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# Yasuyuki Kihara Editor

# Druggable Lipid Signaling Pathways



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Yasuyuki Kihara Editor

# Druggable Lipid Signaling Pathways



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## Introduction: Druggable Lipid Signaling Pathways

Yasuyuki Kihara

#### Abstract

Lipids are essential for life. They store energy, constitute cellular membranes, serve as signaling molecules, and modify proteins. In the long history of lipid research, many drugs targeting lipid receptors and enzymes that are responsible for lipid metabolism and function have been developed and applied to a variety of diseases. For example, non-steroidal anti-inflammatory drugs (NSAIDs) are commonly prescribed medications for fever, pain, and inflammation. The NSAIDs block prostaglandin production by inhibiting cyclooxygenases. A recent innovative breakthrough in drug discovery for the lipid biology field was the development of the sphingosine 1-phosphate receptor modulators (fingolimod, siponimod and ozanimod) for the treatment of multiple sclerosis, which were approved by the United States Food and Drug Administration in 2010, 2019 and 2020, respectively. This review series of "Druggable Lipid Signaling Pathways" provides 9 outstanding reviews that summarize the currently available drugs that target lipid signaling pathways and also outlines future directions for drug discovery. The review chapters include lipid signaling pathways (prostanoids, leukotrienes, epoxy

fatty acids, sphingolipids, lysophospholipids, endocannabinoids, and phosphoinositides) and lipid signaling proteins (lysophospholipid acyltransferases, phosphoinositide 3-kinase, and G protein-coupled receptors (GPCRs)). Drugs targeting lipid signaling pathways promise to be life changing magic for the future of human health and well-being.

#### Keywords

Lipid mediator · Drug discovery · Pharmacology · Biochemistry · Molecular biology

The lipid bilayer membrane that protects DNA from external stress is essential for DNA inheritance and cell survival [1]. Membrane lipids contain glycerophospholipids (phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylgerol), glycerolipids (mono-, ditri-acyl-glycerols), sphingolipids, and sterol lipids [2–4]. Membrane glycerophospholipids are *de novo* synthesized from glycerol-3-phosphate (known as the Kennedy pathway), which produces phosphatidic acid (PA) via lysophosphatidic acid (LPA) by the sequential actions of glycerol-3-phosphate acyltransferase and LPA acyltransferase (LPAAT). Phospholipiases liberate fatty acyls from the glycerophospholipids,





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whose diversity is generated by lysophospholipid acyltransferases (known as Land's cycle) [5–8]. Liberated fatty acyls are further metabolized by cyclooxygenases (COXs), lipoxygenases (LOs), and cytochrome P450, resulting in the generation of prostanoids, leukotrienes, and epoxy fatty acids, respectively [9–11]. Drug discoveries for lysophospholipid acyltransferases are summarized by Dr. Hideo Shindou (Chap. 2).

The first NSAID, acetylsalicylic acid (Aspirin<sup>®</sup>), was commercialized in 1897 before the finding of prostanoids including the prostaglandins (PGs: PGD<sub>2</sub>, PGE<sub>2</sub>, PGF<sub>2 $\alpha$ </sub>, PGI<sub>2</sub>) and thromboxane (TXA<sub>2</sub>) [12]. Prostanoids are derived from arachidonic acid and play important roles in pain, fever, inflammation, cardiovascular diseases, the reproductive system, and others [9, 13, 14]. Dr. Emanuela Ricciotti summarizes the prostanoid pathways and drugs targeting this pathway (Chap. 3). Leukotrienes are also derived from arachidonic acid, whose receptor antagonists such as pranlukast, montelukast, and zafirulukast are prescribed for treating asthma and rhinitis [9, 15–19]. Dr. C. Henrique Serezani provided a review of leukotriene pathways, particularly focusing on metabolic and cardiovascular diseases (Chap. 4). Polyunsaturated fatty acids including arachidonic acid, docosahexaenoic acid, and eicosapentaenoic acid are metabolized by CYP P450 to produce epoxy fatty acids that are further metabolized to hydroxy fatty acids by soluble epoxide hydrolases (sEHs) [20]. Cindy McReynolds et al. introduced novel drugs targeting sEH for the treatment of neuropathic pain and cardiovascular diseases (Chap. 5).

Sphingolipids (sphingoid bases, ceramides, sphingomyelins, cerebrosides) are also essential components of membranes that have a sphingosine backbone with N-acyl chains and/or head groups [21, 22]. Sphingosine 1-phosphate (S1P) is a lipid mediator that controls lymphocyte trafficking and is responsible for immune diseases [23, 24]. Fingolimod is a pro-drug that is metabolized to fingolimod-phosphate by endogenous sphingosine kinases [25]. Fingolimod is the first FDA-approved orally available drug for the treatment of relapsing-remitting multiple sclerosis, which targets S1P receptors [26–28]. Dr. Victoria A. Blaho reviewed drug discoveries in the sphingolipid pathways (Chap. 6).

Lysophospholipid biology is expanding rapidly by finding receptors for each lysophospholipid (LPA, lysophosphatidic acid; LPI, lysophosphatidylinositol; lysoPS, lysophosphatidylserine; LPGlc, lysophosphatidylglucoside) [26, 27]. LPA receptor antagonists and the LPA metabolic enzyme, autotaxin, inhibitors are expected to treat pulmonary fibrosis, pain, cardiovascular, and neurological diseases [29–32], which was summarized by Dr. Keisuke Yanagida (Chap. 7).

Endocannabinoids (anandamide and 2-arachidonoylglycerol) are essential lipid mediators in the central nervous system and immune system [33]. The endocannabinoid receptors were originally discovered as receptors for cannabis components before endocannabinoids were found. Cannabinoids are clinically and recreationally used worldwide. Dr. Matthew W. Buczynski provides an overview of endocannabinoid biology and drug discovery (Chap. 8).

Phosphoinositides (phosphatidylinositol 3-phosphate (PI3P), phosphatidylinositol 4-phosphate (PI4P), phosphatidylinositol 5-phosphate (PI5P), phosphatidylinositol 3,4-biphosphate ( $PI(3,4)P_2$ ), phosphatidylinositol 3,5-biphosphate ( $PI(3,5)P_2$ ), phosphatidylinositol 3,4-biphosphate  $(PI(3,4)P_2),$ and phosphatidylinositol 3,4,5-triphosphate (PIP<sub>3</sub>)) are essential intracellular signaling molecules downstream of a variety of cell surface receptors [34, 35]. These are derived from phosphatidylinositol by the actions of phosphoinositide kinases. Dr. John E. Burke provided a comprehensive summary of this pathway with particular focus on the phosphoinositide 3-kinase (PI3K) and phosphatidylinositol 4-kinase (PI4K) family (Chap. 9).

All the lipid mediators introduced above bind to their cognate GPCRs that are the most attractive targets for drug discovery. This book's editor, Dr. Yasuyuki Kihara, provided a review of druggable lipid GPCRs that summarizes the histories of lipid GPCR identification, drugs targeting lipid GPCRs, and striking drug designs for future GPCR drug discovery (Chap. 10).

Taken together, the book contains 10 chapters that provide a historical overview as well as the recent advances in studies of lipid signaling pathways with particular emphasis on "druggable" targets. The book is aimed at a broad audience from academic to industry researchers and was authored by the next generation of lipid researchers who were trained and mentored by prestigious lipid scientists including Drs. Frank K. Austen, Charles R. Brown, Jerold Chun, Edward A. Dennis, Garret A. FitzGerald, Timothy Hla, Bruce D. Hammock, Loren H. Parsons, Marc Peters-Golden, Takao Shimizu, Gabor Tigyi, Roger L. Williams, and more.

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2

## Biosynthetic Enzymes of Membrane Glycerophospholipid Diversity as Therapeutic Targets for Drug Development

William J. Valentine, Tomomi Hashidate-Yoshida, Shota Yamamoto, and Hideo Shindou

#### Abstract

Biophysical properties of membranes are dependent on their glycerophospholipid compositions. Lysophospholipid acyltransferases (LPLATs) selectively incorporate fatty chains into lysophospholipids to affect the fatty acid composition of membrane glycerophospholipids. Lysophosphatidic acid acyltransferases (LPAATs) of the 1-acylglycerol-3-phosphate O-acyltransferase (AGPAT) family incorporate fatty chains into phosphatidic acid during the de novo glycerophospholipid synthesis in the Kennedy pathway. Other LPLATs of both the AGPAT and the membrane bound O-acyltransferase (MBOAT) families further modify the fatty chain compositions of membrane glycerophospholipids in the remodeling pathway known as the Lands' cycle. The LPLATs functioning in these pathways possess unique characteristics in terms of their biochemical activities, regulation of expres-

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sions, and functions in various biological contexts. Essential physiological functions for LPLATs have been revealed in studies using gene-deficient mice, and important roles for several enzymes are also indicated in human diseases where their mutation or dysregulation causes or contributes to the pathological condition. Now several LPLATs are emerging as attractive therapeutic targets, and further understanding of the mechanisms underlying their physiological and pathological roles will aid in the development of novel therapies to treat several diseases that involve altered glycerophospholipid metabolism.

#### **Keywords**

Phospholipid · LPCAT · LPAAT · Lysophospholipid acyltransferase · AGPAT

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#### 2.1 Function and Diversity of Cellular Membranes

Cellular membranes are comprised mainly of protein and lipids; and glycerophospholipids, along with sphingolipids and cholesterol, are the major lipid components. The glycerophospholipids share a common glycerol-based structure with a phosphate-containing headgroup at the sn-3 position of the glycerol backbone, and two hydrophobic fatty chains attached to the sn-1 and sn-2 positions (Fig. 2.1). This basic structural unit supports formation of lipid bilayers, which serve various cellular functions: to separate the interior of cells from their physical environments; to form compartments within cells that define organelles and structures; to form domains of molecular interactions; and as storage of lipid mediator precursors. Some glycerophospholipids also form monolayers such as outer monolayers of HDL (high-density lipoprotein) particles, LDL (low-density lipoprotein) particles, and lipid droplets; as well as specialized surfactant monolayers such as pulmonary surfactant. A great diversity of glycerophospholipid species exists due to the many possible combinations of headgroups, fatty chains, and linkages of the fatty chains to the glycerol backbone. This diversity varies among cell types and tissues and imparts membranes with unique biophysical and biological properties.

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#### 2.1.1 Glycerophospholipid Classes

Glycerophospholipids possess a phosphatecontaining headgroup esterified to sn-3 of their glycerol backbones. In the simplest glycerophospholipid, phosphatidic acid (PA), the phosphate is the headgroup and no further addition is made. PA is not very abundant in membranes but is a key intermediate in biosynthesis of all other classes of glycerophospholipids. The other classes are formed by esterification of the phosphate group to any of several alcohols (choline, ethanolamine, serine, inositol, or glycerol) forming the glycerophospholipid classes phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylserine (PS), phosphatidylinositol (PI), and phosphatidylglycerol (PG). Cardiolipin (CL) is structurally unique in having a modified dimeric PG structure, with a glycerol backbone esterified to two PA moieties.

The relative amounts of the different glycerophospholipid classes in cellular membranes varies. PC followed by PE are the most abundant glycerophospholipids in membranes, and together typically account for over half of the glycerophospholipids. Other classes of glycerophospholipids are typically less abundant, PI and PS classes each typically account for  $\sim$ 5–10% of all glycerophospholipids, and lesser amounts of CL, PG, and PA (<5% each) are generally present





Basic structures of diacyl-, alkyl-acyl-, and alkenyl-acyl (plasmalogen) -glycerophospholipids are shown. X represents -OH, choline, ethanolamine, serine, inositol, or glycerol for PA, PC, PE, PS, PI, and PG, respectively.

Stereospecific numbering (*sn*) positions of the glycerol backbone are indicated by red arrows. R1 and R2 represent the fatty chains at *sn*-1 and *sn*-2, respectively. Acyl, alkyl, and alkenyl linkages at *sn*-1 are highlighted in blue. GPL, glycerophospholipid

[1]. However, the less abundant classes of glycerophospholipids may have specialized functions and important roles in various biological contexts, such as roles for PS in cell fusion, phagocytosis, and apoptosis [2] and roles for PI in vesicle trafficking [3]. These less abundant classes may also be concentrated within cells in certain structures, domains, or organelles; for example, CL is a major component of the inner mitochondrial membrane, where it has important roles in mitochondrial structure and function [4].

#### 2.1.2 Fatty Chain Diversity

Fatty chains found in glycerophospholipids vary in terms of carbon chain length and double-bond number. The fatty chain compositions of membrane glycerophospholipids varies among organelles, cell types, tissues, and physiological states; and these compositions can strongly affect biophysical properties of the membranes in terms of fluidity, flexibility, fusion, fission, and curvature [5, 6]. Carbon chain lengths affect membrane thickness and microdomain formation, which can strongly affect functions of transmembrane proteins and membrane-associated proteins. Doublebond number affects membrane thickness, viscosity, flexibility, and strength. Compared to unsaturated and monounsaturated fatty chains, polyunsaturated fatty chains in membrane phospholipids impart flexibility and curvature to the membranes. Polyunsaturated fatty acids in membrane glycerophospholipids also represent important sources of precursor molecules that can be de-esterified by phospholipase A (PLA) 1/2 s and converted to lipid mediators [7, 8].

#### 2.1.3 Glycerophospholipid Linkages

In addition to chain length and saturation, the linkages of the fatty chains to the glycerol backbone further increase the diversity of glycerophospholipid species. Acyl linkages are the most

common at both *sn*-1 and *sn*-2. Alkyl and alkenyl linkages may also occur at sn-1, forming what are known as plasmanyl- or plasmenylphospholipids, respectively (Fig. 2.1). Plasmanyland plasmenyl-phospholipids have a different biosynthetic route than diacyl glycerophospholipids. Rather than being synthesized from a PA precursor, as are diacyl species, their synthesis begins in peroxisomes with acylation of dihydroxyacetone phosphate (DHAP) by the enzyme DHAP-acyltransferase (DHAPAT). This reaction produces 1-acyl-DHAP, which is enzymatically converted to 1-alkyl-DHAP and then 1-alkylglycerol-3-phosphate. 1-alkylglycerol-3phosphate is acylated at sn-2 and further metabolized in the endoplasmic reticulum to form the plasmanyl- and plasmenyl-phospholipids [9].

The plasmanyl-phospholipids, with alkyl linkages at *sn*-1, usually are of the PC class of glycerophospholipids. A notable example is platelet-activating factor (PAF; 1-*O*-alkyl-2-acetyl*sn*-glycero-3-phosphocholine). PAF is a potent inflammatory phospholipid mediator, and produced by lyso-PAF acetyltransferase activities of lysophosphatidylcholine acyltransferase (LPCAT)1 or LPCAT2 from lyso-PAF and acetyl-CoA [10, 11].

The plasmenyl glycerophospholipids, commonly known as plasmalogens, have alkenyl linkages at sn-1 and are enriched with polyunsaturated fatty acids at sn-2. This unique structure may impart them with special properties, however determining the biological functions of plasmalogens has often been challenging. Overall, plasmalogens account for 15-20% of all phospholipids in cell membranes and are highly enriched in certain tissues. Plasmalogens of the PE class are generally the most abundant, as well as PC plasmalogens in certain tissues. For instance, in adult humans over half of the PE glycerophospholipids in heart and brain may be plasmalogen; and, while PC in brain is low in plasmalogen, ~25% of PC in heart may be plasmalogen. Other tissues rich in plasmalogens include kidney, lung, skeletal muscle, and ocular lens; and plasmalogens may also have unique roles during development and in immune cells [9].

#### 2.1.4 *De novo* Glycerophospholipid Biosynthesis (Kennedy Pathway)

De novo glycerophospholipid production proceeds through pathways that involve production of PA as a precursor in production of all mammalian diacyl glycerophospholipids. These enzymatic reactions were first described by Kennedy and Weiss in 1956 and are now termed the Kennedy pathway [12]. First, glycerol-3phosphate acyltransferases (GPATs) esterify an acyl chain to glycerol-3-phosphate (G3P) at the sn-1 position to produce lyso-PA (LPA; 1-acylglycerol-3-phosphate). Next, LPAacyltransferases (LPAATs) esterify a second acyl chain to the sn-2 position to produce PA. Newly synthesized PA may be further converted by either of two metabolic routes active in glycerophospholipid biosynthesis. The PA may be dephosphorylated by PA phosphatases (PAPs; also known as lipins) to produce diacylglycerol (DAG), which may be further metabolized to produce PC, PE, PS, and triglyceride (TG). Alternatively, PA may be acted upon by cytidine diphosphate (CDP) -DAG synthase to produce CDP-DAG, which may be further metabolized to produce CL, PI and PG [13] (Fig. 2.2).

#### 2.1.5 PC and PE Are Produced from Diacylglycerol

PC and PE are the most abundant glycerophospholipids, and in the Kennedy pathway two parallel pathways convert DAG to either PC or PE. The Kennedy pathway to produce PC proceeds in three sequential reactions: (a) choline kinase (CK) phosphorylates choline to form phosphocholine; (b) CTP:phosphocholine cytidyltransferase (PCYT1) forms CDP-choline from phosphocholine and cytidine triphosphate (CTP); and (c) CDP choline:1,2-DAG cholinephosphotransferase (CPT) utilizes CDP-choline and DAG as substrates to produce PC. In the analogous Kennedy pathway to produce PE, (a) ethanolamine kinase (EK) phosphorylates ethanolamine to form phosphoethanolamine; (b) CTP:phosphoethanolamine cytidylyltransfer-



**Fig. 2.2** Glycerophospholipid *de novo* synthesis and remodeling pathways

Basic mammalian pathways to produce diacyl-glycerophospholipids is shown (see text for details). Acyl chains at sn - 2 are specified during production of PA from LPA in Kennedy pathway (green circle), and may be extensively remodeled during Lands' cycle reactions (orange circles). Abbreviations: CDP - DAG cytidine diphosphatediacylglycerol, CDP - DGS cytidine diphosphate-diacylglycerol synthase, *DAG* diacylglycerol, *DGAT* diacylglycerol acyltransferase, *G3P* glycerol-3-phosphate, *GPAT* glycerol-3-phosphate acyltransferase, *LPC* lyso-PC, *LPE* lyso-PE, *LPG* lyso-PG, *LPI* lyso-PI, *LPS* lyso-PS, *MAG* monoacylglycerol, *PAP* phosphatidic acid phosphatase, *PEMT* PE methyltransferase, *PSD* PS decarboxylase, *PSS1* PS synthase 1, *PSS2* PS synthase 2, *TG* triglyceride

ase (PCYT2) forms CDP-ethanolamine from CTP and phosphoethanolamine; and (c) CDPethanolamine:1,2-diacylglycerol ethanolaminephosphotransferase (EPT) utilizes CDP-ethanolamine and DAG to produce PE [1].

#### 2.1.6 Additional Reactions to Generate Glycerophospholipid Classes

Other enzymatic reactions occur that mediate conversion of glycerophospholipids between classes. An alternative pathway to produce PC from PE exists that is called the PE methyltransferase (PEMT) pathway. In this pathway, PC production occurs via three sequential methylations of PE, all catalyzed by the enzyme PEMT. This pathway to PC production is only active in liver, where it accounts for ~30% of PC production [14].

PS is produced from PC and PE via base exchange reactions catalyzed by either of two enzymes, PS synthase (PSS) 1 or PSS2. Both enzymes produce PS in regions of the endoplasmic reticulum; PSS1 converts PC to PS, and PSS2 converts PE to PS. PS that has been transported to the mitochondria may be converted back to PE by the actions of another enzyme, PS decarboxylase (PSD) [1].

These pathways for production of PC, PE, and PS all proceed from DAG as a common intermediary. The pathways to produce the other classes of glycerophospholipids PI, CL, and PG all involve a series of enzymatic reactions that utilize CDP-DAG, produced from PA, as a precursor. Thus, PA is a common precursor molecule in de novo synthesis of all diacyl glycerophospholipids. PA is usually maintained at relatively low levels in cells, and newly synthesized PA may be rapidly converted to other glycerophospholipid classes. Therefore, the enzymes that regulate fatty chain compositions of PA also regulate the fatty chain compositions of all glycerophospholipids produced in Kennedy pathway [12].

#### 2.2 Regulation of Acyl Chain Compositions

During Kennedy pathway of glycerophospholipid synthesis, acyl chains are determined first when GPAT incorporates an acyl chains into sn-1 position of G3P to produce LPA, and again when LPAAT incorporates an acyl chain into sn-2 to produce PA. GPAT enzymes preferentially utilize saturated or mono-unsaturated acyl-CoA substrates for incorporation into sn-1, and different LPAAT enzymes vary in their acyl-CoA selectivities to utilize saturated, mono-unsaturated, or poly-unsaturated acyl-CoA substrates for incorporation into sn-2. Thus, GPAT and LPAAT enzyme selectivities are major determinants of fatty chain compositions at sn-1 and -2 of glycerophospholipids formed during the de novo synthesis. However, these selectivities do not fully account for the fatty chain diversity found in cellular membranes. The fatty chain compositions at sn-2 are further modified as part of a glycerophospholipid acyl chain remodeling pathway known as the Lands' cycle.

Rapid turnover of acyl chains in glycerophospholipids was originally described by William Lands in 1958 [15]. In radioactive tracer experiments of PC synthesis in lung tissue, Lands noticed the ratio of fatty acid incorporation to glycerol was several-fold higher in phospholipids compared to TGs. This suggested that in addition to the biosynthetic route leading to production of both TG and PC from a common DAG precursor, another mechanism to allow exchange of fatty acids on PC in absence of *de novo* synthesis may exist. Lands postulated existence of an enzyme system which catalyzes exchange of fatty acids via formation of a lysophospholipid intermediate followed by reacylation. This enzyme system is now known to catalyze the rapid turnover at sn-2 via cycles of PLA2-mediated deacylations and (LPLAT) lysophospholipid acyltransferase -mediated reacylations in a pathway distinct from de novo synthesis. PA production as part of the Kennedy pathway and glycerophospholipid remodeling during Lands' cycle are two distinct mechanisms by which acyl chains of glycerophospholipids are specified. Different sets of LPLATs function in these two pathways, and together these pathways account for the acyl chain diversity that exists in membrane glycerophospholipids.

#### 2.2.1 Distinct Sets of LPLATs Function During *de novo* and Remodeling Pathways

The first identified mammalian LPAATs, LPAAT1 and LPAAT2, were cloned by several independent groups in 1997 based on motifs conserved in homologous sequences from plants, bacteria, yeast, nematodes and viruses [16–20]. These motifs included regions of high homology, now known as 1-acylglycerol-3-phosphate *O*-acyltransferase (AGPAT) motifs I-IV, that are important for substrate binding and enzymatic activity [19, 21, 22]. Originally, eleven mammalian AGPAT family members were identified [23]; however, biochemical

characterization of the recombinant enzymes indicated many of these AGPAT family members primarily produce glycerolipids other than PA. Now five AGPAT family members are thought to function primarily as LPAATs by acylating LPA at sn-2 to produce PA [18, 24-27]. The other AGPAT family members have been reclassified according to their biochemical activities as GPATs, DHAPAT, or Lands' cycle LPLATs (such as LPCATs, LPEATs, LPIATs, LCLATs, and LPGATs) [21, 28]. Subsequently, non-AGPAT family LPLATs were also identified that are membrane bound O-acyltransferase (MBOAT) family members [29]. MBOAT family enzymes have activation motifs that are different from AGPAT motifs [30]. Currently four MBOAT family members are known to function as LPLATs in the Lands' cycle. The LPLATs of AGPAT and MBOAT families which function in the Kennedy pathway and Lands' cycle are summarized in Fig. 2.3.

	Family	LPLAT name	Product	HUGO symbol	Other Symbols
Kennedy pathway	AGPAT	LPAAT1 LPAAT2 LPAAT3 LPAAT4 AGPAT5	PA PA PA, PI PA	AGPAT1 AGPAT2 AGPAT3 AGPAT4 AGPAT5	LΡΑΑΤα LΡΑΑΤβ LΡΑΑΤγ LΡΑΑΤδ LΡΑΑΤε
Lands' cycle	AGPAT	LPEAT2 LCLAT1 LPCAT1 LPCAT2 LPGAT1	PE CL, PG, PI PC, PE, PAF PC, PE, PAF LPG	LPCAT4 LCLAT1 LPCAT1 LPCAT2 LPGAT1	AYTL3, AGPAT7 ALCAT1, AGPAT8 AYTL2, AGPAT9/10 AYTL1, IysoPAFAT NET8, KIAA0205
	MBOAT	LPCAT3 LPCAT4 LPEAT1 LPIAT1	PC, PE, PS PC, PE, PA PE, PS PI	LPCAT3 MBOAT2 MBOAT1 MBOAT7	OACT5, MBOAT5 OACT2 OACT1 LENG4, MBOA7



eling (orange box). Both LPCAT4/MBOAT2 and LPEAT2/LPCAT4 (in red letters) are referred to as "LPCAT4" and sometimes induce confusion in the literature

#### 2.3 LPAAT Enzymes Determine Acyl Chains During *de novo* Synthesis

In de novo synthesis of PA, following esterification of a fatty chain to G3P by GPATs, the next step involving esterification of a second fatty chain, to the sn-2 position, is catalyzed by LPAAT enzymes of the AGPAT family (Fig. 2.2). The first identified mammalian isoforms, LPAAT1 and LPAAT2, were cloned nearly simultaneously by several groups [16–19]. Eberhardt et al. identified motifs in human LPAAT2 that were conserved in homologous sequences from plants, bacteria, yeast, nematodes and viruses [19], and Aguado et al. reported similarly conserved sequences in human LPAAT1 the following year [20]. These regions included the regions now referred to as AGPAT motifs that are conserved in all AGPAT family members and important in substrate binding and enzymatic activity [21]. Mammalian LPAAT1 and LPAAT2 are the most evolutionarily conserved isoforms and suggested to have evolutionarily arisen as part of the earliest TG synthesis pathway, indicating the importance of these isoforms in TG as well as glycerophospholipid production [31].

#### 2.3.1 LPAAT1 Has Essential Functions in Multiple Tissues

LPAAT1 and LPAAT2 share high homology and have similar but not identical biochemical activities to utilize a variety of fatty chain-CoAs in producing PA [32]. LPAAT1 is broadly expressed, while LPAAT2 shows more restricted expression. Both LPAAT1 and LPAAT2 are expressed in adipocytes [32], however genetic loss of LPAAT2 activity causes congenital generalized lipodystrophy (CGL) [33], indicating that LPAAT2 has essential functions in adipocytes that are not compensated for by LPAAT1 [34].

To understand the biological functions of LPAAT1, LPAAT1 knockout (KO) mice were generated and phenotypically analyzed [35]. LPAAT1 KO mice had widespread disturbances in metabolism and glycerophospholipid homeostasis, caus-

ing pathological effects in multiple organ system. The LPAAT1 KO pups were born at less than Mendelian frequency, and those born had reduced body weights that almost did not increase after day 12. The LPAAT1 KO pups had decreased leptin and decreased plasma glucose, and about half died by 4 weeks of age. KO mice had markedly reduced epididymal fat pads, and cervical brown adipose tissue was also reduced but maintained in proportion to the reduced body weights. The LPAAT1 KO mice that survived to adult had reproductive abnormalities including impaired sperm development in males, and ovulation defects in females especially in late follicular maturation. LPAAT1 KO mice had features of seizures/epilepsy, and in hippocampus, where LPAAT1 is normally expressed, LPAAT1 KO mice tended to have reduced CA-region thickness, reduced neuron number, and impaired neurological function. Overall these results indicate LPAAT1 has essential functions in brain and testes, and is required for normal lipid homeostasis [35].

#### 2.3.2 LPAAT2 and Lipodystrophy

LPAAT2 is expressed in several tissues, showing highest expression in adipose tissue, pancreas and liver, and has broad specificity to utilize a variety of fatty acid-CoAs as substrates; including C14:0, C16:0, C18:1, and C18:2 -CoAs to produce PA [32]. LPAAT2 mutations are associated with congenital generalized lipodystrophy (CGL), also known as Berardinelli-Seip lipodystrophy [33]. Four subtypes of the disease are recognized based upon the causative gene mutation (LPAAT2, BSCL2, CAV1, or CAVIN1/PTRF), and LPAAT2 was identified as the causative gene of type 1 CGL through positional cloning [33, 36]. Disease-causing homozygous or compound heterozygous LPAAT2 mutations have been identified that include deletions, nonsense, missense, splice-site and those in the 3'-UTR mutations [34, 37].

CGL is a rare autosomal recessive disorder and the most striking feature is a total lack of subcutaneous body fat from birth. Children with this disorder have increased appetites, undergo accelerated growth, and develop metabolic complications including severe insulin resistance, hypertriglyceridemia, hepatic steatosis and early onset of diabetes. LPAAT2 KO mice have been used to elucidate the pathological mechanisms involved [38]. LPAAT2 KO mice had almost a complete lack of both white and brown adipose tissue, and just 2% body fat compared to 24-29% in wild-type mice. The LPAAT2 KO mice developed extreme insulin resistance, diabetes, and hepatic steatosis. Lipogenic gene expression was increased and fatty acid biosynthesis was accelerated in LPAAT2 KO mouse livers, accompanied by increased monoacylglycerol (MAG) acyltransferase isoform 1, suggesting the MAG pathway for TG production may be hyper-activated under conditions of LPAAT2 deficiency, possibly causing or contributing to the hepatic steatosis. Both LPAAT1 and LPAAT2 are normally expressed in adipose tissue, however LPAAT1 cannot compensate for the observed phenotypic abnormalities in LPAAT2 KO mice, underscoring the essential function of LPAAT2 in this tissue [38].

LPAAT2 functions in TG as well as glycerophospholipid synthesis, and it is possible that LPAAT2 mutations cause CGL primarily by inhibiting TG biosynthesis and storage in adipocytes. The lack of functional adipose tissue in CGL results in TG accumulations in other tissues like skeletal muscle and liver and contributes to the disrupted metabolic homeostasis [39]. It has been suggested that the lipodystrophy due to mutations in LPAAT2 and other CGL-causing genes might be mechanistically caused by defective lipid droplet formation in adipocytes. However, LPAAT2-generated phospholipids may also impact adipocyte function and TG storage, and further studies are required to understand the relative contribution of the LPAAT2-generated TGs and glycerophospholipids to metabolic homeostasis that is disrupted in CGL [34].

#### 2.3.3 LPAAT3 Incorporates DHA into Membranes

Consumption of fish oil, which is rich in very long-chain omega-3 fatty acids such as docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA), is well-known to promote cardiovascular health and have beneficial effects in other tissues [40]. Incorporation of very longchain, highly unsaturated chains like DHA and EPA into membrane glycerophospholipids may impart fluidity and flexibility to the membranes, as well as impact functions of membrane proteins [41]. DHA and EPA also have other biological functions as ligands for lipid sensing molecules such as PPARs [42] and as precursor molecules for specialized pro-resolving mediators [43]. Thus, incorporation of DHA and EPA into membrane glycerophospholipids may both alter membrane properties as well regulate their availability as ligands or precursors of bioactive molecules. We have focused on the functions of DHA in biological membranes, because DHA-CoA is selectively utilized as a substrate by LPAAT3 during glycerophospholipid synthesis [44, 45].

LPAAT3 was originally identified as an enzyme broadly expressed in tissues, regulated by PPAR-alpha in mouse heart [24], and involved in golgi dynamics [46]. Substrate specificity of LPAAT3 was shown to incorporate very long-chain polyunsaturated fatty acids into LPA [25, 44, 45] and to selectively incorporate DHA to increase production of DHAcontaining glycerophospholipids [45, 47–49]. LPAAT3 KO mice were generated, and they show marked and specific reductions in DHAcontaining glycerophospholipids in several tisdemonstrating a central role sues, for LPAAT3 in generation of DHA-containing glycerophospholipids [47, 48].

DHA-containing glycerophospholipids are abundant in several tissues including retina, testes, brain, heart, and skeletal muscle where they may have important physiological functions. DHA deficiency is associated with several human diseases including hyperlipidemia, cardiovascular disease, cognitive dysfunction, retinal degeneration, and male infertility [50]. We have investigated regulation and biological functions of LPAAT3-generated DHA-containing glycerophospholipids in sperm, retina, and skeletal muscle cells [47–49].

#### 2.3.4 LPAAT3 Incorporates DHA into Glycerophospholipids During Sperm Cell Development

Male infertility frequently occurs due to declines in sperm function. Mammalian sperm contains a high amount of very long-chain polyunsaturated fatty acids including DHA, and defective human sperm populations show declines in DHA in both esterified and unesterified fatty acid fractions [51]. Thus, high DHA content in sperm may be required to impart sperm cell plasma membranes with necessary properties for specialized functions involved in sperm cell maturation, morphology, motility, or fusion with the egg [52].

LPAAT3 was investigated as a candidate enzyme to incorporate DHA into sperm cell membranes. LPAAT3 was highly expressed in mouse testicles, and expression increased during development, coinciding with increased enzymatic activities to incorporate DHA into PC and PE [25, 45]. Immunohistochemical analyses indicated LPAAT3 was expressed both in Leydig cells as well as in spermatids, where LPAAT3 levels increased during spermatogenesis. DHA levels and metabolism in the testes were investigated in LPAAT3 KO mice. Microsome fractions from testes of LPAAT3 KO mice had moderately decreased LPAAT activities to utilize arachidonic acid-CoA but greatly decreased activities to utilize DHA-CoA. Moreover, DHA-containing PC, PE, and PS were highly and selectively decreased in testes, establishing the physiological role of LPAAT3 to incorporate DHA into membrane glycerophospholipids [47].

LPAAT3 KO mice showed male infertility due to defective spermiogenesis. LPAAT3 KO sperm had morphological defects, including sperm heads that bent backwards. Scanning electron microscopy revealed abnormal membranous structures wrapped around the sperm heads which should have been removed when the sperm were released into the seminiferous tubules. This suggests DHA-containing glycerophospholipids generated by LPAAT3 impart flexibility to sperm membranes that allows rapid endocytosis required for normal spermiation [47] and may partly explain why omega-3 supplementation promotes male fertility [53].

#### 2.3.5 LPAAT3 and DHA in Visual Function

Retinal tissue is abundant in DHA-containing glycerophospholipids, and DHA may have protective roles to prevent or delay the progression of several retinal disorders [54, 55]. The role of LPAAT3 in visual function was examined in wild-type and LPAAT3 KO mice [48]. In wildtype mice, LPAAT3 was highly expressed in retinas, and protein expression increased during development from age 11 days through 8 weeks. Compared to wild-type tissues, retinal tissues from LPAAT3 KO mice had decreased levels of DHA in several glycerophospholipids (PA, PC, PE, and PS) accompanied by corresponding increases in several arachidonic acid-containing species. Imaging mass spectrometry showed DHA-containing PC was present in outer segments of photoreceptors in wild-type mice but nearly absent in KO mice. Histologically, LPAAT3 KO retinas appeared normal until 2 weeks of age, but by 3-8 weeks of age they showed abnormal retinal layer morphologies including incomplete elongation of the outer segment, decreased thickness of the outer nuclear layers, and disordered disc morphology in photoreceptor cells. LPAAT3 KO mice showed attenuation of visual function as assessed by electroretinography, with 50-80% decreases in a- and b-wave amplitudes at 8 weeks of age. These results established that LPAAT3 has an essential role in visual function by producing DHA-containing glycerophospholipids, which are required to form, organize, and maintain proper disc shape in photoreceptor cells [48].

#### 2.3.6 LPAAT3 and DHA in Skeletal Muscle

Skeletal muscle is adaptive tissue, and adaptation of skeletal muscle to endurance exercise training is associated with metabolic benefits including reduced obesity and improved glucose handling. Although the biological function and mechanism is unknown, several studies indicate that DHAcontaining glycerophospholipids are also increased in endurance-trained muscle and correlates with oxidative status of the muscles [56– 60]. In mice, exercise training increased phospholipid-DHA in glycolytic extensor digitorum longus muscle, while phospholipid-DHA was constitutively high in oxidative soleus muscle even without training [56]. In rats, PE-DHA content was enriched in the oxidative compared to glycolytic vastus lateralis muscles [60]. In human volunteers, a 4 weeks regime of one-leg exercise training resulted in increased DHAcontaining GPLs that was accompanied by increased citrate synthase activity compared to the untrained leg [58].

Endurance training activates transcriptional responses that mediate adaptive responses in skeletal muscle. PPAR-delta and AMPK are activated by exercise and promote increased oxidative metabolic capacity and transitioning of glycolytic myofibers to more oxidative fiber types [61, 62]. PGC1-alpha is activated downstream of AMPK and is a coactivator of PPARdelta. In one study, mice overexpressing PGC1-alpha in skeletal muscle had enhanced levels of several DHA-containing glycerophospholipid species that were also increased by endurance training, indicating exercise-induced transcriptional responses may also enhance DHA incorporation into glycerophospholipids of muscle [56].

The role of LPAAT3 to produce DHAcontaining glycerophospholipids in skeletal muscle was investigated using primary skeletal muscle myoblasts. LPAAT3 expression was transiently upregulated during differentiation into myotubes and functioned to increase DHAcontaining PC and PE [49]. Treatment of differentiated myofibers with PPAR-delta and AMPK agonists also enhanced LPAAT3 expression and increased levels of DHA-containing PC and PE. These results showed LPAAT3 expression is regulated by two mechanisms in myoblasts, transient upregulation as part of the myogenic transcriptional program during myogenesis, and in differentiated myotubes in response to PPAR-delta and AMPK agonists. The PPAR-delta agonist GW1516 and AMPK agonist AICAR are exercise mimicking drugs, and when administered to mice promote endurance and transcriptionally upregulate genes that promote oxidative metabolism [63, 64]. LPAAT3 expression and DHA incorporation was upregulated by these same compounds in cultured myotubes, suggesting LPAAT3 may also be upregulated by exercise-induced pathways to increase DHA in endurance-trained muscle [49].

#### 2.4 Acyl Chain Remodeling by Lands' Cycle Enzymes

In glycerolipids, an asymmetric distribution of fatty acids at sn-1 and sn-2 positions imparts diversity to cellular membranes that cannot be fully explained enzymatic reactions of de novo glycerophospholipid synthesis, and further diversity at sn-2 especially is generated by cycles of deacylation and reacylation reactions known as Lands' cycle (remodeling pathway). PC, the most abundant glycerophospholipid in membranes, may undergo extensive Lands' cycle remodeling mediated by the actions of PLA2s and LPCAT enzymes. Several LPCAT enzymes of both the AGPAT and MBOAT families have been identified, and a growing list of functional roles pertinent to physiological and/or pathological conditions is being assigned to these enzymes, garnering much interest in their biological activities and therapeutic potentials. Similar remodeling of other classes of glycerophospholipids is mediated by other LPLATs classified as LPEATs, LCLATs, LPIATs, or LPGATs, and as their biological activities are being increasingly uncovered, interest in their potential as therapeutic targets is also emerging (Table 2.1).

#### 2.4.1 LPCAT1 Produces Lung Surfactant Essential for Respiratory Function

Pulmonary is surfactant essential for breathing and comprised mainly of lipids (~90%) and protein (~10%), and nearly half of the lipid is PC(16:0/16:0), dipalmitoyl-PC (DPPC) [65]. DPPC along with surfactant proteins form a specialized monolayer in alveolar spaces which

		Human
		disease/in
Enzyme	Major biological functions	vivo studies
LPAAT1	Brain, testes, lipid	[35]
	homeostasis	
LPAAT2	Lipid homeostasis,	[33, 38]
	lipodystrophy	
LPAAT3	Sperm maturation, visual	[47, 48]
	function, muscle	
LPCAT1	Lung surfactant, visual	[76–78, 81]
	function, cancer, non-	
	inflammatory PAF	
	production	
LPCAT2	Inflammatory PAF	[92]
	production, neuropathic pain	
LPCAT3	TG transport, VLDL	[115–119,
	secretion and lipogenesis in	126, 127]
	liver, lipid absorption in	
	small intestine	
LPIAT1	Brain development, liver	[134–136]
	disease modifier	

 Table 2.1
 LPLATs as possible therapeutic targets

reduces surface tension, facilitates gas exchange, and prevents alveolar collapse [66, 67]. Pulmonary surfactant is produced by alveolar type II cells, and deficiency of pulmonary surfactant is associated with several pulmonary diseases. Respiratory distress syndrome, the leading cause of death in pre-term infants, is caused by lack of surfactant in premature lung structures [68, 69].

Identification of the biosynthetic routes of DPPC production in lung had been long sought, and both the Kennedy pathway and Lands' cycle thought to have significant were roles. Involvement of Lands' cycle enzymes was indicated by biochemical activities present in alveolar type II cells and rat lung tissue to incorporate labelled palmitate (C16:0) preferentially into the sn-2 position of DPPC rather than TGs, presumably through acylation of LPC [70, 71]. LPCAT activities had been known to exist in several tissues, and in 2006 the first mammalian LPCAT enzyme was independently identified by two groups [72, 73]. Both studies identified LPCAT1 as the candidate enzyme present in alveolar type II cells that produces DPPC.

LPCAT1 has AGPAT motifs, and Nakanishi et al. cloned mouse LPCAT1 based on homology to other AGPAT family members [72]. Mouse

LPCAT1 was highly expressed in lung and had activity to produce PC using saturated acyl-CoA as donors. Rat LPCAT1 was also highly expressed in lung and enriched in alveolar type II cells rather than macrophages. Later, they also characterized the human LPCAT1 homolog, which was suggested to also produce DPPC in lung [74]. Chen et al. also identified LPCAT1 as an enzyme that was upregulated in mouse and rat lungs shortly before birth. They cloned both the mouse and rat enzymes, which were 99% identical at amino acid level. The enzymes both possessed a  $H(X)_4D$  activation domain sequence that was known to be present in other AGPAT family members [75]. Rat LPCAT1 was overexpressed in mammalian cells and produced DPPC [73].

These studies indicated that LPCAT1 may be responsible for production of DPPC in pulmonary surfactant [72–74]. Additional studies utilizing LPCAT1-deficient mice generated by two different groups have confirmed that LPCAT1 is a major producer of DPPC in pulmonary surfactant [76, 77]. The two LPCAT1-deficient mouse strains showed varying degrees of respiratory dysfunction; this variation may be due to the genetic backgrounds or different gene deletion strategies. Bridges et al. generated mice bearing a hypomorphic allele of LPCAT1. These mice had difficulty to transition to air breathing and showed varying degrees of perinatal lethality due to respiratory distress. Perinatal lethality correlated with decreased LPCAT1 mRNA, decreased disaturated PC in lungs, and functionally poor surfactant [76]. Harayama et al. generated LPCAT1 KO mice lacking exon 3 which contains the  $H(X)_4D$ AGPAT activation domain. These mice had dramatically reduced LPCAT activity to utilize C16:0-CoA. The KO mice had ~40% reduced DPPC in lung but did not show major signs of neonatal lung distress. However, the mice had enhanced susceptibility to a ventilator-induced lung injury model, which was partially rescued by intratracheal administration of DPPC [77]. These studies establish a critical function for LPCAT1 in producing sufficient levels of DPPC in pulmonary surfactant to prevent respiratory distress or failure under different physiological challenges.

#### 2.4.2 LPCAT1 and Cancer

Besides producing DPPC in pulmonary surfactant, LPCAT1 has additional important roles in physiological and disease states. LPCAT1 is important for visual function, and a natural mutation in LPCAT1 in rd11 mice causes rod and cone cell loss, followed by retinal degeneration [78]. LPCAT1 also has a role to produce PAF under noninflammatory conditions [22]. Another reported function of LPCAT1 is to protect against polyunsaturated fatty acid-mediated cytotoxicity [79].

In addition, LPCAT1 has a role in cancer. LPCAT1 expression was reported to be high or involved in progression of a variety of cancers including colorectal adenocarcinomas, prostate cancer, lung adenocarcinoma, hepatocellular carcinoma, oral squamous cell carcinoma, breast cancer, esophageal cancer, gastric cancer, clear cell renal cell carcinoma, and glioblastoma [80-82]. Recently Bi et al. reported LPCAT1 is highly upregulated in a wide array of cancers, and LPCAT1-produced disaturated PCs may be required for proliferative signaling via oncogenic growth factor signaling [81]. Initially they examined the impact of EGFRvIII, an activating mutation of EGFR and common driver in glioblastoma, on membrane compositions in gliocells. In EGFRvIII-transduced blastoma glioblastoma cells, disaturated PC species and LPCAT1 mRNA were increased, and shRNAknockdown of LPCAT1 reduced disaturated PC species, particularly PC(28:0), PC(30:0), and PC(32:0). Knockdown of LPCAT1 in glioblastoma cancer cells harboring EGFRvIII mutations inhibited EGFR phosphorylation and signaling, and this could be reversed by addition of either DPPC liposomes or saturated C14:0/C16:0 fatty acids. Knockdown of LPCAT1 also inhibited glioblastoma cell viability and colony-forming ability, and this was reversed by supplementation of DPPC or a constitutively-active AKT allele. Their results suggest LPCAT1 may promote glioblastoma growth by maintaining high saturated PC levels that support EGFR oncogenic signaling.

The authors went on to show that LPCAT1 amplification is a widespread occurrence across

all human cancers. They examined LPCAT1 expression in publicly available databases, and LPCAT1 was found to have increased copy number in 30% of all cancer patients, and inverse correlations between LPCAT1 expression and overall survival was detected in multiple cancer types. LPCAT1 knockdown reduced cancer cell viability *in vitro*, and inducible genetic depletion of LPCAT1 inhibited tumor growth in mouse xenograft models. Their study suggests LPCAT1 inhibition may be a promising therapeutic strategy for a variety of oncogenic growth factor driven cancers [81].

#### 2.4.3 LPCAT2 Produces PAF

LPCAT2 was identified in 2007 as a PAFproducing enzyme in the AGPAT family [83]. In the following year, LPCAT1, which had already been identified as the first LPCAT enzyme [72], was also reported to also have PAF-producing activity [22, 77]. The enzymes having lyso-PAF acetyltransferase activity had been long-sought following the first identification of PAF in 1972 as the substance responsible for platelet aggregation [84]. LPCAT2 can synthesize not only PAF but also polyunsaturated fatty acid-containing PC [77, 83]. Unlike most other LPLATs, the activity of LPCAT2 is calcium ion-dependent. LPCAT2 is expressed in inflammatory cells, such as macrophages and neutrophils, and the enhancement of its PAF biosynthesis activity by lipopolysaccharide (LPS) stimulation is another characteristic of LPCAT2 [83].

Recent studies demonstrated three distinct mechanisms that regulate LPCAT2 activity and expression level in macrophages (Fig. 2.4). First, LPCAT2 is rapidly activated (within 30 s) after either PAF or adenosine triphosphate (ATP) stimulation via intracellular calcium-stimulated activation of PLC $\beta$ -PKC $\alpha$  signaling. These pathways induce phosphorylation of LPCAT2 at Ser-34, which enhances LPCAT2's PAF biosynthesis activity [85]. Another mechanism of phosphorylation is via toll-like receptor 4 (TLR4) activation. Thirty minutes of stimulation by the TLR4 ligand LPS activates the downstream pathway, MyD88-p38 MAPK-MK2, leading to phosphorylation of LPCAT2 at the same site Ser-34 as  $Ca^{2+}$ -PLC $\beta$ -PKC $\alpha$  signaling [86]. Finally, LPS stimulation for 16 h increases mRNA expression of LPCAT2, which is attenuated by co-treatment with the steroidal anti-inflammatory drug dexamethasone [83]. These studies indicate LPCAT2 is upregulated and shows enhanced PAFproducing activity as part of inflammatory responses, but this is not the case for LPCAT1.

