uncovered a correlation between increases in peripheral blood n-3 DPA concentrations and single nucleotide polymorphisms in the gene encoding for the fatty acid elongase 2 (ELOVL2, 21]. We recently found that, in addition to EPA and DHA, n-3 DPA is substrate for conversion to novel families of bioactive mediators [20]. The aim of the present review is to discuss the actions of these novel families of mediators in regulating key leukocyte responses.

## 7.2 n-3 DPA-Derived SPM Are Novel Resolution Agonists

Events that occur in the early phases of an inflammatory reaction are suggested to determine whether the response is self-limited or perpetuates and becomes chronic [22]. Assessment of events occurring within the circulation during acute self-limited inflammation demonstrated that the concentrations of n-3 DPA were rapidly upregulated during acute inflammation, to an extent that was comparable to essential fatty acids that are involved in the biosynthesis of lipid mediators, including arachidonic acid and DHA. Using a systematic approach coupling structure elucidation with functional readouts we found that endogenous n-3 DPA is converted to bioactive mediators in both mice and human leukocytes that carried pro-resolving properties [20]. These mediators are congenerous with DHA products, namely D-series resolvins ( $RvD_{n-3 DPA}$ ), protectins ( $PD_{n-3 DPA}$ ) and maresins  $(MaR_{n-3 DPA})$ , with unique stereochemistries [20]. In self resolving exudates, the production of these molecules was temporally regulated where for example RvD1<sub>n-3 DPA</sub> (7S,8R,17S-trihydroxy-9E,11E,13Z,15E,19Z -docosapentaenoic acid) PD2<sub>n-3 DPA</sub> (16,17-dihydroxy-7Z,10,13, and 14,19Z- docosapentaenoic acid) displayed a bi-phasic profile, reaching a maximum during peak neutrophil infiltration and late into PD1<sub>n-3 DPA</sub> (10R,17S-dihydroxyresolution. 7Z,11E,13E,15Z,19Z-docosapentaenoic acid), MaR2<sub>n-3 DPA</sub> (13,14-dihydroxy-7Z,9,11, 16Z, 19Z-docosapentaenoic acid) and MaR3<sub>n-3 DPA</sub> (4, 21-dihydroxy-7Z,10Z,12E,16Z,19Z-docosapentaenoic acid) levels were each found to reach a maximum at the 4 h interval and gradually decreased over the next 20 h. The peak in exudate RvD2<sub>n-3 DPA</sub> (7S,16,17S-trihydroxy-8,10Z,12,14,19Z-docosapentaenoic acid) levels coincided with the onset of resolution (the point where PMN levels reach ~50% of maximim neutrophil counts). RvD5<sub>n-3 DPA</sub> (7S,17S-dihydroxy-4Z,8,10Z,13Z,15,19Z-docosahexaenoic acid) levels were found to gradually increase over the course of inflammation-resolution, with a maximum being reached late in the resolution phase. The n-3 DPA product corresponding to  $MaR1_{n-3}$ (7S,14S-dihydroxy-8E, 10E, 12Z, 16Z, DPA 19Z-docosapentaenoic acid) gave levels that were elevated in the peritoneum of naive mice, where upon challenge with zymosan these levels drastically decreased [20]. Of note, each of these molecules displayed leukocyte directed actions whereby incubation of human neutrophils with RvD5<sub>n-3 DPA</sub> or PD1<sub>n-3 DPA</sub> markedly reduced neutrophil adhesion to TNF- $\alpha$  activated endothelial

cells and chemotaxis towards IL-8, to a similar extent as the DHA-derived RvD2 (7S,16R,17Strihydroxy- 4Z,8E,10Z,12E,14E,19Z- docosahexaenoic acid) [20, 23, 24]. RvD2<sub>n-3 DPA</sub> and  $RvD5_{n-3 DPA}$  also regulate the expression of adhesion molecules on peripheral blood leukocytes and platelets including the expression of CD11b on neutrophils and monocytes as well as CD62P and CD63 on platelets [25]. Furthermore, they also regulate the formation of leukocyte-platelet heterotypic aggregates in both human and mouse peripheral blood. The biological actions of these molecules extend beyond the regulation of mechanisms in leukocyte trafficking. Indeed, n-3 DPA-derived SPMs also regulate the uptake of apoptotic cells by macrophages, a key biological action in the resolution of inflammation, with increases in macrophage efferocytosis of up to 70% at doses as low as 1 nM [20, 23]. These mediators also display endothelial directed actions, counteracting the TNF- $\alpha$ - mediated upregulation of adhesion molecules, such as Intercellular Adhesion Molecule 1 (ICAM-1/ CD54), on endothelial cells [20].

## 7.3 Diurnal Regulation of RvD<sub>n-3</sub> <sub>DPA</sub> Controls Vascular Leukocyte and Platelet Activation

Circadian mechanisms are at the heart of a number of physiological functions, including leukocyte and platelet responses [26, 27]. Disturbances to various aspects of these fundamental mechanisms are thought to be responsible for many of the diseases that afflict modern societies, including cardiovascular and metabolic disorders [26-28]. These conditions are characterized by a dysregulated inflammatory response, although the exact mechanisms that underlie this inflammatory state remain of interest. Recent studies demonstrate that the production of RvD<sub>n-3 DPA</sub> are diurnally regulated in the peripheral blood of healthy volunteers [25] (Fig. 7.1). Multivariate analysis of plasma lipid mediator profiles demonstrated a diurnal shift in plasma LM-SPM concentrations. This shift was associated with an



## and monocyte activation Loss of RvD<sub>n-3 DPA</sub> production leads to increased peripheral blood leukocyte and platelet activation and is linked with CVD

Fig. 7.1 Diurnal changes in  $RvD_{n-3 DPA}$  regulates peripheral blood leukocyte and platelet activation protecting from cardiovascular disease. In peripheral blood diurnal changes in acetylcholine (ACh) upregulates 15-lipoxygenase (ALOX15) activity promoting  $RvD_{n-3 DPA}$ biosynthesis that limit the physiological activation of

increase in the amounts of n-3 DPA derived mediators, including RvD1<sub>n-3 DPA</sub> and RvD5<sub>n-3 DPA</sub> from the evening (18:00 h) to morning intervals (7:00 and 9:00 h). These diurnal changes in peripheral blood RvD<sub>n-3 DPA</sub> concentrations were abrogated in mice lacking the main orchestrator of the molecular clock, Aryl hydrocarbon receptor nuclear translocator-like protein 1, in myeloid cells. Of note, the fluctuations in plasma  $RvD_{n-3}$ DPA were associated with a regulation of leukocyte and platelet activation that reaches a maximum between 7:00 and 9:00 h coincident with an increase in RvD<sub>n-3 DPA</sub> concentrations. The production of these mediators was found to be under the control of acetylcholine (ACh), with peripheral blood concentrations of this neurotransmitter also reaching a maximum during the early hours of the morning (i.e. 7:00 h). Furthermore, incubamonocytes, neutrophils and platelets during the early morning hours. Increases in circulating adenosine concentrations in patients with cardiovascular disease inhibit ALOX5 activity disrupting the diurnal changes in plasma  $RvD_{n-3 DPA}$  and increasing peripheral blood leukocyte and platelet activation

tion of whole blood with ACh increased  $RvD_{n-3}$ <sub>DPA</sub> concentrations, including  $RvD2_{n-3}$  <sub>DPA</sub>, under both static and flow conditions.

Assessment of the production of these mediators in patients with cardiovascular disease (CVD) demonstrated significant decreases in plasma  $RvD_{n-3 DPA}$  concentrations and a marked impairment in their diurnal regulation when compared with healthy volunteers. Flow cytometric analysis of peripheral blood leukocyte from patients with CVD demonstrated increases in the expression of CD11b on both neutrophils and monocytes when compared with healthy volunteers. This was coupled with increases in platelet–neutrophil and platelet–monocyte aggregates in peripheral blood from patients with CVD [25]. In addition, we found a significant relationship between peripheral blood  $RvD_{n-3 DPA}$  concentrations and leukocyte and platelet activation, as demonstrated by a negative correlation between RvD<sub>n-3 DPA</sub> and neutrophil CD41, monocyte CD41, and platelet CD63 and CD42b expression. Investigations into mechanisms that lead to the downregulation of peripheral blood RvD<sub>n-3 DPA</sub> in patients with CVD demonstrated a link between peripheral blood adenosine concentrations and the activity of one of the  $RvD_{n-3}DPA$ biosynthetic enzymes, ALOX5. Adenosine, which via the activation of the A2a receptor, downregulates the activity of ALOX5 [29], was increased in peripheral blood from patients with CVD. The role of adenosine in downregulating RvD<sub>n-3 DPA</sub> concentrations was further underscored by experiments where peripheral blood from CVD patients was incubated with adenosine deaminase, leding to the restoration of peripheral blood RvD<sub>n-3 DPA</sub> concentrations [25].

These findings led us to propose  $RvD_{n-3 DPA}$  as endogenous protective signals that control physiological platelet and leukocyte activation. This is further supported by observations made in Apolipoprotein E deficient mice  $(ApoE^{-/-})$  mice fed a western diet. Treatment of these mice with RvD5<sub>n-3 DPA</sub> reduced platelet-leukocytes aggregates in vivo and modulated vascular lipid mediator profiles reducing concentrations of the pro-thrombogenic mediator Thromboxane (Tx)  $A_2$  (measured as its metabolite  $TxB_2$ ) and upregulating the formation of pro-resolving mediators including MaR1 (7S,14S-dihydroxy-4Z, 8E, 10E, 12Z, 16Z, 19Z-docosahexaenoic acid) and aspirin triggered (AT)-LXA<sub>4</sub> (5S,6R,15Rtrihydroxy-7E,9E,11Z,13E-eicosatetraenoic acid). Furthermore RvD5<sub>n-3 DPA</sub> also decreased early aortic lesions in ApoE<sup>-/-</sup> mice. The present findings are in line with published findings demonstrating an altered production of vascular DHA-derived SPMs including RvD2 and MaR1 and impaired resolution responses in the pathogenesis of atherosclerosis [30, 31]. Together these findings demonstrate that alterations in the diurnal regulation of vascular RvD<sub>n-3 DPA</sub> may occur early in the pathogenesis of cardiovascular diseases that results in vascular inflammation and impaired biosynthesis of DHA derived SPM.

## 7.4 PD<sub>n-3 DPA</sub> Regulates Macrophage Phenotype and Function During Monocyte to Macrophage Differentiation

It is now well appreciated that in chronic inflammatory conditions, such as atherosclerosis and rheumatoid arthritis, monocytes play a central role in the initiation, propagation and termination of inflammation [32, 33]. Upon recruitment to the site of inflammation, these cells either differentiate to inflammatory macrophages that propagate the inflammatory response or to resolution phase macrophages that promote the termination of inflammation and restitution of tissue function. Studies investigating mechanism that regulate the differentiation of macrophages demonstrate a role for the PD<sub>n-3 DPA</sub> pathway in regulating the phenotype and function of monocyte-derived macrophages [34] (Fig. 7.2). Using a total organic synthetic approach coupled with lipid mediator profiling, human ALOX15 and ALOX15B were identified as the enzymes that catalyse the first two steps in the  $PD_{n-3 DPA}$ biosynthetic pathway yielding an allylic epoxide. Using total organic synthesis we established the absolute stereochemistry of this epoxide as 16S,17S-epoxy-7Z,10Z,12E,14E,19Zdocosapentaenoic acid [34, 35]. This intermediate was in turn converted to PD1<sub>n-3 DPA</sub> and PD2<sub>n-3</sub> DPA by distinct epoxide hydrolase enzymes, where in human cells epoxide hydrolase 2 (EPHX2) was found to catalyse the conversion of 16S,17SePD<sub>n-3 DPA</sub> to PD2<sub>n-3 DPA</sub>. Experiments investigating the expression of the PD<sub>n-3 DPA</sub> biosynthetic pathway during monocyte to macrophage differentiation found the expression of all three enzymes was upregulated during monocyte to macrophage differentiation. Of note, ALOX15 expression was higher in M2 differentiated cells, whereas the expression of ALOX15B was higher in M1 cells [34].

Pharmacological inhibition and genetic deletion of ALOX15 enzymes in monocytes led to phenotypic and functional changes in monocytederived macrophages. In cells where ALOX15 Fig. 7.2 PD<sub>n-3 DPA</sub> biosynthetic pathway and its regulation of monocyte-derived macrophage phenotype and function. In the PD<sub>n-3 DPA</sub> pathway n-3 DPA is converted to 17-HpDHA and then to 16S, 17S-epoxy-PD<sub>n-3</sub> DPA by either ALOX15 or ALOX15B. This is then hydrolyzed by epoxide hydrolase activity to PD1<sub>n-3 DPA</sub> and PD2<sub>n-3 DPA</sub>. This pathway regulates macrophage phenotype and function during monocyte-tomacrophage differentiation



was inhibited there was a downregulation of several lineage markers including CD206, CD163 and CD64 and a shift in macrophage phenotype [34]. This downregulation in phagocytic receptors was of functional consequence since inhibition of the PD<sub>n-3 DPA</sub> biosynthetic pathway also significantly downregulated the ability of human macrophages to uptake apoptotic cells, a key proresolving action [36, 37]. Of note, this alteration in macrophage phenotype and function was recovered with the reconstitution of components within the PD<sub>n-3 DPA</sub> pathway. Incubation of human monocyte-derived macrophages with either PD1<sub>n-3 DPA</sub> or 16S, 17S-epoxy-PD<sub>n-3 DPA</sub> led to a restoration of several phagocytic receptors macrophage and increased efferocytosis. Furthermore, administration of PD1<sub>n-3 DPA</sub> to ALOX15 deficient mice also restored the phenotype and efferocytic activity of macrophages *in vivo* [34]. Thus, these findings identify the  $PD_{n-3}$ <sub>DPA</sub> pathway as a component in the monocyte-tomacrophage differentiation program that regulates their phenotype and function.

## 7.5 RvTs Are Produced During the Early Stages of Acute Inflammation and Temper Host Immune Responses

Recent studies have described and characterized a new family of bioactive mediators produced from n-3 DPA. This new family of four resolvins is termed the 13-series resolvins (RvT) given that all four molecules display potent host protective actions and carry a hydroxyl group on carbon 13 [38]. RvTs are biosynthesized from n-3 DPA in a process that requires both endothelial cell COX-2 and neutrophil lipoxygenase (ALOX) activity. The role for ALOX enzymes in the biosynthesis of RvT was established using heavy oxygen incorporation [38] with the identity of the ALOX enzymes catalyzing this reaction remaining of interest.

During acute inflammation, cytokines such as TNF- $\alpha$  and IL-1 $\beta$  are released, activating endothelial cells that upregulate the expression of COX-2. Endothelial COX-2 converts n-3 DPA to 13R-hydro(peroxy)-docosa-7Z,10Z,14E,16Z, 19Z-pentaenoic acid (13R-HpDPA); 13R-HpDPA or its reduced alcohol form 13R-hydroxydocosa-7Z,10Z,14E,16Z,19Z-pentaenoic acid (13R-HDPA) is then donated to neutrophils during neutrophil-endothelial cell interactions, whereby it is first converted to 7-hydro(peroxy)-13R-hydroxy-docosa-8,10Z,14E,16Z,19Zpentaenoic acid [38]. This molecule can then undergo а second lipoxygenation reaction to yield 7,13R,20-trihydroxy-docosa-8,10,14E,16Z,18-pentaenoic acid that was coined as RvT1. The hydroperoxide can also, in a lipoxygenase-dependent manner, undergo an epoxidation reaction to yield the allylic epoxide 7,8-epoxy-13-hydroxy-docosa-9,11, 14E,16Z,19Z-pentaenoic acid. This is then enzymatically hydrolysed to 7,12,13-trihydroxydocosa-8,10,14E,16Z,19Z-pentaenoic acid and 7,8,13-trihydroxy-docosa-9,11,14E,16Z,19Zpentaenoic acid, coined RvT2 and RvT3, respectively. Finally, 7-hydro(peroxy)-13R-hydroxydocosa-8,10Z,14E,16Z,19Z-pentaenoic acid is reduced to 7,13R-dihydroxy-docosaalso 8,10Z,14E,16Z,19Z-pentaenoic acid that is coined RvT4 (Fig. 7.3).

RvTs are produced in humans during exercise, that is now seen as a self-resolving inflammatory state, marked by an increase in neutrophil-endothelial interactions with upregulation of plasma RvT [38]. These mediators are also produced during infection when RvT levels are upregulated in plasma from septic patients

when compared to healthy volunteers. RvTs are protective in mice during acute inflammation where a mixture of RvT1, RvT2, RvT3 and RvT4 immediately before or 2 h after intraperitoneal Escherichia coli inoculation resulted in host-protection, increasing survival by >60%. Indeed, RvT limited neutrophil recruitment to the site of inflammation, increased phagocytosis and intracellular ROS levels and upregulated macrophage efferocytosis. Of note, the protective actions of RvTs resulted from the reprogramming of the innate host response since RvT did not display direct bactericidal actions at biologically-relevant concentrations. Additionally, RvT reduced monocyte and macrophage expression of inflammasome components, decreasing caspase-1 and IL-1 $\beta$  expression and lactate dehydrogenase activity, a marker of pyroptosis. RvT also reduced peripheral blood platelet-leukocyte aggregates, an observation associated with reduced systemic inflammation. Exudate macrophage efferocytosis was also increased and a significant reduction in local and systemic eicosanoid levels was found in mice given RvT [38].

Using a total organic synthetic approach, we recently established the complete stereochemistry and biosynthetic role of 13R-HDPA in the RvT pathway [39]. Chirally pure precursors were used in conjunction with stereoselective reactions that installed the configuration at the carbon 13 atom as R and formed geometrically pure double-bond moieties.

Synthetic 13R-HDPA was matched with biogenic 13-HDPA, obtained by incubating n-3 DPA with human recombinant COX-2. Structural evaluation of synthetic 13R-HDPA and biogenic 13-HDPA was carried out using liquid chromatography tandem mass spectrometry (LC-MS/ MS) to attain MRM chromatograms to match retention times and MS-MS spectra to identify matching daughter ions. Chiral LC-MS/MS was used to confirm the stereochemistry around carbon 13, and UV-Vis spectrophotometry was used to match the double bond conjugation system. Incubation of the synthetic material with human leukocytes demonstrated that this was rapidly converted to all four RvTs [39]. These findings



phenotype

mediators

platelet activation

Reduce joint damage

- Counter-regulate the production of inflammatory mediators
- Enhance neutrophil and macrophage phagocytosis
   of bacteria
- Upregulate efferocytosis
- Increase survival from lethal infections

**Fig. 7.3 RvT biosynthesis and actions in mediating the protective actions of statins in infections and inflammatory arthritis.** Production of RvT is initiated via the conversion of n-3 DPA by the endothelial COX-2

confirmed that the stereochemistry around the hydroxyl group on carbon 13 was in the R orientation and the double bond geometry around the conjugated double bond system was found to be in E, Z with the complete stereochemistry established as 13(R)-hydroxy-7Z,10Z,13R,14E,16Z,19Z-docosapentaenoic acid as well as the role of this intermediate in the RvT biosynthetic pathway.

## 7.6 RvT Mediate the Biological Actions of Statins in Infectious-Inflammation and Inflammatory Arthritis

SPMs are implicated in mediating the protective actions of a number of clinically relevant therapeutics including aspirin and statins, whereby aspirin initiates the biosynthesis of epimeric forms of SPMs [40], while lovastatin, for examexpression yielding 13-HpDHA, that can then be converted to 13-HDPA and donated to neutrophils where via ALOX activity this is converted to RvT1–4. Statin mediated S-nitrosylation of COX-2 upregulates 13-HDPA production contributing to the upregulation of RvTs

Reduce peripheral blood monocyte, neutrophil and

Counter-regulate the production of inflammatory

ple, upregulates the biosynthesis of 15-epi-LXA<sub>4</sub> [41]. In addition, atorvastatin was recently found to increase RvT formation during human neutrophil-endothelial cell interactions, as well as in mice during infections. This increase in RvT production resulted from the S-nitrosylation of COX-2 leading to increased 13R-HDPA levels, suggesting that the S-nitrosylation of COX-2 increased catalytic activity of the enzyme. This finding was in concordance with the S-nitrosylation of COX-2 cysteine residues in the presence of atorvastatin [38]. Inhibition of inducible nitric oxide synthase (iNOS) by L-NG-(L-NAME) nitroarginine reduced the atorvastatin-mediated increases in plasma RvT levels after E. coli inoculation. A similar reduction was observed when mice were given celecoxib, a COX-2 specific inhibitor. This highlights the complex regulatory axis of COX-2, as posttranslational modification of the enzyme may

yield mediators with distinct biological activities to the classic eicosanoids.

This mechanism was recently also found to be protective in arthritic inflammation where administration of atorvastatin upregulated RvT concentrations during inflammatory arthritis in both peripheral blood and joints [42]. Of note, this protective mechanism was not unique to atorvastatin and was shared with pravastatin. Atorvastatin administration during ongoing arthritis led to a 43% increase in total RvT amounts in arthritic paws compared to vehicle-treated mice. Pravastatin also increased paw RvT by ~20% with increases in RvT1 and RvT2.

These increases in joint RvT concentrations were also linked with decreases in tissue prostanoids and LTB<sub>4</sub> concentrations. Prostaglandins were reduced by 20-40% by all statins tested when compared to vehicle. Exceptionally,  $PGF_{2\alpha}$ was reduced by ~75% in mice given pravastatin. LTB<sub>4</sub> concentrations were reduced ~50% by atorvastatin and ~15% by pravastatin. Additionally,  $TxB_2$  was reduced 20–50% both statins [42]. The upregulation in RvT concentrations were linked with a reduction in disease severity where in mice administered atorvastatin, disease progression was dampened at day 4 post disease initiation, with disease scores reaching a maximum of  $9.1 \pm 1.2$  at day 5 which was sustained until day 7. When mice were administered pravastatin, disease activity at day 5 was lower compared with mice administered vehicle, with a reduction in disease activity maintained until day 7 measured both as reduction in of clinical score and edema. In addition, both statins also lead to a reduction in joint damage at a histological level.

In inflammatory arthritis atorvastatin and pravastatin administration also regulates both circulating and tissue resident leukocyte responses. In non-classical monocytes, atorvastatin reduced the expression of CD11b by ~18% and platelet-monocyte aggregation (measured by a decrease in CD62P) was reduced by ~24% compared to mice given vehicle [42]. Pravastatin significantly reduced platelet-monocyte aggregation by ~35%, and decreased CD11b expression by ~10%. In classical monocytes, expression of CD11b and CD62P were significantly reduced by ~42% and

~34% respectively in mice given atorvastatin compared to mice given vehicle. In mice given pravastatin, CD11b expression was decreased by ~40% and platelet-monocyte aggregation reduced by ~35%. Compared to vehicle, neutrophil activation markers were significantly reduced by atorvastatin and pravastatin, reducing CD11b expression by ~30% and platelet-neutrophil aggregation by ~24%. Of note, administration of celecoxib that inhibits the upregulation of RvT by pravastatin and atorvastatin reverses the protective actions of these statins on both disease severity and leukocyte responses [42].

## 7.7 Conclusion

The identification of n-3 DPA as a substrate to novel, structurally distinct, mediators that display potent host protective activities demonstrates that complex mediator networks become activated during acute inflammation to ensure tissue homeostasis. This is further underscored by the observation of a selective regulation of distinct lipid mediator pathways in a tissue and cell specific manner. In addition, mounting evidence suggests that some of the beneficial actions of a number of widely used drugs, including statins, is mediated via the regulation of these protective pathways. Given the potent actions of n-3 DPAderived SPMs in regulating systemic and peripheral inflammatory responses, utilizing analogues and mimetics may be useful therapeutics in the prevention and treatment of chronic inflammatory diseases. In addition, strategies to boost their endogenous production potentially via supplementation with n-3 DPA may also be useful in controlling inflammation. While the clinical evidence for this approach is currently limited, recent studies in healthy volunteers provide evidence for its effectiveness, whereby administration of n-3 DPA upregulates peripheral blood concentrations of  $RvD5_{n-3 DPA}$  [43]. Future studies will need to identify the patient populations that will be responsive to this approach and the supplement forms that will be effective in regulating DPA-derived concentrations. n-3 SPM Furthermore, changes in the observation that tissue concentrations of these SPM are altered in disease and that their levels can be upregulated by certain therapeutics (e.g. atorvastatin and pravastatin) suggest that these pathways may also be useful as biomarkers in both patient stratification and measuring the effectiveness of treatment efficacy.

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# Aspects of Prostaglandin Glycerol Ester Biology

Philip J. Kingsley, Carol A. Rouzer, Amanda J. Morgan, Sachin Patel, and Lawrence J. Marnett

#### Abstract

The Cyclooxygenase enzymes (COX-1 and COX-2) incorporate 2 molecules of  $O_2$  into arachidonic acid (AA), resulting in an array of bioactive prostaglandins. However, much work has been done showing that COX-2 will perform this reaction on several different AA-containing molecules, most importantly, the endocannabinoid 2-arachidonoylglycerol (2-AG). The products of 2-AG oxygenation, prostaglandin glycerol esters (PG-Gs), are

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analogous to canonical prostaglandins. This chapter reviews the literature detailing the production, metabolism, and bioactivity of these compounds, as well as their detection in intact animals.

### Keywords

Endocannabinoid · Cannabinoid · Cyclooxygenase · COX-2 · Inflammation · Prostaglandin · Prostaglandin glyceryl ester · Transgenic mouse · Anandamide · 2-Arachidonoyl glycerol

## 8.1 Introduction

The cyclooxygenase (COX) enzymes, which exist as two isoforms (COX-1 and COX-2), incorporate two molecules of  $O_2$  into arachidonic acid (AA), generating the intermediate prostaglandin  $H_2$  (PGH<sub>2</sub>). PGH<sub>2</sub> is further transformed by various prostaglandin synthases to produce the array of canonical prostaglandins familiar to many researchers (Scheme 8.1). Yu [1] and Kozak [2] reported that the arachidonoyl-containing endogenous lipids anandamide (AEA) and 2-arachidonoylglycerol (2-AG) are efficient substrates for COX-2, but not COX-1. These

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Scheme 8.1 Schematic of COX-2-mediated oxygenation of various arachidonoyl-containing lipid species.

 $(a - PGH_2$  derived from AEA or 2-AG is not a substrate for thromboxane synthase. It is unknown if PGH<sub>2</sub>-LPC or PGH<sub>2</sub>-LPE are acted upon by this enzyme)

compounds – referred to as endocannabinoids because they are ligands for the cannabinoid receptors CB1 and CB2 - are processed by COX-2 analogously to AA, generating the corresponding PGH<sub>2</sub> ethanolamide (PG-EA) or glyceryl ester (PG-G). These intermediates are acted upon by most of the prostaglandin synthases, leading to an array of prostaglandin derivatives (Scheme 8.1). Curiously, thromboxane synthase does not accept PGH<sub>2</sub> derivatives; thus, there are no thromboxane analogs produced from endocannabinoids (2). Subsequent to these reports, other researchers identified additional arachidonic acid analogs that are selective substrates for COX-2. These compounds include *N*-arachidonylglycine [3], 2-O-arachidonoyl ether [4], arachidonoyllysophosphatidylethanolamine (AA-LPE), and arachidonyl-lysophosphatidylcholine (AA-LPC) [5].

Our laboratory has a long-standing interest in exploring the biology of these putative COX-2 products, especially those of 2-AG. The hypothesis that PG-Gs are relevant bioactive

lipids is mainly based on three observations: (1) 2-AG is present at high levels in many mammalian tissues (i.e., nmol/g in brain tissue); (2) kinetic studies indicate 2-AG and AA are utilized by COX-2 with similar efficiencies in vitro [2]; and (3) PG-Gs have been shown to possess significant biological activity. This chapter will review research on (i) production of PG-Gs in enzymatic and cellular systems, (ii) biological activity of PG-Gs, (iii) analytical methodology for detection and measurement of PG-Gs, (iv) the presence of PG-Gs in intact animals, and (v) recent work from the Patel and Marnett laboratories involving PG-Gs in the murine central nervous system (CNS). It should be noted that the biochemistry, enzymology, and pharmacology of the PG-EAs, formed from the oxygenation of AEA by COX-2, are distinct from those of the PG-Gs but are beyond the scope of this review. Several groups have published interesting work elucidating the biochemistry of PG-EAs, and recent reviews and original research in this area can be found here [6-9].

## 8.2 PG-Gs in *in Vitro* and Cellular Systems

The majority of reports regarding non-AAderived products of COX-2 oxygenation used both reconstituted enzymatic and cellular systems to characterize the oxygenated products as well as the mechanism of their production. In the initial report of PG-G formation, Kozak et al. [2] used purified murine and human COX-2 for assessment of the kinetics (via O<sub>2</sub> uptake) of 2-AG oxygenation and the identification of COX-2 reaction products. These studies established that, when assayed individually, COX-2 utilizes AA and 2-AG with similar efficiencies  $(k_{cat}/K_m = 2.4 \text{ s}^{-1} \mu \text{M}^{-1} \text{ and } 4.0 \text{ s}^{-1} \mu \text{M}^{-1} \text{ for AA}$ and 2-AG, respectively, for human COX-2 and  $2.5 \text{ s}^{-1} \mu \text{M}^{-1}$  and  $2.3 \text{ s}^{-1} \mu \text{M}^{-1}$  for AA and 2-AG, respectively, for murine COX-2). The authors used the RAW264.7 murine macrophage-like cell line to confirm that the observed enzymatic reactions could also take place in a cellular setting, where 2-AG would be subject to metabolism by several different pathways. Since RAW264.7 cells do not express COX-2 under basal conditions, they were pretreated with interferon- $\gamma$ (INF- $\gamma$ ) and bacterial lipopolysaccharide (LPS) to induce the COX-2 enzyme. The investigators established that exogenous 2-AG can be taken up by cells, processed to PGD<sub>2</sub>-G via COX-2, and secreted into the extracellular medium. They further demonstrated the formation of PGD<sub>2</sub>-G from endogenous 2-AG following stimulation of LPSand IFN-y-pretreated RAW264.7 cells with ionomycin. The formation of PGD<sub>2</sub>-G by the cells was consistent with the fact that they produce predominantly PGD<sub>2</sub> from AA. In subsequent studies, Kozak et al. demonstrated the formation of PGE<sub>2</sub>-G and PGF<sub>2α</sub>-G from exogenous 2-AG by human HCA-7 colon adenocarcinoma cells, which constitutively express COX-2 [10]. In addition, Siegmund et al. reported the synthesis of PGD<sub>2</sub>-G from exogenously provided 2-AG by hepatic stellate cells isolated from mice pretreated with bile duct ligation to induce liver fibrosis. The investigators confirmed that bile duct ligation led to induction of COX-2 expression in the hepatic stellate cells [11].

Rouzer and Marnett [12] further investigated the cellular production of PG-Gs in a more physiologically relevant setting by isolating murine resident peritoneal macrophages (RPMs). These cells are known to have a relatively high level of AA in their phospholipid pool and are able to synthesize COX-2 and generate large amounts of PGs in response to a variety of inflammatory stimuli. Here, RPMs were pretreated with LPS to induce COX-2 expression and then challenged with zymosan, which stimulated the release of 2-AG. The authors showed that PGE<sub>2</sub>-G and PGI<sub>2</sub>-G were produced by RPMs without the addition of exogenous 2-AG, and these PG-Gs were released from the cells. As in the case of RAW264.7 cells, the primary PG-G products in RPMs were consistent with the primary PG products, which were PGE<sub>2</sub> and PGI<sub>2</sub>.

Based on kinetic analyses of COX-2-mediated oxygenation of AA and 2-AG in vitro, which had shown similar enzymatic efficiency for the two substrates, one would predict that the ratio of PG-Gs to PGs produced in cells should be similar to the ratio of available 2-AG to AA. However, in zymosan-stimulated RPMs, the ratio of total PG to PG-G production was roughly 1000:1, whereas the ratio of free AA to 2-AG in these cells was 10:1. The much lower than expected production of PG-Gs relative to PGs based on substrate availability could not be explained on the basis of PG-G hydrolysis [12]. These observations led to more extensive kinetic analyses of 2-AG and AA oxygenation by COX-2 via experiments in which both substrates were present. Results of these kinetic studies were consistent with previously published data suggesting that the homodimeric COX-2 enzyme behaves as a heterodimer with one subunit acting as the catalytic site and the other serving an allosteric function. Specifically, the results supported the hypothesis that AA and 2-AG compete with each other for both the catalytic and allosteric sites and that binding of either substrate in the allosteric site suppresses 2-AG oxygenation and promotes AA oxygenation. Consequently, when both substrates are present, oxygenation of AA is favored over that of 2-AG [13]. It is not clear whether this phenomenon fully explains the

observed relatively low yield of PG-Gs produced by zymosan-stimulated RPMs. In fact, COX-2 requires peroxide-dependent activation before oxygenation of any substrate can occur, and a report from Musee and Marnett indicates that higher levels of peroxide are required to activate 2-AG oxygenation compared to AA oxygenation [14]. Other factors, such as the actual availability of free 2-AG and AA at the COX-2 active site within the cell, may also play a role.

While investigating the phenomenon of substrate-selective inhibition, in which an inhibitor blocks COX-2-dependent oxygenation of 2-AG more strongly than that of AA, Duggan et al. [15] employed a model utilizing dorsal root ganglia (DRG). DRGs were harvested, plated, and treated with a cocktail of compounds that included LPS and IFN-y to induce COX-2. Ionomycin was subsequently added to stimulate release of 2-AG, resulting in the production of PG-Gs. The predominant products of 2-AG oxygenation were PGE<sub>2</sub>-G and  $PGF_{2\alpha}$ -G. Interestingly, ethanolamide derivatives of PGs were also produced by the cells, in addition to free acid PGs. The absolute quantities of the various products were not reported. With this model, the authors showed that within the physiological system of DRGs, the R-profen class of inhibitors acted as substrate-selective inhibitors.

It should be noted that other reports have demonstrated COX-2-dependent effects of 2-AG in a variety of cell systems, suggesting that these effects may be due to conversion of the endocannabinoid to a PG-G. However, in many of these studies, the actual synthesis of a PG-G in the tissue or cells of interest was not confirmed. We have limited this discussion to cases in which PG-G formation was demonstrated analytically.

#### 8.3 Biological Activity of PG-Gs

Concurrent with the elucidation of the production and control of PG-Gs, several investigators have reported interesting and potent biological activities of PG-Gs, both in cellular systems and in intact mammals. However, the discovery of any PG-G-associated biological activity immediately led to the question of whether or not the effects were mediated by known endocannabinoid or prostanoid receptors as opposed to distinct receptors. An initial pharmacologic study ruled out significant activity of PGE<sub>2</sub>-G at the four EP receptors that modulate the effects of  $PGE_2$ , as well as the FP, DP, TP, and IP receptors [16]. More recently, Woodward et al. used the more metabolically and chemically stable amide derivatives of the 1(3)and 2-glyceryl esters of  $PGE_2$  and  $PGF_{2\alpha}$  to show that neither compound has significant activity at any of the prostanoid receptors. The highest activity was noted in the case of PGE<sub>2</sub>-serinolamide (the stable analog of the 2-glyceryl ester of  $PGE_2$ ) at the EP3 receptor, for which an EC<sub>50</sub> of 500 nM was observed.  $EC_{50}$  values were > 3000 nM for all tested analogs at all other receptors [17].

The earliest report of PG-G-mediated biological activity came from Nirodi et al., who found that PGE<sub>2</sub>-G, but not PGF<sub>2 $\alpha$ </sub>-G or PGD<sub>2</sub>-G, caused Ca<sup>2+</sup> mobilization in the murine RAW264.7 macrophage-like cell line at picomolar concentrations. Ca2+ mobilization was secondary to increases in intracellular inositol 1,4,5-trisphospate, and it resulted in the activation of protein kinase C and, subsequently, extracellular signal regulated kinases (ERKs) 1 and 2. Importantly, the authors also showed that  $PGE_2$ did not elucidate these effects [16]. In follow-up studies, Richie-Jannetta et al. demonstrated PGE<sub>2</sub>-G-mediated Ca<sup>2+</sup> mobilization in the H1819 human non-small-cell lung cancer cell line. In these studies, similar activity was observed regardless of whether the PGE<sub>2</sub> moiety was attached at the sn-1 or sn-2 position of the glycerol, and  $PGF_{2\alpha}$ -G exhibited activity similar to that of PGE<sub>2</sub>-G. In contrast, the corresponding free acid prostanoids were inactive [18].

A number of studies have suggested a potential role for PG-Gs in the nervous system. Sang et al. [19] demonstrated that  $PGE_2$ -G,  $PGF_{2\alpha}$ -G, and  $PGD_2$ -G increased miniature inhibitory postsynaptic currents (mIPSCs) in murine hippocampal neurons. Shortly thereafter, the same group reported that these three PG-Gs enhanced miniature excitatory postsynaptic currents (mEPSCs) in hippocampal neurons, an indication of enhanced glutamatergic synaptic transmission [20]. In both cases, 2-AG had the opposite effect, a role for the CB1 receptor was ruled out, and the involvement of both IP<sub>3</sub> and ERKs was implicated. The PGE<sub>2</sub>-G-mediated enhancement of mEPSCs was also found to induce neuronal injury and/or death. Yang et al. also reported an effect of  $PGE_2$ -G,  $PGF_{2\alpha}$ -G, and PGD<sub>2</sub>-G on hippocampal neurotransmission. In their case, an increase in basal synaptic transmission and long-term potentiation in hippocampal slices was observed that, consistent with prior findings, was dependent on IP<sub>3</sub>-mediated Ca<sup>2+</sup> mobilization and ERK signaling [21]. Commensurate with the neurotoxic effects noted by Sang et al., Valdeolivas and colleagues reported that PGE<sub>2</sub>-G was neurotoxic to the M-213-20 fetal rat striatum-derived cell line. Their studies suggested that PGE<sub>2</sub>-G is a mediator of malonatedependent neurotoxicity, which in M-213-2O cells, serves as a model of Huntington's disease [22]. In studies involving tissues other than the hippocampus, Lindgren and colleagues reported that PGE<sub>2</sub>-G induces an enhancement of stimulusevoked neurotransmitter release by the presynaptic neuron at the neuromuscular junction. They further demonstrated that the effect is dependent on production of nitric oxide and does not involve the EP1 or EP2 receptors for  $PGE_2$  [23]. Woodward et al. demonstrated that the amide derivatives of the 1(3)- and 2-glycerol esters of  $PGE_2$  lower intraocular pressure in canine eyes, whereas the comparable derivatives of  $PGF_{2\alpha}$  are much less effective. In the monkey eye, the derivative of the 1(3)-glycerol ester of PGE<sub>2</sub> was more effective than the 2-glycerol ester [17].

Most other actions of PG-Gs have been identified in various models of immune or inflammaresponses. Alhouayek tory et al. [24] demonstrated that PGD<sub>2</sub>-G suppresses while  $PGE_2$ -G and  $PGF_{2\alpha}$ -G increase IL-1 $\beta$  secretion by murine J774 macrophage-like cells. Their accompanying exploration of LPS-stimulated 2-AG metabolism by the cells suggested that 2-AG-dependent decreases in macrophage activation in response to LPS is mediated by PGD<sub>2</sub>-G. In later work, Alhouayek et al. reported that PGD<sub>2</sub>-G reduced symptoms of inflammation in a murine dextran sodium sulfate-induced colitis model; the related compounds  $PGD_2$  and  $PGD_2$ -EA did not have similar effects [25]. Raman and colleagues demonstrated that the nonenzymatic breakdown product of PGD<sub>2</sub>-G, 15-deoxy- $\Delta^{12,14}$ -PGJ<sub>2</sub>-G (15d-PGJ<sub>2</sub>-G), activates the PPARy receptor leading to decreased transcriptional activity of nuclear factor of activated T cells (NFAT), and ultimately, reduced IL-2 expression in the human Jurkat T lymphoblastoid cell line. The researchers suggest that 15d-PGJ<sub>2</sub>-G mediates the 2-AG-dependent suppression of IL-2 production in these cells [26, 27]. In one of the few studies in intact animals, Hu et al. reported that intraplantar administration of PGE<sub>2</sub>-G in rats produced hyperalgesia and allodynia (8). In this study, PGE<sub>2</sub> induced manner hyperalgesia in а similar to  $PGE_2$ -G. However, while  $EP_{1-4}$  receptor antagonists blocked the hyperalgesic effect of PGE<sub>2</sub>, they did not block the hyperalgesic effects of PGE<sub>2</sub>-G, suggesting that the PGE<sub>2</sub>-G response is mediated by a pathway distinct from that of PGE<sub>2</sub>. Nevertheless, this study highlights one of the major challenges of elucidating the role of PG-Gs in vivo. The compounds are subject to hydrolysis by multiple esterases such that the half-life of PG-Gs in biological tissues is short (see below). Consequently, some reports of PG-G-mediated biological effects are actually due to free PGs obtained following hydrolysis. We have limited this discussion to cases in which the observed pharmacology appears to be due directly to the action of PG-Gs.

A common finding in these studies of the biological activities of PG-Gs is that neither 2-AG nor the free acid prostaglandins mediate the same effects, and in many cases, a role for CB or prostanoid receptors was specifically ruled out. This strongly implies that there is one (or several) receptors specific for PG-Gs. In support of this hypothesis, Bruser et al. recently reported that PGE<sub>2</sub>-G is a potent ligand of the P2Y<sub>6</sub> receptor [28]. In this study, the authors identified G proteincoupled receptors (GPCRs) in PGE<sub>2</sub>-G responsepositive cells via RNA sequence analysis. From a pool of these candidate GPCRs, the authors established that the UDP receptor P2Y<sub>6</sub> is also a receptor for PGE<sub>2</sub>-G. In fact, they report that PGE<sub>2</sub>-G activates  $P2Y_6$  with an EC<sub>50</sub> of 1.2 pM, compared to an EC<sub>50</sub> of 78 nM for the canonical ligand, UDP.

## 8.4 Analytical Methodology for PG-G Quantitation

While several types of analytical methodologies have been applied to lipid detection and quantitation in the last several decades, reports of PG-G quantitation have employed almost exclusively LC-MS techniques. Previously, our group produced protocols [29] and reviews [30] regarding this type of analysis, and other researchers have employed similar methodologies. The typical work flow involves homogenization of cells or animal tissue followed by a secondary purification step (often solid phase extraction (SPE)). Finally, an aliquot of the dried and reconstituted sample is injected onto an LC-MS system where the analytes are chromatographed on a reversephase column and detected by mass spectrometry via selected reaction monitoring (SRM) (Note: sometimes researchers use the term "multiple reaction monitoring" (MRM), which is equivalent to SRM).

Our most recent report [31] employed homogenization of brain tissue via sonication in acetonitrile. No secondary purification was employed. Phospholipids are known to be less soluble than eicosanoids in acetonitrile, and it has been our experience that little interference is experienced in the analysis of PG-Gs and related lipids with this method. PG-Gs were chromatographed on a C18 column with ammonium acetate in the mobile phase to promote the generation of the  $[M + NH_4]^+$  ion. For unknown reasons, PG-Gs preferentially co-ordinate with the ammonium cation, and this complex provides several candidate fragment ions (Fig. 8.1), giving the researcher several options for SRM analysis. PG-Gs will also coordinate with Na<sup>+</sup>, but typically sodium complexes give rise to relatively weak product spectra compared to those of H<sup>+</sup> and NH4+ complexes, rendering this ionization method not useful for SRM detection.

In one of the few studies of PG-G detection in samples from an intact animal, Hu et al. (8) measured PGE<sub>2</sub>-G in rat hind paws by homogenizing the tissues in methanol, then subjecting the diluted homogenates to purification via C18 SPE. Samples were finally analyzed on a LC-MS/ MS system, where PGE<sub>2</sub>-G was ionized via



**Fig. 8.1** Product ion spectrum of PGE<sub>2</sub>-G complexed with an ammonium cation (m/z of  $[M + NH_4]^+ = 444.2$ ). SRM analysis may be accomplished by setting the Q1 m/z

to 444 and the Q3 m/z to any of the several product masses observed

co-ordination with the ammonium ion  $([M + NH_4]^+)$  and detected on a triple quadrupole mass spectrometer operating in SRM mode. For analyte confirmation, the authors used an LC system coupled to a quadrupole/time-of-flight mass spectrometer and compared the product ion spectra of the putative, endogenous PGE<sub>2</sub>-G and an authentic standard.

Similarly, Alhouayek et al. [25] homogenized tissues of interest in chloroform and subsequently performed a modified Folch-type extraction. Samples were further purified via reverse-phase SPE, then subjected to LC-MS/MS analysis on a triple quadrupole instrument, again operating the mass spectrometer in SRM mode.

Researchers have quantitated PG-EAs using similar techniques. Gatta et al. [6] quantified  $PGF_{2\alpha}$ -EA in murine spinal cord by homogenizing the tissue and extracting with acetone. The samples were further purified by open-bed chromatography on silica gel. The eluted fraction containing PG-EAs was analyzed on a reversephase LC-MS system (using a C18 column). Interestingly, the analytes were detected as  $[M + Na]^+$  ions by a high-resolution mass spectrometer (an IT-TOF instrument manufactured by Shimadzu). Uraquhart et al. [32] examined rabbit cornea and cornea homogenates for PG-EAs. A Folch-type extraction was used to purify the analytes from the homogenized tissue, and resultant samples were quantified via LC-MS/MS, where several SRM transitions were employed for  $PGF_{2\alpha}$ -EA,  $PGE_2$ -EA, and  $PGD_2$ -EA detection. The authors utilized precursor ion  $[M + H-H_2O]^+$ for all PG-EA species.

#### 8.5 PG-Gs in *in Vivo* Systems

Despite the relative abundance of reports of PG-G generation in both *in vitro* and cellular experimental models, non-traditional COX-2 products (both PG-Gs and other classes) have proven difficult to detect *in vivo*, and few such reports exist in the literature. As previously mentioned, Hu reported the presence of PGE<sub>2</sub>-G in the hindpaw and brain of rats treated with carrageenan [33]. Gatta reported the presence of

PGF<sub>2α</sub>-ethanolamide (PGF<sub>2α</sub>-EA) in the spinal cords of mice subjected to kaolin/ $\lambda$ -carrageenan inflammation of the knee [6]. More recently, Liu reported the presence of several COX-2 derivatives in human myocardium and murine liver [5]. Here, the authors detail the discovery of PGE<sub>2</sub>-LPE and -LPC, as well as the 11-HETE- and 15-HETE- derivatives of AA LPE and AA LPC, which are also COX-2 products.

One potential factor for the relative lack of detectable levels of PG-Gs in vivo is a high susceptibility of PG-Gs to enzymatic hydrolysis, resulting in the generation of the corresponding free PG and glycerol. Kozak et al. reported that the half-life of  $PGE_2$ -G in rat plasma is 14 s, and the half-life for appearance of  $PGE_2$  is 16 s [34]. Additionally, these authors reported that no starting material was detectable in rat plasma 5 min after dosing the animal with 2 mg/kg of PGE<sub>2</sub>-G. Vila reported that monoacylglycerol lipase (MAGL) and fatty acid amide hydrolase (FAAH) both hydrolyze PG-Gs [35], whereas Manna reported that LYPLA2 does this as well [36]. Indeed, several other enzymes have been reported to carry out this reaction, among them ABHD6, ABHD12, CES-1, and PPT1 [37, 38].

As noted above, there also appear to be kinetic limitations on the generation of PG-Gs via COX-2. AA is typically present at higher concentrations in mammalian tissue, with the excess of up to an order of magnitude. This, combined with the AA-dependent allosteric suppression of 2-AG oxygenation by COX-2 [13] and the lower peroxide tone required for AA oxygenation as opposed to 2-AG oxygenation [14] suggests that AA will likely be the preferred substrate of the enzyme under most *in vivo* conditions.

## 8.5.1 PG-Gs in Transgenic Mouse Brain Tissue

Historically, and possibly for the reasons detailed above, in analyses of murine CNS tissue, PG-Gs have proven to be below the limit of detection for both our methods and those of other researchers [33, 39]. We hypothesized that increased levels of the COX-2 enzyme would generate PG-Gs in a mouse brain setting. Towards this end, we acquired the Thy-1 hCOX-2 mouse. These mice overexpress human COX-2 (hCOX-2) primarily in the neurons of the striatum, amygdala, cerebral cortex, and hippocampus [40]. Litters resulting from the breeding of these mice contain both wild-type and transgenic (Tg) overexpressor animals. The experimental data shown below were generated with 60–90 day-old mice that were obtained in this way [31].

Western blotting analysis verified the presence of hCOX-2 in the brain tissue (prefontal cortex and hippocampus) of the Tg animals (Fig. 8.2) [31]. However, PG-Gs were not detected in analyses of Tg or WT brain tissue (Fig. 8.3). We hypothesized that an increase in substrate levels (i.e., 2-AG) may afford detectable PG-G generation. Thus, WT and Tg mice were dosed with the monoacylglycerol lipase (MAGL) inhibitor, JZL184 [41]. In agreement with previous literature reports, 2-AG was increased in the JZL184-dosed subjects (data not shown), and PG-Gs were detected (Fig. 8.3). Levels of PGF<sub>2α</sub>-G, PGE<sub>2</sub>-G, and PGD<sub>2</sub>-G were found to be in the range of 5–50 pmol per g of tissue (wet weight).

The COX-2 dependence of PG-G production was tested by dosing the Tg + JZL184 animals

concurrently with the highly selective COX-2 inhibitor lumiracoxib (LMX) [42]. The LMX-treated animals showed LMX levels in brain tissue of 200–400 pmol/g and an almost complete elimination of PG-G species (Fig. 8.4). Interestingly, PGE<sub>2</sub> and PGD<sub>2</sub> were also markedly reduced.

## 8.5.2 PG-Gs in Response to Systemic Inflammation

Having established a model system in which robust PG-Gs can be observed with Tg mice, we wanted to explore the possibility of observing PG-Gs without genetic manipulation. As previous reports of COX-2 products *in vivo* involved the administration of inflammatory stimuli, we treated WT mice with LPS (3 mg/kg once per day for 2 days) with and without concurrent administration of JZL184. Some of the LPS-treated mice produced PG-Gs, albeit at levels 1–2 orders of magnitude lower than those of the Tg + JZL184 subjects (Fig. 8.5). Note that tissues from animals treated with LPS alone exhibited a trend toward increased PG-G levels, though this did not reach



**Fig. 8.3** Detection and quantitation of PG-G species in Tg mice. PG-Gs are observed only in the Tg + JZL184 subjects (\*\* indicated p < 0.01). (Figure reproduced by

permission from Morgan et al. [31]. Copyright 2018, American Chemical Society)



Fig. 8.4 Effect of LMX on lipid species in brain tissue of Tg + JZL184 animals. (\* p < 0.05, \*\* p < 0.01, \*\*\* *p* < 0.001, \* *p* < 0.0001). *Note*: Figure **d** has a non-zero



d

25

20

15

10

5

0

-5

20

15

10

5

0

1952

1952

PGF<sub>20</sub>-G - pmol/g

h

6-keto-PGF1 or pmol/g

60

20

800

PGD<sub>2</sub> - pmols/g

TOND

19-521

PGD<sub>2</sub>-G pmol/g



Fig. 8.5 Effect of systemic LPS treatment on brain lipid levels of Tg and Tg + JZL184 subjects (\*p < 0.05, \*\*p < 0.01). (Figure reproduced by permission from Morgan et al. [31]. Copyright 2018, American Chemical Society)

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statistical significance when compared to controls. It is interesting to note, however, that there was no statistical significance between PG-G levels in the brains of animals treated with LPS alone and those treated with LPS and JZL184, although levels in the latter animals were statistically different from those in the controls. These findings suggest that LPS treatment increased PG-G levels in the brains of the mice even in the absence of JZL184; however, a larger study will be necessary to test this hypothesis.

## 8.6 Conclusions and Future Directions

The ability of COX-2 to metabolize 2-AG and other ester and amide derivatives of AA is now well established. However, the physiological relevance of this phenomenon remains unsettled. It is clear that PG-Gs exert interesting biological activities in tissues relevant to their site of production. Furthermore, their high potencies in many systems (with EC<sub>50</sub>'s in the pM range) suggest that only very low levels of these lipid mediators may be necessary to exert important physiological functions. Clearly, a major impediment to elucidating the potential relevance of PG-G formation is our inability to detect these compounds in vivo. One should note that this does not preclude relevance. For example, the highly relevant eicosanoids thromboxane A<sub>2</sub> and prostacyclin (PGI<sub>2</sub>) are not detected in tissue or cellular samples. Rather, their production is monitored through the detection of their nonenzymatic breakdown products, thromboxane B<sub>2</sub> and 6-keto-PGF<sub>1 $\alpha$ </sub>. Unfortunately, in the case of PG-Gs, their hydrolysis products are free acid PGs. Thus, it is impossible to know whether PGs detected in a biological sample may have initially been synthesized from 2-AG or AA.

Given these challenges, the Tg mice described here offer an intriguing model that can be used to detect PG-G formation *in vivo*, albeit under conditions that are not totally physiological. Of perhaps greater interest are our results from LPS-stimulated animals suggesting that, eventually, models may be found in which PG-G biosynthesis can be detected and monitored under conditions that will allow us to assess their role in physiological or pathophysiological processes. Such models will also allow further study of additional aspects of COX-2 biology, such as the *in vivo* relevance of substrate selective inhibition.