Although it has been clearly demonstrated that LPCAT1 produces PAF in *in vitro* assays, LPCAT1's activity was not enhanced by inflammatory stimuli [85, 86]. It has been suggested that LPCAT1 may have a role to limit PAF production during the onset of diabetic retinopathy by catalyzing synthesis of alkyl-PC from lyso-PAF and acyl-CoA, thereby limiting lyso-PAF availability for LPCAT2-mediated PAF production [87]. However, further investigations are needed to clarify the roles of LPCAT1 to produce or regulate production of PAF *in vivo*.

#### 2.4.4 LPCAT2 and PAF Production in Neuropathic Pain

Several reports have demonstrated LPCAT2 is involved in various pathological conditions such as allergic asthma [88], colorectal cancer resistance [89], nonalcoholic fatty liver disease [90], and multiple sclerosis [91]. It was recently reported that LPCAT2 is involved in neuropathic pain, a highly debilitating chronic pain syndrome [92]. Neuropathic pain occurs from damage to the nervous system; such as by trauma, cancer, diabetes, infection or chemotherapy; which does not resolve even after normal tissue healing. Unfortunately, although clinical neuropathic pain affects 7-10% of the human population [93], the cardinal symptom allodynia, pain caused by innocuous stimuli, is refractory to currently available treatments [94, 95].

In the 1980s, the involvement of PAF in pain processes was indicated by studies that observed enhancement of pain sensitivity following local injection of PAF into skin of animals [96, 97] and humans [98]. In addition, intrathecal PAF

injection into the spinal cord also produced allodynia, but injection of its precursor lyso-PAF did not [99, 100]. The biological activities of PAF are elicited via its cognate G protein-coupled receptor, PAF receptor (PAFR) [101]. In rodent models of nerve injury-induced neuropathic pain, it has been reported that treatment with PAFR antagonists, such as WEB2086 or CV-3988, alleviate allodynia symptoms [100, 102]. In accord with this, neuropathic allodynia was attenuated in PAFR KO mice [100]. Both PAFR and LPCAT2 are highly expressed in macrophages (in the periphery) and microglia (in the spinal cord). Peripheral nerve injury increases the number of macrophages in the dorsal root ganglia, where cell bodies of primary sensory neurons are present, and also increases microglia in the spinal dorsal horn. Along with these increases, the protein expressions of PAFR and LPCAT2 also rise [92, 100]. Recently, LPCAT2 KO mice were established, and while the abundance of other PCs were similar to wild-type mice, PAF levels in the spinal cord of this mouse were decreased to below detectable levels under normal physiological conditions. Moreover, nerve injury-induced neuropathic allodynia was attenuated in LPCAT2 KO mice, similar to the PAFR KO mice [92]. These results indicate the importance of LPCAT2-PAFR axis in the pathology of neuropathic pain.

Several studies on the pathogenesis of neuropathic pain have reported that peripheral nerve injury significantly increases the expression levels of several ATP receptors (i.e. P2X4R, P2X7R, P2Y12R) and induces ATP release, via vesicular nucleotide transporter, in the spinal dorsal horn [103–106]. Furthermore, increased TLR4 expression and phosphorylation of p38 MAPK in microglia were also observed in response to nerve injury [107, 108]. Nerve injury also induces LPCAT2 PAF-producing activity by activating ATP receptors and TLR4 signaling, and PAF stimulation induces activation of LPCAT2 via PAFR to further enhance PAF production. Therefore, a positive feedback "PAF-pain loop" is suggested, as PAF-induced increases in PAF production resulted in exacerbation and chronicity of neuropathic pain [92] (Fig. 2.4).



Fig. 2.4 Regulatory mechanisms of LPCAT2-produced PAF levels and the PAF-Pain Loop hypothesis (i) PAFR- and/or ATP receptors-mediated second-scale phosphorylation of LPCAT2, (ii) TLR4 and its downstream pathways-mediated minute-scale phosphorylation,

Many pharmaceutical companies have already developed PAFR antagonists as possible drug candidates to treat inflammatory conditions such as asthma, but in most cases these drugs have so far shown limited efficacy [10, 109]. However, in light of LPCAT2's role in the "PAF-pain loop", it may be warranted to re-evaluate the possible clinical utility of these PAFR antagonists as analgesics. Moreover, LPCAT2 may also be a novel therapeutic target for analgesic drugs, suggesting that PAF loop blockers such as PAFR antagonists or LPCAT2 inhibitors might represent a new class of analgesic drugs different from the current classes of nonsteroidal antiinflammatory drugs (NSAIDs) and opioids. Also, because PAF feedback loop may operate not only in neuropathic pain but also in various other pathological conditions with PAF involvement, a recently

and (iii) hour-scale LPCAT2 mRNA upregulation via TLR4. Nerve injury may activate these regulatory systems and increase PAF levels. The increased PAF further enhances PAFR-mediated PAF production, and may result in exacerbation of neuropathic pain (PAF-Pain Loop)

identified selective LPCAT2 inhibitor, TSI-01 [110], and its derivatives also have potential to contribute to the development of novel drugs for PAFrelated diseases. Importantly, the biological significance of the activities of LPCAT2 to produce PCs other than PAF requires further investigation, which may expand our understanding of LPCAT2 as a therapeutic target [92].

#### 2.4.5 LPCAT3 Functions in Small Intestine, Liver and Several Cells

LPCAT3 is a member of the MBOAT family that catalyzes the transfer reaction of acyl group to proteins and lipids [30]. LPCAT3 synthesizes linoleic acid (C18:2) and arachidonic acid (C20:4) containing PC, PE and PS from LPC, LPE and LPS [29, 111–113]. Recently, several reports suggested that LPCAT3 has several important roles in lipid homeostasis [82, 114]. LPCAT3 global KO mice showed neonatal lethality and died between postnatal day 2 and 3 weeks [115-117]. It was found to be caused by nutritional failure in small intestine because the pups were partially rescued by injections of 10% glucose solution or oral gavage with PCs/olive oil [115, 117]. However, the different studies reported different effects of LPCAT3 deficiency on TG accumulation in small intestine. We reported LPCAT3 deletion caused dramatic accumulation of lipid droplets in enterocytes of global LPCAT3 KO pups [116], and Rong et al. observed a similar accumulation in intestine-specific KO pups [115]. In contrast, Li et al. reported no TG accumulation in intestines of LPCAT3 global KO pups [117], nor following intestine-specific LPCAT3 depletion in adult mice [118]. It is unclear why intestinal lipid accumulation was observed in some studies but not others; the differences might reflect the different gene deletion strategies, gene-targeted-regions, or other factors.

The expression of proteins related to lipid absorption in enterocytes, such as NPC1L1, CD36 and FATP4, were decreased in LPCAT3 global KO mice [117] as well as following inducible intestine-specific depletion [118]. Body weight was decreased following intestine-specific LPCAT3 depletion, and total TG and cholesterol levels were also decreased in plasma and serum [115, 119]. In addition, small intestines were longer and intestinal stem cells showed hyperproliferation in the intestine-specific LPCAT3-KO mice [117, 119]. These results suggest that arachidonic acid rich cell membranes synthesized by LPCAT3 have an essential role in intestinal absorption of dietary lipid and may also have a function to limit proliferation of intestinal stem cells. The role in lipid absorption suggests that intestine-specific inhibition of LPCAT3 might be useful therapeutic strategy to а treat hyperlipidemia.

LPCAT3 was also highly expressed in liver [29, 111]. Its expression was regulated by LXR and PPAR-delta in hepatocytes [120–123]. LXR activates lipogenic genes such as SREBP-1c, SCD-1 and FAS [124, 125]; and plasma TG and phospholipids were changed in LXR agonist-treated mouse as well as LXR-alpha/beta double-KO mice [125]. These results suggest that LPCAT3 could contribute to fatty acid homeostasis in liver. In fact, plasma VLDL secretion was increased by hepatic LPCAT3 knockdown in mice [126]; and glucose tolerance was improved and plasma TG levels were decreased by transient overexpression of LPCAT3 in liver [127].

Compared to the changes observed following transient knockdown and overexpression, liver TG was increased and plasma TG, VLDL secretion levels, and VLDL particle size were decreased in LPCAT3 KO mice [115, 116]. These differences between transient LPCAT3 knockdown and LPCAT3 KO mice may reflect residual LPCAT3-generated arachidonic acid- and linoleic acid-containing phospholipids and lysophospholipids that are present under knockdown conditions, due to limited duration or incomplete efficiency of knockdown by the LPCAT3targeting shRNAs. Both the effective transport of TG by MTP (microsomal triglyceride transfer protein) as well as SREBP-1c maturation in the endoplasmic reticulum by protein cleavage can be promoted by arachidonic acid-containing phospholipids synthesized by LPCAT3 [116, 128], further supporting that LPCAT3 inhibition might improve dyslipidemia.

LPCAT3 has also been shown to function or have roles in other pathological conditions. LPCAT3 expression levels inversely correlated with the disease stage of atherosclerosis, and atherosclerosis was facilitated by LPCAT3 deletion in macrophages [123, 129, 130]. LPCAT3 may also function in cancer because intestinal tumorigenesis was promoted by LPCAT3 deletion [119]. LPCAT3 also has important roles in adipocyte differentiation and macrophage polarization [131, 132], indicating LPCAT3 has diverse physiological roles and may be a promising therapeutic target in several diseases.

#### 2.4.6 LPIAT1 Functions in Brain Development and Modifies Liver Disease Risk

LPIAT1 is a MBOAT family member and incorporates arachidonic acid-CoA into LPI to produce arachidonic acid-containing PI [133]. Two independent groups generated global LPIAT1 KO mice and reported the KO mice are small, born at low frequency, and have poor survival. Both groups also reported abnormal brain development and decreased arachidonic acidcontaining PI and PI phosphates in brain [134, 135]. Lee et al. measured LPLAT activities in the KO tissues, and activity to incorporate arachidonic acid-CoA into LPI was almost abolished in several tissues including brain, whereas the activity to incorporate arachidonic acid-CoA into other lysophospholipids in brain was almost unchanged, establishing that LPIAT1 is a predominant LPIAT involved in production of arachidonic acid-containing PI in mice [134]. Lee et al. also performed detailed analyses of the defective brain development and reported delayed neuronal migration, decreased sizes of cerebral cortex and hippocampus, and disordered cortical lamination and neuronal processes [134]. Anderson et al. reported abnormal brain development as well, and arachidonic acid-containing PI and PI phosphates were decreased in both brain and liver. They also reported that in brain, but not in liver, arachidonic acid-containing PC(38:4) and PE(38:4) were both decreased by about half, which might also contribute to the defective brain development [135]. In humans, homozygous inactivating mutations of LPIAT1 are associated with intellectual disability, autism-like symptoms, and epilepsy; indicating a critical role for LPIAT1-generated arachidonic acid-containing PI in brain development in humans as well as mice [136].

LPIAT1 is also suggested to be a genetic modifier of liver disease risk. Liver cirrhosis is a major disease burden worldwide in terms of disability and death and may develop due to a number of different factors that cause chronic liver injury such as hepatitis C, hepatitis B, alcoholism, non-alcoholic steatohepatitis, and autoim-

mune hepatitis. High variabilities in disease progression exist due partly to genetic modifiers, and a common genetic variant of LPIAT1 (rs641738) has been reported to be associated with an array of alcohol and non-alcoholic fatty liver diseases. The role of LPIAT1 rs641738 variant in modifying fatty liver disease is not well understood but apparently involves altering LPIAT1 expression and the acyl chain compositions of membrane glycerophospholipids, which is proposed to affect inflammation-driven hepatic fibrosis and other symptoms in a variety of contexts including alcohol-related cirrhosis [137], non-alcoholic fatty liver disease [138], and hepatitis C [139]. However, results among different studies with different cohorts of patients have been inconsistent with some studies not supporting LPIAT1 rs641738 as a disease-modifying variant, suggesting that liver disease may have different genetic factors in different populations [140]. Additional mechanistic studies are required to understand the roles of LPIAT1 in liver disease and possible function as a genetic modifier.

#### 2.5 Summary and Future Directions

It has become increasingly clear that the glycerophospholipid compositions of cell membranes, including their fatty chain compositions, affects a variety of physiological and disease states. Identification and biochemical characterization of the key enzymes involved, including LPLATs of the AGPAT and MBOAT families, has shed light on how the membrane compositions may be regulated in different biological contexts. Genetic deletion of these enzymes in mice has revealed unique physiological roles of many of these enzymes, and is expected to translate into new understanding of related human physiological and pathological conditions. Development of potent and selective inhibitors/activators of LPLATs will allow further discovery and elucidation of their biological functions, and pave the way to realize their promise as therapeutic targets.

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### Druggable Prostanoid Pathway

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#### Abstract

Prostanoids (prostaglandins, prostacyclin and thromboxane) belong to the oxylipin family of biologically active lipids generated from arachidonic acid (AA). Protanoids control numerous physiological and pathological processes. Cyclooxygenase (COX) is a rate-limiting enzyme involved in the conversion of AA into prostanoids. There are two COX isozymes: the constitutive COX-1 and the inducible COX-2. COX-1 and COX-2 have similar structures, catalytic activities, and subcellular localizations but differ in patterns of expression and biological functions. Non-selective COX-1/2 or traditional, non-steroidal antiinflammatory drugs (tNSAIDs) target both COX isoforms and are widely used to relieve pain, fever and inflammation. However, the use of NSAIDs is associated with various side effects, particularly in the gastrointestinal tract. NSAIDs selective for COX-2 inhibition (coxibs) were purposefully designed to spare

gastrointestinal toxicity, but predisposed patients to increased cardiovascular risks. These health complications from NSAIDs prompted interest in the downstream effectors of the COX enzymes as novel drug targets. This chapter describes various safety issues with tNSAIDs and coxibs, and discusses the current development of novel classes of drugs targeting the prostanoid pathway, including nitrogen oxide- and hydrogen sulfide-releasing NSAIDs, inhibitors of prostanoid synthases, dual inhibitors, and prostanoid receptor agonists and antagonists.

#### Keywords

Prostanoids · Prostaglandin · Cyclooxygenase · NSAID · mPGES-1 inhibitor · Prostanoid receptor agonist/antagonist

#### 3.1 Overview/History

Prostanoids are bioactive oxylipins formed from arachidonic acid (AA, 5,8,11,14-eicosatetraenoic acid), a polyunsaturated omega-6 fatty acid (FA) 20:4( $\omega$ -6) esterified to the membrane phospholipids. Prostanoids include prostaglandin (PG) E<sub>2</sub> (PGE<sub>2</sub>), F<sub>2\alpha</sub> (PGF<sub>2\alpha</sub>), D<sub>2</sub> (PGD<sub>2</sub>), prostaglandin I<sub>2</sub> (PGI<sub>2</sub>), commonly known as prostacyclin, and thromboxane A<sub>2</sub> (TxA<sub>2</sub>) [1]. The era of prostanoid

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research started in the early 1930 with the observation by Kurzrok and Leib that human semen altered the contractile activity of human uterine strips [2]. It followed by the discovery by Goldblatt and von Euler that identified lipid-soluble acids present in the seminal vesicles, named prostaglandins, because erroneously believed to be produced in the prostate gland, that caused smooth musclecontracting and vasodepressor activities [3, 4]. Bergström isolated the first prostaglandins (PGE<sub>1</sub> and  $PGF_{2\alpha}$ ) in 1957 [5], and Bergström and Samuelsson showed in detail how prostaglandins form from AAand determined their structures in 1963 [6]. In 1971, Vane showed that acetylsalicylic acid, the active compound present in aspirinlike drugs, worked by inhibiting the formation of prostaglandins [7]. In 1976, Vane isolated vascular wall-synthesized PGI<sub>2</sub>, which caused blood vessel relaxation and inhibited platelet function by counteracting thromboxane action [8]. Vane, Bergström and Samuelsson received the 1982 Nobel Prize in Physiology or Medicine for their pioneering work on prostaglandins (www.nobel.se/medicine/laureates/1982/index.html).

The synthesis of prostanoids is the result of the coordinated actions of the activity of several enzymes (Fig. 3.1). AA is first released from membrane phospholipids by phospholipase  $A_2$  [9]. Free AA then can be metabolized by prostaglandin endoperoxide G/H synthase (PTGS), also known as cyclooxygenase (COX), into PGH<sub>2</sub>. PGH<sub>2</sub> is an unstable cyclic endoperoxide that is subjected to further metabolism into TxA<sub>2</sub>, PGI<sub>2</sub>, PGD<sub>2</sub>, PGE<sub>2</sub>, and PGF<sub>2 $\alpha$ </sub> by tissue-specific isomerases, synthases and hydrolases, located on the cytosolic surface of the endoplasmic reticulum or in the cytosol. TxA synthase (TxS), PGI synthase (PGIS) and PGF synthase (PGFS) are involved in the biosynthesis of  $TxA_2$ , PGI<sub>2</sub>, PGF<sub>2 $\alpha$ </sub>, respectively. PGE<sub>2</sub> can be generated by the action of cytosolic PGE synthase (cPGES) and microsomal PGES (mPGES)-1 and 2 [10]. PGD<sub>2</sub> is generated mainly by the action of hematopoietic PGDS (H-PGDS) and to a lesser extent by lipocalin-like PGDS (L-PGDS) [11]. There is a preferential coupling of individual synthases to either COX-1 or COX-2: COX-1 has a preference for coupling with TXAS, PGFS and

cPGES; COX-2 has a preference for PGIS and mPGES-1 [12]. Thus, through a combination of regulated expression, tissue selective expression and specific COX-synthase coupling, COX products are formed in a cell-type or disease-state specific manner, such that most cells make one or two dominant prostanoids.

Prostanoids are autacoids, which act locally on surrounding cells, in an autocrine and paracrine fashion, to mediate a diverse range of physiological and pathological processes. Prostanoids are synthesized de-novo in a cell, have a short half-life, on average less than 1 min, and are inactivated in two steps; prostanoid metabolites formed in the liver are eliminated mainly in the urine. The measure of these inert but chemically stable urinary metabolites by mass-spectrometry provides insights into their *in vivo* biology and pharmacology [13, 14].

Prostanoids act through G-protein coupled receptors localized at the plasma membrane or at the nuclear envelope and characterized by different downstream signal transduction pathways. There are four receptors to bind PGE<sub>2</sub> (EP<sub>1,2,3,4</sub>), two receptors to bind PGD<sub>2</sub> (DP<sub>1</sub> and DP<sub>2</sub>) and one receptor each to bind PGF<sub>2a</sub> (FP), PGI<sub>2</sub> (IP) and TxA<sub>2</sub> (TP; with alpha and beta subtypes found only in humans), with additional subtypes generated through alternative splicing on the cell membrane (Fig. 3.1) [15]. Prostanoid receptors are linked to specific G-proteins, which in turn facilitate changes in the concentrations of intracellular signaling [15].

Prostanoid receptors can be categorized in 3 functional clusters that reflect their biological action, cellular signaling and phylogenetic origin:

- DP<sub>1</sub>, EP<sub>2</sub>, EP<sub>4</sub> and IP, the "relaxant" receptors, which signal through Gα<sub>s</sub>-mediated increases in intracellular cyclic adenosine monophosphate (cAMP);
- TP, FP and EP<sub>1</sub>, the "contractile" receptors, which signal through  $G\alpha_q$ -mediated increases in inositol phosphate and intracellular Ca<sup>2+</sup>;
- EP<sub>3</sub> and DP<sub>2</sub>, the "inhibitory" receptors, which signal through Gα<sub>i</sub>-mediated decreases cAMP formation [15].


**Fig. 3.1** Biosynthetic pathway of prostanoids and druggable targets. Drugs marketed for clinical use are shown in blue. Compounds under clinical development are

shown in red. Agonists are indicated with the symbol  $\leftarrow$ . Antagonists/Inhibitors are indicated with the symbol  $\vdash$ 

### 3.2 Cyclooxygenases

COX exists in two isoforms, referred to as COX-1 (the constitutive isoform) and COX-2 (the inducible isoform), that arose from gene duplication early in evolution [1]. COXs are heme-containing glycoproteins, members of the myeloperoxidase superfamily, which possess both cyclooxygenase and peroxidase activities [16]. COXs are encoded by genes localized on different chromosomes. The intron-exon junctions in the two genes are highly conserved and few significant differences are seen in the dimerization, membrane-binding and catalytic domains between COXs from different species. COXs are glycosylated on asparagine in all organisms and the N-glycosylation appears to be necessary for proper protein folding [17]. There is 61% amino acid homology in human COXs.

Both COX isoforms are homodimers that function as conformational heterodimers having allosteric and catalytic subunits. Each COX monomer consists of three structural domains: an N-terminal epidermal growth factor-like domain that functions as a dimerization domain, a membrane binding domain, and a large C-terminal globular catalytic domain, which has the COX and peroxidase active sites [18]. Both COX-1 and COX-2 work as a dimer located in the luminal surface of the endoplasmic reticulum and associated with the inner membrane of the nuclear envelope. COX-2 is also located in the Golgi apparatus and associated with lipid droplets. COX-1 and COX-2 dimers exhibit half-of-sites activity, where each monomer binds distinct ligands [19]. COX-1/COX-2 heterodimers may also exist, but their role in biology remains to be established [20].

Despite the close similarities in structure, catalytic function, and subcellular localization, COX-1 and COX-2 differ markedly in their profiles of expression. There are several transcriptional regulatory elements in the COX-2, but not the COX-1, promoter region [21]. An important structural difference between the active sites of COX-1 and COX-2 is a substitution of isoleucine 523 in COX-1 for a valine in COX-2. The switch of a voluminous amino acid residue (isoleucine) with a less bulky one (valine) opens a hydrophobic pocket adjacent to the active site channel in COX-2 that has allowed the development of selective COX-2 inhibitors [22]. Another difference between COX-1 and COX-2 is the ability of COX-2 to efficiently oxygenate neutral derivatives of AA, such as 2-arachidonoylglycerol and anandamide, two endogenous ligands for the cannabinoid receptors [19]. Moreover, COX-2 has broader substrate specificity than COX-1 and can oxygenate other FAs [19].

In simplistic terms, COX-1 is ubiquitously and constitutively expressed in mammalian tissues and cells, and it is the dominant (but not exclusive) source of prostanoids for physiological functions. COX-2, in contrast, is generally present in mammalian tissues at very low levels, but it is readily induced by inflammatory mediators and mitogenic stimuli, and thus, contributes to the formation of prostanoids in pathophysiological conditions. COX-2 is constitutively expressed in some tissues like the brain, kidney, testis and vasculature [15]. However, both COXs contribute to the generation of autoregulatory and homeostatic prostanoids, and both enzymes can contribute to prostanoid formation during pathophysiological conditions.

# 3.3 Biological Functions of Prostanoids

Prostanoids are implicated in controlling physiological (i.e., gastric cytoprotection, renal function, platelet aggregation and vascular tone) and pathophysiological (i.e., inflammation, pain, fever, asthma) processes [23]. COX-1 is the main isoform expressed in the gastrointestinal tract, where prostanoids play a protective role by regulating the formation of gastric acid and mucosal blood flow and the secretion of gastrin, pepsin, bicarbonate and mucus secretion [24, 25]. Both COXs are expressed in the kidney: COX-1 is present mainly in the cortical and medullary collecting ducts, mesangial cells, arteriolar endothelium, and the epithelium of Bowman's capsule, while COX-2 is localized in the macula densa, podocytes and cortical thick ascending limb. PGE<sub>2</sub> and PGI<sub>2</sub> maintain renal blood flow and glomerular filtration rate, and regulate water and sodium excretion. On the opposite,  $TxA_2$  and  $PGF_{2\alpha}$  reduce renal blood flow and glomerular filtration rate [26]. Both COX-1 and COX-2 are expressed in the vasculature, where prostanoids can promote or limit the interactions between the vessel walls and blood cells and control the local vascular tone. Studies in animal models have revealed that COX-2 is implicated in the development of vascular remodeling, atherothrombotic events and aneurysm formation [23]. In the blood vessels, the main products of both endothelial and smooth muscle cell layers are PGI<sub>2</sub> and PGE<sub>2</sub>. Normal blood flow shear forces make COX-2 responsible for most PGI<sub>2</sub> production in the blood vessels [27, 28]. PGI<sub>2</sub> mediates vasodilatation, inhibits leukocyte adhesion, prevents smooth muscle cell proliferation, and opposes platelet activation. PGE<sub>2</sub> has vasodilatory and antiplatelet properties by activating  $EP_2$  and  $EP_4$ , but it also can favor vascular hyperplasia and vasoconstriction from activation of EP<sub>1</sub> and EP<sub>3</sub> [29]. PGD<sub>2</sub> mediates vasodilation and increases vascular permeability [30], relaxation of vascular and nonvascular smooth muscle [31, 32], inhibition of platelet aggregation [33]. L-PGDSderived PGD<sub>2</sub> can control blood pressure and thrombosis through an autocrine effect on the vasculature or through L-PGDS functioning as a lipophilic carrier [11].  $PGF_{2\alpha}$  is a potent constrictor of both pulmonary arteries and veins in humans. TxA<sub>2</sub> mediates vasoconstrictions and platelet aggregation. TxA<sub>2</sub> is the main product synthetized by platelet COX-1, the only COX isoform expressed in mature platelets. TxA<sub>2</sub> causes vasoconstriction and platelet aggregation. It amplifies further platelet activation by other platelet agonists and the recruitment of other platelets [29]. Consequently, for effective inhibition of platelet activation, platelet TxA<sub>2</sub> blockade must be almost complete (~95%) to limit thrombotic events [34].

Prostanoids are involved in multiple stages of the inflammatory response and they mediate the cardinal signs of acute inflammation: *rubor* (redness), *calor* (fever), *tumor* (swelling) and *dolor* (pain) [23]. They regulate vascular permeability, expression of cellular adhesion molecules, extravasation and release of cytokines and chemokines, and peripheral and central sensitization. Moreover, PGE<sub>2</sub> mediates the resetting of the hypothalamic temperature set-point.

Prostanoid biosynthesis is significantly increased in inflamed tissues. COX-2 expression is markedly upregulated during inflammation and it represents the major source of pro-inflammatory prostanoids, although COX-1 also plays a role in the initial phase of the inflammatory response [35].

 $PGE_2$  and  $PGI_2$  are the predominant proinflammatory prostanoids. Both markedly enhance vascular permeability and leukocyte infiltration by promoting blood flow in the inflamed region. In addition,  $PGE_2$  can cross the blood-brain barrier and mediate the febrile response [36].  $PGF_{2\alpha}$  plays a role in both acute and chronic inflammation [37, 38].

 $TxA_2$  induces lymphocyte activation and adhesion molecule expression, and similarly to PGE<sub>2</sub> and PGI<sub>2</sub>, it can also act as an anti-inflammatory mediator [15].

The chemotactic function of  $PGD_2$ , a major product of mast cells, contributes to inflammation in allergic responses, particularly in the lung.  $PGD_2$  also increases vascular permeability and vasodilation. However,  $PGD_2$  has been shown to have anti-inflammatory proprieties as well [39–41].

Prostanoids play pivotal roles in pain. Prostanoids increase the sensitivity of nociceptors in inflamed tissue and augment pain signal transmission in the spinal cord and in the brain [42]. In particular, PGI<sub>2</sub> and PGE<sub>2</sub> cause peripheral and central hyperalgesia when bound to IP, EP<sub>1</sub>, EP<sub>3</sub>, and EP<sub>4</sub> receptors by reducing the threshold of nociceptor sensory neurons to stimulation. Perhaps PGD<sub>2</sub> and PGF<sub>2α</sub> also contribute to central sensitization [23].

In the lung,  $TxA_2$ ,  $PGD_2$  and  $PGE_2$  can induce bronchoconstriction, while  $PGI_2$ ,  $PGE_2$  and  $PGD_2$ can mediate bronchodilation. They play a major role in allergic responses such as asthma.  $PGE_2$ can have anti-inflammatory and anti-asthmatic effects via activation of EP<sub>3</sub>.

 $PGD_2$  contributes to the characteristic pattern of vascular and cellular changes associated with both the early and late phases of the allergic response via  $DP_2$  [43].

## 3.4 Approved Drugs Targeting the Prostanoid Pathway

Since the major role of prostanoids, particularly PGE<sub>2</sub>, in inflammation, pain and fever, inhibitors of their synthesis have been used successfully as anti-inflammatory agents [44]. The class of drugs, which inhibit COX activity, is known as the non-steroidal anti-inflammatory drugs (NSAIDs). They are among the most used drugs in the world, and the current opioid crisis has placed a new emphasis on their use since they don't cause addiction. The use of prostanoids themselves as therapeutic agents is limited largely due to their short half-life and because systemic administration of these agents is frequently associated with significant adverse side effects. There are, however, a few prostanoid analogs that are currently used in clinic for different therapeutic indications. Moreover, drugs that limit the effect of  $TXA_2$  (TP antagonist and TXAS inhibitors) are currently on the market in Asia but not in the US; a dual TP antagonist and TXAS inhibitor is sold as an antiplatelet drug in Italy.

### 3.4.1 NSAIDs

Aspirin is a prototypic COX inhibitor. It was synthesized serendipitously from salicylic acid, a natural compound with known analgesic activity, more than 100 years ago [45]. After the discovery of the mechanism of action of aspirin in 1971, traditional NSAIDs (tNSAIDs), which block both COX-1 and COX-2, such as ibuprofen, naproxen, diclofenac, were developed to mimic aspirin pharmacological effects [46]. The purposefully designed selective COX-2 inhibitors (coxibs) were developed after the discovery of COX-2 in 1991 [47] and the structural differences between the two COX isozymes as discussed above.

NSAIDs are weak organic acids, highly protein-bound and lipophilic. They are a chemically heterogeneous group of compounds that can be grouped on the basis of their chemical structure [48]. The kinetics, potency and selectivity of COX inhibitors can be assessed in vitro using purified enzyme systems, isolated cellular preparations or whole blood assay [49, 50]. Based on the selectivity for COX isoform blockade, NSAIDs are classified into nonselective COX inhibitors (ibuprofen, naproxen, indomethacin) and selective COX-2 inhibitors (celecoxib, rofecoxib, etoricoxib) [45]. NSAIDs can also be classified based on the kinetics of the interaction with COX-1 and/or COX-2. They can be distinguished into:

- Inhibitors purely competitive with respect to AA (e.g., ibuprofen, piroxicam) [19, 51].
- Time-dependent, slowly reversible noncovalent inhibitors (e.g., indomethacin, flurbi-

profen, naproxen, celecoxib, rofecoxib) [19, 51].

 Irreversible inhibitors (e.g., aspirin). Aspirin irreversibly inhibits COX activity by acetylation of a serine residue in the active site for COX (Ser<sup>529</sup> in COX-1 and Ser<sup>516</sup> in COX-2). This produces a steric blockage that prevents AA access to the active site [51].

Low-dose aspirin (75-100 mg/day) has an effective anti-platelet action. Since platelets do not have a nucleus, they cannot regenerate new COX-1 protein, after it is acetylated by aspirin. Thus, aspirin unique pharmacokinetics (short half-life, about 39 min) and pharmacodynamics (irreversible inhibition of COX isozyme) allow a selective, cumulative inhibition of COX-1-mediated TxA<sub>2</sub> production and platelet function throughout the dosing interval. Since acetylation of platelet COX-1 by aspirin requires initial low affinity anchoring to the Arg<sup>120</sup> residue of the COX channel, a common docking site for all NSAIDs, concomitant treatment with ibuprofen or naproxen can interfere with the antiplatelet effect of low dose aspirin [52]. NSAIDs can cause serious adverse events, primarily gastrointestinal and cardiovascular complications in some individuals, related to the relative selectivity of a drug for COX-1 and COX-2 and the duration of drug exposure [25, 53].

Coxibs were designed to retain the analgesic and anti-inflammatory effects of tNSAIDs, while sparing COX-1 in the gastric mucosa and platelets, and thus reducing gastrointestinal toxicity [54]. The first coxibs, celecoxib and rofecoxib, were approved by the Food and Drug Administration (FDA) in the late 1990s. Three randomized, double-blind clinical trials, based mainly on short-term use with gastrointestinal monitoring, showed that coxibs present less gastrointestinal toxicity than tNSAIDs [55–57]. Subsequently, novel COX-2 inhibitors with improved biochemical selectivity were developed, i.e., etoricoxib, valdecoxib, parecoxib (the prodrug of valdecoxib, the first injectable coxib), and lumiracoxib (structural analog of diclofenac) [58]. Unfortunately, long-term chemoprevention studies, launched to study the beneficial effect of COX-2 inhibitors in the sporadic colorectal adenoma recurrence, revealed that celecoxib and rofecoxib were associated with increased risk for cardiovascular mortality [59, 60]. This prompted a voluntarily withdrawal of rofecoxib from the market in late 2004. In early 2005, the FDA requested that all sponsors of tNSAIDs and coxibs included a black box warning on the drug labels highlighting the potential for increased cardiovascular risk and the well-described gastrointestinal bleeding associated with the drug use [61]. In addition, the FDA asked the maker of valdecoxib to withdraw the drug from the market, and initiated analysis of all available at that time clinical data on celecoxib to determine if additional regulatory action was needed. In the meantime, the European Medicines Agency (EMA) decided that coxibs should be contraindicated in patients with coronary heart disease (CHD) or stroke [54].

Later, placebo-controlled trials showed that all FDA-approved COX-2-selective NSAIDs cause cardiovascular complications, including atherosclerosis, thrombosis, myocardial infarction, stroke, systemic and pulmonary hypertension, heart failure and sudden cardiac death in approximately 1 to 2% of people exposed, but the absolute risk increases with higher drug doses, frequency of use, and established cardiovascular disease [62]. Observational studies consistent with a cardiovascular risk have also been reported for several tNSAIDs, which are highly selective for COX-2 inhibition, such as diclofenac and meloxicam [53, 62].

In 2013, the Coxib and traditional NSAID Trialists' (CNT) Collaboration published a metaanalysis of 754 randomized controlled trials comparing traditional NSAIDs and coxibs for their cardiovascular and upper gastrointestinal effects [63]. Coxibs and tNSAIDs, excluding naproxen, were reported to increase the risk of major vascular events (myocardial infarction, stroke or vascular death) by roughly 40% [63]. Elevated risk from diclofenac was comparable to that from coxibs, and is consistent with diclofenac acting as a COX-2-selective inhibitor [64, 65]. This indicates that any NSAID blocking COX-2 with insufficient inhibition of platelet COX-1 has elevated risk of major coronary events. In contrast, naproxen did not increase the risk of major vascular or coronary events consistent with its aspirin-like COX-1 inhibition in platelets described above [63]. All studied coxibs and tNSAIDs, including naproxen, doubled the risk of hospitalization due to heart failure [63]. Moreover, all studied NSAIDs elevated the risk of upper gastrointestinal complications (perforation, obstruction, or bleeding), with high-dose diclofenac causing a gastrointestinal risk similar to high-dose coxibs [53].

In 2015, after the review of the CNT metaanalyses and other clinical data, the FDA strengthened the warning that non-aspirin NSAIDs can cause heart attacks and stroke [53]. In turn, the EMA extended restrictive labeling from coxibs, implemented in 2005, to diclofenac and high-dose ibuprofen [66]. Two recent attempts to compare the cardiovascular safety of celecoxib with tNSAIDs, Standard Care vs. Celecoxib Outcome Trial (SCOT) and Prospective Randomized Evaluation of Celecoxib Integrated Safety versus Ibuprofen or Naproxen (PRECISION), were undermined by multiple limitations of the trial design [53, 66, 67]. At present, celecoxib is the only coxib remaining on the market in the United States.

Coxibs and most tNSAIDs inhibit COX-2dependent formation of cardioprotective PGs,  $PGI_2$  and  $PGE_2$ , with inconsistent and ineffective platelet  $TxA_2$  suppression [68], except for naproxen. High-dose naproxen affords sustained inhibition of platelet COX-1/TxA<sub>2</sub>, particularly in those individuals who experience a long halflife of this drug [69]. These effects may increase the risk for cardiovascular events through a direct effect on the myocardium and the vasculature and/or by altering hemodynamic stability and renal function [34, 53]. The clinically manifested elements of this hazard (a predisposition to thrombosis, hypertension, cardiac failure, and arrhythmogenesis) have been recapitulated in rodent models in which the COX-2-dependent formation of PGI<sub>2</sub> or its action is disrupted in the vascular or in cardiomyocytes [70, 71].

### 3.4.2 Prostanoid Analogs

A PGE<sub>1</sub> analog, misoprostol, provides gastric cytoprotection during long term NSAID treatment [53]. It is also used as an effective abortifacient in combination with the anti-progesterone mifepristone for medical abortion [72]. Another PGE<sub>1</sub> analog, alprostadil, is used to treat impotence or for maintenance of the ductus arteriosus in neonates awaiting cardiac surgery [73, 74].

PGI<sub>2</sub> analogs, iloprost, epoprostenol, treprostinil, selexipag (the first approved oral IP receptor agonist with a non-prostanoid structure [75, 76]), are on the market for the treatment of pulmonary arterial hypertension (PAH) [77].

Several PGF<sub>2 $\alpha$ </sub> analogs, latanoprost, bimatoprost, travoprost and tafluprost, have been marketed for the treatment of ocular hypertension glaucoma [78–85]. In recent years, and NO-donating  $PGF_{2\alpha}$  analogs have been developed to treat glaucoma in patients that do not respond to the treatment with  $PGF_{2\alpha}$  analogs [86, 87]. Latanoprostene bunod, LBN, was the first drug in this class approved by the FDA in November 2017 [78]. Upon exposure to corneal esterases, LBN is rapidly cleaved into latanoprost and butanediol mononitrate, an NO-donating moiety [88]. NO-mediated vasodilation, antiinflammatory and antiplatelet effects make this class of drugs especially attractive as impaired ocular blood flow and inflammation contribute to glaucoma progression [89, 90]. Another compound in this class is NCX 470, composed of a bimatoprost molecule and the NO-donating moiety 6-(nitrooxy)hexanoic acid [91]. In animal models of glaucoma and ocular hypertension, NCX 470 was more efficacious in reducing intraocular pressure (IOP) than the equimolar doses of bimatoprost, the most efficacious PG analog approved to date [91]. Currently, a clinical trial is ongoing comparing NCX 470 with latanoprost for the safety and efficacy in patients with openangle glaucoma or ocular hypertension (ClinicalTrials.gov Identifier NCT03657797).

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# 3.5 Prostanoid Pathway-Targeting Drugs in Clinical Development

The future of prostanoid-based therapies appears to reside in selective prostanoid synthase inhibitors, mainly mPGES-1 and H-PGDS inhibitors, prostanoid receptor modulators and dual inhibitors (COX/5-lipoxygenase (LO), COX-2/ TP, mPGES-1/5-LO). Moreover, a novel approach to develop NSAIDs with improved safety profiles has focused on linking existing drugs to a molecule of nitric oxide (NO), hydrogen sulfide (H<sub>2</sub>S) or nitric oxide-hydrogen sulfide, and generation of NO, H<sub>2</sub>S, nitric oxide-hydrogen sulfide-(NOSH) NSAIDs [92-94]. NO and H<sub>2</sub>S are gaseous mediators that have protective effects in the gastrointestinal tract and counteract cardiovascular side effects of the NSAIDs on blood pressure [95, 96].

### 3.5.1 Inhibitors of mPGES-1

Cardiovascular side effects from COX-2-selective NSAIDs [53] prompted search for safer but equally effective drugs for pain and inflammation. Scientists focused on the new drug targets in the arachidonic acid cascade, specifically on the downstream effectors of the COX isoforms to block the synthesis or action of PGE<sub>2</sub>. The development of two new classes of analgesics began, the inhibitors of mPGES-1 and antagonists of the EP<sub>4</sub> receptor.

Numerous animal studies showed that NSAID efficacy might be preserved, while the cardiovascular and gastrointestinal risks are reduced, by blocking mPGES-1 downstream of COX-2 [14, 97-104]. Genetic deletion of mPGES-1 was as effective as NSAID treatment in rodent models of inflammatory pain [97, 98]. Similar to interference with COX-2 expression or function, deletion of mPGES-1 in mice suppresses pro-inflammatory PGE<sub>2</sub>; but unlike with COX-2, deficiency in mPGES-1 elevates cardio-protective PGI<sub>2</sub>, reflected by increased urinary metabolite excretion [100]. Both, suppression of  $PGE_2$  and augmentation of PGI<sub>2</sub> in mPGES-1-lacking mice, result from the shunting of the elevated PGH<sub>2</sub> substrate away from mPGES-1 to PGIS [100]. The beneficial cardiovascular outcomes from mPGES-1 deletion in mice include a decrease in the proliferative response to vascular injury [103], reduced a ortic aneurysm formation [101], slowed development of atherosclerosis [100], and protection from thrombosis and hypertension [14]; although contrasting effects on the blood pressure were reported in mice with different genetic backgrounds [105]. Besides that global deletion of mPGES-1 in mice reduces the postischemic brain infarction and neurological dysfunction in a cerebral ischemia/reperfusion model [99]. Finally, mPGES-1 deficiency in mice does not affect ozone-induced airway inflammation or airway hyper-responsiveness suggesting that pharmacological inhibition of mPGES-1 may not predispose patients at risk to airway dysfunction [102]. Taken together, these studies suggest that pharmacological inhibition of mPGES-1 may retain anti-inflammatory effects from PGE<sub>2</sub> suppression, but due to PGI<sub>2</sub> elevation, targeting of mPGES-1 might avoid the cardiovascular risks associated with selective COX-2 inhibitors.

On the other hand, several preclinical studies suggest that mPGES-1-mediated inflammatory response might be beneficial in certain settings, thus, complicating the development of drugs blocking mPGES-1. The whole-body or myeloid cell-specific deletion of mPGES-1 was reported to adversely interfere with cardiac remodeling after myocardial infarction [106, 107]. In a mouse model of myocardial ischemia/reperfusion injury, deletion of mPGES-1 impairs cardiac microvascular perfusion and increases inflammatory cell infiltration [108]. Furthermore, although  $PGE_2$  is the main mediator of pain [109],  $PGI_2$  may contribute to pain responses and even predominate in some rodent models [42, 110]. So even if substrate shunting to PGI<sub>2</sub> offers cardio-protective effects, it might also compromise the analgesic

efficacy of mPGES-1 inhibitors in some settings. Finally, the predominant product of substrate shunting amongst the prostanoids varies by cell type [111], which further complicates development of drugs for systemic inhibition of mPGES-1. Recent preclinical studies suggest that cell-specific targeting of mPGES-1 in macrophages might be advantageous over systemic blockade of the enzyme, and might provide comparable analgesic and anti-inflammatory efficacy with improved toxicity. Deletion of mPGES-1 selectively in macrophages recapitulates the analgesic effects of global mPGES-1 depletion in an inflammatory pain model, restrains the proliferative response to vascular injury [111] and attenuates development of atherosclerosis [112]. Therefore, macrophage mPGES-1 provides a promising therapeutic target alternative to COXs, and requires further investigation.

In 2005, the development of a high-throughput screening assay for novel mPGES-1 blockers at Merck Frosst led to the discovery of a series of phenanthrene imidazole inhibitors, which were among the first synthetic inhibitors of mPGES-1 [104, 113, 114]. Compound MF63 was the most promising lead in this class [113]. MF63 was highly potent and selective for mPGES-1i inhibition in cell-free and cell-based assays; most importantly, MF63 was the first reported mPGES-1 inhibitor to exhibit potency in human whole blood [113]. Due to structural differences in mPGES-1 between human and rat enzymes, MF63 could not be screened in well-established rat models of inflammatory pain. Indeed, despite being highly potent at the human and guinea pig enzymes, MF63 was inactive against rat and mouse mPGES-1. It was not until 2010, when scientists from the Karolinska Institute reported that the entrance to the active site of mPGES-1 in the mouse and rat enzyme contained more bulky and sterically hindered amino acids than the human enzyme [115]. To screen MF63 in vivo, a humanized knock-in (KI) mouse model was generated, where the murine mPGES-1 gene was replaced with a human mPGES-1 minigene [104]. MF63 dose-dependently inhibited pain sensitivity in a hyperalgesia mouse model with comparable potency to a selective COX-2 inhibitor. MF63 was well tolerated by KI mice and squirrel monkeys, and did not cause gastrointestinal lesions in contrast to a nonselective NSAID indomethacin. When dosed orally in guinea pigs, MF63 was efficacious in the models of pyresis, chronic and acute pain with the analgesic efficacy comparable to diclofenac [104].

Pharmacokinetic analysis of MF63 revealed a short plasma half-life in rats and the rhesus monkeys [114]. Based on MF63 structure, a series of derivatives were synthesized with an improved pharmacokinetic profile [114]. Extensive structure-activity relationship (SAR) studies resulted in compound MK-7285, the most active mPGES-1 inhibitor reported to date [114, 116]. MK-7285 [116], was highly selective and potent at the human mPGES-1 enzyme and in the whole blood assay. MK-7285 exhibited improved pharmacokinetics in rats, and enhanced analgesic efficacy over MF63 in a guinea pig pain model [114]. Despite excellent activity in animals and suitability for clinical development, no further studies on the mPGES-1 inhibitor MK-7285 have been reported.

In 2011 and 2012, two potent and selective of mPGES-1, LY3023703 and inhibitors LY3031207 from Eli Lilly advanced in clinical trials for the treatment of osteoarthritis (OA) pain [117–120]. LY3023703 and LY3031207 were the first mPGES-1 inhibitors to reach clinical development. compounds Both were 2-aminoimidazole-based inhibitors that demonstrated analgesic efficacy and robust safety margins in preclinical studies [117]. LY3023703 exhibited high potency in human blood ex vivo, 10,000-fold selectivity against COX-1 and COX-2 enzymes, and analgesic efficacy in a rodent arthritis model [118]. Based on LY3023703 structure, a new mPGES-1 inhibitor, LY3031207, was made with improved physicochemical properties and a superior pharmacokinetic profile. LY3031207 demonstrated high oral bioavailability, quick absorption, sustained plasma levels over a long period, although it was not as potent as LY3023703 [117]. In a single ascending dose study, LY3023703 was well tolerated at the highest dose tested in healthy subjects, but when screened in a multiple ascending dose study, one subject experienced elevated serum aminotransferase levels indicating liver damage [118]. Hepatotoxicity in this subject met criteria for a severe adverse event and precluded further development of LY3023703 [118]. After single doses in healthy subjects, LY3031207 exhibited good tolerability up to 900 mg, but triggered acute liver injury in six subjects in a multiple ascending dose study. Notably, the hepatotoxicity identified in humans contrasted the preclinical toxicology findings in rats and dogs, and thus, could not be predicted from the animal studies. Thus, further development of LY3031207 was terminated due to a rare form of dose-dependent liver injury with hypersensitivity features [120]. Oxidation of the 2-aminoimidazole ring to epoxide reactive metabolites was reported as a cause of hepatotoxicity in both compounds [119]. Taken together, LY3023703 and LY3031207 studies emphasize the limitations of the animal toxicology studies and the need for careful safety monitoring throughout Phase I trials.

The most successful mPGES-1 inhibitor to date that has recently advanced in a Phase IIb clinical trial is a substituted pyrimidine GRC 27864 from Glenmark Pharmaceuticals [121]. GRC 27864 exhibited high potency in the enzymatic assay (IC<sub>50</sub> = 5 nM) and in human whole blood (IC<sub>50</sub> = 376 nM), and inhibited PGE<sub>2</sub> biosynthesis in chondrocytes and synovial fibroblasts taken from patients with rheumatoid arthritis (RA) and OA [121]. GRC 27864 demonstrated significant analgesic efficacy in preclinical models of OA and inflammatory arthritis. When tested in Phase I clinical trial, GRC 27864 was well tolerated at single doses up to 1000 mg in healthy adults (NCT02179645, NCT02361034). Similarly to celecoxib, GRC 27864 inhibited ex vivo LPS-induced PGE<sub>2</sub> in whole blood of treated subjects in a dosedependent manner. This was accompanied by a reduction of PGE-M by both drugs. However, unlike celecoxib, GRC 27864 did not inhibit PGI-M and Tx-M, indicating that GRC 27864 spared PGI<sub>2</sub> with highly selective PGE<sub>2</sub> inhibition. This suggests that systemic inhibition of PGE<sub>2</sub> by GRC 27864 might avoid cardiovascular toxicity associated with NSAIDs selective for COX-2 inhibition [122]. In two additional studies, multiple oral doses of GRC 27864 were well tolerated in healthy adults and elderly subjects without any dose limiting adverse events. GRC 27864 has recently advanced in a Phase IIb dose range finding study to evaluate safety and efficacy in patients with moderate osteoarthritic pain [123].

### 3.5.2 Inhibitors of H-PGDS

 $PGD_2$  is a well-established pro-inflammatory mediator in allergy-associated disorders and muscle dystrophy [124–127]. Beneficial effects of blocking PGD<sub>2</sub> production or action by targeting H-PGDS enzyme or DP<sub>2</sub>/CRTH2 receptors, respectively, have been reported for many allergic diseases including asthma, rhinitis, atopic dermatitis [128–132], as well as Duchenne (DMD) Muscular Dystrophy [133, 134]. However, in contrast to DP antagonists (see below), clinical research on H-PGDS inhibitors is still in its infancy. From a vast plethora of compounds blocking H-PGDS [135] only two H-PGDS inhibitors, ZL-2102 and TAS-205, have recently advanced into clinical development [136].

ZL-2102 is a selective and reversible H-PGDS inhibitor. ZL-2102 was designed to treat chronic obstructive pulmonary disease (COPD), asthma and idiopathic pulmonary fibrosis. Currently, ZL-2102 is in Phase I clinical trial to assess safety, tolerability, and preliminary pharmacokinetics in healthy male subjects (NCT02397005).

Patients with DMD exhibit elevated levels of H-PGDS in necrotic muscle fibers and increased urinary tetranor-PGD metabolite (t-PGDM) with advancing age, suggesting the involvement of H-PGDS/PGD<sub>2</sub> axis in the etiology and progression of this disease [137, 138]. TAS-205 is a highly selective inhibitor of H-PGDS, which reduced muscle necrosis, promoted recovery of locomotor activity, and suppressed urinary t-PGDM in a mouse model of DMD [139]. TAS- 205 was successfully tested over a range of doses in Phase I trial and was considered safe and tolerable in DMD patients [136]. Recently, a Phase IIa study was completed but the results are still to be released on the efficacy of TAS-205 after 24-week repeated oral dosing in patients with DMD (NCT02752048).

### 3.5.3 Inhibitors of TXAS

Several inhibitors of TXAS were created to treat bronchoconstriction by suppressing  $TxA_2$ mediated activation of the airway smooth muscle in asthma [140]. Early animal studies reported efficacy of TXAS inhibitors [140] and one of them, ozagrel hydrochloride (OKY-046), was marketed in Japan for bronchial asthma in adults [141, 142]. However, in the Western studies, TXAS inhibitors dazmegrel (UK-38485) and pirmagrel (CGS-13080) were ineffective in improving the lung function in asthmatics [143, 144]. Furthermore, dazmegrel was under clinical development in Europe for the treatment of thrombosis, ischemic heart disease and arrhythmias, but failed to advance into clinic [145].

### 3.5.4 Dual Inhibitors (COX/LO, COX-2/TP, mPGES-1/LO)

Selective inhibition of one of the pathways in the AA cascade may cause overproduction of undesirable metabolites from other pathways. The shunting of the arachidonate-derived lipids towards leukotrienes, the products of 5-LO pathway, is a well-recognized contributing factor to NSAID-induced asthma and allergic reactions in sensitive patients and gastrointestinal side effects [146]. Therefore, development of multi-target agents with dual inhibitory activity at COXs and 5-LO (dual COX/LO inhibitors) has been ongoing since the 1970s [147].

The design of ligands to inhibit COX-2/5-LO enzymes has been based on the modification of already existing NSAIDs by adding LO pharmacophores or with the development of new scaffolds by computational techniques. Licofelone or ML-3000 was the most successful dual COX/LO inhibitor that showed anti-inflammatory, analgesic and anti-asthmatic effects in several animal models. It reached Phase III clinical trials for the treatment of OA [148], but results were mixed and the drug has never been submitted for regulatory approval.

Flavocoxid is an FDA-regulated prescription medical food composed of a concentrated proprietary mixture of the flavonoid molecules baicalin and catechin extracted from Scutellaria baicalensis and Acacia catechu, respectively, and was shown to inhibit both COX-2 and 5-LO and show antioxidant activity [149, 150]. Flavocoxid successfully completed Phase II clinical trials for the treatment of knee OA [151, 152]. When tested in healthy volunteers, flavocoxid neither affected hemostasis nor inhibited the anticoagulation effects of aspirin, and thus might have utility in cardiovascular patients with chronic inflammation [153]. Lastly, flavocoxid demonstrated favorable gastrointestinal tolerability and a > 30% reduction or cessation in the use of gastroprotective medications by the OA patients [154].

Another strategy that is under consideration is to develop a multitarget drug, COX-2 inhibitor/ TP antagonist, that combines the antiinflammatory activity of a coxib with the antiaggregating and anti-atherotrombotic activities of a TP antagonist, and exploits recognized therapeutic advantages of the coxib as a GI-safer antiinflammatory drug. Since lumiracoxib possesses a competitive antagonism at the TP receptor at high micromolar concentration [155], a series of lumiracoxib derivatives are under evaluation for their COX inhibition and TP antagonism activities [156, 157]. A possible pitfall of this approach could be an increase in bleeding episodes.

Dual inhibition of mPGES-1 and 5-LO or mPGES-1 and Leukotriene C4 Synthase, an enzyme downstream of 5-LO, represent a promising strategy in the development of novel anti-inflammatory drugs [158–160].

### 3.5.5 Prostanoid Receptor Modulators

Another approach to modulate prostanoid action in a more targeted fashion is at the level of the prostanoid receptors. Global inhibition of all the prostanoids, many of which have important homeostatic functions, lies at the basis of NSAIDassociated toxicity. Taking into account cellselective localization of the prostanoid receptors and their diverse functions, pharmacological targeting of a specific prostanoid receptor may ensure better therapeutic efficacy and lower toxicity. For the past decade, major strides have been made in the development of prostanoid receptorbased therapeutics. This section discusses the most clinically advanced modulators of the prostanoid receptors with the compounds currently in clinical development summarized in Table 3.1.

### 3.5.6 DP Antagonists

PGD<sub>2</sub> binds DP<sub>2</sub> receptor that plays a role in the pathogenesis of allergic disorders, such as asthma. DP<sub>2</sub> receptor is highly expressed on various immune cells, while its natural ligand PGD<sub>2</sub> is elevated in the bronchoalveolar lavage fluid of asthmatics and triggers a characteristic cough [126]. Patients with severe asthma patients showed elevated airway remodeling, goblet metaplasia, and cellular migration after DP<sub>2</sub> activation [127]. Thus, blockade of PGD<sub>2</sub>/DP<sub>2</sub> signaling might be a plausible therapeutic strategy to alleviate asthma symptoms.

OC000459 is a potent and highly selective  $DP_2$  antagonist that has been successfully tested in asthmatic patients. In human cell-based studies, OC000459 inhibited mast cell-dependent activation of both Th2 lymphocytes and eosinophils. In clinical trials, OC000459 inhibited allergic airway inflammation by blocking PGD<sub>2</sub>-mdiated elevation in serum and airway

Target	Compound	Therapeutic indication/clinical status	References	
DP2 antagonist	OC000459	Asthma (Phase II completed)	NCT02560610	
DP2 antagonist	BI 671800	Asthma	[162–164]	
		Seasonal allergic rhinitis		
DP2 antagonist	Setipiprant	Androgenetic alopecia (Phase II)	NCT02781311	
EP1 antagonist	ONO-8539	Heartburn, overactive bladder	[210, 211]	
EP2 agonist	CP-533536	Bone healing (Phase II)	NCT00533377	
EP <sub>2</sub> agonist	Taprenepag isopropyl	Ocular hypertension, glaucoma (Phase II)	[170]	
EP <sub>2</sub> agonist	Omidenepag isopropyl	Ocular hypertension, glaucoma (Approved in Japan in 2018; Phase III, USA)	[173, 174]	
EP2 antagonist	PF-04418948	Safety and tolerability (Phase I)	NCT01002963	
EP3 antagonist	DG-041	Antithrombotic, antiulcer agent	[212]	
EP4 agonist	KAG-308	Ulcerative colitis (Phase II)	[180]	
EP4 antagonist	LY3127760	Safety and tolerability (Phase I completed)	[197]	
EP4 antagonist/	gonist/ Grapiprant/ NSCLC adenocarcinoma (Phase I/II);		NCT03696212	
PD-1 blocker	Pembrolizumab	cancer (Phases Ib)	NCT03658772	
EP <sub>4</sub> antagonist/ PD-1 blocker	ONO-4578/ Nivolumab	Advanced or metastatic solid tumors (Phase I)	NCT03155061	
EP <sub>4</sub> antagonist/ antifolate	CR6086/ Methotrexate	RA (Phase II)	[188] NCT03163966	
FP agonist	NCX 470	Ocular hypertension and open-angle glaucoma (Phase II)	[91] NCT03657797	
TP antagonist	Ifetroban	Systemic scleroderma or scleroderma-associated PAH;	NCT02682511	
		aspirin-exacerbated respiratory disease, solid tumors,	NCT03028350	
		DMD, vascular dilation (all in Phase II);	NCT03326063	
			NCT03694249	
		Hepatorenal syndrome, portal hypertension in cirrhotic	NCT03340675	
		patients (the last two are completed)	NCT03962855	
			NCT01436500	
			NCT02802228	

 Table 3.1
 Prostanoid receptor modulators in current clinical development

eosinophils, improved the quality of life, and overall lung function [128–130]. Furthermore, OC000459 reduced nasal and ocular symptoms in patients with allergic rhinitis [131].

BI 671800, a highly specific and potent  $DP_2$ antagonist, was effective in a number of animal models of asthma and allergic dermatitis [161]. When tested in clinical trials, BI 671800 inhibited  $DP_2$ -dependent eosinophil activation by PGD<sub>2</sub> and demonstrated efficacy in treating seasonal allergic rhinitis [162]. Moreover, BI 671800 led to a moderate but significant improvement in the lung function in poorly controlled asthma [163, 164].

Setipiprant, ACT-129968, is another highly potent, selective and orally bioavailable antagonist of  $DP_2$  receptor [165]. In clinical trials, setipiprant was evaluated as a therapy for asthma and seasonal allergic rhinitis. When tested in asthmatic patients, setipiprant decreased allergen-induced airway responses and the assoairway hyperresponsiveness ciated [166]. However, when screened in seasonal allergic rhidose-dependent nitis. setipiprant efficacy observed in Phase II was not confirmed in a Phase III trial [167]. Currently, setipiprant is in a clinical trial for the treatment of androgenetic alopecia in males (NCT02781311).

#### 3.5.7 **Targeting EP Receptors**

**EP<sub>2</sub> Agonists** Activation of EP<sub>2</sub> receptor was reported to reduce intra-ocular pressure (IOP) by affecting both uveoscleral and conventional pathways of aqueous humor outflow [168, 169]. Thus, a series of EP<sub>2</sub> agonists have been successfully tested in animal models of glaucoma and ocular hypertension, and have advanced into clinical development [169–173]. Taprenepag isopropyl, PF-04217329, is a prodrug of a highly selective and potent EP<sub>2</sub> receptor agonist CP-544326 [169]. Taprenepag isopropyl exerted IOPlowering effects in dog, rabbit and non-human primate models of glaucoma and ocular hypertension [169]. In Phase II clinical trial, tapreisopropyl monotherapy significantly nepag lowered IOP and was comparable in its effect to latanoprost; co-administration of taprenepag and latanoprost reduced IOP to a greater degree than latanoptost alone suggesting an additive effect on IOP and a possibility of combination therapy [170]. Another  $EP_2$  agonist in this class is omidenepag isopropyl, DE-117, which stimulates drainage through both pathways of aqueous humor outflow [172]. When tested in the Japanese patients, omidenepag isopropyl demonstrated sustained IOP-lowering effects and was recommended as an alternative treatment for nonresponders to latanoprost [173, 174]. In September 2018, omidenepag isopropyl ophthalmic solution was approved in Japan for the treatment of glaucoma and ocular hypertension; Phase III clinical trials are currently ongoing in the United States [174].

EP<sub>2</sub> agonist CP-533536 was shown effective in bone healing in animals and clinical studies [183, 184]. CP-533536 increased bone formation in rat tibia, and healed long bone segmental and fracture defects in dogs [183, 184]. Subsequently, bone-healing abilities of CP-533536 were evaluated in patients with closed fracture of the tibial shaft (NCT00533377).

**EP**<sub>4</sub> Agonists EP<sub>4</sub> receptor is constitutively expressed in the colonic epithelium and its levels are increased during inflammatory bowel disease (IBD) [175]. Mice deficient in  $EP_4$  receptor are L. L. Mazaleuskaya and E. Ricciotti

EP<sub>4</sub> agonist protects the animals through regeneration of the intestinal epithelium and suppression of the immune response [176]. Based on these findings, it was suggested that an EP<sub>4</sub> agonist could be used for the treatment of patients with IBD. Rivenprost, ONO-4819, a potent and selective EP<sub>4</sub> receptor agonist [177], was tested in patients with mild to moderate ulcerative colitis (UC) for its effects on disease activity and inflammatory response [178]. An improvement in the ulcerative colitis symptoms was observed in three out of four patients, and one patient achieved complete remission. While more studies with larger patient cohorts would be necessary to conclude on the UC efficacy of rivenprost, its clinical development was terminated in 2009 (NCT00296556). A novel EP<sub>4</sub> agonist KAG-308 was reported to be advantageous over rivenprost due to favorable oral bioavailability [179]. KAG-308 showed a profound anti-inflammatory effect in a mouse model of UC, suppressed the onset of colitis and promoted mucosal healing [179]. KAG-308 was successfully tested in healthy volunteers, and the compound advanced in Phase II clinical trials in patients with ulcerative colitis [180].

EP<sub>4</sub> Antagonists Blockade of PGE<sub>2</sub> action through antagonism of its receptor EP<sub>4</sub> presents another alternative to COX-1/2 inhibition in pain management. The EP<sub>4</sub> receptor is the primary mediator of the PGE<sub>2</sub>-triggered sensitization of sensory neurons and inflammation [181–184]. PGE<sub>2</sub>/EP<sub>4</sub> signaling is not the only mechanism involved in pain and inflammation, but animal studies with EP<sub>4</sub> genetic deletion or pharmacological inhibition implicate the role of this receptor in central sensitization, thus, confirming EP<sub>4</sub> involvement in nociceptive responses [181, 182, 185].

Over the past decade, several pharmaceutical companies have been reporting on EP4 antagonists with analgesic and anti-inflammatory properties [110, 186–189]. Grapiprant (CJ-023,423), a potent and highly selective EP<sub>4</sub> antagonist, is among the most advanced compounds in its class

[182]. Grapiprant showed analgesic efficacy in animal models of acute and chronic inflammatory pain in various species including rats, rabbits, cats, dogs and horses [182, 190–193], and has been recently approved by the FDA for OA in dogs [194–196]. Grapiprant is currently in clinical development as a co-therapy for cancer indications (see below).

LY3127760, a highly selective and potent EP<sub>4</sub> antagonist, has been successfully tested in firstin-human studies and advanced in further clinical development [197]. LY3127760 exhibited a superior pharmacological profile than grapiprant with a > ten-fold increase in potency in a human whole blood assay, and comparable analgesic efficacy to diclofenac in rat models of joint pain and arthritis [189]. In Phase I trial, LY3127760 demonstrated a comparable safety profile and similar pharmacodynamic effects on sodium and potassium excretion observed with celecoxib; this supported LY3127760 advancement into Phase II trials [197].

 $PGE_2/EP_4$ signaling can amplify proinflammatory cytokine production and expand inflammatory T lymphocytes, thus, contributing to the onset and progression of RA [185, 198]. Blocking EP<sub>4</sub> receptor with CR6086, a novel EP<sub>4</sub> antagonist with immunomodulatory properties, presents the rational for the use of this class of agents as disease-modifying anti-rheumatic drugs [188]. CR6086 was effective in the rodent models of arthritis, and when used in combination with methotrexate, CR6086 improved the efficacy of a fully immunosuppressive dose of the anti-rheumatic drug [188]. CR6086 is currently tested in a Phase II clinical trial in patients with early RA as a combination therapy with methotrexate (NCT03163966).

Numerous studies reported on the role of  $PGE_2$  signaling via  $EP_2$  and  $EP_4$  receptors in the elevation of exhausted cytotoxic CD8<sup>+</sup> T cells, which cannot mount effective immune responses in chronic viral infections and cancer [199–201]. T cell exhaustion is mediated by multiple inhibitory receptors, such as programmed cell death protein 1 (PD-1), whose major role is to limit T cell activity during inflammation in the peripheral tissues and to prevent autoimmunity. As a

mechanism of immune resistance, tumor cells upregulate PD-1 ligands, which bind to PD-1 on lymphocytes and block T cell-mediated antitumor immune responses. Thus, suppression of  $PGE_2/EP_4$  signaling may be a complimentary strategy to PD-1 blockade, and may potentiate the effectiveness of the cancer immunotherapy. Currently, EP<sub>4</sub> antagonist grapiprant, ARY-007, is being tested in combination with anti-PD-1 immunotherapy pembrolizumab, an IgG<sub>4</sub> isotype PD-1 antibody, in patients with advanced or metastatic non-small cell lung cancer (NSCLC) adenocarcinoma (NCT03696212). Moreover, the safety and tolerability of the grapiprant and pembrolizumab combination is being assessed in patients with advanced or progressive microsatellite stable (MSS) colorectal cancer (NCT03658772). Finally, a novel EP<sub>4</sub> antagonist ONO-4578 is being assessed as a monotherapy or in combination with nivolumab, a fully human IgG<sub>4</sub> PD-1 antibody, in subjects with advanced or metastatic solid tumors (NCT03155061).

### 3.5.8 TP Antagonists

Ifetroban is an orally active, potent and selectiveTP receptor antagonist [202]. In pre-clinical studies, ifetroban exhibited high receptor affinity for TP on different cell-types, including platelets, vascular and airway smooth muscle cells [203]. Ifetroban showed to inhibit platelet aggregation and relax contracted isolated vascular tissues [204] ex vivo. It was studied in animal models of thrombosis, stroke, myocardial ischemia and hypertension [204]. In humans, ifetroban showed to be a long-acting inhibitor of TxA<sub>2</sub> agonistinduced platelet aggregation and platelet shape change in healthy volunteers [205]. Ifetroban is under clinical investigation and phase II studies are undergoing for several therapeutic indications (Table 3.1). The safety and pharmacokinetics of 3 days of intravenous ifetroban was accessed in syndrome patients with hepatorenal (NCT01436500). Moreover, the safety of ifetroban was evaluated in Aspirin Exacerbated Respiratory patients Disease (AERD) (NCT02216357). Recently, the assessment of the

safety and efficacy of 3 months of treatment with ifetroban for portal hypertension in cirrhotic patients was completed (NCT02802228). Currently, the efficacy of oral treatment with ifetroban in AERD patients is under evaluation (NCT03326063 and NCT03028350). Moreover, the safety and efficacy of oral ifetroban in patients with diffuse cutaneous systemic sclerosis or systemic sclerosis-associated PAH are being evaluated (NCT02682511). Furthermore, the assessment of the safety and feasibility of ifetroban administration in patients with malignant solid tumors at high risk of metastatic recurrence is under evaluation (NCT03694249). Two new clinical studies are about to start recruiting patients to evaluate the safety, pharmacokinetics and efficacy of two doses of oral ifetroban in subjects with DMD (NCT03340675) and to study the safety of oral and in patients with established cardiovascular disease (NCT03962855). TP antagonist seratrodast is marketed in Japan and China for the treatment of asthma [206]. However, this drug is not yet licensed for use in other countries. TP antagonist ramatroban, that is also a  $DP_2$ antagonist [207], was initially approved in Japan for the treatment of allergic rhinitis and asthma [208]. Successively, it was approved for the treatment of coronary artery disease [209].

# 3.6 Concluding Remarks

NSAIDs, including both non-selective COX-1/2 and selective COX-2 inhibitors, are currently the major class of drugs targeting the prostanoid pathway. NSAIDs continue to be widely used for pain and inflammation, despite associated cardiovascular and gastrointestinal toxicity. Considering a high demand for pain management medicine, an urgent need for non-addictive analgesics due to the opioid crisis, great health care costs and loss of productivity due to chronic pain conditions, development of new strategies and drugs alternative to existing NSAIDs, is of paramount importance. The ongoing strategies are summarized as followed:

- A new class of drugs, targeting enzymes downstream of COX-1/2, like mPGES-1, promises to retain the same anti-inflammatory efficacy but assures a more favorable cardiovascular safety profile. However, the hallmark of mPGES-1 targeting is substrate shunting towards other terminal synthases with the predominant prostanoid product varying by cell type. What remains to be determined is whether blockade of mPGES-1 affects the signaling networks beyond the prostanoid pathway, and whether substrate shunting leads to functional consequences in a disease state, like chronic pain conditions or cardiovascular syndromes of inflammation. The same concern exists for the drugs targeting H-PGDS, when inhibition of PGD<sub>2</sub> may lead to a concurrent elevation of other eicosanoids. Alternative to systemic inhibition, cell-specific targeting of mPGES-1 in macrophages provides a promising therapeutic target for pain and inflammation with potential cardiovascular benefits. Preclinical studies are currently ongoing to address the therapeutic potential of targeted blockade of macrophage mPGES-1 in inflammatory pain models.
- Modulation of prostanoid receptors is another • active area of therapeutic research in the prostanoid field. Targeting of prostanoid receptors may not have widespread anti-inflammatory effects of NSAIDs. since individual prostanoids and their receptors play compensatory roles, and act sequentially to initiate and sustain the inflammatory response; however, prostanoid receptor modulators may be useful in pathological states where a single prostanoid is the main causative agent. The most clinically advanced therapeutics in this class are DP antagonists for allergic indications, EP<sub>2</sub>/FP agonists for glaucoma and ocular hypertension, and a TP antagonist for various inflammatory conditions. Combinatorial approaches of EP<sub>4</sub> antagonism with other drugs are being investigated in oncology and RA. A promising strategy for various cancer indications is a combination of an EP<sub>4</sub> antagonist with PD-1 blocking immunotherapy.

In addition to novel drug development, alternative strategies are emerging to improve the safety and tolerability of existing NSAIDs. These strategies include a personalized selection of the appropriate NSAID based on each patient's clinical background and genetic makeup, a better selection of NSAID doses and schedules (the lowest effective drug dose used for the shortest period of time), and development of biomarkers that may predict the response to NSAID treatment in individual patients.

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4

# Targeting Leukotrienes as a Therapeutic Strategy to Prevent Comorbidities Associated with Metabolic Stress

Theresa Ramalho, Nayara Pereira, Stephanie L. Brandt, and C. Henrique Serezani

### Abstract

Leukotrienes (LTs) are potent lipid mediators that exert a variety of functions, ranging from maintaining the tone of the homeostatic immune response to exerting potent proinflammatory effects. Therefore, LTs are essential elements in the development and maintenance of different chronic diseases. such as asthma, arthritis, and atherosclerosis. Due to the pleiotropic effects of LTs in the pathogenesis of inflammatory diseases, studies are needed to discover potent and specific LT synthesis inhibitors and LT receptor antagonists. Even though most clinical trials using LT inhibitors or antagonists have failed due to low efficacy and/or toxicity, new drug development strategies are driving the discovery for LT inhibitors to prevent inflammatory diseases. A newly important detrimental

role for LTs in comorbidities associated with metabolic stress has emerged in the last few years and managing LT production and/or actions could represent an exciting new strategy to prevent or treat inflammatory diseases associated with metabolic disorders. This review is intended to shed light on the synthesis and actions of leukotrienes, the most common drugs used in clinical trials, and discuss the therapeutic potential of preventing LT function in obesity, diabetes, and hyperlipidemia.

### Keywords

Leukotrienes · Inflammation · Immune regulation · Clinical trials · Metabolic disorders · Diabetes

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# 4.1 A Brief History of the Leukotrienes (LTs)

Leukotrienes (LTs) are part of a large family of lipids termed eicosanoids, which also include prostaglandins and hydroxyeicosatetraenoic acids (HETEs). Eicosanoids are polyunsaturated fatty acids composed of twenty carbons, aptly named from the Greek word "eicosa", meaning twenty. These lipids are essential mediators in amplifying or dampening inflammation, and promoting tissue remodeling and wound healing. Eicosanoids are not typically stored within cells, but are produced and secreted rapidly after cell activation.

The history of LTs begins in the 1930s with the identification of an alcohol soluble molecule present in the sputum of asthmatic patients which is capable of stimulating smooth muscle cells [1]. A similar phenomenon was described by a substance generated *de novo* from guinea pig lungs by snake venom or antigen-stimulated after ovalbumin sensitization [2, 3]. Due to the slow and long-lasting contraction caused by this substance in the smooth muscle cells of the guinea pig intestine, this unknown substance has been called "Slow Reacting Substance (SRS)." In 1958, Walter Brocklehurst demonstrated that during anaphylaxis caused by antigen challenge in the guinea pig ileum, another substance distinct from histamine was capable of promoting smooth muscle contraction [4]. This contraction was slow, long-lasting, and resistant to antihistamines, and it was, for the first time, considered an effect of "slow-reacting substance of anaphylaxis (SRS-A)" [5, 6]. Only in the 1970s, SRS was identified as a member of the LT class and named as LTC<sub>4</sub> [7, 8].

LTs were named by Samuelsson in 1977, who recognized that leukocyctes produce oxygenated metabolites with three conjugated double bonds in the chemical structure [9]. Therefore, the term leukotrienes were used to identify structures containing three double bonds "tri-enes" that are generated by "leuko"cytes. An extension of these studies led to the characterization of a product derived from arachidonic acid (AA) metabolism, named LTB (12R-dihydroxy-6,14-cis-8,10-transeicosatetraenoic acid) [10, 11]. Later, leukotriene  $A_4$  (LTA<sub>4</sub>) (5,6-epoxy-7,9,11,14-eicosatetraenoic acid) was identified as a precursor required for the formation of LTB<sub>4</sub> and LTC<sub>4</sub>, which for a long time were known as SRS [7, 8].

### 4.2 LT Biosynthesis and Their Pharmacological Inhibitors

LT production occurs mainly in immune cells activated by different receptors, such as FcRs,  $G\alpha_q$ , or  $G\alpha_i$ -coupled receptors and growth factors on the cell membrane [12].

The synthesis of LTs involves several ratelimiting steps that comprise the activation of phospholipase  $A_2$  (PLA<sub>2</sub>) and arachidonic acid (AA) release from phospholipids in the cellular membranes [13, 14] (Fig. 4.1). AA is converted to 5-hydroperoxy-eicosatetraenoic acid (5-HPETE) and subsequently to an unstable intermediate, LTA<sub>4</sub>, by the enzyme 5-lipoxygenase (5-LO). When 5-LO is activated, it translocates from its cytosolic or nucleoplasmic location to the perinuclear envelope, where it acts in concert with 5-LO-activating protein (FLAP), which is required for 5-LO to function enzymatically in intact cells in order to generate  $LTA_4$  [14–16]. In neutrophils, LTA<sub>4</sub> hydrolase (LTA<sub>4</sub>H) is highly active and preferentially generates LTB<sub>4</sub> and dihydroxy LT [17]. In mast cells, eosinophils, basophils, and some types of macrophages, LTA<sub>4</sub> is conjugated with reduced glutathione by LTC<sub>4</sub> synthase to form  $LTC_4$  [18]. Following specific export, LTC<sub>4</sub> is converted by the extracellular enzymes  $\gamma$ -GT and  $\gamma$ -GL to LTD<sub>4</sub>, and LTE<sub>4</sub> by dipeptidase, and are collectively known as cysteinyl leukotrienes (CysLTs) [18].

The primary cellular sources of  $LTB_4$  in both murine and humans are granulocytes, monocytes, and macrophages (Table 4.1) [19], while the main cellular source of CysLTs are eosinophils [20, 21]. However, murine (RAW264.7 and J774) and human (THP1 and U937) macrophage cell lines express low levels of 5-LO and produce barely detectable levels of LTB<sub>4</sub>, which make these cell lines unsuitable models for LT research [22]. Some cell types, even non-immune cells,



**Fig. 4.1** Leukotriene biosynthesis and drug targets. Inflammatory receptor signaling triggers the cPLA<sub>2</sub> activation and release of arachidonic acid (AA) that is further metabolized to LTA<sub>4</sub> by 5-LO and FLAP in a twostep reaction involving the formation of 5(S)HpETE and the intermediate LTA<sub>4</sub>. The enzyme LTA<sub>4</sub>H metabolizes LTA<sub>4</sub>

to LTB<sub>4</sub> or LTC<sub>4</sub> by LTC<sub>4</sub>S. LT biosynthesis can be inhibited pharmacologically by specific inhibitors at various synthesis steps: LT, leukotriene, cPLA<sub>2</sub>, cytosolic phospholipase  $A_2$ ; 5-LO, 5-lipoxygenase; FLAP, 5-LO-activating protein; LTC<sub>4</sub>S, LTC<sub>4</sub> synthase; LTA<sub>4</sub>H, LTA<sub>4</sub> hydrolase

**Table 4.1** Expression of LT synthesis enzymes

Cell types	5-LO	FLAP	LTA <sub>4</sub> hydrolase	LTC <sub>4</sub> synthase
Neutrophil	+++	+	+++	±
Monocyte/macrophage	++	+	+++	+
Dendritic cell	+	+	++	+
Mast cell	+	+	+	++
Eosinophil	+	+	+	++
Endothelial cell	-	-	+	+
Red blood cell	-	-	+	-
Keratinocyte	±	_	+	+

+ indicates relative amounts of enzymes or receptors produced by various cell types. – indicates a lack of expression.  $\pm$  indicates minimal to no expression

have been reported to express some but not all of the LT-synthesis enzymes, which renders these cells incapable of synthesizing leukotrienes independently (Table 4.2). However, these cells may contribute to the synthesis of LTs in a process known as transcellular biosynthesis [23]. Examples of transcellular biosynthesis of LTB<sub>4</sub> are with neutrophils/erythrocytes and keratinocytes/endothelial cells [24–28]. The capabilities of individual cell types to produce various types of LTs depend on the expression of LT synthesis enzymes (Table 4.2).

**5-LO** 5-LO activity is reliant on various signals, including calcium release and phosphorylation, which control the catalytic site and the translocation of 5-LO within the cell [13, 14]. In a resting cell, 5-LO location varies depending on the cell type [29]. In neutrophils and peritoneal macrophages, 5-LO is located in the cytosol, whereas in

Cell type	Cytokines/Growth factors	Bacteria	Opsonized pathogen	Fungi	Viral
Neutrophil	++	++	+++	++	++
Monocyte/macrophage	++	++	+++	++	++
Dendritic cell	+	++	ND	+	+
Mast cell	+	+	ND	+	+
Endothelial cell	±	±	±	±	±

 Table 4.2
 Relative induction of LTs produced in response to various stimuli

+ indicates relative amounts of  $LTB_4$  or cysLTs produced in response to various stimuli or receptors produced by various cell types.  $\pm$  indicates minimal to no production of LTs. *ND* not determined

alveolar macrophages and Langerhans cells, 5-LO is located within the nucleus [30-32]. Upon cell activation, increased intracellular calcium levels induce 5-LO translocation to the perinuclear or plasmatic membrane where it can metabolize AA into LTA<sub>4</sub> [33]. 5-LO activity is triggered by various stimuli such as pathogens, cytokines, and immune complexes (Table 4.2) [34, 35]. Upon infection, pathogens have limited abilities to increase intracellular calcium levels and therefore are weak 5-LO activators alone. However, treating infected cells with a calcium ionophore or opsonized zymosan particles can significantly enhance LT synthesis [36, 37]. The molecular mechanisms that regulate 5-LO activation are reviewed here [38, 39].

The 5-LO pathway has been involved in the development and progression of many pathologic disorders, such as asthma, allergic rhinitis, cardiovascular diseases, and rheumatoid arthritis [15]. Since there is an increasing number of indications that anti-LT drugs can show protective effects, the development of 5-LO inhibitor agents becomes increasingly important. Although many 5-LO inhibitors have been developed, Zileuton (Zyflo, Leutrol – Abbot) is the only 5-LO inhibitor approved to use in humans. However, this inhibitor can induce liver toxicity and has a short half-live (drug needs to be administered up to 4 times a day) [40, 41]. Zileuton is an iron-ligand inhibitor that inhibits enzyme activity through chelation of the central iron atom and/or by stabilizing the ferrous oxidized state [42]. Zileuton inhibits an estimated 26-86% of endogenous LT production [43].

Many other 5-LO inhibitors were also tested for human use to treat asthma, ulcerative colitis, cardiac failure, and irritable bowel diseases, but they all failed in either phase II or III clinical trials. At this moment, the inhibitor MK-0633 is in phase II of a clinical trial to treat asthma, but also show hepatotoxic effects [44].

FLAP Another important alternative to inhibit LT production is to prevent FLAP actions. Merck-Frost discovered the first class of FLAP inhibitors (MK-886) during a screening of indole compounds derived from indomethacin and sulindac. MK-886 works by preventing the binding to arachidonic acid on FLAP and preventing the transfer of the substrate to 5-LO [45]. Further clinical testing was discontinued due to inefficacy since the treatment of asthmatics with MK-886 showed 50% inhibition of  $LTB_4$  in ex vivo-stimulated whole blood and urinary LTE<sub>4</sub> levels [46]. A few years later, Merck developed the second generation of FLAP inhibitors. Like MK-886, MK-0591 blocks 5-LO activity by binding to FLAP, preventing 5-LO activation [47]. The further development of MK-0591 was discontinued after results from further clinical testing showed limited therapeutic potential [47]. Recently, the FLAP crystal structure was resolved, which promises to be very useful in drug design [48]. One FLAP inhibitor, DG031 (Veliflapon, deCODE genetics), is being reformulated for use in phase III clinical trials in the prevention of myocardial infarction [49].

LTA<sub>4</sub>H LTA<sub>4</sub>H is a complex enzyme that exhibits an epoxide hydrolase activity responsible for stereo-specific conversion of LTA<sub>4</sub> to LTB<sub>4</sub>, and an aminopeptidase with preference tripeptides [50]. The most specific and potent LTA<sub>4</sub>H inhibitors are derived from broad-spectrum aminopeptidase inhibitors, with ubenimex (also known as bestatin) representing the unique LTB<sub>4</sub> pathway inhibitor to gain approval to treat human disease [51]. At least six LTA<sub>4</sub>H inhibitors of the current generation have entered clinical trials, with five of these reaching Phase II [51]. Furthermore, the LTA<sub>4</sub>H inhibitors with broad aminopeptidase inhibitory activity have moved the farthest in the clinic. Although the efforts to generate several potent and specific LTA<sub>4</sub>H inhibitors, these drugs have failed to demonstrate clinical efficacy or have harmful side Recently, Acebilustat (CTX-4430) effects. showed functional selectivity for LTA<sub>4</sub>H epoxide hydrolase, and three trials in phase I showed that Acebilustat inhibits ex-vivo stimulated production of LTB<sub>4</sub>, CYP3A4 induction, and reduces inflammatory mediators in the blood and sputum of cystic fibrosis patients [52–54]. These data resulted in advancing Acebilustat to a phase II clinical trial to investigate expiratory volume in cystic fibrosis patients. Also, Acebilustat is being tested in the lesions of patients with acne vulgaris. Although these phase II studies have been finished, the reports were not published yet [52–54]. LTA<sub>4</sub>H expression has been associated as a risk factor for myocardial infarction (MI). It was shown that DG051 (deCODE genetics) have effects on dose-dependent reductions in blood LTB<sub>4</sub> levels in patients with a history of MI or coronary artery disease and that this drug is safe and welltolerated, with an excellent pharmacokinetic profile (phase I study) [51]. Recently, a phase II clinical trial started to test DG051 ability to prevent MI in 400 patients, but whether this drug is effective remains to be published [51].

# 4.3 LT Receptors, Signaling and Their Antagonists

LT receptors are G protein-coupled receptors (GPCR) located on the outer plasma membrane of both structural and immune cells. These receptors comprise a family of structurally related GPCRs that elicit intracellular signaling by activating  $G\alpha_q$  or  $G\alpha_i$  [17] (Fig. 4.2).

CysLTRs The CysLTs/CysLTR axis is initiated by a variety of signals induced by agents that enhance calcium production, TLRs, cytokines, and opsonins and amplified by the inflammatory milieu and therefore could lead to adaptive immune responses [21, 34]. Since cysLTs have brief half-lives in vivo, it is expected that LTC<sub>4</sub> and LTD<sub>4</sub> might exert acute/subacute effects in cells, but due to the high stability of LTE<sub>4</sub>, it is anticipated that this cysLTs might have chronic effects in vivo [21]. CysLTs have been implicated in a myriad of diseases, from cancer to the pathophysiology of bronchial asthma and allergic rhinitis [55]. This is because both a 5-LO inhibitor and CysLT<sub>1</sub> antagonist have proof efficacy to treat these diseases [56–58]. These receptor blockers were developed from functional studies before any components of the pathway had been cloned and molecularly characterized [21].

The receptors for cysLTs are members of the GPCR family, and so far, at least five different receptors have been identified: CysLT<sub>1</sub>, CysLT<sub>2</sub>, P2Y<sub>12</sub>, GPR99, and GPR17. These receptors show different affinities for cysLTs, being that  $CysLT_1$  binds  $LTD_4 > LTC_4 = LTE_4$ .  $CysLT_2$ binds both  $LTC_4 = LTD_4 > LTE_4$  [55]. Recently, GPR17, GPR99, and P2Y<sub>12</sub> were described as a high-affinity receptor for  $LTE_4$  [59] (Fig. 4.2).  $CysLT_1$  is widely expressed in spleen, lungs, small intestine, colon, and skeletal muscle, while CysLT<sub>2</sub> is exclusively detected in heart, adrenals, spleen, lymph nodes, and brain [60]. CysLT<sub>1</sub> is mainly expressed in monocyte/macrophages, neutrophils, and mast cells [21, 61]. Interestingly, CysLT<sub>2</sub> is expressed in eosinophil, muscle cells, and interstitial macrophages [21, 61] (Table 4.3).

CysLT<sub>1</sub> and CysLT<sub>2</sub> are GPCRs that use both pertussis toxin (PTX)-sensitive ( $G\alpha_i$ ) and PTXinsensitive G proteins ( $G\alpha_q$ ) that culminates in decrease cAMP abundance or Ca<sup>2+</sup> mobilization and phospholipase C activation, respectively [55]. These varieties of downstream signaling effectors lead to differential activation of many downstream kinases, such as JNK/AP1 signaling, PI3K, Akt, MAPK/ERK1/2, and different PKCs [55]. The activation of pleiotropic signaling pro-



**Fig. 4.2** Leukotriene receptors and specific antagonists. Leukotrienes bind to its specific receptors (BLT<sub>1</sub>, BLT<sub>2</sub>, CysLT<sub>1</sub>, CysLT<sub>2</sub>, and GPR99) with different affinities, leading to specific cell changes. The pharmacological

agents directed against to prevent receptor signaling. 12-HHT, 12-Hydroxyheptadecatrenoic acid is an eicosanoid that shows a high affinity to  $BLT_2$ 

Cell type	BLT <sub>1</sub>	BLT <sub>2</sub>	CysLT <sub>1</sub>	CysLT <sub>2</sub>
Neutrophil	+	+	±	±
Monocyte/macrophage	+	+	+	+
Dendritic cell	+	+	+	+
Mast cell	+	+	+	+
Eosinophil	+	+	+	+
Endothelial cell	+	+	+	+
Red blood cell	-	-	-	-
Keratinocyte	+	+	+	ND
B Lymphocytes	ND	+	+	ND
CD4 T cells	+	+	+	ND
CD8 T cells	+	+	ND	ND
Hematopoietic stem cells	ND	+	+	ND

 Table 4.3
 Cellular distribution LT receptors

+ detection; - not detected, ± minimal expression of the receptors in various cell types. ND not determined

grams is responsible for the actions of various transcription factors and, consequently, different pathologies [55]. CysLT<sub>1</sub> mediates bronchocon-

striction, mucous secretion, and edema in the airways, being an essential therapeutic target in the treatment of asthma [62]. CysLT<sub>1</sub> abundance can

be influenced by Th2 cytokines and as part of a positive feedback loop [62]. CysLT<sub>1</sub> also amplifies Th2 responses [62].

Since LTE<sub>4</sub> can elicit cellular responses in  $CysLT_1$  and  $CysLT_2$  deficient cells [63], the search for another LTE<sub>4</sub> receptor has been at the center of intense research. Two GPCRs were found to bind to LTE<sub>4</sub>. The first LTE<sub>4</sub> receptor identified was  $P2Y_{12}$  [64]. Genetic deletion of this receptor prevented LTE<sub>4</sub>-mediated production of chemokines and cytokines, as well as ERK1/2 activation in mast cell [21, 63]. GPR99 was initially described as a receptor for alphaketoglutarate, and then demonstrated to be imporant for  $LTE_4$  signaling [21, 59]. GPR99 is a  $G\alpha_{\alpha}$ -coupled receptor expressed in respiratory epithelial cells and mediates mucin release in animal models of asthma [65]. GPR17 is a member of the P2Y receptor family and can recognize both cysLTs and uracil nucleotides [66]. GPR17 activation decreases cAMP, suggesting that this receptor is coupled to  $G\alpha_i$ . Interestingly, it has been suggested that GPR17 inhibits CysLT<sub>1</sub> in models of allergy [67].

CysLT<sub>1</sub> antagonists in the market are montelukast (Singulair), pranlukast (Onon), and zafirlukast (Accolate), and are prescribed to treat asthma and rhinitis. Montelukast, which is administered orally once daily, is the most prescribed antagonist for asthmatic patients [57]. Pranlukast is an orally administered, selective, and competitive CysLT<sub>1</sub> antagonist [68]. This drug is effective for chronic bronchial asthma. Furthermore, pranlukast has also shown to be effective in decreasing nasal eosinophil cationic protein and obstruction [69]. Zafirlukast is approved for the treatment of asthma in patients with 7 years of age or older [70].

**LTB**<sub>4</sub> **Receptors** LTB<sub>4</sub> induces cellular changes via its interaction with two G protein-coupled receptors, BLT<sub>1</sub>, and BLT<sub>2</sub> [71]. LTB<sub>4</sub> was one of the first chemoattractant identified, but the discovery of LTB<sub>4</sub> receptors was challenging. The high-affinity receptor, BLT<sub>1</sub>, was cloned in 1997 from the neutrophil-like HL-60 cells and showed a direct association between LTB<sub>4</sub> and BLT<sub>1</sub> in mediating neutrophil chemotaxis [72]. The lowaffinity LTB<sub>4</sub> receptor, BLT<sub>2</sub>, was also identified by Yokomizo et al. [73]. The genes of both receptors are located close to each other in human as well as mouse genomes [74]. Distribution of BLT<sub>1</sub> and BLT<sub>2</sub> on cells and tissues vary between mouse and human [71]. In human cells,  $BLT_1$ expression is limited to leukocytes, and BLT<sub>2</sub> is ubiquitously found on many cell types (Table 4.3). On mouse cells,  $BLT_1$  expression is detected on leukocytes, and BLT<sub>2</sub> is reported to be limited to the intestinal epithelium and keratinocytes [71, 74]. BLT<sub>1</sub> can be coupled to  $G\alpha_i$ ,  $G\alpha_a$ , or  $G\alpha_{16}$ that results in decreased cyclic AMP (cAMP) levels and increased intracellular calcium levels, respectively [75].  $LTB_4$  activation of  $BLT_1$ enhances antimicrobial effector function activities in macrophages and neutrophils [76]. BLT<sub>1</sub> activation increases host defense during infections caused by different pathogens, including bacteria, viruses, fungi, and protozoan parasites. It does so by enhancing phagocytosis mediated by different phagocytic receptors, including FcyR1, Dectin1, mannose receptor, and CR3 in macrophages and neutrophils [77].  $LTB_4/BLT_1$ axis also enhances phagocyte antimicrobial effectors, such as reactive oxygen and nitrogen species, as well as the production of antimicrobial peptides [76]. Also, we and others have shown that topically or aerosolized LTB<sub>4</sub> can enhance in vivo host defense in the lungs or skin by enhancing phagocyte antimicrobial arsenal [78]. Furthermore,  $LTB_4/BLT_1/BLT_2$  activation is a crucial step in mounting the inflammatory response by activation inflammatory transcription factors, such as NFkB and AP1, and inducing a proinflammatory program characterized by the production of cytokines and chemokines, such as IL-1 $\beta$ , TNF $\alpha$ , IL-6, CXCL1, CXCL2 [79, **80**]. In mice,  $BLT_1$  activation is involved in multiple inflammatory diseases as arthritis [81], autoimmune uveitis [82], atherosclerosis [83], and asthma [84]. Also, it has been shown that the  $LTB_4$ -BLT<sub>1</sub> axis stimulates macrophages by enhancing the expression of the Toll-like/IL1 receptor (TIR) adaptor MyD88 by amplifying STAT1 phosphorylation. This allows the activation of TIRs and therefore potentiates the inflammatory response [79].

Although there are reports that leukocytes in mice do not express BLT<sub>2</sub>, others have detected BLT<sub>2</sub> expression in murine phagocytes [85, 86], but its role in inflammatory response and pathogenesis is poorly understood. Although BLT<sub>2</sub> has been shown to induce pro-inflammatory programs, others have shown that BLT<sub>2</sub> is required to decrease airway eosinophilia and decrease IL-13 abundance in murine asthmatic lungs without influencing IL-4 and IgE production [87]. BLT<sub>2</sub> on mast cells mediates the recruitment and accumulation of these cells in response to LTB<sub>4</sub> production at the sites of inflammation [84]. BLT<sub>2</sub>-deficient mice show susceptibility to drug-induced inflammatory colitis [88] suggesting an enhanced epithelial barrier function developed by BLT<sub>2</sub>. In humans, bladder cancer cells express high levels of BLT<sub>2</sub>, and the treatment with BLT<sub>2</sub> antagonist (LY255283) or BLT<sub>2</sub> siRNA results in apoptosis and inhibits cancer cells proliferation [89], suggesting that BLT<sub>2</sub> antagonists might be candidates for therapeutic agents against cancer.

BLT<sub>2</sub> can also bind to other lipid mediators, indicating that the effects of BLT<sub>2</sub> actions are not limited to LTB<sub>4</sub> actions. BLT<sub>2</sub> plays a beneficial role in skin wound healing through 12-Hydroxyheptadecatrenoic acid (12-HHT) actions that mediate TNF- $\alpha$  and MMP production [71]. 12-HHT is important for keratinocyte wound healing in diabetic mice [90]. Additionally, 12(S)-HETE and BLT<sub>2</sub> effects are important for enhancing VEGF expression and promoting wound healing [91]. Although other lipid mediators promote beneficial wound healing responses through BLT<sub>2</sub> signaling, less is known about specific LTB<sub>4</sub>/BLT<sub>2</sub> effects on phagocyte effector functions during infections.