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9

# Targeting the COX/mPGES-1/PGE<sub>2</sub> Pathway in Neuroblastoma

Karin Larsson, Anna Kock, Per Kogner, and Per-Johan Jakobsson

#### Abstract

The importance of prostaglandin E<sub>2</sub> in cancer progression is well established, but research on its role in cancer has so far mostly been focused on epithelial cancer in adults while the knowledge about the contribution of prostaglandin E<sub>2</sub> to childhood malignancies is limited. Neuroblastoma, an extracranial solid tumor of the sympathetic nervous system, mainly affects young children. Patients with tumors classified as high-risk have poor survival despite receiving intensive treatment, illustrating a need for new treatments complimenting existing ones. The basis of neuroblastoma treatment e.g. chemotherapy and radiation therapy, target the proliferating genetically unstable tumor cells leading to treatment resistance and relapses. The tumor microenvironment is an avenue, still to a great extent, unexplored and lacking effective tar-

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A. Kock · P. Kogner Childhood Cancer Research Unit, Department of Women's and Children's Health, Karolinska Institutet, Stockholm, Sweden geted therapies. Cancer-associated fibroblasts is the main source of prostaglandin  $E_2$  in neuroblastoma contributing to angiogenesis, immunosuppression and tumor growth. Prostaglandin  $E_2$  is formed from its precursor arachidonic acid in a two-step enzymatic reaction. Arachidonic acid is first converted by cyclooxygenases into prostaglandin  $H_2$  and then further converted by microsomal prostaglandin E synthase-1 into prostaglandin  $E_2$ . We believe targeting of microsomal prostaglandin E synthase-1 in cancer-associated fibroblasts will be an effective future therapeutic strategy in fighting neuroblastoma.

#### Keywords

 $\begin{array}{l} Microsomal \ prostaglandin \ E \ synthase-1 \ \cdot \\ Prostaglandin \ E_2 \ \cdot \ mPGES-1 \ inhibition \ \cdot \\ COX-inhibition \ \cdot \ Neuroblastoma \ \cdot \ Cancer-\\ associated \ fibroblasts \ \cdot \ Tumor \ microenvironment \ \cdot \ Targeted \ therapy \ \cdot \ Tumor-promoting \ inflammation \ \cdot \ Cancer \end{array}$ 

## 9.1 Introduction

Prostaglandin  $E_2$  (PGE<sub>2</sub>) is a pro-inflammatory mediator belonging to the eicosanoid family of bioactive lipids and the most abundant lipid mediator in tumor tissue. Numerous studies

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Per Kogner and Per-Johan Jakobsson contributed equally to this work.

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describe upregulation of  $PGE_2$  in different tumors [1–5] and the contribution of  $PGE_2$  to tumor progression is linked to several of the hallmarks of cancer including increased proliferation of tumor cells [6, 7], withstanding apoptosis signals [8], increased angiogenesis [9], invasion and metastasis [10], and evasion of host immune response [11, 12].

Neuroblastoma is a neural crest derived childhood malignancy of the sympathetic nervous system. Neuroblastoma accounts for approximately 6-10% of the childhood cancer cases and 9-15% of the pediatric cancer deaths making it the single most common and deadly tumor of childhood [13, 14]. The disease ranges from localized tumors with favorable biology and high survival to metastatic tumors with aggressive biology and poor prognosis. Neuroblastoma is stratified into three riskgroups, low-risk, intermediate-risk and highrisk groups, depending on clinical age, metastatic stage and histologic appearance with/ without differentiation and biology including genetic aberrations [15]. Two of the most common genetic aberration in the unfavorable highrisk neuroblastoma is amplification of the MYCN oncogene (MYCN-amplified) and loss of the long arm of chromosome 11 (11q-deletion) [16]. Children with high-risk tumors only have a survival rate of 40–50% despite intensive multimodal treatment including intense induction chemotherapy, ablative therapy with stem cell rescue, radiation therapy, immune therapy and attempts to complete surgical removal [17]. The remarkable progression in pediatric oncology with increasing survival of most childhood malignancies during the second half of the twentieth century has stagnated in the last decade highlighting the need for new therapeutic targets and strategies to further increase survival. Intensification of current treatments is not an option since life long side effects and secondary malignancies already pose an increasing problem in surviving children [18].

Chemotherapy and radiation therapy hit the fast proliferating tumor cells that are genetically unstable resulting in clonal evolution and the development of therapy resistance [19]. Stromal

cells that are not targeted by chemotherapy and radiation, continue to produce important mediators such as cytokines, chemokines, growth factors and PGE<sub>2</sub> that sustains inflammation and promote tumor repopulation [20]. It has therefore lately been suggested that therapies targeting genetically stable cells in the stromal compartment will be a promising alternative or an additional therapeutic strategy [21, 22]. This review will address PGE<sub>2</sub>-driven inflammation, its contribution to neuroblastoma progression and inhibition of PGE<sub>2</sub> as a new therapeutic strategy in neuroblastoma treatment.

## 9.2 Prostaglandin E<sub>2</sub> Biosynthesis and Signaling

Arachidonic acid (AA), the initial precursor for prostanoid (prostaglandins and thromboxane) biosynthesis, is an omega-6 fatty acid and released from cellular membranes by phospholipases  $A_2$  (PLA<sub>2</sub>). PGE<sub>2</sub> is synthesized from AA in a two-step enzymatic reaction. In the first step AA is converted by cyclooxygenases (COX)-1 and - 2 into a reactive intermediate, prostaglandin (PG)H<sub>2</sub> via a transition molecule PGG. PGH<sub>2</sub> is then converted into PGE<sub>2</sub>, PGD<sub>2</sub>, PGF<sub>2a</sub>, prostacyclin (PGI<sub>2</sub>) and thromboxane (TXA<sub>2</sub>) by specific terminal synthases i.e. PGE synthases, PGD synthases, PGF synthase, PGI synthase and TX synthase respectively. The key PGE<sub>2</sub> producing synthase is microsomal prostaglandin E synthase-1 (mPGES-1) [23]. During normal conditions mPGES-1 is expressed at low levels but then rapidly induced upon stimuli with proinflammatory cytokines (IL-1 $\beta$ , TNF- $\alpha$ ) [24, 25], endotoxins (LPS) [26], growth factors (EGF) [27] and hypoxia [28]. There is two additional PGE<sub>2</sub> synthases reported, namely cytosolic prostaglandin E synthase (cPGES) and microsomal prostaglandin E synthase-2 (mPGES-2), with no structural relationship to mPGES-1 [29, 30]. While the function of mPGES-2 as a PGE<sub>2</sub> synthase has been shown both for recombinantly expressed enzyme [31] and in mammalian cells [29], the function of mPGES-2 as a  $PGE_2$  synthase in physiological and pathological condi-



**Fig. 9.1** Prostaglandin  $E_2$  biosynthesis. Arachidonic acid (AA) released from cellular membranes is converted to prostaglandin (PG) $E_2$  in a two-step enzymatic reaction. In the first step AA is oxidized by cyclooxygenase (COX) -1 or -2 into the short lived intermediate PGH<sub>2</sub>. In the second step microsomal prostaglandin E synthase-1 (mPGES-1)

tions remains to be proven [32, 33]. PGE synthase activity was found in cPGES purified from rat brain and in mammalian cells transfected with cPGES cDNA [30]. cPGES (also known as p23 or cPGES/p23) is a co-chaperone to Hsp90 and has been linked to cancer but not coupled to any PGE synthase activity *in vivo* [34, 35]. PGE<sub>2</sub> can also be metabolized non-enzymatically from PGH<sub>2</sub> but at a much slower rate than enzymatic conversion by mPGES-1 [36]. The biosynthesis of prostanoids is summarized in Fig. 9.1.

PGE<sub>2</sub> elicit its response by four G-protein coupled receptors, the E prostanoid receptors EP1, EP2, EP3 and EP4. The EP receptors are coupled to G $\alpha$  proteins with stimulatory or inhibitory subunits leading to the activation of a diverse panel of downstream signaling pathways (Fig. 9.2). EP2 and EP4 are coupled with G $\alpha$ s that activates adenylyl cyclase (AC) that in turn leads to cAMP production. EP3 is coupled to G $\alpha$ i that instead inhibits AC. EP1 is coupled to G $\alpha$ q that activates phospholipase C leading to increased Ca<sup>2+</sup> influx [37].

converts  $PGH_2$  into  $PGE_2$ .  $PGH_2$  can also be converted into other prostanoids ( $PGD_2$ ,  $PGF_{2\alpha}$ , prostacyclin ( $PGI_2$ ) or thromboxane ( $TXA_2$ )) by respective terminal synthases.  $PLA_2$ , phospholipase  $A_2$ ; EP, E prostanoid; HETEs, hydroxyeicosatetraenoic acids; EETs, epoxyeicosatrienoic acids; LOX, lipoxygenase; Cyt, Cytochrome

### 9.3 PGE<sub>2</sub> in the Tumor Microenvironment

Solid tumors are not only composed of malignant cells but a complex mix of cellular components including cancer cells, immune cells, endothelial cells, cancer-associated fibroblasts (CAFs) and the non-cellular extracellular matrix (ECM) contributing to the production of growth factors and pro-inflammatory mediators, thus providing the prerequisites for tumor progression. PGE<sub>2</sub> play an important role in the orchestration of the many processes involved in the developing tumor microenvironment [38]. By downregulating Th1 cytokines (IFNy, TNFa and IL-2) and upregulating Th2 cytokines (IL-10, IL-4 and IL-6) PGE<sub>2</sub> shift the balance from the anti-tumor Th1 response towards immunosuppressive Th<sub>2</sub> response [39-41]. PGE<sub>2</sub> both directly and via the shift in cytokine production suppress the cytotoxic activity of cytotoxic T lymphocytes and natural killer cells, inhibits maturation of dendritic cells and promotes immunosuppressive cells like T regulatory cells and myeloid derived



**Fig. 9.2** PGE<sub>2</sub> signaling. PGE<sub>2</sub> formed via COXs and mPGES-1 is released from cells and confer downstream signaling via four E prostanoid (EP) receptors, EP1-EP4, either on the same cell (autocrine) or neighboring cells (paracrine). The EP receptors are G-protein coupled receptors that leads to changes in intracellular Ca<sup>2+</sup> or cyclic adenosine monophosphate (cAMP) levels. EP1

suppressor cells [42–46]. PGE<sub>2</sub> also promotes the polarization of tumor-associated macrophages (TAMs) towards a phenotype close to M2 polarized macrophages with surface expression of CD163 and CD206 [47]. The M2-like TAMs in turn contribute to tumor progression and immune suppression by the production of cytokines and chemokines e.g. IL-6 and IL-10 [48]. CAFs, one of the most abundant cell type within the tumor microenvironment, are recruited and activated by tumor cells and influence several important processes in tumor progression including ECM remodeling, migration and metastasis, immune modulation and angiogenesis via secretion of a plethora of soluble factors, including PGE<sub>2</sub> [49].

results in increased Ca<sup>2+</sup> flux mediated through phospholipase C (PLC), EP2 and EP4 leads to increased cAMP levels and EP3 in decrease levels of cAMP via activation or inhibition of adenylyl cyclase (AC) respectively. To inhibit PGE<sub>2</sub> signaling, either COXs or mPGES-1 can be inhibited or EP receptor antagonists can be used. NSAIDs, nonsteroidal anti-inflammatory drugs

PGE<sub>2</sub> produced by CAFs, TAMs and tumor cells can stimulate vascular endothelial growth factor (VEGF) production in both CAFs and tumor cells and thereby promote angiogenesis [50, 51].

## 9.4 Tumor-Promoting Inflammation in Neuroblastoma

Lately, several investigations about the stromal compartment of neuroblastoma tumors have improved our knowledge about the role of nonmalignant cells in the tumor microenvironment to neuroblastoma progression [21]. In a study by Carlson and coworkers, a shift was found during tumor progression in an experimental MYCNdriven neuroblastoma model, from an adaptive immune response in early lesions to a state of immature innate immune response in larger tumors. Also, a change in the population of infiltrating macrophages, the TAMs, was detected from an M1 macrophage phenotype in early neoplastic lesions to an M2-like macrophage phenotype in the established tumors leading to a gradually increasing immunosuppressive microenvironment [52]. Asgharzadeh and colleagues also illuminated the importance of TAMs in metastatic spread of neuroblastoma. Metastatic MYCN non-amplified tumors had a higher degree of TAM infiltration than non-metastatic tumors and by calculating an inflammation-related gene score, survival rate could be predicted [53]. We also found an increased infiltration of M2-like TAMs (CD163 and CD206 expression) in high-risk neuroblastoma compared to low-risk neuroblastoma [2]. In addition to TAMs, other cell types were also infiltrating the neuroblastoma tumors e.g. dendritic cells, T cells, B cells and CAFs. The CAFs were found in proximity to the dendritic cells and T-cells indicating an interaction between these cell types [2]. The numbers of TAMs and area of CAFs were found to correlate with clinical stage, in a study by Hashimoto et al. They also observed that TAMs resided close to the CAFs, suggesting an interaction also between CAFs and macrophages in the neuroblastoma tumor microenvironment and that these cell together promote neuroblastoma progression [54]. These results were recently confimed in a study by Borriello et al., where they demonstrated a correlation between CD163 expressing cells and CAFs in neuroblastoma tumors and also in this study it was found that the cell types resided in proximity to each other indicating an interaction [55]. In addition to promoting cancer cell growth and interacting with immune cells, CAFs also promote angiogenesis [56]. Zeine et al. found an association between high levels of  $\alpha$ -SMA positive CAFs and microvascular proliferation in neuroblastoma tumors suggesting a role of CAFs in promoting angiogenesis also in neuroblastoma [57].

## 9.5 Prostaglandin E<sub>2</sub> in Neuroblastoma

## 9.5.1 Expression of PGE<sub>2</sub> Producing Enzymes and Receptors in Neuroblastoma

As reported by us previously, mPGES-1 is expressed in human neuroblastoma tumors [2] as well as in experimental neuroblastoma tumors [58]. The highest levels of mPGES-1 was found in a subset of high-risk tumors with 11q-deletion but without MYCN-amplification, compared to high-risk tumors with MYCN-amplification and low-risk tumors without poor prognosis biological features. Colocalization of mPGES-1 with markers such as vimentin, fibroblast specific protein (FSP-1), fibroblast activating protein (FAP) and platelet derived growth factor receptor  $\beta$  $(PDGFR\beta)$  in the tumors suggested that the major source of mPGES-1 expression was cancerassociated fibroblasts [2]. In experimental tumors we also found colocalization of mPGES-1 with PDGFR $\beta$  indicating the validity of these models to study mPGES-1 inhibition in neuroblastoma. Even though we did not find mPGES-1 expression in tumor cells in primary human or experimental neuroblastoma tumors there are reports about mPGES-1 expression in IL-1β stimulated SK-N-SH cells [59, 60], and  $PGE_2$  production in SK-N-SH and SK-N-BE(2) cells when treated with IL-1 $\beta$  and AA [61].

The source of PGH<sub>2</sub>, the substrate for PGE<sub>2</sub> biosynthesis, in neuroblastoma tumors is not yet fully understood. In a study by Johnsen et al., extensive COX-2 expression was found both in neuroblastoma tumors and cell lines that further responded to NSAID therapy *in vitro* and *in vivo* [62]. In a more recent study, we on the other hand primarily found COX-1 expression in the neuroblastoma tumors both on mRNA level and protein level, with the exception of *MYCN*-amplified tumors where COX-2 was the dominant isoform. Interestingly, there were not many cells co-expressing COX-1 and mPGES-1, suggesting transcellular transfer of PGH<sub>2</sub> [2].

The levels of PGE<sub>2</sub> not only depend on COX and mPGES-1 expression but also on the PGE<sub>2</sub> degrading enzyme 15-hydroxyprostaglandin dehydrogenase (15-PGDH). In the subset of high mPGES-1 expressing neuroblastoma tumors with 11q-deletion only low levels of 15-PGDH was detected whereas in the low mPGES-1 expressing tumors (*MYCN*-amplified tumors and lowrisk tumors) high expression of 15-PGDH was detected. The low expression of 15-PGDH probably contributed to the increased levels of PGE<sub>2</sub> found in the 11q-deleted tumors [2].

In a comprehensive study by Rasmuson et al., an abundant expression of all EP receptors in the tumor tissue irrespective of tumor subset was detected. Expression of the EP receptors was found in tumor cells and in the stromal vasculature [61]. In a following study, we also found expression of all EP receptors in neuroblastoma tumors with MYCN-amplification and 11q-deletion. EP1, EP2 and EP3 was found in both tumor cells and stromal cells whereas EP4 showed a clear stromal localization [58]. The reason for this discrepancy could be that in the previous study paraffin embedded material was used while in the latter frozen tumor material was used.

## 9.5.2 COX-Inhibitors in Experimental Neuroblastoma Models *in vivo*

The benefits of COX-inhibition to reduced tumor growth in neuroblastoma experimental models have been demonstrated in several studies, summarized in Table 9.1. Johnsen et al. showed a significantly reduced tumor growth and tumor weight at sacrifice, in nude rats with SK-SY5Y neuroblastoma xenografts, treated with either celecoxib (10 mg/day for 10 days) or diclofenac (250 g/l drinking water for 11 days). They also demonstrated increased apoptosis in the tumors from diclofenac treated rats [62]. In another study, transgenic MYCN+/+ mice were treated with low-dose aspirin for 10 days (10 mg/kg/ day), leading to reduced tumor growth and a decrease in tumor-promoting inflammation [52]. Additionally, a COX-2 specific inhibitor NS-398 (15 mg/kg/day for 4.5 weeks) was found to reduce growth of subcutaneous SK-N-AS xenografts as well as bone metastasis in nude mice. Treatment with NS-398 also reduced expression of VEGF-A and microvessel density [63]. We also showed that diclofenac (250 g/l drinking water for 9 days) significantly reduced tumor growth in mice carrying SK-N-AS neuroblas-

	Target	In vivo model	Treatment		Effects	
Inhibitor			Dose	Time		References
Celecoxib	COX-2	rat xeno, SK-SY5Y	10 mg, <i>p.o.</i>	10 days	Tumor growth↓	[62]
Diclofenac <sup>a</sup>	COX-1/2	rat xeno, SK-SY5Y	250 g/l	11 days	Inhibit growth	
					Apoptosis↑	
Aspirin <sup>b</sup>	COX-1	mice, tg-MYCN <sup>+/+</sup>	10 mg/kg, p.o.	10 days	Tumor growth↓	[52]
					Inflammation↓	
NS-398	COX-2	mice xeno, SK-N-AS	15 mg/kg, <i>i.p.</i>	4.5 weeks	Tumor growth↓	[63]
					Bone metastasis↓	
					Angiogenesis↓	
Diclofenaca	COX-1/2	mice xeno, SK-N-AS	250 g/l	9 days	Tumor growth↓	[2]
Compound III	mPGES-1	mice xeno, SK-N-AS	50 mg/kg, <i>i.p.</i>	8 days	Tumor growth↓	[58]
		mice, tg-MYCN+/+	50 mg/kg, <i>i.p.</i>	10 days	Tumor growth↓	1
					Angiogenesis↓	
					CAF infiltration↓	
					M1/M2↑	

Table 9.1 Overview of neuroblastoma in vivo studies targeting PGE<sub>2</sub> biosynthesis

<sup>a</sup>Mice had free access to drinking water supplemented with diclofenac at the indicated concentration <sup>b</sup>Dose of aspirin administered equivalent to low-dose aspirin in humans. *Xeno*, xenograft; *tg*, transgenic; *p.o.*, oral gavage, *i.p.*, intraperitoneal. In all experiments, inhibitors were administered daily during the indicated time toma xenografts, and that the reduction of tumor growth was associated with a reduction of  $PGE_2$  in the tumor tissue [2].

## 9.5.3 Selective Inhibition of mPGES-1 in Experimental Neuroblastoma Models *in vivo*

In a recently published paper, we investigated the effect of selective mPGES-1 inhibition on neuroblastoma growth [58]. We used two experimental neuroblastoma mouse models, a xenograft model reflecting the 11q-deleted subset of high-risk neuroblastoma and an inflammatory MYCN-driven transgenic model [52, 64]. In both models, daily intraperitoneal injections of the cross-species human/murine mPGES-1 inhibitor Compound III (CIII, 50 mg/kg) for 8-10 days, resulted in reduced tumor growth. We also found interesting changes in the tumor microenvironment upon pharmacological mPGES-1 inhibition with CIII, highlighting the importance of  $PGE_2$  in several aspects of the tumor microenvironment all of which probably contributed to the resulting decrease in tumor growth. Firstly, tumors from CIII treated mice were less vascularized compared to controls, assessed by immunohistochemical (IHC) analysis with an antibody towards the endothelial marker CD31. Secondly, IHC analysis of macrophage polarization markers revealed less pro-tumorigenic M2 phenotype of the TAMs (CD206) in tumors from CIII treated mice compared to controls. A concomitant increase in antitumorigenic M1 phenotype of the TAMs, detected with flow cytometry, confirmed a shift towards a less immunosuppressive tumor microenvironment in CIII treated mice compared to controls. Thirdly, host-derived PGE<sub>2</sub> producing CAFs infiltrating the tumors were positive for PDGFR $\beta$ , EP4 and the IL-1 receptor type I as well as phosphorylated STAT3, describing a pro-inflammatory pro-tumorigenic CAF phenotype. In an in vitro migration assay, IL-1β treatment induced migration of fibroblasts towards tumor cells, a migration that was inhibited either by CIII or an EP4 antagonist, suggesting a role of PGE<sub>2</sub> in recruiting stromal cells to the tumor microenvironment. Inhibition of mPGES-1 in vivo also resulted in decreased presence of PDGFR $\beta$  expressing CAFs, thus not only inhibiting mPGES-1 enzyme activity in CAFs already infiltrating the tumor but, consistent with the *in vitro* data, reducing further recruitment of CAFs. These data together provide strong evidence that mPGES-1/PGE<sub>2</sub> play an important role in the developing tumor microenvironment in neuroblastoma creating an immunosuppressive milieu and contributing to CAF infiltration and angiogenesis.

## 9.6 Clinical Benefit of PGE<sub>2</sub> Blocking Therapy in Cancer Treatment

All anti-tumor treatments strive to induce apoptosis or cell death, either by directly targeting the tumor cells or via the immune system. The cellular stress that follow massive cell death, induced by cytotoxic treatment or irradiation of cells, also leads to induction and release of PGE<sub>2</sub>, stimulating tumor repopulation [65–67]. Proposed mechanisms how PGE<sub>2</sub> support tumor cell survival and repopulation include changing the apoptotic threshold [68], suppression of inflammatory responses [69] and by promotion of cancer stem cells [70, 71]. Several studies have illuminated the benefits of PGE<sub>2</sub> inhibition in combination with chemotherapy. Recently, Kurtova et al. showed that the cytotoxic treatment-induced apoptosis and the accompanied PGE<sub>2</sub> release promoted cancer stem cells repopulation and chemoresistance. Inhibition of PGE<sub>2</sub> with celecoxib (5 mg/kg/day, starting 2 days before cytotoxic treatment and then continuing throughout the experiment) in combination with gemcitabine/cisplatin (GC) administered in several treatment cycles reduced chemotherapy resistance compared to GC treatment alone in a bladder cancer xenograft model [20]. Also in neuroblastoma in vivo studies, there are reports about beneficial combination effects with celecoxib and cytotoxic drugs. Celecoxib (10 mg/day for 12 days) was found to potentiate the antitumor effect of irinotecan and doxorubicin in neuroblastoma (SH-SY5Y) xenografted rats [72]. Additional studies confirmed an enhanced anti-tumor effect of irinotecan when administered in combination with low-dose celecoxib (5 mg/kg/day for 20 consecutive days) in three patient-derived neuroblastoma xenografts [73]. Celecoxib (250 mg/kg/day for 20 days) and a PGE<sub>2</sub> neutralizing antibody was also found to enhance the effect of radiation in a head and neck squamous carcinoma xenograft model [74]. Several recent studies also indicate that inhibition of PGE<sub>2</sub> could be a strategy to enhance the clinical outcome of immune-based therapies [75–77]. Weather mPGES-1 inhibitors will have the same beneficial combinatorial effects as celecoxib remains to be proven.

## 9.7 A Niche for mPGES-1 Inhibition in Cancer Treatment

Although NSAIDs and Coxibs have proved antitumor efficiency in mouse models and epidemiology data supports the benefits of regular NSAID intake to prevent cancer, the severe side effects on the gastrointestinal tract and cardiovascular system has hampered their use as chemopreventing and chemopotentiating agents. In children, there is also a fear of Reye's syndrome that has been associated with viral induced fever and intake of aspirin, which is why the use of aspirin in children below 16 years of age is usually not recommended [78, 79]. In addition, some cytostatic drugs like the anthracyclines are cardiotoxic and therefore may increase the risk of cardiovascular adverse effects seen with Coxibs in adults, also in children [80].

An mPGES-1 inhibitor would potentially have the same anti-tumor properties seen with COX inhibitors without the severe side effects on the gastrointestinal tract and the cardiovascular system, resulting from the inhibition of all prostaglandins. Still, there are no mPGES-1 inhibitors available in the clinic to date. There are three main reasons why the development of mPGES-1 inhibitors has failed to reach the clinic. (*i*) 'Guilt of association' to COX-2 inhibitors. Since mPGES-1 preferentially couples with COX-2 there are concerns that an mPGES-1 inhibitor would have the same deleterious effect on the cardiovascular system. (*ii*) A three amino acid phylogenetic difference between human mPGES-1 and murine mPGES-1 in the catalytic cleft renders most candidate drugs developed to human mPGES-1 inefficient towards murine mPGES-1 and thus obstructing pre-clinical testing [81]. (*iii*) Lack of differentiation to NSAIDs. Researchers have failed to provide compelling evidence of the potential benefits of mPGES-1 inhibition compared to COX-inhibition.

In contrast to COX-2 inhibitors, mPGES-1 inhibitors would not affect the thromboxane/ prostacyclin balance in favor of thromboxane production and would thereby not have the same effect on the cardiovascular system. Indeed, pharmacological inhibition of mPGES-1 with CIII [82], a cross-species human/murine mPGES-1 inhibitor, was even shown to increase production of prostacyclin and reduce vasoconstriction of blood vessels [83]. There are also studies showing chemoprotective effects of prostacyclin and PGD<sub>2</sub>, effects that would be lost upon COX inhibition but would be spared or even enhanced by mPGES-1 inhibition and the potential shunting to prostacyclin and PGD<sub>2</sub>. For comprehensive reviews of pre-clinical mPGES-1 inhibitors see references [84, 85]. For a summary of the advantages and disadvantages with mPGES-1 inhibition versus COX inhibition see Table 9.2.

 Table 9.2
 Advantages and disadvantages with mPGES-1

 inhibition vs COX inhibition in cancer treatment

	mPGES-1 inhibition				
+	Anti-tumor efficiency in vivo.				
+	Selective PGE <sub>2</sub> inhibition.				
+	Cardiovascular safe.				
-	No available inhibitor in the clinic.				
_	Unknown shunting effects.				
-	Poor efficiency of human inhibitors in mouse				
	models.				
	COX inhibition				
+	Anti-tumor efficiency in vivo.				
+	Supportive epidemiologic data.				
-	Inhibit chemoprotective prostacyclin and PGD <sub>2</sub> .				
-	Gastrointestinal side effects.				
-	Cardiovascular side effects.				
-	Fear that aspirin causes Reye's syndrome in				
	children.				
_	Could increase cardiotoxicity of cytotoxic drugs.				

#### 9.8 Conclusions

A link between tumor-promoting inflammation and prostaglandin  $E_2$  is well established in adult tumors [41]. There are recent studies highlighting the contribution of the tumor microenvironment to neuroblastoma progression, but less studies exist that cover the role of PGE<sub>2</sub> in the neuroblastoma microenvironment. We have suggested a role of PGE<sub>2</sub>-driven inflammation in neuroblastoma with CAFs as the main source of mPGES-1 expression [2, 58]. In experimental neuroblastoma tumors, inhibition of CAFderived PGE<sub>2</sub> slows down tumor growth and alters several parameters of the tumor microenvironment in favor of the host; however, further investigations are warranted elucidating underlying mechanism behind the role of PGE<sub>2</sub> in the microenvironment of neuroblastoma.

COX-inhibitors are widely used drugs and have shown promising results in experimental models of neuroblastoma and in occasional clinical reports, but they are with a few exceptions not used in the regular clinical treatment today as adjuvant neuroblastoma therapy. The reason for this could be attributed to the risk of adverse effects with prolonged use of NSAIDs in the adult population and that these risks are not well documented in children. Even though inhibition of PGE<sub>2</sub>, using COX inhibitors or mPGES-1 inhibitors, reduces tumor growth it will not be used as monotherapy in cancer treatment. Instead the great benefit of reducing  $PGE_2$  in the tumor microenvironment lay in sensitizing tumor cells to killing [86]. As an adjuvant treatment, inhibition of PGE<sub>2</sub> have the potential to improve the effects of established therapies, e.g. chemotherapy, radiation therapy and immune therapy leading to increased survival or lowering the doses of these treatments and their associated side effects. Thus, we envision that inhibition of mPGES-1/  $PGE_2$  has the potential to be widely used as a future adjuvant anti-tumor therapy.

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# Metabolomics Biomarkers for Precision Psychiatry

Pei-an (Betty) Shih

### Abstract

The treatment of psychiatric disorders remains a significant challenge in part due to imprecise diagnostic criteria and incomplete understanding of the molecular pathology involved. Current diagnostic and pharmacological treatment guidelines use a uniform approach to address each disorder even though psychiatric clinical presentation and prognosis within a disorder are known to be heterogeneous. Limited therapeutic success highlights the need for a precision medicine approach in psychiatry, termed precision psychiatry. To practice precision psychiatry, it is essential to research and develop multiple omics-based biomarkers that consider environmental factors and careful phenotype determination. Metabolomics, which lies at the endpoint of the "omics cascade," allows for detection of alterations in systems-level metabolites within biological pathways, thereby providing insights into the mechanisms that underlie various physiological conditions and pathologies. The eicosanoids, a family of metabolites derived from oxygenated polyunsaturated fatty acids, play a key role in inflammatory mechanisms and have been implicated in psy-

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Department of Psychiatry, University of California, San Diego, San Diego, CA, USA e-mail: pbshih@ucsd.edu chiatric disorders such as anorexia nervosa and depression. This review (1) provides background on the current clinical challenges of psychiatric disorders, (2) gives an overview of metabolomics application as a tool to develop improved biomarkers for precision psychiatry, and (3) summarizes current knowledge on metabolomics and lipidomic findings in common psychiatric disorders, with a focus on eicosanoids. Metabolomics is a promising tool for precision psychiatry. This research has great potential for both discovering biomarkers and elucidating molecular mechanisms underlying psychiatric disorders.

#### Keywords

Systematic review · Psychiatric disorders · Metabolomics · Eicosanoids · Polyunsaturated fatty acids · Biomarkers

## 10.1 Challenges in Clinical Psychiatry

Psychiatric disorders can impair one's thinking, perceptions, emotions, and behaviors, resulting in significant distress or impairment of personal functioning [1]. The five most common categories of psychiatric disorders are *anxiety disorders*, including generalized anxiety disorder and

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post-traumatic stress disorder; mood disorders, such as depression and bipolar disorder; schizophrenia and psychotic disorders; dementia; and eating disorders, including anorexia nervosa and binge-eating disorder. Psychiatric disorders are prevalent, with an astonishing 46.4% lifetime prevalence of having at least one major psychiatric disorders in the United States [2]. Psychiatric conditions represent a major public health problem due to their associated disabilities [3] and mortality [4]. The estimated global burden of psychiatric disorders accounts for up to 32% of years lived with disability, and more than 13% of disability-adjusted life-years [5]. Moreover, psychiatric disorders are significant predictors of the onset and severity of subsequent serious medical illnesses such as heart disease [6].

Diagnosis in psychiatry is based on a classification system that includes clinical nosologies such as the International Classification of Diseases [7] and the Diagnostic and Statistical Manual of Mental Disorders [8]. The current diagnostic system is universally applied, not only clinically, but also in research and policy settings such as drug-approval and insurance-reimbursement systems. Although these diagnostic criteria are regularly revised to improve validity, more disagreements about diagnosis fundamentals are found in psychiatry than in any other branch of medicine [9, 10]. The heterogeneous presentation of psychiatric disorders is a result not only of phenotypic, biological, and genetic heterogeneity, but also the outcome of complex interactions between environmental and biological factors. A lack of clear understanding about the complex psychopathology contributing to each disorder leads to inadequate or ineffective treatment strategy. Taking depression as an example, although antidepressants provide substantial benefits for many, issues including lack of efficacy, intolerance, delayed therapeutic onset, and risk of relapse are frequently reported. In fact, results from one of the largest randomized trials involving 4041 patients from 41 clinical sites around the country showed that the remission rate from the first line of treatment was only 28% [11]. Clearly, there is a lot of room for improvement in clinical psychiatry.

## 10.2 Omics-Based Strategies in Precision Psychiatry

A promising strategy to overcome obstacles in clinical psychiatry is "precision medicine," an emerging approach that aims to improve health and advance individualized care by taking into account "each person's variability in genes, environment, and lifestyle" [12]. This ambitious initiative requires collecting dense data from a large number of cohort studies, including studies of psychiatric disorders [13]. The rise of biotechnologies that simultaneously measure thousands of data points has been timely in meeting the needs of precision medicine. These highthroughput technologies yield multifaceted data, including genomics, epigenomics, transcriptomics, proteomics, metabolomics and are collectively referred to as "multi-omics" [14]. Used effectively, multi-omics investigation enables exploration of complex interactions in biological systems and their roles in health and disorders.

Among individual "omics" disciplines, the most frequently published in psychiatry are genome-wide association studies (GWAS) [15, 16]. GWAS have revealed evidence of substantial pleiotropy or shared genetic etiology among several psychiatric disorders [17]. Due to the polygenic, multi-factorial nature of psychiatric disorders and the inherent limitations of GWAS design, the genetic loci identified are typically small in effect size and of questionable clinical significance [18]. By itself, GWAS likely remain limited in yielding significant translational advances to improve diagnostic accuracy and treatment effectiveness [19].

A multidisciplinary approach that combines multiple omics data-integrated multi-dimensional omics- is much more likely to offer complementary vantage points to enrich our knowledge of expression and functions of genomic factors associated with a disorder, thus improving diagnosis, prognosis, and treatment development [20]. For example, a recent GWAS meta-analysis revealed a high degree of correlation [average genetic correlation (rg) = 0.40] among bipolar disorder, major depressive disorder (MDD), and schizophrenia [21]. On the other hand, a molecular profiling approach characterizing 181 proteins and small molecules in serum showed excellent potential to distinguish schizophrenia from healthy controls, as well as from subjects with MDD, bipolar disorder, and Asperger syndrome [22]. Studies incorporating both investigation methods in the same study cohort likely will lead to significant improvement in diagnostic accuracy.

Biomarkers are *objective* surrogates of genetic, tissue-specific, and environmental factors, as well as their interactions [23]. An effective biomarker system such as integrated multi-dimensional omics will thus serve as one of the most informative research and clinical tools and move the practice of psychiatry closer to the goal of precision psychiatry [24].

## 10.3 Unique Role of Metabolomics Biomarkers

While GWAS provide information on genomic risk factors that are often unmodifiable, metabolomics studies measure our metabolic state, determined not only by genomic factors but also modified by diet, environmental factors, and host factors such as the childhood experiences and gut microbiome. The metabolic profile serves as a quantifiable, dynamic readout of biochemical state that can inform underlying molecular mechanisms of the disorder or phenotype. As such, metabolomics data have higher relevance to the "disordered state" and may serve well as predictive, prognostic, diagnostic biomarkers [25] for psychiatric disorders. The remainder of this chapter provides a brief summary of the analytical techniques most commonly used in metabolomics studies, and reports on and discusses a selection of psychiatric metabolomics and lipidomic studies. In particular, it highlights a specific class of metabolites called eicosanoids and their unique role in unraveling how disorders are influenced by the interactive relationship between genes and diet [26].

## 10.4 Overview of Metabolomics Analytical Techniques and Methodologies

The likelihood of success for precision psychiatry lies in the accuracy and comprehensive dimensionality of the data. Analytical techniques for metabolomics have come a long way. Nuclear magnetic resonance (NMR), mass spectrometry (MS), and electrochemical detection are commonly used techniques to identify and quantify metabolites [27]. NMR is less sensitive than MS-based methods, yet it is favorable due to the absence of detection bias and is useful in identifying novel metabolite structures [28]. Compared to NMR, MS is superior in mass analysis capabilities and is usually used together with other separation instruments such as gas chromatography (GC), liquid chromatography (LC), or capillary electrophoresis (CE). GC and LC have traditionally been used in metabolomics studies; CE has gained popularity in recent years [27]. In clinical laboratories, liquid chromatographytandem mass spectrometry (LC-MS/MS) is known for high specificity and sensitivity [29]. LC-MS/MS can detect compounds with low molecular weight (such as eicosanoids) with better sensitivity, selectivity, and higher throughput than high performance liquid chromatography or GC-MS [29].

Equally as important as choosing the right instrument for metabolomics measurement are the design and analysis aspects of metabolomics. Metabolomics analysis methods can broadly be categorized in two ways. "Untargeted metabolomics" (global) analysis captures a wide array of detectable metabolites, including those with unknown functions or that have not been seen previously [30]. Untargeted metabolomics offers the unique advantage of discovering novel perturbations and detecting the relationship between interconnected metabolites from multiple pathways in an unbiased fashion [30]. In contrast, a "targeted metabolomics" approach focuses on a narrower, prespecified cluster of metabolites that have been hypothesized to play a role in the disorder studied. Internal standards allow for quantification of analytes in targeted metabolomics, offering better control of sensitivity, stability, and reproducibility of each targeted metabolite. Having some prior knowledge of these metabolites and biochemical pathways means associations identified in targeted analysis can move more quickly to other molecular or translational studies to further define mechanisms underlying the phenotype associations.

Recent advances in these complementary approaches have helped elucidate informative metabolomics biomarkers relevant in psychiatric disorders such as eicosanoids with inflammation regulatory functions. These biomarkers show promise for capturing early biochemical changes in the disease state [31] and enabling early diagnosis of psychiatric disorders. While analytical considerations for generating metabolomics data are beyond the scope of this chapter, it is important to note that metabolites are volatile, with a short half-life, making rigorous quality control of biological samples and assay preparation necessary to ensure validity of the findings.

## 10.5 Metabolomics Studies of Common Psychiatric Disorders

Using an untargeted metabolomics approach and proton NMR (1H-NMR) system, a serum metabolite profile was effective in separating schizophrenia from healthy controls [32]. Moreover, the results seem to reinforce the importance of the glycolysis pathway and a "hyperglutamate hypothesis" previously proposed [33] in schizophrenia. Examining both serum and urinary metabolites, 1H-NMR and gas chromatography with two-dimensional gas chromatography (GC-TOFMS) platforms revealed several pathways implicated in schizophrenia including fatty acid metabolism, carbohydrate metabolism, and amino acid metabolism [34].

Metabolic profiles of cerebrospinal fluid samples from drug-naïve (or minimally treated) first-onset schizophrenia and controls suggest brain-specific alterations in glucoregulatory processes were intrinsic to disease because these dysregulations normalized after treatment with atypical antipsychotic medications in half of schizophrenia patients [35]. Patients with schizophrenia and other psychiatric disorders often experience significant weight gain during their course of treatment [36]. Lipidomic and metabolomic analyses have identified lipids associated with medication-associated weight gain [37] and metabolic predictors of future weight gain [38]. These results emphasize the added usefulness of a metabolomics approach in identifying psychiatric patients at risk of developing metabolic comorbidities [38]. To begin to address the variability in treatment response commonly found in psychiatric disorders, serum metabolites were investigated in 8 schizophrenia patients before and after risperidone monotherapy together with healthy controls. Although the sample size was small, partial least squares discriminant analysis model derived from GC-MS spectra revealed clear separations not only between schizophrenia and controls, but also between risperidone responders and nonresponders [39]. These data suggest a global change of metabolites after risperidone treatment, and disturbances of energy metabolism, antioxidant defense systems, neurotransmitter metabolism, fatty acid biosynthesis, and phospholipid metabolism in schizophrenia, which could be partially normalized by risperidone therapy [39].

In major depressive disorder, at least 17 peripheral blood mononuclear cell -derived metabolites identified in the GC-MC platform were significantly altered when compared with controls, indicating disturbances of energy and neurotransmitter metabolism [40]. In a urinary metabolomics study, the NMR- and GC-MS– based methods identified two sets of metabolites that effectively discriminate "moderate" and "severe" patients from healthy controls, respectively [41]. These metabolites implicate involvement of gut microbial metabolites, glycine biosynthesis, and cell death and survival in MDD [41].

Depression is heterogeneous in its presentation and pathophysiology, affecting people of all ages, including those with medical diseases. Metabolomic analysis of plasma from older adults with and without depression revealed lower levels of several neurotransmitters and medium chain fatty acids in depression. Also, the profile of those with remission from depression was more similar to non-depressed controls than to the depressed individuals [42]. In a medical cohort of patients with heart failure with and without depression, GC-MS and LC-MS platforms revealed higher concentrations of several amino acids and dicarboxylic fatty acids [43], consistent with prior findings in neurotransmitter systems and fatty acid metabolism dysregulation. These results suggest that metabolomics biomarkers might be useful as objective diagnostic tests for depressive disorder. Based on findings in several untargeted metabolomics studies of depression and pharmacometabolomic studies [44, 45], a new study investigating whether these metabolites (sphingomyelins, lysophosphatidylcholines, phosphatidylcholines, and acylcarnitines) could act as predictors of depression recovery found that the addition of metabolites in all predictive models outperformed models without these metabolites [46].

In bipolar disorder, 1H-NMR-based analysis revealed lipids, lipid metabolism-related molecules, and some amino acids that distinguished bipolar subjects, with 7 specific markers as "key metabolites" [47]. A study using dual platform (NMR spectroscopy and GC-MS) revealed 5 urinary metabolite biomarkers with higher accuracy than single-platform derived markers in discriminating bipolar disorder from healthy controls [48]. In another study, an increased proportion of serum sphingolipids and glycerolipids and a decreased proportion of glycerophospholipids were found in bipolar disorder patients when UltraPerformance LC coupled with highresolution MS was used [49]. However, of the top 5 most differential lipids identified, 3 had unknown biology and could not be identified in any databases [49].

## 10.6 Polyunsaturated Fatty Acids in Psychiatric Disorders

While advances in mass spectrometry have expanded our knowledge of the patterns of metabolomic perturbation in psychiatric disorders, nongenetic risk factors such as diet play a major role in neuronal fitness [50–52]. Essential fatty acids represent a modifiable risk factor for neuropathophysiological processes [53, 54]. While a number of hypotheses exist for etiology of psychiatric disorders, inflammation has recently been shown to play a role in common mental disorders such as depression [55] and schizophrenia [56].

Bioactive lipid mediators are a class of underappreciated, under-utilized molecules in studies of inflammation. Specifically, the bioactive metabolites derived from fatty acids, termed eicosanoids, participate in modulation of inflammation [57, 58] and pain [59], and have been shown to affect risks of hypertension [60], cardiovascular diseases [61], cancer [62], anorexia nervosa [63], and schizophrenia [64]. To more comprehensively assess how dietary-based intervention [65] may affect inflammation and psychiatric outcomes [66-68], MS technology has been extended to lipidomics analysis for polyunsaturated fatty acids (PUFA) [69, 70]. These lipids include the 18-carbon "essential" PUFA such as linoleic acid (LA; 18:2n-6) and alpha-linolenic acid (ALA; 18:3n-3), 20-carbon PUFA arachidonic acid (ARA; 20:4n-6) and eicosapentaenoic acid (EPA; 20:5n-3), and 22-carbon PUFA such as docosapentaenoic acid (DPA; 22:5) and docosahexaenoic acid (DHA; 22:6n-3).

The clinical benefits observed when supplementing n-3 PUFA in inflammation-driven diseases were the initial clues that n-3 PUFA may similarly yield symptom relief in psychiatric disorders.

Rheumatoid arthritis patients who took n-3 fatty acids supplementation showed significant clinical benefits compared with those who did not receive n-3 supplementation [71]. Patients with colon cancer who received fish oil supplementation had a significant reduction in IL-6 and TNF-alpha levels and an increase in the percentages of CD3+ and CD+ lymphocytes when compared with the control group [72]. These data suggest that n-3 PUFA might also benefit symptoms in psychiatric disorders [73], which are now recognized as disorders of neuronal inflammation [74–76].

Peripheral levels of PUFA and n-6:n-3 PUFA ratios have been investigated in depressive disorder and bipolar disorder, the two most common mood disorders. The erythrocyte membrane ARA and DHA were significantly reduced in Taiwanese patients with bipolar disorder patients when compared with healthy controls, while no differences in total PUFAs were observed [77]. Similarly, in a sample of Italian patients with bipolar disorder, plasma DHA was significantly lower than that of healthy controls; however, EPA, AA, ALA, and ARA appeared to be elevated. Based on this result, the authors suggest that DHA may be a useful adjuvant for bipolar disorder [78].

To account for the competitive biology between the n-3 and n-6 classes of PUFA, another group analyzed a broad panel of serum lipids including PUFA in individuals with euthymic bipolar, depressive bipolar, major depressive disorder, and non-psychiatric controls. They found that higher AA:EPA and AA:EPA + DHA ratios were consistently found in the group with bipolar depression. Moreover, the AA:EPA + DHA ratio was positively correlated with depression severity in all groups, despite a lack of control on the fasting status of the subjects [79]. In another study, a high n-6:n-3 ratio and low DHA were found to be predictive of suicide risk among depressed patients [80], highlighting the potential prognostic role PUFA markers may play in depression. Lastly, several eloquent metaanalyses have examined evidence of the efficacy of treating depression or depressive symptoms with n-3 PUFA. Some took a conservative position, stating that the antidepressant efficacy of n-3 PUFAs in unipolar and bipolar depression cannot be confirmed until further replication with more "homogeneous" and larger samples [81]. Two independent meta-analyses reported n-3 PUFA supplementation, especially EPA, to be effective in treating major depression disorder and depressive symptoms [54, 82].

Schizophrenia is a serious psychiatric disorder that has been proposed as "neurodevelopmental" based on early subclinical brain imaging characteristics [83]. Decreased levels of AA and DHA were observed in never-medicated first-episode schizophrenia patients compared with medicated patients and healthy controls [84]. In another study using established schizophrenia cases and carefully selected matched controls, DHA, DPA, and DHA:ARA ratio were reduced in patients compared to controls [85].

For another psychiatric disorder, anorexia nervosa, we found the ARA: EPA ratio to be lowered in anorexia nervosa compared with healthy controls [63]. To determine if PUFA levels were "risk factors" or "consequences" of schizophrenia, ultra-high risk individuals (for developing schizophrenia) were followed and dietary intake was assessed. Those who later developed psychosis were found to consume more dietary n-6 PUFAs (LA, AA) and had higher AA:EPA + DHA ratios than those who did not develop psychosis [86]. Similarly, n-3 PUFA supplementation was associated with beneficial effects for anorexia nervosa in several studies [87, 88]. Together, these data support a possible protective role n-3 PUFAs play in preventing onset or worsening of psychotic symptoms. Several mechanisms have been proposed to explain n-3 PUFAs' favorable effect in psychiatric disorders, including antineuronal inflammation [89] and neuronal protection [90].

Although the data in psychiatric literature largely paint a favorable view for supplementation of n-3 PUFA, the verdict on the supplements' therapeutic role in psychiatric disorders cannot be established without randomized clinical trials with well-characterized longitudinal data and large sample size. While many independent studies in the past have supported the benefits of n-3 PUFAs for serious medical disorders such as cardiovascular disease and cancer, the most recent meta-analysis showed that n-3 fatty acids did not reduce the incidence of cancer and cardiovascular events (e.g., stroke, myocardial infarction, and cardiovascular event-related death) [91]. In a large randomized trial including 15,480 diabetic patients without cardiovascular disease, no significant difference was found in the risk of serious vascular events between those who were assigned to n-3 PUFA supplementation and those who were assigned to a placebo [92]. It is thus imperative to conduct further research not only to confirm the effectiveness of n-3 PUFAs in psychiatric disorders but also to explore molecular mechanisms driving clinical benefits in patients and develop biomarkers to classify individuals with high likelihood of benefiting from PUFA supplementation. To achieve these goals, the logical next step is to take advantage of targeted metabolomics technology to focus on a specific class of metabolites, termed eicosanoids [93, 94].

## 10.7 Eicosanoids as Biomarkers for Psychiatric Disorders

While the pattern of association between PUFA and psychiatric disorders may at first seem straightforward, one must understand the functions and mechanisms underlying beneficial effects of any compound to use such benefits clinically. The bioactive lipids family represents the next logical class of molecules to study to elucidate PUFA mechanisms, and to establish a biomarker system that is biologically and clinically informative to guide precision psychiatry.

Major n-6 and n-3 PUFA can be oxygenated by at least 3 different enzymes to synthesize over 120 heterogeneous and pleiotropic bioactive molecules termed eicosanoids [59, 95]. While the word eicosanoid was derived from the Greek word "eikosa," meaning "20," based on the derivatives of the 20-carbon ARA, here "eicosanoid" is applied to also include the oxygenated products of other PUFA including LA, ALA, DHA, and DPA. The 3 enzymatic families that affect PUFA are cyclooxygenases 1 and 2 (COX-1/2); 5-, 12-, and 15-lypooxygenases (5/12/15-LOX); and P450 epoxygenase. The COX-1/2 are known to drive the synthesis of prostanoids such as prostaglandins and thromboxanes, while 5/12/15-LOX produce leukotrienes, lipoxins, and hydroxyeicosatetraenoids, and P450 synthesize HETEs and epoxyeicosatrienoids [95]. The eicosanoids most well-studied for their link to inflammation biology include prostaglandin E2 (PGE<sub>2</sub>), a pro-inflammatory molecule stimulated by COX, and 5-LOX-produced leukotrienes, which contribute to potent inflammation in asthma and other allergic diseases [96]. CYP regulates inflammation by oxidizing ARA with its active heme iron to form anti-inflammatory HETE or epoxy-eicosatrienoic acid (EETs), which is then hydrolyzed into pro-inflammatory dihydroxyeicosatrienoic acids (DHET) by soluble epoxide hydrolase (sEH) [97].

We have demonstrated the effectiveness of a combined use of lipidomics and targeted metabolomics in investigating anorexia nervosa, an illness characterized by rapid weight loss and reduction in food consumption [63]. Higher ratios of dihydroxy to epoxy fatty acids were found in anorexia nervosa patients than in controls, suggesting an upregulation of sEH activity, an elevation in pro-inflammatory eicosanoid profile, and a reduction in anti-inflammatory epoxy fatty acids [63]. Additionally, recovered anorexia nervosa patients showed a partial normalization in PUFA and eicosanoids, implying the resolution of inflammation and that it may be achieved by dietary intervention [26]. This is clinically relevant as well for patients with other types of psychiatric disorders because medication non-adherence rate is notoriously high, up to 80% in schizophrenia [98]. Dietary intervention may be an important alternative treatment modality for patients refusing medications.

The results of the anorexia nervosa study suggest that psychopathology and inflammatory processes in eating disorders are affected by interactions between dietary PUFA and genetically driven metabolism. With additional empirical research, food-based treatment or a nutraceutical strategy may be employed to improve outcomes in clinical psychiatry. Furthermore, as eicosanoid variation reflects *in vivo* cellular inflammation, targeted metabolomics can be applied to develop improved prognosis biomarkers.

Untargeted metabolomics emerged as a useful tool to uncover unsuspected pathways involved in psychiatric disorders, and a targeted metabolomics approach is particularly helpful in characterizing the specificity, direction and magnitude of disease-associated metabolites, which provide molecular insight helpful to develop new treatments. In a pilot study of adolescent major depressive disorder, we characterized eicosanoids in fasting plasma at the baseline visit and final visit after a 2 year follow-up period. While all subjects displayed no difference in depression severity or profile of depression risk factors at the baseline visit, half of the subjects had progressed to significantly worse depression (refractory group) while the other half remitted. Strikingly, the eicosanoids profile in the refractory group revealed a pattern very similar to that found in patients with anorexia nervosa [99], implicating an epoxy fatty acid catalyzing enzyme, soluble epoxide hydrolase (sEH), as a common risk factor for depression and anorexia nervosa.In a study of seasonal major depression [31], quantitative changes of CYP450 pathway eicosanoids during the winter season (when subjects experienced severe depression symptoms) were similar in pattern to the eicosanoids profile we found in the refractory adolescent depression group [99], suggesting that sEH-mediated metabolism of PUFA eicosanoids underlies the psychopathology of depressive disorders [31].

sEH is known as a regulator of inflammatory resolution due to its potent and complex mechanisms in the formation/catabolism of epoxy- and diol eicosanoids [100], but its involvement with psychiatric phenotypes was only recently uncovered through MS-based discovery [31, 99] and sequencing [101]. Another group has since demonstrated that sEH inhibition showed antidepressant effects in both inflammation and social defeat stress models of depression [102] and attenuated behavioral abnormalities (i.e., hyperlocomotion and prepulse inhibition deficits) in an animal model of schizophrenia [103]. Moreover, a higher level of sEH was found in postmortem brain samples from patients with depression, schizophrenia, and bipolar disorder compared with control samples [102], strengthening the role sEH plays in psychiatric pathology.