Although there are specific and potent BLT<sub>1</sub>specific antagonists (such as CP105696 [92] and U75302 [93, 94]) none of them are on the market for clinical use. Etalocib (LY293111) have potency for binding to BLT<sub>1</sub> on isolated neutrophils; however, it has off-target agonist activity toward PPAR $\gamma$  [95, 96] [96–98]. Amelubant (BIIL 284) is a synthetic prodrug that can be converted to the active forms BIIL260 and BILL315. These active forms bind BLT<sub>1</sub> with high affinity, while for BIIL 284 binds BLT<sub>1</sub> weakly. Amelubant was tested in at least 18 clinical trials [99]. In the phase I study, Amelubant showed complete inhibition of LTB<sub>4</sub>-induced BLT<sub>1</sub> signaling [51]. In a COPD study, Amelubant reduced macrophage frequency in spontaneous or induced sputum [51]. These results opened a new opportunity to start a phase II clinical trial in the treatment of COPD [100], rheumatoid arthritis (RA) [101], asthma [102], and cystic fibrosis [103]. However, these trials showed that Amelubant is not effective in tests of exercise endurance in COPD patients [100], asthma tests, and in adults and children with cystic fibrosis was terminated early due to adverse events [104].

### 4.4 Leukotrienes in Metabolic and Cardiovascular Diseases

Obesity, Diabetes, and Insulin Resistance In obesity, hypertrophic adipose tissue stores excess lipids, which trigger inflammation and dysregulate the production of inflammatory mediators [105]. For over a decade, studies have identified high expression of 5-LO and FLAP in adipocytes and adipose tissue (AT)-associated macrophages from subjects with obesity [106, 107]. Increased expression of LT synthesizing enzymes correlates with increased LTB<sub>4</sub> in adipose tissue and LTE<sub>4</sub> in the urine of mice and people with obesity [108]. Increased  $LTE_4$  also correlates with high BMI and leptin (a hormone that controls ingestive behavior and energy balance) [109]. These data suggest that obesity is significantly associated with increased urinary LT levels [109]. A study showed that primary mature adipocytes from both healthy humans and mice, secretes high amounts of both LTB<sub>4</sub> and CyLTs, and it is further increased when mice are fed in a high-fat diet (HFD) [110]. Enhanced LT production enhances T cell recruitment and macrophages infiltration, leading to adipose tissue inflammation and obesity-induced insulin resistance [110]. Pharmacologic and genetic deletion of BLT<sub>1</sub> prevents high fat-induced insulin resistance in liver and skeletal muscle, and prevents inflammation in adipose tissue, while protecting mice from systemic insulin resistance and hepatic steatosis [108] [111]. Importantly,  $LTB_4$  also show detrimental effects induced by low insulin levels. We have shown that 5-LO deficiency protects mice from insulin resistance, and the muscle of those mice have improved insulin signaling which corroborates the lower expression of inflammatory cytokines and higher levels of anti-inflammatory markers in this tissue compared to WT mice in a model of diabetes induced by streptozotocin (STZ) [112].

In type 1 diabetes (T1D), shreds of evidence are not enough to affirm that systemic inflammation caused by  $LTB_4$  is the main reason for insulin resistance. In this case, it is speculated that both features caused by  $LTB_4$  can be interlinked between themselves. However, in HFD-induced production of  $LTB_4$  directly inhibits insulin sensitivity in adipose tissue in a manner dependent on T cell and macrophages activation [113]. This data lead us to speculate that in T1D,  $LTB_4$  may be a common link among metabolic alterations, inflammation, and insulin resistance. Therefore, we speculate BLT<sub>1</sub> antagonist or  $LTA_4H$  inhibition as a novel strategy to improve insulin resistance in metabolic diseases.

Catabolic Diseases T1D is also associated with adipose tissue remodeling [114]. Nevertheless, low levels of insulin lead to a catabolic state characterized by adiposity loss [115]. This catabolic state affects the accumulation of lipids in the circulation of people with T1D positively, and these circulatory lipids do not follow a standard route to the liver [116]. Although replacement of insulin in subjects with T1D mitigates hyperglycemic complications, lipid metabolism is still impaired in T1D, which associates with comorbidities, such as fat depots in blood vessels [117]. Mice overexpressing FLAP in adipose tissue are leaner and show increased energy expenditure, due to browning of white adipose tissue [118]. We have shown that systemic inhibition of BLT<sub>1</sub> with U75302 protects diabetic mice from adiposity loss and hyperlipidemia [114]. Moreover, the liver of diabetic U75302treated mice recovers the levels of fatty acid synthase (FAS) and its transcription factor, SREBP1

[114]. This data reinforces that the blockade of LTB<sub>4</sub> signaling would improve catabolic state and impaired lipid metabolism in diabetic subjects. Moreover, we have shown that in macrophages, LTB<sub>4</sub> promotes massive accumulation of lipid droplets, which reflects a pronounced energetic metabolism associated with uncoupled mitochondrial respiration [114]. Interestingly, T1D mice treated with U75302 downregulated all metabolic parameters observed in macrophages [114]. More studies are being conducted by our group to better integrate LTB<sub>4</sub> effects on lipid metabolism and inflammation. Interestingly, our preliminary data suggest that 5-LO deficiency protects mice from adiposity loss in a model of STZ-induced diabetes. We are speculating that poorly controlled diabetes leads to browning of adipose tissue and therefore, to a catabolic state that could negatively affect the quality of life of people with diabetes [119].

Hyperlipidemia Hyperlipidemia is characterized by a chronic state of inflammation and activation of resident macrophages [120]. Our group has demonstrated that LTB<sub>4</sub> dictates systemic inflammatory response in a model of hyperglycemia [121] in a manner dependent on macrophages [122]. In a murine model of atherosclerosis, the inhibition of the 5-LO pathway in apolipoprotein E-deficient (ApoE-/-) mice reduces liver injury and enhances cardiovascular protection [123-125]. Hypercholesterolemia is a central risk factor for the initiation and progression of atherosclerotic lesions [126]. LTs enhances the progression of hyperlipidemia-dependent vascular disease and are associated with atherogenesis, cardiovascular disease, myocardial infarction, and stroke [123, 127]. Accordingly, the treatment of apoE-deficient mice with BLT<sub>1</sub> antagonist decreases the development of atherosclerosis [128] and reduces infarct size in a murine model of myocardial ischemia/reperfusion injury [129]. Furthermore, endothelial overexpression of CysLT<sub>2</sub> increases vascular permeability, myocardial ischemia/reperfusion damage, and cardioapoptosis peri-infarct myocyte in areas [130–132]. The treatment of mice with the CysLT<sub>1</sub> antagonist montelukast showed cardioprotective capacities in both animal models and clinical trials, suggesting that blocking cysLTs could show beneficial effects in models during cardiac events [133–137].

4.5 Future Directions for Drug Discovery

Since LTs were discovered in the 1970s, and about 20 years since the availability of LT-targeting drugs, several new roles for LTs were discovered. These new insights range from new receptors, new biological functions, and new roles in different disease states. One potential new frontier to be explored is a possible role for LTs in the neuro-immune axis during obesity. There are many potentials for the crosstalk between LTs and sympathetic neuron- associated macrophages (SAMs) and lipid storage. Possibly, LTB<sub>4</sub> may act as a promoter of SAMs NE-uptake activity in adipose tissue of obese subjects. In parallel, in asthma, beta-adrenergic receptors activation is impaired in airway smooth muscle [138], and for this reason,  $\beta$ 2-adrenoceptor agonists are often used for the treatment of asthma [139]. β2-adrenoceptor agonists reduce cysLT synthesis by eosinophils, therefore, a potential cross-talk between  $\beta$ 2-adrenoceptor agonists and LT production or actions could potentially affect the outcome of allergic diseases.

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5

Epoxy Fatty Acids Are Promising Targets for Treatment of Pain, Cardiovascular Disease and Other Indications Characterized by Mitochondrial Dysfunction, Endoplasmic Stress and Inflammation

Cindy McReynolds, Christophe Morisseau, Karen Wagner, and Bruce Hammock

### Abstract

Bioactive lipid mediators resulting from the metabolism of polyunsaturated fatty acids (PUFA) are controlled by many pathways that regulate the levels of these mediators and maintain homeostasis to prevent disease. PUFA metabolism is driven primarily through three pathways. Two pathways, the cyclooxygenase (COX) and lipoxygenase (LO) enzymatic pathways, form metabolites that are mostly inflammatory, while the third route of metabolism results from the oxidation by the cytochrome P450 enzymes to form hydroxylated PUFA and epoxide metabolites. These epoxygenated fatty acids (EpFA) demonstrate largely anti-inflammatory and beneficial properties, in contrast to the other metabolites

formed from the degradation of PUFA. Dysregulation of these systems often leads to chronic disease. Pharmaceutical targets of disease focus on preventing the formation of inflammatory metabolites from the COX and LO pathways, while maintaining the EpFA and increasing their concentration in the body is seen as beneficial to treating and preventing disease. The soluble epoxide hydrolase (sEH) is the major route of metabolism of EpFA. Inhibiting its activity increases concentrations of beneficial EpFA, and often disease states correlate to mutations in the sEH enzyme that increase its activity and decrease the concentrations of EpFA in the body. Recent approaches to increasing EpFA include synthetic mimics that replicate biological activity of EpFA while preventing their metabolism, while other approaches focus on developing small molecule inhibitors to the sEH. Increasing EpFA concentrations in the body has demonstrated multiple beneficial effects in treating many diseases, including inflammatory and painful conditions, cardiovascular disease, neurological and disease of the central nervous system. Demonstration of efficacy in so many disease states can be

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ing the sEH or administration of EpFA mimics that block metabolism are in progress.

cacy by increasing EpFA that include inhibit-

 $PUFA \cdot sEH \cdot Oxylipin \cdot Epoxide \cdot Lipid metabolism$ 

# 5.1 Introduction

# 5.1.1 Production of Hormones and Other Chemical Mediators

Lipids are an important component of human health, providing a source of energy, maintaining cellular integrity and acting as regulators of cell signaling. These bioactive lipids include steroids, diacyl glycerol (DAG), sphingolipids, phosphatidylinositol phosphate (PIP), phosphatidylcholine (PC), and polyunsaturated fatty acids (PUFA). They range in function from energy storage and generation through beta-oxidation (PUFA), cellular proliferation (PIP), insulin regulation (DAG), cellular protection (sphingolipids), pulmonary function (PC), and maintaining cell structure (cholesterol). However, the metabolism of these lipids often produces more potent biological mediators than the parent molecule. For example, PUFAs, which circulate through blood as triglycerides or as free fatty acids, can also be incorporated into adipose tissue or the membranes of cells that are further released upon insult or response to cell signaling, and their metabolism produces potent inflammatory and anti-inflammatory compounds that have profound effects on the body. Due to their potent effects, inhibitors that alter their metabolism represent one of the earliest

drug targets of the pharmaceutical industry. For example, aspirin was discovered in the late 1800s although its mechanism of action as both a reversible and irreversible cyclooxygenase (COX) inhibitor that blocked the formation of prostaglandins (PG) was not identified until the early 1970s, and is still debated [1]. Blocking COX activity and the formation of inflammatory PG compounds resulted in one of the largest selling classes of drugs, NSAIDs, on the market today. In addition to COX metabolism, PUFA are also metabolized by the lipoxygenase (LO) and cytochrome P450 (CYP450) enzymes that have more recently attracted attention for their potential in modulating disease. LO inhibitors are targeted for their ability to inhibit the formation of inflammatory leukotrienes, and Zileuton, a 5-LO inhibitor, is used for the treatment of asthma [2] by blocking the formation of inflammatory leukotrienes. In contrast to COX and LO metabolism, the CYP branch of PUFA metabolism results in the formation of both inflammatory hydroxylated metabolites as well as ant-inflammatory fatty-acid epoxides (Fig. 5.1). Disease altering strategies targeting the CYP450 branch of the pathway focuses on increasing these beneficial epoxy fatty acids (EpFA). However, so far, few drugs specifically targeting this pathway have reached the market although several currently approved drugs alter EpFA concentrations through their action on enzymes and their metabolites in the CYP450 branch of the arachidonic acid cascade. This chapter will focus on the biological activity of these largely beneficial lipid epoxides, as well as strategies for developing pharmaceutical interventions to increase their concentrations in the body.

# 5.1.2 Polyunsaturated Fatty Acids: The Essential Fatty Acids

PUFA are named for the presence of two or more double bonds in the mid-long chain carbon backbone that ranges in length from 16 to 24 carbons or longer. They are considered essential because the body cannot synthesize them naturally and must consume them in order to maintain health;



**Fig. 5.1** Metabolic fate of polyunsaturated fatty acids Free fatty acids are primarily metabolized through  $\beta$ -oxidation, Cyclooxygenase (COX), Lipoxygenase (LOX or LO), and CytochromeP450 (CYP450). A simplistic overview of the biological action of the resulting metabolites is shown in parenthesis.

**COX 1 and COX 2** metabolize PUFA to PGH2 which is the precursor to other inflammatory prostanoids and thromboxanes that regulate the immune system (PGD<sub>2</sub>), increase pain and inflammation (PGE<sub>2</sub>) and control platelet aggregation (PHI<sub>2</sub> and TXA<sub>2</sub>). [108]

**5-LO** metabolizes PUFA to 5-HpETE or **15-LO** to 15-HpETE, both are precursors to inflammatory leukotrienes and cytotoxic leukotoxins. These metabolites are important in exacerbating asthma by acting as powerful bronchoconstrictors, and they can also sustain inflammatory reactions through chemotaxis of inflammatory mediators. LO metabolism of omega-3 fatty acids result in

however, with the proper precursors, PUFAs can be altered and interconverted. Depletion of either omega-3 or -6 PUFA result in serious side effects such as neuronal and vision impairment, skin anomalies, thrombocytopenia and intellectual disability [3]. PUFA in the body are either circulating as free fatty acids or incorporated into glycerides and cellular membranes. Upon injury or stress, PUFA are released from cell membranes by phospholipase acetyltransferases (PLA) and other enzymes. PLA2 liberates PUFA pro-resolving lipid mediators called Resolvins, Protectins and Maresins. [139]

CYP450 metabolizes PUFA to anti-inflammatory epoxy fatty acids (EpFAs), n-terminal hydroxylated n-HETE, ω-1 oxidation, or allylic hydroxylations. 20-HETE regulates blood pressure by acting as a potent vasoconstrictor in kidneys and preventing sodium reabsorption in nephrons [140, 141]. The biological significance of mid-chain hydoxylations is less understood; however, biological significance has been observed with 12-HETE in corneal inflammation neovascularization [142, and 1431. Formation of EpFA, particularly if induced, is primarily accomplished by CYP2C and CYP2J subfamily; however, other CYP enzymes can generate EETs [144]. The EpFA act as homeostatic regulators to other metabolites in this pathway by stabilizing mitochondria, reducing ROS, decreasing ER-stress [20] and inflammation [15], regulating the vascular endothelium [88] and increasing bronchodilation [145]

from the triglycerides to release free fatty acid (FFA), but also PLC and PLD further act to increase FFA in circulation (Fig. 5.2). Once freed from the plasma membrane, FFA are rapidly metabolized by  $\beta$ -oxidation or other enzymatic metabolism [4] (Fig. 5.1). As mentioned above, the three main enzymes responsible for non-catabolic metabolism of PUFA are COX, LO and CYP450. The COX and LO enzymes form primarily inflammatory mediators, and therapeutic interventions focus on blocking the formation of



Fig. 5.2 Formation of EpFA

Polyunsaturated fatty acids (PUFAs) differ in both structure and function based on number of carbons and location of double bonds. They are incorporated as glycerides in fat cells, cellular membranes or circulating micelles and are liberated to free fatty acids by different phospholipases (PL) that act upon different areas of the glyceride or phospholipid (A). EpFA are formed through the oxygenation of FFA by CYP450. The metabolism of Arachidonic Acid (AA, 20:4 n-6) by cytochrome P450 yields EpFAs, epoxyeicosatrienoic acids (EET), which are further degraded by the soluble epoxide hydrolase into dihydroxyeicosatrienoic acids (DHET). The epoxide and diol on the 11,12 position is shown, but similar regioisomers are possible on all the double bonds in the PUFA. The n-6 fatty acid linoleic acid, LA, has been attributed to largely inflammatory epoxides, EPOMES; however, recent studies show that they are only toxic in the presence of sEH, suggesting that the diols of LA, DIHOMES, are responsible for this inflammatory action [137]. The 18:3 omega-3 fatty acid, linolenic acid (ALA), does not seem to have this same inflammatory action. The omega-6 fatty Adrenic Acid, AdA, is named for its abundance in the adrenal gland. Less is known about this PUFA and its metabolites, although the AdA EpFA, dihomoEETs are thought to regulate blood flow to the adrenal gland [138]. n-3 fatty acids alpha eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) form EpFA epoxyeicosatetraenoic acids (EEQs) and epoxydocosapentaenoic acids (EDPs) respectively. Omega-3 EpFA are largely beneficial with anti-inflammatory and pain resolving properties in vitro and in vivo. Little biological activity has been associated with the diols of Ada (dihomoDHET) or the diols of EPA and DHA, dihydroxyeicosatetraenoic acids (DHEQs) and dihydroxydocosapentaenoic acids (DiHDPAs) respectively. (see [86] for review)

these compounds. In contrast, the CYP450 metabolism results in the formation of both hypertensive and inflammatory hydroxylated compounds, as well as and anti-hypertensive and anti-inflammatory epoxide compounds. Therapeutic interventions discussed here focus on increasing the concentration of the anti-inflammatory epoxide metabolites.

# 5.2 Epoxy Fatty Acids Are Therapeutic Targets for Disease

# 5.2.1 Epoxy Fatty Acids (EpFA) Are Important Signaling Molecules That Are Regulated by Their Metabolism

EpFA are formed from the activity of CYP450, a large class of metabolizing enzymes that oxidize fatty acids as well as xenobiotics using heme as a

co-factor. The addition of molecular oxygen results in the formation of compounds from the epoxidation of double bounds, end terminal hydroxylation or allylic oxidation [5] each with unique biologies and roles in disease. EpFA have positive beneficial effects on maintaining endothelium function, inflammation and cellular oxidative stress. As early as 1986 and continuing through present day, CYP450 metabolites were identified as influencing blood pressure and renal function by regulating vascular smooth muscle proliferation through MAP kinase signaling pathways [6], anti-aggregation of platelets by decreasing leukocyte adhesion to endothelial cells [7], and regulating vascular tone. Vascular tone, in part, is regulated by the balance of hydroxylated and epoxygenated CYP450 PUFA metabolites. The 20-hydroxy-fatty acids (20-HETE) act as vasoconstrictors by hyperpolarizing vascular smooth muscle cells through activation of the protein kinase C pathway, while the epoxy fatty acids hyperpolarize vascular endothelium through activation of voltage-gated potassium (BK) channels. In this way, the two metabolites act as homeostatic regulators to prevent pathological changes in vascular tone [8, 9]. Although increased 20-HETE results in endothelium dysfunction and increased hypertension, increased EpFA decrease blood pressure, but has not been shown to cause hypotension [10, 11]. This provides strong evidence that EpFA are homeostatic regulators of endothelium function [12, 13]. EpFA also show other beneficial biologies, including potent anti-inflammatory effects and decreasing the endoplasmic-reticulum (ER) stress response pathway [14]. EpFA act as anti-inflammatory agents by reducing the nuclear translocation of NF-kappaß, thereby preventing the transcription of a number of inflammatory cytokines and synthesis of inflammatory eicosanoids [15, 16]. Furthermore, the diol metabolite of EpFA metabolism drives monocyte chemotaxis in response to monocyte chemoattractant protein, MCP-1. Thus preventing the metabolism of EpFA by the sEH further regulates inflammation by decreasing monocyte infiltration [17]. EpFA have demonstrated a wide range of beneficial effects in animal models of disease

[18] which is not fully explained by antiinflammatory or endothelial homeostasis, but possibly explained by the regulation of ER-stress by EpFA. ER-stress is a protective mechanism deployed by the cell to overcome cellular stress and prevent deleterious mutations. The ER-stress pathway is a homeostatic mechanism regulating cellular responses to the presence of increasing misfolded protein resulting from oxidative, physiological or pathological stressors. Although a fundamental mechanism in maintaining homeostasis, this response is often upregulated in disease, and if not controlled, will result in increased inflammation or activation of cell death pathways. Preventing or reducing the inflammatory and apoptotic branches of ER-stress is associated with many beneficial disease treatments [19], and EpFA have demonstrated the ability to reduce ER-stress [20]. These ubiquitous mechanisms (inflammation, endothelial function, and ER-stress) underlie many diseases and are regulated by EpFA, which may explain why preclinical models investigating the role of EpFA indicate beneficial results in many different diseases when these lipid mediators are maintained.

In normal cell systems, and increasingly in disease, EpFA are rapidly removed from circulation either because they are re-incorporated back in cellular membranes, metabolized by betaoxidation, or further degraded by epoxide hydrolases [21]. Metabolism enzymes generally increase polarity of compounds to aid in their elimination from the body, and the metabolism of PUFA are no different. After metabolism by the CYP450, the EpFA are further degraded by epoxide hydrolases into the corresponding polar vicinal diols which diffuse from the cells or are rapidly conjugated and removed from the body. In many diseases, the sEH activity is upregulated compared to healthy controls, thus inhibiting its activity in disease settings indicate a potential target for increasing EpFA as a potential therapy.

The epoxide hydrolases are catalytically active dimers that convert xenobiotic or PUFA epoxides to corresponding diols through an exothermic, 2-step hydrolysis reaction (Fig. 5.3) [22]. There are four structurally related isozymes in the epoxide hydrolase family of enzymes



**Fig. 5.3** Mechanism of epoxide to diol metabolism by the soluble epoxide hydrolase (sEH)

Two acidic tyrosines are oriented by pi-stacking to bind to and polarize the epoxide moiety. sEH inhibitors functionally mimic transient intermediates and the transition state

(EPHX1-4) in mammals, in addition to other enzymes that have hydrolase activity such as the leukotriene A<sub>4</sub> hydrolase (LTA<sub>4</sub>H), cholesterol hydrolase, and Peg1/MEST. LTA<sub>4</sub>H metabolizes leukotriene A4 into the leukocyte recruiter, leukotriene B4, to help in the resolution of inflammation. While the functions of PEG/MEST and EPHX4 are not known, isozymes EPHX 1-3 are capable of metabolizing EpFA and differ in cellular location and substrate preference. EPHX1 (mEH), is named for its cellular location: it is found in microsomal membrane fractions in tissue and is active on polyaromatic hydrocarbons found in a variety of xenobiotic epoxides and is also capable of metabolizing EpFA. Conversely, EPHX2 is similarly named as the soluble epoxide hydrolase (sEH) after its predominant location in the cytosolic and peroxisomal fractions of the cell. The EH activity is located at the C-terminus portion of the protein, and the N-terminal portion of sEH has phosphatase activity while the N-terminus of mEH is anchored to the membrane. While mEH is capable of metabolizing both aromatic and aliphatic epoxides, catalytic turnover by the sEH is greater for mono and disubstituted epoxides, making EpFA a good substrate for this enzyme. However, trans, di, tri and even tetra-substituted epoxides can be turned over sometimes with a low Km [23]. Cholesterol epoxides and the squalene epoxide precursor to lanosterol are also substrates of mEH, although

of the enzyme (middle panel). The NH groups of the urea, amide, carbamate or other electronegative groups possibly encourage a salt bridge formation, for example between a polarized urea and the catalytic aspartic acid, likely stabilized by hydrogen bonds with the tyrosine. [146]

the cholesterol epoxide hydrolase and lanosterol synthase are the primary routes of metabolism for these compounds [24]. EPHX3 is also capable of hydrolyzing EpFA with similar efficiency (Kcat/Km) as that of sEH, but a > 10x higher Km indicates that EpFA of arachidonic acid (AA) and presumably other PUFA are a weak substrate for EPHX3 compared to their affinity for sEH or mEH [25].

# 5.2.2 Human Polymorphisms Altering Epoxide Hydrolase Activity Affect EpFA Concentrations and Correlate Epoxides with Disease States

Most EH related mutations in humans that are associated with disease states are associated with EPHX2 (sEH). There are four main mutations that affect enzyme activity, two that do not alter function, and as many as 20 less characterized non-coding mutations that can occur in up to 20% in human populations [26, 27]. The four most common coding mutations result in two gain of function mutations (K55R and C154Y) and two reduced function mutations (R287Q and R103C mutations results in decreased dimerization). These mutations affect the velocity of epoxide hydrolysis while leaving the selectivity for substrate binding and phosphatase activity

apparently unchanged [28, 29] Considering that the concentration of the sEH enzyme (ranging from 3 nM in lung to 400 nM in liver) is often higher than that of the EpFA substrate (low nM in tissue [30–32]), and the concentration of EH enzymes, such as EPHX1 and 3, can convert epoxides to diols, it should be taken into consideration that mutations that only slightly affect enzyme efficiency may not significantly affect EpFA concentration. However, mutations in the sEH and prevalence of SNPs associated with different diseases suggest that this enzyme plays an important role in disease, as described below.

### Mutations in sEH Are Biomarkers of Anorexia

Nervosa In a genome wide association study of patients with anorexia nervosa (AN), investigators identified rare mutations in non-coding regions of the EPHX2 that correlate with disease susceptibility. The activity of the mutations was not determined, but investigations in the levels of epoxide:diol ratios found they were decreased in ill AN patients compared to recovered AN or healthy populations, suggesting an upregulation in the conversion of epoxides to diols. Furthermore, the loss of function mutation, R287Q, occurred less frequently in AN patients compared to healthy populations, further correlating increased sEH activity to higher risk of severe AN [33-36]. Although the exact mechanism for the involvement of EpFA in AN is unknown, considering the impacts of diet and aversion to food in this disease, understanding the role of altered lipid signaling in this disease is of increasing interest.

**Reduced sEH Activity Protects Against Familial Hypercholesterolemia** Familial hypercholesterolemia (FH) is a hereditary disease that causes increased plasma cholesterol concentrations resulting from a defective hepatic low-density lipoprotein receptor (LDLR). In a targeted analysis approach that studied the prevalence of the reduced function sEH mutation, R287Q, in 8 generations of families with FH, Sato et al. discovered that family members with the R287Q mutation had normal cholesterol levels compared to members with the normal 287R

allele. Cholesterol was unchanged in healthy humans with the R287Q mutation [37]. Preclinical investigations further support the role that sEH has in reverse cholesterol transport, and possibly explain the protective effects on inhibiting its activity in LDLR related disease. For example, in Ldlr-/- mice that mimic the FH disease, treatment with the sEH inhibitor (sEHI) t-AUCB decreased atherosclerosis plaques through increasing HDL synthesis and efflux of cholesterol from adipose lesions compared to vehicle treated controls. Further investigation demonstrated that sEHI treated mice had increased ATP binding cassette transporter A1, which is responsible for HDL synthesis through efflux of cellular cholesterol to extracellular apoA1 [38].

sEH Mutations Are Associated with Outcome Measures in Vascular Disease Impaired vascular function contributes to heart disease, agerelated vascular decline, blood pressure and stroke. EpFA act as vasodilators by opening calcium-activated potassium channels that relax the vascular smooth muscle and are thought to mitigate vascular disease [39]; therefore, it is hypothesized that decreased EpFA would contribute to heart disease, and in fact gain-offunction sEH polymorphisms are associated with increased cardiovascular diseases. For example, pregnant women with preeclampsia had higher frequency of the K55R gain of function mutation and lower methylation of the EPHX2 promotor region, causing higher expression, than healthy pregnant women [40]. In another study that analyzed sEH polymorphisms with frequency of stroke in African American and Caucasian populations participating in the Atherosclerosis Risk in Communities study, investigators identified a rare EPHX2 mutation in African Americans that was not found in Caucasian populations. The mutation resulted in increased sEH activity and a twofold to threefold increased risk of stroke. Although the infrequency of the mutation complicated statistical analysis, and larger sample sizes were needed to determine significance. Additional haplotypes in the sEH gene correlated with both increased and decreased risk of stroke

in both races [26]. Although the effect of these gene sequences on enzyme activity is not known, further studies analyzed site-directed mutagenesis on survival rates of ischemic cells in vivo and found that decreased sEH activity with the R287Q mutant conferred to increased survival after inducing a simulated stroke environment of depleted glucose and oxygen [41]. This mutation was also associated with lower risk of stroke in Europeans [42]. Although a large Danish study failed to identify correlations in sEH SNPs and stroke, myocardial infarction or ischemic heart disease [43]. A large study in Swedish men found correlations between the gain-of-function mutation, K55R, with increased risk of stroke [44]. Additionally, Hawaiian Asians with dementia but without prior ischemic injury compared to healthy age-matched controls had increased 14,15 DHET in cortical brain tissue from patients with dementia; however, heterozygous carriers of the reduced function R287Q SNP had increased markers for plaques compared to healthy patients [45]. These data are at odds for understanding if sEH activity protects or contributes to the progress of AD especially considering that dementia correlates with a decreased EET:DHET ratio, suggesting a negative role of sEH in this disease. However, because the R287Q mutation affects dimerization, it's possible that these heterozygous carriers still have functional sEH protein.

In addition to the sEH, the mEH also hydrolyses EpFA into corresponding diols, although with much less efficiency. As discussed later, the association of the mEH in the lipophilic endoplasmic reticulum membrane and with the cytochrome P450 that oxidize epoxy fatty acids may result in greater mEH contribution to diol formation than anticipated from the concentration and kinetic constants of the mEH. Mutations in mEH are also associated with several diseases, including cancer, preeclampsia, seizure, neurological disease, drug-dependence and COPD. However, because this enzyme is primarily responsible for metabolizing aromatic xenobiotic epoxides, it is uncertain if these associations are a result of decreased epoxides in the body, or from accumulation of toxic xenobiotics (reviewed in [46]). Interestingly,

sEH expression in the brain is mostly localized in glial cells of the brain, while mEH is found more throughout the brain, suggesting either a specific role of sEH or more significant contribution of mEH to EpFA metabolism in the brain [47]. Recent studies demonstrate that sEH activity outside the brain can influence depression. In this study, overexpression of sEH in the liver resulted in increased depression in mice, and genetic deletion of sEH in the liver had a positive effect in treating stress-induced depression. This study suggests that peripheral-acting EpFA can influence CNS diseases [48].

# 5.2.3 Laboratory Knockout Models Identify Beneficial Effects of Increasing EpFA in Treating Preclinical Models of Disease

A homozygous mouse model deleting EPHX2 stabilize EpFA and further demonstrate biological activity of increasing EpFA in disease. The first incidence using sEH-/- mice observed decreased blood pressure on a high-salt diet compared to wild-type mice [49], and sEH<sup>-/-</sup> mice are used to further demonstrate that increasing EpFA and decreasing diol formation resolves multiple disease states. For example, sEH null mice demonstrate beneficial effects in decreasing inflammation, maintaining the vascular endothelium, and resolving neuroinflammatory diseases. Specifically, genetic sEH -/- mice demonstrated accelerated wound healing, reduced inflammation in inflammatory bowel disease and LPSinduced inflammatory models, improved insulin signaling in a Type II model of diabetes, reduced cisplatin-induced kidney damage, reduced niacin flushing, reduced arteriosclerosis, smaller infarct size in cerebral artery occlusion/reperfusion injury, decreased hepatic and arterial fibrotic disdecreased depression, ease, autism, and Parkinson's disease (see [50, 51] for review). Recently, tissue specific sEH knockout models demonstrate the local effect that EpFA have on tissues. Mice with podocyte specific sEH knockout were protected from hyperglycemia-induced renal injury resulting from high fat diet or STZ-

induced diabetic hyperglycemia [52]. In further support of the importance of this pathway in disease, the analgesic effects of morphine were attenuated in CYP-null mice that lack the ability to generate EpFA, and in mice administered compounds that inhibit fatty acid oxidizing CYPs [53–55]. Thus genetic models that increase EpFA concentrations through deletion of their metabolism support the beneficial effects of EpFA in treating disease, and models that decrease the ability of animals to form EpFA reduce these beneficial effects, suggesting an essential role of EpFA in disease.

# 5.3 Clinical Approaches for Increasing EpFA Concentrations

The EpFA to diol ratio are reduced in several disease sates suggesting that increasing the EpFA concentrations in the body could provide beneficial effects in preventing or treating disease (Table 5.1). There are many different approaches for increasing concentrations of fatty acid epoxides for the treatment of disease. Strategies include direct administration of PUFA or EpFA, inhibition of EpFA metabolism through chemical inhibitors of sEH (sEHI), induction of EpFA formation through CYP modulators, or directly mimicking the fatty acid epoxide.

### 5.3.1 PUFA Supplementation

Omega-3 supplementation is a widely investigated approach for improving health or treating disease, and the resulting fatty acid epoxides are thought to account for some of the beneficial effects observed with their supplementation [31]. However, randomized clinical trials often fail to support the efficacy observed in meta-analysis of diet behaviors and disease risk [56]. Increased sEH activity in disease would increase EpFA metabolism, thus limiting efficacy and may account for the inconsistent therapeutic benefits reported with omega-3 supplementation. This is possibly due to lipid peroxidation products in **Table 5.1** Altered ratios of EpFA: diol correlate to disease outcomes

#### Alzheimers disease (AD) [130]

AD patients with and without type 2 diabetes (T2D) had increased DHET compared to healthy controls. However, there were no effects following adjustments for multiple comparisons.

### Arthritis [131]

In synovial fluid of arthritic vs. normal joints, 11,12-DHET and 14,15-DHET were higher in affected joints of people with unilateral osteoarthritis. In addition, these and 8,9-DHET were associated with worse progression over 3.3 years.

### Anorexia Nervosa [34, 35]

Ill anorexia nervosa patients have higher DHA diol metabolites 19,20 DiHDPE:EpDPE compared to either recovered AN patients or healthy human subjects, while both ill and recovered AN patients have higher ALA diol metabolites 15,16 DiHODE:EpODE ratios compared to healthy subjects.

#### Peripheral arterial disease [132]

Increased 8,9 DHET correlated with increased risk of coronary and cerebrovascular events in patients with peripheral arterial disease.

#### Coronary artery disease [133]

Decreased EETs in patients with obstructive coronary artery disease compared to healthy controls

### Depression [134]

In patients with major seasonal depression syndrome, sEH-derived oxylipins (12,13 DiHOME, 7,8- and 19,20 DiHDPE), in addition to other eicosanoids, increased in winter compared to summer-fall, while 14,15 EET and corresponding diol both decreased in the winter.

#### Preeclampsia [135]

In preeclamptic women 14,15-DHET was higher in urine samples compared to healthy pregnant women. **Vascular dementia** [136]

In patients with cognitive impairment, an increase in 9,10- and 12,13 DiHOME: EpOME was associated with poor performance in function but not memory.

some omega-3 lipids. Omega-3 lipids are inherently unstable and subject to oxidation, often as much as 200% increase in PUFA peroxides after only 22 days of storage [57], and further oxidation results in aldehydes that are not tested for in commercial settings [58]. The oxidized products are associated with cellular stress and increased cellular toxicities and are hard to detect or control outside of sophisticated analytical labs and thus not a well-controlled approach for improving health or treating disease [59]. Similarly, supplementation with EpFA is also subject to oxidation and provides further challenges because EpFA are also rapidly degraded by acid hydrolysis in the stomach or are eliminated through first-pass metabolism in the liver. An alternative administration route, for example direct application to affected tissue, would avoid first-pass metabolism; however, other metabolizing enzymes would still contribute to rapid elimination. For example, enteric coating to bypass the acid in the gut may provide options for treatment of intestinal diseases; however, metabolizing enzymes in the gut or microbiota containing epoxide hydrolases would further limit their effectiveness. Ocular therapy provides another application to avoid first-pass metabolism; however, recent studies have implicated increased sEH expression as contributing to disease progression in a mouse model of diabetic retinopathy as well as in samples from humans with diabetic retinopathy [60]. Thus, ocular application to treat retinopathy would be susceptible to sEH metabolism possibly demonstrating that disease treatment by direct EpFA supplementation will be difficult due to sample stability and metabolic instability.

### 5.3.2 Increase Formation of EpFA

Clinical and preclinical strategies for investigating biological activity of EpFA have focused on preventing their metabolism either through inhibition of the sEH enzyme or through synthesizing stable EpFA mimics. A third approach involves increasing their formation through CYP450 activity. Preclinical data indirectly suggests that increased CYP activity could reduce certain pathologies. In a mouse model of inflammatory pain, co-administration of a CYP modulator, omeprazole, and the sEHI, TPPU, resulted in increased efficacy compared to either compound administered alone. Omeprazole induces CYA1A1, 1A2, 2B1 and 3A1 and inhibits 2D2 and 2C. CYP2C is a more efficient at forming epoxides of AA (12/8 ratio of epoxidation/ hydroxylation) compared to the other CYP isoforms which form hydroxylated metabolites in greater amounts than EpFA; however, because the other isoforms also form EpFA, increasing

their activity would also increase EpFA as well as hydroxylated PUFA metabolites [61]. This is consistent with the results published in this study showing that the EpFA and hydroxylated metabolites were increased in the plasma of mice treated with both compounds [62]. Hydroxylated metabolites, especially hydroxylated metabolites of 18:2 linoleic acid (LA), are often associated with increased inflammation and oxidative stress [63–66], which brings up another complication with targeting CYP induction to increase EpFA in that it could also increase the production of inflammatory PUFA metabolites that could negate the beneficial effects of EpFA. Preclinical studies demonstrate that administration of ketoconazole, an inhibitor of CYP2A6, 2C19 and 3A4, reduces pain in an inflammatory mouse model by reducing the formation of hydroxy octadecadienoic acid (HODE), the monohydroxy metabolite of LA that causes hyperalgesia through activation of TRPV1 channels [61, 67]. These studies demonstrate that increasing CYP activity is a complicated approach given the promiscuity of the CYP enzymes for forming both anti-inflammatory **EpFA** and preinflammatory hydroxylated PUFA metabolites, as well as influencing the metabolism of other xenobiotics. Thus, increasing CYP activity does not present a viable strategy for clinical utility, and clinical approaches designed to increase EpFA should take into consideration drug-drug interaction potentially affecting EpFA formation if patients are currently taking CYP modulators.

### 5.3.3 Stabilizing EpFA Through Small Molecule Inhibitors of SEH

To overcome metabolic instability of EpFA, sEH inhibitors (sEHI) were identified that mimic the transition state of the epoxide ring opening. The pharmacophore of sEHI consist of a urea, carbamate, or amine heterocycle that mimic the interaction of the substrate and enzyme by forming one or more hydrogen bonds between the NH and aspartate (Fig. 5.3.) The inhibitors contain hydrophobic regions that allow interaction with the

enzyme and maintain high specificity over the mEH, while specifically placed polar side groups increase druggable properties such as water solubility and metabolic stability and increased oral bioavailability. The first generation of sEH inhibitor, 12-(3-adamantan-1-yl-ureido)-dodecanoic acid (AUDA) [68], was a small molecule designed to mimic to 14,15 EET with a dodecanoic acid to mimic the aliphatic chain and carboxylic acid present at the  $\alpha$  end of the fatty acid, an adamantine to mimic the  $\omega$  hydrophobic end of the fatty acid, and urea to act as a mimic to the epoxide and also inhibitor to the sEH enzyme [69]. AUDA is a potent sEHI, with an IC<sub>50</sub> of 3-60 nM, but is short lived in the body ( $T_{1/2} = 2.9$  h in canine PK) due to oxidation of the adamantine and beta oxidation of the alkyl chain, thus limiting its use in vivo to conditions where long half-life is not required. Since AUDA also mimics epoxy fatty acids, it shows biological activity in tissues lacking sEH. Such dual action may improve efficacy, but it complicates interpretation when AUDA is used to investigate physiology [70]. Second generation sEHI replaced the adamantine with a more stable benzyl-trifluoromethoxy and alkyl chain with a benzenesulfonamide to maintain potency with the sEH enzyme while improving solubility and PK stability. ([71] for review). The most potent inhibitors of the sEH are reversible and tight binding with a slow off-rate from the enzyme and sub-nanomolar potency. They also show improvements in PK for increased chances of testing clinical relevance for treating disease. Kinetic studies demonstrate optimization of new inhibitors by targeting drug occupancy time on the enzyme and demonstrate that inhibitors remain bound to the enzyme long after they are detectable by classical PK techniques. These data correlate with in vitro half-life measurements and provide novel techniques for selecting potent lead compounds for clinical development [72].

### 5.3.4 Mimics of EpFA

As an alternative to blocking the metabolism of EpFA in order to increase their concentrations, another strategy focuses on creating more stable

mimics of EpFA while retaining the active moiety of the original compound. Epoxy fatty acid mimics investigated in clinical trials often replace the epoxide with functional groups that retain beneficial effects in vivo while also blocking  $\beta$ -oxidation by adding functional groups to the  $\alpha$ -hydroxy portion of the fatty acid. Mimics of epoxy fatty acids remove the complexity of enzyme potency and off-rate kinetic parameters of small molecule sEHI that can complicate translation from the lab bench to clinical efficacy, but due to the unknown target for EpFA activity and complex structure diversity of EpFA, selecting one isomer for development could be overly simplistic. Many of the mimics were based on earlier studies in agricultural chemistry where various groups resistant to epoxide hydration were used to replace the epoxide of natural juvenile hormone while presumably retaining efficacy at the putative receptor [73].

## 5.4 Clinical Development of Compounds That Alter EpFA Concentrations

One of the first identified biological targets of EpFA action was modulation of the microvasculature and inflammation which underlies many pathological disease states. Clinical targets testing efficacy of increasing EpFA include hypertension, cardiovascular pulmonary disease, stroke, diabetes and pain. Preclinical studies provide evidence that altering concentrations of regulatory lipid mediators formed from metabolism of PUFA could provide beneficial effects in many other diseases, including neurological disease and bone degeneration. Despite the unknown target, multiple clinical trials investigating the therapeutic potential of both small molecule inhibitors of the sEH as well as EpFA mimics have been initiated. These trials are highlighted in Table 5.2 and the mechanisms are explained in detail below along with the benefits and liabilities of these approaches.

Small molecule sEH inhibitors		Clinical Trials
AUDA	ОН СТАНКА	<i>Clinical trial NCT00654966: Microvessel Tone in patients with heart failure.</i> Status: Complete. Healthy humans and patients with heart failure challenged with topical urotensin II, a potent vasoconstrictor, and treated with sEHI [74].
TPPU		This compound has not been investigated in clinical trials but is the most frequently used compound in preclinical research.
AR9281		Clinical trial NCT00847899: Evaluation of sEHI in Patients with Hypertension and Impaired Glucose Tolerance. Status: Complete. Single and multiple day testing up to 8 days at doses up to 1.2 g/day (400 mg every 8 h) were well tolerated [129]. Data from Phase II clinical trials not published.
GSK2256294		Clinical trial NCT01762774: A Study to Assess the Safety, Tolerability, PK and PD of Single and Repeat Doses of GSK2256294 in Healthy Volunteers and Adulate Male Moderately Obese Smokers. Status: Complete. Doses were well tolerated and attenuated smoking related endothelial dysfunction.
EC1728 ( <i>t</i> -TUCB)	$\overset{F}{\underset{F}{\overset{O}{\overset{O}{\overset{O}{\overset{O}{\overset{O}{\overset{O}{\overset{O}{\overset$	Clinical trials are in development for companion animals.
EC5026	F F F F F F F F F F F F F F F F F F F	Clinical trial NCT04228302: Safety, Tolerability, and Pharmacokinetics of Oral EC5026 in Healthy Subjects. Status: Enrolling
EpFA Mimics		Summary of results
CMX020		Clinical trial ACTRN12615000885594: A Study to Evaluate the Safety and Analgesic Efficacy of Oral CMX-020 in Subjects with Symptoms of Sciatica Resulting from Lumbosacral Radiculopathy. ACTRN12616001435471: A Phase 2 Study to Assess the Efficacy and Safety of CMX-020 in Treating Osteoarthritis. Status: Phase 1 studies complete. Enrolling for Phase 2.
OMT-28	Structure not disclosed	Clinical trial NCT03906799: Study on OMT-28 in Maintenance of Sinus Rhythm in Patients with Persistent Atrial Fibrillation. Status: Enrolling
Icosabutate		Clinical trial NCT04052516: A Phase 2b Study of Icosabutate in Fatty Liver Disease. Status: Phase 1 studies complete. Enrolling for Phase 2b.
Vascepa (ethyl-EPA)		Status: approved for the treatment of hypertriglyceridemia.

Table 5.2 Clinical development candidates of small molecule sEHI and EpFA mimics

# 5.4.1 Small Molecule sEHI in Clinical Development

The clinical trials registry lists six clinical trials completed with small molecule soluble epoxide hydrolase inhibitors tested in diseases mostly affected by endothelial dysfunction. The following sections will highlight the small molecule sEHI investigated in these clinical strategies to increase EpFA as a mechanism for treating disease. AUDA Based on the observation that EpFA open potassium channels and hyperpolarize vascular endothelium resulting in vasodilation [39], investigators in Australia conducted clinical trial NCT00654966 as an exploratory study in humans to determine if AUDA increases EpFA to protect against heart failure by increasing blood flow in the microvasculature. After topical challenge with a potent vasoactive peptide, urotensin II (UII), blood flow was measured in healthy humans or patients with heart failure (HF) treated with and without topical AUDA. UII causes vasodilation and increased blood flow in healthy humans but vasoconstriction and reduced blood flow in patients with HF. AUDA alone caused increase blood flow when administered at the intermediate dose of 0.1 µM in both healthy and HF patient populations. When administered with UII, AUDA was able to reverse the reduced blood flow observed in HF patients, although not back to levels observed in healthy subjects, and significantly increased blood flow in healthy subjects more than when UII was administered alone [74]. The increased vasodilation observed from this study indicate many potential benefits in addition to heart failure that increasing EpFA would have in patients; for example, diabetics and hypertensive patients would benefit from increased vasodilation; however, poor PK probably prevented this molecule from being a viable drug candidate.

AR9281 (UC1153) AR9281 offered some advantages as a clinical candidate including low IC<sub>50</sub> on the rodent sEH, easy synthesis, a surprisingly high water solubility, high selectivity for the sEH, and low mammalian toxicity; however, its poor target occupancy and the speed with which it was metabolized to synthetically complex metabolites were clear liabilities. In preclinical models, AR9281 reduced hypertension and renal injury in an angiotensin induced model of hypertension in rats [75]. Multiple clinical trials were launched by Arete Therapeutics to test the v and efficacy of AR9281 for treating hypertension. Published results from the Phase 1 study found that AR9281 was well tolerated at doses up

to 1000 g/day but was rapidly cleared from the body, with a half-life of only 3-5 h in humans. However, high plasma concentrations well above the IC<sub>50</sub>, and *ex vivo* assays monitoring sEH activity showing 90% inhibition of the enzyme up to 24 h at the top dose, justified advancing the compound to Phase 2 human efficacy studies. The results of the Phase 2 efficacy studies in hypertensive patients with glucose intolerance were not published, and Arete Therapeutics closed shortly after completing the study, so one assumes that the compound failed to show efficacy. One possible speculation for lack of efficacy was the high metabolic clearance of the compound. For example, the ex vivo determination of the IC<sub>90</sub> was based on a 60 min assay; however, AR9281 is a reversible inhibitor that has a kinetic  $T_{1/2}$  on the enzyme of 6 min [76]. Thus, the ex vivo data may not be representative of the in vivo environment where the inhibitor is rapidly metabolized and cleared from the body. Additional measurements of diols in the urine of subjects were combined from all treatments and compared to pretreatment levels and placebo treated subjects as a marker of target engagement. The diols of human subjects treated with AR9281 modestly decreased compared to pretreated controls, while placebo treated subjects remained unchanged. Epoxide concentrations were not detectable in the urine; thus, the ratio of epoxide:diol change was not monitored and thus impossible to determine if the decrease in diol levels was due to treatment effect or other independent variables. Overall, the data from the Phase 1 trial did not demonstrate convincing data that AR9281 effectively inhibited sEH activity, possibly explaining the lack of efficacy in phase 2 trials. There are situations where rapid clearance such as that demonstrated with adamantane containing compounds like AR9281 and AUDA offer clinical advantages; however, these have not been explored.

**GSK225629A4** GSK225629A4 is a potent sEHI that attenuated leukocyte infiltration in mice after exposure to cigarette smoke [77]. Based on this information, clinical trials were

initiated to test safety and endothelial dysfunction in both healthy humans and obese smokers at doses of 2-20 mg administered as a single or repeat oral dose for 14-days. Endpoints included safety and endothelial dysfunction measured by forearm venous occlusion plethysmography after intra-articular challenge with vasodilator, bradykinin. Overall, GSK225629A4 was well tolerated with favorable PK and  $T_{1/2}$  equal to 19–30 h. in healthy humans and 41-49 h in overweight smokers. One significant adverse event was reported, but ultimately considered non-drug related as the subject had a history of this event prior to the clinical trial. Otherwise, only mild-moderate adverse events of headache and contact dermatitis were reported. Headache occurred with similar occurrence between the placebo and treated groups, and contact dermatitis around the site of ECG electrode placement was reported in nine healthy patients receiving active compound and none in the placebo or obese smokers receiving active or placebo compound. Ex-vivo sEH activity was measured in the plasma of treated patients as a function of EET hydrolysis after 30-min incubations with 14,15 EET, and investigators found that >80% inhibition of EET to diol hydrolysis was observed after repeat dosing in all dose cohorts. In obese smokers, vasodilation after bradykinin injection was reduced compared to healthy subjects, as expected. After administration of GSK225629A4 vasodilation improved in a dose and time dependent manner in obese smokers after 1 and 14-d administration compared to placebo control. Although some limitations need to be considered, such as small sample size and non-smoking obese control subjects. Furthermore, as an added marker of safety, the sponsor measured VEGF and plasma fibrinogen after single and repeat dosing in response to potential safety concerns from increased angiogenesis [78, 79] and tumor metastasis [80] in preclinical settings. Both plasma VEGF and fibrinogen were similar across all treatment groups potentially indicating that preclinical angiogenesis observations may not be clinically relevant. Overall, these data suggest that GSK225629A4 is a safe compound with potential efficacy in patients with COPD, a disease

exacerbated by cigarette smoke, or other disease affected by dysfunction of the microvasculature.

Given the successful safety profile of GSK225629A4, independent investigators have secured rights to initiate clinical trials with the GSK compound to investigate insulin resistance and stroke as described below.

**Insulin Resistance** Preclinical data suggests that anti-inflammatory properties of EETs reduce inflammation in adipose tissue resulting in decreased insulin resistance in several, but not all, rodent models [81–83]. Based on this information, a group at Vanderbilt University in Nashville, Tennessee initiated a Phase 2 clinical trial to investigate the therapeutic potential of GSK225629A4 ability to improve insulin sensitivity in response to glucose infusion. The study is currently recruiting patients, and there are no reported data from the study.

**Subarachnoid Hemorrhage (SAH)** Numerous preclinical studies have investigated the role of soluble epoxide hydrolase in exacerbating stroke symptoms and the utility of inhibiting the sEH as a potential treatment option. (Reviewed in [84]) As a result of these data, investigators at the Oregon Health and Science University initiated a Phase 1 and 2 clinical trial with GSK225629A4 in patients with aneurysmal SAH to evaluate effects on length of hospital stay, incidence of new stroke, disposition upon discharge and outcome measures. The study recently finished recruiting patients, but no results have been published.

**Neuropathic Pain** As new mechanisms for explaining EpFA beneficial effects has been discovered, clinical activities are targeting diseases with complicated etiologies. For example, the newest clinical development programs that are scheduled to start at the end of 2019 focus on treating neuropathic pain, a disease attributed to pathological ER-stress. EC5026 is the newest sEHI being developed for clinical utility. Recent press releases announced FDA approval of an IND application from EicOsis to test their small molecule inhibitor, EC5026, for the treatment of neuropathic pain in humans, and EC1728 for treating inflammatory and neuropathic pain in companion animals. Many review papers have described the therapeutic potential of increasing epoxy fatty acids for the treatment of both neuropathic and inflammatory pain (reviewed in [18, 85, 86]). Considering the devastating impacts of the opioid epidemic and lack of effective and safe pain medications, there is considerable interest in the outcomes of these clinical trials.

## 5.4.2 EpFA Mimics in Clinical Development

CMX-020 is a mimic similar to AUDA that is also designed around 14,15 EET. This compound maintains most of the original structure except the olefin on the 14,15 carbon is replaced with a dimethylcarbamoyl and the  $\alpha$  hydroxy group is replaced with a cyclopropyl amine to prevent beta-oxidation. In preclinical studies, CMX-020 undergoes rapid elimination, with most of the drug eliminated 1-h after administration; however, the compound exhibits potent pain-relieving properties preclinically in the acetic assay writhing assay and tail flick assay, comparable to that of morphine [87]. It is unknown if CMX-020 metabolism results in epoxy-fatty acid mimics as a result of CYP450 epoxidation, or if CMX-020 acts to inhibit the sEH, similar to carbamates such as GSK225629A4. Based on the potent analgesic effects of CMX-020 and despite the rapid elimination profile, multiple clinical studies were initiated to test the safety and efficacy of CMX-020 in treating painful conditions such as osteoarthritis and sciatic nerve pain in Australia. Results have not been published.

Focused mimics based on the structure of one regioisomer of one PUFA describe the challenges of developing a mimic to a fatty acid epoxide. While CMX-20 chose to mimic the omega-6 AA epoxides, other companies, described below, selected omega-3 fatty acids as the background for their mimics. The epoxides of omega-3 fatty acids are thought to account for some of the beneficial effects of omega-3 supplementation in the diet, and animal models show that they have

more potent activity in *in vitro* and animal models than the omega-6 epoxides [31]. In addition to choosing which omega position of the fatty acids to model the mimic, further complications arise when identifying which regioisomer to target. For example, 11,12 and 14,15 EET are commonly associated with having vasodilator activity compared to the other regioisomers of arachidonic acid [88].

Omeicos is focused on developing another epoxy mimic by creating a transition state mimics of the 17,18 EPA omega-3 epoxide. Their lead compound, OMT-28, is actively recruiting patents for a Phase 2 clinical trial to treat atrial fibrillation. Although the exact structure is not disclosed, detailed structure activity relationship identified important characteristics studies needed to exert antiarrhythmic effects. Atrial fibrillation is a type of arrhythmia initiating from the top chambers of the heart and can lead to increased risk of blood clot, stroke, and heart failure. In vitro models using neonatal rat cardiomyocytes have been used to investigate the anti- or arrhythmic effects of certain drugs and demonstrate that omega-3 fatty acids and the R,S isomer of the 17,18 epoxide of EPA decreased the contraction rate in these cells [89], indicating a potential ability to alleviate atrial fibrillation. These studies further demonstrate the complexity of EpFA biology that could potentially complicate the identification of an active mimic.

Other approaches that mimic the PUFA of omega-3 or -6 fatty acids have been developed. For example, Icosabutate, developed by Northsea Therapeutics, and Vascepa (icosapent ethyl, or ethyl-EPA), an approved product sold by Amarin, are structurally engineered fatty acids both being developed to lower triglycerides in the body. Icosabutate mimics EPA with the addition of 2-bromo butyric acid on the  $\alpha$  end, while Vascepa adds a methyl group to the  $\alpha$  end to prevent  $\beta$ -oxidation; otherwise, both structures are unaltered compared to EPA. Northsea data presented at the International Liver Congress in 2018 show the compound remains in the non-esterified form longer than EPA as expected, but was metabolized primarily by CYP2C enzymes, suggesting that epoxides are likely formed in the metabolism

of this compound [90]. Multiple clinical trials were completed with Icosabutate testing the safety and potential drug-drug interactions with CYP inducers and inhibitors, as well as efficacy in hypertriglyceridemia (NCT01893515) and NASH (NCT04052516). Patients with hypertriglyceridemia receiving 600 mg once daily for 12-weeks had significantly lower triglyceride, very low-density lipoprotein cholesterol, and Apo C-III levels [91]. The NASH study recently started dosing and results are not yet available. There is more published information in icosapent ethyl considering that it is an approved drug for reducing the risk of cardiovascular disease in patients with hypertriglyceridemia. In a placebo controlled clinical trial enrolling 8179 patients, administration of 2 g twice daily of icosapent ethyl significantly reduced ischemic events, including reduced incidence of death [92, 93].

Similar to risks in choosing a mimic to omega-3 or 6 fatty acid, identifying the regioisomer and stereoisomer to mimic further complicates the process. Omeicos is in a unique position by having structure-activity relationship information for atrial fibrillation, but without knowing the target of EH activity, translating this information to other disease areas should not be assumed.

## 5.4.3 New Therapeutic Approaches Targeting EpFA Through Polypharmaceutical Approaches

Pharmaceutical targets to the COX and LO enzymes focus on preventing the formation of inflammatory prostaglandins and leukotrienes, respectively. NSAID drugs inhibit COX-1 and-2 enzymes and are potent anti-inflammatory compounds by preventing the formation of inflammatory prostaglandins; however, these inhibitors are often accompanied by toxic side effects associated with enzyme distribution. COX-1 enzymes are in most cells and protect the GI mucosa by regulating acid secretion through the EP3 receptor. Inhibition of COX-1 increases gastric release, thus causing GI-toxicity and increased ulcer formation. COX-2 enzymes are found in lymphocytes, red blood cells and synovial cells and are thought to regulate pain and inflammation. Selectively inhibiting COX-2 was thought of as a desirable approach to reduce pain and inflammation while avoiding GI complications. However, while selective inhibition of COX-2 avoided gastro-intestinal ulcer formation, chronic use increased the risk of stroke and cardiovascular disease. Further investigation into the mechanism of this toxicity found that COX-1 inhibition decreases the vasoconstrictor thromboxane A2 synthesis; while COX-2 inhibition decreases the vasodilator, prostacyclin. Non-selective inhibitors would decrease both vasoregulators and maintain homeostasis, while selective COX-2 inhibitors would decrease only prostacyclin, resulting in platelet aggregation and vasoconstriction [94, 95]. Vasodilatory effects of EpFA suggest further protection against endothelial dysfunction associated with COX-2 inhibition, but recent studies suggest an additional mechanism for decreasing COX toxicities results from the reduction of ER-stress [96]. NSAIDs increase ER-stress which has been attributed to the toxicities associated with NSAID use, including cardiovascular toxicity [97-99]. ER-stress also increases COX transcription, which creates a feedback inflammatory mechanism perpetuated by COX-2 activation of IRE1a, a key protein involved in activating the ER-stress pathway. Blocking ER-stress, as has been demonstrated with EpFA, prevent the upregulation of COX, and dual inhibition of sEH and COX are an attractive therapeutic strategy for increasing the benefit of NSAIDs while reducing their toxicity. Many preclinical studies demonstrate the advantages of dual COX-sEH inhibition. For example, the sEH inhibitor, t-AUCB, or NSAID inhibitor, Celecoxib, administered alone do not affect tumor volume or metastasis in a Lewis lung carcinoma mouse model of cancer while treatment with both significantly reduced both tumor volume and metastasis. Previous studies demonstrated that sEH null mice have increased metastasis and tumor volume [100], presumably through increased angiogenesis and VEGF expression; however, clinical trials with GSK's sEHI failed to show translation of VEGF

increases in mice to human patients [101]. Furthermore, preclinical studies identify that EETs are angiogenic and induce endothelial cell proliferation [102–104] through metabolism by COX that produces a potent angiogenic metabolite [105]. Thus, dual inhibition would prevent the formation of this metabolite and could explain the added benefit in tumor models. Additional benefits have been observed in improving survival after tumor-induced cytokine surge in mice. Inflammation is a protective mechanism to eliminate foreign toxicants from the body; however, an intense and rapid inflammatory response, as occurs in sepsis, can be deadly. CAR-T therapy is a promising treatment of cancer that activates the body's immune system to recognize tumor cells as foreign material. The body mounts an aggressive immune attack to eliminate these tumor cells; however, if too effective, the outcomes also result in sepsis and death. Preclinical studies demonstrate that the dual COX/sEHI, p-TUPB, improves survival rate in a cancer cell debris model of cytokine-surge in mice [106].

Dual inhibition with COX and sEH is an attractive target for treating disease by minimizing the toxicities associated with NSAIDs while also increasing the efficacy of both compounds [107]. Many NSAIDs and coxibs lead to mitochondrial dysfunction, which in turn increases the production of reactive oxygen species. They have also been shown to increase ER-stress [99], which can induce the transcription of COX2 and prostaglandin synthase [108] leading to an increase in inflammatory eicosanoids and cytokines. Thus, the most widely used drugs in the world are themselves inflammatory. Anti-inflammatory sEHI block this inflammation axis both at the level of the mitochondria and the endoplasmic reticulum. Thus, when used with NSAIDS and coxibs should make these drugs not only safer but also improve their anti-inflammatory activity. Multiple rodent studies have shown that sEHI synergize with NSAIDs and coxibs to reduce inflammatory pain and extend the utility of NSAIDs and coxibs to include neuropathic pain. The sEHI also reduce gastrointestinal and cardiovascular side effects of cyclooxygenase inhibitors. Since prescription and over the counter

COX inhibitors are so commonly used in pain management, this interaction is likely to be seen in the clinic if patients in trials are continued on standard of care treatment.

Exploiting this interaction commercially will be more complex. Regulatory pathways require that novel therapeutics demonstrate stand-alone efficacy before being combined with other targets, thus the pathway toward human treatment with NSAID-sEHI combinations is complicated. A polypharmaceutical approach: where one compound inhibits both COX and sEH, such as PTUBP, would lessen this challenge; however, the FDA closely monitors NSAID cardiovascular toxicity and requires extensive cardiovascular safety studies and lengthy clinical trials prior to testing in humans, thus developing this dual target under the current regulatory environment would likely be more expensive and risky than other targets. For example, this regulatory scrutiny resulted in the FDA not approving a potent NSAID, etoricoxib, after the FDA advisory committee recommended further cardiovascular risk assessment, despite etoricoxib approval in other countries [109].

Other targets in the fatty acid metabolism pathway provide attractive opportunities for treatments. For example, inhibition of LO is currently approved for the treatment of asthma. Leukotrienes, the main target of LO metabolism, are potent inflammatory agents that potentiate bronchoconstriction and exacerbate an asthma attack. Inhibiting LO activity through direct inhibition (e.g. Zileuton) or through the inhibition of 5-lipoxygnase activating protein (FLAP) is an approved treatment for asthma [110]. sEHI has also shown efficacy for treating asthma [111]. Interestingly, Zileuton and the FLAP inhibitors, Zafirlukast and Montelukast, also have weak activity for inhibiting the sEH (0.9–1.95  $\mu$ M), but at concentrations likely achieved at therapeutic doses [112]. Identifying improved dual LO-sEHI with greater potency for the sEH is an attractive target for improving asthma treatments.

The fatty acid amide hydrolase enzyme (FAAH) is a complicated target for drug therapy. The endocannabinoids, a bioactive class of lipids formed through the addition of an amide to the

carboxylic acid of PUFA. For example, N-arachidonoyl phosphatidylethanolamine (NAPE), and related amides are associated with beneficial effects in a variety of disease models including inflammation, pain, asthma, epilepsy, neurological disease, among others (see [113] for review). Because FAAH metabolizes endocannabinoids, therapeutic approaches of inhibiting this enzyme were considered for treatments of some diseases. Over ten clinical trials have been initiated to test efficacy of FAAH inhibitors, but after significant toxicities and one death were reported in a Phase 1 study of a claimed FAAH inhibitor in France, all clinical trials were put on hold. Although the exact cause of the toxicity is unknown, recent reports suggest that off-target effects on lipases caused the toxicity [114]. Renewed interests in FAAH as a target for pain came after a case study identified a woman with a knock-out mutation in FAAH were thought to result in her inability to feel pain [115]. Administration of both sEH and FAAH inhibitors show synergistic effects in animal models of pain [116] and continued efforts to develop a dual inhibitor suitable for clinical development are ongoing [117].

sEH inhibitors are more effective in reducing pain in the presence of cAMP. Dual phosphodiesterase 4 (PDE4) and sEH inhibition also show synergistic effects in decreasing pain in animal models [118]. PDE inhibitors (PDEi) have been developed for the treatment of inflammation by preventing the metabolism of cyclic adenosine monophosphate (cAMP); however, increasing cAMP has also been associated with increased pain states. Interestingly, PDE4 and 5 inhibitors increase EpFA through lipase activity, releasing arachidonate and possibly EETs from phospholipids, and could possibly explain the mechanism for analgesic effects of PDEi despite increases in cAMP [118]. In laboratory settings, investigators demonstrated that decreasing EpFA concentrations through CYP450 inhibition while treating with PDEi resulted in increased pain states. Conversely, increasing EpFA concentrations through sEHI resulted in synergistic increases in pain relief. Efforts are ongoing to identify dual inhibitors of PDE4 and sEH, and recent advances

identified MPPA, a compound with potent inhibition on both enzymes that is also efficacious in an LPS model of inflammatory pain [119].

While some compounds are synthesized specifically to inhibit an enzyme, others are identified after approval as having off-target effects against desirable or undesirable enzymes. For example, sorafenib and regorafenib are receptor tyrosine kinases that have anti-angiogenic properties by inhibiting VEGFR-2 and other kinases. They are approved for the treatment of hepatocellular carcinoma and renal cell carcinoma, and both are potent inhibitors of the sEH (12 and 0.5 nM IC<sub>50</sub>, respectively). The other approved small molecule inhibitor of VEGFR, sunitinib, is not an sEH inhibitor. Although the biological relevance of this dual activity is difficult to compare with other kinases that do not affect sEH because kinases are in general promiscuous inhibitors of many kinases. Both sorafenib and regorafenib are known for being difficult to formulate and for often serious side effects of their use. Clinical doses of these Raf-1 and pan-kinase inhibitors are likely to inhibit most sEH activity and increase EpFA in vivo. It is likely that without the sEH inhibition, these kinase inhibitors would have even worse side effects. It follows that the side effects of these two kinase inhibitors could be dramatically reduced by increasing dietary  $\omega$ -3 and limiting dietary  $\omega$ -6 lipids. The kinase inhibition is not ubiquitous to the urea pharmacophore that inhibits sEH; however, Sorafenib and regorafenib are unique compared to other published sEH inhibitors used in preclinical or clinical studies in their ability to inhibit kinases, as can be predicted from structure activity relationships [120]. Although recent publications indicate that TPPU is a weak inhibitor of p38 kinase  $(IC_{50} = 0.98 \ \mu M)$ . The p38 kinase is a mitogenactivated protein kinase and activates inflammatory cytokines, and inhibition of this kinase would explain many of the beneficial effects seen in the preclinical studies using this compound; however, p38 is also regulated by oxidative stress, and the study failed to show if the activity was an indirect result of reducing oxidative stress vs. direct inhibition of the kinase given that the in *vitro* assays were conducted below the  $IC_{50}$  of 100 nM [121].

# 5.5 Summary and Future Directions for Targeting EpFA as Treatments for Disease

The newest innovations in inhibiting the sEH focus on identifying natural compounds with inhibitory activity, or polypharmaceutical approaches targeting multiple enzyme pathways. The inhibitors being tested for sEH inhibition focus on a central pharmacophore of either a urea, amide, or carbamate, and few new patents have been filed with different pharmacophores. Instead, new technologies focus on identifying new targets of disease, poly-pharmaceutical approaches developing a single compound to inhibit multiple targets [122], or inhibitors isolated from natural products. Inhibiting the sEH affects a regulatory pathway, ER stress, and is a relatively safe target that could offer benefits when combining with other targets. In some cases, efforts for developing dual targets to provide added benefits or safety have been intentional, while others have been discovered as off-target effects after developments. Both approaches are described below.

Current clinical approaches are focused on developing small molecule inhibitors or EpFA mimics; however, future approaches are investigating polypharmaceutical approaches, thus capitalizing on the low toxicity of alerting this pathway. Yet despite widespread interest in targeting this pathway, few new pharmacophores are identified that lack a carbamate or urea as the active moiety. Recently, natural products have been identified as a new source of sEH inhibitors that hold promise for future nutraceutical development; however, these products have relatively poor potency, with  $IC_{50}s$  in the  $\mu M$  range, which would require g/day amounts of dosing. Techniques are being considered to improve production and isolation of natural sEHI or identify more potent natural sEHI [123, 124].

Many early sEHI, such as AUDA, were designed as mimics of specific EpFA. This dual action was clearly demonstrated in earlier publications [125]. Subsequent synthesis led to compounds that inhibited the EH without mimicking EpFA or compounds that mimicked specific EpFA without inhibiting sEH. Shen and Hammock discussed the advantages and limitations of each of these approaches [126]. The resulting molecules made biological data much easier to interpret when they were used as physiological probes, and likely simplified patent positions as well. Possibly it is worth reconsidering dual acting compounds. For example, one could have an sEHI pharmacophore which would increase EpFA systemically, while also targeting mimicry of 17,18 EEQ or 19,20 EDP to control atrial fibrillation [127]. Such compounds would offer the advantages of stabilizing all EpFA while allowing direct action of the EpFA mimic in tissue with a reduced ability to epoxidize PUFA.

In summary, lipid epoxides and their mimics or stabilizers are of increasing interest in treating disease due to their many beneficial and homeostatic functions as well as limited observed toxicities. However, their multimodal mechanism of action, including effects on angiogenesis and cancer, raises caution for monitoring safety in clinical trials. Furthermore, few studies report toxicities associated either with direct supplementation of EpFA, or inhibition of sEH; however, one study reported that sEH null mice displayed reduced survival in a cardiac arrest model compared to wild type mice [128] demonstrating one of the few examples of increased toxicities in preclinical models modulating the sEH. While the most recent advances are focused on investigating the polypharmaceutical advantages of increasing EpFA, other approaches that could increase EpFA include altering the release and reincorporation into the cell membrane and could provide attractive benefits to the current clinical approaches being investigated (Fig. 5.4.). Currently small molecule inhibitors of sEH are being tested in clinical settings to investigate the effects of increasing EpFA concentrations in the body as a way of treating pain, diabetes, and reducing the symptoms of subarachnoid hemor-



**Fig. 5.4** Possible ways of increasing natural epoxy fatty acid chemical mediators to prevent and treat disease Increasing EpFA concentrations in the body have been associated with treating many diseases. The figure above demonstrates potential pathways of increasing their concentrations through increasing their biosynthesis or through preventing their metabolism. EpFA can be increased by increased PUFA consumption, increasing

rhage. Other strategies focus on mimicking the beneficial EpFA and are targeted in clinical investigations for treating pain, fatty liver disease, hypertriglyceridemia, and atrial fibrillation. Overall, previous clinical trials targeting strategies to increase EpFA lack on-target toxicities, and most studies using sEH knock-out animals lack toxic side effects, which increases confidence in the safety of increasing EpFA concentrations in the body. The combined safety profile and wide-ranging efficacy in treating disease encourage continued investigation in the beneficial effects of this pathway as a treatment option.

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release from lipid membranes, or increased formation through CYP450 activity. Inhibiting the metabolic enzymes that convert EpFA to more polar compounds that are rapidly eliminated from the body, or supplementing the diet with EpFA mimics that prevent degradation by  $\beta$ oxidation are other ways in increasing the concentrations of the beneficial fatty acids

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**Conflict of interest statement** The University of California holds patents on the sEH inhibitor used in this study as well as their use to treat inflammation, inflammatory pain, and neuropathic pain. KM Wagner, CB McReynolds, and BD Hammock are employees of EicOsis L.L.C., a startup company advancing sEH inhibitors into the clinic.

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6

# Druggable Sphingolipid Pathways: Experimental Models and Clinical Opportunities

Victoria A. Blaho

### Abstract

Intensive research in the field of sphingolipids has revealed diverse roles in cell biological responses and human health and disease. This immense molecular family is primarily represented by the bioactive molecules ceramide, sphingosine, and sphingosine 1-phosphate (S1P). The flux of sphingolipid metabolism at both the subcellular and extracellular levels provides multiple opportunities for pharmacological intervention. The caveat is that perturbation of any single node of this highly regulated flux may have effects that propagate throughout the metabolic network in a dramatic and sometimes unexpected manner. Beginning with S1P, the receptors for which have thus far been the most clinically tractable pharmacological targets, this review will describe recent advances in therapeutic modulators targeting sphingolipids, their chaperones, transporters, and metabolic enzymes.

### **Keywords**

Sphingolipid  $\cdot$  S1P  $\cdot$  Fingolimod  $\cdot$  Siponimod  $\cdot$  Ozanimod

### 6.1 Introduction

The family of bioactive sphingolipid molecules is immense, but all are characterized by the same core component, the sphingoid backbone, which is simply an amino alcohol with a long carbon chain [1]. The canonical sphingolipid, sphingosine, can be enzymatically modified to add fatty acids, phosphorous-containing head groups (e.g., phosphocholine), sugar moieties, and changes in acyl chain saturation [1-3]. Flux through the sphingolipid pathway has far-ranging effects, from cellular architecture to multi-organ system coordination [4, 5]. The ubiquity of sphingolipids presents both challenges to and opportunities for their manipulation. Unlike other bioactive lipids with proposed shunting to different enzymatic pathways, the flow of sphingolipids rarely has an alternative for degradation or synthesis other than reversal  $\begin{bmatrix} 6-11 \end{bmatrix}$ .

Subsequently, while inhibition of a particular enzyme stops generation of a specific product, the biological outcome could be the result of increased concentrations of upstream precursors and not necessarily the most immediate parent molecule. For instance, a great deal of effort has focused on the inhibition of two enzymes, the sphingosine kinases (Sphk1/2), for the treatment of cancer. Although the desired decrease in product may be achieved, an increase in the parent molecule of the Sphk substrate is commonly credited with affecting the biological outcome.

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Like a malfunctioning traffic light, a blockage at one sphingolipid node can often have repercussions throughout the metabolic pathway (Fig. 6.1). This review will present known mechanisms for therapies that target sphingolipid signaling pathways, including our current understanding of sphingosine 1-phosphate (S1P) receptor modulators, S1P chaperones and transporters, and sphingolipid metabolic enzymes [12–14].

### 6.1.1 Sphingosine 1-Phosphate (S1P) and Its Receptors, S1P<sub>1-5</sub>

Unlike the on-demand production of other bioactive lipids, the signaling molecule sphingosine 1-phosphate (S1P) is omnipresent in blood and lymph circulation, with both human and murine concentrations of 18:1 S1P in the mid-nanomolar to low micromolar range [15–18]. Blood plasma concentrations of other powerful bioactive lipids, such as prostaglandin  $E_2$  (PGE<sub>2</sub>) and leukotriene  $B_4$  (LTB<sub>4</sub>), are approximately 10 times less than S1P [19]. Despite high plasma concentrations, tissue concentrations of S1P are far lower than circulating levels, setting up an "S1P gradient" in which small alterations in local S1P concentrations are sensed by finely-tuned mechanisms within specific cell types, potentially triggering dramatic effects [20–22].

The five S1P receptors (S1PR),  $S1P_{1-5}$ , are members of the rhodopsin class of G proteincoupled receptors (GPCR). This family of proteins constitutes 40% of drug targets [23–27]. The first S1PR, S1P<sub>1</sub>, was cloned from endothelial cells (EC) owing to its critical role in endothelial cell and vascular biology [28, 29]. Lack of S1pr1 results in embryonic lethality due to hemorrhage from immature vasculature [30]. Induced S1pr1<sup>-/-</sup> in endothelial cells (EC) causes increased vascular leakage and inflammatory molecule expression, and S1pr1<sup>-/-</sup> tumor vessels have disordered architecture and poor perfusion [31–33]. Conversely, overexpression of EC S1P<sub>1</sub> reinforces the vascular barrier, increasing perfusion of tumor vessels [31, 33]. As one of the genes regulated by the transcription factor KLF2,

a hemodynamic responsive protein, EC *S1pr1* also signals in response to fluid shear stress [31, 32, 34].

In the vasculature, as well as in other cell and tissues types,  $S1P_1$  and  $S1P_2$  signaling counteract each other, with  $S1P_3$  signaling acting as a modifier [35–37]. Effects on the vasculature are of great importance in understanding the mechanisms and potential side effects of S1PR modulating drugs. The literature regarding S1PR and the vascular system is vast, and the reader is referred to several recent excellent reviews on the topic for more detailed descriptions [33, 38, 39].

Although the first S1PR was cloned from EC, S1PR modulating drugs work primarily through immune cell modification [23, 28]. There are currently three FDA-approved S1PR modulating drugs: the first-in-class FTY720 (fingolimod/ Gilenya), BAF312 (siponimod/Mayzent), and RPC1063 (ozanimod/Zeposia) are approved for treatment of the relapsing-remitting form of multiple sclerosis (RRMS) (Fig. 6.2) [12, 40–42]. A New Drug Application (NDA) has been submitted for a fourth compound, ACT128800 (ponesimod), also for the treatment of RRMS [43, 44]. Siponimod is also approved for secondary progressive MS (SPMS), the stage of MS disease progression after RRMS. While numerous S1PR modulators are utilized as pharmacological tools in the laboratory, most were not tested in the clinical setting due to poor solubility, in vivo stability, half-life, or specificity. The side effects of fingolimod and siponimod illustrate why increasing target specificity is a driving factor behind the continued development of S1PR modulators.

FTY720 is a sphingosine analogue derivative of a fungal metabolite and must be phosphorylated (FTY720P) for recognition by S1PRs [45, 46]. Although FTY720P activates all S1PRs except S1P<sub>2</sub>, S1P<sub>1</sub> binding FTY720P causes its polyubiquitination and degradation, resulting in "functional antagonism" [47]. In humans, FTY720 has a long *in vivo* half-life of greater than 100 hours, combined with low oral clearance and a high volume of distribution that is likely due to absorbance into lipid-rich tissues and cell membranes [48–51]. Lymphopenia is the most striking effect of FTY720 treatment and the



Fig. 6.1 Sphingolipid metabolism, signaling pathways, and pharmacological interventions

(a) De novo sphingolipid synthesis begins in the endoplasmic reticulum (ER) membrane with the condensation of the fatty acyl-CoA palmitoyl-CoA and the amino acid serine to form 3-ketodihydrosphingosine. The reaction is catalyzed by the pyridoxal 5'-phosphate (PLP)-dependent heterodimeric enzyme serine palmitoyl-CoA transferase (SPT), which consists of the SPTLC1 subunit and either SPTLC2 or SPTLC3. SPT activity is enhanced by SPTssa or SPTssb and additional vitamin  $B_6$  ( $B_6$ ) and is homeostatically inhibited by the ORMDL1-3 proteins. If alanine or glycine are utilized instead of serine, toxic 1-deoxysphinganine or 1-deoxymethylsphinganine, respectively, are produced. Generation of these toxic deoxysphingolipids can be reduced by supplementation with L-serine. 3-ketodigydrosphingosine is then reduced by 3-ketodihydrosphingosine reductase (KDSR) to dihydrosphingosine. (b) Acylation of dihydrosphingosine by the (dihydro) ceramide synthases (CerS) 1-6 generates dihydroceramide. All CerS can be inhibited by fumonisin B1 (FB1) and P053 specifically inhibits CerS1. (c) Dihydroceramide is then desaturated by dihydroceramide desaturase (Des1/2) to ceramide. This reaction can be inhibited by Lau7b, Nanofen, or fenretinide (4-HPR). (d) Ceramide is hydrolyzed to sphingosine by ceramidases (CDases) according to subcellular location. Sphingosine can be converted back to ceramide by CerS1-6 or (e) phosphorylated by sphingosine kinases (Sphk1/2) to sphingsosine 1-phosphate (S1P). Sphk1 and 2 are inhibited by SKI-II, dimethylsphingosine (DMS) or D,L-threodihydrosphingosine (tDHS). Sphk1 is specifically inhibited by PF543 or LCL351 and Sphk2 is specifically inhibited by ABC294640 (ABC). (f) Intracellular S1P can be dephosphorylated by S1P phosphatases (SPP1/2) or irreversibly degraded by retro-aldol cleavage of the C2-C3 bond by S1P lyase to form (2E)-hexadecenal and phosphoethanolamine (PE). S1P lyase is a PLP-dependent enzyme whose activity can be increased by B<sub>6</sub> supplementation or inhibited by LC2951, 2-acetyl-4-tetrahydroxybutylimidazole (THI), or 4-deoxypyridoxine (DOP). (g) S1P can be actively transported out of cells by Spns2 or from red blood cells and platelets by Mfsd2b. (h) Extracellular S1P can be dephosphorylated by lipid phosphate phosphatase 3 (LPP), which is non-specifically inhibited by sodium orthovanadate (Na<sub>3</sub>VO<sub>4</sub>) or propranolol. (i) S1P in circulation is carried by albumin or the HDL-bound S1Pspecific chaperone apolipoprotein M (ApoM). (j) Albumin-S1P, ApoM-S1P, or synthetic ApoM-Fc-S1P can activate cell surface S1P receptors, S1P<sub>1-5</sub>. The multiple S1PR agonists and antagonists in clinical use or testing are described in more detail in Fig. 6.2



\*metabolites of FTY720, RPC1063, and MT1303 bind to the S1P receptors

**Fig. 6.2** S1P receptor modulators and their clinical uses There are six drugs that target S1P receptors (S1PRs) and are FDA-approved for clinical use or currently undergoing clinical testing: fingolimod (FTY720), siponimod (BAF312), ozanimod (RPC1063), etrasimod (APD334), amiselimod (MT1303), and ponesimod (ACT128800; abbreviated "ACT"). Generic drug names are given on the left. FTY720, BAF312, etc. are the experimental compounds actually administered, but FTY720, RPC1063, and MT1303 must be metabolized to an active form in

greatest contributor to its mechanism of action: it restricts lymphocytes from exiting the lymphoid organs, preventing them from trafficking to attack other organs [15, 52–55]. Lymphopenia is largely the result of lymphocyte-expressed S1P<sub>1</sub> functional antagonism, since mature B and T cells use S1P<sub>1</sub> to sense and migrate toward the high circulating S1P concentrations [56]. In the animal model of MS, experimental autoimmune encephalomyelitis (EAE), and in MS patients treated with FTY720, autoreactive lymphocytes are prevented from entering circulation and reaching the central nervous system (CNS) [45, 57].

A phase III trial comparing FTY720 to cyclosporine in the prevention of renal transplantation rejection found that although higher doses are generally well-tolerated compared to high doses of other classical immunosuppressants, kidney function was consistently lower in FTY720-

order to bind to the S1PR. For each compound, the relative potency of it or its active metabolite is shown below each receptor. For instance, the active metabolite of FTY720, FTY720P, has the greatest effect on S1P<sub>1</sub>, the second strongest effect on S1P<sub>5</sub>, relatively similar potency at S1P<sub>3</sub> and S1P<sub>4</sub>, and no binding to S1P<sub>2</sub>. Conditions for which each drug has undergone clinical trials are listed on the right. Listed in **bold** are conditions for which that drug is a currently FDA-approved treatment

treated cohorts and small increases in pulmonary resistance were also documented [58]. The most frequently observed adverse effect in clinical studies of FTY720/fingolimod was macular edema, which, along with the other adverse events, directly correlated with dose, whereas efficacy did not [50, 59, 60]. This indicates that the escalating dose results in increased engagement of the S1PR in order of their affinity for FTY720P: S1P<sub>1</sub> > S1P<sub>3</sub> > S1P<sub>4</sub> ≥ S1P<sub>5</sub> [61, 62]. With increasing S1PR engagement comes greater signaling complexity, since cells are likely to express multiple S1PR [23].

S1PR modulators may also find use in the treatment of neurological disorders other than MS. In the mSOD1<sup>G93A</sup> model of amyotrophic lateral sclerosis (ALS), treatment of mice with 0.1 mg/kg FTY720 significantly delayed progression of neurological deterioration and
extended survival [63]. In brains of Alzheimer's disease patients (AD), *S1PR1* mRNA was significantly decreased, but *S1PR3* was increased [64]. An increase in brain S1P<sub>3</sub> may partially explain why FTY720 treatment could effectively reduce brain A $\beta$  plaques and neuroinflammation and improve neurological function in multiple mouse models of AD [65–67]. In a mouse model of AD, FTY720 treatment reduced the numbers of activated microglia and astrocytes [67]. Astrocyte-intrinsic S1P<sub>1</sub> may be key to FTY720's efficacy in neurological disorders, since a subset of astrocytes are also activated during EAE and reduced with FTY720 treatment [68].

The possibility of using FTY720 as an anticancer therapy has been enthusiastically pursued since early reports of in vitro and in vivo proapoptotic activity [69-71]. The immunosuppressive effect of FTY720 was originally attributed to induction of T cell apoptosis [69, 70, 72, 73]. Subsequently, FTY720 has been tested for efficacy in cancer cells derived from, and cancer models affecting, almost every organ system including leukemia, prostate, glioma, breast, mesothelioma, non-small cell lung carcinoma, pancreatic, and colorectal [70, 71, 73–81]. Rather than affecting S1PR signaling, the proposed antitumoral/pro-apoptotic effect of FTY720 is inhibition of sphingosine kinases and activation of protein phosphatase 2A (PP2A) [81-84]. A recent study used NMR spectroscopy to characterize the direct interaction of FTY720 with SET, a PP2A inhibitor [85].

The recommended dosage for Gilenya (FTY720, fingolimod) is 0.5 mg once daily, and multiple clinical trials examining the long-term effects of FTY720 administration in patients have completed been or are ongoing (NCT01201356, NCT02720107, NCT00662649, NCT01281657, NCT02307877, NCT03216915, NCT02232061, NCT01442194). Clinical trials have confirmed that adverse events, both common (acute bradycardia, macular edema, renal dysfunction) and uncommon (fatal infection, seizure, lymphoma) are dose-dependent while efficacy and effectiveness are not [59, 60, 86-88]. Adverse events are not commonly recapitulated in mice, and mouse studies investigating the use

of FTY720 in cancer models have frequently (although not always) used extended dosing of 10 mg/kg. However, the approximate conversion of a 10 mg/kg dose for a mouse reveals that this is equivalent to a single oral dose of 56 mg in a human – greater than 100 times the approved dose and 10 times the highest dose administered in clinical trials [89, 90]. Currently, two clinical trials are investigating the use of FTY720 treatment during cancer, but with the goal of reducing chemotherapy-induced neuropathy (NCT03943498, NCT03941743). No other S1PR modulators are undergoing clinical trials for cancer as the targeted condition.

There is potential for modulating S1PR signaling for the treatment of viral infections, particularly HIV. T cells from the lymph nodes (LN) of HIV patients showed impaired migratory activity, including toward S1P, possibly explaining HIV lymphadenopathy [91]. CD69 expression usually inversely correlates with that of S1P<sub>1</sub> because their physical interaction down-regulates surface  $S1P_1$  and  $S1P_1$  expression suppresses that of CD69, yet both CD69 and S1P1 were decreased in cells from viremic HIV patients compared to control cells [91, 92]. KLF2, the primary transcription factor responsible for T cell S1PR1 gene activation, was also down regulated in LN, but surprisingly, mRNAs for S1PR1 and KLF2 from purified T cells were not decreased and antiretroviral therapy (ART) improved responsiveness to S1P [91, 93]. In vitro, cells expressing S1P<sub>1</sub> allowed greater HIV replication and treatment with the S1P<sub>1</sub> agonist SEW2871 resulted in reversal of latency and reactivation of viral replication in peripheral blood cells and LN, whereas FTY720P decreased in vitro virus production by monocyte-derived dendritic cells [94]. An early study found that FTY720 administration to simian immunodeficiency virus (SIV)-infected macaques did not affect viremia and proviral DNA [95]. However, a more recent study reported that FTY720 treatment of SIV-infected rhesus macaques initiated after at least 4 months of combination ART (cART) both increased LN numbers of cytotoxic T cells and decreased the infection of LN T follicular helper (Tfh) cells, as determined by level of proviral DNA [96]. The authors suggested that FTY720 treatment could be started concurrently with cART or cytotoxic T cell activating IL-2 or IL-15 therapies, and by decreasing the number of circulating cells with viral RNA, the viral reservoir allowed into circulation would be decreased. FTY720 may also protect from HIV-associated dementia in the context of inflammation. Human neural progenitor cells (hNP1) exposed to HIV and treated with FTY720P had decreased expression of immune and inflammatory response-related genes [97]. Thus, FTY720 treatment at doses relevant to human patients, particularly in the context of cART, has potential for increasing immune responses that would be beneficial for controlling HIV replication and suppressing inflammatory responses that would be neurotoxic.

S1P<sub>2</sub> expression is also necessary for regulating migration of many cell types and coordinates S1P responsiveness with  $S1P_1$  for proper positioning of various B and T cell subsets within the lymphoid organs, including germinal center B cell (GCB) confinement, and suppression of their over-proliferation and apoptosis [98]. Tonsilderived T central memory (TCM) and T resident memory (TRM) cells are chemorepulsed in vitro by S1P via S1P<sub>2</sub> signaling, which counters promigratory CXCL12 responses [99]. Both TCM and TRM are defined by markers known to counter-regulate S1P1 responses: TCM are CCR7<sup>+</sup> and TRM are CD69<sup>+</sup> [100, 101]. Immunohistochemically, expression of S1P<sub>1</sub> and  $S1P_2$  are mutually exclusive and vary between different diffuse large B cell lymphoma (DLBCL) types [102]. S1PR2 mutations were present in more than 25% of diffuse large B cell lymphoma (DLBCL) patients, and the S1PR2 mutations present in GCB-DLBCL resulted in altered protein expression or an inability to bind the G protein  $G\alpha_{13}$ , leading to loss of GCB confinement [103, 104]. Expression of a negative regulator of S1PR2, the transcription factor FOXP1, correlates with poor survival in activated B cell (ABC)-DLBCL patients [105]. A subset of Tfh with high PD-1 expression coordinates S1P<sub>2</sub> and CXCR5 signaling to localize to the GC, indicating that S1P<sub>2</sub> mutations could impair antibody production and lymphomagenesis through altered T-B cell interactions [106].

Follicular B cells (FBC) utilize  $S1P_1$  to migrate to the marginal zone (MZ) from the follicle, whereas MZ B cells (MZB) use S1P<sub>1</sub> signals to shuttle between the MZ and follicle [107, 108]. MZB S1P<sub>1</sub> phosphorylation by G proteincoupled receptor kinase 2 (GRK2) results in their desensitization to S1P, permitting them to respond to other chemotactic signals [108]. GRK2 also inhibits MALT1, a protease and scaffold protein positive regulator of NF-kB, impairing the survival of DLBCL cells [109, 110]. Since ABC-DLBCL expression of GRK2 positively correlated with patient survival, altered S1P-directed migratory patterns may be related to anti-apoptotic signaling [110].

In vitro studies repeatedly indicated that  $S1P_3$  would be the primary regulator of bone marrow (BM) B cell egress; however, *in vivo* studies determined that agonism and subsequent down-regulation of  $S1P_1$  allowed  $S1P_3$  signals to be misinterpreted as the dominant BM egress signal [111, 112]. In a mouse model of autoantibody production, immature B cells in the BM use  $S1P_3$  to migrate from the parenchyma to the sinusoids, but only if they are not autoreactive [112]. Subsequently,  $S1P_1$  signaling draws them from BM into circulation [111]. Mature B cells also use  $S1P_3$  to position themselves within the MZ, in addition to using  $S1P_1$  as their cue to migrate to the MZ [113].

In human leukemia cells (CLL (chronic lymphocytic leukemia), pre-B-ALL (pre-B cell acute lymphoblastic leukemia), and CLL (chronic lymphocytic leukemia)), S1P<sub>1</sub> was down regulated by 10-fold and had impaired *in vitro* chemotaxis toward S1P as compared to control cells [114]. *S1PR4* mRNA was co-expressed with that of *S1PR1* and its over-expression appeared to modulate S1P<sub>1</sub>-directed chemotaxis [114]. Highly expressed by lymphocytes, S1P<sub>4</sub> appears to have only modulatory effects on S1P<sub>1</sub>-induced migration in most lymphocyte types, but may be critical for the regulation of lymphocyte proliferation and activation. T cell S1P<sub>4</sub> can suppress proliferation and IL-2 and IL-4 production initiated by anti-CD3/CD28 activation and signaling, providing a partial explanation for the skewing of  $S1pr4^{-/-}$  immune response to Th2 and away from Th17 [115, 116]. S1P<sub>4</sub> is not a critical regulator of B cell migration or activation in the spleen, but some peritoneal B cell subsets rely on S1P<sub>4</sub> signaling, rather than S1P<sub>1</sub>. Peritoneal B1a, B1b, and B2 B cells all expressed *S1pr4* mRNA, although only B1a and B1b cells appeared to use either S1P<sub>1</sub> or S1P<sub>4</sub> for migratory cues [117]. Although *S1pr4<sup>-/-</sup>* animals had normal numbers of B cells in circulation, the numbers of B1a and B1b peritoneal cells were significantly reduced, as was the level of secretory IgA in the small intestine [116, 117].

S1P<sub>4</sub> signaling may play a greater role in the innate immune system by regulating inflammatory responses. A missense variant of the human S1PR4 was discovered that correlated with decreased numbers of neutrophils in circulation [118]. Dendritic cells (DC) utilize  $S1P_4$  for their migration to lymph nodes in cooperation with CCL21 [116]. High concentrations of S1P in *vitro* (>3  $\mu$ M) inhibited neutrophil and macrophage 5-lipoxygenase (5-LO), a leukotriene biosynthetic enzyme critical for innate immune function and activated in multiple inflammatory and autoimmune disorders, including arthritis and asthma [119]. Whole blood cell mRNA profiling of patients after aneurysmal subarachnoid hemorrhage found higher S1PR4 transcript levels correlated with a greater risk of vasospasm, a major cause of severe cognitive defects and mortality, the pathogenesis of which may be linked to neutrophil recruitment and activation [120, 121]. Neutrophils are also of interest in psoriasis because of their induction of Th17 responses as well as direct pro-inflammatory activities [122]. S1pr4<sup>-/-</sup> mice had less inflammation in an imiquimod model of psoriasis as a result of decreased production of the macrophage and neutrophil chemokines CCL2 (MCP-1) and CXCL1 (KC), possibly because of decreased NF-kB activation [123].

*S1pr4<sup>-/-</sup>* mice had decreased pathology in the dextran sulfate sodium (DSS) colitis model, which correlated with decreased IL-6 production

and a skewing from Th17 to increased Th2 differentiation, although their CD4<sup>+</sup> and CD8<sup>+</sup> cells had increased *in vitro* migration toward an intermediate S1P concentration (0.1  $\mu$ M), and their DC had increased migration toward draining lymph nodes [116]. The S1PR agonist etrasimod activates S1P<sub>1</sub> > S1P<sub>5</sub> > S1P<sub>4</sub> with no activity at S1P<sub>2</sub> or S1P<sub>3</sub> and decreased inflammation in a T cell transfer model of colitis [124]. Etrasimod has also shown efficacy at a dose of 2 mg in clinical trials for treatment of moderate to severe active ulcerative colitis (UC), including histologic remission [125].

## 6.2 S1P Chaperone: Apolipoprotein M (APOM)

An ideal pharmacological target is one that has minimal impact on other components of the pathway. With this qualifier, the S1PR present the best option, since agonism or antagonism of a single receptor could be anticipated to impact only the signaling of the remaining S1PR, rather than changing flux within the entre sphingolipid metabolic pathway. The target with the second lowest possibility of large pathway perturbation is the primary S1P chaperone, apolipoprotein M (ApoM), the other chaperone being the nonspecific lipid transporter albumin [126, 127].

High concentrations of S1P can be found in plasmas of both blood and lymph, known to be bound to protein and lipoprotein fractions [128]. Although ApoM is present in the lymph, *Apom<sup>-/-</sup>* mice do not have significantly altered lymph S1P concentrations compared to the 60–70% drop in blood S1P, indicating that either all lymph S1P is bound to albumin or there is another lymph-specific S1P chaperone [16]. In the blood of mice constitutively lacking both albumin and ApoM, S1P is bound to ApoA4 [129]. A recent study of human males described a third pool of ApoM, neither lipoprotein nor protein associated, in blood, although it is unclear what the purpose is of this ApoM population [130].