The discovery of an association between cytochrome P450-associated bioactive lipid mediators and psychiatric disorders is made possible in part because of advances in technology, but the involvement of eicosanoids in psychiatric disorders was reported as early as the 1980s. Using low throughput techniques such as radioimmunoassay, elevated levels of PGE and PGE2 were identified in schizophrenia [104, 105], whereas PGD2, PGE2, and PGF2 $\alpha$  and TXB2 were found to be elevated in major depressive disorder [106– 109]. Almost 40 years later, the field can now take advantage of both untargeted and targeted liquid chromatography-mass spectrometry-based methods to monitor a much larger number of potential markers. A recent schizophrenia study that investigated 158 markers including PUFA, eicosanoids, and related mediators from enzymedependent or independent pathways uncovered 23 metabolites that were significantly altered in patients compared with healthy controls [64]. While some abnormal markers were reversed antipsychotic treatment, anandamide, after oleoylethanolamine, and ARA were identified as having the best potential for differentiating patients from controls [64].

Leveraging what is already known about the biology of bioactive lipids and the plethora of physiological and homeostatic processes they participate in, several drugs have already been developed to inhibit the production of proinflammatory mediators, including nonsteroidal anti-inflammatory drugs (NSAIDS) that reduce the activity of both COX-1 and COX-2 [110], cysteinyl leukotriene (cysLT) receptor antagonists that reduce bronchoconstriction caused by cycLT and pro-inflammatory cytokines in the pulmonary system [111], and COX-2 inhibitors [112]. In fact, administration of COX-2 inhibitor celecoxib has been shown to improve symptoms in schizophrenia [113], possibly through inhibiting conversion of ARA into prostanoids. Additionally, COX-2 inhibitors may be effective as an adjunctive treatment by accelerating the onset of antidepressant effects for bipolar depression and refractory major depression [114, 115].

## **10.8 Conclusions**

While an untargeted metabolomics strategy has gained popularity for its ability to screen new and unsuspected pathways involved in psychiatric disorders, evidence of a role for eicosanoids in psychiatry is accumulating. Eicosanoids participate in the modulation of inflammatory processes and affect the risk of a number of neuropsychiatric disorders. Characterizing the eicosanoid signature in major psychiatric disorders and subtypes within can lay the foundation for individualized treatment approaches. Much work is needed to develop psychiatric multi-omics biomarkers that would not only predict risk, but could also offer an individual-specific course of disorder and responses to therapeutics. For example, studies identifying metabolomic changes during the course of psychiatric disorders are lacking. Additionally, almost all studies used biospecimens taken from blood or urine and not from the organ of disease origin, the brain. This limits researchers' ability to identify brain regionspecific metabolite changes and mechanisms in human samples. Follow-up studies using model animals are critical to further research metabolome read-out and neuronal mechanisms to better define pathophysiology of psychiatric disorders. That being said, when coupled with other omics strategies, metabolomics provides a platform for clarifying the relationship among host factors (e.g., genetic variation), substrates (e.g., dietary profile), and downstream metabolomic perturbation and implicated biology. The end knowledge will improve the clinical utility of a multi-omics biomarker system on diagnostic, prognostic, and therapeutic fronts.

While emerging data already indicate beneficial effects of pharmacological agents such as COX-2 and sEH inhibitors, another unique characteristic of eicosanoids is that their substrate availability required for synthesis can be altered by dietary intake or supplementation of PUFA. This opens the door for development of a nutraceutical approach in psychiatric therapeutics. Although there are still many challenges to be addressed and further studies are required to elucidate the complex role of eicosanoids in the psychopathology of psychiatric disorders, metabolomics coupled with other multi-omics approaches can (1) provide deeper insights into the biological underpinnings of psychiatric disorders, (2) be used as powerful diagnostic, diseasemonitoring, and treatment response biomarkers, and (3) bring precision psychiatry closer to reality by enabling improved drug discovery and development processes, thereby advancing pharmacometabolomics, nutrigenomics, and metabolomic engineering technologies.

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11

# Cytochrome P450 Eicosanoid Signaling Pathway in Colorectal Tumorigenesis

Weicang Wang, Katherine Z. Sanidad, and Guodong Zhang

#### Abstract

Colorectal cancer (CRC) is the third most common cancer and the second leading cause of cancer-related death in the United States. It is important to discover novel cellular targets which are crucial in the pathogenesis of CRC, which could facilitate development of mechanism-based strategies to reduce the risks of CRC. Emerging studies support that the cytochrome P450 (CYP) monooxygenase/ soluble epoxide hydrolase (sEH) pathway and their eicosanoid metabolites play critical roles in colonic inflammation and CRC, and could be therapeutically explored for treating or preventing CRC. Here in this review, we discuss recent studies about the roles of the CYP/sEH eicosanoid pathway in the pathogenesis of colonic inflammation and CRC.

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#### Keywords

Colorectal cancer · Colonic inflammation · Cytochrome P450 · Soluble epoxide hydrolase · Eicosanoids

## 11.1 Introduction

Colorectal cancer (CRC) is a serious health problem: there were ~140,250 new cases and ~50,630 deaths in the United States in 2018 [1], emphasizing the need for discovering novel cellular targets which are crucial in the pathogenesis of CRC. Colonic inflammation is a major risk factor for developing CRC, therefore, targeting the pathological components involved in colonic inflammation is a promising strategy to reduce the risks of CRC [2]. Eicosanoids, which are endogenous lipid signaling molecules produced from enzymatic metabolism of polyunsaturated fatty acids (PUFAs), play essential roles in inflammatory responses and were recently implicated in cancer [3, 4]. The most prominent CRCassociated eicosanoids are prostaglandins, which are produced by the cyclooxygenase-2 (COX-2) enzyme that is overexpressed in most human CRC samples [4]. Genetic knockout of Cox-2 reduces polyp formation in azoxymethane (AOM)- or Apc mutation-induced CRC models [5, 6]. Furthermore, clinical and epidemiological

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studies support that pharmacological inhibitors of COX-2, such as nonsteroidal anti-inflammatory drugs (NSAIDs), are effective in reducing the risk of CRC [4]. These results support the critical importance of eicosanoid signaling in CRC. However, the gastrointestinal and cardiovascular toxicities induced by the COX-2 inhibitors have limited their clinical applications [7]. Besides COX-2, the roles of other eicosanoid pathways in colonic inflammation and CRC are not well understood [8]. It is therefore important to discover novel eicosanoid signaling pathways involved in the pathogenesis of CRC.

Besides being substrates of COX-2, PUFAs are also substrates of cytochrome P450 (CYP) monooxygenases (predominately the CYP2C and CYP2J isoforms), which convert them to epoxygenated fatty acids (EpFAs). EpFAs include epoxyeicosatrienoic acids (EETs) produced from arachidonic acid (ARA,  $20:4\omega-6),$ epoxyoctadecenoic acids (EpOMEs) from linoleic acid (LA, 18:2ω-6), epoxyoctadecadienoic acids (EpODEs) from  $\alpha$ -linolenic acid (ALA,  $18:3\omega$ -3), and epoxydocosapentaenoic acids (EDPs) from docosahexaenoic acid (DHA, 22:6 $\omega$ -3) [9]. EpFAs are metabolically unstable with a half-life of several seconds in vivo, in part because they could be rapidly metabolized by soluble epoxide hydrolase (sEH) to generate the corresponding fatty acid diols [10]. Currently, the CYP/sEH eicosanoid pathway is being explored by academic laboratories and pharmaceutical companies for clinical applications. For example, GlaxoSmithKline is conducting human clinical trials to test an sEH inhibitor GSK2256294; the company has found that this drug candidate is well-tolerated and causes sustained inhibition of sEH in humans [11]. Other novel classes of sEH inhibitors are also being considered for human trials [12]. In addition, recent studies have shown that some FDA-approved drugs are potent inhibitors of CYP monooxygenases [13].

Emerging research supports that the CYP/sEH pathway plays critical roles in regulating inflammation, angiogenesis, tumor growth, and tumor metastasis [14–17], and could be involved in the pathogenesis of colonic inflammation and CRC [18–21]. A better understanding of the roles of

this previously unappreciated pathway in the pathogenesis of CRC could help to develop new strategies for cancer treatment or prevention. In this review, we will discuss the roles of the CYP/ sEH eicosanoid pathway in the pathogenesis of colonic inflammation and CRC, as well as obesity-associated colonic inflammation and CRC.

## 11.2 Expression of CYP Monooxygenases and sEH in Colonic Inflammation and CRC

Our recent study has shown that CYP monooxygenases are overexpressed in colon tumor tissues and colon cancer cells [21]. Compared with control healthy mice, the expressions of mouse CYP monooxygenases, such as Cyp2c38, Cyp2c39, Cyp2c55, Cyp2c65, Cyp2c70, Cyp2j6, Cyp2j9, and Cyp2j13, are increased in colon tissues of AOM/dextran sulfate sodium (DSS)-induced CRC mice [21]. In addition, the concentrations of CYP-produced EpFAs are increased in both the plasma and colon tissues of AOM/DSS-induced CRC mice [21]. Furthermore, we find that compared with normal human colon cells (CCD-18co), the expression of CYP2C8, CYP2C9, CYP2C19, and CYP2J2 is increased in human CRC cells (HCT116 and Caco-2) [21]. These results support that the CYP monooxygenase pathway is upregulated in mouse and cell culture models.

The expressions of CYP monooxygenases in human CRC are more complicated. We analyzed gene expression of CYP monooxygenases (CYP2C8, CYP2C9, CYP2C19, and CYP2J2) in the Cancer Genome Atlas (TCGA) database, and found that their expressions were not increased in colorectal adenocarcinoma [21]. However, we must note that the expression and activity of the CYP enzymes are regulated by multiple mechanisms, including transcription, translation, and post-translational modification, not only the mRNA expression levels [22]. Indeed, Enayetallah et al. report that CYP2C9 is detected in 13 out of 17 human colon tumor samples,

while it is not detected in matched benign samples [23]. In addition to CRC, previous studies have shown that CYP monooxygenases are overexpressed in other tumor tissues, such as breast, liver, and stomach tumors [16, 23]. There could be many mechanisms by which CYP monooxygenases are overexpressed in tumor tissues. The expression of CYP monooxygenases has been shown to be elevated by hypoxia [10], which is a common feature of tumor tissues [24]. It is feasible that the hypoxic tumor microenvironment could contribute to the increased expression of CYP monooxygenases in tumor tissues.

In humans, the expression of sEH is increased in colonic dysplasia and adenocarcinomas in ulcerative colitis (UC) patients [18]. sEH has been detected in ~40% of human colon adenocarcinomas (7 out of 17 samples) with relatively high expression levels, but is not detected in matched benign samples (0 out of 4 samples) [23]. More studies are needed to characterize the expression of sEH and the concentrations of CYP/sEH-produced eicosanoid metabolites in colonic inflammation and CRC.

## 11.3 Roles of CYP/sEH Eicosanoid Pathway in Colonic Inflammation and CRC

Recent research has shown that sEH plays a critical role in colonic inflammation and CRC. In the DSS-induced mouse model, sEH<sup>-/-</sup> mice have reduced colonic inflammation (as assessed by mucosal erosion and lymphoplasmocytosis) and carcinogenesis (tumor incidence and volume) compared with wild-type mice [18]. Similarly, in an interleukin 10 (IL-10) deficiency-induced CRC model, sEH<sup>-/-</sup> IL-10<sup>-/-</sup> mice have reduced colonic expression of pro-inflammatory cytokines and formation of ulcers and carcinomas compared with sEH<sup>+/+</sup> IL-10<sup>-/-</sup> mice [19, 20]. Together, these results support that sEH could colonic contribute to inflammation and inflammation-associated CRC. This is largely in agreement with previous studies which show that inhibition of sEH reduces inflammatory responses in various disease models. For example, in obese mice, pharmacological inhibition of sEH reduces the infiltration of macrophages and expression of pro-inflammatory cytokines in epididymal fat and liver [25, 26]. Deletion of sEH also leads to reduced infiltration of neutrophils, decreased levels of pro-inflammatory cytokines and less neuronal damage in an intracerebral hemorrhage mouse model [27]. Together, these studies demonstrate sEH is involved in many inflammationassociated diseases.

More studies are needed to better characterize the roles of sEH in cancer. Panigrahy et al. have shown that pharmacological inhibition or genetic deletion of sEH increases tumor growth and metastasis in xenograft models by stimulating tumor angiogenesis [15]. However, this finding is different from the results observed in the DSS and IL-10<sup>-/-</sup> mouse models [18-20]. The different results could be, at least in part, due to the differences in mouse models. The phenotypes in the DSS and IL-10<sup>-/-</sup> mouse models are strongly associated with inflammation, therefore, inhibition of sEH would reduce inflammatory response and attenuate inflammation-associated CRC [18-20]. In other models such as xenograft models, inhibition of sEH could upregulate angiogenesis and increase tumorigenesis [15]. However, the pro-angiogenic effects of sEH inhibition were mainly observed in mouse models [15]. A recent human clinical trial has shown that even at 100% inhibition of sEH, there is no change of the plasma concentration of vascular endothelial growth factor (VEGF), which is an important biomarker of angiogenesis [11]. Since sEH inhibitors are currently being evaluated in human clinical trials [11, 12], it is of critical importance to better understand the roles of sEH and sEH inhibitors in tumorigenesis.

Recent studies also support the critical roles of CYP monooxygenases in tumorigenesis. In a xenograft tumor model, overexpression of human CYP2C8 or CYP2J2 in endothelial cells led to increased xenograft tumor growth of B16F10 melanoma and T241 fibrosarcoma [15]. Using a Lewis lung carcinoma (LLC) resection-induced tumor metastasis model, endothelial expression of human CYP2C8 or CYP2J2 increases lung metastases [15]. Together, these results support the pro-tumorigenic and pro-metastatic effect of CYP monooxygenases.

Our recent studies also support a potential role of CYP monooxygenases in the tumorigenesis of CRC [21]. Compared with AOM/DSS-induced  $Cyp2c^{+/+}$  mice, the AOM/DSS-induced  $Cyp2c^{+/-}$ mice have lower tumor numbers and total tumor burden, as well as reduced expression of CYP monooxygenases and concentrations of CYPderived fatty acid epoxides in colon tissues, supporting the roles of Cyp2c monooxygenases in colon tumorigenesis [21]. Consistent with the results observed in transgenic mouse models, we also find that pharmacological inhibition of CYP monooxygenases suppresses AOM/DSS-induced colon tumorigenesis in mice [21]. Together, these results support that CYP monooxygenases contribute to the tumorigenesis of CRC.

## 11.4 Effects of CYP-Produced Eicosanoids on Inflammation and CRC

The metabolism of PUFAs by CYP monooxygenases leads to the formation of EpFAs [9]. The major EpFAs in tissues and plasma include EpOMEs produced from LA, EETs from ARA, and EDPs from DHA. Emerging research supports that these eicosanoid metabolites have potent effects on inflammation and tumorigenesis with the details discussed below.

Previous studies show that EpOMEs have a series of detrimental actions such as inducing chemotaxis, inflammation, cardiovascular diseases, and pulmonary injury [28–33]. In human studies, EpOMEs, which are termed "leukotoxins," are associated with multiple organ failures and adult respiratory distress syndrome in severe burn patients [29, 31, 34]. Notably, at a concentration as low as 10 nM, EpOMEs enhance neutrophil chemotaxis, suggesting potent pro-inflammatory effects of EpOMEs [33]. Regarding CRC, our recent study shows that treatment with 12,13-EpOME exaggerates AOM/ DSS-induced CRC in mice [21], supporting the pro-CRC actions of EpOMEs. EpOMEs can be further metabolized by sEH to form the corresponding fatty acid diols termed dihydroxyoctadecenoic acids (DiHOMEs) [10]. Similar to EpOMEs, DiHOMEs have also been shown to induce chemotaxis, tissue injury, and cause mortality in animal models [34, 35].

The biological actions of EETs are more complicated, as they have been shown to have anti-inflammatory effects (negatively associated with tumorigenesis) and pro-angiogenic effects (positively associated with tumorigenesis). Indeed, many studies have shown that EETs have potent anti-inflammatory effects. In a murine carotid artery model, treatment with 11,12-EET decreases tumor necrosis factor- $\alpha$  $(TNF-\alpha)$ -induced mononuclear cell adhesion to the arterial endothelium [36]. Treatment with 14,15-EET inhibits TNF-induced degradation of I $\kappa$ B $\alpha$  in primary human lung tissue [37] and reduces LPS-activated IL-1β and TNF-α expression in mouse macrophages [18]. Together, these results support the anti-inflammatory effects of EETs. The effects of EETs on tumor inflammation are not well characterized and require more studies. Previous studies have shown that inhibition or deletion of sEH attenuates DSS- or IL-10 knockout-induced CRC [18-20]; these results could be, at least in part, due to the anti-inflammatory effects of EETs. On the other hand, EETs have pro-angiogenic effects, and therefore could promote tumor growth and metastasis. In an orthotopic cancer model, treatment of 14,15-EET at a dose as low as 15 µg/kg/ day increases orthotopic PC3M-LN4 prostate tumor growth in SCID mice [15]. In transgenic adenocarcinoma of the mouse prostate (TRAMP) mice, administration of 14,15-EET at a dose of 15 µg/kg/day promotes prostate tumor growth, suggesting that EETs increase tumor growth in vivo [15]. In addition, treatment with 14,15-EET increases tumor metastasis in a LLC resection model [15]. More studies are needed to further characterize the role of EETs in tumorigenesis.

Opposite to the effects of EpOMEs and EETs, our studies have shown that  $\omega$ -3 PUFA-produced EDPs inhibit angiogenesis, tumor growth, and

tumor metastasis [38]. 19,20-EDP inhibits tube formation, migration, and production of matrix metalloproteinases (MMPs) in endothelial cells, and suppresses VEGF- and basic fibroblast growth factor (bFGF)-induced angiogenesis in a Matrigel plug assay in mice, demonstrating its anti-angiogenic effect [38]. Treatment with stabilized 19,20-EDP also suppresses primary tumor growth and tumor metastasis in mice [38].

Furthermore, our recent study showed that treatment with EDPs suppresses growth of MC38 xenograft colon tumors, supporting the anti-CRC effects of EDPs [39]. Consistent with our results, a recent study by Yanai et al. has shown that systematic treatment with EDPs inhibits pathological angiogenesis in a mouse model of macular degeneration [14].

To date, the molecular mechanisms for the biological actions of EpFAs are not well understood. Many eicosanoids act by binding to specific cellular targets. For example, COX-2produced prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) and lipoxygenase (LOX)-produced leukotriene  $B_4$  (LTB<sub>4</sub>) act by binding to their G-protein coupled receptors [40]. The direct cellular target(s) of CYP monooxygenase metabolites are not well understood, hampering our understanding of their mechanisms of action. Previous studies show that EETs bind to cell membrane-bound proteins in a high-affinity, specific, and saturable manner [41– 43], and some of the biological actions of EETs are G protein-dependent [43-46]. These results support that the CYP monooxygenase metabolites also act via interactions with specific cellular proteins; however, the identities of the cellular targets are not well understood. Beyond EETs, no study has investigated the cellular targets of other CYP monooxygenase metabolites (such as EpOMEs). Identification of their direct cellular targets could greatly enhance our understanding for the molecular mechanisms of the CYP monooxygenase pathway. In addition, the identified cellular targets could also serve as novel molecular targets for preventing or treating cancer and other human diseases.

Besides the EpFAs, their down-stream metabolites, termed fatty acid diols, have also

been shown to be biologically active and could contribute to the biological actions of CYP monooxygenases and sEH. Recent studies have that dihydroxyeicosatrienoic shown acids (DHETs), which are metabolites of EETs produced by sEH, have pro-inflammatory effects [10, 47]. Treatment of 5,6-DHET, 8,9-DHET, 11,12-DHET, or 14,15-DHET at a dose of 3 µM stimulates primary human monocyte migration *in vitro* [50]. Similar to the pro-inflammatory effects of ARA-produced DHETs, recent studies show the DHA-produced dihydroxydocosapentaenoic acids (DHDPs) promote progression of retinopathy in mice [48, 49]. Treatment of 19,20-DHDP induces retinal angiogenesis by increasing tip cell, sprouting, and filopodia numbers in mice, all of which contributes to proliferative retinopathy [48]. Moreover, in an ex vivo whole mount retina model, treatment with 19,20-DHDP increases vascular endothelial cell permeability and pericyte migration into extravascular space, both of which are disease markers for diabetic retinopathy [49]. In cultured murine brain microvascular endothelial cells, treatment of 19,20-DHDP decreases junction formation between cells and reduces expression of N-cadherin, which could contribute to effect of 19,20-DHDP on vascular permeability during diabetic retinopathy [49]. Overall, these studies demonstrate that fatty acid diols are bioactive eicosanoids which could contribute to the pathogenesis of many diseases.

Together, these results support that CYPproduced eicosanoid metabolites, including EpOMEs, EETs, and EDPs, have potent effects on tumorigenesis. These results could help to establish a novel mechanistic linkage between fatty acid intake and cancer risks. For example, animal experiments have shown that a high dietary intake of LA increases AOM-induced colon tumorigenesis, suggesting its potential adverse effect on CRC [50–54]. Here our study about the promoting effects of LA-produced EpOMEs on CRC suggests that the formation of EpOMEs could contribute to the promoting effects of LA on the risks of CRC [21].

# 11.5 Roles of CYP/sEH Eicosanoid Pathway in Obesity-Induced Colonic Inflammation

More than one-third of US adults (34.9% or 78.6 million) are obese [55], and obese individuals have a 30-60% higher risk of developing CRC [56, 57]. Considering the obesity epidemic and the potential lethal consequence of CRC, obesity-enhanced CRC is a serious health problem in the US. However, the mechanism by which obesity increases the risks of CRC is not well understood, and there are few effective strategies to prevent obesity-enhanced CRC [58]. Using LC-MS/MS-based metabolomics, our recent research suggests that sEH could be a novel therapeutic target of obesity-induced colonic inflammation [59]. In a high fat diet (HFD)-induced obesity model in C57BL/6 mice, we find that the expression of sEH and the concentrations of sEH-produced fatty acid diols are significantly increased in the colon tissues of HFD-induced obese mice [59]. Furthermore, pharmacological inhibition or genetic ablation of sEH abolishes HFD-induced colonic inflammation in mice, with reduced expression of proinflammatory cytokines (*Il-1* $\beta$  and *Tnf-* $\alpha$ ) and/or decreased infiltration of immune cells in colon tissues [59]. Furthermore, we find that the inhibition or ablation of sEH attenuates HFD-induced activation of Wnt signaling pathway in colon tissues [59].

Considering the critical roles of colonic inflammation and Wnt signaling in the pathogenesis of CRC, these results support that sEH could be a potential therapeutic target of obesityenhanced CRC. This notion is supported by previous studies, which show that inhibition of sEH has beneficial effects on colonic inflammation, CRC, and obesity, supporting that targeting sEH is a promising strategy to reduce the risks of obesity-enhanced CRC. Previous studies have shown that: [1] compared with normal colon tissues, the expression of sEH is increased in human CRC samples [18, 23]; [2] pharmacological inhibition or genetic ablation of sEH attenuates colonic inflammation and CRC [18–20]; and [3] sEH is overexpressed in the liver and adipose tissues of obese mice [60, 61]. In addition, pharmacological inhibition or genetic ablation of sEH attenuated various adverse consequences of obesity, including endoplasmic reticulum stress, metabolic syndrome, fatty liver, hepatic steatosis, inflammation, endothelial dysfunction, and diabetes [25, 26, 60, 62–68]. Together, these results support that targeting sEH could be a promising strategy to reduce the risks of CRC in obese individuals. Further studies are needed to characterize the roles of sEH in obesity-enhanced CRC.

In our studies, we find that the colonic expressions of CYP2C and CYP2J monooxygenases are not altered in HFD-treated mice [59]. However, considering that the fatty acid diols are down-stream metabolites of CYP monooxygenases, it is feasible that inhibition of CYP monooxygenases could also reduce obesity-induced colonic inflammation and associated tumorigenesis. Targeting CYP monooxygenases could be an alternative approach to reduce the risks of obesity-enhanced CRC. This approach could minimize potential adverse effects of sEH inhibition on angiogenesis [15], and further studies are needed to better characterize the roles of the CYP/sEH eicosanoid pathway in obesityenhanced CRC.

## 11.6 Conclusion

CRC is the third most common cancer and the second leading cause of cancer-related death in the US [1], emphasizing the need for discovery of novel cellular targets which are crucial in the pathogenesis of colon cancer. Recent research by us and others support that CYP monooxygenases, sEH, and associated eicosanoid metabolites (EpFAs and fatty acid diols) play critical roles in regulating angiogenesis, tumor growth, and tumor metastasis [14–17], and could be involved in the pathogenesis of colonic inflammation and CRC [18–21] (Fig. 11.1). Currently pharmaceutical companies and academic laboratories are targeting the CYP/sEH eicosanoid pathway to develop therapeutic drugs. Further understanding about the roles of the CYP/sEH eicosanoid pathway in colonic inflammation and CRC could facilitate



the development of novel therapeutic strategies in the prevention or treatment of CRC. In addition, our research supports that the omega-6-series EpFAs (e.g. EpOMEs) are associated with increased inflammation and CRC [21], while the omega-3-series EpFAs (e.g. EDPs) are associated with decreased CRC [39] (Fig. 11.1), providing a potential mechanism-based nutritional strategy to reduce the risks of CRC.

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Contributions of 12/15-Lipoxygenase to Bleeding in the Brain Following Ischemic Stroke

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## Abstract

Ischemic strokes are caused by one or more blood clots that typically obstruct one of the major arteries in the brain, but frequently also result in leakage of the blood-brain barrier and subsequent hemorrhage. While it has long been known that the enzyme 12/15-lipoxygenase (12/15-LOX) is upregulated following ischemic strokes and contributes to neuronal cell death, recent research has shown an additional major role for 12/15-LOX in causing this hemorrhagic transformation. These findings have important

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implications for the use of 12/15-LOX inhibitors in the treatment of stroke.

## Keywords

Lipoxygenase · Eicosanoid · 12-HETE · 15-HETE · Ischemic stroke · Hemorrhage · Hemorrhagic transformation · Ischemia · Blood-brain barrier · Tissue plasminogen activator · tPA · Neuroprotection · Warfarin · STAT6

Strokes are typically classified into two major subtypes. Of these, ischemic strokes caused by blockage of a major artery account for around 85% of cases, while the remainder are caused by hemorrhage which can be either intracerebral or subarachnoid, depending on the location of the vessel rupture. However, even among the ischemic strokes a substantial number go on to include subsequent bleeding, leading to increased brain injury. This hemorrhagic transformation frequently occurs when tissue plasminogen activator (tPA) is used to lyse the obstructive blood clot, contributing to catastrophically low usage of this potentially lifesaving therapy - only a minor percentage of ischemic stroke patients receive thrombolytic treatment. Mechanisms involving the enzyme 12/15-lipoxygenase (12/15-LOX) contribute to the hemorrhagic transformation of

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ischemic strokes both in the presence and absence of tPA, as will be discussed in this mini-review.

The liberation of polyunsaturated fatty acids including arachidonic acid in the brain following a stroke has been recognized since the early 1970s [1]. These give rise to a dizzying spectrum of eicosanoids and related compounds produced by lipoxygenases, cyclooxygenases, and cytochromes P450, including prostaglandins, leukotrienes, and hydroxyeicosatetraenoic acids (HETEs). Increased levels of 12-HETE were found along with leukotrienes C4 and D4 in gerbil brains following an experimental stroke [2]. We have similarly seen massively increased levels of 12-HETE specifically on the infarcted side of the brain in mice both 12 and 24 h after onset of ischemia (Fig. 12.1). Therapeutically, initially 5-LOX was seen as the most promising target, mostly due to a much better understanding of leukotriene biology compared to the much less studied 12/15-LOX. However, two independent findings changed this perception: In 2004, a Japanese study found that Alox5 knockout mice developed the same level of ischemic injury following experimental stroke as matched wild type mice [3]. Around the same time, the group of Chandan Sen at Ohio State University [4] and our group [5, 6] found that Alox15 knockout mice were protected against the consequences of an experimental stroke, developing smaller

infarct sizes (Sen group 90% reduction 72 h after stroke onset, van Leyen group 40% infarct size reduction measured 24 h after initiation of experimental stroke). Moreover, subsequent studies from our lab found that the mRNA encoding 12/15-LOX was up-regulated 2.2 fold in mice 24 h after an experimental stroke [7]. Immunohistochemistry showed the increased 12/15-LOX signal both in neurons, and in endothelial cells [8]. Early work focused on injury to neurons, initially with the discovery that 12/15-LOX contributes to a form of cell death termed oxidative glutamate toxicity or oxytosis in neuronal cells [9]. More recently, a related redox pathway termed ferroptosis was introduced, which is characterized by the loss of glutathione peroxidase 4 (Gpx-4) activity [10] and in which 12/15-LOX is also involved. The commonalities and differences between these two pathways have yet to be clearly defined [10-12]. Glutathione as the major intracellular antioxidant in neurons is clearly important for both pathways, and glutathione levels also drop on the ischemic side of the brain following stroke, which presumably contributes to the activation of 12/15-LOX. The function of 12/15-LOX in this neuronal cell death pathway is to damage mitochondria and other organelles, for which the 12/15-LOX is uniquely qualified: in stress reticulocytes produced during severe anemia, as well as when



**Fig. 12.1** (a) 12-HETE was significantly increased in the infarcted ipsilateral hemisphere of mice both 12 and 24 hours after transient focal ischemia, compared to sham-operated mice (\*p < 0.05, \*\*\*p < 0.001; sham, n = 6 brains; 12 h, n = 3 brains; 24 h, n = 5 brains). (b) The

identity of 12-HETE was confirmed by high-performance liquid chromatography (HPLC)/mass spectrometry analysis. The smaller peak for 15-HETE in the HPLC profile (top panel) is also a 12/15-LOX product. (Reprinted with permission from reference Rai et al. [24])

incubated in vitro, the enzyme attacks mitochondrial membranes [13–16], priming the mitochondria for further degradation via the ubiquitin/ proteasome system. This is one of three pathways by which reticulocytes lose their organelles during maturation to become functioning erythrocytes, the others being degradation via autophagic vacuoles and exosome formation [17, 18]. The redundancy of these pathways may be the reason why no outright defects in erythropoiesis were found in Alox15 knockout mice [19].

Beyond causing cell death in neurons, however, it has in recent years become clear that 12/15-LOX also contributes to vessel injury in rodent models of stroke. Alox15 knockout mice develop 51% less edema following experimental stroke than their wild type counterparts, and 30% less immunoglobulin G (representative of blood proteins) extravasates into the brain parenchyma [8]. Several years later, we made the striking observation in a mouse model of thrombotic stroke that tPA infusion intended to lyse the occluding thrombus led to massive brain hemorrhage in these mice, which was reduced by 82%through simultaneous administration of a 12/15-LOX inhibitor, LOXBlock-1 [20] (Fig. 12.2). We have expanded on these results by investigating the effects of 12/15-LOX inhibition on both bleeding and infarct size in this thrombosis model, and found that LOXBlock-1 also improved behavioral scores in the mice [21].

This finding led us to systematically study mouse models of stroke where reperfusion following the ischemic event is associated with increased bleeding. In the classical filament model of transient focal ischemia, a filament is inserted into the internal carotid artery to partially block the middle cerebral artery on one side of the brain, which leads to a reduction of blood flow and ischemia in the striatum and cortex. The filament is then removed after a pre-specified time to allow for reperfusion. When the mouse is sacrificed after 24 h an infarct is detected, the size of which is determined by the duration of the ischemia. Typically, this model does not lead to significant bleeding, but so called hemorrhagic transformation of the ischemic stroke can be induced, for example when mice are fed with the

anticoagulant warfarin [22, 23]. Warfarin is a vitamin K inhibitor that is frequently given to patients with atrial fibrillation to reduce their risk of blood clot formation and subsequent stroke. While warfarin reduces the risk of stroke in these patients, this anticoagulant can cause excessive bleeding leading to increased injury when a stroke does occur. Moreover, thrombolysis with the clotbuster tissue plasminogen activator (tPA) is contraindicated in effectively anticoagulated patients on warfarin (international normalized ratio of coagulation time (INR) > 1.7) because tPA itself has bleeding as a side effect, thus eliminating the only drug currently approved by the FDA as a treatment option. Mice pretreated with warfarin via their drinking water for 24 h prior to experimental stroke develop severe hemorrhage both when the mice receive a tPA infusion following removal of the filament, or in the absence of tPA when the stroke is severe enough (3 h of filament occlusion; Fig. 12.2) [23]. Along with the increased hemorrhage, we also found 25% higher levels of 12/15-LOX in the brains of the warfarin-treated mice. The increase was seen mostly in the vasculature, consistent with the idea that the increased vessel leakage following warfarin pretreatment is due to 12/15-LOX.

Consistent with the idea of 12/15-LOX as contributor to hemorrhage, 41% less bleeding was seen following warfarin pretreatment in Alox15 knockout mice [23]. In wild type mice, a similarly drastic reduction in hemorrhage by 38% was detected when the mice were treated with the second generation 12/15-LOX inhibitor ML351 [24], administered intraperitoneally at the time of reperfusion, 3 hours after onset of ischemia. The reduction in bleeding remained significant even when the results were adjusted to account for the reduced infarct size in the ML351-treated mice, confirming that there is a specific effect on hemorrhage. When ML351 was administered along with tPA in warfarin pretreated mice, hemorrhage was similarly reduced by 59%. Taken together, these results demonstrated that increased 12/15-LOX in the brain vasculature can contribute to excessive bleeding in the brain, which is reduced by treatment with a 12/15-LOX inhibitor.



**Fig. 12.2** Examples of stroke models associated with increased hemorrhage. (a) Thrombosis was induced when 10% ferric chloride solution was topically applied to the brain. An infusion of tissue plasminogen activator (tPA) 2 h later led to distinct hemorrhage in vehicle-treated mice after 24 h, visible both on the surface of the brain (top) and in sections (below). In contrast, when mice were intraperitoneally injected with the 12/15-LOX inhibitor LOXBlock-1 (50 mg/kg), significantly less hemorrhage was detected in the brain. (b) Pretreatment of mice for

Much work remains to be done to elucidate the mechanism by which 12/15-LOX contributes to increased hemorrhage after an ischemic stroke. Important open questions include the selective up-regulation of 12/15-LOX in brain vascular endothelial cells following warfarin administration, both with and without subsequent tPA infusion. Is this a direct effect of warfarin and/or tPA, or are intermediate factors involved? Also, in neurons signal transducers and activators of transcription (STATs), specifically STAT1 and

24 h with the anticoagulant warfarin added to the drinking water causes massive hemorrhage following a severe form of experimental ischemic stroke with 3 h of occlusion of the middle cerebral artery. This is again visible both on the surface, as well as in brain sections. Mice treated with the 12/15-LOX inhibitor ML351 (50 mg/kg) develop far less hemorrhage (bottom right). Quantitation graphs represent hemorrhage area measured in brain sections and are reprinted with permission from references [24] (top) and [23] (bottom)

STAT6 are involved in up-regulating 12/15-LOX under ischemic conditions [7]. Are the same STATs active here, or is a different form of regulation relevant? Finally, what happens after 12/15-LOX is up-regulated in the endothelial cells and how does this lead to vessel rupture? In addition to destroying endothelial cells of the brain vasculature by damaging mitochondria, there may be a second injury mechanism induced by the signaling function of 12/15-LOX via metabolites of arachidonic acid. Both 12-HETE and its immediate precursor 12-HPETE are known as second messengers [25], activated along the semaphorin pathway [26, 27]. In neurons, this can lead to axon retraction [28, 29], but under some conditions also to cell death [30]. Semaphorin 3A has also been reported to increase vascular permeability in experimental stroke models [31]. Downstream of 12-HETE and 12-HPETE, secretion of destabilizing matrix metalloproteinases (MMPs) may play a role [32]. Both the molecular details of this signaling pathway, and the relative contributions of both pathways to vascular injury require further study.

Because 12/15-LOX contributes to both neuronal cell death and to vessel leakage following a stroke, 12/15-LOX inhibition appears to be a particularly promising approach to stroke therapy by targeting two separate modes of injury, killing two birds with one stone. Both our group [20, 23,24, 33, 34] and others [35, 36] have in recent years focused on developing improved inhibitors of 12/15-LOX, and it will be exciting to see if these novel molecules can turn the tide in the seemingly endless war to combat stroke. The finding that we can reduce bleeding subsequent to an ischemic stroke in the rodent model broadens the spectrum of patients that could be treated with a 12/15-LOX inhibitor. In addition to its use as a stand-alone neuroprotective treatment that could already be given in the ambulance on the way to the hospital, 12/15-LOX inhibition could also be combined with tPA thrombolysis to make the use of tPA safer. By removing the most serious side effect of tPA, this approach may lead to significantly more patients receiving tPA treatment. Furthermore, the recently introduced endovascular treatment in which a stent retriever is used to remove the obstructing blood clot could also be rendered more effective by adding a 12/15-LOX inhibitor, because even after thrombus removal cognitive deficits are seen in many patients who could benefit from the added neuroprotection[37]. Finally, besides the more common ischemic strokes there may also be a place for 12/15-LOX inhibition in the treatment of hemorrhagic strokes. We have recently completed a study to investigate the function of 12/15-LOX in subarachnoid hemorrhage, where

we found increased 12/15-LOX in the brains of mice 24 h after hemorrhage induction (92  $\pm$  60 12/15-LOX positive cells/field vs. 2  $\pm$  2 in shamoperated controls, p < 0.05) [38]. In this case, 12/15-LOX expression was detected mostly in macrophages however, rather than in neurons and endothelial cells; the injury mechanism may thus differ from that in ischemic stroke. Regardless, Alox15 knockout mice developed 72% less injury than wild type mice, and 12/15-LOX inhibition also reduced injury by 55% compared to vehicle-treated mice in this model of hemorrhagic stroke.

In conclusion, despite different triggers – in the presence or absence of anticoagulant, with or without tPA treatment – 12/15-LOX is activated in various models of stroke-related hemorrhage. In addition to its benefits in infarct size reduction, 12/15-LOX inhibition may thus independently reduce hemorrhagic conversion of ischemic strokes by protecting the vasculature.

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# Systematic Understanding of Bioactive Lipids in Neuro-Immune Interactions: Lessons from an Animal Model of Multiple Sclerosis

# Yasuyuki Kihara

## Abstract

Bioactive lipids, or lipid mediators, are utilized for intercellular communications. They are rapidly produced in response to various stimuli and exported to extracellular spaces followed by binding to cell surface G proteincoupled receptors (GPCRs) or nuclear receptors. Many drugs targeting lipid signaling such as non-steroidal anti-inflammatory drugs (NSAIDs), prostaglandins, and antagonists for lipid GPCRs are in use. For example, the sphingolipid analog, fingolimod (also known as FTY720), was the first oral disease-modifying therapy (DMT) for relapsing-remitting multiple sclerosis (MS), whose mechanisms of action (MOA) includes sequestration of pathogenic lymphocytes into secondary lymphoid organs, as well as astrocytic modulation, via down-regulation of the sphingosine 1-phosphate (S1P) receptor, S1P<sub>1</sub>, by in vivo-phosphorylated fingolimod. Though the cause of MS is still under debate, MS is considered to be an autoimmune demyelinating and neurodegenerative disease. This review summarizes the involvement of bioactive lipids (prostaglandins, leuplatelet-activating kotrienes. factors.

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lysophosphatidic acid, and S1P) in MS and the animal model, experimental autoimmune encephalomyelitis (EAE). Genetic ablation, along with pharmacological inhibition, of lipid metabolic enzymes and lipid GPCRs revealed that each bioactive lipid has a unique role in regulating immune and neural functions, including helper T cell (T<sub>H</sub>1 and  $T_{\rm H}17$ ) differentiation and proliferation, immune cell migration, astrocyte responses, endothelium function, and microglial phagocytosis. A systematic understanding of bioactive lipids in MS and EAE dredges up information about understudied lipid signaling pathways, which should be clarified in the near future to better understand MS pathology and to develop novel DMTs.

## Keywords

$$\label{eq:linear} \begin{split} & \text{Neuroimmunology} \cdot \text{Autoimmunity} \cdot \\ & \text{Neuroinflammation} \cdot \text{Neurodegeneration} \cdot \\ & \text{Demyelination} \cdot \text{Inflammation} \cdot \text{Microglia} \cdot \\ & \text{Astrocyte} \cdot \text{Blood-brain barrier} \cdot \text{Eicosanoid} \cdot \\ & \text{PLA}_2 \cdot \text{PGE}_2 \cdot \text{LTB}_4 \cdot \text{PAF} \cdot \text{LPA} \end{split}$$

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## 13.1 Neuro-immune Interactions and Their Failures

The central nervous system (CNS) is separated from the peripheral immune system by the blood-brain barrier (BBB) and it is also immunologically inactive which provides immune privilege [1] despite the existence of autoimmune demyelinating diseases such as multiple sclerosis (MS). Recent studies clearly show the communication pathways between the CNS vs. peripheral immune system through a lymphatic system in the meninges [2] and tunnels connecting the brain and the skull [3]. Furthermore, an animal model of MS proposed that pathogenic T cells penetrate into the CNS via the fifth lumber spinal cord [4]. Failure of homeostatic neuroimmune interactions exerts pernicious effects on the CNS, resulting in the development of several diseases including MS [4], Alzheimer's disease [5], and social behavior impairment [6]. In this section, MS and its animal model, experimental autoimmune encephalomyelitis (EAE), is introduced.

#### 13.1.1 Multiple Sclerosis

Publications in the 1830s described a disease exhibiting multiple, irregular foci of discoloration and shrinkage throughout neuroaxis [7]. In 1868, a French neurologist, Jean-Martin Charcot, gathered prior clinical depictions and framed the disease as sclérose en plaques (multiple sclerosis in French) [8]. The pathologic hallmarks of MS are myelin loss (demyelination), accompanied by inflammation within the CNS, which are called plaques or lesions. Introduction of magnetic resonance imaging (MRI) in 1981 [9] conquered the chaos in diagnosing MS, understanding MS pathogenesis, and evaluation of treatment. The current standard of MS diagnosis, the McDonald criteria [10, 11], uses MRI to identify CNS damage as seen over time and location. In 1983, John F. Kurtzke developed the Expanded Disability Status Scale (EDSS) [12, 13] that quantify the disabilities in MS patients whose symptoms are variable and numerous including fatigue, walking difficulties, numbness/tingling, vision problems, and dizziness/vertigo. Surprisingly, many of these symptoms were recorded in documents about St. Lidwina of Schiedam (1380–1433), which is thought to be the oldest depiction of MS [14].

Based on the disease course, MS is classified into four types: (1) clinically isolated syndrome (CIS), (2) relapsing-remitting MS (RRMS), (3) secondary progressive MS (SPMS), and (4) primary progressive MS (PPMS) (nationalmssociety.org). Currently, about 2.3 million people live with MS around the world, with a higher prevalence in North America and Europe (>100/100,000 inhabitants) compared to Asia and Africa (2/100,000 population) [15]. MS affects more women than men (3~4:1 ratio) (nationalmssociety.org). Although involvement of genetic and environmental factors in MS pathogenesis have been proposed, the cause of MS is still under By 2018, the Food and Drug debate. Administration (FDA) has approved 16 medications as disease-modifying therapies (DMTs). However, daclizumab, an anti-CD25 monoclonal antibody (Ab), was withdrawn from the market worldwide in March 2018 [16]. Additional details and updated information about MS and its treatment can be found on the National Multiple Sclerosis Society's website (nationalmssociety. org). Since MS is traditionally considered to be an autoimmune disorder, immunomodulation is the mechanism of action (MOA) of most MS-drugs such as natalizumab (anti-VLA4 Ab) [17], alemtzumab (anti-CD52 Ab) [18], ocrelizumab (anti-CD20 Ab) [19], interferon  $\beta$  (IFN- $\beta$ ) [20], fingolimod [21, 22], and dimethyl fumarate (DMF) [23, 24]. However, a growing body of literature supports that some MS drugs, such as fingolimod [25], IFN- $\beta$  [26], and DMF [27], exhibit direct effects in the CNS. Exploring and developing CNS-targeted MS-drugs is meaningful for finding a cure for progressive forms of MS that show more neurodegenerative features than RRMS. Neuro-immune interactions underlying MS are far more complex than previously understood, and thus further exploration of the communications between the immune and nervous systems is highly desirable.

## 13.1.2 Experimental Autoimmune Encephalomyelitis

A breakthrough in understanding MS pathogenesis and MS drug development was the establishment of an animal model of MS, now called experimental autoimmune (or allergic) encephalomyelitis (EAE), by Thomas Rivers in 1933 [28]. The study provided the first evidence of cell-mediated immune CNS damage. Recapitulation of EAE by transfer of lymph node cells [29] guided several important findings that include EAE induction with T cells reactive against myelin basic protein (MBP) [30] and definition of encephalitogenic epitopes of MBP [31]. Further investigation revealed CD4<sup>+</sup> T recognize helper type 1  $(T_{\rm H}1)$ cells oligodendrocyte-specific proteins or peptide fragments (such as MBP; proteolipid protein, PLP; myelin oligodendrocyte glycoprotein, MOG) [32, 33] that are responsible for EAE induction and progression. In 2005, interleukin-23 (IL-23)-derived IL-17 producing encephalitogenic T cells, which are now known as  $T_H 17$ cells, were found to play key roles in CNS autoimmunity [34].

EAE susceptibility varies in mouse strains and may be explained by the major histocompatibility complex H2 haplotypes [35]. The most commonly used mouse strains in the scientific field are  $T_H1$ -prone C57BL/6 (H2b) and CD4<sup>+</sup> T helper type 2 ( $T_H$ 2)-prone Balb/c (*H2d*) mice. Both active immunization with MOG peptide ( $MOG_{35-55}$ ) and passive immunization by adoptive transfer of encephalitogenic T cells in C57BL/6 mice display monophasic disease course [23, 36–39]. All the knockout studies introduced below used the C57BL/6 genetic background unless otherwise stated. Balb/c mice are not susceptible to EAE, but some controversial results are reported [40]. SJL mice harboring H2s present a relapsing-remitting disease course when immunized with PLP peptide (PLP<sub>139-151</sub>) [35]. Non-obese diabetic (NOD) mice harboring  $H2g^7$  immunized with MOG<sub>35-55</sub> display progressive MS-like disease signs [35]. This needs careful consideration since NOD mice develop spontaneous diabetes at a higher rate.

Failure of neuro-immune communication results in T cells attacking CNS elements, particularly oligodendrocytes, which causes demyeneurodegeneration. lination and Although immunological aspects of these diseases have been well-studied, it remained unknown whether CNS cells are actively involved in the disease. By using genetically engineered mice harboring a tetracycline-controlled c-Fos reporter (a green fluorescent protein-histone H2B fusion protein under a tetO promoter controlled by a c-Fos inducible tetracycline transactivator), we identified that astrocytes were activated by EAE insults at the initial phase of disease course [41]. We named the astrocytes that experienced c-Fos activation during EAE as immediate-early astrocytes (*ieAstrocytes*) [41]. The number of *ieAstrocytes* increased linearly with EAE progression, indicating that astrocytes are the key CNS cell type in EAE pathogenesis [41]. Although there are several differences between MS and EAE, both diseases share the pathological, clinical features, which justify EAE as an MS model to study neuro-immune interactions. In the following sections, the roles of bioactive lipids in neuroimmune interactions from EAE studies that used knockout (KO) mice or pharmacological tools are summarized.

## 13.2 Arachidonic Acid Cascade in EAE and MS

Arachidonic acid (AA) cascade is a pathway that produces eicosanoids from  $\omega$ -6 polyunsaturated acid (PUFA), AA (5Z,8Z,11Z,14Zfatty eicosatetraenoic acid) [42]. Eicosanoid is the general term used for potent bioactive lipids that have 20 (eicosa in Greek) carbon units in their structure, which include prostaglandins (PGs), thromboxanes (TXs), leukotrienes (LTs), hydroxyl eicosatetraenoic acids (HETEs), and epoxyeicosatrienoic acids (EETs). Figure 13.1 summarizes the relationship between AA cascade and EAE/MS pathology.



Fig. 13.1 EAE phenotypes in AA cascade-KO mice

#### 13.2.1 Phospholipase A<sub>2</sub>s (PLA<sub>2</sub>s)

PLA<sub>2</sub>s including cytosolic PLA<sub>2</sub>s (cPLA<sub>2</sub>), secreted PLA<sub>2</sub>s (sPLA<sub>2</sub>) and calcium-independent  $PLA_{2}s$  (iPLA<sub>2</sub>), hydrolyze the *sn*-2 position of membrane glycerophospholipids to liberate fatty acyls including AA [43]. Among them, group IVA cPLA<sub>2</sub> (cPLA<sub>2</sub> $\alpha$ ; gene name, *Pla2g4a*) is a key enzyme to produce eicosanoids, since its deficiency lacks the ability of producing eicosanoids, resulting in resistance to various disease models [43]. Several lines of evidence, such as (1) up-regulation of Ca<sup>2+</sup>-dependent PLA<sub>2</sub> activity and PLA<sub>2</sub> mRNAs (cPLA<sub>2</sub> $\alpha$ , cPLA<sub>2</sub> $\beta$ , cPLA<sub>2</sub> $\zeta$ , and sPLA<sub>2</sub>-V) in EAE spinal cords (SCs) [38], (2) cPLA<sub>2</sub> $\alpha$  expression in brain endothelium and infiltrated immune cells in EAE mice [44], and (3) increased sPLA<sub>2</sub> activity in both MS and EAE urine [45], suggest active involvement of these enzymes in EAE. Using cPLA<sub>2</sub> $\alpha$ -KO mice [46], Marusic et al. revealed the requirement of both peripheral and neuronal cPLA<sub>2</sub> a in EAE development and progression [47]. No other PLA<sub>2</sub>-KO mice have been tested for EAE. Pharmacological inhibition of PLA<sub>2</sub>s (Pan inhibitors, AACOCF3 and FKGK2; cPLA<sub>2</sub> $\alpha$  inhibitor, WAY-196025; sPLA<sub>2</sub> inhibitor, CHEC-9; and iPLA<sub>2</sub> inhibitor, FKGK11) also blocked EAE development and

progression [44, 47–50]. These results suggest that eicosanoids, which are produced down-stream of  $PLA_2$ , should have unique roles in EAE and MS.

#### 13.2.2 Cyclooxygenases (COXs)

COXs (COX-1 and COX-2; gene names, *Ptgs1* and *Ptgs2*, respectively) insert two molecular oxygen into AA to produce an unstable endoperoxide intermediate, PGH<sub>2</sub>, which in turn metabolizes to PGD<sub>2</sub>, PGE<sub>2</sub>, PGF<sub>2</sub>, PGI<sub>2</sub>, and TXA<sub>2</sub> by isomerases and terminal synthases [51]. Acetylsalicylic acid (Aspirin<sup>®</sup>) is the first nonsteroidal anti-inflammatory drug (NSAID) synthesized by Bayer in 1897 [52]. The MOA of aspirin is suppression of prostaglandin synthesis by inhibiting COXs, which was revealed by John Vane in 1971 [53].

There were no beneficial effects of aspirin in guinea pig EAE [54, 55], while a high dose sodium salicylate, a major metabolite of aspirin, showed efficacy in guinea pig EAE [56]. Two clinical trials in the early 1960's examined aspirin's efficacy in MS failed [57, 58]. However, mouse EAE studies tested other NSAIDs including indomethacin and naproxen (non-selective COX inhibitors) that clearly demonstrated the involvement of COXs in EAE [50, 59]. Miyamoto et al. reported that COX-2-KO mice showed equivalent disease course with controls [59]. The study also demonstrated that a COX-2 selective inhibitor, celecoxib, prevented EAE in mice, while COX-2-KO mice were not rescued by celecoxib. Thus, the MOA of celecoxib in EAE suppression is independent from COX-2 inhibition [59]. Recently, the efficacy of low-dose aspirin (1 ~ 3 mg/kg), which is commonly used for lowering cardiovascular risks [60], on the EAE phenotype was reported [61]. The study revealed that low-dose aspirin prevented loss of regulatory T cells  $(T_{reg})$  by stimulating IL-11 production, and also suppressed T<sub>H</sub>1/T<sub>H</sub>17 differentiation, resulting in EAE amelioration [61]. However, since this MOA of low-dose aspirin is not tested in COX-1/2-KO mice and eicosanoid levels were not quantified, it remains unclear if the efficacy of low-dose aspirin is related to COX-1/2 inhibition. Considering the results from cPLA2 $\alpha$ -KO and COX-2-KO studies, COX-1 may play some role in EAE, but EAE has not been tested in COX-1-KO mice to date.

#### 13.2.3 Prostaglandins (PGs)

PGs are produced downstream of COX-1/2 and are functionally coupled with terminal PG synthases to produce each PG efficiently [62–64], followed by binding to their specific receptors (a member of the superfamily of G-protein coupled receptors (GPCRs)), to elicit a variety of biological responses [42].