In mice, the 60–70% ApoM-S1P bound to lipoprotein is usually associated with HDL; how-

ever, human lipoprotein studies have found that while S1P is usually highly correlated to ApoM, the lipoprotein class that ApoM is found on may vary based on several factors, including sex, race, age, and disease. The correlation of HDL antiinflammatory activity with S1P content has driven the search for diseases in which ApoM could be outcome predictive, including coronary artery disease (CAD), type 1 (TI) and type 2 diabetes (T2D), metabolic syndrome (MetS), lupus, nephropathy, and insulin resistance IgA [131–139].

There are diseases where altered ApoM or ApoM-HDL concentrations appear to correlate with increased disease severity or mortality. ApoM and HDL-S1P were both decreased in T2D and mortality of African Americans with T2D inversely correlated with ApoM or S1P levels [135, 140]. MetS patients without diabetes have both higher TG and lower S1P [130, 133]. Although the ratio of ApoM to ApoA1, an HDLspecific protein, was unchanged in MetS patients, the molar ratio of S1P:ApoM was 30% decreased compared to controls [132]. CAD patients also have normal HDL but decreased plasma S1P [141, 142]. In post-menopausal women, although plasma S1P concentrations are the same as in pre-menopausal women, they have increased ApoM, resulting in a greater than 25% decrease in the S1P:ApoM ratio, a characteristic accompanied by endothelial dysfunction and metabolic syndrome [143]. Interestingly, women with very low TG and low LDL had an increased risk of hemorrhagic stroke, but there was no significant correlation between total cholesterol or HDL and hemorrhagic stroke risk [144].

Alternatively, although the absolute concentration of ApoM may be the same, a shift in the lipoprotein particle that it associates with can be indicative of a loss of anti-inflammatory or atheroprotective quality. T1D patients can have normal or above normal HDL concentrations, but are still at increased risk of cardiovascular disease (CVD) [145, 146]. Female T1D patients had ApoM on less dense HDL particles which are believed to be less atheroprotective and in some cases, pro-inflammatory [147, 148]. While still capable of activating the S1P<sub>1</sub>-ERK pathway and inducing S1P<sub>1</sub> internalization in endothelial cells, T1D HDL was ineffective at activating AKT, a major inducer of endothelial nitric oxide synthase (eNOS), the enzyme responsible for production of homeostatic nitric oxide production induced by S1P<sub>1</sub> signaling [149]. MetS patient ApoM was more frequently found on LDL, having been transferred from the HDL particles [150]. A study investigating the impact of a hypercholesterolemic diet on HDL content in a porcine model of ischemia reperfusion found that less ApoM was present in HDL particles from hypercholesterolemic pigs versus controls [151].

MetS patient HDL, which has lower S1P in addition to other lipidome alterations, was also less effective at activating eNOS [150, 152, 153]. Once S1P was loaded exogenously onto MetS HDL, the ability to activate eNOS was restored [132]. Loading S1P onto S1P-poor HDL of CAD patients also restored S1PR signaling to levels achieved with HDL from control patients [154]. Another group found that recombinant HDL without sphingomyelin (SM), a metabolic S1P precursor present in high concentrations in the HDL particle, is not sufficient to activate eNOS, but the phosphorylation of eNOS is not directly proportional to HDL SM content, since too much SM will decrease eNOS phosphorylation [155]. These effects may be due to providing the S1P precursor as well as the biophysical effect SM has on the HDL particle itself. High SM content in a lipid layer reduces fluidity, which would alter the flexibility of the HDL particle and subsequently cell membranes to which it transferred lipid cargo to [156, 157]. In control patients, S1P and ApoM are usually enriched on the smaller HDL3 particles, in which the ratio of S1P to SM is over 30 times greater than that of HDL2 [158, 159].

The link between ApoM and metabolism has recently become even more complex than attempting to correlate plasma ApoM concentrations with S1P and lipoproteins. The *Ldlr*<sup>-/-</sup> (LDL receptor) mouse is a key mouse model of atherosclerosis, and the impact of ApoM-S1P on vascular integrity and endothelial cell health would imply that *Apom*<sup>-/-</sup> mice would be more prone to atherosclerotic disease, but *Apom*<sup>-/-</sup>*Ldlr*<sup>-/-</sup> double knockout mice are protected from atherosclerosis [160]. Our current understanding of the roles ApoM may play in lipoprotein metabolism indicate that defective LDL regulation, as in the setting of LDLR deficiency, lead to a compensatory increase in plasma ApoM, which in turn, resulted in increased circulating LDL, promoting a pro-atherogenic phenotype that was mitigated by concomitant ApoM deficiency [161]. The impact of ApoM expression in other models of atherosclerosis, such as *Apoe* or LDLR-related protein 1 (*Lrp1*) knockouts, is dependent on the LDL metabolism in each model [160–162].

Soon after its discovery, APOM was identified as a leptin-modulated gene [163], the expression of which positively correlated with leptin measurements in human plasma and was suppressed in the obesity model, leptin receptor-deficient (ob/ob) mice [164]. More recently, it was reported that Apom<sup>-/-</sup> mice had increased brown adipose tissue (BAT) and were protected from dietinduced obesity, a phenotype reversed by  $S1P_1$ agonist administration [165]. A study of tissue from almost 500 human patients found adipose ApoM was produced by adipocytes and secreted to plasma, with ApoM levels inversely correlating with obesity, metabolic syndrome, and T2D [166]; however, it is unclear if S1P is involved in this adipocyte-derived ApoM signaling. In a mouse model of diabetes, insulin administration reversed the decrease in ApoM levels [167]. It is likely that ApoM and insulin cross regulate each other, since APOM<sup>Tg</sup> mice have increased circulating insulin, which can be reduced by treatment with the  $S1P_{1/3}$  antagonist VPC23019 [168].

In systemic lupus erythmatosus (SLE), low plasma ApoM correlated with the presence of disease activity markers, including nephritis, leukopenia, and anti-double stranded DNA antibodies (anti-dsDNA) [138, 169]. In an *in vivo* model of immune complex deposition, the reverse Arthus reaction (RAR), mice lacking endothelial cell (EC) S1P<sub>1</sub> developed a stronger response [170]. Surprisingly, *Apom* knockout alone did not impact the magnitude of the RAR generated, but when treated with a low dose of S1P<sub>1</sub> antagonist the response was significantly greater. Conversely,

patients with IgA vasculitis had increased serum ApoM but those with nephritis as a complication had lower ApoM levels than those without [171]. The authors suggest that renal tubular epithelial cell destruction triggered by renal inflammation may have led to decreased ApoM production.

The vascular role of ApoM impacts the development of inflammation and responses to infection in addition to direct signaling on immune cells. In sepsis patients, ApoM produced in the liver drastically drops within 12 h and S1P and ApoM in plasma drop at 6–12 h in both human patients and a baboon model of lethal sepsis [172, 173]. The most severe cases of infection tend to have the lowest ApoM levels, and this drop in ApoM-S1P may contribute to the defects in vascular barrier function that occur in sepsis. ApoM deficiency does not result in gross vascular permeability in the same way that loss of EC S1P<sub>1</sub> does [16, 31, 174]. While larger molecules cannot diffuse freely across the BBB of Apom<sup>-/-</sup>, paracellular transport of much smaller molecules (<0.07 kDa) was increased in specific vessel types, as was transcytosis; however, not all of the vessels were responsive to S1P<sub>1</sub> agonist rescue [175]. The differences in regulation of vascular bed permeability are dramatically illustrated by the pulmonary vascular leakage seen in  $S1P_1$ EC-specific knockout (ECKO) animals as compared to the small effect on the BBB of the same animals [16, 174, 176]. In sepsis, effects on barrier integrity within organs such as those in  $S1P_1$ ECKO versus ApoM KO mice highlight the necessity for more detailed characterization of the effects of both the S1PR and its chaperones [177].

*APOM* mRNA has been identified in EC but protein, if produced, is below the limit of detection and the inflammatory stimulus TNFα does not change this mRNA production [178]. The authors put forth the hypothesis that this distinctive expression may imply a purpose for endothelial versus hepatic ApoM, particularly in an inflammatory context such as sepsis, where the plasma levels of ApoM and S1P decrease, as does HDL [173, 179]. The ability of EC to make and retain their own ApoM while producing and secreting their own S1P would allow for some tissue-intrinsic control in response to the drastic systemic decreases in ApoM-S1P seen in sepsis.

#### 6.2.1 ApoM-Fc

Disease modulation through targeting of ApoM signaling pathways has recently been demonstrated by administration of a recombinant ApoM fused to a modified immunoglobulin Fc domain (ApoM-Fc) [180]. ApoM-Fc has improved in vivo stability versus a traditional recombinant ApoM protein and has similar in vitro properties as ApoM-HDL. The effects of ApoM-Fc appear to be endothelium-centric: it reduced infarct size in the middle cerebral artery occlusion (MCAO) model of stroke, preserved cardiac function in a model of myocardial ischemia/reperfusion, and reduced pulmonary inflammation in the RAR model of immune complex injury [170, 180]. Since immune cell numbers were not affected, particularly lymphocytes, it is possible that ApoM-Fc cannot access the hematopoietic compartment and therefore may provide a tool for differential delivery of ApoM-S1P to EC, sparing the immune system. Subsequent iterations of ApoM-Fc may aim to target endothelial subtypes or the specific S1P receptors they express. However, since ApoM prevents excessive bone marrow lymphopoiesis and HDL is known to affect survival of mature T cells, T regulatory cell (Treg) differentiation, and antigen presentation to T cells, modification of ApoM-Fc or development of a novel ApoM mimetic that targets lymphocytes and/or their progenitors, could be beneficial for direct immunosuppression [16, 181–183].

#### 6.2.2 ApoM Receptor Megalin

To date, the lipocalin receptor megalin is the only known ApoM receptor but it does not appear to be involved in recognition of ApoM outside of the kidney [184]. In this context, megalin is believed to rescue only locally synthesized ApoM from secretion in the urine, but it is also involved in the resorption of albumin from urine, a role that can be modified by a high glucose diet that reduces megalin expression [184–187]. Reported competitive inhibitors of megalin include cilastatin and receptor-associated protein (RAP) [188–190]. Although modulation of megalin expression or activity may provide an indirect mechanism for altering the S1P signaling axis, since this could impact both albumin and ApoM metabolism, without identifying ways of creating specificity for these two proteins the impact on the resorption of other megalin binding partners makes this a less attractive therapeutic target.

#### 6.2.3 Megalin and Vitamin D<sub>3</sub>

Vitamin  $D_3$  is either ingested or synthesized in the skin from 7-dehydrocholesterol, then undergoes sequential metabolism to  $25(OH)D_3$  (calcidiol) in the liver and is then converted to the active metabolite, 1,25-dihydroxyvitamin D  $(1,25(OH)_2D_3; \text{ calcitriol})$  in the kidney [191, 192]. Megalin, also known as LDL receptorrelated protein 2 (LRP2), is involved in renal of 25(OH)D<sub>3</sub> for conversion uptake to  $1,25(OH)_2D_3$  through binding vitamin D binding protein (DBP) and may be expressed in other tissues, allowing their vitamin D metabolism [188, 193, 194]. Low  $D_3$  has been correlated to glucose intolerance and increased risk of diabetes and CVD, although the effect of  $1,25(OH)_2D_3$  or  $D_3$ on circulating lipid profiles is unclear [195–197]. A recent meta-analysis of 41 randomized controlled trials found that D<sub>3</sub> supplementation lowered LDL and TG, but in many studies D<sub>3</sub> had no effect on circulating HDL, in others it raised HDL; however, the trend was actually toward decreased HDL in response to D<sub>3</sub> supplementation [198]. One group reported that increased deoxysphingolipids, particularly deoxysphinganine (deoxydihydrosphingosine) are predictive of T2D development in non-obese individuals and correlate with increased TG and glucose, whereas another found that total dihydroceramides (dhCer), particularly C18:0, were elevated at least five years before T2D onset [199, 200]. In another T2D patient cohort, after 6 months of  $D_3$ 

supplementation plasma 25(OH)D<sub>3</sub> was increased, as were C18 dhCer (d18:0/18:0) and C18 Cer (d18:1/18:0), but there was no effect on plasma S1P or dihydrosphingosine 1-phosphate (dhS1P, dihydrosphinganene) [201]. Yet monocytes from T2D patients stimulated ex vivo in the presence of 1,25(OH)<sub>2</sub>D<sub>3</sub> secreted less S1P, had decreased mRNA S1PR1 and S1PR2 mRNA and increased S1PR3 and S1PR4 mRNA [202]. A study of overweight and obese Asian-Australians found that individuals with low D<sub>3</sub> may benefit from D<sub>3</sub> supplementation by developing increased glucose tolerance; however, supplementation does not offer added protection in patients that are at risk of developing diabetes but already have levels of circulating  $D_3$  that are within the normal range [203].

As the chaperone for S1P, ApoM has emerged as not only a critical component of the signals triggered by S1P binding to its receptors, but also as a potential target for pharmaceutical manipulation. GPCRs are the most popular pharmacologic targets but the inability to selectively bind a single S1PR or a group of S1PR expressed by a specific tissue or cell type has led to a search for other points of modification within the S1P-S1PR signaling pathway. Manipulating the S1P chaperone is an unconventional approach that may provide the opportunity to target subpopulations of cells that are more likely to be exposed to blood or lymph plasma, such as endothelial or immune cells [129, 170, 180].

## 6.3 S1P Transporters

#### 6.3.1 Spinster 2 (Spns2)

Although the ABC transporters may be involved in the subcellular localization of S1P or its secretion by a limited subset of cells, multiple studies have determined that they are not involved in efflux from the major cell sources of S1P: EC, red blood cells (RBC), and platelets [176, 204– 206]. There are now two confirmed S1P transporters, spinster 2 (Spns2) and Mfsd2b. Spns2 is the EC S1P transporter and the secreted S1P modulates specific biological effects of blood and lymph [21, 207]. Spns2<sup>-/-</sup> are lymphopenic, although not to the same extent as mice lacking the S1P biosynthetic enzymes, Sphk1/2. S1P produced by Sphk and secreted by lymphatic EC Spns2 binds naïve T cell S1P<sub>1</sub> and promotes their migration and survival through maintenance of mitochondrial numbers [22, 208]. High endothelial venules (HEV) are blood vessels specialized in regulating lymphocyte trafficking into secondary lymphoid organs at homeostasis and tertiary lymphoid organs under inflammatory and disease conditions, including cancer [209]. DC recruited to HEV by CCL21 produce lymphotoxin- $\beta$ receptor (LT $\beta$ R) ligands to activate HEV LT $\beta$ R, which in turn promotes HEV function and EC survival [209]. HEV EC require Spns2 to secrete S1P, which then acts in an autocrine fashion, activating S1P<sub>1</sub> signaling and increasing CCL21 production to recruit DC [18].

## 6.3.2 Major Facilitator Superfamily Domain Containing 2b (Mfsd2b)

Two groups recently reported the characterization of major facilitator superfamily domain containing 2b (Mfsd2b) as the S1P transporter in RBC and platelets [210, 211]. Unlike Spns2<sup>-/-</sup>,  $Mfsd2b^{-/-}$  mice were not lymphopenic, despite a 50% drop in blood plasma S1P, approximately the same decrease as seen in Spns2-/-. Intriguingly, Apom<sup>-/-</sup> mice had a 65% decrease in blood plasma S1P and albumin/ApoM double knockout mice had a 75% decease in blood plasma S1P and both have significantly more lymphocytes in circulation, further emphasizing the need to better understand the microenvironmental regulation of S1P concentrations by key cell types through production, secretion, and degradation [16, 129]. Mfsd2b also transports docasahexanoic acid (DHA) in the form of lysophosphatidic acid (LPA) precursor molecule lysophosphatidylcholine (LPC), the binding of which is dependent upon the phosphocholine head group and transports LPC from the plasma into brain parenchyma [212]. Mice lacking Mfsd2b also have increased transcytosis by EC involved in the BBB, resulting in leaky CNS vasculature without a breakdown in tight junction (TJ), a phenotype also reported in *Apom*<sup>-/-</sup> mice [175, 213]. Mfsd2b also suppressed endocytic vesicle formation without affecting TJ by altering the lipid composition of the cell membranes themselves, making assembly of caveolae domains less favorable for vesicle formation [214].

#### 6.4 S1P Metabolism

#### 6.4.1 S1P Lyase (SPL)

Terminal metabolism of intracellular S1P occurs through cleavage of the C2–3 bond by the ER membrane-bound S1P lyase (SPL), yielding phosphoethanolamide (PE) and (2E)-hexadecenal [215]. Almost all mammalian cells express some level of SPL. For example, the brain, kidneys, and splenic and thymic stromal cells have high expression, whereas splenic and thymic immune cells have low expression [216, 217]. Platelets lack SPL and RBC appear to have little to no SPL activity, allowing these two cell types to carry S1P cargo without the danger of degradation [218, 219].

Unlike most of the S1PR, mutations in the SPL gene SGPL1 are known to cause human disease, such as a form of Charcot-Marie-Tooth disease, the most common hereditary peripheral neuropathy, with the earliest manifestations including weakness in the feet and lower legs [220–222]. More commonly, SGPL1 mutations manifest as nephrotic syndromes, such as congenital nephrotic syndrome with adrenal calcification and steroid-resistant nephrotic syndrome (SRNS) and adrenal insufficiency, often present with comorbidities of icthyosis, immunodeficiency, gastrointestinal disorders, and neurological deterioration, recently named nephrotic syndrome type 14 (NPHS14) or SPL Insufficiency Syndrome (SPLIS) [223–227].

SPL inhibitors targeted for the clinic have been developed based on the chemical structure of 2-acetyl-4-(tetrahydroxybutyl)imidazole (THI), an SPL inhibitor commonly used in experimental settings and a component of caramel food coloring [228, 229]. Most known SPL inhibitors, parental compounds including THI and 4-deoxypyridoxine (DOP), act by blocking the binding site of cofactor pyridoxal 5' phosphate (PLP), the active form of vitamin  $B_6$  [228, 230]. Both DOP and THI must be metabolized to a form compatible with the PLP site of SPL. Ohtoyo et al. hypothesized that THI is metabolized by the gut microbiota to an intermediate form before phosphorylation and SPL binding, providing an explanation for why THI will not block SPL activity *in vitro* or under B<sub>6</sub>-rich conditions [231, 232]. There are over 100 PLP-dependent enzymes in eukaryotes, one of which is serine palmitoyltransferase (SPT), a complication for data interpretation and the design of SPL inhibitors because SPT is the initiating enzyme in the *de novo* biosynthesis of sphingolipids [232, 233]. Most recently, creation of the compound RBM10-8 was reported as an SPL inhibitor structurally based on S1P that acts as an enzyme substrate, irreversibly binding in the active site by forming a covalent bond [234]. Although RBM10-8 would not require metabolism for activity, its in vivo utility and specificity have not yet been studied.

SPL activity is critical for normal and pathological development of the nervous system. Neuron-specific knockdown of the Drosophila SPL, *sply*, caused progressive axonal degradation similar to that seen with SMN deletion, the gene responsible for spinal muscular atrophy (SMA) in humans [220, 235]. Mice with Sgpl1 deleted in neuronal progenitors, ependymal cells, and oligodendrocytes with Nestin-Cre (Sgpl<sup>Nes-Cre</sup>) had accumulation of brain S1P, decreased PE, and behavioral abnormalities concomitant with alterations in the hippocampus, increased microglial activation, and decreased neuronal autophagosome formation [236–239]. Microglia from these mice also had decreased expression of beclin-1, ATG7, and LC3-II, rendering them defective in autophagy induction [239, 240]. Similarly, autophagic flux in neurons from Sgpl1<sup>Nes-Cre</sup> mice could be restored ex vivo by incubation with exogenous PE [237].

The effect of SPL on neuronal autophagy is notable in the context of several neurodegenera-

tive diseases, since inducers of autophagy are being investigated as possible therapeutics to degrade toxic protein plaques or aggregates [241]. Mice transgenic for mutant human FUS protein (FUS (1-359)), an RNA/DNA-binding protein responsible for altered splicing and cytoplasmic aggregation of target mRNAs in amyotrophic lateral sclerosis (ALS), had significantly increased Sgpl1 mRNA and decreased Sphk2 [242, 243]. Sph was significantly increased in brains and spinal cords of FUS (1-359) mice, and although S1P concentrations were not significantly different, this may have been due to a dramatic increase in SPL activity [243]. Loss-of-function mutations in a FUS target gene, MECP2, are the genetic cause of the X-linked neuroregressive disorder Rett syndrome [242, 244]. Plasma from Rett syndrome patients had significantly higher S1P and dhS1P, as well as Sph and dhSph [245]. Rett syndrome patient fibroblasts had defective autophagosome formation and mice lacking Mecp2 ( $Mecp2^{-/y}$ ) developed cerebellar intracellular aggregates as they aged, concurrent with clinical phenotype development [246]. When incubated in vitro with THI, mouse primary neurons expressing exon 1 of mutant huntingtin (mHTT), the same abnormal splice product seen in brains of Huntington's disease patients, had increased autophagy and conlonger sequently, survival compared to control-treated cells [247]. In brain tissue from AD patients, Sphk1 was decreased and SPL1 was increased, potentially resulting in a net decrease in S1P concentrations [248]. SPL expression correlated histologically with focal amyloid β deposits in the entorhinal cortex and changes in SGPL1 mRNA were already significantly increased in brains of patients with the lowest clinical dementia ratings [248, 249].

Model organisms have helped to clarify how the loss of SPL activity can manifest in various organ systems besides the nervous system. *Drosophila* lacking functional Sply are flightless and have a decreased number of dorsal longitudinal flight muscles (DLM) [250]. In a mouse model of post-menopausal osteoporosis, administration of LX2931 (LX3305) restored bone volume by increasing osteoblast activity, subsequently increasing cortical bone thickness and mechanical bone strength [251]. In a collagen-induced arthritis mouse model, LX2931 prevented development of clinical disease and had a small ameliorative effect on joint swelling and inflammation without affecting anti-collagen antibody titers [252]. Phase I and II clinical trials were conducted where rheumatoid arthritis patients received oral LX3305, but results have not published (NCT00847886, NCT00903383, NCT01417052).

SPL also has roles in immune homeostasis because of its control over S1P concentrations. Global Sgpl1<sup>-/-</sup> mice have increased circulating and tissue S1P as well as pro-inflammatory cytokine production [253]. Drosophila lacking methyltransferase 2 (Mt2) activity had reduced Sply activity as they aged, resulting in increased total S1P and Cer concentrations, altered hematopoiesis and immune cell morphology, and defective antibacterial immune responses [254]. Although present in very low numbers, thymic parenchymal CD11c<sup>+</sup> DC with SPL activity were found to be major regulators of the S1P gradient required for T cell egress [255]. While mature T cellintrinsic SPL also affected thymic S1P concentrations and had a moderate effeon egress, thymic stromal epithelial cells expressing large amounts of SPL protein were not involved in maintaining the S1P gradient required for T cell egress. Treatment of mice with SPL inhibitor for only three days showed a trend toward decreased numbers of double positive thymocytes (CD4<sup>+</sup>CD8<sup>+</sup>), and prolonged SPL inhibitor administration resulted in significant depletion of CD4+CD8+ cells in the thymus [20, 256].

Subcutaneous administration of an SPL inhibitor in an imiquimod-induced mouse model of psoriasis was as effective as cyclosporine at decreasing redness and epidermal thickness [257]. In the DSS/azoxymethane (DSS/AOM) mouse model of colitis-associated cancer, gut epithelium-specific knockout of *Sgpl1* resulted in increased disease severity and tumor formation accompanied by increased numbers of macrophages and Th17 T cells [258]. Loss of SPL in bone marrow immune cells also resulted in increased colonic inflammatory lesions composed of infiltrating myeloid cells and T cells and loss of crypt architecture; however, Sgpl1-/- mice that received wild-type bone marrow cells developed more severe colitis, more tumors, and had increased mortality [259]. Conversely, administration of DOP or THI decreased inflammation, T cell recruitment, and Crohn's disease-like pathology in mice that overexpress  $TNF\alpha$  in intestinal epithelium (TNF<sup>iAARE</sup>) [256, 260]. Results from studies of SPL in colitis models corroborate the hypothesis of a key role for S1P in the numerous clinical studies assessing the efficacy of S1PR modulating drugs etrasimod (APD334), ozanimod (RPC-1063), and amiselimod (MT-1303) in ulcerative colitis (UC) and Crohn's disease [125, 261-263].

The vascular nature of the lung and its role as an interface between the host and microorganisms indicates that regulation of S1P would be crucial in this organ. For instance, severity of cystic fibrosis (CF) is potentially influenced by altered regulation of S1P. CF varies in the number of organ systems it affects, but the greatest morbidity and mortality are due to progressive lung inflammation and dysfunction arising from defective cystic fibrosis transmembrane conductance regulator (CFTR) protein [264]. 352 of the greater than two thousand mutations in the CFTR gene are causative for CF, although severity of symptoms is typically based on the mutation, the most common of which is  $\Delta$ F508 (https://cftr2. org/) [265]. Although bacterial infections are usually associated with CF, viral infections can also capitalize on defective mucus clearance and host immunity [266]. Mice expressing  $\Delta$ F508 showed increased lethality when infected with an enterovirus (coxsackievirus B3 Nancy) despite viremia levels similar to controls [267]. Yet  $\Delta$ F508 mice had increased viral titers in lymphoid tissues, decreased IFN $\alpha$  production, and decreased virus-specific IgM and IgG titers.

Defects in antiviral activation could be linked to SPL activity. IKKɛ-mediated inhibition of influenza A (IVA) virus replication was regulated by SPL, which enhanced type I interferon (IFN) responses *in vitro* in response to viral RNA [268]. However, the authors stated that enzymatic activity was not necessary for the antiviral effect.

Another group found  $\Delta$ F508 mice had lungs with decreased S1P but high basal innate and adaptive immune cell infiltration [269]. Administration of LX2931 reduced immune cell numbers in the lungs of  $\Delta$ F508 mice, including inducible NOS (iNOS)<sup>+</sup> granulocytes, reducing the cellular infiltrate to wild-type levels. Work from a different group contradicted the implication that SPL inhibition would have beneficial anti-inflammatory effects in CF, reporting that S1P was a negative regulator of CFTR cell surface expression and activity, making SPL inhibition particularly counterproductive in CF patients [270]. A study of patients with community-acquired pneumonia (CAP) found elevated circulating S1P compared to patients without pneumonia [271]. This was not a general response to lung dysfunction, because chronic obstructive pulmonary disease (COPD) patients only had increased S1P concentrations if they developed pneumonia. A clinical trial (NCT03473119) is currently underway to determine if plasma S1P concentrations could serve as a reliable biomarker in CAP cases.

Infection with the malaria parasite Plasmodium spp. may also engage the sphingolipid pathway. In a malaria model using infection with Plasmodium berghei, humanized mice with decreased SPL activity (hSGPL1-/-) had approximately the same level of parasitemia but almost no mortality. Curiously, administration of LX2931 did not have a significant effect on survival in experimental cerebral malaria, but FTY720 treatment of hSGPL-/- mice had a small survival benefit, particularly when coadministered with the anti-malarial drug artesamate [272]. Compared to children with uncomplicated malaria, children with cerebral malaria have decreased plasma S1P, possibly due to a drop in platelet numbers [272].

The potential for therapeutic manipulation of SPL-derived disorders is dependent upon how the lyase deficiency manifests. For instance, administration of the SPT inhibitor L-cycloserine decreases the amount of substrate entering the S1P biosynthetic pathway, reducing the amount of SPL substrate available, but reportedly inhibits SPL in addition to SPT [227]. However, patients with non-functional SPL could potentially bene-

fit from such a compound. Conversely, as in the autophagy studies cited earlier, if a lack of SPL products is causing disease, it may be possible to administer those molecules to patients. A recent retrospective study of SPLIS patients supplemented with vitamin  $B_6$  found 30% of patients responded positively with increased SPL activity and decreased sphingolipids, emphasizing that SPL variant should determine treatment regimen [273].

## 6.4.2 Sphingosine 1-Phosphate Phosphatases (SPP1/2)

There are other, nondegradative enzymes that metabolize S1P by dephosphorylation: the S1P phosphohydrolases, SPP1 and SPP2, are specific for long chain sphingoid bases, and LPP3 (discussed below), which is nonspecific and better characterized with regard to LPA metabolism [274]. Both SPP1 and SPP2 localize to the ER but are expressed in different cell types [275-277]. For instance, SGPP1 mRNA is highly expressed in human placenta and has moderate expression in liver and skeletal muscle, whereas SGPP2 mRNA is highest in heart [277]. Both SGPP1 and SGPP2 mRNAs are highly expressed in human kidney. In mice, northern blotting showed Sgpp1 to be highly expressed in liver with little expression in skeletal muscle [275]. Differential expression was evident in the endometrium of women with endometriosis, where SGPP1 was increased and SGPP2, along with SGPL1, were decreased in endometriosis [278]. SPP1 over-expression in vitro led to Cer accumulation and apoptosis, whereas knockdown of SGPP1 in MCF7 cells caused S1P and dhS1P accumulation and induced an ER stress response, leading to autophagosome formation [276].

Mice lacking *Sgpp1* on a pure C57Bl/6 genetic background are viable, but have severely stunted growth and detachment of an abnormally thin stratum corneum from thickened subcorneal layers [279]. Loss of SPP1 activity caused almost no significant changes in the epidermal sphingolipidome profile, with only C26 Cer significantly decreased and trends toward decreased C24 Cer

and increased S1P and dhS1P. Keratinocytes were hyperproliferative and differentiated abnormally in response to increased epidermal Ca2+ concentrations. Sgpp1-/- mice maintained on a mixed C57/129sv genetic background reportedly did not have the same epidermal defects [280]. In studies utilizing these Sgpp1-/- and Sgpp2-/mice on a mixed background, compared to wild-type controls, Sgpp1-/- animals developed increased DSS-induced colitis and their colons had increased proinflammatory cytokines TNF, IL-6, and IL-1b. Conversely, cytokines in colons of Sgpp2<sup>-/-</sup> animals did not increase with DSS administration, resulting in decreased colitis severity. Both Sgpp1 and Sgpl1 were downregulated in bone marrow-derived DC stimulated with lipopolysaccharide (LPS) [281]. While naïve DC showed nuclear SPP1 staining, LPS stimulation caused its translocation from the nucleus to the cytosolic compartment. There are currently no drugs that can specifically target either SPP1 or SPP2.

## 6.4.3 Lipid Phosphate Phosphatase 3 (LPP3)

Lipid phosphate phosphatase (LPP3) also dephosphorylates S1P, but shows substrate promiscuity, metabolizing various extracellular phospholipids [282]. LPP3 has a cytoplasmic motif targeting it to the basolateral membrane [283]. Global loss of *Plpp3*, the LPP3 gene, is embryonic lethal because of abnormal Wnt/β-catenin signaling generating vascular defects [284]. Constitutive endothelial/hematopoieticspecific deletion using the Tie2-Cre yields a similar phenotype [285]. Transcriptional regulation of PLPP3 by NF-kB can be induced by inflammation in the monocyte-like cell line THP-1 [274]. However, a SNP in a regulatory element for endothelial PLPP3 was identified as protective against coronary artery disease (CAD) and ischemia/stroke [286]. The protective allele sequence created a binding site for KLF2, the same transcription factor regulating S1pr1. Modulation of LPP3 expression in primary human aortic EC in vitro altered extracellular and intracellular S1P concentrations [287]. In the thymus, LPP3 produced by both endothelial and epithelial cells is necessary for maintaining the S1P gradient utilized by T cells for egress into circulation [285]. Despite difficulties in characterizing the physiological roles of LPP3-mediated S1P metabolism, it is believed to be the primary dephosphorylating enzyme for FTY720P, although SPP1 is also able to do so [288]. There are no published LPP3-specific inhibitors and compounds that have been used, such as sodium orthovanadate and propranolol, are too nonspecific for clinical use [289].

#### 6.5 Biosynthetic Enzymes

## 6.5.1 Sphingosine Kinases 1 and 2 (Sphk1/2)

The sphingosine kinases, Sphk1 and Sphk2, are differentially expressed by cell and tissue type and although both generate S1P from sphingosine, they show different subcellular localization patterns [5, 290, 291]. The topic of Sphk is quite broad, so this review will address biology directly relevant to common inhibitors and the development of new compounds [14, 292-295]. The Sphks have long been targets for inhibition but isoform specificity, which is particularly important, has been lacking. Double null Sphk1/2<sup>-/-</sup> is embryonic lethal because of massive hemorrhage [296]. When *Sphk1* alone is deleted, circulating S1P concentrations go down, although compensatory activity by Sphk2 prevents tissue S1P concentrations from changing substantially [297]. Sphk1<sup>-/-</sup> animals also develop lymphopenia when administered FTY720, demonstrating that Sphk2 is the kinase responsible for the majority of FTY720 phosphorylation in vivo [297]. Contrary to expectation, deletion of Sphk2 resulted in increased, rather than decreased, circulating S1P concentrations [298]. The proposed mechanism for this increase is a regulatory pathway where S1P is dephosphorylated by LPP3 and some of the Sph is subsequently taken up by cells and rephosphorylated by Sphk2 [298, 299]. The Sphks can also display a differential substrate preference: Sphk1 will preferentially metabolize dhSph over Sph [300]. When cells overexpressing Sphk1 were incubated with FTY720, intracellular dhS1P and S1P increased, but dhSph and Sph concentrations remained the same [300]. This occurred because Sphk2 is 30 times more efficient at phosphorylating FTY720 and FTY720 itself can act as a Sphk inhibitor at micromolar concentrations [46]. Of note is that Spns2 expression is high in the same tissues where Sphk2 is expressed and where FTY720P is secreted, illustrating the interconnectedness of the entire sphingolipid metabolic system [300].

While the search for S1PR inhibitors tends to focus on vascular and autoimmune diseases, the development of Sphk inhibitors is driven by cancer research [301]. The primary anti-tumoral mechanism of action of Sphk inhibition is believed to be an increase in intracellular Cer, triggering cancer cell apoptosis. D,L-threodihydrosphingosine (tDHS) or N,N, dimethylsphingosine (DMS) act as competitive nonspecific inhibitors [290, 302]. The most frequently used inhibitor is SKi (also referred to as SKI-II), which inhibits both Sphk1 and 2 [303]. Like many Sphk inhibitors subsequently developed, it must be present in micromolar concentrations for full potency and since it inhibits both Sphks there are unwanted and unexpected effects [304]. The block on catalytic activity by Sphk1 inhibitors correlates with its degradation, a unique mechanism where inhibitor binding induces polyubiquitnylation, targeting Sphk1 to the proteasomal degradation pathway [305-307]. The binding of inhibitors induces a conformational change in Sphk1, allowing ubiquitnylation of Lys183 and subsequent binding of the Kelch-like protein 5 (KLHL5)-cullin 3 ubiquitin ligase complex [308]. While *Klhl5* knockdown reduced Sphk1 degradation, KLHL5 expression was correlated with decreased chemotherapy sensitivity [309]. SKi also inhibits another enzyme in the sphingolipid metabolic pathway, Des1, in a noncompetitive manner at submicromolar concentrations, which may account for the cellular accumulation of dhCer with the use of this inhibitor [310].

Several Sphk1-specific inhibitors with improved specificity and/or potency have been described. LCL351 is a sphingosine analogue that has 10 times greater inhibitory activity for Sphk1 versus Sphk2, but still requires low micromolar concentrations for inhibition [311]. Although not clinically viable, LCL351 is a useful Sphk1-specific tool. Patients with UC have increased Sphk1 expression and *Sphk1<sup>-/-</sup>* mice develop less severe DSS-induced colitis [312]. LCL351 administration prevented the development of DSS-induced colitis, reducing colonic neutrophil recruitment in combination with a decrease in colon S1P concentrations, although circulating S1P concentrations were slightly elevated [311].

PF543 is a Sph competitive Sphk1 inhibitor at low nanomolar concentrations and was used in the crystallization of Sphk1 [313, 314]. Incubation of 1483 (squamous cell carcinoma) cells with nanomolar concentrations of PF543 did not increase Cer concentrations but did increase Sph in direct correlation with the S1P decrease [314]. Since PF543 did not induce apoptosis in cancer cell lines A549 (lung adenocarcinoma), Jurkat (T cell acute lymphoblastic leukemia), LN229 (glioblastoma), MCF7 (invasive ductal carcinoma), or U937 (acute monocytic leukemia) but did inhibit S1P generation, this illustrated that the pro-apoptotic effect of Sphk inhibition was not a result of lost S1P, but the increase in Cer [314]. PF543 also decreased the severity of DSS-induced colitis, concurrent with the decrease in S1P concentrations [315, 316]. EC in isolated rat aortic and coronary arteries transiently exposed to hypoxic conditions upregulated Sphk1, increasing S1P and vasodilation that was blocked by PF543 [317]. In vivo, PF543 blocked S1P production and increased cardiac Sph concentrations in the angiotensin II (AngII)dependent model of arterial hypertension and cardiac remodeling [318]. At a dose of 1 mg/kg, PF543 blocked development of cardiac hypertrophy and decreased S1P<sub>1</sub> protein in the heart with a subsequent decrease in activated STAT3 and ERK1/2 [318]. Despite the intense interest in Sphk1 inhibitors, none have made it to clinical trials.

However, ABC294640 (ABC), an Sphk2 inhibitor, has been in multiple clinical trials since

it was first reported in 2010 [319]. The first clinical trial, in patients with solid tumors (cholangiosarcoma, colon, pancreatic), found a dose of 500 mg twice a day was well tolerated [320]. An important finding was that after trial initiation, a protocol amendment was needed requiring fasting blood glucose below 160 mg/dL because of doselimiting hyperglycemia [320]. Experimentally, ABC suppressed the development of cancer in the DSS/AOM colon cancer model, decreased chemoresistance in breast and ovarian cancer models. and suppressed inflammation in models of arthritis and lupus [257, 321–327]. Some ABC efficacy may be due to its accumulation in tumor tissues, since the half-life in human plasma is only 5.5 h [319]. Currently, ABC (Opaganib/Yeliva) is being investigated in two clinical trials: ABC plus androgen antagonist in metastatic castrationresistant prostate cancer (NCT04207255) and alone or in combination with hydroxychloroquine sulfate advanced cholangiosarcoma in (NCT03377179). So far, no changes have been posted for the second trial with regard to possible during hydroxychloroquine shortages the COVID-19 pandemic [328].

Sphks could also be targets for inhibition during some viral infections, although efficacy is likely to be pathogen- and manifestation-specific. Influenza A virus (IAV) infection increased Sphk2 expression and activation in vitro and treatment with ABC during IAV infection increased survival and decreased lung viral titers [329]. Inhibition with non-specific DMS had the same effect, and although SKi treatment did not result in the same magnitude of survival increase, it did significantly decrease viral titers better than ABC, indicating that Sphk1 and Sphk2 may be responsible for different aspects of IAV viral reproduction and host response [329, 330]. Dengue virus type 2 (DENV2), a positive-sense single-stranded RNA virus, actively downregulated Sphk1 transcription, decreasing the activation of IFN-responsive genes [331]. In vitro, DENV2 replicates less efficiently in Sphk2<sup>-/-</sup> mouse embryonic fibroblasts, which did not produce IFN $\beta$  in response to viral infection, but lack of Sphk2 did not impact viral replication in vivo or survival [332]. IAV and DENV2 have different modes of transmission, different cycles, and are not related, but similar responses involving Sphks *in vitro* implicate a more general role in the anti-viral immune response [333].

#### 6.5.2 Ceramide Synthases (CerS)

Production of Cer can occur through two pathways, one of which is the salvage pathway: reacylation of Sph by Ceramide synthases (CerS) [334, 335]. Alternatively, Cer is produced de novo from dhCer, which will be covered in the following section. There are six CerS, which are ER membrane-bound enzymes that catalyze the N-acylation of sphingoid bases and require phosphorylation of C-terminal residues for catalytic activity [336-338]. Each of the CerS exhibit different cellular expression patterns and acyl chain preferences, and inhibition or deletion of one CerS typically results in up-regulation of another and production of different Cer species [336, 339]. CerS2 is the most ubiquitously expressed and produces C20-C26 Cer [334, 340]. Knockout or knockdown in MCF7 cells resulted in accumulation of dhSph and Sph, increases in CERS4, 5, and 6, and decreased very long chain (VLC) Cer [336, 341]. CerS2 overexpression increases VLC Cer production, causing insulin resistance and oxidative stress in cardiomyocytes [342]. Conversely, CerS1 has the most restricted expression and is highest in the CNS, skeletal muscle (SkM), and testis and generates only C18 Cer, which decreases with CerS1 knockdown [334, 340, 343]. Mutations in CERS1 have been linked to progressive myoclonus epilepsy and CerS1 interactions with mutant heat shock protein (Hsp27) result in decreased mitochondrial Cer, leading to neurodegeneration in Charcot-Marie-Tooth variant 2F disease [344–346].

There are two inhibitors of CerS, the most specific of which is P053, an FTY720 derivative and selective noncompetitive inhibitor of CerS1 [347]. P053 selectively decreased C18 Cer in SkM while liver and adipose Cer concentrations were not affected. P053 also decreased triacylglycerol (TAG) by 50% in SkM of HFD-fed mice but did not affect TAG in SkM of normal chowfed mice [347]. P053 may not effectively cross the BBB since it is found in much lower concentrations in brain tissue versus SkM and has less of an effect on brain C18 Cer production. CerS1specific inhibition also increased mitochondrial capacity and enhanced fatty acid oxidation in SkM while decreasing whole body fat mass, despite HFD consumption and no effect on insulin resistance [347]. However, genetic deletion of *Cers1* in SkM did show increased insulin and glucose tolerance with HFD feeding, in addition to reduced adiposity [348].

The other CerS inhibitor is fumonisin B1 (FB1), a fungal toxin with a deoxysphingoid base structure and known carcinogenic activity [349–351]. FB1 inhibits all six CerS, leading to increased S1P, dhS1P, Sph, and dhSph, and decreased Cer and dhCer [11, 352]. It also causes accumulation of 1-deoxysphinganine, possibly compounding neurological sequelae of CerS inhibition, similar to production of deoxysphingolipids associated with hereditary sensory and autonomic neuropathy type 1 (HSAN1) [351, 353].

## 6.5.3 Dihydroceramide Desaturase (Des1 and 2)

De novo Cer synthesis occurs by insertion of a 4,5 trans double bond into the sphingoid backbone of dihydroceramide (dhCer) by the dihydroceramide desaturases, Des1 and Des2 [354, 355]. CerS are responsible for the production of the dhCer substrate, so their inhibition affects both salvage and *de novo* pathways [356]. Compared to Des1, far less is known about Des2, which in addition to desaturase activity can also exhibit C4-hydroxylase activity and synthesize phytoceramides (phytoCer) [357]. Membrane-bound cytochrome  $b_5$  affinity and complex formation may determine which of these enzymatic activities Des2 engages in [358]. Des2 is highly expressed in the digestive tract, kidneys, and skin, where phytoCer are critical [355, 358]. DEGS2, the Des2 gene, is also expressed in the adult brain and was significantly upregulated in brains of schizophrenia patients and downregulated in major depressive disorder patients [359]. A *DEGS2* missense mutation also correlated with cognitive deficits in schizophrenia patients [360].

Des1 is ubiquitously expressed and its activity is most associated with insulin resistance and cancer [361]. Palmitate upregulates *Degs1* mRNA in SkM myoblasts, increasing Cer and subsequently inducing insulin resistance, which was reversible by oleate incubation [362]. Cells and mice lacking Degs1 have increased dihydroxysphingolipids and uncoupled nutrient and apoptosis signaling [363]. Degs1-/- mice crossed with the obesity model ob/ob mice had significantly increased dhCer and decreased Cer in liver, white adipose tissue, and serum [364]. ob/ ob Degs1<sup>-/-</sup> animals subsequently had lower fat mass, blood glucose, and improved liver function. Accumulation of dhCer in plasma had previously been proposed as a biomarker for diabetes progression [199].

Des1 is the target of the synthetic retinoid chemotherapeutic, fenretinide (4-hydroxyphenyl retinamide (4-HPR)) [365-367]. 4-HPR also increases activity of SPT, leading to the accumulation of cytotoxic dhCer [14, 368, 369]. In HEK293 cells, 4-HPR induced polyubiqutinylation of Des1, increasing enzymatic activity but targeting it for degradation, making Des1 activity dependent upon the rate of degradation induced by polyUb [310, 370]. Metabolites of 4-HPR differentially affect the 4-HPR target enzymes [371]. The 3-keto-HPR metabolite inhibits all targets, stearoyl CoA desaturase (SCD1),  $\beta$ -carotene oxyegnase (BCO1), and Des1, but the N-[4-methoxyphenyl]retinamide metabolite (MPR) specifically affects BCO1. SCD1 converts saturated fatty acids (FA) to monounsaturated FA, particularly palmitic acid or stearic acid to palmitoleic or oleic acid, respectively, but was also reported to decrease Cer in cardiomyocytes [372–374]. However, SCD1 deficiency decreased Cer and mRNA for SPT components in SkM, so its inhibition by 4-HPR may contribute to effects attributed to Des1 inhibition in vivo [373, 375].

This target combination may also explain results of 4-HPR treatment in CF. 4-HPR decreased inflammation and corrected the FA imbalance and Cer deficiencies seen in *CFTR*<sup>-/-</sup>

mouse models and in CF patients [376–378]. A new oral formulation of 4-HPR by Laurent Pharmaceuticals, Lau-7b, is currently in phase II trials for CF (APPLAUD, NCT03265288) and reportedly normalized blood and lung polyunsaturated FA (PUFA) and Cer concentrations in mouse models of asthma [379]. Similar to the  $Degs1^{-/-}$  mice, 4-HPR has been shown to prevent or partially reverse obesity, insulin resistance, and hepatic steatosis by blocking Cer synthesis [380–382]. The effects of 4-HPR in obese patients have been investigated in a clinical trial, with results under review by the FDA in January 2020 (NCT00546455).

The most extensive clinical testing of 4-HPR has been in clinical trials for a wide range of cancers: neuroblastoma, glioblastoma, lymphomas, leukemias, recurrent ovarian and prostate, lung, bladder, head and neck, and breast (Clinicaltrials. gov search "fenretinide"). A new formulation of 4-HPR complexed with 2 hydroxypropyl- $\beta$ -cyclodextrin (Nanofen) was recently described [383]. Nanofen had improved bioavailability and efficacy in lung tumor xenograft models, having led to C18 dhCer accumulation and inducing tumor apoptosis.

#### 6.5.4 Ceramidases (CDases)

The enzymes that convert dhCer to dhSph or Cer to Sph are ceramidases (CDases), which hydrolyze the N acyl linkage between the FA and the sphingoid base [14, 384]. The CDases are categorized based on their optimal catalytic pH: neutral ceramidase (NCDase), alkaline ceramidases (Acer), and acid ceramidase (ACDase). Like the CerS, the CDases have substrate specificity and subcellular localization. Sph can be converted to Cer by ACDase, NCDase, and Acer1-3, whereas dhSph and phytoSph are converted from their dhCer and phytoCer precursors by Acer2 & 3 [384, 385].

Defects in ACDase lead to Faber disease and SMA with progressive myoclonic epilepsy [386]. mRNA for two CDases, *Asah1* (ACDase) and *Asah2* (NCDase), are altered in the brains of ALS model *FUS* (1-359) mice [243]. Knockout of ACDase (*Asah1<sup>-/-</sup>*) is embryonic lethal, and conditional *Asah1<sup>-/-</sup>* mice have elevated ovarian Cer levels, leading to decreased fertility [387, 388].