We applied targeted lipidomics using liquid chromatography tandem mass spectrometry (LC-MS/MS) in combination with transcriptomics to identify a key eicosanoid pathway that is involved in EAE [37]. Lipidomics identified a metabolic shift from the PGD<sub>2</sub> pathway in naïve spinal cords (SCs) to the PGE<sub>2</sub> pathway in EAE SCs [37]. Among the three PGE<sub>2</sub> synthases, microsomal PGE synthase 1 (mPGES-1; gene name, *Ptges*) mRNA was uniquely up-regulated in EAE SCs. mPGES-1 protein was expressed in microglia/macrophages in both EAE and MS

lesions [37]. mPGES-1 deficiency almost completely inhibited PGE<sub>2</sub> production in EAE SCs, while doubling PGI<sub>2</sub> production. mPEGS-1-KO mice showed EAE amelioration and impairment of  $T_H 1/T_H 17$  differentiation [37]. Later, another group reported essentially the same results using the same mPGES-1-KO mice. They proposed that mPGES-1 in vascular endothelial cells controls IL-1β signaling in both CD4<sup>+</sup> T cells and endothelial cells, resulting in EAE exacerbation [65–67]. EAE phenomics using 8 PG receptor KO mice was reported [68], which identified a significant suppression of EAE only in PGE<sub>2</sub> receptor 4 (EP<sub>4</sub>; gene name, Ptger4)-KO mice on the mixed background of C57BL/6 and 129/Ola. EAE phenotypes in other  $PGE_2$  receptors (EP<sub>1</sub>,  $EP_2$ , and  $EP_3$ ) were equivalent to their matching controls [68]. Prophylactic administration of the EP<sub>4</sub> antagonist (ONO-AE3-208) prevented mice from developing EAE, while the therapeutic paradigm showed little effect on EAE development and severity [68]. The efficacy of ONO-AE3-208 was greater in EP<sub>2</sub>-KO mice than wild-type (WT) mice, suggesting a redundancy of  $EP_4$  and  $EP_2$ [68]. Indeed,  $PGE_2$  facilitated  $T_H1$  differentiation and IL-23-induced T<sub>H</sub>17 expansion through both  $EP_2$  and  $EP_4$  [69]. These results clearly demonstrate that the mPGES-1-PGE<sub>2</sub>-EP<sub>2/4</sub> axis is an exacerbating pathway in EAE and MS.

Although the EAE phenomics study concluded no aggravation or facilitation of EAE in any PG receptor KO mice except for EP4-KO mice, the clinical score of PGI<sub>2</sub> receptor (IP; gene name, Ptgir)-KO mice appeared to show a right shift (delayed onset and/or milder EAE) as compared to controls [68]. Indeed, another group reported a similar trend with significant differences between IP-KO mice vs. controls [70]. They also demonstrated that PGI<sub>2</sub>-IP signaling induces IL-17A production in naïve CD4+ T cells and promotes  $T_{\rm H}17$  differentiation [70]. The decreased PGI<sub>2</sub> in EAE SCs could be explained by down-regulation of PGI synthase (PGIS; gene name, Ptgis) mRNA that is abundant in endothelial cells [37], suggesting a direct neuroprotective role of PGI<sub>2</sub> in the CNS. Muramatsu et al. reported that knockdown of PGIS and IP by siRNA delivered directly into the CNS, delayed recovery

from motor dysfunction associated with EAE [71]. Furthermore, PGI<sub>2</sub> promoted neurite elongation *in vitro*. Systemic administration of an IP agonist, iloprost, improved motor deficits in EAE, indicating that vascular endothelial cell-derived PGI<sub>2</sub> promotes neuronal rewiring in EAE via the PGIS-PGI<sub>2</sub>-IP pathway [71]. Collectively, PGI<sub>2</sub> shows anti-immune and neuroprotective effects.

 $PGD_2$  is the most abundant eicosanoid in the CNS [72]. The decreased  $PGD_2$  in EAE SCs might be associated with reductions in lipocalintype PGD synthase (L-PGDS; gene name, *Ptgds*) mRNA that is highly expressed in oligodendrocytes (OLs) [37]. L-PGDS deficiency in a genetic demyelinating mouse model (twicher mice harboring a homozygote for a nonsense point mutation of the galactosylceramidase) showed increases of apoptotic neurons and OLs [73]. Moreover, increased L-PGDS expression was reported in remyelinated lesions of MS brains [76], indicating an anti-apoptotic and proremyelinating property of the L-PGDS-PGD<sub>2</sub> pathway in OLs. No difference in EAE signs between  $PGD_2$  receptor  $(DP_1;$  gene name, *Ptgdr1*)-KO mice vs. controls was reported [68], while DP<sub>1</sub>-KO mice appeared to show a slightly severer disease course than controls. This requires a more careful evaluation of the EAE phenotype in DP<sub>1</sub>-KO mice. Moreover, little is known about the roles of L-PGDS, hematopoietic-type PGD synthase (H-PGDS; gene name, Ptgds2), and another PGD<sub>2</sub> receptor (DP<sub>2</sub>/CRTH<sub>2</sub>; gene name, *Ptgdr2*) in EAE.

Although PGD<sub>2</sub> levels decreased in EAE SCs, one PGD<sub>2</sub> metabolite, 15-deoxy- $\Delta^{12,14}$ -PGJ<sub>2</sub>  $(15d-PGJ_2)$ , was substantially increased in EAE SCs [37]. 15d-PGJ<sub>2</sub> binds selectively to one of three peroxisome proliferator-activated receptors, PPAR $\gamma$  (gene name, *Pparg*), which inhibits pro-inflammatory cytokine production [75]. Both PPAR $\gamma$ -hetero [76, 77] and PPAR $\gamma$  antagonist treated mice developed severe EAE [77]. Furthermore, prophylactic and therapeutic administration of 15d-PGJ<sub>2</sub> [78], as well as prophylactic treatment of a PPARy agonist (troglitazone) [79], ameliorated EAE [78], indicating that 15d-PGJ<sub>2</sub> production in EAE SCs might be a defensive reaction as an innate response.

#### 13.2.4 Lipoxygenases (LOs)

LOs (5-LO, 8-LO, and 12/15-LO; gene names, Alox5, Alox8, and Alox12, respectively) insert one molecule of molecular oxygen into the 5, 8, 12, and 15 positions of AA, to produce hydroperoxy eicosatetraenoic acids (HpETE) [80, 81]. 5-LO catalyzes the two-step conversion of AA to LTA<sub>4</sub> that are metabolized to LTs and HETEs by enzymatic and non-enzymatic reactions, respectively [80]. LTs elicit their biological actions by binding to their specific GPCRs [42]. In addition to LTs, LOs also produce specialized proresolving mediators (SPMs) including AA-derived lipoxins, docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA)-drived resolvins (RvDs and RvEs, respectively), and DHA-derived neuroprotectin (NPD<sub>1</sub>) [82-84].

Gene expression profiling in MS lesions and EAE brains identified an up-regulation of the 5-LO gene [85]. 5-LO-KO mice on a 129 genetic background showed severe disease as compared to controls on the 129S1/SvImJ background [86]. 12/15-LO-KO mice on a mixed B6:129S2 background also showed severe disease as compared to controls on a C57BL/6 J background [86]. These severe phenotypes may be accounted for by a metabolic shift towards the COX-PG pathway in 5-LO-KO mice, and/or by a reduction of SPMs in 12/15-LO-KO mice. However, the mismatched genetic backgrounds between KO vs. controls make it difficult to conclude roles of these LOs. On the other hand, the FDA-approved anti-asthma drug, zileuton, which is an 5-LO selective inhibitor, effectively delayed EAE onset and ameliorated EAE [49], suggesting that LTs produced by 5-LO may worsen EAE.

#### 13.2.5 Leukotrienes (LTs)

LTs are produced downstream of 5-LO. LTA<sub>4</sub> hydrolase (LTA<sub>4</sub>H; gene name, *Lta4h*) metabolizes LTA<sub>4</sub> to LTB<sub>4</sub> [87]. Cysteinyl LTs (cys-LTs) are produced by LTC<sub>4</sub> synthase (LTC<sub>4</sub>S; gene name, *Ltc4s*) that conjugates reduced glutathione to LTA<sub>4</sub>, resulting in LTC<sub>4</sub> formation that is

metabolized to  $LTD_4$  followed by  $LTE_4$  [88, 89]. Levels of these 5-LO metabolites in naïve SCs were very low as compared to COX metabolites, which were further declined in EAE SCs [37]. Therefore, LTs may not play pivotal roles in EAE. However, mRNAs of the LTB<sub>4</sub> receptor 1  $(BLT_1; gene name, Ltb4r1)$  and the cys-LT receptor 1 (CysLT<sub>1</sub>; gene name, Cysltr1) were highly up-regulated in EAE SCs from disease onset through the acute phase [37, 39], implying accumulation of immune cells expressing these receptors into the CNS. The BLT<sub>1</sub> antagonist, CP-105,696, prevented EAE and suppressed eosinophil infiltration into the CNS in a dose-dependent manner [90]. We reported that BLT<sub>1</sub>-KO mice showed delayed onset, less severe EAE, and reduced  $T_H 1/T_H 17$  responses than controls [39]. Moreover, BLT<sub>1</sub>-KO SCs from asymptomatic EAE mice showed no T cell, neutrophil, or macrophage infiltrations, whereas those cells were found in asymptomatic WT EAE controls [39]. These results suggest that  $BLT_1$  is responsible for immune cell recruitment into the CNS in the early phase of the disease. EAE studies using KO mice of LTA<sub>4</sub>H, LTC<sub>4</sub>S, BLT<sub>2</sub> (gene name, *Ltb4r2*), CysLT<sub>1,2,3</sub> (gene name, *Cysltr1*, Cysltr2, Cyltr3/Oxgr1/Gpr99) are not available at this time.

## 13.3 Platelet-Activating Factor (PAF) in EAE and MS

PAF (1-O-alkyl-2-acetyl-sn-glycero-3-phosphocholine) is a potent lipid mediator that activates immune cells and induces vascular hyperpermeability, hypotension, and bronchoconstriction via its specific GPCR, PAF receptor (PAFR; gene name, Ptafr) [91, 92]. PAF production through a remodeling pathway requires membrane phospholipid hydrolysis by PLA<sub>2</sub>s that (1-O-alkyl-sn-glycero-3supply lyso-PAF phosphocholine), which in turn metabolizes to PAF by acetyl-CoA:lyso-PAF acetyltransferase (LysoPAFAT; gene name, Lpcat2) [93]. PAF is rapidly degraded to lyso-PAF by PAF acetylhydrolase (PAF-AH; gene name, Pafah1b1, Pafah1b2, Pafah1b3) [94]. Although a clinical

trial using ginkgolide B, a PAFR antagonist extracted from Ginkgo biloba, showed no efficacy for the treatment of acute exacerbations of MS [95], several lines of evidence support an involvement of PAF in MS/EAE to certain extent, including (1) elevated PAF levels in cerebrospinal fluids (CSF) and plasma of RRMS patients [96], (2) up-regulation of PAFR mRNA in chronic MS plaques [97], (3) a relationship between PAFR gene missense mutation vs. the susceptibility for MS [98], and (4) an efficacy of PAFR antagonist (BN52021) on EAE [99]. We found increased activity of PAF producing enzymes (PLA<sub>2</sub> and LysoPAFAT) and unchanged PAFAH activity in EAE SCs as compared to controls, resulting in a significant elevation of PAF levels [36, 38]. We also tested EAE in PAFR-KO mice that showed a lower incidence and less severe disease than controls [36]. PAF-PAFR signaling promoted cytokine and chemokine production in SCs before disease onset [36]. In addition, PAF accelerated phagocytotic activity and its associated TNF-α production in macrophages via PAFR [36]. Another group independently confirmed these results using the same PAFR-KO mice [100]. These results suggest a dual role of PAF-PAFR signaling in EAE development and progression.

## 13.4 Lysophospholipid (LP) Mediators in EAE and MS

LP is a derivative of a phospholipid in which one acyl chain is missing from the glycerol backbone combined with a phosphate head group, such as lysophosphatidic acid (LPA, 1 or 2-acyl-snglycero-3-phosphate), lysophosphatidylserine (LysoPS), lysophosphatidylinositol (LPI), and lysophosphatidylcholine (LPC) [101]. Since LIPID MAPS® classifies sphingosine 1-phosphate (S1P) in the sphingolipid group [102], it is technically not a lysophospholipid. However, S1P is included here based on the IUPAR (International Union of Basic and Clinical Pharmacology) GPCR classification [103]. Figure 13.2 summarizes the relationship between LPs and EAE/MS pathology.



Fig. 13.2 EAE phenotypes in LP signaling-KO mice. (a) LPA pathway. (b) S1P pathway

#### 13.4.1 Lysophosphatidic Acid (LPA)

LPA is produced by three distinct pathways: (1) de novo synthesis from glycerol-3-phosphate (G3P) by G3P acyltransferase (GPAT; gene names, Gpam, Gpat2, Gpat3 and Gpat4) [93, 104], (2) head group removal from LPs by autotaxin (ATX; gene name, *Enpp2*) [105, 106], and (3) hydrolysis of phosphatidic acid (PA) by PA-specific PLA<sub>1</sub> (PA-PLA<sub>1</sub> $\alpha$ ; gene name, *Liph*) [105, 107]. LPA levels in blood (0.1 µM in plasma  $\sim 10 \ \mu\text{M}$  in serum) are of sufficiently high concentration to activate six cognate GPCRs (LPA<sub>1-6</sub>; gene names, Lpar1-6) [101, 108-111], in which LPA1 dissociation constants (Kd) for LPA approximated subnanomolar range [112]. Although LPA was isolated and identified from soy beans in 1978 [113], it has not been well-studied in MS and EAE until recently. In 2017, Schmitz et al. reported a meticulous investigation of the relationship between LPA and MS and EAE [114]. LPA concentrations quantified by LC-MS/MS were significantly reduced in the serum of MS patients, regardless of disease type, and EAE mice on an SJL/J background as compared to their controls [114]. Moreover, unsaturated LPA levels in serum were responsive to some DMTs (fingolimod and natalizumab), which were also observed in EAE mice on an SJL/J background [114]. In a spontaneous relapsing-remitting EAE model (T cell receptor (TCR) transgenic mice carrying TCR specific for MOG<sub>92-106</sub> in the context of I-A<sup>s</sup> in SJL/J genetic background; TCR<sup>1640</sup> mice [115]), unsaturated LPAs in plasma and SCs were highly elevated during the first remission, followed by suppression in the second relapse [114]. Receptor expression profiles in spleen cells of EAE mice identified a suppression of LPA<sub>2</sub> protein expression on CD4<sup>+</sup> T cells and myeloid cells [114]. LPA1 mRNA in spleen, LPA2 and LPA<sub>3</sub> mRNA in white blood cells, and LPA<sub>2</sub>, LPA<sub>3</sub>, LPA<sub>4</sub> and LPA<sub>5</sub> mRNA in SCs were upregulated in EAE mice [114]. In LPA<sub>2</sub>-KO mice on a C57BL6 x Sv129 mixed background, about 25% developed EAE with increased T cell and myeloid cell infiltration into the SCs, while their matching WT controls showed very mild disease course because Sv129 mice are resistant to EAE [114]. LPA<sub>2</sub> agonist, GRI-977,143, effectively ameliorated EAE SJL in mice [114]. Controversial, small cohort studies were also reported that LPA levels increased in serum of RRMS patients, while they were determined by ELISA or phosphate quantification [116, 117]. ATX activity was elevated in the CSF and serum of RRMS patients [118]. A naturally occurring LPA analog, cyclic phosphatidic acid (cPA, 1-acyl-sn-glycero-2,3-cyclic phosphate), is reported to activate LPA receptors [119]. Treatment using a metabolically stable analog of cPA (2ccPA) in both a prophylactic and therapeutic manner ameliorated EAE and reduced inflam-
mation in the SCs [120], which may be mediated via LPA<sub>2</sub>. The EAE course of LPA<sub>4</sub>-KO mice was equivalent to controls (unpublished observation). The EAE disease course in LPA<sub>1</sub>, LPA<sub>3</sub>, LPA<sub>5</sub>, and LPA<sub>6</sub> deficiency, as well as LPA-producing and degrading enzyme deficiency, need to be studied to characterize their roles in EAE.

# 13.4.2 Sphingosine 1-phosphate (S1P)

S1P is produced from sphingosine (2-amino-4-octadecene-1,3-diol) by the action of sphingosine kinases (Sphks; gene name, *Sphk1*, *Sphk2*) [121]. S1P is enriched in blood plasma (low micromolar range), where S1P binds to albumin (gene name, *Alb*) and apolipoprotein M (ApoM; gene name, *Apom*) tethered to high-density lipoprotein (HDL) at a ratio of approximately three to seven [122]. S1P levels in lymph and tissues are lower than in blood (nanomolar range), which generates an S1P gradient between the circulatory system and tissues [122]. The biological significance of this gradient was recognized about 10 years after the discovery of fingolimod (trade name, Gilenya<sup>TM</sup>), originally called FTY720.

In 1995, fingolimod was first synthesized from an immunosuppressive natural product, myriocin (ISP-I), which was isolated from culture broths of Isaria sinclairii [123–125]. Chiba et al. reported that fingolimod strikingly reduced the number of circulating lymphocytes [125], while the molecular basis of fingolimod activity remained unclear at that time. This immunosuppressive effect of fingolimod was clinically tested for preventing organ graft rejection, while phase III clinical trials did not support a superior efficacy of fingolimod in renal transplantation as compared to the prior standard treatment [126]. During 1998–2000, five S1P receptors (S1P<sub>1-5</sub>: gene names, S1pr1-5) that belong to rhodopsin family GPCRs were identified [101, 108]. In 2002, the MOA of fingolimod was independently proposed by two pharmaceutical companies, Merck and Novartis [127, 128]. Both groups clearly demonstrated that phosphorylated fingolimod (fingolimod-P) was generated in vivo after

administration of fingolimod. Moreover, fingolimod-P was identified as a high affinity agonist to four out of the five known S1P receptors (S1P<sub>1</sub>, S1P<sub>3</sub>, S1P<sub>4</sub>, and S1P<sub>5</sub>). Brinkman et al. also reported the efficacy of fingolimod in EAE by a prophylactic treatment paradigm [127]. In 2003, Sphk2 was reported to show a greater effect of fingolimod phosphorylation as compared to Sphk1 [129]. In 2004, Jason Cyster's group revised the MOA of fingolimod from agonism to functional antagonism based upon findings that (1)  $S1P_1$  was required for lymphocyte egress from lymphoid organs to circulation, and (2) fingolimod treatment down-regulated S1P<sub>1</sub> cell surface expression [130, 131]. These studies provided a basis for the biological significance of the S1P gradient in lymphocyte trafficking between circulatory and lymph systems, which are supported by other studies using S1Pgenerating (Sphks) and -degrading (S1P lyase; gene name, Sgpl1) enzyme KO mice [132, 133]. Additional studies provided more evidence of S1P<sub>1</sub> involvement in MS and EAE. Proteomics analysis on MS brain tissue identified S1P<sub>1</sub> phosphorylation on a C-terminal serine residue that is crucial for receptor internalization [134]. A knock-in mouse harboring alanine mutations on S1P<sub>1</sub> C-terminal serine residues (S1P<sub>1</sub>-S5A mice) [135] developed more severe EAE than controls with an enhanced T<sub>H</sub>17 immunity. S1P<sub>1</sub> floxed mice (S1P<sub>1</sub><sup>flox/flox</sup>) were used to study cell-specific roles of S1P1 in EAE, since global S1P1-KO mice were embryonically lethal due to impairment of maturation T<sub>H</sub>17-specific vascular [136]. S1P<sub>1</sub>-KO mice (IL-17A-Cre: S1P<sub>1</sub><sup>flox/flox</sup> mice) were completely resistant to EAE development [137]. On the other hand,  $T_{reg}$ -specific S1P<sub>1</sub>-KO mice (Foxp3-Cre: S1P1 flox/flox mice) developed systemic autoimmunity, since T<sub>reg</sub> cells were retained in lymphoid organs and reduced in peripheral tissues. Also, S1P<sub>1</sub> deletion, as well as fingolimod treatment, promoted to effector T<sub>reg</sub> cell conversion from central T<sub>reg</sub> cell. Tamoxifeninducible Treg-specific S1P1-KO mice (Foxp3-CreER<sup>T2</sup>: S1P<sub>1</sub><sup>flox/flox</sup> mice) developed severe EAE [137]. The immunological roles of ApoM-bound S1P were investigated using ApoM-KO mice, which revealed that ApoM-S1P suppresses

expansion of Lin-Sac-1+cKit+ hematopoietic progenitor cells (LSKs) and common lymphoid progenitors (CLPs) through S1P<sub>1</sub> [138]. This immune stimulation led to exacerbation of EAE in mice lacking ApoM, while less severe EAE was observed in ApoM transgenic mice (driving with endogenous promoter). Although endothelium-specific S1P<sub>1</sub>-KO mice (Cdh5-Cre-ER<sup>T2:</sup> S1P1 flox/flox mice) showed pulmonary vascular leakage, EAE disease course in these mice were equivalent to their matching controls [138]. Collectively,  $S1P_1$  signaling is responsible for homeostatic lymphocyte trafficking and lymphopoiesis, whose functional antagonism by fingolimod reduces circulating pathogenic T cells, resulting in EAE/MS amelioration.

Given the fact that fingolimod penetrated and accumulated in the CNS [139] where S1P receptors are abundant (S1P<sub>1</sub> in astrocytes and S1P<sub>5</sub> in oligodendrocytes) [36], direct CNS effects of fingolimod were expected. In 2011, Jerold Chun's group reported EAE amelioration and no fingolimod efficacy in CNS-specific S1P<sub>1</sub>-KO mice (Nestin-Cre: S1P1 flox/flox mice) and astrocytespecific S1P<sub>1</sub>-KO mice (GFAP-Cre: S1P<sub>1</sub><sup>flox/flox</sup> mice), while neuron-specific S1P<sub>1</sub>-KO mice (Synapsin-Cre: S1P<sub>1</sub><sup>flox/flox</sup> mice) did not show such phenotypes [140]. Most recently, we identified a novel functional astrocyte, *ieAstrocyte*, in EAE SCs, whose formation was significantly blocked by fingolimod administration and S1P<sub>1</sub> deficiency [41]. These results suggest that  $S1P_1$ inhibition on astrocytes appears to be another MOA of fingolimod, which seems to be desirable for the treatment of progressive type of MS (PPMS and SPMS). Development of S1P receptor modulators in next generation compounds are designed to have a receptor subtype selectivity, such as the  $S1P_1/S1P_5$  specificity in siponimod, ponesimod, and ozanimod, and S1P<sub>1</sub> specificity in KRP-203 and GSK2018682 [108]. Among these, the phase III clinical trial (EXPAND) demonstrated that siponimod reduced the risk of disability progression in SPMS patients [141], which might be mediated through direct CNS action. Several reviews have been published that summarize direct CNS effect of fingolimod and S1P receptor modulators [21, 25, 108, 140].

Knockout and antagonist studies targeting  $S1P_3$ ,  $S1P_4$ , and  $S1P_5$  have not been reported, but the EAE phenotype in S1P<sub>2</sub>-KO mice was reported [142, 143]. Microarray analysis searching for sexually dimorphic genes in the CNS of naïve SJL mice identified higher S1P<sub>2</sub> expression levels in female vs. male [142]. S1P<sub>2</sub> expression increased in brain endothelial cells of EAEinduced female mice and female MS patients, which enhanced permeability BBB to Na-Fluorescein [142]. Therapeutic treatment with the  $S1P_2$  antagonist (JTE-013) ameliorated EAE in SJL mice [142]. Furthermore, S1P<sub>2</sub>-KO mice on a C57BL/6  $\times$  129S mixed background showed milder EAE course than controls [142]. Using the same S1P<sub>2</sub>-KO mice, another group also reported that S1P<sub>2</sub> deficiency ameliorated EAE, increased the number of oligodendrocytes in EAE lesions, and decreased fibrinogen extravasation and macrophage infiltration [143].

#### 13.5 Conclusions

Collectively, this review provides an overview of lipid signaling pathways in MS and EAE. Each bioactive lipid, lipid metabolic enzyme, and lipid GPCR play key roles in regulating immune and neural functions. One of the most important contributions to the lipid biology field in neurodegenerative diseases was the development of fingolimod for the treatment of RRMS patients. Although most DMTs are immunomodulatory, fingolimod shows dual regulatory roles in the immune and nervous systems. Considering the neurodegenerative features of progressive forms of MS, not only immunomodulation, but also neuroprotection and neuroregeneration, should be explored. Unfortunately, we still have a lot to learn about the roles of lipid mediators including (EETs, HETEs, SPMs, cannabinoids, and lysophospholipids), lipid metabolic enzymes (PLA<sub>2</sub>s, COX-1, PGDS, LysoPAFAT and other acyltransferases, diacylglycerol lipase, Sphks, and ATX), lipid GPCRs (DP<sub>2</sub>, BLT<sub>2</sub>, CysLT<sub>1, 2, 3</sub>, cannabinoid receptors, fatty acid receptors, LPA1, 3, 5, 6, S1P<sub>3-5</sub>, and other LP receptors), and more in EAE and MS. Among them, several proteins (L-PGDS,

LPA<sub>1</sub>, S1P<sub>5</sub>, and GPR17) that are highly expressed in oligodendrocytes and anti-inflammatory/proresolving lipid mediators (EETs and SPMs), are attractive neuroprotective targets to study in EAE/MS.

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# Role of Bioactive Sphingolipids in Inflammation and Eye Diseases

14

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# Abstract

Inflammation is a common underlying factor in a diversity of ocular diseases, ranging from macular degeneration, autoimmune uveitis, glaucoma, diabetic retinopathy and microbial infection. In addition to the variety of known cellular mediators of inflammation, such as cytokines, chemokines and lipid mediators, there is now considerable evidence that sphingolipid metabolites also play a central role in the regulation of inflammatory pathways. Various sphingolipid metabolites, such as ceramide (Cer), ceramide-1-phosphate (C1P), sphingosine-1-phosphate (S1P), and lactosylceramide (LacCer) can contribute to ocular inflammatory diseases through multiple pathways. For example, inflammation generates Cer from sphingomyelins (SM) in the plasma membrane, which induces death receptor ligand formation and leads to apoptosis of retinal pigment epithelial (RPE) and photoreceptor cells. Inflammatory stress by reactive oxygen species leads to LacCer accumulation and S1P secretion and induces proliferation of retinal endothelial cells and eventual formation of new vessels. In sphingolipid/lysosomal storage disorders, sphingolipid metabolites accumulate in lysosomes and can cause ocular disorders that have an inflammatory etiology. Sphingolipid metabolites activate complement factors in the immune-response mediated pathogenesis of macular degeneration. These examples highlight the integral association between sphingolipids and inflammation in ocular diseases.

#### Keywords

Inflammation · Sphingolipid · Ceramide · Ceramide-1-phosphate · Sphingosine-1phosphate · Lactosylceramide · AMD · Uveitis · Diabetic retinopathy · Glaucoma

# 14.1 Introduction

Inflammation is a defensive mechanism of a host organism against infectious agents and injury. Inflammatory mechanisms represent a network of complex processes requiring the involvement of different metabolic and signaling pathways to

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resolve damage to tissue or to fight against infection. However, inflammation may also be detrimental if it progresses out of control. Host organisms have evolved different signaling mechanisms to respond appropriately against a range of threats by utilizing specialized immune cells such as neutrophils, resident and recruited macrophages, dendritic cells, and lymphocytes [57]. Host immune machinery is activated against microbial pathogens and recognizes molecular structures found in pathogens, known as Pathogen-Associated Molecular Patterns (PAMPs) [80], whereas signals released from stressed and damaged host cells are known as Damage Associated Molecular Patterns (DAMPs) [175]. Both PAMPs and DAMPs are recognized by molecular structures on immune cells, known as Pattern recognition receptors (PRR). The Tolllike receptors (TLR) are important class of PRR [82] that recognize bacterial (pathogen) membrane lipopolysaccharides and viral RNA as well as endogenous molecules that are secreted from damaged or dying cells [126]. After activation, TLRs recruit downstream signal adaptor proteins, including Myeloid differentiation primary response 88 (MyD88) and TIR-domain containing adapter inducing interferon  $\beta$  (TRIF), which leads to activation of kinases, such as Inhibitor of kappa B (IkB) and Mitogen activated protein kinase (MAPK), downstream transcription factors, such as Nuclear factor kappa B (NF-kB), Activator protein-1 (AP-1), and interferon regulatory factor family proteins. These factors can stimulate transcription of several amplifiers and effectors [155]. Different types of cytokines, such as Tumor necrosis factor (TNF)- $\alpha$ , Interleukin (IL)-1 $\beta$  and IL-6, and chemokines, e.g., C-C motif chemokine ligand 2 (CCL2), C-X-C motif chemokine ligand 1 (CXCL1), and C-X-C motif chemokine ligand 10 (CXCL10) act as amplifiers and effector molecules in this mechanism. Another member of the innate immune sensor is the NOD-like receptor (NLR), which is a component of the inflammasome multiprotein complex [125]. The third type of pattern recognition receptor is Retinoic acid inducible gene 1 (RIG1) [87]. Cooperative interactions of inflammasomes and complement cascades play significant roles in immune surveillance and inflammatory processes [10]. During complement-mediated targeted cell lysis, there is an initiation of strong opsonization of the foreign pathogen or apoptotic cell/cellular compartment, followed by induction of proinflammatory signaling by anaphylatoxins, which lead to recruitment of macrophages and eventually phagocytosis of the pathogen through the formation of the membrane attack complex (MAC) [129]. Thus, the inflammasome-complement pathway eliminates the pathogen and clears and eliminates potential mediators of damage and injury. Acute and chronic inflammation can influence vascular permeability of the cell. Activation of proinflammatory cytokines up-regulates selectins (e.g., P-selectin) and integrin ligands, e.g., Vascular cell adhesion molecule 1 (VCAM-1) and Intercellular adhesion molecule 1 (ICAM-1), on the lumen of endothelial cells. These are sensed by selectin ligands, e.g., P-selectin glycoprotein ligand 1 (PSGL1) and integrins, e.g., Lymphocyte function-associated antigen 1 (LFA1) on the surface of leukocytes, and promote loosening of tight junctions between endothelial cells while permitting transfer of solutes to peripheral tissues and leukocyte infiltration through the blood-brain barrier [127]. Inflammasome activation can also regulate synthesis of various eicosanoids, such as prostaglandins (PGs), thromboxane, hydroxyeicosatetraenoic acid (HETEs) and leukotrienes [128]. In addition to inflammasome-mediated canonical activation of caspase-1-dependent maturation of proinflammatory cytokines IL-1β and IL-18, caspase-1 independently activates cytosolic phospholipase A2 (cPLA2) that stimulates eicosanoid synthesis. In this mechanism, there is formation of a membrane pore, which drives rapid Ca2+ influx. The influx of Ca2+ then activates cPLA2 and generates arachidonic acid (AA) from membrane phospholipids. This arachidonic acid is further converted to prostaglandins and thromboxanes by cyclooxygenases-1 (COX-1) and COX-2, and leukotrienes and HETEs are converted by lipoxygenases [163]. The generation of eicosanoids is responsible for increasing vascular permeability and leucocyte recruitment during diverse homeostatic and pathological processes [30]. Thus, during injury or disease, the immune cells become reactive and their PRRs are activated, which leads to generation of innate inflammatory mediators including complement pathway, chemokines and cytokines, and inflammatory enzymes. These proinflammatory mediators stimulate immune cells to proliferate, migrate and induce expression of adhesion molecules on endothelial cells, which promote loosening of tight junctions and eventually infiltration of immune cells leading to recovery from injury or infection from pathogens or otherwise pathological changes in diseased state.

# 14.2 Sphingolipid Metabolites and Inflammation

Sphingolipids serve both structural and regulatory roles in eukaryotic cells [31, 56]. The sphingolipid metabolites Ceramide (Cer), Sphingosine-1-phosphate (S1P), Ceramide-1 phosphate (C1P), and Lactosylceramide (LacCer) are the major signaling molecules regulating key physiological functions and a variety of pathological processes, mainly related to inflammatory responses or inflammation-associated diseases [55]. Cer acts as a potent pro-inflammatory agent, whereas C1P and S1P can regulate either inflammation or participate in anti-inflammatory functions. LacCer plays a role as a signaling molecule in inflammation-induced proliferation or angiogenesis. Immune cell mediated secretion of proinflammatory cytokines stimulate inflammatory sphingolipid metabolic enzymes to convert sphingomyelin (SM) into Cer. Cer is then converted into either S1P or C1P or glycosphingolipid. The schematic diagram of sphingolipid metabolism and the biosynthetic enzymes involved in this process has been presented in Fig. 14.1. The conversion of different sphingolipid metabolites varies with cell type. These inflammatory sphingolipid mediators then induce different types of inflammatory transcription factors (e.g., NFkB) or they may activate cyclooxygenase -2, leading to production of pro-inflammatory prostaglandins. In this review, we provide an overview of the significant body of research that reveals involvement of sphingolipid metabolites in inflammation and their role in ocular diseases.

#### 14.2.1 Ceramides

Sphingolipid metabolism is regulated by cascades of enzyme activation within different cellular compartments wherein Cer occupies a central position. [56, 109] Cer plays a structural role by regulating membrane properties and its permeability [161] leading to promotion of raft fusion [46]. Cer- enriched platforms facilitate clustering of receptor molecules and their ligands [65]. This in turn helps the induction of apoptosis by clustering of CD95/Fas death receptor ligand [47]. In addition to its structural role, Cer acts as a second messenger by activating a diverse set of kinases and phosphatases [132]. The de novo Cer biosynthesis pathway is an anabolic pathway, which begins with condensation of serine and palmitoyl-CoA catalyzed by Serine palmitoyltransferase (SPT) in the endoplasmic reticulum (ER). The catabolic pathway of Cer generation occurs in the plasma membrane and lysosome via degradation of sphingomyelin (SM) to Cer and phosphorylcholine by sphingomyelinase. The third pathway is the lysosomal salvage pathway involving complex sphingolipids. Ceramide synthases play a significant role in the salvage pathway, thereby bypassing the formation of dihydroceramide. The fourth pathway of Cer biosynthesis occurs in liver mitochondria. The first report of the involvement of Cer in the inflammatory process demonstrated intracellular induction of a proinflammatory cytokine, TNF- $\alpha$ , which induced sphingomyelinase and, in turn, elevated Cer [75, 94]. Sphingolipidomics and transcriptomics studies revealed that lipopolysaccharide (LPS) induces inflammation through TLR4 in macrophage cell lines by inducing an increase in Cer [29]. In macrophages, the LPS-induced TLR4-mediated increase in de novo Cer biosynthesis is necessary for autophagosome formation, which could play a role in innate immunity [140]. Production of Cer subsequently activates a proinflammatory transcription factor, NFkB, the



Fig. 14.1 Sphingolipid Metabolites in Ocular Diseases. The name of the disorders are presented in red and enzymes responsible for these metabolites are presented in blue. The de-novo Ceramide (Cer) biosynthesis is mediated by Serine palmitoyltransferase (SPT). In salvage pathway Ceramide synthase isoenzymes (CerSs) plays role in formation of Cer from Sphingosine. Sphingomyelin phosphodiesterase isoenzymes (SMPDs) converts Sphingomyelin (SM) to Cer. Sphingomyelin synthase (SmS) is the enzyme that converts Cer to SM. Ceramide kinase (CerK) and Ceramide-1-phosphate phosphatase (C1PP), respectively converts Cer to Ceramide-1-phosphate or vice versa. Conversion of Sphingosine-1-phosphate (S1P) is mediated by

ubiquitously expressed transcription factor in mammalian cells [139]. The induction of NFkB encodes different cytokines, such as IL-1β, IL-6, IL-8, as well as chemokines, Monocyte chemoattractant protein-1 (MCP-1) including proinflammatory enzymes Cyclooxygenase -2 (COX-2), which is involved in the production of prostaglandins [169]. All these factors play important roles in inflammation. Another family of transcription factors, CCAAT/enhancer binding proteins (cEBP), is also activated by Cer in hepatocytes and macrophages. In hepatocytes, proinflammatory cytokine IL-1ß induced CCAAT activation through Cer-mediated Extracellular signal regulated kinase 1/2 (ERK-1/2) pathway [42]. Cer can lead to induction of COX-2 via cEBP activation in macrophages stimulated with LPS [25]. Cer also plays a role in obesity by

Sphingosine kinase isoenzymes (SPHKs) and for reverse reaction Sphingosine-1-phosphate phosphatase (S1PP) plays its role. Addition of glucose moiety with Cer is mediated by Glucosylceramide synthase (GCS). Lactosylceramide synthase (LCS) converts Glucosylceramide (GlcCer) to Lactosylceramide (LacCer) and Lactosylceramidase (LCdase) converts LacCer to GlcCer.GM3 ganglioside formation is mediated by GM3 synthase. Complex Gangliosides are generated by other carbohydrate moiety adding enzymes, which we discussed in our earlier review. AMD Age-related macular degeneration, DR Diabetic Retinopathy, DTS Dysfunctional Tear Syndrome, MS Multiple Sclerosis, RP Retinitis Pigmentosa

modulating inflammatory pathways. The Nlrp3 dependent inflammasome pathway increased caspase-1 activity through lipotoxicity-associated ceramide production in macrophage and adipose tissue of obese mice [162]. In mouse models, it has been reported that increases in Cer production leads to TLR-4 dependent insulin resistance by inhibiting Akt [60]. Stimulation of protein kinase C  $\zeta$  (PKC $\zeta$ ) by Cer is another pathway which inhibits Akt activity [39]. In summary, these studies support a strong link between Cer and inflammation-related disorders.

#### 14.2.2 Ceramide-1-P

Ceramide-1-phosphate (C1P) is mitogenic and anti-apoptotic for different cell types [44].

Interestingly, C1P can have a dual regulatory role by serving as an intracellular second messenger to regulate cell survival and/or as an extracellular receptor ligand to stimulate chemotaxis [43]. In inflammation, CIP also behaves in a promiscuous manner, either as a pro-inflammatory or antiinflammatory agent. The biosynthesis of C1P takes place in the trans-Golgi network through phosphorylation of Cer by Ceramide kinase (CerK). The role of C1P in inflammation was first reported in A549 lung adenocarcinoma cells, where it stimulated release of arachidonic acid (AA) and subsequent production of proinflammatory eicosanoids [120]. C1P-mediated inflammation is directly regulated by activation of cytosolic phospholipase-A2 $\alpha$  (cPLA2 $\alpha$ ), an enzyme that releases AA from membrane phospholipids [121]. Further studies demonstrated that C1P-mediated activation of group IV cPLA2 proinflammatory enzyme is chain lengthspecific; C1P bearing an acyl chain of 6 carbon or higher, activated cPLA2 $\alpha$  in vitro, whereas CIP with a shorter acyl chain length ( $C_2$ -C1P) was unable to activate this proinflammatory enzyme [150, 166]. Interestingly, prostaglandin production is a coordinated function of C1P and S1P, where S1P stimulates COX-2 activity and then cPLA2α functions in synthesis of AA to produce prostaglandins [122]. The interaction of C1P in proinflammation has also been proposed in some studies. It has been shown that, compared to wild type mice, CerK knock-out mice generate decreased level of proinflammatory cytokines, IL-6 and TNF- $\alpha$  in high fat diets and show normal insulin signaling [98]. These knock out animals show higher expression of insulin receptors and glucose transporter GLUT4 and decreased signaling of MCP-1 in infiltrating macrophages of adipose tissue. However, the role of C1P in proinflammation is complex, as other studies have demonstrated that C1P may also reduce inflammation. C1P was shown to inhibit tumor necrosis factor (TNF)-converting enzyme or TACE, which is the major metalloprotease for cleaving pro-TNF to its active form that plays a role in inflammation [79]. Also, exogenous use of C1P was shown to suppress production of IL-6, IL-8, TNF, and IL-1 $\beta$  in LPS treated human

peripheral blood mononuclear cells [54]. The bimodal behavior of C1P in pro- and antiinflammation could provide a novel therapeutic strategy for modulating inflammation associated with different diseases.

#### 14.2.3 Sphingosine-1-P

To date, Sphingosine-1-phosphate (S1P) is the best-described mediator within the sphingolipid pathway. Unlike Cer, which promotes apoptosis, S1P is responsible for suppressing apoptosis [146]. As an extracellular and intracellular messenger, S1P plays diversified roles in inflammation, cancer, atherosclerosis, autoimmunity, and angiogenesis [153]. The diversified actions of S1P are mainly regulated by five widely expressed S1P G-protein-coupled receptors, S1PR(1–5) [147]. S1P is produced by phosphorylation of free sphingosine by Sphingosine kinase isoenzymes 1 and 2 (SphK1 and SphK2). Topologically, SphK1 is a cytosolic protein and may also be localized at the plasma membrane and endocytic membrane trafficking network, whereas SphK2 mainly resides in the nucleus, mitochondria or in the ER [53]. It has been well documented that S1P gradient in circulation plays major role in lymphocyte migration and trafficking [12]. Usually, in the blood and lymph S1P level is higher than in tissues, which is important for maintaining vascular integrity. The maintenance of circulating lymphocytes is balanced through S1P; lymphocytes are attached through S1P with their receptors in the lymphoid organ to prevent their egression into blood. In inflamed tissues, there is production of S1P by SphK1 in endothelial cells. Simultaneously, S1PR1 is also activated by inflammatory signals, which in turn lead to disbalance in circulating lymphocytes [133]. The synthetic S1P analog FTY720 (Fingolimod) prevents egression of lymphocytes in circulation and accumulation in the lymph nodes [131]. Thus, FTY720 acts as an immunosuppressive drug in inflammation and autoimmune diseases. The role of S1P in inflammation varies with cell type. It plays an important role during activation of mast cells and the subsequent development of inflammatory responses [111]. The involvement of S1P in inflammation is supported by the fact that loss of generation of S1P leads to decreased levels of proinflammatory cytokines (TNF- $\alpha$ , IL-6) and proinflammatory factor, arachidonic acid, in SphK2 deficient fetal liver mast cells [112]. TNF- $\alpha$  induced proinflammatory enzyme, COX2 and production of prostaglandin E2 are regulated by activation of the Sphk1/S1P axis [120]. In addition, in an animal model of inflammation, S1P levels were decreased in dextransulfate induced colitis of Sphk1-lacking mice [143]. TNF- $\alpha$  mediated activation of Sphk1 is responsible for activation of inflammatory transcription factor NFkB. S1P binds and stimulates ubiquitin E3 ligase TRAF2 activity, resulting in Lys-63 linked polyubiquitination of Receptor interacting protein-1 (RIP-1), leading to phosphorylation of IKK complex and activation of NFkB [6]. Similarly, in Rheumatoid arthritis, S1P/S1P receptor 1 signaling upregulates proinflammatory receptor activator of NFkB ligand (RANKL) [154]. Contrary to its role in inflammation, S1P has also been reported to have antiinflammatory effects by causing a switch from pro-inflammatory macrophage subtype M1 to anti-inflammatory subtype M2. [130]. In mice, it has been reported that lymphopoiesis and neuroinflammation has been restrained by HDL-bound S1P [18]. Although lots of information supports the role of the S1P/Sphk1 axis in activation of NFkB, nevertheless it has also been reported that downregulation of SphK1 enhances chemokine CCL5, which plays an active role in recruiting leukocytes in inflammatory sites. Downregulation of Sphk2 reduced CCL5 expression. In this mechanism p38MAPK may play a significant role without affecting NFkB [2]. Another complexity in S1P biology is that not all tissues respond in a similar fashion to regulation of SIP production. For example, in a mouse model, deletion of Sphk1 decreases S1P in blood, whereas deletion of *Sphk2* increases it [86, 143]. Although we have progressed significantly in various aspects of S1P research, we are still lacking in a comprehensive understanding of the involvement of SIP mechanistic pathways in inflammation related diseases.

#### 14.2.4 Lactosylceramide

Lactosylceramide (LacCer) acts as a common precursor of all types of the lactose series of complex glycosphingolipids (GSLs) (e.g. the gangliosides and globotriosylceramide). It acts as a bioactive lipid in various physiological processes ranging from inflammation, proliferation, expression of adhesion molecules, angiogenesis and endocytosis [17]. LacCer is synthesized from ceramide generated by the *de novo* pathother way and from sphingolipids. Glucosylceramide (GlcCer) is the first glycosylation product of ceramide generated at the cytosolic surface of the Golgi. GlcCer is then translocated to the lumen of the Golgi and LacCer synthase [UDP-Galactose: glucosylceramide  $\beta$ 1,4 galactosyl transferase ( $\beta$ 4GalT)] converts GlcCer to LacCer. LacCer is an important signaling component in astrogliosis and induction of inflammatory mediators in neuroinflammatory diseases. The proinflammatory facarachidonic acid is generated tor by LacCer-mediated activation of cytosolic phospholipase A2 $\alpha$  [103]. The inflammatory mediators TNF  $\alpha$  [116] and LPS/IFN- $\gamma$  [117] activate LacCer, which in turn induces inflammatory factors, namely inducible nitric oxide synthase enzyme (iNOS) that eventually generates nitric oxide(NO) and causes neuroinflammation. In this LacCer-mediated inflammatory mechanism, Ras-NFkB-MAPK [117] and Ras-ERK1/2 [116] pathways play significant roles. LacCer also induces inflammatory mediator, NADPH oxidase and generates reactive oxygen species (ROS) from endothelial cells [16] and from neutrophils [9]. Inflammation stimulates proliferation and migration of immune cells and induces expression of adhesion molecules on endothelial cells. LacCer induces expression of Platelet endothelial cell adhesion molecule-1 (PECAM1) on endothelial cells in the microenvironment of monocyte accumulated cells at the site of inflammation [45]. This LacCer-mediated expression of PECAM1 is regulated by cross-talk between activation of PKC- $\alpha/\zeta$  and stimulation of phospholipase A2. The inflammation induced LacCer activation plays a role in PECAM1 expression

and induces angiogenesis. LacCer mediated induction of angiogenesis has been shown in Human umbilical vein endothelial cells (HUVEC). Loss of the LacCer synthase gene in HUVEC cells leads to reduction of angiogenesis by reduction of PECAM1 expression when induced with Vascular endothelial growth factor (VEGF) [124]. LacCer serves as a lipid second messenger in VEGF induced angiogenesis, separate from S1P mediated pathway [77]. LacCer also contributes to mitochondrial dysfunction and generation of ROS in murine model of diabetes [107]. This information suggests that LacCer acts as a connecting modulator between inflammation and angiogenesis by expression of cell adhesion molecules and eventually, angiogenesis.

# 14.3 Sphingolipids in Ocular Disease

# 14.3.1 Ocular Inflammation

Interestingly, ocular tissues prevent and resolve inflammation by different mechanisms. The barrier between circulating blood and the retina, lack of a direct lymphatic drainage pathway, and the intraocular microenvironment limit local immune and inflammatory responses and make the eye an immune-privileged tissue [148]. A major population of innate inflammatory cells involved in ocular inflammation are macrophages [27], whereas adaptive immune elements, CD4+ and CD8+ T cells, express effector function in the eye [119]. In the most common ocular inflammatory disease, uveitis, inflammation is associated with Th1 and Th17 cells [21] along with different innate effectors, such as monocytes and neutrophils. In Age-related macular degeneration (AMD), innate/complement inflammatory responses play a significant role [32] along with adaptive immune responses [108]. Diabetic retinopathy (DR) is another inflammatory and a classical microvascular disease, where presence of microglia has been reported in the outer nuclear layer and photoreceptor layer [173].

# 14.3.2 Sphingolipidoses and Ocular Inflammation

There are similar reports on ocular inflammation from metabolic diseases, which often cause neurodegeneration and visual impairment. Many of these diseases are lysosomal storage disorders resulting in functional impairment of lysosomal enzymes or co-factors responsible for accumulation of sphingolipid metabolites in the cell [23]. Sphingolipids are fatty amino alcohols, which regulate cell survival, growth, inflammation, senescence and apoptosis [89]. In the mouse model of GM1 and GM2 gangliosidoses, there is microglial activation leading to elevation of proinflammatory cytokines TNF- $\alpha$ , IL-1 $\beta$  [68]. The GM1 and GM2 Gangliosides are sialic acidcontaining glycosphingolipids, which plays important role in cell-cell recognition, adhesion and signal transduction. The loss of beta hexosaminidase A and hexosaminidase B causes accumulation of gangliosides in the brain and nerve cells during Tay Sachs and Sandhoff disease, the lysosomal storage disorders [171]. The accumulation of gangliosides in patients' retinas has been reported in Tay Sachs [104] and Sandhoff disease [135]. Accumulation of glucocerebroside has been observed in Gaucher patients leading to pathological abnormalities in the eye ranging from ocular motor apraxia [35] to corneal opacity [51] followed by infiltration of monocytes/macrophages [40]. In Krabbe's disease (globoid cell leukodystrophy or galactosyl ceramide lipidosis), neuroinflammation is the major component of pathogenesis. A reduction of retinal ganglion cells and nerve fiber layers of the retina are observed in Krabbe's disease [34]. In murine models, there is a generation of numerous proinflammatory molecules, including Major histocompatibility complexes (MHC) [95], TNF- $\alpha$ , IL-6 [84], and Monocyte chemoattractant protein-1 (MCP 1), and IL-10 [167]. Activated microglia produce an inflammatory signaling mediator, Prostaglandin D<sub>2</sub> (PGD<sub>2</sub>), which activates astrocytes in mouse models of Krabbe's disease [101]. Monoglycosylsphingolipid (Psychosine) plays a significant role as an inflammatory component in the pathogenesis of

Krabbe's disease [152]. Niemann-Pick is a lysosomal storage disease caused by a mutation in the acid sphingomyelinase gene leading to dysfunction of sphingolipid signaling [81]. In Neimann-Pick Type A, ocular abnormalities range from corneal opacification to retinal opacification with a macular cherry red spot [164]. Whereas in the case of Neimann-Pick Type B, the ocular manifestation is mainly retinal with pathological features including macular halos and cherry-red maculae [96]. Optic nerve pallor and perimacular gray discoloration in Neimann-Pick Type C have been observed, both clinically and histologically. In knock-out mouse models of Neimann-Pick disease, there is enhancement of microglial activity and upregulation of IL-1 $\beta$  from astrocytes [15]. In Farber disease, there is accumulation of ceramide in the joints, liver, throat, CNS and retina due to deficiency of ceramidase [41]. The pathological changes are observed in retinal ganglion cells with gross distention and inclusions [172]. Fabry disease is a deficiency of α-galactosidase A which leads to accumulation of globotriosylceramide. The most common ocular condition arising from this is cornea verticillate [144]. Overall, these observations suggest a role for sphingolipids in ocular inflammatory diseases.

# 14.3.3 Sphingolipids and Autoimmune Eye Diseases

Uveitis is an autoimmune eye disease where the uvea is pathologically affected. There is inflammation of the uvea, which composes the middle layer of eye including the iris, ciliary body and choroid. There are different types of uveitis, which is classified according to International Uveitis Study Group (IUSG) Classification, which includes Anterior Uveitis, Intermediate Uveitis, Posterior Uveitis and Panuveitis [66]. Anterior Uveitis is acute type and it is most common kind of uveitis where anterior chamber is inflamed. It mainly affects the iris and is often called as Iritis. Iridocyclitis and Anterior cyclitis are also included in this category of Anterior

Uveitis. In Intermediate Uveitis there is chronic inflammation, which affects the vitreous. It includes Pars planitis, Posterior cyclitis and Hyalitis. During Posterior Uveitis inflammation affects retina, choroid and optic nerve. It could be chronic and recurrent in nature. The disease named Chorioretinitis. Retinochoroiditis. Retinitis and Neuroretinitis are under the category of Posterior Uveitis. Pathologically, Posterior Uveitis involves breakdown of bloodretinal barrier (BRB), whereas in other forms of uveitis do not [37]. Like Posterior uveitis pathology, in Experimental Autoimmune Uveitis (EAU), there is an extensive breakdown of BRB and release of retinal autoantigen [49]. The EAU follows classical example of organ-specific autoimmune disease that resembles Posterior Uveitis in humans [22]. In case of Panuveitis, the inflammation affects entire uvea. The inflammation associated with uveitis is due to infiltration of both innate and adaptive immune cells [61]. Using a murine model of uveitis, it has been confirmed that T cells are involved and that Th17 and Th1 play a significant role in the inflammatory mechanism. Th17 and Th1 recruit different innate effector molecules: Th17 recruits neutrophils and Th1 recruits monocytes; both cause tissue destruction with independent mechanisms of pathology, with proinflammatory cytokines playing a major role [119]. Interestingly, FTY720, a structural analog of Sphingosine (Sph) and an FDA-approved therapeutic drug for Multiple sclerosis (MS), has been found to be effective in a rat model of experimental autoimmune uveitis [26]. The exact mechanism of FTY720 is still unknown, but it acts in a complex way on sphingolipid metabolism. Sphk2 phosphorylates FTY720 to FTY720-P, which is a mimetic of S1P and inactivates S1P receptor mediated signaling [91]. It also inhibits *de novo* ceramide synthesis and also acts to inhibit ceramide synthase enzymes [23]. This same drug was earlier used in experimental treatment of Vogt-Koyanagi-Harada (VKH) uveitis patients to suppress production of granulocyte monocyte colony stimulating factor by T cells [134]. The T cell clones (TCC) from aqueous humor (AH) or peripheral blood mononuclear cells (PBMCs) from VKH patients produced significantly higher level of proinflammatory cytokines IL-6, IL-8 and IFN-y in comparison with healthy donors. This finding suggests a role for sphingolipid in inflammation and lymphocyte migration in uveitis. Recently, in a Wister rat model of endotoxin-induced uveitis (EIV), increased levels of proinflammatory cytokines IL-6 and TNF- $\alpha$  were noted in the aqueous humor [165]. Increased levels of ceramides C24:0 and C24:1, and sphingomyelin C24:0 were also reported in the aqueous humor. In the retina, similar length carbon chain species of ceramide also have been noticed in EIV rats. Increased levels of proinflammatory transcription factor NFkB were also observed in the retina of EIV rats. These observations suggest that infiltration of innate and adaptive immune cells induces inflammation, which could be mediated through modulation of sphingolipid metabolites. Thus, sphingolipids may play a major role in uveitis pathology.

Multiple Sclerosis is an autoimmune disease. Inflammation-related retinal atrophy is one of the pathological features related to MS. Significant loss of retinal ganglion cells and the presence of human leukocyte antigen-DR positive cells in the retina, with activation of microglia are characteristic abnormalities associated with MS [48, 160]. In the central nervous system (CNS), oligodendrocytes are the myelin forming cells, which are affected during MS by activation of glial cells and infiltration of lymphocytes and macrophages, to apoptosis of oligodendrocytes. leading Sphingolipids are the major component of myelin sheath and there are multiple pathophysiological roles of sphingolipids in MS. In MS patients, increased levels of ceramide have been reported in oligodendrocytes [141] in association with an increase in sphingosine in white matter [102]. In addition to NSMase- Ceramide upregulation in MS, sphingosine kinase 1- S1P receptor signaling regulates astroglial proliferation and gliosis [168]. As S1P- S1P receptor 1 is a main pathway of lymphocyte egression in MS, application of Fingolimod or FTY720, an immunosuppressive S1P receptor agonist drug reduces lesion formation patients in MS [73]. Neutral Sphingomyelinase (NSMase) activation and pro-

duction of ceramide has been linked with types of neuroinflammation other than MS, including those that are connected to NFkB regulated pathways that cause blood brain barrier disruption, vascular leakage, and lymphocyte migration with upregulation of ICAM1, VCAM1 and selectin [67]. Although Fingolimod is currently used in the treatment of MS, one of the common side effects of this drug is Fingolimod-associated macular edema (FAME) [90]. Retinal hemorrhages and retinal vein occlusion can also occur in Fingolimod treated patients. Although information pertaining to molecular mechanisms associated with FAME is still lacking, a possible mechanism could be disruption of cell-to-cell and cell-to-matrix adhesion complexes in retinal vessels resulting in stress in vascular permeability and subsequent macular edema [97, 113]. While our current understanding of MS is incomplete, there appears to be a strong correlation between MS related retinal degeneration and ceramide-related inflammatory pathways.

# 14.3.4 Sphingolipids and Degenerative Retinal Diseases

Progressive damage to the retina and death of photoreceptors is a hallmark for degenerative retinal diseases, including Age-related macular degeneration (AMD) and Retinitis Pigmentosa (RP). AMD is associated with several pathological disorders, ranging from inflammation, malfunctioning of autophagy and chronic oxidative stress leading to degeneration of retinal pigment epithelium (RPE) and ultimately photoreceptor death with vision loss [99, 123]. RPE is the pigmented cell layer, which is attached to underlying choroid and provides nourishment to overlying retinal visual cells. It also functions in phagocysecretion and immune modulation. tosis, Photoreceptor cells function in visual phototransduction and visual signal generation. There are two types of photoreceptor cells in mammalian retinas, rods and cones, along with second and third order neurons, bipolar and ganglion cells, respectively. During early stage of AMD there is accumulation of extracellular deposits called drusen in the retina, between RPE and Bruch's membrane. Drusen formation is linked to chronic low-level inflammation and complement activation during initial stages in the pathogenesis of AMD [7, 69]. Activation and secretion of various cytokines and chemokines, e.g., IL-1β, IL-6, TNF-α, CXCL8 play a significant role in initiation of inflammation [83]. The later stage of disease progression is classified as either 'Dry AMD' or 'Wet AMD'. Dry AMD is limited to damage of the macula region of the retina caused by atrophy whereas wet AMD also includes both macular atrophy as well as choroidal neovascularization (CNV). Inflammation mediated by complement factor plays an important role in AMD. In addition to this, genetic mutations associated with complement factor gene is among the major risk factors in AMD pathogenesis. One such factor in AMD is the inheritable genetic mutation, Y402H in complement factor H (CFH) [52, 76]. Other variants are present in C3, CFB, C2 genes, associated with susceptibility to AMD [8]. These mutations are associated with a reduction of anti-inflammatory iC3b component and an increase of proinflammatory cytokines TNF- $\alpha$ and IFN- $\gamma$  [24]. RPE also plays role in autophagy by autophagic degradation of photoreceptor outer segments (POS) in the process called heterophagy [70]. In aging, the function of RPE declines and results in accumulation of POS, which eventually forms lipofuscin in lysosomes leading to malfunctioning of lysosomes, generation of oxidative stress and retinal inflammation [36]. Oxidative stress-induced Cer biosynthesis genes are involved in photoreceptor cell death [13]. Increased Cer levels in RPE cells raises the level of inflammatory factor and ROS, which leads to mitochondrial permeabilization and activation of caspase-3, followed by apoptosis [72]. Use of desipramine protects photoreceptor death by reducing inflammatory factors and oxidative stress augmented by Cer, as desipramine inhibits sphingomyelinase's ability to convert sphingomyelin to Cer [136]. Similarly, overexpression of Acid ceramidase (ASAH1) in ARPE19 cells (Human retinal pigment epithelial cell line) protects from oxidative stress by reducing Cer level

[151]. On the other hand, overexpression of Sphingomyelin phosphodiesterase 3 (SMPD3) enhances Cer production, which in turn leads to enhancement of RPE cell death by increasing inflammatory factors and stress [174]. In mouse models, it has been reported that cholesterol mediates activation of acid sphingomyelinase, which disrupts autophagy in RPE and leads to early onset macular degeneration [159]. Increases in Cer eventually promote inflammatory factors and oxidative stress, which prevent proper endosomal recycling of complement regulatory proteins after complement attack and disrupt endosomal biogenesis [156]. Aberrant endosomal biogenesis mediates complement activation in the RPE cells in murine model of macular degeneration [74]. In Rd10 mouse models, inhibition of de novo Cer biosynthesis by myriocin lowers retinal Cer levels and restricts photoreceptor death in RP [149]. Accumulation of POS increases oxidative stress and activates CFB, leading to AMD associated neovascularization [157]. The inflammatory factor also activates complement factor C3 and aggravates AMD pathogenesis [105]. Ceramide induces retinal degeneration, whereas choroidal neovascularization (CNV) is promoted by administration of alpha-galactosylceramide into the vitreous cavity of C57BL/6 mice [58]. Similarly, S1P2 receptor deficient mice do not develop neovascularization in the murine model of ischemia driven retinopathy [142]. The blockage of S1P by sonepcizumab, a humanized monoclonal antibody, also significantly reduces CNV in mouse models [170]. In summary, sphingolipids appear to play a significant role in retinal degenerative diseases by increasing inflammation, generating oxidative stress and deregulating lysosomal function in RPE and triggering photoreceptor cell death and/ or neovascularization.

# 14.3.5 Sphingolipids and Diabetic Retinopathy

Diabetic retinopathy is a microvascular disease affecting retinal vascular degeneration and defective repair of retinal endothelial cells with persistent low-grade inflammation. It has been reported that activated retinal glial cells and pigment epithelial cells express proinflammatory cytokines and VEGF in diabetes, which contributes to damage of retinal vasculature [1, 20, 100]. In addition to this, activation of circulating myelomonocytic cells from bone marrow increases leukocyte adhesion and contributes to retinal inflammation [85, 138]. There is also myeloid derived monocyte infiltration in diabetic retinas and exacerbation of inflammation by secreting proinflammatory cytokines, which further activates resident microglia, astrocytes and Muller glia in the retina [1, 59, 145]. The proinflammatory cytokines secreted from these cells cause endothelial cells to produce Acid sphingomyelinase (ASMase). Endothelial cells produce up to 20-fold more secretory sphingomyelinase than macrophages in response to cytokine stimulation [92]. The increase in ASMase regulates cytokine-mediated inflammation by generation of Cer in diabetic human and animal models [115]. Using different inhibitors, it has been observed that ASMase plays a major role in diabetic retinopathy. Increases in ASMase by TNF- $\alpha$ and IL-1 $\beta$  induce VEGF and ICAM-1 in Human retinal endothelial cells (HREC) and regulate retinal microangiopathy [114]. Retinal vascular permeability is mediated by very long chain ceramide, which is decreased in diabetic conditions due to decreases of biosynthetic enzyme, an Elongation of very long-chain fatty acids protein 4 (ELOVL4) [71, 158]. The streptozocininduced rat models exhibit decreased levels of Cer concomitant increase and а of Glucosylceramide (GlcCer). The inhibition of glucosylceramide synthase increases the viability of retinal neuronal cells and insulin sensitivity in retinal neurons [38]. In addition to this it has also been observed that the pharmacological inhibition glucosylceramide of synthase increases insulin sensitivity in Zucker diabetic fatty (ZDF) rat [3]. Thus sphingolipid, more specifically Cer and GlcCer, play significant role in inflammation and retinal neovascularization in diabetic retinopathy.

#### 14.3.6 Sphingolipids and Glaucoma

Glaucoma is a neurodegenerative disease where retinal ganglion cells (RGC) and their axons in the optic nerve are affected. The major risk factor of glaucoma is elevation of intraocular pressure (IOP). The neuroinflammatory responses during early stages of glaucoma are mediated by astrocytes, resident microglia, and other monocytederived cells in the optic nerve head (ONH). Proteomic analysis of human glaucomatous retinas revealed upregulation of TLR signaling, where TLR2, TLR3 and TLR4 was observed in microglia and astrocytes from glaucomatous retinas [88]. In DBA/2J (Dilute Brown Non Agouti, which develops progressive eye abnormalities that closely mimic hereditary glaucoma) mice in early stages of glaucoma, 11 of the 13 TLRs were upregulated in the optic nerve head (ONH) [62, 64]. As there was upregulation of TLR, the downstream factors such as MyD88, MAPK and NFkB all were activated, which in turn lead to activation of proinflammatory cytokines. In RGC degeneration, Fas ligand also is a major effector in DBA/2J mice models [50]. In disease pathology apart from monocytes derived cells [63], the complement cascade system plays a significant part in inflammation in DBA/2J animal models. Upregulation of C1 complex was observed in microglial cells in ONH in DBA/2J glaucomatous mice [62]. The second component of the complement cascade that plays a damaging role is complement component C5, a necessary component for MAC generation. Although there is incomplete information on role of sphingolipids in glaucoma development, it has been reported that in the aqueous humor there are native sphingolipid species. The levels of sphingomyelin and sphingoid base were reduced in hypertensive state from normotensive conditions, whereas S1P and ceramide levels increased in a hypertensive state [33] in DBA/2J mouse models. Data pertaining to sphingolipid composition of human aqueous humor [5] and trabecular meshwork [4] have also been generated. There is still a significant lack of information regarding the sphingolipid biology in glaucoma.

# 14.3.7 Sphingolipids and Dry Eye Syndrome

Dysfunctional tear syndrome (DTS), commonly known as dry eye disease, is caused by tear deficiency or excessive evaporation [19]. In addition to this, ocular surface inflammation due to increase in tear osmolarity plays a major role in DTS [78]. The tear film performs diversified functions, ranging from maintaining light refraction, supplying the cornea with nutrients and oxygen, lubrication of the cornea and conjunctiva, and ocular surface protection against foreign materials [110]. There are three different layers in tear film composition: the carbohydrate-rich glycocalyx layer, the intermediate aqueous layer, and the superficial tear film lipid layer (TFLL) [28]. Meibomian glands are the major source of TFLL lipids. Meibomian Gland Dysfunction (MGD) is a complex multifactorial disorder arise from combination of five different pathophysiological mechanisms; these are eyelid inflammation, conjunctival inflammation, corneal damage, microbiological changes and dry eye disease resulting from tear film instability [14]. Mass spectrometry (MS) data from dry eye disease patient reveals the role of sphingolipid in maintaining TFLL integrity [78]. In patient meibomian samples, significant increases of SM levels were observed compared to normal subjects. The individual short chain GlcCer species were significantly increased in patient meibomian samples. Whereas in case of meibomian keratoconjunctivitis (MKC), increased levels of Cer were reported due to abnormal hyperkeratinization [93]. Similarly, increased Cer levels disrupt stability and elasticity of TFLL [11]. However, patients with chronic blepharitis had been reported with decreased amount of cerebrosides in their meibomian gland [106]. In animal models, very long chain ceramides (acylceramide) in TFLL prevent dry eye disease, as transgene ELOVL1 mice developed corneal opacity with vascular invasion, accompanied by epidermalization of the cornea due to lower level of acylceramide in epidermis and in the meibomian gland [137]. Recently, our lab has reported increase in Cer/S1P ratio from poor quality meibomian gland tear film as compare to the good quality individuals [118]. The sphingolipid metabolites in meibomian gland tear film could serve as clinical signature of different types of eye diseases.

#### 14.4 Summary and Conclusion

This chapter summarizes our current understanding of inflammation and its correlation with sphingolipid metabolites in eye diseases. Although ocular immune privilege protects the eye and retina from inflammation, the modulation and accumulation of different sphingolipid metabolites can perturb the ocular antiinflammatory environment and lead to ocular pathology in different lysosomal storage disorders, autoimmune diseases, age related macular degeneration and diabetic retinopathy, suggesting an involvement of sphingolipid metabolites in maintaining homeostasis of the eye. Fig. 14.1 shows a schematic diagram of sphingolipid metabolism and involvement of different sphingolipid metabolites in ocular diseases. The bioacsphingolipid ceramide tive acts as а proinflammatory lipid, whereas C1P and S1P have both pro- and anti-inflammatory functions. LacCer, on the other hand, acts as an angiogenic sphingolipid and induces neovascularization. In ocular diseases, ceramides are found to be inflammatory factors for stimulating proinflammatory cytokines and in some cases, proinflammatory cytokines induce the formation of ceramide that may be ultimately responsible for retinal cell death. GlcCer, LacCer, and S1P have been found to be associated with the cross talk between immune cells and endothelial cells that eventually develop neovascularization in 'wet AMD' and diabetic retinopathy. The loss of homeostasis in diseased conditions leads to stress in the endoplasmic reticulum, mitochondria, lysosomes and ultimately to activation of different proinflammatory factors. A more complete understanding of sphingolipid metabolites and their role in inflammation will help in our understanding of the etiology and pathobiology of various eye diseases that have inflammatory links.

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# Roles of Ceramides and Other Sphingolipids in Immune Cell Function and Inflammation

# 15

# Sabrin Albeituni and Johnny Stiban

# Abstract

Ceramides are bioactive sphingolipids that support the structure of the plasma membrane and mediate numerous cell-signaling events in eukaryotic cells. The finding that ceramides act as second messengers transducing cellular signals has attracted substantial attention in several fields of Biology. Since all cells contain lipid plasma membranes, the impact of various ceramides, ceramide synthases, ceramide metabolites, and other sphingolipids has been implicated in a vast range of cellular functions including, migration, proliferation, response to external stimuli, and death. The roles of lipids in these functions widely differ among the diverse cell types. Herein, we discuss the roles of ceramides and other sphingolipids in mediating the function of various immune cells; particularly dendritic cells, neutrophils, and macrophages. In addition, we highlight the main studies describing effects of ceramides in inflammation, specifically in various inflammatory settings including insu-

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lin resistance, graft-versus-host disease, immune suppression in cancer, multiple sclerosis, and inflammatory bowel disease.

#### Keywords

Ceramides · Immune cells · Sphingolipids · Inflammation · Disease

# Abbreviations

3KS	3-keto-sphinganine		
acyl-CoA	fatty acyl-coenzyme A		
aSMase	acid sphingomyelinase		
ATM	adipose tissue macrophages		
C1P	ceramide 1-phosphate		
CerS	ceramide synthases		
CNS	central nervous system		
COX-2	cyclooxygenase-2		
CTL	cytotoxic T lymphocytes		
CXCR2	C-X-C motif chemokine receptor		
	type 2		
DAG	diacylglycerol		
DC	dendritic cells		
DSS	dextran sulfate sodium		
EAE	autoimmune encephalomyelitis		
ERK	extracellular signal-regulated		
	kinases		

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fMLP	N-formylmethionine-leucyl-		
	phenylalanine		
GalCer	galactosylceramides		
G-CSF	granulocyte-colony stimulating		
	factor		
GI	gastrointestinal		
GVHD	Graft-Versus-Host Disease		
HIV	human immunodeficiency virus		
IBD	Inflammatory Bowel Disease		
IFNγ	interferon gamma		
IL-	interleukin		
iNOS	inducible nitric oxide synthase		
IRS-1	insulin receptor substrate-1		
JNK	c-Jun N-terminal kinase		
LacCer	lactosylceramide		
LipC6	nanoliposome-loaded C <sub>6</sub> -ceramide		
LPS	lipopolysaccharide		
MAPK	mitogen-activated protein kinase		
M-CSF	macrophage-colony stimulating		
	factor		
MDSC	myeloid-derived suppressor cells		
MS	Multiple Sclerosis		
NETs	neutrophil extracellular traps		
Nlrp3	Nod-like receptor pyrin domain-		
1	containing-3		
NO	nitric oxide		
PI3K	phosphatidylinositol 3 kinase		
РКВ	protein kinase B		
ΡΚϹζ	protein kinase C zeta		
PRR	pattern recognition receptors		
ROS	reactive oxygen species		
S1P	sphingosine 1-phosphate		
Sa	sphinganine		
SK	sphingosine kinase		
SLs	sphingolipids		
SMase	sphingomyelinase		
So	sphingosine		
SPT	serine palmitoyltransferase		
TAM	tumor-associated macrophages		
TCR	T cell receptor		
TEM	tumor microenvironment		
TGFβ	transforming growth factor beta		
TLRs	toll-like receptor		
TNFα	tumor necrosis factor alpha		
T <sub>reg</sub>	regulatory CD4+ T cells		
	-		

# 15.1 Introduction

Ceramides are sphingolipids (SLs) that along with sterols and glycerolipids constitute the "fluid" part of the plasma membrane of eukaryotic cells. Ceramides are biologically active metabolites of the SL family, composed of a sphingoid base that mainly consists of the 18-carbon amino alcohols sphinganine (Sa) or sphingosine (So) covalently bound to a long fatty acyl side-chain [1, 2]. Conjugation of various headgroups to ceramide leads to the production of sphingomyelin (choline phosphate group), ceramide 1-phosphate (C1P) (phosphate group), glucosylceramide (glucose), galactosylceramides (GalCer) (galactose), or diverse glycolipids of the ganglioside and globoside families (addition of various saccharides) [1, 3, 4]. Apart from the differences in the headgroups, the variations in the number of carbons of the sphingoid base, the length of the fatty acyl sidechain, and location of double bonds lead to the diversification of ceramide structure and biological function [5].

In eukaryotic cells, ceramide generation occurs via three main pathways: de novo synthesis, sphingomyelin hydrolysis, and the salvage pathway [6, 7]. In the *de novo* biosynthetic pathway, ceramide synthesis is first mediated by serine palmitoyltransferase (SPT) that transfers serine to fatty acyl-coenzyme A (acyl-CoA), leading to the generation of 3-keto-sphinganine (3KS), which is then reduced by 3KS reductase producing the saturated amino alcohol Sa. Sa is later N-acylated through the action of any of the 6 identified ceramide synthases (CerS) forming dihydroceramide which is finally converted to ceramide via the action of dihydroceramide desaturases [8-10]. The second major reaction that results in ceramide production is sphingomyelin hydrolysis. In this reaction ceramides are generated via hydrolysis of the phosphocholine head group from sphingomyelin by sphingomyelinase (SMase) enzymes [11, 12]. The third major pathway by which ceramide is produced is the SL recycling or salvage pathway. In this pathway, complex SLs are catabolized to So which is subsequently *N*-acylated to ceramide. A more complex network of enzymes involving SMases, ceramidases, and CerS are implicated in the pathway [13].

In mammals CerS family consists of 6 enzyme isoforms, named CerS1-6 [9, 14, 15]. Different CerS are distributed differentially in cells and tissues in the body (Fig. 15.1) [14, 16]. All CerS transfer acyl-CoA of variable lengths to the amine group of a sphingoid base [2]. Each CerS has a higher specificity towards the transfer of acyl-CoA of a certain length [9]. CerS1 shows specificity towards the transfer of  $C_{18}$ -CoA [17]; CerS2 is specific to  $C_{20-26}$  [16]; CerS3 acylates sphingoid bases with very long-chain fatty acyl CoAs (>26) [18]. CerS4 is specific for the transfer of  $C_{18-22}$  acyl CoAs [19], whereas the preferred substrates for CerS5 and CerS6 are C14-18 CoAs [20], and C<sub>14-16</sub> CoAs [16], respectively. Even though the specificity of CerS towards different CoAs has been well established, little is known about the CerS regions that determine such specificity, because the crystal structure of different CerS has not been solved. However, it has been recently reported by Tidhar et al., that 11 key amino acid residues might be critical in determining the acyl chain length specificity of CerS2, CerS4, and CerS5 [21].

Functional CerS are important players for the wellbeing of cells. Loss of CerS has led to abnormalities in mouse models (Table 15.1): CerS1 knockout mice suffered from reduced ganglioside levels and Purkinje cell loss leading to impaired behavioral and motor development [17, 22]. CerS2 knockout mice developed hepatocarcinoma and cerebral degeneration [28–30]. In addition, CerS3 loss resulted in disruption of the skin barrier and spermatogenic arrest [18, 31]. While CerS4 deficient mice developed alopecia [32] due to destabilization in epidermal stem/progenitor cell homeostasis [35]. Interestingly, CerS5 loss led to improved adipose tissue health and function after consumption of high fat diet [20]. Deficiency of CerS6 led to behavioral abnormalities and abnormal clasping of the hind limbs in mice [34].

Ceramides are the simplest SLs composed of two hydrophobic tails and a simple rather than complex hydrophilic head, consisting of a hydroxyl group [36]. Because ceramides are



**Fig. 15.1** Tissue distribution of CerS isoforms in mice. Tissue distribution of all CerS isoforms based on mRNA levels [14, 16]. The percentage next to organ pictures represents the relative amount of each CerS isoform in that organ

Deficient CerS		
isoforom	Abnormality <sup>a</sup>	Reference(s)
CerS1	Purkinje cell loss; motor development impairment	Ginkel et al. [17] and Zhao et al. [22]
CerS2	Delayed liver regeneration after partial hepatectomy	Jin et al. [23]
	Increased intestinal permeability	Chen et al. [24]
	Pheochromocytoma	Park et al. [25]
	Impaired neutrophil migration	Barthelmes et al. [26]
	Enhanced liver tumorigenesis	Chen et al. [27]
	Cerebral degeneration, myelin sheath defects	Imgrund et al. [28] and Pewzner-Jung et al. [29, 30]
CerS3	Skin barrier deformation	Jennemann et al. [18]
	Blocked spermatogenesis	Rabionet et al. [31]
CerS4	Altered lipid composition in skin; alopecia	
CerS5	Improved glucoseGosejacobhomeostasis and adiposeet al. [20]tissue health followinghigh fat diet <sup>a</sup>	
CerS6	Protection against the development of colitis <sup>a</sup>	Scheffel et al. [33]
	Behavioral problems	Ebel et al. [34]

 Table 15.1
 Cellular abnormalities resulting from CerS

 deficiency
 Image: Cers Section 1.1

<sup>a</sup>Abnormality may not necessarily be detrimental to cells, it may be beneficial, but still it is a change from normal conditions

hydrophobic and usually composed of a  $C_{18}$  sphingoid base and a long  $C_{14-26}$  N-linked-fatty acyl group, these lipids are embedded in the membrane making it harder to study their physiological functions. For this reason, more permeable ceramide analogs with short chains have been used in the laboratory ( $C_2$ ,  $C_6$ , and  $C_8$ ) to better understand ceramide biological function [37]. Nevertheless, numerous studies have been performed on the biophysical effects of ceramides in membranes ([30, 38–40]; Stiban et al.

[41]). In all, ceramides are not mere structural components in membranes. Along with So, sphingosine 1-phosphate (S1P), C1P and lysosphingomyelin, ceramides have been implicated as bioactive lipids [42] that act as second messengers and regulate cellular functions including apoptosis and stress responses [43], tumor cell death and metabolism [44], and cytokine signaling and inflammation [45, 46]. Interestingly, numerous evidences point to the ability of self-assemble ceramides to into proteinpermeable channels [47] in artificial membranes [48, 49], mitochondria [50–53] and lysosomes [54] that are upstream to caspase-dependent apoptotic cell death.

Despite the enormous progress in understanding the effects of ceramides in regulating key events in cellular biology, their role in regulating immune cell function and inflammatory diseases has only gained momentum in the last two decades. Herein, we discuss the main research findings describing the roles of ceramides in regulating the function of various immune cells, including dendritic cells (DC) and neutrophils, and the modulation of T cell function and macrophages in different disease settings. In addition, we will address the main findings highlighting ceramide function in various inflammatory diseases.

# 15.2 Ceramides and Other SLs in Immune Cell Function

#### 15.2.1 Dendritic Cells

Unraveling the mechanisms of DC development, differentiation, maturation, antigen uptake, processing, and presentation have lied in the core of immunology research since their discovery by Steinman more than four decades ago [55, 56]. The main function associated with DC is linking the innate and adaptive immune responses through the uptake of foreign antigens and subsequent presentation to T cells in order to mount effective inflammatory and immune responses. In early studies, the role of ceramides in regulating DC function was initially associated with induction of apoptosis by C2-ceramide [57]. Similarly, induction of DC apoptosis was linked to increased accumulation of ceramides in DC cultured with tumor supernatants, subsequently leading to down regulation of the following survival signaling pathways, phosphatidylinositol 3 kinase (PI3K), Akt kinase, Bcl- $x_L$ , and NF- $\kappa$ B [58]. However, induction of ceramide accumulation in DC by factors that cause DC maturation including, CD40L, interleukin 1 $\beta$  (IL-1 $\beta$ ), tumor necrosis factor alpha (TNF $\alpha$ ), and the gram-negative bacterial endotoxin lipopolysaccharide (LPS) did not induce DC apoptosis [59, 60]. These controversial findings were later reconciled by Franchi and colleagues demonstrating that ceramideinduced cell death in DC is only exacerbated in the absence of serum, while in the presence of serum and LPS, DC survival was achieved by the action of cellular ceramidases that deacylate ceramides to So, thus, preventing ceramide accumulation and DC apoptosis [61].

The study of ceramides in DC gained further attention due to the structural resemblance between the toxic component of LPS, lipid A, and ceramide (Fig. 15.2) [62]. It was suggested that LPS mediates its function by mimicking ceramides since, similar to LPS inducing DC maturation, C2-ceramide reduces micropinocytosis and antigen presentation to T cells by DC [60]. However, while both LPS and  $C_2$ -ceramide induce c-Jun N-terminal kinase (JNK), only LPS activates extracellular signal-regulated kinases (ERKs) and NF- $\kappa$ B. In addition, LPS stimulates the production of ceramides regardless of whether macrophages are genetically responsive or unresponsive to LPS [63]. Therefore, this further supported that LPS exerts its function by inducing ceramide accumulation and not by interacting with ceramide-producing enzymes or as a structural mimic of ceramide.

Moreover, ceramides play important roles in DC during viral infections. GalCer on epithelial cells binds the human immunodeficiency virus (HIV)-1 envelope glycoproteins gp120 [64, 65]



**Fig. 15.2** Structural similarity between Lipid A of LPS and ceramides. Two representative ceramides are included for comparison, the most abundant  $C_{16}$ -ceramide and the phosphorylated  $C_{12}$ -ceramide 1-phosphate. The blue triangle identifies the comparable

structure to ceramides. The 2D structures were obtained from PubChem and were redrawn to increase resolution. *PubChem CID:* 9877306 (*Lipid A*), 71314646 ( $C_{16}$ -ceramide) and 5283580 ( $C_{12}$ -ceramide *1*-phosphate).

and gp41 [66, 67]. In addition, GalCer is essential in the formation of membrane lipid rafts that allow for the internalization of HIV-1 through endocytosis and transcytosis [68]. Interestingly, GalCer is present in monocyte-derived immature DC and human primary DC isolated from mucosa, suggesting that DC mediates HIV-1 transfer to its target cells through GalCer [69]. Ceramides also stabilized the membrane for measles virus entry in DC, as Dendritic Cellspecific intercellular adhesion molecule-3-grabbing non-integrin ligation on DC results in sphingomyelinase activation and subsequent ceramide accumulation in DC exposed to either mannan or measles virus [70].

The role of ceramides was further extended beyond viral entry in DC. It has been demonstrated that local administration of a ceramide analog C<sub>8</sub>-ceramide causes the induction of DC maturation, secretion of the pro-inflammatory cytokines IL-12p70 and TNF $\alpha$ , and enhanced virus-specific T cell responses in murine models of chronic lymphocytic choriomeningitis virus clone 13 and influenza virus [71].

Collectively, these findings demonstrated that DC apoptosis, maturation, and antigen presenting capacity, are finely tuned by the action of endogenous ceramides or treatment with exogenous ceramide analogs. In addition, ceramides are key structural components of lipid rafts in DC required for binding, uptake, and internalization of viruses. These steps are key for initiating DC response allowing for viral internalization, virus peptide processing, and presentation to T cells that subsequently kill virus-infected cells. Since these findings strongly suggest that ceramides are key effectors of DC function, it is important to note that future studies elucidating the role of ceramides on the various DC subsets (e.g. plasmacytoid DC, migratory classical DC, tissue resident classical DC) could be of great therapeutic relevance in numerous immunologic diseases.

#### 15.2.2 Neutrophils

Neutrophil extravasation, migration, production of cytokines and superoxide, and formation of

neutrophil extracellular traps (NETs) in response to inflammatory stimuli are crucial for mounting an effective frontline immune response against invading microorganisms, especially extracellular pathogens [72]. Since the isolation of the free long-chain base So from human neutrophils [73], the role of ceramides in mediating and regulating neutrophil function has gained considerable traction. This was particularly due to early studies linking TNFa signaling, a potent inducer of superoxide and apoptosis in neutrophils [74], to ceramide function [75]. In HL-60 human promyelocytic leukemia cells, TNFa causes early sphingomyelin hydrolysis and ceramide production [76]. In addition, in a cell-free system both sphingomyelin content and ceramide concentration were reported to be increased in response to TNFa [77]. It was therefore hypothesized that ceramides might regulate neutrophil function in response to  $TNF\alpha$ . However, later studies have proposed that ceramides activated a negative feedback loop to inhibit superoxide production in human neutrophils. It has been shown that ceramides not only did not mediate TNFainduced superoxide production in human neutrophils [78] but also  $C_2$ -ceramide inhibited the 20:4 (n-6)-mediated superoxide formation in human neutrophils [79]. C2-ceramide also inhibited respiratory burst of N-formylmethionineleucyl-phenylalanine (fMLP)-stimulated adherent neutrophils [80-82]. Modulation of neutrophil response to polarity in response to a chemotactic agent such as fMLP has been shown to be dependent on neutral sphingomyelinase activity that converts sphingomyelin to ceramide through the modulation of Rac1/2/ RhoA GTPases [83]. These combined results suggested that induction of ceramides might delay the response of neutrophils to  $TNF\alpha$  to allow for neutrophil extravasation and migration prior to superoxide production.

Ceramides have also been implicated in the modulation of phagocytosis and migration in neutrophils. C<sub>2</sub>-ceramides reduced phagocytosis of IgG-opsonized erythrocytes by fMLP-activated neutrophils through the inhibition of MAP kinase activation and tyrosine phosphorylation of ERK1 and ERK2 [84]; and by inhibiting

phospholipase D (PLD) function required for phagocytosis [85, 86]. Similarly, in COS-1 monkey kidney immortalized cells transfected with  $Fc\gamma IIA$  receptor, inhibition of ceramide synthesis led to enhanced phagocytosis [87]. On the other hand, chemotaxis, phagocytosis and NETs formation in fMLP-stimulated neutrophils were enhanced by the selective estrogen receptor antagonist, tamoxifen, through induction of ceramide accumulation, and subsequently protein kinase C zeta (PKC $\zeta$ ) activation [88]. These conflicting findings might suggest the opposing roles of various ceramides on neutrophil function.

A more direct role of ceramides is also prevalent in neutrophils. Ceramides are pro-apoptotic metabolites whose concentration in cells rises prior to the execution of the apoptotic pathway. Neutrophil apoptosis is mediated by C16- and  $C_{24}$ -ceramides via caspase activation. This is correlated with the ability of granulocyte-macrophage colony-stimulating factor, a neutrophil survival factor, to reduce the accumulation of ceramides in neutrophils [89]. During early neutrophil apoptosis ceramide is generated by acid SMase (aSMase). In aSMase -/- mice, neutrophil apoptosis is delayed compared to WT mice [90]. In an anti-microbial setting, *Pseudomonas* auroginosa release pyocyanin that induce reactive oxygen species (ROS), which subsequently activates mitochondrial SMase, therefore, increasing mitochondrial ceramide levels and inducing cytochrome c release from mitochondria. This initiates cell death in neutrophils [91]. In addition, the enzyme sphingomyelin synthase, which mediates the transfer of choline phosphate to ceramide from phosphatidylcholine, leads to the production of sphingomyelin and diacylglycerol (DAG) [92, 93] and mediates neutrophil killing of fungus *Cryptococcus neoformans* [94].

Nevertheless, the aforementioned negative regulation by ceramides was not reported upon stimulation with the glycosphingolipid, lactosylceramide (LacCer). In neutrophils, LacCer compose more than two thirds of the glycolipid molecules in the plasma membrane and is mainly associated with a pro-inflammatory phenotype [95]. This large composition was later demon-

strated to be not only relevant in supporting the membrane structure but also as a transducer of cellular signals. In vitro studies have revealed that LacCer enhances the upregulation of the integrin, CD11b, on neutrophil surface, inducing neutrophil adherence to endothelium, and mediating the production of ROS through activation of NADPH oxidase [96]. NADPH oxidase activation in neutrophils results from the association of LacCer in lipid rafts with the Src family kinase Lyn, and subsequent activation of PI3K, mitogen-activated protein kinase (MAPK) and PKC [97]. In addition, LacCer with long-chain fatty acids  $(C_{24})$  are required for the coupling of Lyn to LacCer lipid rafts resulting in the production of superoxides and induction of migration in neutrophils [98–100]. Association of Lyn with the LacCer containing C<sub>24</sub>-fatty acid chain is necessary for the phagocytosis of mycobacteria by neutrophils. Interestingly, LacCer-enriched lipid rafts are modulated by pathogenic bacteria to evade neutrophil-mediated killing. For instance, Mycobacterium tuberculosis prevented phagolysosome formation in neutrophils through binding of bacterial mannose-capped lipoarabinomannan to LacCer rafts in neutrophils [101].

In addition, inhibition of inflammation in neutrophils has also been associated with SL biology. Ceramides inhibit immune cell responses by binding to CD300f inhibitory receptor in sepsis [102], LPS-induced skin inflammation [103], allergic responses [104], and experimental colitis [105]. Interestingly, disruption of ceramide-CD300f binding induces neutrophil infiltration in sepsis and skin inflammation [102]. Ceramide metabolites have also been implicated in the modulation of neutrophil function. For instance, chemotactic migration of neutrophils in response to IL-8 and fMLP is inhibited by S1P, an immediate metabolite of ceramide [102]. Moreover, IL-8 gene expression and secretion was shown to be induced by S1P in lung H441 epithelial cells [107]. Similarly, C1P dampens inflammation in a model of LPS-induced lung inflammation. Particularly, C<sub>16</sub>-C1P and synthetic C<sub>8</sub>-C1P analog inhibit NF-κB activation in neutrophils and LPS-mediated IL-8 production [108].

These observations make it difficult, at a first glance, to conclude whether ceramides induce or inhibit neutrophil function. It is important to note that neutrophils are short-lived innate immune cells that sense extracellular pathogens early on during infection. Therefore, early on during activation, it is possible that ceramide induction in neutrophils leads to a delay in the production of TNFa allowing for neutrophil extravasation. However, it is not yet clear whether, as neutrophil activation progresses, a certain threshold of ceramides is required to turn on the apoptotic program in neutrophils. Data using ceramide analogs must be interpreted with caution, since the use of ceramide analogs might not correspond to the physiologic concentration of ceramide during infection. Nevertheless, the importance of understanding ceramide biology in neutrophils has started to attract more attention, especially in studies describing ceramide inhibitory role in multiple models of inflammation including models of sepsis, skin inflammation, allergic responses, and experimental colitis. Thus, these results may possibly be opening new doors for the inclusion of novel ceramide inhibitors that dampen neutrophil activation in diseases in which neutrophils are the main cause of pathophysiology. The effects of different SLs on neutrophil function are summarized in Table 15.2.

#### 15.2.3 Macrophages

As the name implies, macrophages or the 'big eaters', along with DC and monocytes, compose the mononuclear phagocytic system [109, 110]. Due to their phagocytic nature, macrophages have the capacity to engulf debris, dead cells, and foreign pathogens [110, 111]. The heterogeneity and plasticity of macrophages enable these cells to mount a spectrum of pro-inflammatory or antiinflammatory responses to various stimuli [111, 112]. Due to their vast distribution throughout the body, understanding macrophage biology has been a high pursuit since their description by Metchnikoff in the late 1800s. It is therefore not surprising that such a cell type with high membrane activity has recently gained considerable attention from lipid biochemists and immunologists alike [113, 114].

Macrophages recognize pathogen-associated molecular patterns through pattern recognition receptors (PRR), including toll-like receptors (TLRs) [115, 116]. The role of ceramides in modulating the ability of macrophages to sense and respond to microbes has been documented. Global lipidome analysis revealed that ceramides accumulated in all cellular membranes of activated macrophages in response to TLR4 stimulation with Kdo2-lipid A [117–119]. Furthermore, ceramide production was induced in macro-

SL	Function	Modulation	Reference(s)
Ceramide	Superoxide production	Inhibition	Robinson et al. [79], Nakamura et al. [82], Ahmed and Berridge [80], and Fuortes et al. [81]
	Extravasation and migration	Activation	
	Phagocytosis	Inhibition	Suchard et al. [84], Hinkovska-Galcheva et al. [85], Suchard et al. [86]
	Chemotaxis	Activation	Corriden et al. [88]
	Apoptosis	Activation	Manago et al. [91]
	Inflammation	Inhibition	Izawa et al. [102], Shiba et al. [103], Izawa et al. [104], and Matsukawa et al. [105]
LacCer	Adherence to endothelium	Activation	Arai et al. [96]
	ROS production	Activation	Iwabuchi and Nagaoka [97], Chiricozzi et al. [98], Iwabuchi
	Migration	Activation	et al. [99], and Sonnino et al. [100]
S1P	Chemotaxis	Inhibition	Kawa et al. [106]
C1P	Inflammation	Inhibition	Baudiss et al. [108]

Table 15.2 SLs in Neutrophil Function

phages stimulated with TLR4 in combination with palmitate, suggesting that lipotoxic conditions induce de novo ceramide synthesis in macrophages. Increased ceramide production was also associated with induced TNF $\alpha$  and IL1 $\beta$  production by macrophages [150]. In addition, palmitate and LPS synergistic effect was also shown to induce NLRP3 inflammasome activation, resulting in induced IL-1 $\beta$  and IL-18 production [121] in a manner independent of the SPT subunit Sptlc2 [122]. Interestingly, ceramide accumulation has also been implicated in macrophage response to oxidative stress in a TLR2-dependent manner [123]. In the aforementioned study, ceramide accumulation led to suppression of mitochondrial respiration shifting the use of the citric acid cycle metabolites to the production of the antioxidant glutathione.

Ceramide accumulation has also been associated with induced cell death in macrophages [124]. It has been demonstrated that apoptosis in adipose triglyceride lipase-deficient macrophages is mediated by increased C<sub>16</sub>-ceramide concentrations [125]. Interestingly, withdrawal of macrophage-colony stimulating factor (M-CSF) from bone marrow-derived macrophages resulted in enhanced SPT activation and ceramide production prior to apoptosis [126]. This finding was further supported by the partial rescue of aSMasedeficient macrophages following M-CSF withdrawal, suggesting that apoptosis was at least in part mediated by ceramides. Additionally, ceramide accumulation was shown to mediate apoptosis in macrophages exposed to a lipotoxic diet consisting of saturated fatty acids [127].

Altogether, these studies suggest a crucial role for ceramides in modulating macrophage function and metabolism early and late during infection. The ability of ceramides to induce downstream signaling for the production of proinflammatory cytokines following an infection, allows macrophages to persist and orchestrate activation of immune cells that subsequently produce survival factors such as M-CSF. Once the infection is cleared and macrophage survival factors are no longer high, ceramides mediate macrophage apoptosis winding down the cycle of immune cell activation.

# 15.3 Ceramides and Other SLs in Inflammatory Diseases

Most of what is known today about the roles of ceramides and other SLs in modulating immune cell responses arises from a plethora of studies performed by lipid biochemists around the world. In the current era of lipidomics and targeted lipid therapeutics, lipid biology and metabolism have also started to attract many immunologists worldwide. In this section we present the main studies highlighting the roles of SLs in some major inflammatory diseases.

#### 15.3.1 Insulin Resistance

Insulin Resistance refers to the impaired response of cells to insulin, resulting in a reduced uptake of glucose and glucose accumulation in the bloodstream. Insulin resistance is the main hallmark of type 2 diabetes mellitus and is highly associated with induction of cardiovascular disease, obesity, and various types of cancer [128]. Early studies established a strong link between ceramide accumulation and insulin resistance by demonstrating that SLs inhibited glucose transport into 3T3-L1 mouse adipose fibroblasts [129] and that bacterial SMase and the shortchain ceramides, C2 and C6, reduced insulininduced tyrosine phosphorylation of insulin receptor substrate-1 (IRS-1) downstream the glucose transporter, GLUT4, in insulin-sensitive rat hepatoma Fao cells [130]. Interestingly, inhibition of IRS-1 was later demonstrated to be mediated by TNFa via induction of tumor necrosis factor receptor and SMase activity [131]. However, inhibition of IRS-1 activity by ceramides seems to be a result of protein kinase B (PKB) activity rather than direct inhibition of IRS-1 function [132–136]. Further investigation of the mechanisms of PKB inhibition by ceramides demonstrated that C<sub>2</sub>-ceramide inhibited nuclear translocation of Akt1 [137], reduced phosphorylation of serine 473 in PKB [138], inhibited translocation of Akt/PKB to the plasma membrane and promoted dephosphorylation of Akt/PKB by protein phosphatase 2A [139–141].
Recent studies have also demonstrated induction of PKR/JNK activation [142, 143].

Further investigations aimed to determine whether ceramides induce insulin resistance. Analysis of muscle biopsies from insulin intolerant obese individuals revealed an increased accumulation of ceramides [144-147]. In addition, exogenous C2-ceramide induced apoptosis in skeletal muscle myotubes, reducing the cell capacity to uptake glucose, a process that can be reversed by the CerS inhibitor, fumonisin  $B_1$ [148, 149]. In muscle cells, C<sub>2</sub>-ceramide also mediated insulin resistance by inhibiting Rac activation, thus reducing GLUT4 translocation to the plasma membrane in response to insulin [150]. These studies suggested that targeting ceramide accumulation could protect muscles against insulin resistance. In line with this hypothesis, Bruce and coworkers demonstrated that overexpression of sphingosine kinase 1 (SK1) led to reduced ceramide accumulation and insulin resistance in mice given high-fat diet [151]. Inhibition of CerS and ceramide synthesis with the S1P analog, FTY720 [152], also reduced insulin tolerance in mice on high-fat diet [153]. Furthermore, in obese rodents, blockade of *de novo* ceramide synthesis with the SPT) inhibitor, myriocin, improved glucose tolerance [128, 154].

Since CerS are required for *de novo* ceramide generation, several studies have focused on the role of CerS in inducing insulin tolerance. Overexpression of CerS1, CerS2, CerS4, CerS5, and CerS6 in L6 myotubes induced ceramide production; however, none of the CerS was able to inhibit insulin signaling [139]. Given the opposing role of CerS2 and CerS6 in inflammation, current studies have been focusing on the role of these CerS in insulin resistance in vivo. CerS2 haploinsufficient mice have altered patterns of ceramide acylation, leading to reduced levels of very-long-chain ceramides and increased levels of long-chain C<sub>16</sub>-ceramide as a compensatory mechanism leading to insulin resistance when fed with high-fat diet [155]. In agreement with these findings, CerS6 expression and levels of  $C_{16}$ -ceramide are induced in the adipose tissue of obese humans. Moreover, CerS6- and CerS5deficient mice fed with high-fat diet are protected from obesity, glucose intolerance, and insulin resistance suggesting that targeting CerS6 could be beneficial for the treatment of obesity and type 2 diabetes [20, 156]. It is worth noting that the products of CerS5 (C16-ceramide) and CerS2 (C<sub>24</sub>-ceramide) antagonized each other's ability to form channels in mitochondrial outer membranes to induce apoptosis [157]. This may be another mechanism by which different CerS affect insulin resistance and tolerance differentially.

Ceramide accumulation has been linked to inflammatory pathways mainly involving signaling events downstream of TLR4. More specifically, Holland et al., was the first to provide a link between lipotoxicity and inflammation in the of intolerance induction insulin [158]. Particularly, saturated fatty acids induced de novo ceramide synthesis via TLR4 activation, which also altered the metabolic program of skeletal muscle, inducing insulin resistance. However, Galbo et al. showed that lipid-induced insulin resistance is a result of increased accumulation of DAG and induced DAG-PKCe signaling rather than induced TLR4-ceramide pathway [159]. These conclusions were based on the observation that knockdown of TLR4 or the adaptor protein MyD88 prevented hepatic steatosis in mice fed with a saturated fat diet through reduction of appetite but not hepatic insulin signaling. When mice were given saturated fat by oral gavage, loss of TLR4 or MyD88 did not protect mice from hepatic insulin resistance. Interestingly, another link between ceramides and inflammatory pathways in insulin tolerance involves stimulation of the Nod-like receptor pyrin domain-containing-3 (Nlrp3) inflammasome [160]. In obese mice, ceramides activated Nlrp3 inflammasome and IL-1ß secretion through caspase-1 activation in adipose tissue macrophages in a Nlrp3-dependent manner. This induction subsequently led to T cell activation. However, this study does not exclude the possibility that inducers other than ceramides present in the diet induced caspase-1 activation. Further studies are required to establish whether ceramides are truly sensed by PRR in immune cells.

#### 15.3.2 Graft-Versus-Host Disease

Graft-versus-host disease (GVHD) is a major complication of allogeneic hematopoietic stem cell transplantation. It is an inflammatory response mediated primarily by donor T cells, resulting in destruction of host tissues including skin, liver, and gastrointestinal (GI) tract [161]. The role of ceramides in mediating T cell cytotoxic function has only been recently explored two studies of mouse models in of GVHD. Rotolo et al. reported that aSMase in the host mediated GVHD [162]. Adoptive transfer of allogeneic T cells to aSMase-deficient hosts reduced morbidity and mortality. This induction in survival resulted from reduced inflammatory responses, cytokine storm, CD8+ T cell proliferation and activation, and apoptosis of host hepatocytes, skin and intestinal cells. Interestingly, aSMase is required for the formation of ceramide-rich platforms on target cells for cytotoxic T lymphocytes (CTL) efficient killing. Further investigation of requirement of ceramide bioactive function in donor T cells by Sofi and colleagues demonstrated that CerS6deficient donor T cells reduced GVHD [163]. In addition, T cells lacking CerS6 had an aberrant T cell receptor (TCR) signal transduction due to the reduction of tyrosine phosphorylation and CD3-PKCθ colocalization required for T cell proliferation and response to pro-inflammatory particularly cytokines, interferon gamma (IFN<sub>y</sub>). Furthermore, inhibition of Cer6S with its specific inhibitor, ST1072 [164], reduced T cell proliferation and IFNy production. This could also be a result of reduced IL-2 secretion by aSMase-deficient T cells upon TCR stimulation as previously reported [165]. Moreover, aSMase has also been described to be required for proper TCR signaling downstream CD3/ CD28 activation in CD4+ T cells, since blockade of aSMase bioactivity with imipramine impaired PLC<sub>γ1</sub>, JNK, ERK, Akt, and mTOR phosphorylation downstream TCR [166]. More studies are required to further elucidate the roles of the aSMase and lipid metabolism in driving T cell activation and its role in GVHD pathogenesis.

# 15.3.3 Immune Suppression in the Tumor Microenvironment

Immunotherapy has recently been employed as a novel strategy to eradicate tumors. During tumor development, immune cell responses include massive tumor infiltration and production of cytokines in an attempt to contain tumor growth and kill tumor cells. If not contained, tumor growth leads to the establishment of a tumor microenvironment (TEM) characterized by induced hypoxia [167] and lactic acid accumulation leading to suppression of effector CD8+ CTL [168]. CD8+ T cell responses are inhibited by suppressive immune cells of various types that initially infiltrated the tumor to contain growth but reversed its effector phenotype in the TEM. Among these suppressive immune cells are tumor-associated macrophages (TAM), myeloid-derived suppressor cells (MDSC), and regulatory CD4+ T (Treg) cells [111]. Recently, it has been appreciated that tumor cells gain advantage over immune cells by altering their glucose and lipid metabolism. Despite many studies describing the effects of alterations in glucose metabolism in immune cell function, only recently has similar alterations in immune cell lipid metabolism been considered [169].

S1P has been implicated in the polarization of macrophages to an M2 anti-inflammatory phenotype in the TEM. During tumor progression, apoptotic cells are released in the TEM serving as a source for S1P [170]. Interestingly, S1P released from engulfed apoptotic cells by macrophages induces macrophage survival through the activation of PIRK, ERK/2, and Ca+2 [171] and polarization to an M2 phenotype through the inhibition of inducible nitric oxide synthase (iNOS) and reduction of TNF $\alpha$  and IL-8 production [172–175]. Knock down of the S1P-producing enzyme, sphingosine kinase 2 (SK2) in MCF-7 breast carcinoma cells delayed tumor growth in a xenograft model in nude mice by promoting macrophage polarization to an M1 pro-inflammatory phenotype characterized by increased expression of nitric oxide (NO), TNF $\alpha$ , IL-12, and major histocompatibility

complex class II and reduced expression of IL-10 and CD206, which are markers associated with macrophage suppression [176].

Modulation of TAM function by ceramides has been also achieved in a mouse model of hepatocellular cancer through the administration of nanoliposome-loaded C<sub>6</sub>-ceramide (LipC6) [177]. LipC6 exerts its modulatory function by acting as a ROS scavenger, therefore inducing macrophage polarization from an M2 to an M1 phenotype and resulting in reversal of CD8+ T cell exhaustion and induction of CD8+ cytotoxic function against tumor cells. The effect of ceramides has also been explored in suppressive MDSC in mice bearing CMS4-metastic tumors. Treatment of tumor-bearing mice with acid ceramidase inhibitor, LCL521, reduced MDSC accumulation in tumors without reducing tumor growth. In addition, LCL521 treatment led to an increased accumulation of C<sub>16</sub>-ceramide that resulted in cathepsin-mediated cell death of tumor and MDSC-like J774 cells [178]. Suppression of CD8+ T cell function in tumors also results from suppression mediated by T<sub>reg</sub> cells. To our knowledge, there have been no studies reporting the effect of ceramides on T<sub>reg</sub> cell function in tumor-bearing mice. However, recent studies have described the effect of ceramide accumulation on  $T_{\mbox{\scriptsize reg}}$  cells in healthy WT and aSMase-deficient mice. Treg cell frequency and suppressive function are induced in aSMase-deficient mice [179]. In addition, this was associated with increased percentage of induced  $T_{reg}$  (i $T_{reg}$ ) cells from aSMase-/- CD4+ T cells treated with transforming growth factor beta (TGF $\beta$ ) and IL-2. Moreover, aSMase product C<sub>6</sub>-ceramide induced a Th17-associtated cytokine in CD4+ T cell hampering T<sub>reg</sub> cell induction, suggesting that aSMase is a negative regulator of  $T_{reg}$  cell development [180]. The relevance of these findings remains to be further explored in models of inflammation for further development of lipidtargeted therapies.