NCDases are present in humans, mice, and pathogens, including *Pseudomonas aeruginosa* and *Mycobacterium tuberculosis* [389, 390]. Mice lacking NCDase (*Asah2<sup>-/-</sup>*) were relatively normal and demonstrated the critical role of NCDase in the intestines [391]. *Asah2<sup>-/-</sup>* have high circulating endotoxin and inflammation of the gut epithelium in the DSS colitis model [327].

Loss of each of the alkaline CDases (Acer1-3) manifests in different tissues. Acer1 is critical for epidermal Cer regulation, and Acer1-/- mice have progressive alopecia due to altered hair follicle cycling and have increased energy expenditure with decreased body fat [392, 393]. Acer2<sup>-/-</sup> mice have significantly decreased circulating Sph, dhSPh, S1P, and dhS1P [394]. In vitro, Acer2 displays broad substrate specificity and is upregulated by serum deprivation [395]. Acer3 preferentially hydrolyzes C18:1 Cer and is highly expressed in brain, increasing with age [396]. Acer3<sup>-/-</sup> mice appear mostly normal until they age beyond 8 months, at which point C18:1 Cer is significantly decreased in addition to Sph and S1P. As their brain sphingolipid composition changes, Acer3-/- mice develop impaired balance, motor coordination, and grip strength due to Purkinje cell degeneration [396]. In humans, ACER3 deficiency manifests in childhood as progressive leukodytrophy [397]. Although CDase inhibitors exist for laboratory use, none have been advanced to the clinic [398-400].

## 6.5.5 Serine Palmitoyl-CoA Transferase (SPT)

The initial reaction in the *de novo* sphingolipid biosynthetic pathway is the condensation of the amino acid serine and palmitoyl-CoA by serine palmitoyltransferase (SPT) to 3-ketodihydrosphingosine [401, 402]. The essential components of SPT are the protein subunits SPTLC1 and SPTLC2 or 3, with SPTLC1 being ubiquitously expressed and SPTLC2 and 3 showing some tissue specificity [403, 404]. SPTLC2 and 3 contain the PLP consensus motif for cofactor binding and whichever is included in the heterodimer (SPTLC1 plus SPTLC2 versus 3) determines whether longer fatty acyl-CoAs (palmitoyl and larger) are incorporated (SPTLC2) or shorter myristoyl or lauroyl (SPTLC3) are selected [405, 406]. Other components of the enzyme complex are the proteins SPT small subunit a and b (SPTssa/b), which bind to the SPTLC complex conferring optimal catalytic activity [407]. A mutation in SPTssb results in increased SPT activity and over-production of C20 long chain bases, resulting in abnormal membranes and vacuoles in the brain, leading to ataxia and early death [408]. SPT activity is negatively regulated by the ORMDL proteins, which are always complexed with the SPT holoenzyme and act through conformational changes in response to sphingolipid concentrations, particularly D-erythro Cer [409-411].

ORMDL deficiency in mice is not lethal and null animals appear normal at weaning [412]. Ormdl3<sup>-/-</sup> mice have significantly increased brain sphingolipids, particularly Cer and Sph, but dhCer is increased only in Ormdl1/3-/- doublenull mice. These mice have smaller body weights, exhibit neurological defects, and their sciatic nerves contain significantly greater concentrations of dhSph, dhCer, Cer, and Sph. Altered sphingolipid concentrations manifest as abnormal sciatic nerve morphology with excessive (redundant) myelination, a phenotype recapitulated in mice with an inducible constitutive SPT [412]. SNPs in ORMDL3 and a cis gene, GSDML, are linked to non-allergic childhood asthma [413]. DNA methylation sites in *ORMDL3* were also independently correlated with childhood asthma and DNA methylation regions in the 5' UTR of ORMDL3 were significantly less methylated in CD8<sup>+</sup> T cells and children with asthma [414].

Mutations in *SPTLC1* or 2 are responsible for hereditary sensory and autonomic neuropathy (HSAN1) types 1A and 1C, respectively, characterized by damage to peripheral neurons leading to progressive neuropathy, ulcerations, and weakness [415–417]. The most prevalent mutations change SPT substrate amino acid preference, but others change affinity for acyl-CoAs of different chain lengths and increase basal activity [405, 418–420]. Mutations causing substrate preference to change from serine to alanine or glycine result in accumulation of neurotoxic 1-deoxysphingolipids, such as 1-deoxysphinganineand1-deoxymethylsphinganine [418–421]. HSAN1C patients also have decreased CD8<sup>+</sup> T cell sphingolipid synthesis upon activation and impaired proliferation and survival [422].

Dietary supplementation of 10% L-serine deoxysphingolipids decreased plasma and improvement in motor and coordination testing in mice with the C133W HSAN1 mutation, whereas L-alanine supplementation led to accumulation of deoxysphingolipids and motor function deterioration [423]. In a randomized controlled trial, 400 mg/kg/day of L-serine resulted in improvement of disease scores concomitant with dramatic, significant decreases in deoxysphingolipids plasma [423. 424]. Surprisingly, despite improvement in neuropathy, L-serine-treated patients had no decrease in ulcers and a higher frequency of skin infections and osteomyelitis, which the authors suggested could be due to permanent nerve damage occurring before supplementation [424]. L-serine supplementation has been shown to increase D-serine in plasma and CSF in a mouse model of GRIN2B encephalopathy, a Rett-like syndrome [425]. Considering the frequent overlap of substrate specificity for various sphingolipid enzyme inhibitors, a relatively simple diet modification that is efficacious in severe diseases related to SPT activity would be a preferred treatment.

## 6.6 Glycosphingolipids

The glycosphingolipids (GSL) are a large subfamily of sphingolipid molecules created by attachment of glycans to a ceramide moiety that anchors them in the lipid bilayer, primarily in the plasma membrane [1, 426]. Galactosylceramides (GalCer) and glucosylceramides (GlcCer) are synthesized in the Golgi by  $\beta$ -linkage of the respective galactose or glucose sugar moiety to the primary hydroxyl of a ceramide [427, 428]. GlcCer can then be metabolized to lactosylceramide (LacCer), which serves as the base molecule for the more complex GSL: globo/isoglobo-, ganglio/isoganglio-, and lacto/neolacto-series [428, 429]. Clinically, the GSL are most widely recognized for their roles in lipid storage diseases: Fabry, Tay-Sachs, Sandhoff, Gaucher, Krabbe, Niemann-Pick C, and GM1 and GM2 gangliosidosis [430, 431]. The complexities of the glycosphingolipid metabolic pathways are such that interested readers are directed to the detailed reviews referenced in this section.

## 6.7 Summary

The known contributions of sphingolipids to all aspects of biological homeostasis and pathogenesis have continuously expanded since their first description almost a century and a half earlier [432]. The generation of animal models and the increasing depth of genetic sequencing have allowed researchers and clinicians to discover unexpected phenotypes and rare mutations in the sphingolipid metabolic and signaling pathways responsible for diseases in every biological system. Although the greatest successes in sphingolipid pharmaceutical targeting have been S1PR modulating drugs, the development of new compounds and modification of old ones have generated promising results. Complex rules governing sphingolipid flux combine with cellular and subcellular specialization to create a network that is, unfortunately, at times irreducible. However, the restricted utilization of sphingolipid biosynthetic and signaling pathways also provides opportunities for targeted therapeutic exploitation.

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## Druggable Lysophospholipid Signaling Pathways

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#### Abstract

Lysophosphatidic acid (LPA) has major roles as a bioactive signaling molecule, with multiple physiological and pathological roles being described in almost every major organ system. In this review we discuss LPA signaling pathways as emerging drug targets for multiple conditions relevant to human health and disease. LPA signals through the six G proteincoupled receptors LPA<sub>1-6</sub>, and several of these receptors along with the LPA-producing enzyme including autotaxin (ATX) are now established as therapeutic targets with potential to treat various human diseases as exemplified by several LPA signaling targeting compounds now in clinical trials for idiopathic pulmonary fibrosis and systemic sclerosis. Several crystal structures of LPA receptors and ATX have been solved, which will accelerate development of highly selective and effective LPA signaling targeting compounds.

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Department of Molecular Therapy, National Center of Neurology and Psychiatry, Tokyo, Japan e-mail: wvalentine@ncnp.go.jp We also review additional bioactive lysophospholipid (LPL) signaling molecules including lysophosphatidylserine and lysophosphatidylinositol, which represent the next wave of LPL druggable targets. An emerging theme in bioactive LPL signaling is that where the ligand is produced and how it is delivered to the cognate receptor are critical determinants of the biological responses. We will also discuss how connecting the production and function of bioactive LPLs will identify new therapeutic strategies to effectively target LPL signaling pathways.

#### Keywords

GPCR · LysoPS · LPI · Lysophosphatidylglucoside · Lysophosphatidylcholine · GPR55 · GPR34 · P2Y10 · GPR174

## 7.1 Introduction

Lysophospholipids (LPLs), glycerophospholipids with just one fatty chain, include lysophosphatidic acid (LPA), lysophosphatidylcholine (LPC), lysophosphatidylethanolamine (LPE), lysophosphatidylserine (lysoPS) and lysophosphatidylinositol (LPI) (Fig. 7.1). LPLs were recognized in the early 1900s as cytolytic substances derived from



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H,-OH



2-Arachidonoyl-LPI



**Fig. 7.1** Chemical structures of LPL ligands Representative structures of LPLs including LPA, lysoPS, LPI and LysoPtdGlc are shown. Note that the acyl chain

can be linked to either the sn-1 or sn-2 position of the glycerol backbone

phospholipids which were incubated with snake venom; their production was later shown to be through an enzymatic phospholipase A (PLA) activity in the venom. Indeed, the prefix "lyso-" comes from this cytolytic activity of LPLs, and their actions on cells were initially associated primarily with their detergent-like properties. However, by the middle of the twentieth century, researchers started to become aware of potential roles for LPLs as bioactive molecules which, when applied to cells or tissues, evoked physiological responses that were independent of their lytic and other detergent-like properties. In 1960, Vogt reported the contraction of isolated rabbit duodenum by LPA [1], and subsequently Tokumura et al. reported vasopressor activities of several molecular species of LPA and their structure-activity relationships [2]. In 1989, Moolenaar and colleagues found that the mitogenic action of LPA involves G proteins [3], and the existence of a specific G protein-coupled receptor (GPCR) for LPA was proposed. From the late 1990s, pioneered by studies by Chun and colleagues [4], various receptor targets have been identified for bioactive LPLs. Since then, numerous physiological and pathological roles of LPL signaling have been elucidated, and these extensive "bench" works are now about to be translated into the "bedside"; as exemplified by ongoing clinical drug trials targeting LPA signaling in order to treat fibrotic diseases. Moreover, recent successes in crystallization of LPA receptors and LPA-producing enzymes will further accelerate rational design of novel potent modulators of LPA and other LPL signaling pathways.

In this chapter, we will discuss the druggablepotential of LPL signaling pathways, especially by reviewing the physiological and pathological roles of LPA signaling that have been revealed by studies utilizing genetic and pharmacological tools *in vivo*. We will also discuss findings from crystal structures of LPA receptors and an LPAproducing enzyme. Lastly, we will discuss other bioactive LPLs, such as lysoPS and LPI, which may be the "next-generation" of LPL signaling targets for drug discovery.

## 7.2 Bioactive LPA Synthesis Pathways *In Vivo*

LPA is not a single molecular entity; many LPA species exist which differ in the chemistry of their hydrocarbon chains and linkages to the glycerol backbone. The biological activities of these LPA species also differ, largely because multiple LPA receptors (LPA<sub>1-6</sub>) exist which differ in their selectivities for the different LPA species [5]. For example, LPA<sub>3</sub> [6] and LPA<sub>6</sub> [7] receptors are more potently activated by LPA with their acyl chain at the sn-2 position (2-acyl-LPA) rather than at the sn-1 position (1-acyl-LPA). In addition, LPA<sub>5</sub> receptor shows preference for alkyl-ether-linked LPA (alkyl-LPA) rather than acyl-LPA [5]. Therefore, not only the LPA levels but also where and how the LPA was produced will determine LPA receptor activation and the biological actions of LPA in various settings.

LPA is an intermediate in phospholipid biosynthesis and can be synthesized via multiple pathways, and at least two pathways are known to have important roles in the production of LPA which functions as a bioactive lipid mediator [8]. In one pathway, LPA is extracellularly produced from other LPLs such as LPC by autotaxin (ATX), a secreted enzyme with lysophospholipase D activity [9, 10]. In the other pathway, LPA is produced from intramembrane phosphatidic acid (PA) by the actions of membrane-bound, PA-selective  $PLA_{1\alpha}$  (mPA-PLA\_{1\alpha}) [11]. These two pathways produce compartmentally distinct pools of LPA (extracellular production by ATX versus intramembrane production by mPA- $PLA_{1\alpha}$ ), and the produced LPA species also differ between these pathways. ATX produces both 1and 2-acyl-LPA, while only 2-acyl-LPA is produced by mPA-PLA<sub>1 $\alpha$ </sub>, indicating that the LPA species produced by these two pathways may differ in their activities on various LPA receptors and therefore have distinct biological roles. In addition to ATX- and mPA-PLA<sub>1 $\alpha$ </sub>-dependent LPA production, other pathways have also been suggested to contribute to production of LPA as a bioactive lipid mediator, including conversion of PA to LPA via secretory-type or cytosolic PLA2; however, *in vivo* evidence is lacking and awaits future validation [12].

#### 7.3 LPA Receptor Repertoire

In 1996, Chun and colleagues provided the first report that a member of the endothelial differentiation gene (EDG) family of GPCRs represents a functional receptor for LPA [4], which is now referred to as LPA<sub>1</sub>. Subsequently, two additional EDG family GPCRs were also identified as LPA receptors, LPA<sub>2</sub> [13] and LPA<sub>3</sub> [14]. LPA<sub>1-3</sub> share 50–58% amino acid identity with each other and comprise the EDG family of LPA receptors. In 2003, Shimizu and colleagues discovered a fourth LPA receptor, LPA<sub>4</sub>, from an orphan GPCR, GPR23/p2y9, that has low homology to EDG family LPA receptors but is in the P2Y purinergic GPCR cluster [15]. This has led to the identification of two additional LPA receptors from the P2Y cluster, LPA<sub>5</sub> [16] and LPA<sub>6</sub> [7]. LPA<sub>4-6</sub> share 35–55% amino acid identity with each other and constitute the non-EDG family of LPA receptors. Depending on the functional coupling of a given LPA receptor to different G proteins, namely  $G\alpha_s$ ,  $G\alpha_i$ ,  $G\alpha_q$ , and  $G\alpha_{13}$ proteins, LPA binding activates diverse signaling cascades involving adenylyl cyclase, phosphoinositide 3-kinase, phospholipase C, and Rho-family GTPase. The G protein-coupling selectivity of each receptor is summarized in Table 7.1.

## 7.4 Crystal Structures of ATX and LPA Receptors

Rational drug design frequently relies on computer modeling techniques, which are greatly aided when a high-resolution structure of the target protein is known. Recent studies have successfully resolved crystal structures of ATX, LPA<sub>1</sub>, and LPA<sub>6</sub>. Their high-resolution structures will increase not only our understanding of substrate/ligand recognition but also provide precious information for the rational design of novel potent modulators of these targets.

Ligand	Receptor	Previous names	Gene name (human/mouse)	Coupling Ga protein family
LPA	LPA <sub>1</sub>	EDG2, Vzg-1	LPAR1/Lpar1	$G\alpha_i, G\alpha_q, G\alpha_{13}$
	LPA <sub>2</sub>	EDG4	LPAR2/Lpar2	$G\alpha_i, G\alpha_q, G\alpha_{13}$
	LPA <sub>3</sub>	EDG7	LPAR3/Lpar3	$G\alpha_i, G\alpha_q$
	LPA <sub>4</sub>	P2Y9, GPR23	LPAR4/Lpar4	$G\alpha_s, G\alpha_i, G\alpha_q, G\alpha_{13}$
	LPA <sub>5</sub>	GPR92, GPR93	LPAR5/Lpar5	$G\alpha_q, G\alpha_{13}$
	LPA <sub>6</sub>	P2Y5	LPAR6/Lpar6	$G\alpha_{13}, G\alpha_s^{a}, G\alpha_i^{a}$
lysoPS	lysoPS1	GPR34	LYSOPSR1/Lysopsr1	Gα <sub>i</sub>
	lysoPS <sub>2</sub>	P2Y10	LYSOPSR2/Lysopsr2	Gα <sub>13</sub>
	lysoPS <sub>2L</sub>	A630033H20	pseudo gene/not determined	Gα <sub>13</sub>
	lysoPS <sub>3</sub>	GPR174, FKSG79	LYSOPSR3/Lysopsr3	$G\alpha_s, G\alpha_{13}$
LPI	LPI1	GPR55	LPIR1/Lpir1	Gα <sub>13</sub>

Table 7.1 LPL receptor repertoire

<sup>a</sup>Has not been validated in multiple studies



matic activity

nel" structures

# Fig. 7.2 Schematic views of ATX structure revealed by crystallographic studies

(a) Schematic presentation of the active site, the hydrophobic "pocket" and "tunnel" structure, with bound LPL substrate. The hydrophobic "tunnel" structure is proposed to be essential for effective delivery of LPA to receptor targets

(b) Binding modes of conventional ATX inhibitors to ATX. Many conventional ATX inhibitors occupy either

7.4.1 Structure of ATX

Crystal structures of ATX were first reported in 2011 by two independent research groups [17, 18]. ATX was found to have a unique structural component, a hydrophobic "tunnel" structure, in addition to the hydrophobic "pocket" that accepts LPL substrates (Fig. 7.2a). The structures revealed that ATX probably contains LPA molecules in the hydrophobic "tunnel", which would serve as a second binding site of LPA. Significantly impaired cell motility-stimulating activity was observed in an ATX mutant with the "tunnel" precluded, even though it showed similar activity to wild-type (WT) ATX in enzymatic assays [18]. Addition of ATX to cultured cells had been shown to induce cell motility even without pro-

duction of detectable levels of LPA in the culture medias [10], which supports the possibility that ATX-derived LPA might directly access LPA receptors via the hydrophobic "tunnel" structures even without diffusion into the media. Thus, ATX may function not only as an LPA-producing enzyme, but also as an LPA carrier or chaperone protein to facilitate effective stimulation of LPA receptors.

the orthosteric site (model on left) or the hydrophobic "pocket" (model on right) and thereby inhibit the enzy-

(c) Binding mode of GLPG1690 to ATX. GLPG1690 is

the most successful ATX inhibitor in clinical trials at present and targets both the hydrophobic "pocket" and "tun-

The resolved structures of ATX enabled a design of a wave of selective inhibitors based on the three-dimensional architecture of the enzyme; and additional crystallographic studies followed, resolving structures of ATX with various inhibitors [19–32]. Currently we can find about 40 different crystal structures of ATX deposited in the Protein Data Bank (http://www.rcsb.org), provid-

ing further insights in their various binding sites and unique inhibitory mechanisms. Most of the classical ATX inhibitors target the hydrophobic substrate binding sites or solely inhibit the catalytic activity [33] (Fig. 7.2b). Given that ATX has at least two important functional domains, the hydrophobic "pocket" that is the site of LPL substrate acceptance and the "tunnel" structure which may be involved in LPA delivery, development of inhibitors that target both structures may be expected to yield more efficacious drugs. GLPG1690 is one such molecule [30] (Fig. 7.2c) and the most successful ATX inhibitor in clinical trials at present, and it is suggested that the clinical success of GLPG1690 is not independent from its unique inhibitory mode; blocking both "pocket" and "tunnel" [33].

#### 7.4.2 Structures of LPA<sub>1</sub> and LPA<sub>6</sub>

Following the pioneering work on crystal structure of the antagonist-bound sphingosine 1-phosphate (S1P) receptor S1P<sub>1</sub> [34], crystal structures for various GPCRs with lipid ligands have now been reported, including LPA<sub>1</sub> and LPA<sub>6</sub>, which are EDG- and non-EDG-LPA receptors, respectively [35]. These two receptors share low amino acid sequence homology, and their crystal structures have revealed contrasting features including the access route of LPA into the binding site (Fig. 7.3). Here we briefly discuss the structural characteristics of LPA<sub>1</sub> and LPA<sub>6</sub>, including comparisons with other lipid-binding GPCRs.

In 2015, the crystal structures of LPA<sub>1</sub> bound to three different antagonist compounds were reported [36]. Recent structural analyses on lipid GPCRs have revealed that many of them have a "gap" structure that is embedded in the membrane lipid bilayer, which is proposed to provide a route for the lipid ligand to access the binding pocket of the receptor by lateral diffusion within the membrane [35]. However, structural analyses with molecular dynamics simulations indicate absence of a "gap" structure in LPA<sub>1</sub> and support an open access route for ligand entry from the extracellular space to the binding pocket [36]. The unique open access route from the extracellular space might also facilitate effective accommodation of LPA extracellularly delivered by lipid chaperones including ATX. Absence of an intramembrane "gap" structure was also observed in antagonist-bound BLT<sub>1</sub> [37], agonist-bound EP3 [38], and agonist-bound  $CB_1$  receptors [39]. However, a "gap" structure was present in  $CB_1$ when it was bound with an antagonist [40] or inverse agonist [41], suggesting that the "gap" structure formed by transmembrane helices is not fixed and its presence may depend on the recep-



**Fig. 7.3** Models for LPA access to LPA<sub>1</sub> and LPA<sub>6</sub> based on their crystallographic structures

LPA<sub>1</sub> lacks an intramembrane "gap" structure, supporting a model of open access route from the extracellular space.

On the other hand, LPA<sub>6</sub> potentially accommodates LPA delivered either by open access from the extracellular space or lateral diffusion from the lipid bilayer
tor's ligand-dependent conformational state [39]. A similar scenario was also suggested for agonistbound EP<sub>3</sub>, which showed a totally enclosed ligand binding pocket in its crystal structure [38]. Therefore, further crystallization of LPA<sub>1</sub> in different ligand-bound states may be necessary to determine whether LPA<sub>1</sub> actually lacks the lateral diffusion access route. The structure of LPA<sub>1</sub> is also characterized by its "baggy" large globular ligand binding pocket, which may facilitate broader ligand recognition not only among various LPA species but also phosphorylated endocannabinoids [36]. Many lipid GPCRs, including LPA<sub>1</sub>, possess an extracellular "lid" structure over the ligand pocket formed by the N-terminus and/or second extracellular loop of the receptors, which is proposed to regulate or limit extracellular access of lipid ligands [35]. However, the extracellular "lid" structure of LPA1 is proposed to be relatively flexible and less restrictive, which might facilitate access of LPA delivered by carrier or chaperone proteins including ATX [36].

The crystal structure of LPA<sub>6</sub> was resolved in 2017, and, in contrast to LPA<sub>1</sub>, revealed an intramembrane "gap" structure, suggesting a lateral diffusion mode of LPA access to the ligand binding site [42]. LPA<sub>6</sub> notably lacks the abovementioned "lid" structure, suggesting that LPA could have open access from the extracellular space, in addition to the lateral diffusion access [42]. Currently, the biological significance of the potential "dual" access routes of LPA into the ligand binding pocket of LPA<sub>6</sub> is unclear. LPA<sub>6</sub> signaling in hair follicles is induced by 2-acyl-LPA derived from membrane-embedded PA by the enzymatic activity of mPA-PLA<sub>1 $\alpha$ </sub> [43] (described in Sect. 7.5.10). Indeed, mPA-PLA<sub>1 $\alpha$ </sub> over-expression induced LPA<sub>6</sub> activation by increasing membrane LPA levels without LPA secretion [42], suggesting that mPA-PLA<sub>1 $\alpha$ </sub>derived LPA accesses the binding pocket of LPA<sub>6</sub> via the lateral diffuse route. On the other hand, ATX-derived LPA delivered to endothelial LPA<sub>6</sub> is known to have important roles in angiogenesis [44] and lymphocyte homing into secondary lymphoid organs [45]. Delivery of LPA by ATX to LPA receptors is proposed to occur from the extracellular space, suggesting that the open access route rather than lateral diffusion may be utilized to deliver ATX-derived LPA to  $LPA_6$  on the plasma membrane of endothelium.

Since LPA<sub>1</sub> and LPA<sub>6</sub> belongs to distinct families of LPA receptors, it follows that their contrasting structural features may reflect the common characteristics either of EDG or non-EDG family LPA receptors. However, there are several concerns about simply applying their properties as family-specific (EDG versus non-EDG) characteristics of LPA receptors. For example, S1P<sub>1</sub>, an EDG-family S1P receptor with high sequence homology to LPA<sub>1</sub>, has a lateral diffusion ligand route and no ligand access from the extracellular space [34]. Furthermore, in contrast to the broad ligand recognition of LPA<sub>1</sub> with its "baggy" ligand binding pocket, LPA<sub>3</sub>, also an EDG-family receptor, has a rather strict ligand selectivity and clearly prefers 2-acyl LPA [6], possibly suggesting a more restrictive agonist binding pocket. Determining the crystal structures of additional LPA receptors will elucidate their mechanisms of ligand binding and facilitate rational design of drugs to effectively and selectively target LPA receptors.

# 7.5 Pathophysiology of LPA Signaling

After the cloning of the first LPA receptor, numerous studies have assessed the roles of LPA signaling both in vitro and in vivo. Especially, in vivo genetic tools including knock-out (KO) animals have revealed roles of LPA signaling in virtually every organ system. In addition, a rapidly growing number of ATX inhibitors and LPA receptor modulators have been developed, and their effects have been tested in vivo. These studies have further revealed diverse pathophysiological roles of LPA signaling and have been instrumental in targeting LPA pathways in clinical applications. Indeed, studies with Lpar1-KO mice have led to clinical trials of LPA<sub>1</sub> antagonists and ATX inhibitors for fibrosis patients. In this section, we discuss roles of LPA signaling in pathophysiology across organ systems, especially focusing on the knowledge obtained from studies that utilized genetic and pharmacological approaches.

#### 7.5.1 Fibrosis

Fibrosis is a major feature and cause of morbidity for a number of diseases including idiopathic pulmonary fibrosis (IPF), systemic sclerosis, progressive kidney diseases, and diabetes; thus effective treatment of fibrotic disorders represents a highly unmet and urgent medical need. LPA signaling pathway is a potential therapeutic target for fibrosis, and indeed multiple small molecule drugs are currently being evaluated in clinical trials. Profibrotic roles of LPA have been extensively studied since the first reports on the roles of LPA<sub>1</sub> in lung [46] and renal [47] fibrosis in 2007–2008. In the bleomycin-induced lung fibrosis model, Lpar1-KO mice were protected from disease progression and mortality. The LPA-LPA<sub>1</sub> axis seems to be involved in multiple pathological aspects of fibrosis including fibroblast recruitment/proliferation, extracellular matrix accumulation, epithelial apoptosis, myofibroblast differentiation, and vascular leak [46, 48]. Of note, it seems that the profibrotic action of LPA involves induction of connective tissue growth factor, another important player and potential drug target for fibrosis, through the LPA<sub>1</sub>-G $\alpha_{13}$ -ROCK-serum response factor axis. Indeed, genetic deletion or pharmacological inhibition of the players in this axis successfully diminished fibrosis development in murine fibrosis models [47, 49–51].

The profibrotic role of LPA<sub>1</sub> is not limited to the bleomycin-induced lung fibrosis model, and *Lpar1*-KO mice also displayed significant protection from lung fibrosis induced by radiation [52] or lung allograft [52] as well as various models of renal [47, 49], skin [53] and peritoneum [50] fibrosis, indicating that LPA-LPA<sub>1</sub> signaling has a fundamental role in the process of fibrosis. Moreover, beneficial effects of LPA<sub>1</sub> antagonists have also been observed in various rodent models of fibrosis including fibrosis in lung [54–59], kidney [55, 60], skin [53, 61], and peritoneum [50]. Although LPA<sub>1</sub> seems to be the primary player mediating the profibrotic LPA action, other LPA receptors may also have roles in fibrosis. For example, Lpar2-KO mice showed protection from bleomycin-induced lung fibrosis [62] but not from dermal fibrosis [53].

It is likely that profibrotic LPA is mainly derived from the ATX-dependent pathway, and elevated ATX levels were observed in lungs of bleomycin-challenged mice and also IPF patients [63]. Indeed, conditional genetic deletion of *Enpp2*, which encodes ATX, specifically in bronchiolar epithelial cells or myeloid cells resulted in protection from bleomycin-induced lung fibrosis [63]. Of note, systemic ATX levels do not seem to contribute to pulmonary fibrosis, because liver-specific Enpp2 over-expression increased systemic ATX levels without affecting fibrosis development [63]. On the other hand, hepatocytespecific Enpp2-KO mice displayed diminished disease progression in liver fibrosis models [64, 65]. Therefore, profibrotic LPA may be locally supplied at the site of fibrosis rather than systemically supplied. In addition to LPA<sub>1</sub> antagonists, many studies have shown the beneficial effects of ATX inhibitors on different types of fibrosis including lung [59, 63, 66], kidney [60, 67], skin [68, 69], liver [27], and synovial joint [70] fibrosis.

As mentioned above, the LPA-LPA<sub>1</sub> profibrotic pathway is a promising druggable target to treat fibrotic diseases. Treatment with BMS-986020, an LPA<sub>1</sub> antagonist from Bristol-Myers Squibb, significantly slowed the rate of respiratory function decline in Phase 2 clinical trials for IPF patients [71]. However, the appearance of cholecystitis in three patients receiving the drug lead to early termination of the study. The cholecystitis was determined to be a drug-specific side effect not related to LPA<sub>1</sub> antagonism, and the study suggested it was possible to slow decline of lung function in IPF patients by targeting LPA<sub>1</sub>. Later, Bristol-Myers Squibb developed a novel LPA1 antagonist BMS-986278 that does not have hepatobiliary toxicity [72], and it entered into Phase 1 clinical trials with healthy volunteers that were ongoing or completed in 2019 (NCT03429933, NCT03712540, and NCT03981094). Another LPA<sub>1</sub> antagonist, SAR100842 from Sanofi, was well tolerated with an acceptable safety profile in a Phase 2 trial for systemic sclerosis patients, and was associated with numerically improved clinical scores suggestive of potential clinical benefits [73].

Several ATX inhibitors are also being tested in clinical trials to slow or halt progression of fibrotic diseases. One such compound, GLPG1690 (Ziritaxestat) from Galapagos NV is currently under clinical trials for patients with fibrotic diseases. In a Phase 2 study for a small cohort of IPF patients (FLORA study), GLPG1690 showed a halt of disease progression and favorable safety profile and tolerability [74]. Two larger Phase 3 clinical trials started from December 2018 to test the efficacy of GLPG1690 in IPF patients, which combined have a total of ~1,500 patients and more than 200 clinical sites worldwide (ISABELA1 and ISABELA2 studies) [75]. In 2019, Galapagos NV also started a Phase 2 trial with GLPG1690 in systemic sclerosis patients (NOVESA study, NCT03798366). **BBT-877** from Bridge Biotherapeutics is another ATX inhibitor in clinical trial, and was found to be well-tolerated and safe in a Phase 1 trial with healthy volunteers [76]. In July 2019, Boehringer Ingelheim obtained a license from Bridge Biotherapeutics to develop this drug beyond Phase 1. Lastly, BLD-0409 (PAT-409) from Blade Therapeutics (previously ATXCo, a spin-off of PharmAkea Therapeutics) is a Phase 1-ready ATX inhibitor for patients with fibrotic diseases, and the trial will start from January 2020 (NCT04146805).

### 7.5.2 Central Nervous System

The gene encoding LPA<sub>1</sub> was originally called ventricular zone gene-1 due to its enriched expression in the ventricular zone of the developing brain [4]. Indeed, LPA<sub>1</sub> is highly expressed in neural progenitor cells (NPCs) in developing brain, and Lpar1-KO mice have defects in cortical development including a reduction in proliferation, premature NPC maturation, and increased apoptosis [77]. Importantly, ex vivo or in vivo LPA application studies have revealed an important role for LPA signaling in pre-natal and newborn brain damage, a serious health issue that affects millions of babies each year and may be caused by hypoxia, bleeding, or infection. In ex vivo mouse brain slice culture experiments,

hypoxia-induced cerebral cortical disruption including displacement of mitotic NPCs was blocked by either genetic depletion of Lpar1 or application of  $LPA_1$ antagonists [78]. Furthermore, in vivo injection of LPA to either fetal or neonatal brains produced hydrocephalus phenotype, which was ameliorated in Lpar1- or Lpar3-KO mice and mice treated with LPA<sub>1</sub> antagonists [79, 80]. Since intraventricular bleeding often precedes hydrocephalus formation, and LPA is abundant in blood, LPA may be one of the key causative mediators of the post-hemorrhagic hydrocephalus. Prenatal intracerebral hemorrhage is an identified risk factor for schizophrenia, and prenatal mice receiving intraventricular injections of serum or LPA showed schizophrenialike behavior as adults and had altered expression profiles of genes relevant to schizophrenia; these effects were blocked by a LPA<sub>1/3</sub> antagonist [81]. Thus, LPA receptors blockage is a potential strategy to prevent infant and neonatal brain damage from various insults.

High levels of LPA<sub>1</sub> expression was also observed in NPCs in brain of adult mice, as revealed in a LPA<sub>1</sub>-GFP reporter mouse line [82]. Intracerebroventricular infusion of LPA resulted in increased adult hippocampal neurogenesis [82, 83] and cell proliferation [83] in WT but not in *Lpar1*-KO mice nor in LPA<sub>1/3</sub> inhibitor-treated mice [83]. Hippocampal neurogenesis was also reduced in adult Lpar1-KO mice under normal conditions [84]. Possibly reflecting the developmental or adult neurological defects, Lpar1-KO mice displayed various behavioral defects closely related to psychiatric and mental diseases including reduced prepulse inhibition (PPI) (a marker of schizophrenic disorders) [85], spatial memory defects [86-88], reduced exploratory behavior [86, 87], increased anxiety-like behavior [86, 87, 89], impaired fear extinction [90], and altered substance abuse behavior [91, 92]. Since Lpar1-KO mice suffer from altered neurodevelopment, as described above, it is plausible that these phenotypes are due to altered neurodevelopment or neuroadaptation. However, some studies have shown LPA signaling manipulation also causes acute effects on neuronal function. In rodents, intracerebroventricular infusion of LPA potentiates hippocampal-dependent memory [93], increases anxiety-like responses [94, 95] and decreases cocaine-induced conditioned place preference [83]. Furthermore, administration of an LPA<sub>1/3</sub> antagonist decreased context-dependent fear extinction [90], and increased anxiety-like behavior [96] or alcohol consumption [92, 97], all of which mimic the Lpar1-KO mice phenotypes 89, 90, 92, [86, 87, 96]. Intracerebroventricular injection of an LPA<sub>1/3</sub> antagonist also led to progressive increases of cocaine-induced conditioned place preference [83]. These results demonstrate neurodevelopment-independent effects of the LPA-LPA<sub>1</sub> axis in memory, fear extinction, anxiety and substance abuse.

In addition to LPA<sub>1</sub>, a neuropsychiatric role of LPA<sub>2</sub> has been demonstrated with relevance to the function of plasticity related genes (PRGs), neuron specific membrane proteins located at the postsynaptic density of glutamatergic synapses. PRGs are highly homologous to lipid phosphate phosphatases (LPPs), ecto-phosphatases that degrade LPA and S1P [98]. However, PRGs generally lack ecto-phosphatase activities, and rather are proposed to modify synaptic phospholipid levels by promoting their uptake into the intracellular compartment [98]. Prg1-KO mice display epileptic seizures caused by neuronal hyperexcitability, leading to reduced body weight and increased mortality [99]. Neuronal hyperactivity in these mice was rescued by in utero electroporation of WT PRG1 but not by PRG1 pointmutated to disrupt the putative interaction with lipid phosphates [99]. Of note, the phenotypes of Prg1-KO mice were rescued by global deletion of Lpar2 [99], astrocyte-specific deletion of Enpp2 [100], or ATX inhibitors [100]. Mono- or bi-allelic removal of Prg1 also induces behavioral abnormalities including reduced PPI and social interaction, higher exploratory behavior, and higher motor activity with running and jumping (referred to as rodent "Forrest Gump") [101]; these abnormalities are reverted by genetic or pharmacological inhibition of LPA<sub>2</sub> or ATX [100–102]. Therefore, it is proposed that PRG1 normally functions to limit bioavailability of synaptic LPA which is produced by astrocytic ATX and induces neuronal activation via LPA<sub>2</sub>. Notably, a loss-of-function single nucleotide polymorphism (SNP) was identified in the human *PRG1* gene that is associated with an endophenotype for mental disorders [102].

These studies indicate LPA signaling may have important roles in mental and neurological disorders; however, there are several controversial and unsolved issues. For example, reduced PPI is observed under conditions of both loss (in Lpar1-KO mice [85]) and gain (in Prg1heterozygous mice [100]) of LPA signaling, while genetic or pharmacological inhibition of ATX under normal physiological conditions did not alter animal behavior, including PPI, of WT mice [100]. PRG1 and ATX display spatially restricted expressions at postsynaptic neurons [99] and peri-synaptic astrocytic processes [100], respectively, suggesting that the microenvironmental LPA levels may be tightly regulated. Therefore, it is plausible that spatially distinct pools of LPA have different roles in the regulation of neuronal activities by signaling through different LPA receptor subtypes. Furthermore, in addition to LPA<sub>1</sub> and LPA<sub>2</sub>, other LPA receptors which are also enriched in brain and neuron [103] may participate in neuronal function. Indeed, Lpar5-KO mice display altered behaviors including anxiolytic effects, reduced social exploration, increased behavioral flexibility, and increased motivational behavior [104]. Thus, more comprehensive understanding of LPA signaling in the brain including functions of the various LPA receptors in their different microenvironments is required to enable development of LPA signalingbased therapies to treat mental and neurological disorders.

#### 7.5.3 Pain

Neuropathic pain, intractable pain directly caused by damage or disease of the somatosensory nervous system, is challenging to treat with currently available therapies. LPA signaling plays a central role in the initiation of neuropathic pain and therefore represents a potential therapeutic target to treat this debilitating condition. In rodents, intrathecal injection of LPA itself induces behavioral allodynia and hyperalgesia accompanied by demyelination [105]. Importantly, *Lpar1*-KO mice were resistant to both the nociceptive response and demyelination not only in LPAinduced model of neuropathic pain but also in a partial sciatic nerve injury model [105]. Behavioral allodynia and demyelination were attenuated by pre- but not post-injury blockage of  $LPA_{1/3}$  [106, 107] or its downstream signaling molecules Rho/ROCK [105, 107], highlighting the essential role of LPA<sub>1</sub> signaling in the initiation of neuropathic pain [105]. Mechanistically, LPA<sub>1</sub> signaling in Schwann cells at the dorsal root activates multiple cascades that decrease myelin gene mRNA expression and increase proteolysis of myelin proteins, leading to the subsequent demyelination [105, 108].

ATX mediates the production of LPA which acts as an initiator of neuropathic pain. Indeed, Enpp2-heterozygous mice displayed improved recovery from neuropathic pain [109]. It's been known for nearly fifty years that direct injection of LPC into the spinal cord induces demyelination [110], and this procedure is still commonly used in animal models for studying demyelination and remyelination processes. Notably, LPC did not exhibit demyelinating activity in Lpar1-KO mice, and Enpp2-heterozygout mice displayed much milder phenotypes in a LPCinduced demyelination model [111]. In WT mice, LPA levels showed drastic increases after injury in spinal dorsal horn and dorsal roots but not in spinal nerve or sciatic nerve, and these increases were attenuated both in Enpp2-heterozygous mice as well as in PLA<sub>2</sub> inhibitor-treated mice [112, 113]. These observations suggest that the demyelination initiator LPA and its precursor LPC are locally produced during nerve injury.

*Lpar3*-KO mice are also protected from LPCor LPA-induced demyelination. Notably, these mice did not show an initial increase in LPA levels at the spinal dorsal horn following nerve injury [112]; this suggests that LPA<sub>3</sub> facilitates feed-forward amplification of LPA production following nerve injury, a mechanism known to involve microglial activation [114]. Genetic or pharmacological interventions have also demonstrated the involvement of the LPA-LPA<sub>1/3</sub> axis in models of neuropathic pain induced by chemotherapeutic agents [115], osteoarthritis [116], and stroke [117, 118]. Given the pivotal role of the ATX-LPA<sub>1/3</sub> axis in the initiation stage of neuropathic pain, blockage of this pathway represents a therapeutic target for prevention and treatment of neuropathic pain.

In addition to LPA<sub>1</sub> and LPA<sub>3</sub>, the role of LPA<sub>5</sub> in neuropathic pain has been established. *Lpar5*-KO mice were protected from neuropathic pain development in peripheral nerve injury models [104, 119] as well as in a cuprizoneinduced multiple sclerosis model [120]. Intrathecal injection of a selective LPA<sub>5</sub> agonist itself induced pain [121] while injection of a LPA<sub>5</sub> antagonist had an analgesic effect [121, 122] in rodent neuropathic pain models. Despite their protection from neuropathic pain development, Lpar5-KO mice did not show decreased myelin sheath aberrations following nerve ligation [119], unlike what had been observed in *Lpar1*-KO mice [105]. Instead, *Lpar5*-KO mice showed abolished neuronal cAMP response element-binding protein phosphorylation at dorsal horn after nerve ligation [119], indicating a role for LPA<sub>5</sub> in central neurons during neuropathic pain induction. The analgesic effects achieved by genetic deletion or pharmacological inhibition of LPA<sub>5</sub> are not limited to neuropathic pain models but has also been demonstrated for inflammatory pain [121], supporting the central involvement of LPA<sub>5</sub> in pain-signal transmission and responses. Therefore, pharmacological targeting of LPA<sub>5</sub> may represent an attractive strategy to manage pain for broad range of pain conditions including neuropathic and inflammatory pain.

## 7.5.4 Cardiovascular System

The importance of ATX-derived LPA in vascular development was demonstrated by multiple studies that showed that *Enpp2*-KO embryos die due to severe vascular defects [123–126]. Overexpression of *Enpp2* also caused embryonic lethality with severe defects in angiogenesis and

vessel formation [127]; therefore, tight regulation of ATX expression and LPA production seems to be essential for proper embryonic angiogenesis. This is further supported by the fact that genetic removal of LPP3, an LPA degrading enzyme, causes embryonic lethality that is accompanied by vascular defects resembling those of Enpp2overexpressing embryos [128]. Since the vascular defects in Enpp2-KO embryos are reminiscent of *Gna13* (encoding  $G\alpha_{13}$  protein)-KO embryos [129–131],  $G\alpha_{13}$ -coupled receptor targets were postulated to mediate the actions of angiogenic LPA. One of the target receptors for angiogenic LPA is LPA<sub>4</sub> since embryos deficient for *Lpar4*, a  $G\alpha_{13}$ -coupled LPA receptor, partially phenocopied the vascular defects in Enpp2-KO embryos [132]. However, the penetrance of lethal vascular defect in *Lpar4*-KO embryos is ~30%, indicating the existence of at least one more angiogenic LPA receptor existed that links ATXproduced LPA to  $G\alpha_{13}$  signaling [132]. Very recently, Yasuda et al. established that LPA<sub>4</sub> and LPA<sub>6</sub> synergistically function to contribute to sprouting angiogenesis, and Lpar4/Lpar6-double KO mice almost completely phenocopy the vascular defects observed in Enpp2- or Gna13-KO embryos [44]. The role of endothelial LPA<sub>4</sub> in vascular development has been further highlighted in studies of tumor vasculature. In murine lung carcinoma [133] or glioblastoma [134] cell implantation models of tumors, LPA application promoted intra-tumor vascular network formation and improved drug delivery into tumors, which effect was not observed in Lpar4-KO mice [133]. Therefore, activation of the LPA-LPA<sub>4</sub> axis in endothelial cells may be a promising target to normalize vasculature in tumors, which has potential to facilitate anti-tumor drug delivery, improve anti-tumor immunity, and also normalize hypoxic environments which may promote cancer progression. Abnormal or excessive angiogenesis plays major roles in the development or pathologies of numerous diseases including cancer, arthritis, and blindness; and vascularization/vascular architecture is often a critical factor affecting delivery of drugs to treat various conditions. Therefore, modification of the LPA<sub>4/6</sub> axis in endothelial cells holds great promise as a therapeutic strategy to treat various diseases associated with disturbed angiogenesis or vascular maturation.

Historically, the vasoactive role of LPA was first identified in a soybean extract in 1978 [2], and hypertension has long been noted as a major physiological effect of LPA. This LPA-induced altered hypertensive effect was not in Lpar1/Lpar2-double KO mice [135], and the molecular mechanisms including LPA receptor subtypes which mediate the hypertensive actions of LPA had long been elusive. Recently, Kano et al. have utilized a variety of LPA receptorselective agonists and LPA receptor-KO mice to show that the hypertensive response to LPA is mediated mainly by LPA<sub>4</sub>, while LPA<sub>6</sub> is also crucial for normal vasoactivity [136]. Of note, elevated levels of plasma LPA or ATX have been reported in acute coronary syndrome [137, 138] and pregnancy, especially in women facing preterm delivery [9]. Therefore, the ATX-LPA<sub>4/6</sub>-G $\alpha_{13}$ axis may be a major contributor to hypertension in these clinical conditions, and this pathway will be a promising drug target for blood pressure control.

Neointimal formation is a pathological vascular remodeling process that occurs after arterial injury, and it is a major cause of restenosis after stenting or angioplasty. LPA has a major role in neointima formation, and infusion of LPA itself induced neointimal formation in uninjured rodent arteries [139, 140]. The LPA-induced vascular remodeling was blunted by either a LPA<sub>1/3</sub> antagonist [141] or genetic depletion of *Lpar1* but not *Lpar2* or *Lpar3* [142], indicating a major role of  $LPA_1$  in this process. However, the roles reported for various LPA receptors in neointimal responses after injury may be complex and often varies among studies. An LPA<sub>1/3</sub> antagonist reduced carotid wire-induced neointima formation in Apoe-KO mice, possibly by inhibiting mobilization and recruitment of smooth muscle progenitor cells [141]. However, in a carotid artery ligation model, Lpar1-KO mice showed enhanced neointimal formation, possibly by upregulation of LPA<sub>3</sub> [135]. In the same study, *Lpar1/Lpar2*double KO mice but not Lpar2-KO mice were partially protected from the development of intimal formation [135], suggesting that LPA promotes neointimal formation by signaling that is cooperatively regulated by LPA<sub>1</sub>, LPA<sub>2</sub> and possibly LPA<sub>3</sub>. Exaggerated vascular injuryneointima formation was also observed in mice with smooth muscle cell (SMC)-specific deletion of LPP3, indicating a biological role for LPP3 to limit LPA-induced responses following vascular injury [143]. Additionally, a non-GPCR-mediated role of LPA was postulated whereby PPAR $\gamma$  may promote neointima formation by working as an intracellular receptor target of LPA independently of LPA<sub>1</sub> or LPA<sub>2</sub> [140, 144]. The variable and inconsistent roles reported for several LPA receptors in different neointima formation models may reflect the complexity and diversity of LPA signaling responses that occur in various cell types and vascular beds during different phases of vascular remodeling. Furthermore, exaggerated hypoxia-induced pulmonary vascular remodeling was observed in Lpar1/Lpar2-double KO and *Enpp2* heterozygous mice [145], indicating additional roles for the ATX-LPA<sub>1/2</sub> axis in vascular remodeling in lung that are distinct and rather opposite from those in the systemic vasculature. To better understand these discrepancies, it may be necessary to examine the role of LPA receptors utilizing cell type-specific KO approaches for several different cell types including endothelium, SMCs, and inflammatory cells.