### 15.3.4 Multiple Sclerosis

Multiple sclerosis (MS) is a chronic inflammatory disease that results in demyelination due to autoim-

mune responses against myelin in the central nervous system (CNS) [181]. In experimental autoimmune encephalomyelitis (EAE), de novo synthesis of  $C_{16}$ -ceramide by CerS6 is required for the production of pro-inflammatory TNF $\alpha$  and iNOS in macrophages in response to IFNy [182]. Upregulation of CerS6 in EAE led to further speculations on its role in driving MS. Interestingly, upregulation of CerS6 and TNFa mRNA expression was found to be higher in females compared to male littermates in spontaneous relapsing remitting EAE [183]. This increase was correlated with the ability of females to initiate anti-inflammatory responses during the course of the disease, suggesting that CerS6 could promote anti-inflammatory responses. This observation was later confirmed with experiments showing that EAE progression is worsened in CerS6 knockout mice [184]. In addition, EAE was enhanced in chimeric mice in which only leukocytes were CerS6-deficient, providing further evidence that leukocytes lacking CerS6 drive the exacerbated phenotype. Moreover, expression of genes driving leukocyte migration and CNS infiltration (e.g. CCL2, CCL5, CXCL2) was increased, especially in CerS6-deficient neutrophils due to increased C-X-C motif chemokine receptor type 2 (CXCR2) in response to granulocyte-colony stimulating factor. On the contrary, CerS2-deficient mice had delayed development of EAE. This delay in disease onset was correlated with the reduced expression of CXCR2 in CerS2-deficient neutrophils [26]. In addition, the induction of ceramides was also associated with disease development in EAE, since aSMase deficiency protected mice from disease [185]. Collectively, these findings suggest that CerS6 and CerS2 have opposing roles in driving disease progression in EAE.

Excitingly, the S1P receptor agonist, fingolimod FTY720, was FDA approved in 2010 as a first-line therapy for the treatment of MS [186, 187]. FTY720 is phosphorylated *in vivo* by SK to form FTY720-P, which binds with a high affinity to S1P receptors and competes with its natural ligand, S1P. Therefore, FTY720 functionally antagonizes S1P by strongly binding to S1PR leading to internalization and inhibition of the receptor [188–190]. By modulating the S1P receptor, fingolimod prevented autoreactive S1P expressing inflammatory T cells from exiting the lymph nodes, therefore, inhibiting CNS infiltration by autoreactive T cells. Subsequently, this resulted in reduced destruction of myelin sheath surround the axons of nerve cells [188–191]. This is a perfect example of the potential outcome of modulating lipid metabolism in immune cells driving forward the era of lipid therapeutics.

#### 15.3.5 Inflammatory Bowel Disease

Inflammatory Bowel Disease (IBD) is a group of diseases, including ulcerative colitis and Crohn's disease, characterized by chronic inflammation of gastrointestinal tract. Pathology is mediated by leukocytes infiltration and massive production of pro-inflammatory cytokines leading to intestinal damage [192, 193]. The first link between SL metabolism and IBD originated from studies showing that TNF $\alpha$ , a cytokine that induces the generation of S1P and synthesis of cyclooxygenase-2 (COX-2) [194, 195], was induced in patients with IBD [192, 196]. In addition,  $TNF\alpha$ blockade alleviated clinical symptoms in mouse models of disease [197, 198]. Since ceramides also induced the activation of MAPK, a key inducer of inflammatory responses [199], follow up studies demonstrated that inhibition of ceramide accumulation by targeting SMase or S1P receptor diminished clinical manifestations of disease in mouse models of colitis. For example, in a dextran sulfate sodium (DSS) model of colitis, inhibition of SMase with a sphingomyelin analogue-7 reduced the formation of ceramide, levels of cytokines, and intestinal injury [200]. In addition, administration of FTY720 reduced disease symptoms in a mouse model of colitis, associated with a reduced production of the pro-inflammatory cytokine IL-12p70 and Th1 cytokines, and upregulation of CD4+ Foxp3+ suppressive  $T_{reg}$  cells [201]. Furthermore, administration of a new S1P receptor agonist, KRP-203, resulted in reduced lymproduction phocyte infiltration and of pro-inflammatory Th1 cytokines in the colonic mucosa [202]. Similarly, chemical and genetic inhibition of SK1 that is responsible for the production of S1P reduced manifestations of colitis,

COX-2 expression, and neutrophil infiltration [203–205]. In support of these findings, high SK1 expression has also been reported in intestinal mucosa of patients with ulcerative colitis [205]. Currently, modulators of S1P receptor, such as ozanimod (RPC1063) and etrasimod (APD334) are being tested in clinical trials for the treatment of IBD [206, 207], further emphasizing the importance of investigating the role of SL metabolism in this disease setting.

Along with inhibition of S1P receptor function, modulation of CerS has also been explored in IBD, particularly CerS2 and CerS6. In a mouse model of colitis, loss of CerS2 destabilized the epithelial barrier and tight junction in the intestinal membrane leading to increased intestinal permeability. CerS2-deficient mice have reduced expression of junctional adhesion molecule A [208] and tight junction protein ZO-1 [209]. This outcome is associated with reduced levels of very-long acyl chain ceramides (C24) and increased levels of long-chain sphingoid bases and  $C_{16}$ -ceramides [208]. These findings further suggest that CerS2 is protective against colitis as opposed to EAE in which CerS2-deficient mice are protected [26]. Interestingly, further exploration of the role of CerS6 in colitis has led to opposing conclusions. Scheffel et al. reported that the transfer of CerS6-deficient CD4+ T cells is protective in colitis [33]. On the contrary, Helke et al. showed that in a model of DSSinduced colitis, loss of CerS6 exacerbates inflam-[210]. Interestingly, pathology mation in CerS6-deficient mice is not a result of reduced intestinal permeability but is associated with enhanced neutrophil infiltration. However, more studies are needed to further elucidate the role of CerS in various models of colitis and its implementation in the development of CerS targeted therapies in humans with IBD.

# 15.4 Conclusions and Future Directions

While it has been thoroughly reviewed in other cells, the roles of ceramides in immune cells have not been proportionally presented. In this chapter we attempted to summarize the significant effects of ceramides in immune cells and immune diseases. Numerous studies have highlighted the importance of ceramides in a variety of pathways necessary for the development, function, and metabolism of immune cells. Ceramide accumulation has been described as a key step mediating and regulating various immune cell functions, including regulation of immune cell responses to viruses, bacteria, and other foreign pathogens, migration, phagocytosis, and cytokine production. For instance, ceramides have been implicated in the modulation of responses to LPS, cytokine production, antigen presentation, and viral entry in DC; control of migration, cytokine and superoxide production, and formation of NETs in neutrophils; and response to TLR stimulation, inducing apoptosis, and regulating oxidative stress in macrophages. Moreover, ceramide functions extend to T cells, stabilizing the T cell receptor complex and mediating T cell responses during inflammation. Ceramide metabolites and upstream regulators including CerS in immune cell function have also been thoroughly described in the literature, further emphasizing the important role that ceramides play during inflammation.

Investigating the roles of ceramides and other SLs as modulators of the biology and metabolism of immune cells has unraveled new avenues in targeting ceramides in life-threatening inflammatory diseases that negatively impact the life of millions around the globe. For instance, recently, the FDA approved the CerS inhibitor, FTY720, as the first-line therapy for MS patients. This certainly has raised an interest among immunologists and lipid biochemists alike in developing novel inhibitors to target ceramide metabolism in various models of inflammation in the laboratory to hopefully translate such findings in the clinic.

It is also strictly important to consider the multiple effects of a plethora of ceramide species on the function of a certain immune cell or different cells when targeting ceramides in disease. Despite the encouraging routes that ceramide research has taken, further studies and collaborations between scientists of multidisciplinary fields are still needed to elucidate the mechanisms of ceramides in immune cell function and other cell types. Since diversity of ceramides, similar to other membrane and bioactive lipids, arises from the different possible combinations of head groups and/or degree of saturation, the effect of each type of SL and ceramide on every immune cell opens endless possibilities in targeting various ceramides to retune immune cell function in cancer, transplantation, diabetes, MS, IBD and many other diseases.

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16

# Bioactive Lipids in Cancer, Inflammation and Related Diseases

Acute and Chronic Mild Traumatic Brain Injury Differentially Changes Levels of Bioactive Lipids in the CNS Associated with Headache

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#### Abstract

Headache is a common complaint after mild traumatic brain injury (mTBI). Changes in the CNS lipidome were previously associated with acrolein-induced headache in rodents. mTBI caused similar headache-like symptoms in rats; therefore, we tested the hypothesis that mTBI might likewise alter the lipidome. Using a stereotaxic impactor, rats were given either a single mTBI or a series of 4 mTBIs 48 h apart. 72 h later for single mTBI and 7 days later for repeated mTBI, the trigeminal ganglia (TG), trigeminal nucleus (TNC), and cerebellum (CER) were isolated. Using HPLC/MS/MS, ~80 lipids were measured in each tissue and compared to sham controls. mTBI drove widespread alterations in lipid levels. Single

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mTBI increased arachidonic acid and repeated mTBI increased prostaglandins in all 3 tissue types. mTBI affected multiple TRPV agonists, including N-arachidonoyl ethanolamine (AEA), which increased in the TNC and CER after single mTBI. After repeated mTBI, AEA increased in the TG, but decreased in the TNC. Common to all tissue types in single and repeated mTBI was an increase the AEA metabolite, N-arachidonoyl glycine, a potent activator of microglial migration. Changes in the CNS lipidome associated with mTBI likely play a role in headache and in long-term neurodegenerative effects of repeated mTBI.

## Keywords

mTBI · Endocannabinoids · TRP · Lipidomics · Lipoamine · Acyl amino acid · Acyl amide · Docosahexaenoyl ethanolamine · N-arachidonoyl glycine · BV-2

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# 16.1 Traumatic Brain Injury, Headache, and Endogenous Cannabinoids

~40 million people worldwide endure a mild traumatic brain injury (mTBI; also known as concussion) each year [1], accounting for over 75% of brain injuries [2]. Headache is a common complaint after mTBI [2–6]. In studies of TBI patient populations in the United States, around 70% of participants reported having headaches during the first-year post-injury [3, 5]. Demonstrating that post-mTBI headache is a global phenomenon, a study of TBI patients in China found that, regardless of TBI severity, 58% of patients had headaches at 3 months post-injury, 54% at 6 months, and 49% at 1 year [6]. In contrast, only 12% of the patients reported pre-injury headaches [6]. Often, post-mTBI headaches are migraine-like [4, 6-9]. For example, in the study by Xu and colleagues, around 70% of the headaches described by TBI patients were classified as migraine-type [6]. Activation of the trigeminovascular system (TVS), the trigeminal innervation of cranial vasculature [10], is hypothesized to underlie migraine pain [11]. Sensitization can occur after repeated TVS activation [11]. After the initial mTBI, there is a secondary inflammatory biochemical insult that occurs days later [12, 13]. These biochemical changes may promote headaches through the activity of inflammatory mediators, many of which are bioactive lipids, that are produced during chronic immune responses [4, 8].

Bioactive lipids such as endogenous cannabinoids (eCBs), the endogenous activators of CB<sub>1</sub> and CB<sub>2</sub> cannabinoid receptors [14–17], help regulate inflammation [17] and have emerging roles in the TVS [18]. Brain levels of the eCB 2-arachidonoyl glycerol (2-AG) [15, 16] significantly increased in a mouse model of TBI, starting at 4 h post-injury [19]. As 2-AG was neuroprotective after TBI [12, 19, 20], it was hypothesized that the increase in 2-AG was a compensatory mechanism to mitigate the damage of pro-inflammatory mediators released after injury [19]. The effects of 2-AG were mostly mediated by CB<sub>1</sub> [19]. However, CB<sub>2</sub> agonists were also neuroprotective in rodent TBI models by reducing blood-brain barrier disruption, as measured by sodium fluorescein uptake, which prevented the entry of pro-inflammatory immune cells, and by attenuating microglial activation, as measured by immunohistochemistry [21]. Cannabinoid receptor activation is hypothesized to reduce headache pain [4, 18], suggesting convergent biochemistry between headache and TBI.

## 16.2 Lipoamines as Endogenous Activators of Transient Receptor Potential (TRP) Channels

TRP channels are ubiquitous ligand-gated ion channels that serve a variety of functions throughout the body [22–31]. There are 28 known TRP channels in mammalian systems; however, they are arguably understudied to date as their endogenous ligands, distributions, and signaling properties are still in question [26, 29, 31]. In the context of disease, and more specifically the symptom of pain, TRP vanilloid type 1 (TRPV1) has been the focus of intense study and may represent the TRP channel being the most studied overall [23, 27, 28, 31-34]. More than a dozen bioactive lipids have been shown to activate TRPV1 [31, 35–40]. Our group recently identified 8 of these [41]. Given the ubiquity of TRPs, it is not surprising that they appear to have interconnected responses with other TRPs and GPCRs. A combination of TRPV1-TRP ankyrin 1 (TRPA1) activity has been observed in an animal model for headache wherein ablation of TRPV1 in the trigeminal ganglia (TG) inhibited TVS activation driven by TRPA1 agonists [42]. We recently showed that TRPA1 activation by acrolein drives increases in TRPV1 endogenous bioactive lipids in the CNS [43].

Many endogenous TRPV ligands are lipoamines, which are conjugations of fatty acids and amines [22, 44–46]. The eCB *N*-arachidonoyl ethanolamine (AEA) [14] is a lipoamine that activates TRPV1, as well as cannabinoid receptors [35]. Additional lipoamines activate TRPV1 such as the *N*-acyl ethanolamines (NAEs) *N*-oleoyl ethanolamine (OEA) [37, 38], *N*-linoleoyl ethanolamine (LEA), and *N*-docosahexaenoyl ethanolamine (DEA) [41], and certain lipoamines derived from arachidonic acid (AA) such as *N*-arachidonoyl GABA (A-GABA) [41] and *N*-arachidonoyl taurine (A-Taur) [39]. *N*-arachidonoyl serine (A-Ser) was neuroprotective in a mouse model of TBI, and these effects were attenuated with a TRPV1 antagonist, as well as a CB<sub>2</sub> antagonist [47, 48].

# 16.3 Bioactive Lipid Levels Change in a Model of Headache

Showing cross-talk with TRPV1, TRPA1 is expressed in sensory neurons [49]. The TRPA1 agonist acrolein is an irritant and a major component of air pollution [50, 51]. Molecular mechanisms of inflammatory pain and hypersensitization of the TVS caused by irritants like acrolein partially depend on TRPA1 activity [52, 53]. In a rat model of headache driven by exposure to acrolein, TVS sensitization [53] and headache-like behaviors [54] were correlated with altered levels of bioactive lipids in the TVS and the cerebellum (CER), such as eCBs and endogenous lipoamine TPRV1 ligands [43]. TVS tissues analyzed were the TG, where cell bodies of trigeminal nerve fibers are located [10], and the trigeminal nucleus caudalis (TNC), part of the brainstem which receives sensory signals from the TG and projects them onto thalamo-cortical pathways [55]. These experiments provided evidence that acrolein exposure drives changes in CNS lipids, supporting a working hypothesis that both TRPA1 and TRPV1 activity play a role in headache.

Exposure to a single mTBI caused headachelike symptoms in rats [56, 57]. Specifically, mTBI caused periorbital allodynia, meaning that stimuli that were non-nociceptive before the injury became painful after the injury [56, 57]. Providing more evidence of alterations in the TVS that could support headache post-TBI, levels of pro-nociceptive peptides were upregulated in the TNC after TBI [56, 57]. Periorbital allodynia was a marker of headache-like symptoms

measured in the acrolein model [54], showing these very different models have similar effects on measures of headache-like pain in rodents. Given that headache driven by acrolein exposure was linked to alterations in bioactive lipids [43], we wanted to know whether headache caused by a very different model, mTBI, would drive similar alterations in lipid levels and whether the effects of repeated mTBIs would differ from the effects of a single mTBI. To test the hypothesis that acute and repeated mTBI alters the CNS lipidome, we performed targeted lipidomics screens of the TG, TNC and the CER, from rats exposed to single or repeated mTBI. Analyzing 74 lipoamine structural analogs, 2-acyl glycerol structural analogs, prostaglandins (PGs), and free fatty acids through targeted high-pressure liquid chromatography-coupled tandem mass spectrometry (HPLC/MS/MS) we were able to determine how this lipidome is modified. Both single and repeated mTBI modified many bioactive lipids including increased levels of the AEA metabolite [58] and GPR18 ligand [59], N-arachidonoyl glycine (NAGly), and alterations of TRPV1 and CB ligands. Increased levels of PGs were associated with repeated mTBI. These findings may shed new light on how bioactive lipids in the CNS play a role in headache associated with TBI.

# 16.4 mTBI Protocols, Tissue Collection, and HPLC/MS/MS Analysis

All animal procedures were approved by the Institutional Animal Care and Use Committee of Indiana University School of Medicine and were in accordance with the ethics guidelines set by the International Association for the Study of Pain [60]. In total, 24 adult male (170–250 g) Sprague-Dawley rats (Harlan, Indianapolis, IN, USA) were used: 12 were assigned to the single mTBI paradigm and 12 were assigned to the repeated mTBI paradigm. Rats were housed in pairs with food and water available ad libitum, and were kept on a standard light/dark cycle. Using an Impact One stereotaxic impactor (Leica Microsystems, Wetzlar, Germany) with a 3 mm

diameter tip, mTBI was induced by 4.0 m/s impact to 2.0 mm depth on the right hemisphere adjacent to bregma and sagittal sutures. This was performed once on single mTBI rats and performed 4 times, with 48 h between each impact, on repeated mTBI rats. 6 of the 12 rats in each paradigm (single or repeated) received mTBI and the other 6 received a sham treatment.

To better model concussion, the injury was a closed-head injury and the rats did not undergo craniotomy [61]. Confirming a mild injury, the impact did not damage the skull. As reviewed by Fehily and Fitzgerald, other rodent models of repeated mTBI use similar parameters [62]. For example, a study by David Brody's group described modeling repeated mTBI in mice by striking the exposed, intact skull with a rubber tip at 5.0 m/s to a depth of 3.3 mm [63]. Although this injury caused cognitive deficits, lasting microglial activation and disruption to whitematter axonal cytoskeletal integrity, there was no damage to the skull or any readily observable damage to the underlying brain tissue [63]. Bolton and Saatman tested various impact depths in a closed-head mouse model of repeated mTBI and found that 2.0 mm impact depth did not damage the skull but caused gliosis which was worsened when mTBI was repeated every 24 h [64]. Thus, our parameters are consistent with models employed by other groups studying mTBI in rodents. Rats were sacrificed via decapitation, either 72 h after the single mTBI or 1 week after the last session in repeated mTBI. Brains were immediately removed. Following removal of the brain, the left TG was removed from the skull and frozen on dry ice. The brains were dissected into targeted regions: TNC and CER, and frozen on dry ice. TG, TNC and CER samples were stored at -80 °C before being processed for lipid extraction.

Tissue extracts were performed as previously described [41, 43, 46, 65–72]. Lipids were analyzed using an Applied Biosystems API 3000 triple quadrupole mass spectrometer with electrospray ionization (Foster City, CA, USA) as previously described [43]. Levels of each compound were determined by running each sample using a multiple-reactions monitoring method

(MRM) tailored for each group of structurally similar compounds (Fig. 16.1). HPLC/MS/MS data was analyzed using Analyst software (Applied Biosystems) as previously described [41, 43, 46, 65–72]. Chromatograms were generated by determining the retention time of analytes from the C18 analytical column with a [M-1] or [M+1] parent peak and a fragmentation peak corresponding to the programmed values. Extraction efficiency was calculated with the d<sub>8</sub>NAGly or d<sub>8</sub>AEA-spiked recovery vial as a standard as done previously [41, 43, 46, 65–72]. For each individual lipid in the TG, TNC and CER, concentrations in moles per gram of wet tissue weight adjusted for percent recovery from mTBI animals were compared to sham using a one-way ANOVA. Statistical tests were carried out using SPSS Statistics (IBM, Armonk, NY, USA) and significance was defined as p < 0.05and trending significance was defined as p < 0.10. Using ANOVAs instead of more flexible t-tests provides more constraints on this type of larger data sets.

As a first level of analysis presented here, the percentage of the detected lipids affected by single and repeated mTBI in each tissue type was calculated. To calculate the percent of the lipids detected that were unaffected by mTBI, the number of changes (p < 0.10) in a tissue type for a specific condition (single or repeated) was first subtracted from the number of lipids detected in that tissue (which represents the number of possible changes). This number was then divided by the number of lipids detected and multiplied by 100. For example, in the TNC in the repeated mTBI condition, there were 73 lipids detected and 29 of them changed with repeated mTBI, meaning that 44 did not change. 44 divided by 73 times 100 is 60.27%, so 60.27% of the detected lipidome did not change with repeated mTBI in the TNC. This percentage can be viewed in the left, blue columns of Fig. 16.2. The next portion of Fig. 16.2 (middle, green) gives the percentage of the lipids detected in each tissue that increased in mTBI. Sticking with the repeated mTBI TNC, of the 29 changes that were detected, 14 of them were increases. 14 is then divided by the number of lipids detected (73 in this case) and multiplied

N-acyl alanine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl alanine	326.5	88.09		
N-stearoyl alanine	354.55	88.09		
N-oleoyl alanine	352.53	88.09		
N-linoleoyl alanine	350.52	88.09		
N-arachidonoyl alanine	374.5	88.09		
N-docosahexaenoyl alanine	398.56	88.09		
N-acyl dopamine	[M - H] <sup>.</sup>	Fragment		
N-oleoyl dopamine	416.3	123.2		
N-arachidonoyl dopamine	438.4	123.2		
N-acyl ethanolamine	[M + H] <sup>+</sup>	Fragment		
N-palmitoyl ethanolamine	300.29	62.1		
N-stearoyl ethanolamine	328.3	62.1		
N-oleoyl ethanolamine	326.3	62.1		
N-linoleoyl ethanolamine	324.3	62.1		
N-arachidonoyl ethanolamine	348.3	62.1		
N-docosahexaenoyl ethanolamine	372.6	62.1		
N-acyl GABA	[M - H] <sup>-</sup>	Fragment		
N-palmitoyl GABA	340.54	102.1		
N-stearoyl GABA	368.58	102.1		
N-oleoyl GABA	366.57	102.1		
N-linoleoyl GABA	364.54	102.1		
N-arachidonoyl GABA	388.57	102.1		
N-docosahexaenoyl GABA	412.59	102.1		
N-acyl glycine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl glycine	312.26	74.2		
N-stearoyl glycine	340.3	74.2		
N-oleoyl glycine	338.3	74.2		
N-linoleoyl glycine	336.3	74.2		
N-arachidonoyl glycine	360.3	74.2		
N-docosahexaenoyl glycine	384.3	74.2		
N-acyl leucine	[M - H] <sup>-</sup>	Fragment		
N-palmitoyl leucine	368.58	130.1		
N-stearoyl leucine	396.63	130.1		
N-oleoyl leucine	394.61	130.1		
N-linoleoyl leucine	392.6	130.1		
N-docosahexaenoyl leucine	440.64	130.1		
N-acyl methionine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl methionine	386.62	148.2		
N-stearoyl methionine	414.64	148.2		
N-oleoyl methionine	412.65	148.2		
N-linoleoyl methionine	410.64	148.2		
N-arachidonoyl methionine	434.66	148.2		
N-docosahexaenoyl methionine	458.68	148.2		
N-acyl phenylalanine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl phenylalanine	402.59	164.1		
/v-stearoyl phenylalanine	430.65	164.1		
/V-oleoyi phenylalanine	428.63	164.1		
/V-Inoleoyl phenylalanine	426.61	164.1		
N-arachidonoyl phenylalanine	450.64	164.1		
N-docosahexaenoyl phenylalanine	474.66	164.1		

N-acyl prolino	[M _ H]-	Fragmont		
	252 52	114 12		
	220 50	114.12		
	300.39	114.12		
/v-oleoyi proline	3/8.31	114.12		
/V-linoleoyl proline	376.56	114.12		
N-arachidonoyl proline	400.58	114.12		
N-docosahexaenoyl proline	424.6	114.12		
N-acyl serine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl serine	342.3	74		
N-stearoyl serine	370.3	74		
N-oleoyl serine	368.3	74		
N-linoleoyl serine	366.27	74		
N-arachidonoyl serine	390.3	74		
N-docosahexaenoyl serine	414.3	74		
N-acyl taurine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl taurine	362.6	124		
N-stearoyl taurine	390.6	124		
N-oleovl taurine	388.6	124		
N-arachidonovl taurine	410.6	124		
N-acyl tryptophan	[M - H]	Fragment		
N-palmitovl tryptophan	441.63	203.1		
N-stearoyl tryptophan	469 68	203.1		
	467.67	203.1		
M-lineleovi tryptophan	465.65	203.1		
A arashidanovi tryptophan	490.67	203.1		
	409.07 512.60	203.1		
	IM L1-	Eragmont		
		Flagment		
/v-paimitoyi tyrosine	416.59	160.16		
iv-stearoyi tyrosine	440.00	180.18		
	444.63	180.18		
	442.61	180.18		
/V-arachidonoyi tyrosine	466	180.18		
N-docosahexaenoyl tyrosine	490.66	180.18		
N-acyl valine	[M - H] <sup>.</sup>	Fragment		
N-palmitoyl valine	354.31	116.31		
N- stearoyl valine	382.6	116.14		
N-oleoyl valine	380.59	116.14		
N-linoleoyl valine	378.58	116.14		
N-docosahexaenoyl valine	426.62	116.14		
2-acyl glycerol	[M + H]⁺	Fragment		
2-palmitoyl glycerol	331.5	239.5		
2-oleoyl glycerol	357.5	265.2		
2-linoleoyl glycerol	355.5	245		
2-arachidonoyl glycerol	379.3	287.5		
Free Fatty Acids	[M - H] <sup>.</sup>	Fragment		
Oleic acid	281.5	263		
Linoleic acid	279.5	261		
Arachidonic acid	303.5	285		
PhosphoNAEs	[M - H] <sup>-</sup>	Fragment		
PhosphoLEA	403.5	58.5		
Prostaglandins	[M - H] <sup>.</sup>	Fragment		
PGE <sub>2</sub>	351.2	315		
PGF2	353.3	309.2		
6-keto-PGF <sub>1α</sub>	369.3	206.9		

**Fig. 16.1** Lipids in HPLC/MS/MS screening library with parent ion and fragment ion masses. Lipids are grouped by amide family and all members of that lipid family are screened in a multiple reactions monitoring (MRM) method. The parent ion mass is also listed: negative ionization mode, resulting in a  $[M - H]^-$  parent ion, is used for all methods except the *N*-acyl ethanolamine and 2-acyl glycerol methods, which uses positive ionization and generates a parent ion with a mass of  $[M + H]^+$ . The

parent ion is the only ion allowed to pass through the first quadrupole of the API3000. The parent ion is then fragmented into the collision chamber and an abundant fragment can be selected as the fragment ion. Only the selected fragment ion can pass from the collision chamber into the third quadrupole. Therefore, unknown lipids are matched to known standards according to retention time from the analytical column and according to their mass fingerprint

		0/ Lipida	0/ Lipido	0/ Lipido	
		% Lipius	% Lipias	% Lipias	
		detected	detected	detected	
		unchanged	increased	decreased	
		by mTBI	by mTBI	by mTBI	
Cerebellum	Single	53.85%	46.15%	0.00%	
	Repeated	75.64%	21.80%	2.56%	
Trigeminal Ganglia	Single	77.50%	18.75%	3.75%	
	Repeated	63.64%	35.06%	1.30%	
Trigeminal Nucleus	Single	63.16%	36.84%	0.00%	
	Repeated	60.27%	19.18%	20.55%	

Fig. 16.2 Summary of effects of single and repeated mild traumatic brain injury (mTBI) on lipid levels in the rat cerebellum, trigeminal ganglia, and trigeminal nucleus caudalis. The left, blue column represents the percentage of the lipids detected within each of tissue type (row) with concentrations that were unaffected by single

by 100 to yield the percentage increased (19.18%). The right portion of Fig. 16.2 shows the percentage of the lipids detected that decreased with single or repeated mTBI. The percentage was calculated by taking the number of lipids with decreased concentrations in each tissue and dividing it by the number of lipids detected in that tissue. For the TNC, 15 lipids decreased with repeated mTBI, giving a percentage of 20.55% for the proportion of the lipidome that decreased. When the 3 different percentages for a tissue are added, they should equal 100. For the repeated mTBI TNC, 60.27 plus 19.18 plus 20.55 equals 100.

Analyzed lipidomics data from the TG, TNC, and CER are represented in tabular format illustrating both the direction and magnitude of change. For example, the mean level of AEA was  $9.20 \times 10^{-11}$  moles per gram in the CER of the rats subjected to a single mTBI and  $7.86 \times 10^{-11}$  moles per gram in the corresponding sham CER.  $9.20 \times 10^{-11}$  divided by  $7.86 \times 10^{-11}$  is 1.17, assigning it 1 up arrow in the figures because the magnitude of change was between 1 and 1.5 times higher than sham. Providing an example of a decrease, the average level of AEA in the TNC of rats exposed to repeated mTBI was  $5.22 \times 10^{-12}$  moles per gram and the average level of AEA in the TNC of the sham rats was  $7.32 \times 10^{-12}$  moles per gram;  $5.22 \times 10^{-12}$  divided by  $7.32 \times 10^{-12}$  equals 0.71, and the reciprocal of 0.71 is 1.41, meaning that the decrease is between 1 and 1.5 times sham levels and giving it 1 down arrow on our scale.

or repeated mTBI. The middle, green column represents the percentage of lipids detected that increased with single and repeated mTBI and the right, orange column represents the percentage of lipids detected that decreased with single and repeated mTBI relative to sham. See Methods for more details on how percentages were calculated

Immortalized BV2 microglia cells were a gift from Dr. N. Stella at University of Washington, Seattle. Boyden migration chamber assays and analyses were performed identically to those previously described in our laboratory [59, 73].

## 16.4.1 mTBI Has Broad Effects on the CER, TG, and TNC Lipidome

Of the 74 lipoamines in our screening library (Fig. 16.1), over 50 were detected in the TG, TNC, and CER. If a lipid was detected in the samples from injured rats it was also found in the corresponding sham samples. In both single and repeated mTBI, 78 lipids were detected in the CER (92% of the 85 lipids in the screening library). For the TG and TNC, different numbers of lipids were detected after single and repeated mTBI. In the TG, 80 lipids were detected in the single condition (94%) and 77 in the repeated condition (91%). Fewer lipids were detected in the TNC (single: 76 lipids – 89%; repeated: 73 lipids – 86%). Tables listing the lipids detected and their mean levels in each tissue type in sham and mTBI tissues are available upon request from the authors.

The first level of analysis examined the proportion of the lipids detected that were unchanged, upregulated, or downregulated with mTBI relative to sham. Effects of single mTBI on the lipidome were mostly tissue-dependent (Figs. 16.2, 16.3, 16.4, and 16.5). The highest percentage of changes in lipid levels occurred in the CER (36 lipids – 46% of the lipids detected), followed by the TNC (28 lipids – 37%). The area with the lowest percentages of changes in lipid levels was the TG (18 lipids – 22.5%). All of the changes driven in the TNC and CER were

increases in a lipid's concentration. In contrast, changes measured in the TG included decreases (15 increases, 3 decreases).

Repeated mTBI affected a similar number of the detected lipids (Figs. 16.2, 16.3, 16.4, and 16.5). However, the specific tissue most affected shifted in repeated mTBI. The highest percent-

	Cerebellum		Trigeminal Ganglia		Trigeminal Nucleus	
Lipid Species	mTBI X 1	mTBI X 4	mTBI X 1	mTBI X 4	mTBI X 1	mTBI X 4
N-acyl ethanolamine						
N-palmitoyl ethanolamine						$\downarrow$
N-stearoyl ethanolamine						
N-oleoyl ethanolamine				$\downarrow$		
N-linoleoyl ethanolamine	$\uparrow$			$\uparrow$	$\uparrow$	$\downarrow$
N-arachidonoyl ethanolamine	$\uparrow$			$\uparrow$	$\uparrow$	$\downarrow$
N-docosahexaenoyl ethanolamine	$\uparrow$	$\downarrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\downarrow$
N-acyl glycine						
N-palmitoyl glycine					$\uparrow$	
N-stearoyl glycine		$\uparrow$	$\uparrow$		$\uparrow$	$\downarrow$
N-oleoyl glycine	$\uparrow$		$\uparrow$		$\uparrow$	
N-linoleoyl glycine					$\uparrow$	
N-arachidonoyl glycine	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$
N-docosahexaenoyl glycine	$\uparrow$			$\uparrow$	$\uparrow$	
N-acyl taurine						
N-palmitoyl taurine	$\uparrow$				$\uparrow$	
N-stearoyl taurine	$\uparrow$	$\downarrow$			$\uparrow$	
N-oleoyl taurine	$\uparrow$				$\uparrow$	$\uparrow$
N-arachidonoyl taurine	$\uparrow$			$\uparrow$	$\uparrow$	$\uparrow$
2-acyl glycerol						
2-palmitoyl glycerol		$\uparrow\uparrow$		$\uparrow$	$\uparrow\uparrow$	
2-oleoyl glycerol				$\uparrow$		$\checkmark$
2-linoleoyl glycerol		$\uparrow$		$\uparrow$	$\uparrow$	
2-arachidonoyl glycerol				$\uparrow$	$\uparrow$	
Free Fatty Acids						
Oleic acid	$\uparrow$			$\uparrow$		
Linoleic acid	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\downarrow$
Arachidonic acid	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$	
Prostaglandins						
PGE <sub>2</sub>		$\uparrow$		$\uparrow$	$\uparrow\uparrow$	
PGF <sub>2α</sub>	$\uparrow$	$\uparrow\uparrow$	$\uparrow$	$\uparrow\uparrow$		$\uparrow$
6-ketoPGF <sub>1α</sub>	$\uparrow$	$\uparrow$	$\downarrow$	$\uparrow\uparrow$	$\uparrow$	$\uparrow$

Fig. 16.3 Comparison of effects of single or repeated mild traumatic brain injury (mTBI) on levels of *N*acyl ethanolamines, *N*-acyl glycines, *N*-acyl taurines, 2-acyl glycerols, free fatty acids, and prostaglandins. Levels of targeted bioactive lipids in the cerebellum, trigeminal ganglia, and trigeminal nucleus caudalis of rats given a single mTBI (mTBI  $\times$  1) or 4 repeated mTBIs (mTBI  $\times$  4) were compared to respective sham rats. Cells with shaded arrows indicate a significant or trending change in that lipid with mTBI. The arrow color indicates the direction of change relative to sham. Green colors represent increases, whereas orange colors represent decreases. Darker colors represent significant changes of p < 0.05 and lighter colors represent trending changes of p < 0.10, as determined by one-way ANOVA. The number of arrows indicates the magnitude of the difference between mTBI and sham. One arrow indicates a magnitude difference of less than 1.5 fold and 2 arrows indicate a 1.5–1.99 fold change. A blank cell indicates that there was no change in the lipid's level due to mTBI. See Methods for more detailed description of analysis



Fig. 16.4 Comparison of effects of single or repeated mild traumatic brain injury (mTBI) on levels of *N*docosahexaenoyl ethanolamine (DEA) and *N*arachidonoyl glycine (NAGly). Panel A shows bar graphs for mean levels in moles per gram tissue of DEA in the cerebellum (CER), trigeminal ganglia (TG), and tri-

geminal nucleus caudalis (TNC) of rats exposed to a single mild traumatic brain injury (single mTBI – black bars) or sham (open bars) and of rats exposed to a series of 4 mTBIs (repeated mTBI – black bars) or sham (open bars). Error bars are  $\pm$  standard error of the mean. Asterisk (\*) indicates a difference between mTBI and sham of p < 0.05

age of changes occurred in the TNC (29 lipids -40% of the lipids detected), followed by the TG (28 lipids - 36%). Unlike in single mTBI, where the most changes were detected in the CER, in repeated mTBI the CER had the fewest changes detected (19 lipids -24%). The ratio of increases and decreases also shifted, with decreases occurring in every tissue type. In the TG and CER, most of the changes were increases (27 increases of 28 changes for TG and 17/19 for CER). The TNC stands out, because it was the only tissue type where most of the changes were decreases, suggesting functional specialization in this area that can potentially underlie a more dynamic response to injuries (15/29; Figs. 16.2, 16.3, 16.4, and 16.5). Given that the CER was the most affected area after a single mTBI, a single mTBI may therefore have a stronger effect on bioactive lipid production in sites closer to the injury, such as the CER, whereas the effects of repeated mTBI on bioactive lipid levels may spread to more distant areas.

# 16.4.2 Effects of mTBI on Bioactive Lipids with Relatively More Well-Studied Biosynthetic Pathways and Protein Targets

## 16.4.2.1 N-Acyl Glycine Lipid Species Are Upregulated After mTBI

Levels of NAGly increased in all 6 groups in the mTBI experiments (Figs. 16.3 and 16.4). Increases in NAGly were also found after repeated exposure to low levels of the environ-

mental toxin, acrolein [43]. This means that increases in NAGly may serve as a marker of headache caused by very different stimuli, mTBI and TRPA1 activation. There are multiple pathways that regulate NAGly levels. NAGly is a metabolite of AEA and can be formed from AEA via 2 enzymatic pathways, one mediated by alcohol dehydrogenase and the other mediated by fatty acid amide hydrolase (FAAH) [58]. Indeed, in FAAH knockout (KO) mice, brain levels of NAGly are significantly reduced, whereas AEA levels are significantly higher compared to wild-type (WT) [69]. The concurrent reduction in AEA and other NAEs and increase in NAGly in the TNC after repeated mTBI could potentially be driven by an increase in AEA metabolism via FAAH. NAGly production can also be mediated by glycine N-acyl transferase enzymes [75] and by the newly-characterized enzyme peptidase M20 domain containing 1 (PM20D1) [76, 77]. PM20D1 regulates mitochondrial uncoupling via regulation of endogenous lipoamines. As mitochondrial dysfunction is a hallmark of neuroinflammation after TBI [13], the relationship between PM20D1, TBI, and lipoamine regulation should be further investigated.

All other *N*-acyl glycine lipids that changed with a single mTBI showed an increase (Fig. 16.3). After a single mTBI, *N*-oleoyl glycine (O-Gly) increased in all 3 tissue types, along with the increase in NAGly, which was still present after repeated mTBI. Alterations in O-Gly have previously been associated with TBI in rodent models, as O-Gly was upregulated in the mouse insular cortex 24 h after TBI [78]. Levels

**Fig. 16.4** (continued) whereas the hash sign (#) indicates a difference between mTBI and sham of p < 0.10, as determined by one-way ANOVA. After single mTBI, DEA increased in all 3 tissue types, corresponding to green cells with 1 up arrow in Fig. 16.4. After repeated mTBI, DEA decreased in the CER and TNC, corresponding to orange cells with 1 down arrow in Fig. 16.4, but increased in the TG, corresponding to a green cell with 1 up arrow in Fig. 16.4. **Panel B** shows bar graphs for mean levels in moles per gram tissue of NAGIy in the cerebellum (CER), trigeminal ganglia (TG), and trigeminal

nucleus caudalis (TNC) of rats exposed to a single mild traumatic brain injury (single mTBI – black bars) or sham (open bars) and of rats exposed to a series of 4 mTBIs (repeated mTBI – black bars) or sham (open bars). Error bars are  $\pm$  standard error of the mean. Asterisk (\*) indicates a difference between mTBI and sham of p < 0.05 whereas the hash sign (#) indicates a difference between mTBI and sham of p < 0.10, as determined by one-way ANOVA. In all 3 tissue types, levels of NAGly increased after single and repeated mTBI, corresponding to green cells with 1 up arrow in Fig. 16.4

	Cerebellum		Trigeminal Ganglia		Trigeminal Nucleus	
Lipid Species	mTBLX 1	mTBLX 4	mTBLX 1	mTBLX 4	mTBLX 1	mTBLX 4
N-acyl alanine						
N-palmitovl alanine	$\wedge$		$\uparrow$			$\uparrow$
N-stearoyl alanine	· · · ·		<u> 个 个 </u>			×
<i>N</i> -oleovl alanine	· 个	$\uparrow$	· · ·			<b>↓</b>
N-arachidonovl alanine	<u>.</u> 		- 			· 个
N-docosahexaenovl alanine		ተተ				
N-acyl GABA						
N-palmitovi GABA			, sk	<u> </u>	$\uparrow$	
N-stearoyl GABA	$\wedge$		Ť	<u>↑</u>		J.
N-oleovi GABA	· · · ·		J.			, ,
N-linoleovl GABA	· 个		BAI	BAI		Ť
N-arachidonovl GABA	<b>小</b>	$\wedge$			$\uparrow$	$\wedge$
N-docosahexaenovl GABA						, sk
N-acyl leucine						*
N-palmitovl leucine				$\uparrow$		
N-stearoyl leucine				· · ·		J
N-oleovl leucine				•		¥
N-linoleovl leucine		$\wedge$				Ť
N-docosabexaenovl leucine		· · ·				
N-acyl methionine						
N-palmitovl methionine	$\wedge$					
N-stearoyl methionine	· · ·		$\uparrow$			
<i>N</i> -oleovl methionine			· 个			
<i>N</i> -arachidonovl methionine						$\uparrow$
<i>N</i> -docosahexaenovl methionine		BAL		<u> </u>	BAL	BAL
N-acyl phenylalanine						
N-stearovl phenylalanine						J.
N-oleovl phenylalanine					$\uparrow$	Ť
N-arachidonovl phenylalanine	$\uparrow$		$\uparrow$	$\uparrow$	$\uparrow$	$\uparrow$
<i>N</i> -docosahexaenovl phenvlalanine						ΨΨ.
N-acyl proline						
N-oleovl proline		$\uparrow$				$\uparrow$
N-arachidonoyl proline	BAL	BAL	BAL	$\uparrow\uparrow$	BAL	BAL
N-acyl serine						
N-palmitoyl serine	$\uparrow$				$\uparrow$	
N-stearoyl serine	$\uparrow$					
N-oleoyl serine	$\uparrow$					
N-linoleoyl serine				$\uparrow$		
N-arachidonoyl serine	$\uparrow$	$\uparrow$		$\uparrow$		
N-acyl tryptophan						
N-stearoyl tryptophan				$\uparrow$		
N-acyl tyrosine						
N-palmitoyl tyrosine					$\uparrow$	
N-oleoyl tyrosine	$\uparrow$					
N-linoleoyl tyrosine	$\uparrow\uparrow\uparrow$					BAL
N-arachidonoyl tyrosine	$\uparrow$				$\uparrow$	$\uparrow$
N-acyl valine						
N-palmitoyl valine	$\uparrow$					
N- stearoyl valine	$\uparrow$		$\uparrow$		$\uparrow$	
N-docosahexaenoyl valine	$\uparrow\uparrow$				BAL	BAL
phosphoLEA						
phosphoLEA	BAL	$\uparrow\uparrow$	BAL	$\uparrow\uparrow$		

Fig. 16.5 Effects of single and repeated mild traumatic brain injury (mTBI) on additional bioactive lipids in the cerebellum, trigeminal ganglia, and trigeminal nucleus. Specifically, this heatmap shows effects of mTBI on members of the *N*-acyl alanine, *N*-acyl GABA, *N*-acyl leucine, *N*-acyl methionine, *N*-acyl phenylalanine, *N*-acyl proline, *N*-acyl serine, *N*-acyl tryptophan, *N*-acyl tyrosine, and *N*-acyl valine families of bioactive lipids, and effects on phosphoLEA. Levels of targeted bioactive lipids in the cerebellum, trigeminal ganglia, and trigeminal nucleus caudalis of rats given a single mTBI (mTBI  $\times$  1) or 4 repeated mTBIs (mTBI  $\times$  4) were compared to respective sham rats. Only lipids that had significant or trending changes with either single or

of the TRPV1 agonist *N*-docosahexaenoyl glycine (D-Gly) [41] also increased in the CER and *N*-stearoyl glycine (S-Gly) also increased in the TG. The TNC had the most changes in *N*-acyl glycine levels after a single mTBI, with levels of all 6 *N*-acyl glycines increasing. After repeated mTBI, the increase in NAGly was the only increase in an *N*-acyl glycine in the TNC. In the TNC, S-Gly decreased after repeated mTBI, which was the only mTBI-driven decrease measured in *N*-acyl glycines. S-Gly changed in the opposite direction in the CER, increasing after repeated mTBI. D-Gly increased in the TG only (Figs. 16.3 and 16.4).

## 16.4.2.2 NAGIy and Additional N-Acyl Glycine Lipids Drive Microglial Migration

NAGly drives dose-dependent migration in BV2 microglia via activation of GPR18, which can be inhibited by A-Ser [59]. A-Ser's effects on microglia could underlie some of its reported neuroprotective actions after mTBI [47, 48] because microglial migration is understood to be a marker of neuroinflammation [47]. Other studies have shown an increase in microglial activation after mTBI, with microglia rapidly migrating towards damaged tissue [79]. However, the utility of the microglial response is complex [13]. Initially, microglia may be useful at clearing away damaged axonal tissue, which can promote regeneration of damaged axons [13]. However, sustained microglial activation does not seem to be as beneficial and appears to promote inflammation rather than regeneration [13, 79]. The fact that the increase in NAGly was widespread, occurring in sites distant from the injury, and sus-

**Fig. 16.5** (continued) repeated mTBI in at least 1 tissue type are shown here. Cells with shaded arrows indicate a significant or trending change in that lipid with mTBI. The arrow color indicates the direction of change relative to sham. Green colors represent increases, whereas orange colors represent decreases. Darker colors represent significant changes of p < 0.05 and lighter colors represent trending changes of p < 0.10, as determined by one-way ANOVA. The number of arrows indicates the

tained up to 1 week after repeated mTBI suggests broad increases in neuroinflammation [79]. Microglia can release pro-inflammatory lipid signaling molecules such as PGs [4]. It is possible that the increases in PGs observed after repeated mTBI are a consequence of increased microglial activation. Experiments are planned to see if microglia release PGs when incubated with NAGly.

Novel data shown here demonstrates that NAGly is not the only *N*-acyl glycine that can induce microglial migration. At 10 µM, N-palmitoyl glycine, S-Gly, O-Gly, N-linoleoyl glycine, NAGly, and D-Gly induced migration in BV-2 microglia (Fig. 16.6a, b). This demonstrates how BV2 microglia might not be responding to the identity of the acyl chain but are instead sensitive to glycine-containing lipoamines. Follow-up studies should examine how combining these compounds affects migration, as levels of multiple N-acyl glycines change with mTBI. Unpublished data from the Hurley lab confirmed that there were increased numbers of microglia in the corpus callosum of mTBI rats, suggesting some effects on migration (personal communication). Highlighting potential cross-talk between TRPA1 and microglia, endogenous TRPA1 ligands released by microglia in the spinal cord are hypothesized to contribute to central sensitization after a peripheral nerve injury. Both TRPA1 antagonists and blockers of microglia can reduce central pain hypersensitivity in animal models [80]. Therefore, it is worth investigating whether TRPA1 antagonists or microglial blockers can similarly reduce headache pain secondary to TBI.

magnitude of the difference between mTBI and sham. One arrow indicates a magnitude difference of less than 1.5 fold, 2 arrows indicate a 1.5–1.99 fold change, and 3 arrows indicate a 2–2.99 fold change. A blank cell indicates that there was no change in the lipid's level due to mTBI. BAL stands for below analytical limits and means that lipid was not detected in all samples in that tissue type. See Methods for more detailed description of analysis

A. Number of Migrated BV-2 Microglia



B. Number of Migrated BV-2 Microglia



Fig. 16.6 Cellular migration activity of *N*-acyl glycines in BV2 microglial cells. Panel A: At 10  $\mu$ M, *N*-docosahexaenoyl glycine (DocGly), *N*-arachidonoyl glycine (NAGly), *N*-linoleoyl glycine (LinGly), and *N*-oleoyl glycine (OIGly) caused cellular migration that was significantly greater than the vehicle control. 7 plates were analyzed with 20 repeats for each condition per plate. \* indicates a mean difference significant at the 0.05

# 16.4.3 N-Docosahexaenoyl Ethanolamine (DEA) May Play a Key Role in the Effects of mTBI with a Potential Implication in Resolving Pathways

As the most affected NAE, the TRPV1 agonist DEA [41] increased in all single mTBI groups but decreased in the CER and the TNC with repeated mTBI. The eCB AEA increased in the CER and TNC after a single mTBI, but not in the TG. LEA also increased in the CER and TNC, meaning that multiple TRPV1 agonist NAEs [41] were elevated in these tissues after a single mTBI. Repeated mTBI drove a tissue-specific mixture of increases and decreases in NAEs, with increases restricted to the TG. The only change in NAEs in the CER was a decrease in DEA. In contrast, DEA increased in the TG, along with LEA and AEA. OEA decreased slightly in the TG. In contrast to single mTBI where LEA, AEA, and DEA increased, these NAEs decreased in the

level when compared to vehicle. **Panel B:** At 10  $\mu$ M, *N*-arachidonoyl glycine (NAGly), *N*-linoleoyl glycine (LinGly), *N*-stearoyl glycine (StrGly), and *N*-palmitoyl glycine (PalGly) caused cellular migration that was significantly greater than the vehicle control. 4 plates were analyzed with 20 repeats for each condition per plate. \* indicates a mean difference significant at the 0.05 level when compared to vehicle

TNC after repeated mTBI, along with *N*-palmitoyl ethanolamine (Figs. 16.3 and 16.4). Reductions in NAEs in the TNC after repeated mTBI could be driven by a decrease in biosynthesis via *N*-acyl phosphatidyl ethanolamine-specific phospholipase D (NAPE-PLD) [70]. In NAPE-PLD KO mice, brain levels of NAGly either stayed the same or increased while AEA decreased [70], consistent with what was seen in the TNC after repeated mTBI. Increased levels of PGs in the TNC after repeated mTBI (Fig. 16.3) are also consistent with NAPE-PLD blockade, as NAPE-PLD KO mice have higher levels of PGs in the CNS compared to WT [70].

The omega-3 fatty acid, docosahexaenoic acid (DHA) is a precursor for DEA and can be neuroprotective after TBI [81–85]. For example, rats were subjected to an impact acceleration injury, which causes diffuse axonal injury [81]. For the next 30 days, injured rats were given vehicle or DHA [81]. In rats supplemented with DHA, plasma levels of DHA increased and the ratio of AA to eicosapentaenoic acid, a general

marker of inflammation, decreased [81]. In rats given vehicle, plasma levels of DHA were significantly reduced [81]. DHA had a protective effect and decreased the number of amyloid precursor protein-positive and caspase-3 positive (apoptotic) neurons in the brainstem [81]. The same group performed a similar follow-up study, but here they gave rats DHA for 30 days before the injury instead of after the injury [83]. Similar results were uncovered, with DHA having a neuroprotective effect against TBI, suggesting that DHA can also be used as a prophylactic to protect the brain against the consequences of injury [83].

In another study, rats were given a DHAsupplemented diet or a control diet for 30 days before receiving a mild fluid percussion injury [82]. Rats on the control diet experienced learning difficulties after the injury, as measured by the Morris water maze, whereas rats that received DHA did not show these deficits [82]. Furthermore, injury-related decreases in BDNF, CREB, and synapsin I, were not measured in the DHA-supplemented rats and lower levels of oxidized proteins were measured in the hippocampus of the DHA-rats, suggesting a reduction in oxidative stress [82]. DHA also appears to protect against inflammation after TBI, as rats that were given daily injections of DHA for 21 days showed a reduction in markers of activated microglia, which were elevated after TBI [85]. Of the activated microglia that were still present in the CNS of the DHA-treated rats, more of these expressed the anti-inflammatory marker CD206 and fewer expressed the proinflammatory marker CD16/32 [85]. On the other hand, when rats are raised on a diet low in DHA and other omega-3 fatty acids, they show worsened recovery from TBI-related motor deficits and increased neuronal death compared to rats on a control diet, as well as a 70% loss of DHA in the brain [84]. This data is an important reminder that diet can influence levels of bioactive lipids and that a diet rich in omega-3 polyunsaturated fatty acids can have measurable health benefits. Although metabolites of DHA were not quantified, the authors hypothesized that some of DHA's neuroprotective effects are due to conversion into pro-resolving mediators such as D-series resolvins and neuro-protectin [81].

The primary biosynthetic pathways for these DHA-derived lipids, 15-lipoxygenase DHA (15-LOX)can convert into 17S-hydroperoxydocosahexaenoic acid (17S-H(p)-DHA), whereas cyclooxygenase 2 can convert DHA into the enantiomer, 17R-hydroperoxydocosahexaenoic acid (17R-H(p)-DHA)5-lipoxygenase [86]. (5-LOX) converts 17S-H(p)-DHA to resolvin D1, whereas the same enzyme converts 17R-H(p)-DHA into aspirin-triggered resolvin D1 [86]. Alternatively, 17S-H(p)-DHA and 17R-H(p)-DHA can first be converted into epoxide intermediates which are then hydrolyzed to produce neuroprotection D1 [86]. Resolvin D1 can reduce immune cell infiltration and reduces inflammatory pain [87]. Likewise, neuroprotectin D1 reduces inflammatory pain and can also inhibit pain signals via TRPV1 at intrathecal doses of just 0.1-10 ng [88]. Given that TRPV1 ligands are elevated after a single mTBI, it is possible that neuroprotectin D1 could reduce TVS sensitization and therefore decreases headache pain.

Pro-resolving mediators are currently being investigated as neuroprotective therapies for brain injuries [89], as they are highly potent antiinflammatory bioactive lipids [90]. Treating mice with diffuse axonal injury with aspirin-triggered resolvin D1 for 3 days pre-injury and 7 days postinjury partially rescued the cognitive deficits and motor deficits, as measured by the novel object recognition task and the rotorod task [90]. Neuroprotectin D1 formation increased in the mouse hippocampus after cerebral artery occlusion, where it inhibited immune cell infiltration and pro-inflammatory gene induction [91]. Neuroprotectin D1 also inhibited cytokine production in neuronal cell cultures [91]. Highlighting the neuroprotective effect of this bioactive lipid, the infarct volume in the hippocampus was significantly reduced 48 h after the cerebral artery occlusion injury in mice given intracerebroventricular infusions of neuroprotectin D1 [91].

Decreases in DEA after repeated mTBI could potentially be driven by conversion to oxygenated metabolites. DEA has been identified as a precursor for several bioactive lipids, which are formed via similar pathways as the biosynthesis of resolvins and neuroprotectin from DHA [92]. For example, incubating mouse brain homogenates with DEA gener-17-hydroxydocosahexaenoyl ethanolamide ated 4,17-dihydroxydocosahexaenoyl (17-HDHEA), ethanolamide, as well as smaller amounts of 7,17-dihydroxydocosahexaenoyl ethanolamide. 10,17-dihydroxydocosahexaenoyl ethanolamide (10,17-diHDHEA), and 15-hydroxy-16(17)-epoxydocosapentaenoyl ethanolamide (15-HEDPEA) [92]. 10,17-diHDHEA and 15-HEDPEA were agonists at CB<sub>2</sub> with EC<sub>50</sub>'s in the low nanomolar range and blocked platelet-leukocyte aggregation formation in human whole blood at concentrations of just 10pM [92]. As CB<sub>2</sub> ligands were neuroprotective after TBI [21], it is possible that these DEA-derived lipids have neuroprotective effects via that receptor. Highlighting the potency of these resolving lipids, injections of 15-HEDPEA reduced lung injury after reperfusion at doses as low as 1  $\mu$ g/mouse [92]. Given that these lipids are so potent, they might be bioactive at concentrations below the detection limits of our HPLC/MS/MS system. It might instead be a more viable strategy to measure the activity of 5-LOX after mTBI and acrolein exposure, as this is a rate-limiting enzyme for the formation of resolvins from DHA and might also be important for the formation of oxygenated metabolites of DEA [93]. Indeed, blocking 5-LOX with siRNA in head and neck squamous cell carcinoma cell lines attenuated the formation of reactive oxygen species and blocked the ability of DEA to inhibit cell proliferation [93]. 15-LOX is also an important enzyme to monitor, because it mediates the conversion of DEA to 17-hydroperoxydocosahexaenoyl ethanolamide, a precursor for the CB<sub>2</sub> agonists 10,17-diHDHEA and 15-HEDPEA, as well as 17-HDHEA [92].

The fact that multiple NAEs were altered with mTBI is important because there are emergent signaling properties when multiple TRPV1-ligand NAEs are combined in that the potency is increased when multiple agonists are present [43]. Multiple NAEs also changed in brain tissues of rats in a model of peripheral inflammation

[41] and in a rodent model of headache driven by acrolein exposure [43], suggesting that these molecules are sensitive to inflammatory insults. The actions of multiple NAEs at TRP channels may override the analgesic effects of AEA via CB<sub>1</sub> [18], and prolonged exposure to elevated levels of NAEs has been associated with a nociceptive phenotype in response to capsaicin [66].

## 16.4.4 Additional Bioactive Lipids Effected by mTBI

#### 16.4.4.1 N-Acyl Taurines

All 4 *N*-acyl taurines, including the TRPV1 and TRPV4 agonist [39] A-Taur, increased in the CER and TNC after a single mTBI. However, none of the targeted *N*-acyl taurines changed in the TG. Fewer changes in *N*-acyl taurines were measured after repeated mTBI and there were no longer increases in all 4 *N*-acyl taurines in the CER and TNC. Instead, *N*-stearoyl taurine decreased in the CER and A-Taur increased in the TG, which was the only change in *N*-acyl taurines associated with mTBI in the TG. A-Taur also increased in the TNC, as did *N*-oleoyl taurine (Fig. 16.3) [43].

#### 16.4.4.2 2-Acyl Glycerols

After a single mTBI, 2-acyl glycerol levels were only affected in the TNC. Here, there were increases in the eCB 2-AG, as well as 2-palmitoyl glycerol (2-PG) and 2-linoleoyl glycerol (2-LG). This makes the TNC the only tissue where levels of both of the eCBs, AEA and 2-AG, were affected by a single mTBI. Whether levels of 2-acyl glycerols increased or decreased after repeated mTBI was dependent on tissue type. Changes in 2-acyl glycerols were increases in the CER and the TG, but decreases in the TNC. In the CER, 2-PG and 2-LG increased. In contrast, all 4 2-acyl glycerols in the screening library significantly increased in the TG. Only 1 change in 2-acyl glycerol levels was measured in the TNC – a reduction in 2-oleoyl glycerol (Fig. 16.3).

As 2-AG has been shown to be neuroprotective in multiple TBI studies [12, 19, 20], increases in 2-AG in the TG after repeated mTBI and in the

TNC after single mTBI may be part of a neuroprotective and regenerative response that mediates some of the moderate spontaneous recovery that occurs after TBI [74]. mTBI also impacted structurally analogous lipids to the eCB 2-AG, especially in the in the TG, where repeated mTBI increased 4 different 2-acyl glycerols. This implicates eCB system enzymes as potential mediators of mTBI's effects on lipid levels because these enzymes regulate lipid levels beyond eCB substrates [69, 70, 94]. A decrease in 2-acyl glycerol hydrolysis via monoacylglycerol lipase (MAGL) could increase 2-acyl glycerol levels, and we have shown that MAGL deletion causes widespread increases in 2-acyl glycerols in the mouse brain [69]. However, these increases in 2-acyl glycerols likely came at the expense of levels of AA and PGs [69]. Increases in AA and PGs were measured in the TG after repeated mTBI, making MAGL inhibition an unlikely mechanism.

Diacylglycerol lipases (DAGL) synthesize 2-acyl glycerols from their diacylglycerol (DAG) precursors, so an increase in DAGL activity could upregulate 2-acyl glycerols [95]. The DAGL $\alpha$ isoform appears more important for biosynthesis of 2-AG in the brain, whereas the DAGL $\beta$  isoform appears more important in the periphery [96]. There is evidence that levels of AA and AEA can change in the same direction as 2-AG upon a change in DAGL activity. Along with 2-AG levels, AEA levels were downregulated in the cerebellum, striatum, and hippocampus of a line of DAGL $\alpha$  KO mice [97]. Another line of DAGLα KO had an 80% reduction in whole brain 2-AG and AA levels and a 40% reduction in AEA [98]. A third line of DAGL $\alpha$  KO had reduced levels of 2-AG and AA in the forebrain, but did not detect a significant reduction in AEA in this area, hinting at some regional specificity for the contribution of DAGL $\alpha$  activity to AEA levels [99]. Reductions in whole-brain 2-AG, AA, and AEA also occur when DAGL $\alpha$  is pharmacologically inhibited [100]. It isn't yet known whether increasing DAGL activity causes concurrent increases in AA and AEA, which occurred in the TG after repeated mTBI.

Follow-up studies can determine if the effects of mTBI are abolished when DAGL is inhibited

or deleted. If effects on the lipidome require DAGL, then more direct measurements of DAGL activity can be performed after mTBI or acrolein exposure. Recently, a fluorescent probe was developed to measure DAGL activity [101]. This probe can be used in activity based protein profiling (ABPP) assays in mouse brain proteasomes [102]. By performing ABPP after acute and repeated mTBI and after acute and chronic acrolein exposure, the impact on DAGL activity can be quantified. ABPP can also be employed to detect off-target serine hydrolase activity [103], which may reveal a more widespread impact of mTBI on enzymes important for maintaining levels of eCBs and other bioactive lipids.

## 16.4.4.3 The Potential Link Between TRPV1 and 2-Acyl Glycerol Lipids

What upstream changes can affect DAG production? Phospholipase C (PLC) intracellular pathways stimulate the release of DAGs from membrane phospholipids [104]. An earlier study demonstrated that TBI increased PLC activity in the cat brain [105]. Activation of TRP receptors can drive PLC pathways [36]. Indeed, we have shown that capsaicin activation of TRPV1 increases 2-acyl glycerol production [43]. Increases in levels of multiple TRPV1 ligands like LEA, AEA, and DEA in the TG after repeated mTBI could potentially increase PLC signaling, leading to an increase in DAG substrates for 2-acyl glycerol production. AA itself can also activate PLC pathways [106] and levels of AA were upregulated after repeated mTBI in the TG.

#### 16.4.4.4 Free Fatty Acids and PGs

After a single mTBI, increases in AA and linoleic acid (LA) were common to all 3 tissues. Oleic acid (OA) also increased in the CER, meaning that all 3 free fatty acids screened for increased after single mTBI in this tissue type. After repeated mTBI, it was the TG that had increases in all 3 free fatty acids. AA and LA increased in the TG, but OA did not significantly change in this tissue. The only decrease in free fatty acid levels was restricted to the TNC, where LA decreased after repeated mTBI (Fig. 16.3). PGs were also affected by mTBI. A single mTBI increased levels of 2 different PGs,  $PGF_{2\alpha}$  and 6-ketoPGF<sub>1 $\alpha$ </sub> in the CER. In the TG,  $PGF_{2\alpha}$  increased, whereas 6-ketoPGF<sub>1 $\alpha$ </sub> decreased. This was the only measured decrease in PG levels. In contrast, 2 PGs increased in the TNC,  $PGE_2$  and 6-ketoPGF<sub>1 $\alpha$ </sub>. After repeated mTBI,  $PGF_{2\alpha}$  and 6-ketoPGF<sub>1 $\alpha$ </sub> increased in all 3 tissue types. In the CER and TG,  $PGE_2$  also increased, such that all 3 PGs in the screening library increased in the CER and TG (Fig. 16.3).

Increases in AA in CNS tissues were measured after mTBI. AA can be directly released from phospholipids via phospholipase  $A_2$ , or indirectly via PLC [107]. Levels of AA are elevated in the CSF of TBI patients and higher levels of AA 1 week post-injury were correlated with worse outcomes [108]. Increased levels of AA are hypothesized to underlie increases in PGs in the brain after TBI [105] and here there were increases in levels of all 3 PGs in the CER and TG after repeated mTBI, where levels of AA also increased.

Levels of bioactive lipids are differentially affected by mTBI, mostly increasing after single and repeated mTBI. However, decreases in bioactive lipid levels were more common after repeated mTBI compared to single mTBI, especially in the TNC. After a single mTBI, certain changes were measured in all 3 tissue types and all of these were increases relative to sham. Specifically, DEA, O-Gly, NAGly, LA, and AA increased. After repeated mTBI, fewer changes were common to all 3 tissue types, although levels of PGs increased in all 3 tissues, along with NAGly. Thus, DEA levels changed in every tissue type and NAGly was upregulated in the CER, TG, and TNC, after a single or repeated mTBI (Figs. 16.3 and 16.4).

# 16.4.5 Effects of mTBI on Lipoamine Families That Include a TRPV Ligand

The following section summarizes some of the effects on the lipids that were measured in these models but are lipids that have members that have some activity at TRP channels. Many of these lipids have little data about them beyond those generated by our laboratory from which to compare; therefore, we will have to rely on those few reports. The lipids are subdivided into lipoamine "families" as characterized by the amine moiety and each section is labeled with this family for ease of referencing those that might be of particular interest to a reader.

N-Acyl GABAs N-linoleoyl GABA (L-GABA), and N-docosahexaenoyl GABA A-GABA, (D-GABA) are ligands at TRPV1 [41]. However, D-GABA did not change after single mTBI. After single mTBI, change in L-GABA was restricted to the CER, where it increased along with A-GABA and 2 additional N-acyl GABAs. Changes in N-acyl GABAs were decreases in the TG after single TBI and were restricted to *N*-acyl GABAs that lack TRPV1 activity. N-palmitoyl GABA changed in the opposite direction in the TNC, as it increased after a single mTBI, along with A-GABA. Fewer N-acyl GABAs changed in the CER after repeated mTBI, as an increase in A-GABA was the only detected change. Decreases in N-acyl GABAs were no longer found in the TG after repeated mTBI and instead 2 N-acyl GABAs with saturated acyl moieties increased. On the other hand, 3 N-acyl GABAs decreased in the TNC, including D-GABA. This was the only change in D-GABA associated with mTBI. However, A-GABA increased in the TNC. This means that increases in A-GABA were present in the CER and TNC after both single and repeated mTBI, but other changes in *N*-acyl GABAs were sensitive to the number of mTBIs (Fig. 16.5).

*N-Acyl Prolines* Although *N*-docosahexaenoyl proline is a TRPV1 antagonist [41], this lipid was not detected in any tissue type. This is likely to do with a poor signal to noise characteristic of our mass spectrometric analysis than due to a lack of endogenous production given that all other combinations are measurable. Even with the poor signal to noise of this lipoamine family in general, we are still able to measure many of the members

and showed that those *N*-acyl prolines only changed after repeated mTBI. *N*-oleoyl proline increased in the CER and TNC, whereas *N*-arachidonoyl proline (A-Pro) increased in the TG, which was the only tissue where it was detected in all samples (Fig. 16.5).

*N-Acyl Serines* A single mTBI increased 4 different *N*-acyl serines in the CER, including A-Ser. The only other change in an *N*-acyl serine after a single mTBI was an increase in *N*-palmitoyl serine in the TNC. Repeated mTBI increased A-Ser in the CER and TG. *N*-linoleoyl serine also increased in the TG but no changes in *N*-acyl serines were measured in the TNC in the repeated mTBI paradigm. Levels of the TRPV1 agonist *N*-docosahexaenoyl serine [41] did not change with mTBI (Fig. 16.5).

*N-Acyl Tryptophans N*-acyl tryptophans containing polyunsaturated acyl chains are agonists at TRPV4 [41]. However, these particular lipids were either not detected or unchanged by mTBI. The only mTBI-driven change in an *N*-acyl tryptophan was an increase in *N*-stearoyl tryptophan measured in the TG after repeated mTBI (Fig. 16.5).

**N-Acyl Tyrosines** Multiple N-acyl tyrosines increased in the CER and TNC after single mTBI. The CER had the most changes, with increases in N-oleoyl tyrosine (O-Tyr), and the TRPV4 agonists [41] N-linoleoyl tyrosine (L-Tyr) and N-arachidonoyl tyrosine (A-Tyr). Although O-Tyr does not directly activate or inhibit a TRPV channel, a mixture of N-acyl tyrosines including O-Tyr activated TRPV2, TRPV3, and TRPV4 in transfected HEK cells [41]. Thus, the elevated levels in multiple N-acyl tyrosines might affect signaling via TRPV2-4. The increase in L-Tyr was a larger magnitude change than the other increases, with levels of L-Tyr being twice as high in the mTBI CER relative to the sham CER. On the other hand, no changes in N-acyl tyrosines were measured in the TG. In the TNC,

single mTBI increased levels of the TRPV2/4 agonist *N*-palmitoyl tyrosine [41] and A-Tyr. An increase in A-Tyr in the TNC was the only change in *N*-acyl tyrosines measured after repeated mTBI (Fig. 16.5).

*N-Acyl Valines* In all 3 tissue types, exposure to a single mTBI increased levels of the TRPV3 antagonist [41] *N*-stearoyl valine (S-Val). In the CER, levels of *N*-palmitoyl valine and *N*-docosahexaenoyl valine, which is also a TRPV3 antagonist [41], additionally increased. Repeated mTBI did not affect *N*-acyl valine levels (Fig. 16.5).

To summarize the effects mTBI on endogenous TRPV ligands, more endogenous TRPV ligands were affected after a single mTBI compared to after repeated mTBI,. A single mTBI elevated levels of TRPV ligands, whereas repeated mTBI produced a mixture of increases and decreases in levels of TRPV ligands. In the mTBI model, changes in TRPV ligands common to all 3 tissue types were only uncovered after a single mTBI, specifically, the TRPV1 agonist DEA [41] and the TRPV3 antagonist S-Val [41] increased.

## 16.4.6 Effects of mTBI on Orphan Bioactive Lipids

Those lipids for which we have no known molecular targets and are collectively described as "orphan lipids" are discussed here. Some of these lipoamine families have multiple members that demonstrate consistent changes across models and represent potentially important targets to focus future research efforts.

*N-Acyl Alanines N*-acyl alanine species were responsive to mTBI. *N*-acyl alanines did not change in the TNC after a single TBI, whereas 4 different *N*-acyl alanines increased in the CER and TG. The increase in *N*-arachidonoyl alanine (A-Ala) was of a larger magnitude than the other increases, with levels of A-Ala being over twice as high in the mTBI CER and TG compared to sham. In contrast, none of the *N*-acyl alanines changed in the TG after repeated mTBI and only 2 changed in the CER. In the repeated condition, the TNC had the most changes, with increases in 4 *N*-acyl alanines, including A-Ala, and with a decrease in *N*-stearoyl alanine (Fig. 16.5).

*N-Acyl Leucines N*-acyl leucines only changed after exposure to 4 mTBIs and did not change after a single mTBI. *N*-linoleoyl leucine and *N*-docosahexaenoyl leucine increased in the CER, whereas *N*-palmitoyl leucine and *N*-stearoyl leucine (S-Leu) increased in the TG. In contrast, S-Leu decreased in the TNC, as did *N*-oleoyl leucine (Fig. 16.5).

*N-Acyl Methionines* Alterations in *N*-acyl methionines were restricted to the CER and TG after a single mTBI. 2 *N*-acyl methionines increased in each of these tissue types and *N*-stearoyl methionine increased in both tissue types. These changes were no longer present after repeated mTBI. Only the TG and TNC had changes in *N*-acyl methionines in this condition. There was a large increase in *N*-docosahexaenoyl methionine in the TG and a more modest increase in *N*-arachidonoyl methionine (A-Met) in the TNC (Fig. 16.5).

*N-Acyl Phenylalanines* In all 3 tissue types, a single exposure to mTBI increased *N*-arachidonoyl phenylalanine (A-Phe). Single mTBI also increased *N*-oleoyl phenylalanine in the TNC only. Changes in *N*-acyl phenylalanines were not measured in the CER after 4 mTBIs and increases in A-Phe were restricted to the TG and TNC. 2 additional *N*-acyl phenylalanines decreased in the TNC (Fig. 16.5).

**PhosphoLEA** PhosphoNAEs are intermediates for NAE production [109]. PhosphoLEA is the only phosphoNAE that is available in the screening library. This lipid only changed after repeated mTBI. Specifically, repeated mTBI increased phosphoLEA in the CER and TG (Fig. 16.5) [43]. Interestingly, these increases did not always accompany an increase in LEA.

Multiple orphan lipids, which lack molecular targets, change with mTBI suggesting that a wider variety of signaling systems may be affected. Those orphan lipids that stand out include A-Phe, which increased in all 3 tissue types after a single mTBI. mTBI affected certain lipoamines derived from AA, both orphan and with known molecular targets. For example, A-Ala robustly increased in the CER and TG following a single mTBI, A-Met increased in the TNC after repeated mTBI, and A-Pro increased in the TG after repeated mTBI. In all 3 tissue types, a single exposure to mTBI increased levels of A-Phe. Increases in A-Phe were also found in the TG and TNC after repeated mTBI. mTBI might therefore have more of an effect on enzymes that preferentially act on substrates containing AA.

# 16.5 Effects on Bioactive Lipids Change Over Time But Are More Similar When Headache-Like Symptoms Are Present

Effects of mTBI and acrolein exposure were quite different when comparing acute acrolein exposure effects to mTBI effects. Specifically, levels of bioactive lipids were more likely to decrease after the acute acrolein exposure [43]. These lipids tended to increase after mTBI. One explanation for these differences is that the tissue was collected immediately after the single 4 h acrolein exposure, whereas tissue was collected at least 72 h later in the case of mTBI. It wasn't until after repeated acrolein exposure that headache-like behaviors appeared [54], whereas after the single mTBI exposure, there were measurable headache-like behaviors. Similar alterations in lipid levels were observed between the models at time points when headache behavior was measurable (4 acrolein exposures or 1 mTBI exposure). One key finding is that chronic acrolein exposure increased levels of multiple TRPV ligands and increased levels of NAGly [43], as did mTBI. Thus, bioactive lipids may serve as a marker for the physiological changes in headache, regardless of the original stimulus that disrupted the TVS. Follow-up studies should examine whether there are similar changes in lipid levels immediately after the mTBI, as these could give insight into the lipid milieu that eventually gives rise to inflammation and pain.

Providing further evidence that the effects of painful insults on bioactive lipids are dynamic and dependent on time post-insult, in another rodent model of inflammatory pain, we also observed decreases in bioactive lipids in CNS tissues 1 h after intraplantar carrageenan application [41]. For example, A-GABA decreased in the cerebellum and brainstem and OEA decreased in the thalamus. At 3 h post-carrageenan, increases were observed in multiple NAEs in all 6 brain areas tested (striatum, hippocampus, cerebellum, thalamus, midbrain, and brainstem) [41]. These effects at 3 h included increases in NAGly in the striatum, hippocampus, and cerebellum [41]. Therefore, the effects of peripheral insults on bioactive lipids take some time to centralize, whereas the effects of central insults like mTBI may take some time to fully permeate the periphery. Overall, the effects of peripheral inflammation, acrolein exposure, and mTBI on bioactive lipids look more similar when painrelated behaviors emerge.

#### **16.5.1 Implications for Therapeutics**

Current therapeutics for headache are not particularly effective, underscoring the need to better understand the mechanisms that cause headache and develop new drugs that target these mechanisms [110]. TRPA1 may represent a novel target for treating headache [111]. Studies in the TRPA1 KO mouse [52] suggest that TRPA1 is required for pain and hypersensitivity associated with chronic inflammation, as TRPA1 functions as a gatekeeper of the release of endogenous inflammatory mediators from sensory neurons [24]. Systemic pretreatment with the TRPA1 antagonist AP-18 prevented the sensitization of the TVS due to chronic acrolein [11]. In acrolein-exposed rats treated with AP-18, changes in dural blood flow in response to either TRPA1 or TRPV1 agonist challenges did not sensitize the responses, implicating TRPA1 in the process of sensitization regardless of the exact receptor action of the agent [11]. The biochemical similarities between the 2 models (acrolein and mTBI), such as increases in NAGly [43], as well as the similarities in central and peripheral sensitization [11, 54], suggest that the same therapy may work in both models. A follow up study will test the hypothesis that pretreatment with AP-18 prevents headache driven by mTBI.

Novel headache therapeutics that block microglial activation are currently being developed [13, 112]. It is possible that attenuating microglial activation could be a therapy for headache due to mTBI, as both share changes in neuroinflammatory mediators that drive microglial activation [4, 13]. Strengthening the hypothesis that blocking microglial migration represents a strategy for treating mTBI, A-Ser, which attenuated NAGly-driven microglial migration [59], was also neuroprotective after TBI [47, 48]. A-Ser levels were elevated in the CER and TG post-repeated mTBI, potentially representing a compensatory strategy to reduce the microglial activation and migration that occurs after TBI. Because GPR18 activation drives microglial migration [59], it should be tested whether GPR18 antagonists are effective at preventing microglial migration after mTBI, as this might represent a novel strategy to reduce inflammation. FAAH inhibition also represents a strategy to reduce NAGly levels [69, 113]. Lipidomics studies have revealed that genetic [69] and pharmacological [113] inhibition of FAAH increases levels of AEA and other NAEs but at the expense of other AA-derived lipoamines such as NAGly. Treatment with the FAAH inhibitor URB597 reduced microglial and astrocytic activation after TBI in rats and was associated with improvement in behavioral measures [20]. The contribution of NAGly to these findings has not yet been investigated.

Cannabis-based medicines also represent a strategy to reduce inflammation and increase neuroprotection after mTBI, as well as reduce headache [4]. 85.1% of medical cannabis patients in Colorado who were recommended cannabis due to migraine experienced a reduction in migraine frequency [114]. Cannabidiol (CBD) might be a suitable candidate plant cannabinoid to treat headache, as it lacks abuse liability or intoxicating effects [4, 18]. Potentially reducing the inflammation associated with headache, CBD has known anti-inflammatory properties [4, 115]. Interestingly, CBD can block microglial migration driven by GPR18 [59], so it might be able to reduce neuroinflammation by blocking a target for NAGly and additional N-acyl glycines. As CBD has anti-epileptic properties [116], it might also protect against excitotoxicity that occurs after TBI [13].

## 16.6 Conclusions

In a rodent model of mTBI, there were widespread changes in levels of many bioactive lipids in the TVS and in the CER. Most of the mTBIdriven changes in lipids were increases. Some of these lipids are active at cannabinoid receptors or at TRPV1 receptors, with potential implications for the development of pain post TBI. Other lipids that were affected by mTBI act on microglia, which could play a role in the microglial activation and inflammation seen after mTBI. The most robust example being the AEA metabolite NAGly, which was upregulated in every tissue type screened after mTBI. NAGly is a potent inducer of migration in microglia, and global changes in NAGly levels could contribute to neuroinflammation and headache. Finally, the effects on DEA may provide an insight into the regulation of DHA-derived lipids such as the resolvins and further indicates that no lipid is an island. The interconnectedness that is a continuous theme in our understanding of bioactive lipids is particularly highlighted in the novel data presented in this chapter and also provides a new platform for thinking about how the long-term effects of mTBI has on lipid signaling.

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17

# Novel Anti-inflammatory and Vasodilatory ω-3 Endocannabinoid Epoxide Regioisomers

Lauren N. Carnevale and Aditi Das

#### Abstract

Accumulating evidence suggests that diets rich in  $\omega$ -3 polyunsaturated fatty acids (PUFAs) offer protection against vascular inflammation, neuroinflammation, hypertension, and thrombosis. Recently, biochemical studies have demonstrated that these benefits are partially mediated by their conversion to  $\omega$ -3 endocannabinoid epoxide metabolites. These lipid metabolites originate from the epoxidation of  $\omega$ -3 endocannabinoids, docosahexanoyl ethanolamide (DHEA) and eicos-

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Division of Nutritional Sciences, University of Illinois Urbana-Champaign, Urbana, IL, USA e-mail: aditidas@illinois.edu form epoxydocosapentaenoic acidethanolamides (EDP-EAs) and epoxyeicosatetraenoic acid-ethanolamides (EEQ-EAs), respectively. The EDP-EAs and EEQ-EAs are endogenously produced in rat brain and peripheral organs. Additionally, EDP-EAs and EEQ-EAs dose-dependently decrease proinflammatory IL-6 cytokine and increased anti-inflammatory IL-10 cytokine. Furthermore, the EEQ-EAs and EDP-EAs attenuate angiogenesis and cell migration in cancer cells, induce vasodilation in bovine coronary arteries, and reciprocally regulate platelet aggregation in washed human platelets. Taken together, the  $\omega$ -3 endocannabinoid epoxides represent a new class of dual acting molecules that display unique pharmacologi-

ethanolamide

cytochrome P450 (CYP) epoxygenases to

(EPEA)

by

#### Keywords

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apentaenoyl

 $\begin{array}{l} Cytochrome \ p450 \cdot Epoxygenase \ \cdot \\ Neuroinflammation \ \cdot Endocannabinoid \ \cdot \\ Epoxyeicosatrienoic \ acids \ \cdot \ Cannabinoid \\ receptors \ 1 \ and \ 2 \ \cdot \ Omega-3 \ fatty \ acids \end{array}$ 

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#### Abbreviations

2-AG	2-arachidonoyl-glycerol		
2-DHG	2-docosahexaenoyl-glycerol		
2-EPG	2-eicosapentaenoyl-glycerol		
AA	arachidonic acid		
AEA	anandamide		
cAMP	cyclic adenosine monophosphate		
CB1	cannabinoid receptor 1		
CB2	cannabinoid receptor 2		
CYP	cytochrome P450		
DHA	docosahexaenoic acid		
DHEA	docosahexaenoyl ethanolamide		
eCB	endocannabinoid		
EDP-EA	docosapentaenoic acid ethanolamide		
EEQ-EA	epoxyeicosatetraenoic aci		
	ethanolamide		
EPA	eicosapentaenoic acid		
EPEA	eicosapentaenoyl ethanolamide		
FAAH	fatty amide hydrolase		
GPCR	G-Protein coupled receptor		
MAGL	monoacylglycerol lipase		
sEH	soluble epoxide hydrolase		
$\Delta^9$ -THC	$\Delta^9$ -tetrahydrocannabinol		

#### 17.1 Introduction

#### 17.1.1 The Endocannabinoid System

The main psychoactive component of Cannabis sativa,  $\Delta^9$ -tetrahydrocannabinol ( $\Delta^9$ -THC), was identified in 1987. Howlett's group showed that the neurobehavioral effects of  $\Delta^9$ -THC were mediated through a G-protein (Gi/o) coupled receptor (GPCR). Shortly thereafter, Pfizer developed the synthetic cannabinoid, CP 55,940. Later, CP 55,940 and  $\Delta^9$ -THC helped identify a cannabinoid (CB) receptor [1]. The first identified cannabinoid receptor, termed cannabinoid receptor 1 (CB1), is the most abundant GPCR located within the central nervous system (CNS) [1–3]. More specifically, it is found at high levels in the hippocampus, pre-frontal cortex, dorsal root ganglion, cerebellum, and substantia nigra. Although CB1 is most abundant in the CNS, it is found to a lesser extent in the cardiovascular, [4,

5] pulmonary, intestinal, and reproductive tissues [6]. Three years after CB1 was cloned, a second cannabinoid receptor, termed CB2, was identified. While both CB1 and CB2 are GPCRs ( $G_{i/o}$ ) activated by phytocannabinoids, their tissue distribution and resulting physiological effects differ. For example, CB2 is primarily expressed in the spleen and immune cells with the highest levels occurring in B lymphocytes, macrophages, and natural killer cells [6–8]. Furthermore, during times of injury or stress, the resident immune cells, microglial cells, express CB2 thereby suggesting a role in abating neuroinflammation. These results prompted the design of CB2 agonists to modulate neuroinflammation [9].

The discovery of CB1 and CB2 prompted the researchers to identify the endogenous ligands of these receptors. The first endocannabinoid identified was arachidonoyl ethanolamide (AEA), which was extracted from pig brain and could readily displace the potent cannabinoid receptor ligand, [<sup>3</sup>H]-HU243 ( $K_i = 52$  nM). AEA was identified to be an agonist at the CB1 receptor and was later named anandamide. The name anandamide was derived from 'ananda,' the Sanskrit word for 'bliss' due to the compound's ability of modulate neurobehavioral activity [10]. Accordingly, AEA and all future ligands for CB1 and CB2 were collectively termed the endocannabinoids (eCBs) since they are endogenously produced molecules that bind and activate cannabinoid receptors. The second eCB, 2-arachidonoyl glycerol (2-AG), was discovered just shortly after AEA. It was shown to activate the CB2 with greater potency than at the CB1 [11]. Since the discovery of AEA and 2-AG, several other eCBs have been discovered, including, but are not limited to, 2-arachidonoylglycerylether N-arachidonoyl dopamine (noladin ether), (NADA), N-oleoylethanolamide (OEA), 2-docosahexaenoyl glycerol, (2-DHG), virodhamine (O-AEA), eicosapentaenoic acid ethanolamide (EPEA) and docosahexaenoyl ethanolamide (DHEA) [10, 12–15]. Several other eCB congeners have been identified that may not directly bind cannabinoid receptors but can bind to other receptors such as TRPPV1, GRP119, GPR55, and GPR18. In addition, many of these receptors interact with phytocannabinoids [5, 16, 17].

Cellular eCB levels are carefully regulated through multiple biosynthetic and degradative enzymes. For instance, the eCBs originate from dietary  $\omega$ -3 and  $\omega$ -6 polyunsaturated fatty acids (PUFAs). PUFAs are class of lipids that contain two or more cis carbon-carbon double bonds (points of unsaturation) and are identified as  $\omega$ -3 or  $\omega$ -6 based on the location of the first carboncarbon double bond from the terminal methyl group.  $\omega$ -6 eCBs derived from arachidonic acid (AA), such as AEA and 2-AG, are the most well studied eCBs. With the recent interest in the dietary effects of  $\omega$ -3 PUFAs, there has been an increased interest in  $\omega$ -3 eCBs. The  $\omega$ -3 eCBs are derived from the  $\omega$ -3 PUFA docosahexaenoic acid (DHA), eicosapentanoic acid (EPA, timnodonic acid), or  $\alpha$ -linoleic acid (ALA).

Following their uptake, PUFAs are mobilized via transport proteins to tissues where they esterified and are temporarily stored in the cell membrane (Fig. 17.1). For example, AEA is stored as its membrane precursor N-arachidonoyl phosphatidylethanolamine (NAPE) [18] and is released from the membrane by phospholipase D. This catabolic process yields a free eCB [19]. After biosynthesis, the eCBs are tightly regulated by degradative enzymes through hydrolytic inactivation [20]. For example, fatty acid amide hydrolase (FAAH) catalyzes the hydrolytic cleavage of AEA to form AA and ethanolamine [21]. FAAH is the principal AEA and DHEAhydrolyzing enzyme distributed throughout the nervous system [22] On the other hand, monoacylglycerol lipase (MAGL) is the degradative



Fig. 17.1 Overview of the  $\omega$ -3 Endocannabinoid Epoxide Biosynthetic Pathway. Dietary consumption of  $\omega$ -3 polyunsaturated fatty acids results in the storage of DHA and EPA esters within the plasma membrane. Upon cleavage by a phospholipase, DHA and EPA are cleaved from their membrane precursor and undergo biosynthesis

to the eCBs DHEA and EPEA, respectively. The metabolism of DHEA and EPEA by cytochrome P450 epoxygenases produces six (DHEA) or five (EPEA) constitutional isomers at each carbon-carbon double bond. DHEA epoxide metabolites are termed EDP-EAs while the EPEA epoxide metabolites are termed EEQ-EAs

enzymes for 2-AG and 2-DHG [20, 23]. Overall, these enzymes convert the eCBs back into their free fatty acid form, which can be esterified and stored in the phospholipid membrane bilayer or used for cellular functions [24].

Based on the widespread tissue distribution of the cannabinoid receptors there is a plethora of biochemical processes that utilize cannabinoid signaling [25–27]. The main role of CB1 is to mediate neurobehavioral activities, such as appetite regulation and executive functions, while the prominent function of CB2 is to mediate an antiinflammatory immune response. More specifically, CB2 is involved in neuroinflammation through its immunoregulatory activity in murine brain microglia [5, 28]. Overall, these activities suggest that CB1 and CB2 are neuroprotective [29–32]. prevalence Given the of neuroinflammatory-based diseases such as Alzheimer's disease (AD), multiple sclerosis (MS), and Parkinson's disease (PD), selective agonists for CB2 activation or modulation of eCB levels have promising therapeutic potential for the control of neuroinflammation [29, 33–37]. Additionally, accumulating evidence suggests that eCBs target alternative receptors such as the nuclear peroxisome proliferator-activated receptors (PPAR) and the heat sensing receptor transient vanilloid type-1 (TRPV1), [38-40] prompting studies regarding their role in nociceptive pain.

While the eCBs directly bind to CB1 and CB2 receptors, they also serve as substrates for the eicosanoid synthesizing enzymes. Cyclooxygenases, lipoxygenases, and epoxygenases oxidize fatty acids to bioactive metabolites that have novel physiological and cannabinoid receptor activities that are unique compared to their parent molecule [5, 41]. Previously, the Serhan group reported the metabolism of DHEA by the lipoxygenase pathway. DHEA is metabolized to 10,12-diHDHA-EA and 15-HEDPEA, which reduce leukocyte infiltration (chemotaxis) during inflammation. They can activate the CB2 receptor with EC<sub>50</sub> values at 3.9 nM and 1 nM, respectively [42]. In this chapter, we will discuss the monooxygenation of eCBs by epoxygenases to produce eCB epoxide metabolites with novel anti-inflammatory and potential anti-pain properties as well as vasoactive activities.

## 17.1.2 Endocannabinoid Metabolism by Cytochrome P450 (CYP) Epoxygenases

In humans, there are 57 CYPs which are involved in xenobiotic metabolism, steroid synthesis, and fatty acid metabolism [43]. These enzymes are distributed throughout the human body, with the highest levels reported in the liver. In 2008, the Hollenberg group was the first to demonstrate the metabolism of AEA by CYPs [44]. This represented a novel metabolic pathway for AEA that led to the formation of the emerging class of  $\omega$ -6 derived eCB epoxides. Importantly, it was demonstrated that the AEA epoxide, 5,6-EET-EA, had 300-fold selectivity for the CB2 compared to CB1 and 1000fold greater affinity for CB2 compared to AEA, indicating unique biological activity of the epoxides compared to their parent molecule [44]. To identify CYPs involved in the conversion of both AEA and 2-AG, the Hollenberg lab utilized LC-MS/MS to determine that CYP isoforms, CYP3A4, CYP4F2, and CYP2D6, metabolize AEA in human liver and kidney microsomes as well as in brain microsomal and mitochondrial preparations [45]. Furthermore, the Das group discovered the role of cardiac CYP, CYP2J2, in the metabolism of 2-AG and AEA. This finding inspired future studies on CYP2J2-mediated  $\omega$ -3 and  $\omega$ -6 eCB metabolism [12, 13, 46]. CYP2J2 converts PUFAs to bioactive fatty acid epoxides which display anti-inflammatory activities and enhance wound repair [47–49]. CYP epoxygenases mediate the metabolism of eCBs to eCB epoxides [13, 50, 51]. More recent studies have shown that CYP2J2 and other CYPs metabolize  $\omega$ -3 eCBs such as DHEA and EPEA to more potent anti-inflammatory epoxide metabolites, as illustrated in Figs. 17.1 and 17.2. This metabolic pathway consists of CYP epoxygenases, which belong to the cysteinato-hemoprotein



**Fig. 17.2** Endocannabinoid Signaling Regulates Inflammation and Arterial Tone. Inflammatory stimuli such as LPS up-regulates cytochrome P450 expression which metabolize eCBs DHEA and EPEA to epoxide metabolites (19,20-EDP-EA and 17,18-EEQ-EA, respec-

superfamily and diflavin enzyme, CYP reductase (CPR), which shuttles electrons from NADPH to the CYP [52].

#### 17.2 Endocannabinoid Epoxides

#### 17.2.1 ω-3 Endocannabinoid DHA Ethanolamide (DHEA)

Encouraged by studies that identified AEA-like fatty acid ethanolamides across several tissues, the Di Marzo group sought to identify their  $\omega$ -3 eCB counterparts. This group demonstrated that  $\omega$ -3 eCB, DHEA is located in bovine retina. Furthermore, DHEA was found at twofold higher levels compared to AEA in the brain (3.77 ± 0.66 ng/g and 1.88 ± 0.46 ng/g, respectively) [15, 53]. Additionally, DHEA has been detected under peripheral inflammation in rat contralateral spinal tissue [54]. More recently, a targeted lipidomics method using liquid chromatography tandem mass spectrometry (LC-

tively). These metabolites are more potent at CB2 than their eCB parent molecule and display CB2 selectivity. 19,20-EDP-EA and 17,18-EEQ-EA diminish proinflammatory NO and IL-6 while they elevate antiinflammatory marker IL-10. In addition, DHEA, EPEA as well as their epoxide metabolites are vasoactive

MS/MS) detected DHEA in rat brain  $(128.9 \pm 27.9 \text{ pmol/g})$ , heart  $(57.7 \pm 24.4 \text{ pmol/g})$ , kidney (49.6 ± 22.2 pmol/g), spleen  $(22.9 \pm 1.3 \text{ pmol/g})$ , liver  $(195.1 \pm 48.7 \text{ pmol/g})$ , pig brain (265.5  $\pm$  100 pmol/g), and human plasma (13.3  $\pm$  0.4 pmol/mL). Interestingly, dietary supplementation with DHA increased the levels of DHEA at the expense of AEA, thereby providing a method for elevating the levels of  $\omega$ -3 eCBs in vivo [13, 15]. Although an exact biosynthetic pathway for DHEA has yet to be determined, it is believed that DHEA is produced in a similar manner to AEA. It has been suggested that membrane а precursor, N-docosahexaenoyl phosphatidylethanolamine (NDHPE) is hydrolyzed by phospholipase D2 to produce free DHEA, however, more studies are required to confirm this hypothesis [55]. Since DHEA is structurally similar to AEA and showed a high potential for physiological relevance, there was significant interest in investigating its physiological activities in vitro and in vivo. Additionally, DHEA displays immunemodulatory activity in RAW264.7 cells. DHEA dose-dependently reduced monocyte chemoat-tractant protein 1 (MCP-1) mRNA, prostaglandin and thromboxane  $B_2$  levels produced by COX-2 [56].

## 17.2.2 @-3 Endocannabinoid DHEA Epoxides (Epoxydocosapentaenoic Acid-Ethanolamide, EDP-EA)

Recently, the Das group showed that DHEA is a substrate for enzymes in the CYP epoxygenase pathway. They designed a targeted lipidomics LC-MS/MS method in the multiple reaction monitoring mode (MRM) to simultaneously detect and quantify five DHEA epoxide (EDP-EA) regioisomers in rat brain, heart, kidney, spleen, liver tissues as well as in mouse microglial cells. These isomers share the same molecular weight but differ in the order in which their atoms are connected. Due to the reported upregulation of CYP epoxygenases in LPSstimulated microglia, the Das lab sought to investigate these molecules under inflammatory conditions [44, 57]. By monitoring the production of EDP-EAs in LPS-stimulated microglia treated with DHEA, they confirmed that EDP-EAs are produced by CYPs as inhibitors of CYPs reduce their levels. It was further demonstrated that the CYP isozyme, CYP2J2, is responsible for this action. Current research is going on to identify other brain CYPs that are involved in eCB metabolism. Interestingly, the production terminal of the epoxide, 19,20-EDP-EA is favored over the other regioia reconstituted CYP2J2-CYP somers in Reductase (CPR) Nanodisc system and by brain microsomes [13]. More research is needed to further understand why certain regioisomers are preferred by CYPs.

As previous studies consistently showed DHEA as a weak ligand at both CB1 and CB2, the Das lab tested to see if DHEA and its epoxide metabolites activated or bound to CB receptors [56]. Using the PRESTO-Tango assay, they

showed that epoxygenation of DHEA by CYP epoxygenases led to an altered CB1 and CB2 activity profile compared to the DHEA parent molecule. For example, 19,20-EDP-EA was observed to be more potent at CB2 compared to DHEA and had a ten-fold lower activity at CB1 (EC<sub>50</sub> at CB1: 108 nM and CB2: 280 nM) (Fig. 17.2) [13]. As 19,20-EDP-EA, was observed to display an altered cannabinoid receptor profile compared to DHEA, it would be interesting to characterize the other five DHEA epoxide regioisomers produced by the cross-talk of CYP metabolism pathways. From similar studies on other regioisomers, it is expected that DHEA epoxide regioisomers and enantiomers will display different activities at the CB1 and CB2 receptors.

## 17.2.3 Anti-Inflammatory Activity of DHA Ethanolamide Epoxides (EDP-EAs)

Multiple studies indicate that eCBs combat microglial-promoted neuroinflammation via CB2 activation [58]. In fact, there is a current drive towards the development of CB2-selective agonists to combat the inflammatory pathology associated with progression of neurodegenerative disease. As the DHEA epoxides (EDP-EAs) are naturally produced by microglia and the microglia express CYPs, the Das group examined the antiinflammatory effects of these molecules in an in vitro model of neuroinflammation. As mentioned briefly above, microglial cells are the innate immune cells of the brain, which continuously survey the brain parenchyma for harmful stimuli. When harmful stimuli are encountered, microglia exhibit a pro-inflammatory phenotype to promote defense. As microglia clear the harmful stimuli, a phenotype change occurs that promotes an inflammation-resolution phase. This phenotype switching mechanism is classically known as macrophage polarization. Out of the EDP-EAs tested, 19,20-EDP-EA showed the most potent dose-dependent reduction of pro-inflammatory markers. (Fig. 17.2). Correspondingly, it decreased pro-inflammatory cytokine IL-6 and increased the production of IL-10 [13]. Additionally, the antiinflammatory effects of 19,20-EDP-EA were confirmed using freshly isolated primary piglet microglial cells stimulated with LPS, which suppressed IL-6 production, and thus corroborated the findings in immortalized BV-2 cells. Based on these findings, it is possible that the DHA-derived eCB epoxides mediate anti-inflammatory activities in addition to other pathways. Taken together, this indicates that the EDP-EAs and their stable derivatives may be utilized for treating neuroinflammatory conditions.

# 17.2.4 Vasoactivity of DHA Ethanolamide Epoxide (EDP-EA)

It is well known that CYP epoxygenases convert  $\omega$ -3 PUFAs to PUFA epoxides. For example, DHA is converted to DHA epoxides (EDPs). These molecules are vasoactive in nature, and are more effective at relaxing pre-constricted vessels compared to CYP-derived AA epoxides (EETs) [59]. The Das lab demonstrated that CYP epoxygenase-mediated metabolism of DHEA produced vasodilatory eCB epoxides, a 19,20-EDP-EA. Compared to 19,20-EDP, as shown in Fig. 17.1, EDP-EA had a two-fold higher EC<sub>50</sub> at relaxing bovine coronary arteries (Fig. 17.2) [13]. Although CYP-derived DHEA epoxides are vasoactive molecules, they do so with reduced potency relative to their parent molecule. Furthermore, 19,20-EDP-EA exerts antiangiogenic effects in HMVEC cells. Angiogenesis plays several roles in pathological and nonpathological states. As eCBs are regarded as anticancer molecules through their anti-angiogenic effects, the Das lab tested the ability of 19,20-EDP-EA to inhibit angiogenesis in HMVEC cells. 1 µM and 3 µM 19,20-EDP-EA decreased tubulogensis by 31 and 75%, respectively. Previous to this study, the anti-angiogenic actions of the EDP metabolites were attributed to their inhibition of VEGF-stimulated cell migration via an unknown epoxyeicosanoic metabolic pathway [13].

## 17.2.5 ω-3 Endocannabinoid EPA Ethanolamide (EPEA)

The report that several fatty acid ethanolamides other than AEA have unique activities at the cannabinoid receptors sparked a study in 1996 by the Martin and Razdan groups, which sought to examine the structure-activity relationships of AEA analogs at CB1 [60, 61]. Previous to this study, AEA was the only endogenously produced fatty acid ethanolamide to bind and activate the cannabinoid receptors. By understanding the structural requirements necessary for ligands to bind CB1 it would be possible to develop more potent ligands for both biological and therapeutic applications. Cannabinoid structure-activity relationships (SAR) indicated that a phenolic hydroxyl, a lipophilic side chain, and an appropriately oriented carbocyclic ring system are required for cannabinoid receptor activity. One of the AEA analogs tested in their study was EPA ethanolamide (EPEA). Based on molecular dynamic simulations, EPEA was suggested to possess some affinity for CB1 [61].

Alongside these studies, the Di Marzo group determined the in vivo localization of EPEA in mouse brains. EPEA was detected at  $0.18 \pm 0.09$  pmol/mg of brain lipid extract, which was the lowest level of all of the fatty acid ethanolamides detected in their study. EPEA was found at five-fold lower levels than DHEA [53]. Compared to EPEA, its parent molecule EPA was found at  $443 \pm 167$  ng/g mice brain. However, dietary supplementation with EPA increased the endogenous levels of EPEA, thereby providing a dietary delivery method for elevating  $\omega$  -3 eCBs [15]. Furthermore, when mice were fed a high  $\omega$  -3 diet consisting of DHA and EPA phospholipids, the levels of EPEA increased in adipose tissue, corroborating the link between diet and the eCB system. More recently, a targeted lipidomics method using LC-MS/MS detected EPEA in rat brain  $(6.2 \pm 1.6 \text{ pmol/g})$ , heart  $(9.4 \pm 6 \text{ pmol/g})$ , kidney  $(37.1 \pm 21 \text{ pmol/g})$ , spleen  $(9.2 \pm 4.1 \text{ pmol/g})$ , liver (80.8  $\pm$  20.1 pmol/g), and pig brain  $(2.2 \pm 0.4 \text{ pmol/g})$  [13]. Interestingly, EPEA is found at a significantly lower level than DHEA in rat brain (DHEA: 128.9  $\pm$  27.9 pmol/g). Together, these findings support that supplementation with  $\omega$  -3 fatty acids can modulate eCB levels and may increase the bioavailability of DHA and EPA for physiological function.

Although the biosynthesis of EPEA has not been proved, the well-studied transacylation-PDE pathway suggests that *n*-acyl ethanolamides are biosynthesized from glycerophospholipids via *N*-acylphosphatidyl ethanolamine (NAPE). Through this pathway, a  $Ca^{2+}$ -dependent *N*-acyltransferase and NAPEhydrolyzing PLD render the fatty acid ethanolamide free from its membrane precursor [56]. This pathway is similar to the biosynthesis of AEA and may support the idea of a conserved biosynthesis for fatty acid ethanolamides.

## 17.2.6 ω-3 Endocannabinoid Epoxide Epoxyeicosatetraenoic Acid-Ethanolamide (EEQ-EA)

In 2017, the Das lab showed that EPEA, like DHEA, is a substrate for the CYP epoxygenase pathway. Using a targeted lipidomics LC-MS/MS approach they detected and quantified all five EPEA epoxide (EEQ-EA) regioisomers in rat brain, heart, kidney, spleen, liver tissues as well as in mouse microglial cells. They found that LPS-stimulated and **EPEA-treated** mouse microglia could convert EPEA to the EEQ-EAs via CYP epoxygenases. They further determined that one of the CYP isozymes responsible for this action is CYP2J2. Using recombinantly expressed proteins, CYP2J2-CPR Nanodiscs showed a favored production of 17,18-EEQ-EA, as shown in Fig. 17.1, compared to other regioisomers [13].

To further characterize EPEA and its epoxide metabolites, we were interested in testing whether the EEQ-EAs were eCBs. Previous studies consistently showed EPEA as a weak agonist for CB1 and CB2 [56]. Through the PRESTO-Tango assay, the Das lab showed that epoxidation of EPEA by CYPs led to an altered CB1 and CB2 activity compared to their parent molecule EPEA. For example, 17,18-EEQ-EA had a lower EC<sub>50</sub> at CB2 than EPEA (EC<sub>50</sub> 17,18-EEQ-EA: 1.4 nM and EC<sub>50</sub> EPEA: 2.1 nM). However, compared to EPEA (EC<sub>50</sub> CB1: 0.1 nM), 17,18-EEQ-EA had a lower potency at CB1 (EC<sub>50</sub> CB1: 18.5 nM), thus showing a CB2-selectivity for 17,18-EEQ-EA [13] (Fig. 17.2). As mentioned above, discovering novel CB2-selective molecules may aid in the development of anti-inflammatory therapeutics that overcome any potential psychoactive activities that may be mediated through CB1 activation.

## 17.2.7 Anti-inflammatory Activity of EPA Ethanolamide Epoxides (EEQ-EAs)

Since EPA and EPEA have been shown to possess anti-inflammatory activities, the antiinflammatory activities of EEQ-EAs were studied in brain microglia. When BV-2 microglia were stimulated with LPS, the levels of EPEA and total EEQ-EA were elevated. Interestingly, EPEA levels significantly surpassed DHEA levels after 12 h of LPS stimulation (DHEA: 6.7 ± 4.6 pmol/10<sup>6</sup> cells and EPEA:  $2042 \pm 939.2 \text{ pmol}/10^6 \text{ cells}$ ). Furthermore, in LPS-stimulated BV-2 cells, 17,18-EEQ-EA (10 µM) dose-dependently reduced NO in a CB2dependent manner, which was attenuated with CB2 antagonist, AM-630, treatment. In addition, 17,18-EEQ-EA dose-dependently decreased IL-6 and increased IL-10 (Fig. 17.2). Interestingly, 17,18-EEQ-EA was a more potent inhibitor of NO production than EPA epoxide (17,18-EEQ). This evidence shows that the CYP epoxygenase pathway may play be responsible for the antiinflammatory nature of EPA through conversion of EPEA to its epoxide metabolite. Lastly, similar to 19,20-EDP-EA, the effects of 17,18-EEQ-EA were confirmed in freshly isolated piglet microglia cells, thereby corroborating the antiinflammatory effects of 17,28-EEQ-EA in primary cells.

# 17.2.8 Vasoactivity of EPA Ethanolamide Epoxide (EEQ-EA)

Since it is known that CYP epoxygenases metabolizes EPA to vasoactive epoxide metabolites, the Das lab tested the vasodilatory activity of eCB EPEA and eCB epoxide 17,18-EEQ-EA in isolated bovine coronary arteries [59, 62]. Utilizing isometric tension measurements to monitor the ability of these molecules to relax preconstricted arteries, they determined that 17,18-EEQ-EA, like 19,20-EDP-EA, dosedependently relaxed constricted bovine coronary arteries (Fig. 17.2). On the other hand, the ED<sub>50</sub> values determined from 17,18-EEQ-EA was two-fold greater than the ED<sub>50</sub> value of 17,18-EEQ (ED<sub>50</sub> of 17,18-EEQ: 0.47 ± 0.01  $\mu$ M and  $ED_{50}$  of 17,18-EEQ-EA:  $1.1 \pm 0.6 \mu$ M), thus showing that eCB epoxides are vasoactive but not as potent as their PUFA epoxides. It has been previously been shown that EPA epoxides act as endothelial-derived hyperpolarizing factors that inhibit platelet aggregation. To followup with these observations, the Das lab revealed that 17,18-EEQ-EA dose-dependently inhibits platelet aggregation and angiogenesis [13]. Overall these endocannabinoid epoxides are vasoactive.

### 17.3 Anti-tumorigenic Properties of the ω-3 Endocannabinoid Epoxides

A particular consequence of unresolved inflammation is the progression towards tumor formation. The microenvironment of a tumor is highly inflammatory and contains a carcinogenic milieu that promotes tumor progression via proinflammatory cytokines, growth factors, and several adhesion molecules [63]. Several studies have reported the anti-inflammatory, proresolving, and anti-tumorigenic activity of  $\omega$ -3 fatty acids, DHA and EPA [64, 65]. Upon conversion to their epoxides, the EEQs and EDPs have

been shown to be anti-proliferative, antitumorigenic, and can inhibit metastasis [66, 67]. The Das lab recently revealed that DHEA and EPEA epoxides display anti-cancer activities. EDP-EAs are not only abundant in osteosarcomaderived lung tumors (20-80% increased levels compared to healthy lungs) but they also possess anti-inflammatory and anti-tumorigenic properties in an *in vitro* model of osteosarcoma [68]. More specifically, Roy et al. examined the ability EDP-EA regioisomers 7,8-EDP-EA, of 10,11-EDP-EA, and 13,14-EDP-EA to inhibit migration of cancer cells and induce apoptosis. Additionally, in 143B human osteosarcoma cells, 10,11-EDP-EA showed the highest ability to induce apoptosis in a CB1-dependent manner (EC<sub>50</sub> at CB1: 0.43 nM). A time-dependent scratch assay revealed that 10,11-EDP-EA has anti-migratory potential, an indicator of metastasis. In order to increase the stability of 10,11-EDP-EA, derivatives were synthesized to prevent degradation by FAAH. Based on a previous characterization of CB1-binding and metabolic stability of AEA's functional groups, a R-1'-methyl isomer (10,11-EDP-IA), a cyclopropyl derivative (10,11-EDP-CA), and a *n*-propyl derivative (10,11-EDP-NA) was prepared. Through LC-MS/MS quantification of metabolites, the rate of hydrolysis of 10,11-EDP-EA to 10,11-EDP was decreased by nearly 100-fold with the derivatives 10,11-EDP-NA, 10,11-EDP-IA, and 10,11-EDP-CA. Furthermore, these stable derivatives were successful at inhibiting migration in osteosarcoma cells and reduce angiogenesis. Taken together, this novel class of eCB epoxides have shown potential to reduce tumor progression through activation of the CB1 receptor. In addition, this was one of the first studies to demonstrate the potential utility of cannabinoid-like molecules in the treatment of bone cancer. Furthermore, these studies provide the grounds for future work to determine the CB1-dependent anti-pain behavior of these molecules, which would be highly beneficial for the development of multi-modal bone cancer therapies.

# 17.4 Conclusions and Future Perspectives

The inflammatory response leads to release of lipid mediators that help in regulating the inflammation. There is a strong interest in identifying anti-inflammatory lipid mediators that can resolve the ongoing inflammation. In this chapter, we review a novel class of anti-inflammatory lipid mediators that emanate from the cross-talk of the two important biochemical pathways: the CYP-epoxygenase pathway and the endocannabinoid biosynthetic pathway. The  $\omega$ -3 eCBs, DHEA and EPEA are metabolized by CYP epoxygenases to form the epoxides, EDP-EA and EEQ-EAs. These eCB epoxides are multifunctional molecules as they can target multiple receptors including the cannabinoid receptors and unknown epoxide receptor. Their effects on inflammation resolution, cancer and vasodilation have briefly been explored through multiple studies and show promise for the development of therapeutics for cerebrovascular and neuroinflammatory diseases.

Although evidence points to CB1 and CB2 receptors as the primary modulator of the antiinflammatory and vasodilatory effects of the omega-3 eCB epoxides, the studies also indicate that the eCB epoxides are anti-inflammatory and vasoactive through an unknown receptor. In order to target hypertension and other vascular conditions through the eCB system, identification of this receptor and competing metabolic enzymes would be highly beneficial. Hence, it is important to establish the receptor systems through which molecules elicit their physiological these response. Additionally, it is critical to map all the primary synthetic and degradative pathways of these eCB epoxides. While it was shown that these eCB epoxides are substrates for two degradative pathways mediated by sEH and FAAH, it is possible that they are synthesized and stored in membrane and released by phospholipases. Current therapeutics, such as FAAH and sEH inhibitors, increase the endogenous levels of PUFA epoxides and eCBs, and have since shown promise for the treatment of inflammatory-based

disease, hypertension, and nociceptive pain [21, 69, 70]. It needs to be evaluated if FAAH and sEH inhibitors increase the levels of these dual functional endocannabinoid epoxides.

Although it was shown that the  $\omega$ -3 eCBs, DHEA and EPEA are metabolized by CYP epoxygenases to form the epoxides, the identity of the specific CYP enzyme is unclear. It has been shown that the  $\omega$ -6 eCB 2-AG, AEA and  $\omega$ -3 eCBs DHEA and EPEA are metabolized by CYP2J2 to produce epoxide metabolites [50, 71]. Several papers from Hollenberg laboratory have identified other CYPs such as CYP3A4 and CYP2D6 are involved in metabolizing eCBs [51]. However, there needs to be a systematic approach to delineate which CYPs are involved in the endocannabinoid metabolism in the body.

The EDP-EA and EEQ-EA metabolites were successfully detected in several tissues. Detection of lipid metabolites is often challenging as these lipid metabolites are unstable and the levels at which they are detected in blood and tissues are lower than their endogenous levels at the site of formation and site of action. The levels of EDP-EA and EEQ-EA in the tissues are within the pmol/g tissue range, however, their local concentration is likely to be greater than plasma levels. This is because they are locally produced and act in a localized manner on the receptors unlike most hormones and neuropeptides. For instance, it is hypothesized that eCBs are synthesized ondemand from their esterified membrane precursors in response to a variety of chemical and neuronal stimuli and are rapidly degraded by FAAH and sEH. Local measurement of lipid metabolite is technically challenging. As a result, the levels of these molecules extracted from tissues does not mirror the local concentrations in the intracellular and synaptic environment. In addition, it is important to note that many of these lipids are esterified in the membrane yet the levels that are reported within the literature reflect the abundance of free lipids often in healthy tissues. Future studies are needed to discern eCB and eCB epoxide levels in disease states as the expression of the enzymes such as CYP epoxygenases change during inflammation. Another cause for the differences in the levels of the lipid metabolites is the extraction efficiency. While large-scale lipidomics studies can identify a variety of lipid types, the solvent extraction method can create a bias against certain molecules based on their chemical structure and solubility. Although optimization of an efficient solvent system is imperative, detection limits and low extraction yields can occur when working on the pmol/g tissue scale.

In summary, the discovery of the eCB epoxides is the initial step in evaluating the role of CYP epoxygenase mediated metabolism of endocannabinoids to generate multi-functional lipid metabolites. There are other endocannabinoids such as noladin ether and endocannabinoid-like molecules such as N-arachidonoyl dopamine (NADA) and *N*-arachidonoyl serotonin (AA-5-HT) that closely interact with FAAH and CB1 [72–74]. Future investigations on the production of novel CYP-mediated bioactive eCB metabolites are imperative for a complete understanding of the CYP epoxygenase pathway. As these endocannabinoid epoxides are dual functional molecules exhibiting the classical epoxyeicosanoid and endocannabinoid activities, their bifunctional nature imparts the ability to simultaneously target multiple signaling pathways. This ability to target different pathways makes them more potent than other lipid metabolites. Hence, the discovery of these novel lipid metabolites also prompts the discovery of new scaffolds that can serve as templates for multi-target drugs. These therapies may be useful for the treatment of inflammatory pain and other conditions in which eCBs receptors are targeted.

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18

# **Overview of Lipid Biomarkers** in Amyotrophic Lateral Sclerosis (ALS)

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#### Abstract

Amyotrophic lateral sclerosis (ALS) is a multifactorial neurodegenerative disease involving motor neuron (MN) degeneration in the spinal cord, brain stem and primary motor cortex. The existence of inflammatory processes around MN and axonal degeneration in ALS has been shown. Unfortunately, none of the successful therapies in ALS animal models has improved clinical outcomes in patients with ALS. Therefore, the detection of blood biomarkers to be used as screening tools for disease onset and progression has been an expanding research area with few advances in the development of drugs for the treatment of ALS. In this review, we will address the available data analyzing regarding the relationship of lipid metabolism and lipid derived- products with ALS. We will address the advances on the studies about the role that lipids plays at the onset, progression and lifespan extension of ALS patients.

#### Keywords

ALS · Lipid biomarkers · Mass spectrometry · Cell signaling

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#### 18.1 Introduction

Amyotrophic lateral sclerosis (ALS) is a neurodegenerative disease without treatment and a short life expectancy upon clinical symptoms appear [1]. This underscores the necessity for an expansion of the current knowledge and underlying biological mechanisms driving disease. Recent research shows the presence of inflammatory processes around motor neurons (MN) and axonal degeneration, being evident through the accumulation of reactive astrocytes and activated microglia [2]. Many treatments have been tested on different ALS animal models. Unfortunately, no successful therapy with promising results in animal models has improved clinical outcomes in patients with ALS [3]. This is partly due to the lack of specific blood biomarkers, which can act as screening tools to identify individuals at risk of developing the disease, as well as the lack of clinical studies. The development of novel medical treatments has lead to an increase in life expectancy, especially in the western world. However, the former is accompanied by an increment on the appearance of cognitive dysfunctions related to aging in addition to the development of these neurodegenerative diseases. Overall, changes represent a significant challenge from the scientific and medical point of view. The current review aims to analyze the recent data

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obtained about lipid help in the development of drugs for the treatment of ALS.

#### 18.2 Amyotrophic Lateral Sclerosis

Amyotrophic lateral sclerosis is a multifactorial neurodegenerative disease caused by genetic and non-inheritable components leading to MN degeneration in the spinal cord, brain stem and primary motor cortex [1]. It is well established that ALS affects both cortical as well as cranial and spinal MN with variable evolution. The majority of ALS cases are sporadic, however there exists a 10% of familial cases, some of which arise from mutations of the protein Superoxide Dismutase 1(SOD1) [1]. The average age of onset of the disease is 55 years, beginning later in women than men, and with 90% of the patients dying within 5 years after the appearance of the clinical symptoms. For a definitive diagnosis of ALS the progressive spread of symptoms involving upper and lower motor neurons is required, according to the revised El Escorial and the Awaji criteria [4, 5]. The most used clinical scores for disease progression is the ALS functional rating scale-revised (ALSFRS-R) [5]. This scale is employed to evaluate the pace of disease progression, predict survival and assess the effects of disease-modifying drugs in therapeutic trials. The scale is based on clinical symptoms so it is imperative to discover biomarkers that allow early diagnosis of the disease. In addition, biomarkers will aid for therapeutic drug design to improve the quality of life of those affected due to the lack of effective pharmacological treatments for ALS [5]. The pathogenesis of ALS consists of two stages: an early neuroprotective stage and a later neurotoxic stage. Multiple mechanisms have been described for MN death including glutamate toxicity, mitochondrial dysfunction, protein misfolding and apoptosis [6]. However, ALS appears as a composite syndrome where the aberrant cellular pathways may not be ascribed solely from a protein misfolding issue, but cellular physiology aspects like deficiencies in RNA

processing and compromised mitochondria homeostasis, increased oxidative stress, excitotoxicity, reduced neurotrophic support, and glial inflammatory responses [7]. Familiar ALS has been studied using active (SOD1<sup>G93A</sup>, SOD1<sup>G37R</sup>) mice mutants which have a phenotype characterized by progressive paralysis and death caused by the degeneration of MN, in addition to gliosis within the spinal cord, brain stem and cortex [6]. These features suggest a gain of toxic function of the mutant SOD might play a role in the neurodegenerative process. In addition, oxidative stress is an important contributor to neuronal death in ALS involving astrocytes [8]. Current research has shown that ALS is not a single cell type disease, since it involves microglia and astrocytes surrounding the MN. In fact, our laboratory reported astrocytes promote neuronal loss by mechanisms involving alterations in mitochondrial functionality, increased production of nitric oxide and nerve growth factor [2, 8–13]. Glial cells are the principle innate immune cell of the CNS and pathology associated with these cells is referred to as neuroinflammation, a hallmark of ALS [14, 15].

Importantly, there exists an increase of neurotoxic molecules such as pro-inflammatory cytokines, reactive oxygen species (ROS) and pro-inflammatory lipid-derived compounds. These molecules may cause further neuronal damage leading to further glial cell activation resulting in a positive feedback loop of neuroinflammation. Indeed, neuroinflammatory processes have been detected in ALS patients as well as in transgenic models of the disease [16]. Based on this background, many treatments aim to inhibit or reduce the pro-inflammatory action of microglia and astrocytes and counteract the progression of the disease. Unfortunately, none of the successful therapies in ALS animal models has improved clinical outcomes in patients with ALS [3]. This can be ascribed to different factors. For example, decreasing or deleting single proinflammatory factors such as TNF- $\alpha$ , IL1- $\beta$ , and inducible nitric oxide synthase has had little-to-no effect on overall survival of SOD1<sup>G93A</sup> mice [8, 12]. These suggest that a multiplicity of proinflammatory cytokines can compensate the absence of any single factor, and it is unlikely that continuing efforts to target a single factor in humans will provide significant therapeutic benefit in patients with ALS. Considering the importance of the disease and the fact that inflammatory processes are involved, the identification of blood biomarkers to identify individuals at risk of developing the disease or for their recruitment in clinical studies in order to analyze benefits in the development of drugs for the treatment of ALS would be of biological relevance. Below we will discuss the identification and use of lipid-derived products as biomarkers since research in the field and the optimization of lipidomic techniques are giving novel and important new data for using them as disease biomarkers.

## 18.3 Role of Lipids in Central Nervous System and ALS

Lipids are implicated in a wide variety of biological processes and can be classified into five categories: fatty acids, triacylglycerols (TAGs), phospholipids, sterol lipids and sphingolipids. The brain requires a near constant source of metabolites to maintain function, and contains the second highest concentration of lipids in the human body [17]. Although the consensus is that glucose metabolism almost completely satisfies the brain energy requirements, it has recently been shown that approximately 20% of the total energy requirement of the brain is met through the oxidation of fatty acids, and that this fatty acid oxidation may take place entirely in astrocytes [18]. Besides this fact, perhaps the most essential role for lipids in the brain is as components of the membrane cellular machinery. This is important in the brain since changes in membrane fluidity and many signaling processes occur in specific intracellular compartments. Importantly, fatty acids and their derivatives have been well characterized as drivers of intracellular signaling processes [19].

Two major polyunsaturated fatty acids (PUFAs) are present at high levels at the brain:

arachidonic acid (AA) and docosahexaenoic acid (DHA). Since these PUFA are the precursors of important cell signaling molecules. As examples, DHA and AAs can be oxidized to give rise to prostaglandins or leukotrienes. The oxidation of DHA produces neuroprotectinD1, a signaling molecule that promotes cell survival under stress. The latter is part of the denominated specialized pro-resolving lipid mediators (SPM) giving to these PUFA precursors an important role in neuroinflammation [20, 21]. The presence of these compounds has been implicated in neuronal signaling processes controlling neurogenesis, brain vesicular activity, central glucose homeostasis, mood and cognition [22]. Other example is Prostaglandin  $E_2$  (PGE<sub>2</sub>), synthetized by Prostaglandin Endoperoxide H Synthase-2 (PGHS-2) from AA, which promotes inflammation after binding to its receptor [23]. Their role as biomarkers or footprints of ALS will be discussed later.

In many neurodegenerative diseases, an accumulation of ceramides has been observed. The latter is considered toxic, since it has been shown to promote neuronal death by oxidative stress and apoptosis in both animal models and patients [24–28]. Moreover it has been proposed in SOD1<sup>G93A</sup> mice that sphingomyelin-associated ROS production leads to MN death through the p75 factor [12]; in addition, it is reported that an increase of sphingomyelin in the spinal cord of ALS patients mediates MN death via oxidative stress [24]. From a structural-functional point of view, it has been shown that membrane fluidity in the brain and spinal cord decreases significantly over the course of disease in ALS mice [29]. In fact, neuronal membranes rich in phosphatidylethanolamine and phosphatidylserine are significantly less fluid. Thus, the increase in DHA results in more rigid membranes with an important impact of signaling activities in ALS brains [30].

Along with neuronal degeneration, alterations of lipid metabolism have been reported in ALS. Different studies have shown that muscle denervation has a role in the promotion of abnormal lipid metabolism. In fact, Body Mass Index (BMI) at diagnosis remains the only metabolic independent prognostic factor for survival in ALS [31]. Studies to determine the role of lipid supplementation and serum lipid profile on ALS onset, progression or fate [4, 32–34] have been carried out, but with unfavorable outcomes. For example, supplementation with omega-3 fatty acids (e.g. eicosapentaenoic acid, EPA, before clinical symptoms appear, in SOD1<sup>G93A</sup> mice increased the progression of the disease and shortened life span of the transgenic animals [35]. In addition, markers of oxidative stress such as 4-hydroxynonenal were also observed [36]. High fat diets exert a modest decrease in disease progression in a mouse model of ALS [37, 38]. In contrast to other pathologies, such as cardiovascular diseases, dyslipidemia is a good prognostic factor for ALS. When looking to ALS transgenic mice, they are leaner, hypolipidemic and present a higher metabolic intake of fatty acids in muscle than control animals [34].

Dyslipidemia, reduced body mass and increased resting energy expenditure are often present in ALS patients [39, 40]. Importantly, ALS is characterized by important alterations in energy homeostasis [37]. Leptin levels in ALS patients appeared significantly decreased, suggesting lower fat reserves [41]. Reports from the literature show a high LDL/HDL cholesterol ratio or elevated content of total cholesterol and triglycerides in ALS patients that were associated with better prognosis or slower disease progression [33, 42].

In summary, neuronal lipid metabolism in ALS is dysregulated affecting energy use, structural integrity, and signaling processes. Oxidative stress is increased since neurons metabolize a greater proportion of lipid substrates. When looking at the structural level, altered lipid metabolism leads to cytoskeletal defects and neuromuscular junction denervation. Finally, altered lipid metabolism disrupts important biological signaling processes, altering neurotransmitter synthesis and release and impairing intracellular transport.

# 18.4 Lipidomic Analysis in ALS Animal Models and Patients

Metabolomics studies search for small molecules present in cells, tissues or biological samples, whereas the observation of modifications in the levels of these molecules, in addition to physiological modifications of signaling pathways may help to elucidate where these changes are occurring, (e.g. intracellularly). When these molecules are lipids, the studies are called Lipidomics [43]. The chance that a small molecule (e.g. fatty acid) can be used as a biomarker relies on the existing communication between the brain and the periphery. The former must be accompanied to the capacity of different metabolites to cross the blood-brain barrier (BBB) and therefore be detected in plasma. In addition to the noninvasive capacity to obtain blood samples from patients, promotes that the metabolites present in plasma are an ideal source of biomarkers as molecular traces of the disease. Besides, in neurodegenerative diseases the hemato-encephalic barrier can be compromised, increasing the possibilities that these metabolites can be detected in plasma [43].

Lipidomic studies have shown that different classes of lipids can be used as biomarkers of ALS onset and progression when compared to healthy volunteers or other neurodegenerative patients, as well as to follow preliminary studies with pharmacological compounds that have impact on signaling pathways involved in neuroinflammation. Below we will discuss these biomarkers in terms of the complexity of the lipids analyzed and the oxidative status of these products.

# 18.4.1 Saturated and Unsaturated Fatty Acids

Nutritional status in conditions such as obesity and cancer can be followed by looking the blood palmitoleate to palmitate (16:1/16:0) and stearate to oleate (18:0/18:1) ratios [4, 44, 45]. Recent studies have shown that levels of 16:1 and 18:1 fatty acids, as well as of the enzyme that introduces the instaurations at the carbon chain, stearoyl-CoA desaturase, are significantly increased in blood cells from ALS patients compared to healthy controls [4, 44, 45]. It is important to note that the ratio of different monounsaturated fatty acids was strongly increased in ALS patients. In particular, 16:1 and 18:1 levels increased significantly in blood cells, and higher oleate levels were also observed in serum [4]. Fatty acids levels in the blood correlated with ALSFRS-R, the 16:1/16:0 ratio in blood cells negatively correlated with ALSFRS-R decline over a six-month period [4]. Circulating free fatty acids were more abundant in ALS patients, suggesting increased lipid breakdown by adipocytes [46]. In fact, a decline of ALSFRS-R was also significantly associated with the levels of 16:1 itself. Survival rates were greater when associated to higher 16:1/16:0 ratios, with a prolonged life expectancy of almost 11 months in the population of patients with a high 16:1/16:0 ratio, as compared to patients with low 16:1/16:0 ratio. Higher levels of palmitoleate itself were also significantly associated with extended life span. In contrast to what was observed for the 16:1/16:0 ratio, no changes in survival were observed associated to the 18:1/18:0 ratio [4]. Moreover, BMI or circulating leptin content did not correlate with ALSFRS-R decline, nor prognosticated survival based on multivariate analysis. In fact, statistical analysis showed that blood cell 16:1/16:0 ratio was an independent prognostic factor for survival with age, BMI, site of onset and ALSFRS-R as variables [4]. The 16:1/16:0 index is an easy-tohandle parameter that predicts survival of ALS patients. The enzymatically and nonenzymatically oxidation of unsaturated fatty acids increase during oxidative stress and may reflect the presence of an inflammatory process. Lipid peroxidation susceptibility, assessed by the peroxidability index (PI) [47], was 16% lower in the blood cell fraction of ALS patients as compared to controls, independent of the omega-6/ omega-3 (AA/EPA) index which did not show significant modification [4].

#### 18.4.2 Complex Lipids

Complex lipids as triglycerides (TG), total cholesterol (TC), phospholipids (PL) were all analyzed as biomarkers of ALS onset, progression or drug effect on clinical symptoms [43]. The levels of TG and TC in ALS patients were comparable to those found in control subjects. A recent study analyzed the composition of lipids in cerebrospinal fluid (CSF) from ALS patients compared to controls [43]. In this study, the authors demon-PC(36:4), strated that phosphatidylcholine ceramide and glucosylceramide levels were higher in ALS patients than in control subjects. Bioinformatics and statistical analysis showed six different metabolites that can be followed as distinctive between ALS and control groups. These compound corresponded to the PC derivatives PC (36:2p), PC(36:4p), PC(40:6p), the sphingomyelin (SM) derivatives SM(d34:0), and SM(d39:1), and TG the (Triglyceride) (16:1/18:1/18:2) [43]. The PC and SM compounds levels were higher in ALS patients, in contrast to TG which was lower in ALS patients than in controls. It is worth noting the higher level of PC (36:4p and 36:4e) was the strongest discriminant factor identified by all the statistical approaches used [43]. However, and importantly, higher levels of SM(d43:2) were associated to a lesser decline of the ALSFRS-r score [43].

Similar studies were performed using transgenic ALS mice. In these experiments, the results were quite different from those of humans, highlighting the difficulties in transferring the data obtained in animals to humans. In this case the complex lipids, which were found to be discriminant between control and ALS mice, were PC (36:2), PC(36:4), PC(40:6). These three lipids were found in higher levels in the ALS groups than in controls [43].

We have previously discussed that accumulation of ceramides (Cer) are toxic for MN [16]. By contrast, increasing the formation and accumulation of Cer-derived agents may be protective by reducing ceramide synthesis thus limiting the direct toxic effect on MN [16]. The membrane lipids Glycosphingolipids (GSLs) are a heterogeneous lipid groups formed through the covalent linkage of a glycan moiety to Cer, especially abundant in the CNS with important bioactive metabolic roles, growth factor signaling and participation on neuroinflammation [48, 49]. All of these activities are thought to participate in ALS disease pathogenesis. When cervical spinal cord gray and white matter samples from ALS patients were analyzed, the major isoforms of Cer, e.g. GalCer, GlcCer, LacCer, GM3, GM1, GL3, and SPM were significantly elevated [16]. This increase was not due to changes on the enzymes activities that catalyze the formation of these products. These results were confirmed by using an inhibitor of the enzyme that produces GlcCer, which increased Cer levels and accelerated disease progression in SOD1<sup>G93A</sup> mice [16].

#### 18.4.3 Oxidized Lipids

Oxidized lipids can be used as blood biomarkers for diseases progression or drug treatments. Importantly, oxidized lipids involves enzymatic derived compounds with relevant biological and signaling actions. Arachidonic acid is the precursor of a wide variety of anti- or pro-inflammatory compounds when metabolized by the PGHS or Lipoxygenase (LOX) pathways. These compounds can be followed in small samples of blood and used as disease biomarkers [43, 50]. In fact, ALS mice as well as patients with sporadic ALS have increased levels of prostaglandin E<sub>2</sub>  $(PGE_2)$  [23]. This compound is formed by the action of PGE synthase-1 on PGH<sub>2</sub> synthesized by oxidation of AA by PGHS. Furthermore, the protein levels of microsomal PGE synthase-1 and PGHS-2, which catalyze PGE<sub>2</sub> biosynthesis, are significantly increased in the spinal cord of ALS mice [23]. In ALS patients,  $PGE_2$  levels are increased in the serum and the CSF [51]. The pharmacological inhibition of PGE<sub>2</sub> receptor or the silencing of the gene coding for PGHS-2 can lower neuroinflammation in SOD1G93A mice, preserve motor functions and extend survival [52, 53]. Since  $PGE_2$  can exert different biological actions depending of the tissue, its use as a blood or tissue disease biomarker needs further studies.

The involvement of AA metabolites in ALS was also supported by the increased mRNA and protein levels of 5-lipoxygenase (5-LOX) observed in SOD1<sup>G93A</sup> mice at 120 days of age. Of therapeutic interest, oral administration of the 5-LOX and tyrosine kinase inhibitors nordihydroguaiaretic acid, significantly extended lifespan and slowed motor dysfunction in this animal model [15]. We have recently reported changes on the levels of some of AA-derived compounds in SOD1<sup>G93A</sup> mice [50]. In addition, we have recently published changes in levels of LOXderived products in SOD1<sup>G93A</sup> mice at different stages of the disease. We observed, when the clinical symptoms appear, a significant increase of 12-hydroxyeicosatetraenoic acid (12-HETE) in both plasma and brain whereas no changes were observed in age-matched non-transgenic mice. Similarly, 15-hydroxyeicosatetraenoic acid (15-HETE) levels were also higher in SOD1<sup>G93A</sup> brains. Prostaglandin levels were also increased at day 90 in plasma from SOD1G93A compared to non-Tg being similar in both types of animals at later stages of the disease [50].

Unexpected results also were reported when analyzing oxidized lipids in ALS mice models. In a recent study, the neuroprotective effect of EPA was analyzed [35]. The treatment with EPA resulted in an enhancement of neuroinflammation, faster disease progression and hastened death for SOD1<sup>G93A</sup> mice [35]. The authors propose that the observed results are due to the greater susceptibility to be peroxidized and therefore toxic end products of EPA.

#### 18.5 Conclusions

ALS is a neurodegenerative disease, with a short life expectancy, for which efficient treatments are still missing. Since many factors affect the onset and progression of the disease, it is important to find biomarkers that may aid the design of drugs that specifically influence and mitigate the damage, prevent MN loss and neuromuscular denervation. The high presence at CNS, the capacity to cross the BBB and be found at plasma suggest that lipid products can be used as prognostics indicators of ALS. The analysis we did in this review suggests that the benefits of detecting these biomarkers may help in designing and performing clinical trials whose aim should be not only increase life expectancy but also quality of life.

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# Flavonoids Ability to Disrupt Inflammation Mediated by Lipid and Cholesterol Oxidation

19

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Keywords

Flavonoids · Cardiovascular disease · Inflammation · Lipid oxidation · Cholesterol oxidation · LDL · Macrophages · Oxysterols · Resveratrol · Dietary antioxidants · Oxidative stress

#### 19.1 Introduction

Flavonoids are plant secondary metabolites that act as protectants against harmful effects of UV-B radiation inasmuch as biotic stress, conferring at the same time pigmentation of fruits and leaves [67]. The term "flavonoid" refers to phenolics having a basic skeleton of diphenylpropane (C6-C3-C6), which consists of two aromatic rings linked through three carbons that usually form an oxygenated heterocycle [25, 52]. Flavonoids are broken down into several different sub-categories based on their chemical structure. The main subclasses commonly found in food

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I. G. Medina-Meza (⊠) Department of Biosystems and Agricultural Engineering, Michigan State University, East Lansing, MI, USA e-mail: ilce@msu.edu 3-ols, proanthocyanidins, and anthocyanins [44, 67]. Figure 19.1 depicts the major classification of flavonoids according to their chemical structure. Their occurrence in food matrices has been extensively reviewed [39, 44], and has been subject of extensive research in the last decades. Table 19.1 contains a few examples of compounds from each of the subcategory, with the fruit (berry) in which they are commonly found. The monomeric unit of flavonoids can dimerize and polymerize to form other important high molecular weight molecules; this is the case of proanthocyanidins, that are polymers of flavan-3ols or flavanols. Not only do these compounds act as plant protectants, but they can also be very beneficial to human health. Cohorts studies performed in the early '90 have shown that dietary consumption of flavonoids was inversely associated with morbidity and mortality from coronary heart disease [31, 32]. These findings have opened an intensive field of research on the effects of flavonoids and flavonoids-rich food extracts in cardiovascular diseases (CVD) progression, particularly in the modulating CVDassociated oxidative stress and inflammation. In this short review, we will summarize the current findings in flavonoids beneficial effects in preventing CVD through inhibition of initial stages of CVD progression. Given the magnitude of scientific literature in the field, we will focus on two

items are: flavonols, flavones, flavanones, flavan-

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Fig. 19.1 Main classification of phenolic compounds

strictly mechanistic aspects: inhibition of chemical-induced LDL oxidation, and the effect of flavonoids in the monocyte/macrophages activation pathways.

## 19.2 Flavonoid Absorption and Bioavailability

The average US daily flavonoid intake is 189.7 mg/d, subdivided in flavan-3-ols (87%), flavanones (7.6%), flavonols (6.8%), and others [12]. Quercetin is the most important contributor to the estimated intake of flavonoids, mainly from the consumption of apples and onions [52]. Data regarding flavonoids bioavailability – i.e. the portion of the compound ingested that is digested, absorbed and metabolized – are still incomplete. Plasma or urine concentration of a certain compound is typically used to character-

ize its bioavailability [46]. In terms of flavonoids, the primary route of administration is ingestion. Once ingested, flavonoids undergo sulfation, methylation and glucuronidation in the small intestine and liver by respective enzymes [26, 44]. These metabolic forms are the ones commonly found in plasma, rather than the aglycone [10, 38, 44, 46, 64]. Several studies performed in humans have shown that after ingestion of flavonoid-rich food, maximum plasma levels are observed after 1.5-2 h; however, only sub- or low-micromolar concentration of the corresponding aglycone are retrieved. This is the case of green tea catechins (0.6-1.8 µM, depending on the considered compound) [74], quercetin from a vegetable and fruit-enriched diet  $(0.14 \,\mu\text{M})$  [17], as well as from ingestion of apples and onions  $(1.5-3.4 \mu M)$  [33], among others. From these studies, it is clear that only a small percentage of flavonoids (<2%) of the initial intake is

Flavonoid subclass	Compound	Berry species
Flavonols	Kaempferol	Blueberry, sour cherry, cranberry, raspberry, strawberry
	Quercetin	Blueberry, sour cherry, cranberry, raspberry, strawberry
	Myricetin	Blueberry, cranberry, strawberry
	Isoharmnetin	Sour cherry
Flavones	Apigenin	-
	Luteolin	-
Flavanones	Hesperitin	-
	Narigenin	Strawberry
Flavan-3-ols	(-)-Epicatechin	Blueberry, sour cherry, cranberry, raspberry, strawberry
	(-)-Epicatechin 3-gallate	Strawberry
	(-)-epigallocatechin	Cranberry, raspberry, strawberry
	(-)-epigallocatechin 3-gallate	Cranberry, raspberry, strawberry
	(+)-catechin	Blueberry, sour cherry, cranberry, raspberry, strawberry
	(+)-gallocatechin	Strawberry
Proanthocyanidins	Monomer	Blueberry, cranberry, raspberry
	Dimer	Blueberry, cranberry, raspberry
	Trimer	Blueberry, cranberry, raspberry
	4-6mers	Blueberry, cranberry, raspberry
	7-10mers	Blueberry, cranberry, raspberry
	Polymers	Blueberry, cranberry,
Anthocyanidins	Cyanidin	Blueberry, sour cherry, cranberry, raspberry, strawberry
	Delphinidin	Blueberry, cranberry, raspberry, strawberry
	Malvidin	Blueberry, cranberry, raspberry, strawberry
	Pelargonidin	Blueberry, cranberry, raspberry, strawberry
	Peonidin	Blueberry, sour cherry, cranberry, raspberry, strawberry
	Petunidin	Raspberry, strawberry

**Table 19.1** Individual flavonoids according to their subclass, as found in common berries

absorbed. Compounds that are not absorbed from the intestine migrate to the colon wherein they interact with the microflora. The flavonoids that re-enter circulation can now be broken into low aglycones by the microbiota and further into low molecular weight compounds that can be absorbed [64].

Different polyphenols have different absorption rates and metabolic conversions due to their variable structures. Regarding flavonols, studies performed in the Caco-2 model cell line have shown that the several glycosylated forms are poorly absorbed [15, 26]. Aglycones can pass through the gut wall because microflora hydrolyzes the sugar moiety [25]. However, there is also a compound specificity in the absorption mechanism, i.e. quercetin and daidzein glucosides seemed to be directly absorbed by active transport [26]. Not only does polyphenol structure affect the absorption, but so can the dose and food matrix in which they are contained. It has been found that the absorption efficiency can actually decrease as the dose increases, suggesting that there is an absorption saturation point [10]. Because of the overall poor absorption and low bioavailability of flavonoids, a variety of strategies have been explored in order to improve these inefficiencies. Increasing metabolic stability, intestinal absorption and changing the absorption site have been considered to improve flavonoid bioavailability [52, 64].

## 19.3 Lipid and Cholesterol Oxidation in LDL and Atherosclerosis

# 19.3.1 Chemical-Induced Oxidation of LDL

There is a generous literature regarding *ex vivo* or *in vitro* oxidation of LDL, and it is out of the scope of this chapter a detailed revision of the field, which can be found elsewhere [42]. Here,

we will summarize the main strategies used to assess LDL oxidation and how these experimental setups are relevant for flavonoids-centered antioxidant studies. LDL are complex macromolecules, made of a lipid core surrounded by a single non-exchangeable lipoprotein, known as apolipoprotein (ApoB). The average lipid core has been calculated to contain 600 molecules of free cholesterol, 1600 molecules of cholesteryl esters (mainly arachidonate and linoleate esters), 700 molecules of phospholipids (64% PC, 1.5% PE, 26% SM, and 11% LPC), 180 molecules of triacylglycerides (TAGs), and approximately 10 molecules lipophilic of the antioxidant  $\alpha$ -tocopherol [37, 42]. Several exchangeable lipoproteins are also associated to LDL particle, and their function is to modulate interactions with specific cell receptors [7, 16]. In particular, high concentrations of ApoC-III in ApoB lipoproteins have been reported among patients with coronary disease and coronary atherosclerotic lesions, as well as metabolic syndrome and type 2 diabetes [16, 61].

*Ex vivo* and *in vitro* oxidation of LDL is an experimental strategy largely adopted to either characterize products of lipid oxidation, or assess the ability of antioxidants to dampen oxidation itself. Oxidation can be triggered via several mechanisms, including but not limited to free radicals generation, Fenton reaction, and peroxynitrite oxidation agents [19].  $\alpha, \alpha'$ azodiisobutyramidine dihydrochloride (AAPH) has been widely used as ROS inducer, since it degrades to highly reactive radical species that oxidized molecular oxygen to peroxy radicals [19]. Fenton reaction is triggered by micromolar solution of Cu<sup>2+</sup> (or less commonly Fe<sup>2+</sup>) salts, which are able to abstract a proton from preformed lipid peroxides to generate peroxyl radicals [28]. Finally, peroxynitrite is obtained from a variety of precursor, including linsidomine (SIN-1) [62, 65]. Oxidation of LDL can potentially affect each of its constituents, including the apoB, and cross-reactions between different fractions (i.e. protein/lipid chemical interaction) can exponentially multiply the chemistry of the oxidative products, to a variety of lipids with reported biological activity [42]. LDL can be mildly or highly oxidized (MM-LDL and the proper ox-LDL, respectively), although there is no general consensus about the active species present in each stage [11, 42, 50].

#### 19.3.2 Cholesterol Oxidation in LDL

Cholesterol is a natural occurring compound that has several crucial functions within the body. It is a key component of all cellular membranes, a precursor to steroid hormones and is involved in many signal transduction pathways [27]. Cholesterol transport in humans is a complex process. LDL are the lipoproteins that carry esterified cholesterol from the liver to the peripheral tissue [71]. In humans, a balance of cholesterol is critical for many physiological processing, since accumulation of this molecules in cell membrane can affect the function of a variety of enzymes, transporters and receptors. Cholesterol is susceptible of being oxidized by naturally occurring oxidative agents, like reactive oxygen and nitrogen species (ROS and RNS, respectively), that can alter its chemical backbone by oxygenating carbons at several positions. Commonly, auto-oxidation of cholesterol (i.e. by chemical and physical means) occurs at position C-7 proximal to the C5-C6 double bond, or to the C-25 tertiary carbon [45, 47]. However, first oxidative derivatives can be further oxidized and go subsequent chemical rearrangements. To date, more than 80 compounds, broadly known as cholesterol oxidation products (COPs) have been identified. COPs are more polar than the parent cholesterol, thus present different chemical and biophysical properties in cell environment. Their different chemistry is the major source of health-associated issues, since they can interfere with cholesterol homeostasis at several level. It is not the scope of this chapter to detail the putative biological effects due to the exposure of COPs, as from cell, in vivo and (marginally) clinical studies. The reader can refer to our recent review [45] or other compelling works in the area. Briefly, in vitro works using several cell lines have reported that administration of high concentration of COPs – either individually or as a mixture of compounds – can trigger several physiological responses able to induce pro-inflammatory, pro-fibrogenic, and pro-apoptotic effects. A consistent body of literature has also assessed the cytotoxic, mutagenic and carcinogenic properties of COPs. As aforementioned, cholesterol homeostasis is strictly linked to COPs accumulation in fluids and cell compartments [45].

## 19.3.3 OxLDL Activate Monocytes/ Macrophages Pathway

The mechanism by which LDL activates monocytes in the intima towards their conversion to macrophages is still controversial, although a rough phenomenological description has been provided [59]. There is scientific consensus that oxLDLs, rather than the parent LDL, are the primary stimulus leading endothelial activation and subsequent inflammatory response. Under particular conditions, LDL can cross the endothelial tissue of the blood vessels and being incorporated into the intima. According to the current response-to-injury hypothesis, oxidation of LDLs favors the expression of cell adhesion molecules by endothelial cells, such as the cell adhesion molecule-1 (ICAM-1) and the vascular adhesion molecule-1 (VCAM-1) [59]. These cell adhesion molecules favor LDL migration towards the intima. ROS and RNS-induced action on LDLs can also occur at the intima level [23, 40]. oxLDL-induced activation of macrophages is the second stage of atherosclerosis development. Both chemical and enzymatic oxidative processes act on the whole LDL chemical structure, including phospholipids, cholesterol (free and esterified), apolipoprotein and TAGs [11]. Lipids species derived from oxidation are responsible to "activate" monocytes, via specific interaction with membrane receptors. Extensive oxidation is necessary for LDL to bind macrophages receptors SR-A or CD36, including up to 50% cholesterol oxidation, apoB fragmentation, and diffused oxidation of unsaturated fatty acids [6, 37]. Isoprostane are one of

the biomarkers of oxidative stress: PL-esterified isoprostanes are known to have pro-inflammatory action, and stimulate monocyte adhesion to the endothelial cell [1, 2]. Oxysterols, in particular 7-ketocholesterol,  $7\alpha$ -OH and  $7\beta$ -OH cholesterol, and cholesterol epoxides are abundant in LDL, and are believed to exert cytotoxic effects on monocyte-macrophages ([5, 13]). Although toxic, ROS-induced COPs (particularly B-ring derivatives) seem unable to activate liver-X receptors (LXR-α and β) and peroxisome-proliferator-activated (PPARs) receptors in macrophages, and so trigger the anti-atherogenic response [6, 37, 69]. On the other side, enzymatic side-chain COPs like 22-OH, 25-OH and 27-OH cholesterols can trigger both LXR $\alpha$  and PPARs [69], which is explained by specific structural requirements needed for these ligand-receptor interactions to occur [36]. Other inflammatory mechanisms have been proposed for B-ring oxysterols, as 7-keto and 7-OH cholesterol isomers. A increasing literature body has demonstrated that B-ring oxysterols can stimulate inflammatory signaling in monocytes by interacting with Toll-like receptors [18], particularly TLR-4 [34]. 7β-OH cholesterol stimulate the increase of IL-8 secretion via the MEK/ERK1/2 pathway [69].

Oxidation of the fatty acid moiety of cholesteryl-esters also forms compounds – like 9-oxononanoyl cholesterol – able to activate adhesion of monocytes [5, 11]. These oxidative CE (OxCE) are also able to trigger inflammation through several mechanisms, including TLR-mediated response, as recently discussed in detail by Miller and Shyy [50].

The discussed inflammatory responses trigger the differentiation of monocytes, as well as their recruitment from the vascular vessels to the arterial wall, *via* trans-endothelial migration [43, 59]. The monocyte recruitment molecular process is still under debate, and involve several signaling mechanisms, as discussed elsewhere [43]. In the intima, monocytes then differentiate into macrophages, that uptake oxLDL *via* scavenging receptors, resulting in the transformation of macrophages to foam cells. Accumulation of foam cells and platelets is the boundary stone for the formation of the atherosclerotic lesions known as fatty streaks.

#### 19.4 Flavonoids Against LDL Oxidation

## 19.4.1 Mechanisms of Flavonoids Action Against Lipid Oxidation

Several studies in recent years have examined the relation between flavonoids and oxidation or inflammation. The powerful antioxidant activity exhibited by flavonoids is due to their action as free radical scavengers, singlet oxygen quenchers, and metal ion chelators [26]. Several *in vitro* systems have been used to evaluate the antioxidant potential of flavonoids. In this chapter, we will focus in LDL oxidation and macrophages activation.

LDL oxidation, as aforementioned, is the first critical step in triggering the inflammatory cascade that finally brings to atheroma formation and consequent CVD manifestation. Early works by Frankel's group [20, 48] have extensively explored the ability of fruits flavonoids extracts to dampen oxidation in LDL. Flavonoids possess lower redox potential than lipids, and are thus oxidized by ROS and RNS, resulting in more stable and less-reactive ortho-semiquinone radical compared to lipid radicals and peroxy radicals [3, 4, 29]. When evaluated individually, several pure flavonoids (catechin, quercetin, cyanidin, caffeic acid, and ellagic acid) showed up to 95% inhibition of Cu<sup>2+</sup>-induced hexanal production in micromolar ranges ( $2.5-7.5 \mu M$ ). However, specific binary and ternary mixtures of flavonoids showed antagonistic effects, particularly if caffeic and ellagic acids coexisted in equal amounts [48]. Dissimilarities among flavonoids AO activity can be explained taking into account differences in their chemical structures; particularly, structural variation in the C-ring and the oxidative state of C3 seemed to confer different reactivity [29, 48]. A structure-activity relationship (SAR) study by Vaya et al. [68]

showed that the contribution of the different functional groups to the inhibition of LDL oxidation is well correlated to the energy needed to form the flavonoid radical by abstraction of a hydrogen atom. In other words, it is possible to classify flavonols according to their inhibition potential towards radical and copper induced oxidation, being more effective those compounds having two adjacent hydroxyls at the B-ring, like quercetin and catechin. Solubility and partitioning behavior of flavonoids could also play a role in defining their scavenging activity, considering that their effectiveness as LDL oxidative protectors relies in their ability to physically interact with the lipid core [48]. However, Paganga et al. [54] demonstrated that superiority of quercetin vs. catechin in inhibiting LDL peroxidation cannot be accounted to partitioning considerations, but to the exceptional ability of the former to chelate copper. Another interesting SAR study was performed by Yi and coworkers [75], where twenty-three 4-oxo-flavonoids (i.e. C-4 is oxidized to ketone function) were assessed against oxLDL-induced endothelial dysfunction. Similarly to the previous studies [48, 49, 68], flavonols – morin, myricetin, fisetin and quercetin – showed higher activity in micromolar range. The promising "hits" shared higher oxy-functionalization at the flavan ring: 3',4'-o-dihydroxyl on B-ring, a 3-hydroxyl on C-ring, a 2,3-double bond and a 5,7-m-dihydroxyl on the A-ring were all required for the observed inhibitory effect.

#### 19.4.2 Dietary Flavonoids and LDL Oxidation

A substantial amount of literature has used grape and wine as flavonoids-enriched matrix to leverage their LDL-protectant function, mainly supported by early hypothesis regarding the socalled "French paradox" formulated by epidemiologists in the early '80. The "French paradox" is the observation of low coronary heart disease (CHD) death rates despite high intake of dietary cholesterol and saturated fat in southern French diet [58]. Red wine contains up to 250 mg/mL phenols, depending on type and variety [44]. Experiments performed using Petit Syrah wine showed that 5 µM concentration of individual catechin, myricetin, epicatechin, rutin and quercetin were able to inhibit LDL oxidation by  $Cu^{2+}$  in the range 60–75% [63], higher than  $\alpha$ -tocopherol. More interesting, procyanidins (i.e. oligomeric forms of flavonols) were higher inhibitors of hexanal formation (up to 80% at 5  $\mu$ M), which can be explain by their better ability to interact with the LDL constituents. A more extensive work performed on 14 grapes varieties demonstrated similar effects on the inhibition of hexanal generation, with the additional information that the inhibitory potential was positively correlated with the content of phenols, and in less extent anthocyanins and flavonols [49]. An interesting paper by Frémont and co-workers more deeply investigated the effects of wine extract and individual flavonoids in *in vitro* LDL oxidation by copper and AAPH [21]. Their results discriminated between chelating agents (resveratrol), which are active against Cu<sup>2+</sup> oxidation, and radical scavengers (catechin) that inhibit AAPH lipid peroxide formation. Furthermore, in their studies highly unsaturated cholesteryl-esters, rather than phospholipids, were mostly affected by both oxidation mechanisms, and this was demonstrated by altered electrophoresis mobility of apoB after oxidation. These effects were negligible in white wines, which contain lower amounts of flavonoids, although imposing a longer grapeskin contact during winemaking can led to "redlike" white wines with analogue antioxidant capacity [22]. Beside grape, other flavonol-rich dietary extracts have been tested as antioxidants against LDL chemically-induced oxidation. Viana et al. [70] used an extract of Vaccinium myrtillus containing anthocyan, catechin, chalcone and other flavonoids to dampen Cu<sup>2+</sup>induced LDL oxidation. They showed a significant increase of the lag phase of lipid peroxidation associated with the presence of vitamin E, indicating that the effects of flavonoids are limited to the early stages of oxidation, when intrinsic antioxidants are still present. Similar results have been obtained with flavonoids extract from different species of berries [30, 51], as well as other fruits [44].

An obvious following step in CVD-related flavonoids research are in vivo and clinical studies. Various studies have exposed either animal models or humans subjects to flavonoids-enriched diets, recording controversial results that partially debunked the "anti-oxidative claim" [44]. Part of this controversy is due to the lack of reliable biomarkers for measuring plasma antioxidant activity, lack of long-term studies and underestimation of gut and liver biotransformation [44, 73]. A few examples of in vivo works follow, and a good critical review can be found elsewhere [44].

O'Reilly and co-workers coupled in vitro assessment of a flavonoid mixture against Cu<sup>2+</sup> oxidation of LDL with dietary intervention study. All the tested flavonoids - including quercetin, luteolin, catechin, and kaempferol, among others - showed sub-micromolar ability to halve TBARS value and decrease LDL peroxides. Surprisingly, when 32 subjects were exposed to a high-flavonoids diet, no significant effects were found in ex vivo LDL oxidation [53]. From the in vitro effects on LDL, Pignatelli and others [56] administered red and white wine to 20 healthy volunteers, finding a significant reduction in plasma conjugate dienes, as well as urinary PGF-2α-III, a marker of oxidative stress. Flavonols from concentrated cranberry juice decreased plasma oxLDL and cell adhesion molecules ICAM-1 and VCAM-1 in 30 men, over three successive periods of 4 weeks [60]. In their review, Lotito and collaborators [44] list a few works that failed to demonstrate in vivo efficacy of flavonoids in inhibit plasma oxidation. The conclusion is that, although epidemiology studies are fairly convincing about their antioxidant effects, is unlikely that flavonoids per se acts against LDL oxidation, given their poor bioavailability. Likely, observed effects are due to upregulation of endogenous antioxidants enzymes, like those of the uric acid biosynthetic pathway.

# 19.4.3 Flavonoids and Inflammatory Activation Pathways

The immune system is integrated by a highly complex regulated group of cells that may interact in a cell-cell manner and may also respond to intercellular messages including hormones and cytokines. Diet, pharmacological agents, pollutants, and food chemicals display remarkable actions, at both pharmacological and biochemical level, that affect the function of inflammatory and immune cells, including macrophages [24]. We already discussed the function of monocytes and derived-macrophages in triggering the inflammatory effect during the formation of the atheroma and CVD progression. Macrophage can proliferate in the presence of a specific growth factor, M-CSF, and in the presence of an inducer such as lipopolysaccharide (LPS), they stop proliferating adopt a phenotype that is characterized by the expression of early cytokines and NO [14]. Several flavonoids - as genistein - can interact with enzymes and receptors involved in the generation of the inflammatory processes, especially tyrosine and serine-threonine protein kinases. In monocytes, those are responsible for the production of cytokines, such as TNF- $\alpha$ , IL-6 and IL-1β. Kaempferol and quercetin inhibitory effects against tyrosine kinases was reflected in a significant antiproliferative effects on M-CSFactivated macrophages [14]. Aglycones and conjugated-derivative showed anti-inflammatory activity: an interesting study by Kawai and co-workers [38] found that quercetin-3-glucoronide and quercetin disrupt expression of CD36 in murine macrophages cell lines. In vivo studies on mice showed that epigallocatechin-3gallate can inhibit LPS-induced and interferon- $\gamma$ -activated nitric oxide synthase (iNOS) gene expression, inasmuch as iNOS activity in cultured macrophages, and so reducing nitric oxide production and subsequently oxidative stress [8]. Direct inactivation of iNOS was explained also by the ability of certain flavonoids to bind arginine and the iNOS cofactor tetrahydrobiopterin [8]. A more extended study performed by Hämäläinen and co-workers [35] showed that

several flavonoids - including kaempferol, genistein, quercetin and dadzein - were able to reduce STAT-1 and NF-kB activation (both iNOS transcription factors), and suppress iNOS expression, whereas others (including naringenin and pelargonidin) had no effect on STAT-1. A similar mechanism has been proposed to explain the strong inhibition of NO generation and iNOS expression in activated macrophages by resveratrol [66], although a similar study contradicts these findings [72]. Resveratrol can dampen the pro-inflammatory phenotype by activating sirtuin-1, a type III histone deacetylase that suppresses NF-kB factor [55]. Resveratrol downstream regulation mode of the mitochondrial biogenesis via sirtuin-1 activation seems to be strongly dose-dependent [9, 57]. It is important to notice that these *in vitro* studies, as well others [41] were performed at relatively high concentration of resveratrol, far from the ones normally observed in plasma after ingestion (see Sect. 19.2).

#### **19.5 Conclusions**

A few considerations follow from the above review. First, several epidemiology studies conducted in the last decades have demonstrated health benefits due to regular intake of flavonoidrich foods. Second, the chemistry of flavonoids makes them prone to show radical-scavenging and metal-chelating properties, that can be successfully used to dampen in vitro lipid oxidation, in particular Cu2+ and free radical-induced oxidation of plasma LDL. This has been achieved both using fruit and vegetable extracts, as well as individual pure flavonoids standards, with inhibitory concentration in the order of 5-10 µM. However, clinical studies performed in healthy subjects were only partially able to replicate these in vitro and ex vivo findings by administration of a variety of dietary regimes with high content in flavonoids. The lack of in vitro-in vivo correlation can be attributed to several factors, that can be summarized in: i) reduced adsorption (0 to  $1-2 \mu M$  in plasma) and short lifetime, that make unlikely an actual antioxidant effect, ii) biotransformation to flavonoids-conjugates, with unknown or reduced biological activity. In order to positively merge the in vitro observations with the diffused epidemiological studies, research should be focused in validate those speculated mechanisms in more physiological settings. Among various aspects worth of research interests, the authors believe that priority should be given to a deep understanding of the "fate" of flavonoids in our organism, a critical effort that should consider adsorption, bioavailability, and the actions of intrinsic metabolism, inasmuch as gut microbiota. Also, the "flavonoids effect" should be better contextualized in the overall diet, thus facilitating the comprehension of combined effects between other macro and micro-nutrients, that can potentially act as synergistic/antagonist. Thus, a holistic rather than a criterion-based approach can led to more realistic outcomes and expectations on the consumer.

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