LPA is abundant in the lipid rich core of human atherosclerotic lesions [146]. Exogenous application of LPA accelerated disease progression in a murine model of atherosclerosis by enhancing recruitment of inflammatory cells, whereas administration of LPA<sub>1/3</sub> antagonist suppressed atherogenesis by reducing inflammatory cell recruitment [147, 148] as well as plasma cholesterol levels [148]. Beneficial effects of a LPA<sub>1/3</sub> antagonist were also observed in a murine model of calcific aortic valve stenosis, which shares common pathophysiological mechanisms with atherosclerosis [149]. In addition, a recent study has shown that Lpar4-KO mice are protected from development of atherosclerosis, probably by changes in macrophage populations that are involved in the process [150, 151]. An important role of LPP3 in atherosclerosis was indicated by a genome-wide association study (GWAS) which identified a heritable SNP in *PPAP2B*, the gene encoding LPP3, as a susceptibility locus for cardiovascular disease [152]. Indeed, SMC- or hepatocyte-specific deletion of LPP3 led to exacerbated plaque formation in murine models of atherosclerosis [151, 153]. Together with the fact that endothelium-specific deletion of LPP3 increases vascular inflammation [154], it is likely that both systemic levels of LPA as well as LPA produced locally in the vascular walls have important roles in progression of atherosclerosis.

LPA also has important functions in heart, that are not well characterized. Cardiomyocytespecific deletion of LPP3 in mice resulted in shorter life span due to heart failure, indicating deteriorative roles for excessive LPA signaling on normal cardiac homeostasis [155]. However, exaggerated cardiac dysfunction and infarction size were observed in Lpar3-KO mice [156] or mice treated with a LPA<sub>1/3</sub>-antagonist [157] in myocardial infarction models, indicating that cardio-protective roles of LPA<sub>1</sub> and/or LPA<sub>3</sub> may exist. Although the specific roles of LPA signaling related to myocardial infarction remains elusive, a six-fold increase in serum LPA levels was reported in patients following acute myocardial infarction [158]; therefore, LPA pathways represent a promising and emerging potential drug target for myocardial infarction and other heart diseases.

#### 7.5.5 Respiratory System

LPA signaling is involved in multiple processes that impact both development and pathologies of the respiratory system. *Lpar1*-KO mice displayed alveolarization defects reminiscent of the alveolar dysplasia that occurs in bronchopulmonary dysplasia due to reduced alveolar septal elastogenesis [159], which may be related to the profibrotic action of LPA<sub>1</sub> observed in pulmonary fibrosis as discussed above (Sect. 7.5.1). Likewise, *LPAR1*-hypomorph (*LPAR1*<sup>M318R/M318R</sup>) rats displayed enlarged alveoli [160], confirming the importance of LPA<sub>1</sub> in alveolar development.

Roles of LPA<sub>1</sub> have been implicated not only in chronic fibrogenic lung pathology (Sect. 7.5.1) but also in non-fibrogenic acute lung injury (ALI). In an endotoxin-induced ALI model, LPA levels in bronchial lavage (BAL) fluid were elevated [161], and *Lpar1*-KO and LPA<sub>1/3</sub> antagonisttreated mice [162] as well as LPAR1-hypomorph rats [163] showed reduced BAL cytokine levels and immune cell infiltration into alveolar spaces following ALI challenges. Unlike the lung fibrosis models, LPA<sub>1</sub> blockage did not affect vascular leak induction in ALI models, indicating that LPA<sub>1</sub> may promote ALI mainly by its proinflammatory properties. A pro-inflammatory role of LPA<sub>1</sub> is also implicated in rodent hyperoxia-induced ALI models [160, 164]; however, the involvement of ATX in ALI is not as clear as that of LPA<sub>1</sub>. Although chronic systemic overexpression of Enpp2 exacerbated lung inflammation in an endotoxin-induced ALI model [161], the contribution of endogenous ATX on the acute inflammatory phase appeared to be minor based on the results from genetic or pharmacological targeting of ATX in ALI models [161]. Rather, it is suggested that increased ATX may predispose or promote pulmonary inflammation differentially under acute or chronic inflammatory conditions, which may involve distinct LPA receptors expressed in various cell types during different phases of lung injury.

Increased LPA levels in BAL fluid is also observed in a murine model of allergic airway inflammation and humans with asthma [165]. In a Schistosoma mansoni egg-driven asthma model, *Lpar2*-heterozygous mice showed reduced airway goblet cell metaplasia, eosinophil infiltration into BAL, and prostaglandin (PG) synthesis compared to WT mice [166]. Reduction of allergic lung inflammation in *Lpar2*-KO mice was also observed in a triple-allergen-driven asthma model [165]. Pharmacological ATX blockage or haploinsufficiency of Enpp2 also bestowed a protective effect, while *Enpp2* over-expression exacerbated airway inflammation in the same model [165], indicating a pro-inflammatory role of the ATX-LPA<sub>2</sub> axis in asthma. However, antiinflammatory roles of LPA<sub>2</sub> have also been reported. In a murine model of ovalbumin-driven

allergic asthmatic inflammation, Lpar2-KO mice displayed more severe airway inflammation, possibly due to increased dendritic cell (DC) activa-Furthermore, pharmacological tion [167]. activation of LPA<sub>2</sub> showed protective effects in a house-dust mite-driven model of murine allergic airway inflammation [168], supporting a potential anti-inflammatory role of LPA2. The reasons for the discrepancies are unknown but might be due to differences in nature of the antigens used, immunization protocols, or genetic backgrounds of the mice used. Although LPA2 was shown to be a negative regulator of DC activation and allergic lung inflammation [167], LPA<sub>2</sub> has also been shown to enhance motility of T cells, which may promote their stimulation by antigen-bearing DCs in lymph node (LN) [169, 170] (discussed in Sect. 7.5.11). Together these studies suggest that LPA<sub>2</sub> may mediate either pro- or antiinflammatory signaling during allergic reactions, which may vary between cell types and disease stage. A distinct neuronal mechanism is also reported to be important for LPA-mediated airway hypersensitivity in asthma, whereby direct activation of carotid body by LPA involving transient receptor potential vanilloid 1 and LPAspecific receptors was sufficient to induce vagal activity followed by acute bronchoconstriction [171].

### 7.5.6 Gastrointestinal Tract

LPA is involved in the homeostatic maintenance of gastrointestinal tissues. Detailed analysis on basal intestinal phenotype of *Lpar1*-KO mice revealed shortened intestinal villi and defective proliferation and migration of intestinal epithelial cells (IECs) [172]. *Lpar1*-KO mice also displayed epithelial barrier dysfunction accompanied by enhanced bacterial infiltration and cytokine gene induction in intestine [173]. Concordantly, inducible global deletion of *Enpp2* from adult mice lead to intestinal inflammation and aberrant IEC proliferation, which was accompanied by weight loss and increased mortality [174]. In addition, gastrointestinal application of LPA promoted gastric would repair [175] and reduced stress-induced gastric ulcer formation in rats [176]. These studies revealed a major role for ATX/LPA signaling in gastric wound healing, which may occur mainly via LPA<sub>1</sub> because the effect was absent in *Lpar1*-KO mice [172].

Inflammatory bowel disease (IBD), which includes ulcerative colitis and Crohn's disease, is a multifactorial intestinal disorder characterized by diffuse accumulation of lymphocytes in mucosa. Given the protective roles of ATX and LPA<sub>1</sub> reported in intestinal homeostasis including barrier maintenance, it follows that LPA signaling might also have protective roles in the context of IBD. Indeed, recovery from dextran sulfate sodium (DSS)-induced colitis was delayed in *Lpar1*-KO mice or LPA<sub>1</sub>-antagonist treated mice [172]. However, other studies have indicated that detrimental roles of LPA signaling also exist in IBD. Global deletion of *Enpp2* [174] or pharmacological inhibition of ATX [177] protected mice from DSS-induced colitis. A beneficial effect by ATX inhibition was also reported in a murine model of Crohn's disease [178]. Notably, mucosal accumulation of lymphocytes, a characteristic of IBD inflammation, was diminished by ATX inhibition or gene deletion in these studies. As discussed later (Sect. 7.5.11), ATX has important roles in homing of lymphocytes to secondary lymphoid organs, thus it is plausible that the ATX-LPA receptors axis boosts mucosal lymphocyte accumulation to promote IBD progression. Therefore, immuno-modulation by ATX inhibitors or LPA receptors antagonists may hold clinical promise for treatment or control of IBD.

IECs, especially those in crypt compartment, abundantly express LPA<sub>2</sub> [179]. LPA administration displayed protective effects from choleratoxin-induced diarrhea by inhibiting cystic fibrosis transmembrane conductance regulator (CFTR)-dependent Cl<sup>-</sup> secretion [180]. This protective role of LPA was absent in *Lpar2*-KO mice, confirming the essential role of LPA<sub>2</sub> [179, 180]. LPA<sub>2</sub> has a unique carboxyl terminal PDZbinding domain which is thought to allow formation of a macromolecular complex with the Na<sup>+</sup>/ H<sup>+</sup> exchanger regulator factor 2 (NHERF2) and other proteins to facilitate effective and compartmentalized inhibition of CFTR [180]. Indeed, Lpar2, Nherf2 and Cftr are all more abundantly expressed in crypts rather than in villi compartments of intestine, and the protective role of the LPA-LPA<sub>2</sub> axis was absent in *Nherf*2-KO mice [179]. LPA<sub>2</sub> also has a unique protective role in radiation-induced intestinal injury. Oral administration of LPA or a stable analogue of LPA clearly reduced radiation-induced apoptosis of IECs in WT but not Lpar2-KO mice [181, 182]. In addition, Lpar2-KO mice showed increased rate of radiation-induced apoptosis and higher mortality, indicating that endogenous LPA also plays an essential role in radioprotection. Mechanistically, it is proposed that radiation increases systemic ATX activity, which facilitates LPA-dependent DNA damage repair via LPA<sub>2</sub> activation [183]. Therefore, LPA<sub>2</sub> agonists represent a promising therapeutic tool to promote recovery from radiation injuries due to environmental exposures or cancer therapy, and various chemically stable LPA<sub>2</sub> agonists are being developed as exemplified by Rx-100 and Radioprotectin-1 [184].

LPA<sub>5</sub> mRNA is also abundant in the intestinal tract. In contrast to LPA<sub>2</sub>, which is enriched in crypts, LPA<sub>5</sub> expression is enriched in the villus compartment of the intestine. LPA acting on IECs in the villus compartment has a protective role in diarrhea by inducing fluid absorption via activation of Na<sup>+</sup>/H<sup>+</sup> exchanger 3 (NHE3) [185]. This effect is absent in IEC-specific Lpar5-KO mice [186] but intact in *Lpar2*-KO mice [187], confirming the essential role of LPA<sub>5</sub> expressed on IECs for LPA-dependent enhancement of fluid absorption. Thus, LPA<sub>2</sub> and LPA<sub>5</sub> have protective roles in diarrhea via different mechanisms: inhibition of fluid secretion at crypt segment is LPA2dependent while activation of fluid absorption at villus segments occurs via LPA<sub>5</sub>. Like LPA<sub>2</sub>, LPA<sub>5</sub> also contains a PDZ-binding domain at its carboxyl terminus and interacts with NHERF2, which is necessary for the stimulation of NHE3 [187]. Indeed, the fluid absorption effect by LPA-LPA<sub>5</sub> axis was abolished in *Nherf2*-KO animals [187]. Of note, bioactive LPA and LPA precursors are present in a variety of herbal medicines and food stuffs such as cabbage where they have

been suggested to have beneficial health effects that include promoting healing of gastric ulcers [188]. Thus, modulation of NHE3 by LPA<sub>5</sub> ligands including both drug-like compounds as well as natural sources enriched in certain foods hold promise for the treatment or prevention of diarrhea, as well as other gastric conditions which can be modulated by LPA signaling.

### 7.5.7 Metabolic Disorders

The involvement of ATX in the development of obesity and metabolic disorders has been extensively studied by many research groups. Notably, adipose tissue is a major source of systemic ATX, as revealed by adipocyte-specific Enpp2-KO mice which display a 50-70% reduction in blood ATX [189–192]. Therefore, ATX can be classified as an adipokine based on its LPA production. Adipocyte-specific *Enpp2*-KO mice [189–192] as well as global *Enpp2*-heterozygous mice [191, 193] display improved systemic metabolism including protection from obesity-induced hepatosteatosis, while systemic [194] or adipocytespecific [191] overexpression of *Enpp2* increases adiposity in murine obesity models. Furthermore, obesity-related cardiac hypertrophy and dysfunction were also attenuated by pharmacological ATX inhibition [195] or *Enpp2* hemizygous deletion [193], indicating broad roles for ATX existing in several tissues that are impacted by metabolic disorders.

Important roles for LPA<sub>1</sub> and LPA<sub>4</sub> in promoting metabolic disorders have been reported. LPA administration acutely inhibited insulin secretion and lowered glucose tolerance in mice, which was inhibited by pre-injection of a LPA<sub>1/3</sub> antagonist [196]. Chronic inhibition of LPA<sub>1/3</sub> also decreased glucose tolerance in a murine model of obesity [196]. Although *Lpar1*-KO mice weighed less, they had higher adiposity than WT mice under low fat diet conditions [197, 198]. Under high fat diet (HFD) conditions, *Lpar1*-KO mice are protected from development of obesity, possibly due to decreased food intake [198]. In addition to LPA<sub>1</sub>, the impact of LPA<sub>4</sub> on obesity-related metabolic disorders was recently evaluated [199]. Lpar4-KO mice showed enhanced expression of mitochondrial and adipogenic genes along with increased production of adiponectin when fed a standard diet. In a HFD-induced obesity model, *Lpar4*-KO mice displayed a metabolically healthy obese phenotype, including improved glucose homeostasis and reduced hepatosteatosis, which was mediated through continuous healthy expansion of adipose tissue. Nonalcoholic steatohepatitis is a progressive form of fatty liver disease that is characterized by inflammation and fibrosis, and there are currently no approved pharmacological therapies. Together with the beneficial effect of LPA<sub>1</sub> and ATX inhibition on liver fibrosis (Sect. 7.5.1), LPA signaling may have potential to solve multiple aspects of this unmet and urgent medical need.

#### 7.5.8 Reproduction

The critical role of LPA<sub>3</sub> signaling in female reproduction has been established. Lpar3-KO female mice showed severe reproductive defects including delayed implantation and aberrant embryo spacing [200]. Similar phenotypes have been observed in mouse models where PG synthesis is genetically or pharmacologically blocked [201]. Indeed, reduced mRNA levels of cyclooxygenase-2 (COX-2), a key enzyme for PG synthesis, as well as reduced PG amounts are observed in uteri of *Lpar3*-KO mice [200]. Of note, exogenous PG rescued the delayed implantation but not the aberrant embryo spacing in Lpar3-KO mice, suggesting that LPA<sub>3</sub> regulates implantation timing and embryo spacing independently. An LPA<sub>3</sub>-selective agonist induced a potent contractile response in isolated uteri from WT but not *Lpar3*-KO mice [202]. Therefore, it is possible that LPA<sub>3</sub>-dependent uterine contraction may be needed for proper embryo spacing in a PG-independent manner. More detailed roles of LPA<sub>3</sub> in female reproductive tissue were further investigated by Aikawa et al. They studied the effects of an LPA<sub>3</sub>selective agonist and an ATX inhibitor on reproductive tissues of WT as well as Lpar3-KO mice [203]. In their study, the authors proposed a model whereby ATX-dependent production of LPA at the embryo-epithelial boundary leads to activation of epithelial LPA<sub>3</sub>, which contributes to successful decidualization through induction of COX-2 and heparin-binding epidermal growth factor at the epithelial layer, followed by BMP2 and Wnt4 induction at the stromal layer. Notably, these downstream targets of LPA<sub>3</sub> have been implicated in the progression of endometriosis, and in fact Lpar3-KO mice displayed less developed endometrial tissues in a mouse endometriosis model [203]. Therefore, the ATX-LPA<sub>3</sub> axis is a potential therapeutic target not only for female infertility but also other female reproductive tissue conditions such as endometriosis.

The male reproductive system is also regulated by LPA signaling. In testis, Lpar1, Lpar2 and *Lpar3* are highly expressed in germ cells. Male Lpar1-, Lpar2-, and Lpar3-single gene-KO mice all displayed mild reductions in sperm counts compared to age-matched WT mice; sperm reductions were even more pronounced in compound-KO mice lacking any two of these receptors [204]. The triple LPA receptor-KO males showed the most pronounced reductions, with over 60% of these males having azoospermia at 8 months age despite normal testosterone levels, suggesting that the reduced sperm counts were caused independent of systemic changes in endocrine function. Mechanistically, activation of these LPA receptors seems to protect germ cells from apoptosis and support sperm production in a partially redundant manner through multiple and convergent roles [204]. Male infertility accounts for 40-50% of all infertility and affects approximately 7% of all men. More precise elucidation of the molecular mechanisms by which LPA signaling promotes healthy sperm counts, including the sources of LPA and whether those LPA levels are altered in various conditions affecting sperm counts such as aging, may lead to new therapeutic tools to treat or prevent male infertility.

#### 7.5.9 Bone

The first in vivo role of LPA signaling was demonstrated in Lpar1-KO mice, which display dwarfism as well as cranial deformities including shorter snouts and more widely spaced eyes [205]. In a follow up study, extensive analyses of the bone phenotypes in Lpar1-KO mice revealed additional abnormalities in ribs and vertebrae, which included fused rims and abnormal attachment of the ribs to the sternum [206]. Lpar1-KO mice showed decreased masses of trabecular and cortical bones without mineralization deficiency, indicative of true osteoporosis due to decreased osteoblast differentiation and osteogenesis. More recently, Nishioka et al. revealed further details about the molecular mechanisms underlying the cranial deformities in Lpar1-KO mice [207]. They found that *Lpar1* is highly expressed in chondrocytes, and Lpar1-KO mice displayed dyschondroplasia in skull, costa, and femur. Because these bones are largely formed by endochondral ossification, in which cartilage is replaced by bone, and disturbed chondrocyte and cartilage phenotypes preceded defective bone tissue formation in Lpar1-KO mice, the authors concluded that impaired bone development in Lparl-KO mice is mainly caused by dyschondroplasia. Enpp2 expression is also enriched in chondrocytes and typical cartilage, and bone abnormalities of Lpar1-KO mice are phenocopied by genetic reduction of Enpp2. Mechanistically, the ATX-LPA<sub>1</sub> axis in chondrocytes supports integrin-dependent fibronectin assembly which is essential for chondrocyte proliferation. Although the skeletal phenotypes of *Lpar1*-KO mice can be attributed to functional defects in chondrocytes and possibly osteoblasts, a role of osteoclastic LPA<sub>1</sub> is also possible. In fact, systemic treatment with a LPA<sub>1</sub> antagonist prevents osteoclast-mediated bone loss in an ovariectomy-induced osteoporosis mouse model [208].

LPA<sub>4</sub> is another LPA receptor involved in bone formation, and has been shown to regulate osteoblast function. *Lpar4*-KO mice displayed increased bone volume, trabecular thickness, and trabecular number [209], indicating that LPA<sub>4</sub> may have an opposing role to LPA<sub>1</sub> on osteoblast differentiation and development of bone mass. The inhibitory role of LPA<sub>4</sub> on bone formation was attributed to its  $G\alpha_s$ -coupled signaling [209]; however,  $G\alpha_s$  stimulation generally enhances osteogenesis [210], in contrast to the antiosteogenic role of LPA<sub>4</sub>. LPA<sub>4</sub> has been shown to couple primarily to  $G\alpha_{13}$  in several biological contexts including angiogenesis [44, 132], vascular normalization [133, 134], and metabolic disorders [199]; and it will be important to determine whether  $G\alpha_{13}$ -coupled signaling may also mediate actions of LPA<sub>4</sub> pertinent to bone formation. Elucidation of the mechanisms that coordinate the opposing actions of LPA<sub>1</sub> and LPA<sub>4</sub> on osteoblasts and determining whether these mechanisms are altered in disease condition such as osteoporosis are critical questions to be addressed in future studies. Determination of the sources of LPA that stimulate each receptor will enable a fuller understanding of the roles of LPA signaling pathway in bone pathophysiology, which may aid in the development of LPA signaling-based therapies for bone diseases.

## 7.5.10 Skin and Hair

In addition to the role in skin fibrosis (Sect. 7.5.1), LPA plays important roles in skin wound healing, itch response, and hair development. In rodents, topical application of LPA thickened the skin epidermis [211] and accelerated skin wound healing [212, 213]. LPA also promoted skin barrier function in a mouse model of dry skin [214]. Notably, LPLs containing high amount of LPA promoted skin moisturizing capacity of human skin [215]. Therefore, LPA may serve as a novel therapeutic target for skin barrier dysfunction. Although these observations reveal beneficial aspects of LPA application on skin, dermal injection of LPA can cause itchiness and scratching behavior in rodents [216-222]. Genetic and pharmacological approaches have identified LPA<sub>1</sub> [220], LPA<sub>5</sub> [221], and transient receptor potential channels [221] as molecular targets of LPA that mediate pruritic responses. Increased blood

levels of both ATX and LPA have been reported in murine models of atopic dermatitis [220, 223] as well as in human atopic dermatitis patients [224, 225], indicating a possible role for LPA in initiation or exacerbation of pruritic skin disease. Furthermore, serum ATX levels were found to be markedly elevated in patients with cholestatic pruritus [226], and LPA was suggested to be a potential pruritogen in these patients [219].

Studies on human hereditary hair disorders and detailed studies utilizing KO mice have established a critical role for LPA signaling in hair development. In 2006, LIPH, encoding mPA-PLA<sub>1 $\alpha$ </sub>, was identified as a causative gene for human autosomal recessive woolly hair/hypotricosis (ARWH/HT) [227]. This was followed by numerous reports on various LIPH mutations in ARWH/HT patients [228-256]. In 2008, P2RY5 (former official gene name of LPAR6) was also identified as a causative gene for ARWH/ HT [257, 258], and various mutations have been reported [253, 259–271]. In accordance with the findings from human genetics, LIPH has been identified as the causative genes for the rex hair coat phenotype in rabbits [272] and LPAR6 is causative for the curly coat phenotype of Cornish Rex cats [273], indicating a fundamental role for the LIPH-LPA<sub>6</sub> axis in hair development across several species. Using Liph-KO mice having wavy hairs, Inoue et al. revealed the detailed molecular mechanism underlying mPA-PLA<sub>1</sub>  $LPA_6$  axis [43]. At hair follicles, the predominant LPA species are 2-acyl ones, and they are almost completely lacking in *Liph*-KO [43] but not in *Enpp*2-KO mice [274], indicating a critical role of mPA-PLA<sub>1 $\alpha$ </sub> rather than ATX in LPA production at hair follicles. At the inner root sheath of hair follicles, mPA-PLA<sub>1 $\alpha$ </sub>-derived LPA activates  $LPA_6$ , an LPA receptor that prefers 2-acyl type LPA species, leading to  $G\alpha_{13}$ -dependent ectodomain shedding of TGF $\alpha$ , a key process for hair development. Together with the "ligand lateral diffusion" hypothesis suggested by the crystal structure of LPA<sub>6</sub> (Sect. 7.4.2), the mPA-PLA<sub>1 $\alpha$ </sub>-LPA<sub>6</sub> axis-dependent model of hair development represents a more complete model of LPAsignaling in a specific biological context, connecting the production and function by describing how the LPA is produced, delivered to receptors, and exerts biology.

# 7.5.11 Hematopoiesis and Immune Function

The roles of LPA signaling in hematopoiesis were evaluated by pharmacological blockage of LPA<sub>2</sub> and LPA<sub>3</sub> in mice. LPA<sub>2</sub> agonists decreased while LPA3 agonists increased red blood cell number in mice, indicating the opposing roles of these receptors in regulation of erythropoiesis [275]. However, a beneficial effect of LPA<sub>2</sub> activation for hematopoiesis has also been reported in a mouse model of irradiation [276]. Administration of a potent LPA2 agonist after irradiation increased peripheral white blood cell and platelet counts and reduced mortality. LPA has critical roles in the maintenance and regulation of hematopoietic stem cells (HSCs), which include both cell-autonomous mechanisms as well as modulation of the HSC niche microenvironment. The importance of LPA signaling in the HSC niche was revealed by a study which found that Lpar4-KO mice have decreased numbers of HSCs in bone marrow and spleen [277]. The Lpar4-KO mice showed delayed hematopoietic recovery and increased mortality after chemicalor radiation-induced myelosuppression. The importance of LPA<sub>4</sub> in stromal cells that support HSC stem cell proliferation was elucidated by bone marrow transplantation experiments.

During their patrol through the body, lymphocytes continuously migrate from circulation into secondary lymphoid organs including LNs via specific type of blood vessels called high endothelial venules (HEVs). An extremely high amount of ATX is expressed in HEV endothelial cells (ECs) [278–280], and ATX plays essential role in lymphocyte transendothelial migration. Local [280] but not circulatory [279] ATX blockage attenuates lymphocyte entry into LNs, indicating the important role of LPA locally produced by ATX in the transendothelial migration of lymphocytes. The locally produced LPA seems to act in an autocrine manner on HEV ECs that express LPA<sub>4</sub> and LPA<sub>6</sub>. Indeed, *Lpar4*- and *Lpar6*-KO mice displayed compromised lymphocyte transmigration across HEV EC layers [45]. T cells, after homing to LNs, dynamically move within the LNs which facilitates effective detection of antigens. Even here, LPA signaling is important for intranodal T cell movement via LPA2dependent signaling. Pharmacological inhibition of ATX slows down intranodal T cell motility [281, 282]. Fibroblastic reticular cells (FRCs) in HEVs express high amounts of ATX [281] and are proposed to be the source of the LPA responsible for the intranodal T cell movement regulation. Indeed, intranodal T cell motility was decreased significantly in FRC-specific *Enpp2*-KO mice [170]. Furthermore, *Lpar2*-KO T cells that have been adoptively transferred into WT mice display attenuated motility in LNs [169, 170]. An important role for LPA<sub>2</sub> in T cell trafficking and homing is also postulated to function in neuroinflammation. In a murine experimental autoimmune encephalomyelitis (EAE) model, Lpar2-KO mice displayed exaggerated disease progression which was accompanied by enhanced T cell infiltration into the spinal cord, suggesting defective lymphocyte homing in these mice [283]. Accordingly, an LPA<sub>2</sub> agonist reduced clinical signs of EAE, possibly by enhancing T cell homing [283]. Taken together, these studies suggest that LPA produced locally by ATX from several distinct cell types coordinately regulates lymphocyte movement into and within the LNs, via actions on specific LPA receptors on several cell types.

CD8 T cell cytotoxicity is often inhibited by prolonged antigen-specific stimulation associated with chronic infections and cancer. Recent studies have revealed that LPA, which is elevated in inflammation and cancer, inhibits activation of cytotoxic T cells via binding to LPA<sub>5</sub>. LPA suppresses T cell receptor-mediated CD8 T cell signaling and cytotoxic activity *in vitro*, but this effect was abolished in *Lpar5*-KO cells [284, 285]. Genetic deletion of *Lpar5* in CD8 T cells enhanced their antigen-specific stimulation *in vivo*, while *in vivo* administration of a stable analogue of LPA dampened antigen-specific CD8 T cell responses [284, 285]. CD8 T cell cytotoxic activity was increased in Enpp2-heterozygous mice [285], further supporting that the ATX-LPA-LPA<sub>5</sub> axis has an inhibitory role on CD8 T cell immunity. LPA5-dependent signaling also suppresses B cell activation in response to antigen receptor signaling and antibody responses [286]. Pharmacological suppression of the adaptive immune resistance is attracting attention due to recent successes in overcoming immunotolerances that limit the ability of the immune system to combat cancer. Notably, tumor-bearing mice transplanted with Lpar5-KO T cells displayed improved control over tumor progression [284, 285], and targeting of LPA<sub>5</sub> may be a key therapeutic strategy to unlock the potential of cancer immunotherapy.

#### 7.6 LysoPS Receptors

The bioactivity of lysoPS was originally identified in 1979 as an activity which enhances mast cell degranulation [287]. Since then, several studies have elucidated the underlying mechanisms for the actions of lysoPS on mast cells. Similar to LPA, lysoPS was postulated to possess specific receptor(s), as indicated by biological responses to lysoPS that showed stereoselectivity [288]. However, it was not until 2006 that Sugo et al. identified the first cell-surface GPCR target of lysoPS, GPR34 (now called lysoPS<sub>1</sub>) [289]. Lysopsr1/GPR34 mRNA expression was found to be remarkably high in mast cells [289]; however, mast cell responses to lysoPS were not altered in Lysopsr1/Gpr34-KO mice, indicating the presence of additional lysoPS receptor(s) [290]. In 2012, Aoki, Inoue, and colleagues developed an excellent GPCR-ligand screening methodology that succeeded in identifying three additional lysoPS receptors: P2Y10 (lysoPS<sub>2</sub>), A630033H20Rik (lysoPS<sub>2L</sub>, a pseudogene in humans) and GPR174 (lysoPS<sub>3</sub>) [291]. Their group further developed unique lysoPS analogues which differentially activate lysoPS<sub>1/2/3</sub> [292]. Notably, they identified an analogue with extremely high potency (>20-fold compared to authentic lysoPS) for mast cell activation, however this compound did not activate any of the known lysoPS receptors [293]. Thus, the receptor target of lysoPS responsible for mast cell degranulation is still enigmatic, and there may be additional unidentified lysoPS receptors, either GPCR or non-GPCR, in mast cells.

# 7.7 Putative Bioactive lysoPS Synthesis Pathways *In Vivo*

LysoPS can be produced from phosphatidylserine (PS) by enzymes with PLA activities. Currently, the identification of the specific enzyme(s) and synthesis pathway(s) to produce bioactive lysoPS in vivo are not firmly established; however one candidate enzyme is PS-specific PLA<sub>1</sub> (PS-PLA<sub>1</sub>) [294]. PS-PLA<sub>1</sub> shows the highest homology with mPA-PLA<sub>1 $\alpha$ </sub>, a bioactive LPA-producing enzyme [11]; and a positive correlation between lysoPS and PS-PLA<sub>1</sub> concentration has been observed in plasma from acute coronary syndrome patients [295] as well as in gastric cancerous ascites [296]. In in vitro experiments, exogenous application of PS-PLA<sub>1</sub> strongly enhanced mast cell degranulation, clearly mimicking the bioactive effects of lysoPS [297]. Another candidate enzyme for bioactive lysoPS production  $\alpha/\beta$ -hydrolase domain-containing is 16A (ABHD16A), a principle PS lipase in mammalian cells and tissues. Indeed, reduced lysoPS levels are observed by genetic removal or pharmacological blockage of ABHD16A in tumor cell lines, macrophages, and mouse brain [298]. Although both PS-PLA<sub>1</sub> and ABHD16A produce lysoPS, further studies, perhaps linking the phenotypes of the specific enzyme- and receptor-KO mice, will be required to determine the enzymes that supply ligands for the lysoPS receptors in vivo.

# 7.8 Pathophysiology of lysoPS Signaling

Compared with LPA, much less is known about the roles of lysoPS signaling *in vivo*. However, recent studies with KO mice have started to unveil the biological significance of lysoPS, especially in the immune system.

Similar to the role for LPA, lysoPS signaling seems to be essential in the pathogenesis of neuropathic pain, likely through effects on microglial function. In nerve injury models of neuropathic pain, Lysopsr1/Gpr34-KO mice show reduced pain as well as microglia-associated pro-inflammatory gene expression [299]. Consistent with this, intrathecal administration of an antagonist for lysoPS<sub>1</sub>/GPR34 suppresses neuropathic pain [299]. Notably, increased lysoPS levels accompanied by dramatically enhanced microglial activation had been observed in brains of mice gene-deficient for ABHD12, a principle lysoPS lipase in brain [300]. Although it is not clear whether the enhanced microglial activation is mediated through lysoPS<sub>1</sub>/GPR34, it is plausible that lysoPS signaling plays proinflammatory roles in microglia. In addition, *Lysopsr1/Gpr34*-KO mice display altered microglial morphology reminiscent of activated microglia even under non-inflammatory conditions [301]. Furthermore, freshly isolated microglia from Lysopsr1/Gpr34-KO mice displayed defective phagocytosis activity [301], suggesting that basal activities of lysoPS<sub>1</sub>/GPR34 may be necessary to maintain microglia in a homeostatic non-phagocytic state that is required to initiate phagocytosis upon stimuli [302]. This scenario may also explain the higher brain pathogen burden of Lysopsr1/Gpr34-KO mice in a murine model of pulmonary infection of fungus [290].

Considering that enhanced levels of brain lysoPS is suggested to contribute to neuroinflammatory disease caused by inactivating mutations of ABHD12 [298, 300], further understanding of lysoPS signaling in microglia will help to establish novel therapeutic approaches toward various inflammation-related neurological diseases.

Studies with *Lysopsr3/Gpr174*-KO mice have revealed important roles for lysoPS signaling in T cell function. Under homeostatic condition, increased frequency of *Lysopsr3/Gpr174*-KO regulatory T cells (Tregs) was observed in sites where thymus-derived and peripherally induced Tregs can accumulate [303]. In *in vitro* experiments, production of IL-2, which is necessary for the growth and differentiation of Tregs, was clearly suppressed by lysoPS in T cells from WT mice but not in T cells from Lysopsr3/Gpr174-KO or Gnas (gene encoding  $G\alpha_s$  protein)-KO mice [304, 305]. Notably, basal levels of IL-2 production were increased in Lysopsr3/Gpr174-KO T cells even without addition of exogenous lysoPS [304, 305]. Furthermore, in *in vitro* culture experiments of CD4 T cells purified from WT mice, lysoPS was almost exclusively detected in cells and levels were further increased after antigen stimulation, while very little lysoPS was detected in culture medias [304]. These results suggest that a T cell intrinsic lysoPS-lysoPS<sub>3</sub>/GPR174 axis restrains T cell proliferation partly by suppressing IL-2 production in a  $G\alpha_s$ -dependent manner. The absence of this "downer" signaling on Tregs likely contributes to protective effects observed for Lysopsr3/Gpr174-KO mice in EAE [303] and cytokine storm of sepsis [306]. Recent GWAS studies have linked human SNPs in LYSOPSR3/GPR174 and LYSOPSR2/P2RY10 (adjacent locus to LYSOPSR3/GPR174) to two different autoimmune diseases; Graves' disease [307–309] and rheumatoid arthritis [310], respectively. Considering the pivotal role of Tregs in limiting excessive immune responses and preventing autoimmunity, unlocking the Tregs "downer" signaling by inhibition of the lysoPSlysoPS<sub>3</sub>/GPR174 axis may be a promising therapeutic strategy to combat various autoimmune diseases.

# 7.9 LPI and Lysophosphatidylglucoside (LysoPtdGlc)

**Dual LPL Ligands for LPI**<sub>1</sub>/**GPR55** GPR55 was an orphan GPCR belonging to the P2Y cluster that was cloned from human brain [311]. In early 2000's, GPR55 was proposed as a new cannabinoid receptor by two patent reports (reviewed in [312]). Since then, numerous studies have sought to elucidate the biological roles of GPR55, especially its potential as an atypical cannabinoid pharmacological target. However, the identity of GPR55 as a cannabinoid receptor is still under debate by conflicting reports [313]. Firmly establishing the natural ligand specificity of GPR55 had been elusive for many years, which had hampered our understanding of pathophysiological roles of GPR55.

### 7.9.1 LPI

In 2009, Oka et al. identified LPI as a high affinity ligand for GPR55 [314]. In brain, two major LPI species are 1-stearoyl-LPI (18.9 nmol/g of tissue) and 2-arachidonoyl-LPI (8.29 nmol/g of tissue) [315]. In structure-activity relationship experiments, 2-arachidonoyl-LPI has much higher activity than 1-stearoyl-LPI and is proposed to be a natural ligand for GPR55 [315]. The identity of GPR55 as a LPI receptor has been confirmed by various studies from many independent groups, and GPR55 has now been assigned with the provisional name LPI<sub>1</sub> and the gene name LPIR1 by a nomenclature review for LPL receptors [316]. Of note, LPI<sub>1</sub>/GPR55independent actions of LPI are also reported [317, 318], suggesting that additional receptor target(s) for LPI may exist.

LPI can be produced from phosphatidylinositol (PI) by various PLAs; however, a bona fide enzymatic pathway for synthesis of LPI which functions as a LPI<sub>1</sub>/GPR55 ligand is not yet established. One promising candidate enzyme to produce bioactive signaling LPI is DDHD domain containing 1 (DDHD1), a brain-enriched intracellular enzyme that can produce 2-acyl type LPLs, including 2-arachidonoyl-LPI, in vitro [319]. Importantly, Ddhd1-KO brain displays a clear reduction of arachidonoyl- or docosahexaenoyl-LPI but not of other LPI species [320]. Ddhd1-KO mice show reduced mechanical nociception [320], which may be related to the impaired nociception that was also observed in Lpir1/Gpr55-KO mice in several pain models [321, 322] (Sect. 7.10.2). However, given that brains of Ddhd1-KO mice display reductions of additional LPLs including lysoPS [320], future analyses will be needed to conclude whether DDHD1 supplies LPI as a bona fide natural ligand for LPI<sub>1</sub>/GPR55.

# 7.9.2 LysoPtdGlc: Repulsive Axon Guidance Cue

As developing dorsal root ganglion axons of sensory neurons enter the spinal cord, they become segregated to project to distinct positions of the spinal cord without mixing; nociceptive axons to lateral positions and proprioceptive axons to dorsomedial positions. This developmental process is thought to be facilitated by the coordinated chemoattraction and chemorepulsion of individual axons; however, the molecular mechanism including the guidance cues had been elusive. In 2015, Guy et al. identified that LysoPtdGlc, a glial cell-derived glycosylated LPL molecule, acts as a spatially repulsive signaling cue during pathfinding of nociceptive axons [318]. In a screening assay that examined over one hundred GPCRs, LPI<sub>1</sub>/GPR55 was identified as a receptor target of LysoPtdGlc. Importantly, injection of a LysoPtdGlc neutralizing antibody against induced guidance errors of the nociceptive afferents, and the same phenotype was completely recapitulated in Lpir1/Gpr55-KO mice, validating the ligand-receptor interaction in vivo.

The LysoPtdGlc that acts as a spatial cue for nociceptive axons is likely to be produced from phosphatidylglucoside (PtdGlc) via an unidentified enzyme with PLA<sub>2</sub> activity. PtdGlc is a component of plasma membrane of radial glia, and specifically localized in the dorsomedial position of spinal cord [318]. This confined distribution of PtdGlc facilitates the confinement of LysoPtdGlc to the position where proprioceptive afferents will project; by repulsing LPI<sub>1</sub>/GPR55-positive nociceptive afferents and thereby aiding their guidance to the lateral positions. Thus, fine spatial compartmentalization of LysoPtdGlc is a key feature for the accurate repulsive guidance of nociceptive afferents via LPI<sub>1</sub>/GPR55, and may distinguish a role of LysoPtdGlc that is distinct from that of LPI, another LPI<sub>1</sub>/GPR55 ligand. Further detailed analyses on the molecular mechanism underlying LysoPtdGlc (and PtdGlc) confinement as well as regulation of LPI synthesis is warranted to more fully understand the biological complexities that have shaped a "dual" LPL ligand system for LPI<sub>1</sub>/GPR55 signaling.

# 7.10 Pathophysiology of LPI<sub>1</sub>/ GPR55 Signaling

After the first proposal of LPI<sub>1</sub>/GPR55 as new cannabinoid receptor, numerous studies have assessed the in vivo roles of LPI1/GPR55, especially in the context of pharmacology of cannabinoid ligands. However, considering the debates on the identity of LPI1/GPR55 as a cannabinoid receptor [313], studies that utilize Lpir1/Gpr55-KO mice will provide more confident information on the specific roles of LPI<sub>1</sub>/ GPR55. Such studies have already validated important roles for LPI<sub>1</sub>/GPR55 existing in the nervous system (Sects. 7.10.1 and 7.10.2), gastrointestinal tract [323-326], cardiovascular system [327-329], pancreas [330-332], cancer [333–335], bone [336], salivary gland [337], lymphocytes [338, 339], and metabolic disorders [340, 341]. Below, we discuss the role of LPI<sub>1</sub>/ GPR55 signaling in the nervous system as revealed by studies using Lpir1/Gpr55-KO mice.

### 7.10.1 Central Nervous System

Roles for LPI<sub>1</sub>/GPR55 are implicated in neurogenesis and synaptic function. In vivo infusion of O-1602, an atypical cannabinoid agonist for LPI<sub>1</sub>/GPR55, into hippocampus of adult WT mice increases NSC proliferation as well as immature neuron generation, but this effect is abolished by genetic deletion of Lpir1/Gpr55 [342]. Notably, Lpir1/Gpr55-KO mice display reduced basal rates of NSC proliferation and immature neuron generation [342], indicating that endogenously activated LPI<sub>1</sub>/GPR55 normally facilitates homeostatic and continuous neurogenesis in the adult mouse hippocampus. LPI<sub>1</sub>/GPR55 is also involved in synaptic function. LPI<sub>1</sub>/GPR55 is expressed within submicron proximity to glutamatergic synaptic vesicles, and application of LPI or O-1602 enhances presynaptic Ca<sup>2+</sup> elevation and glutamate release in acute hippocampal slices from WT but not from Lpir1/Gpr55-KO mice [343]. Even without ligand application, Lpir1/Gpr55-KO slices show decreased post-burst synaptic potentiation that is

thought to depend on presynaptic Ca<sup>2+</sup> elevation [343]. Therefore, activation of LPI<sub>1</sub>/GPR55 by an endogenous ligand seems to positively regulate a presynaptic Ca<sup>2+</sup> elevation that leads to enhanced neurotransmitter release. In addition, LPI enhances long-term potentiation, likely by postsynaptic modification, in hippocampal slices from WT but not Lpir1/Gpr55-KO mice [344]. Furthermore, Lpir1/Gpr55-KO mice display neuronal projection abnormalities not only in nociceptive afferents [318] (Sect. 7.9.2), but also in retinal ganglion cells targeting towards the visual thalamus [345]. Therefore, it is likely that in addition to its roles in the peripheral nervous system, LPI<sub>1</sub>/GPR55 also modulates anatomical neuronal circuits in the central nervous system during development. A major challenge for future research is to identify the endogenous ligand (LPI versus LysoPtdGlc) that signals through LPI<sub>1</sub>/GPR55 to regulate these several processes in the central nervous system. Although behavioral tests with Lpir1/Gpr55-KO mice did not reveal any memory defects [344], increasing LPI<sub>1</sub>/GPR55 signaling may be a promising therapeutic strategy for memory disorders such as dementia and Alzheimer's disease.

### 7.10.2 Pain

Like LPA and lysoPS receptors, LPI<sub>1</sub>/GPR55 has important roles in pain. Intraplantar injection of LPI in hind paws of mice causes a marked mechanical hypersensitivity lasting for 6 days without causing local inflammation [322]. The nociceptive hypersensitivity triggered by LPI is completely abolished in Lpir1/Gpr55-KO mice as well as sensory neuron-specific Gna13-KO or Gnaq/Gnall (encoding  $G\alpha_0/G\alpha_{11}$  proteins)-double KO mice [322]. Importantly, unlike LPA, LPI did not cause demyelination. Mechanistically, it is hypothesized that activation of the LPI1/ GPR55-G $\alpha_{13}$  and G $\alpha_q/_{11}$  axis in peripheral sensory neurons in dorsal root ganglia leads to hyperexcitability and sensitization of sensory neurons. Accordingly, Lpir1/Gpr55-KO failed to develop mechanical hyperalgesia in several different pain models including a partial nerve ligation model of neuropathic pain [321], an inflammatory pain model [321], and a tumorassociated pain model [322]. In addition, microinjection of LPI into intra-periaqueductal gray caused thermic hyperalgesia, which was blocked by pre-treatment with a LPI<sub>1</sub>/GPR55 antagonist [346]. Therefore, LPI<sub>1</sub>/GPR55 has pronociceptive roles not only at peripheral but also at central levels. Although these studies have revealed pronociceptive role of LPI<sub>1</sub>/GPR55, Lpir1/Gpr55-KO mice display mild thermic hyperalgesia under normal conditions [321, 347, 348], suggesting an analgesic role of LPI<sub>1</sub>/GPR55 signaling exists under homeostasis. Together with the pivotal role of LPI<sub>1</sub>/GPR55 for nociceptive afferent guidance (Sect. 7.9.2), this indicates that  $LPI_1/GPR55$  is involved in multiple levels of nociception, from neural network formation to central sensation. As mentioned above, some of the major constituents of cannabis, including cannabidiol and tetrahydrocannabinol, are reported to be ligands for LPI<sub>1</sub>/GPR55 [313]. Considering the increasing focus and debates concerning the usage of cannabinoids for pain relief, further understanding the details of LPI<sub>1</sub>/GPR55-dependent regulation of nociception may be essential to guide development and usage of novel cannabinoid-based pain relievers.

# 7.11 Conclusion

Here we have reviewed some of the many roles of LPLs, especially LPA, in physiology and pathophysiological states that hold potential as druggable signaling pathways. Targeting of bioactive LPA signaling pathways including the LPA-synthesizing enzymes and individual receptor subtypes holds potential to treat or ameliorate a wide range of disease of conditions, as exemplified by the current clinical trials of ATX inhibitors and LPA<sub>1</sub> antagonists for fibrotic diseases. Development of highly selective and effective compounds has been aided by the solved crystal structures of LPA1, LPA6 and ATX; and will be accelerated by future solving of additional LPA receptor structures. Besides for LPA signaling pathway molecules, more recently identified bioactive LPL receptor targets LPI<sub>1</sub> and lysoPS<sub>1-3</sub> are emerging as promising therapeutic targets, and other as yet unidentified receptors may also exist to mediate effects of various LPL signaling molecules. These receptors, along with the enzymes that regulate production and availability of their ligands, will be the next wave of druggable targets of LPL signaling pathways. Determining the bona fide LPL receptor subtype and ligand source mediating biological responses remains an ongoing challenge in many instances, and future studies utilizing various cell type-specific KO mice or receptor-subtype-compound KOs will be highly beneficial to unravel some of these complexities. This will aid not only in novel drug development, but also for avoidance of unwanted side effects and may allow potential drug repositioning. Furthermore, it is expected that where and how the LPL ligand is produced and how it is delivered to its cognate receptor are critical determinants of biological outputs. Elucidating the biological mechanisms that mediate precise regulation of LPL signaling required for physiological responses will reveal exciting new opportunities to pharmacologically target LPL signaling pathways to treat human diseases.

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# Druggable Targets in Endocannabinoid Signaling

8

Ann M. Gregus and Matthew W. Buczynski

### Abstract

Cannabis and cannabinoid-based extracts have long been utilized for their perceived therapeutic value, and support for the legalization of cannabis for medicinal purposes continues to increase worldwide. Since the discovery of  $\Delta^9$ -tetrahydrocannabinol (THC) as the primary psychoactive component of cannabis over 50 years ago, substantial effort has been directed toward detection of endogenous mediators of cannabinoid activity. The discovery anandamide of and 2-arachidonoylglycerol as two endogenous lipid mediators of cannabinoid-like effects (endocannabinoids) has inspired exponential growth in our understanding of this essential pathway, as well as the pathological conditions that result from dysregulated endocannabinoid signaling. This review examines current knowledge of the endocannabinoid system including metabolic enzymes involved in biosynthesis and degradation and their receptors, and evaluates potential druggable targets for therapeutic intervention.

#### Keywords

$$\label{eq:endocannabinoid} \begin{split} & Endocannabinoid \cdot GPCR \cdot CB_1 \cdot CB_2 \cdot \\ & FAAH \end{split}$$

# 8.1 Cannabinoids as Therapeutics

For centuries, cannabis and cannabinoid-based extracts were thought to possess therapeutic value. In recent years, the use of medical marijuana has increased for a wide variety of disorders in the United States, and changes in the legal landscape and public opinion support expanding its recreational availability nationwide. The 2010, a resolution adopted by the American Medical Association advocated reconsideration of marijuana as a Schedule I controlled substance given the potential therapeutic value of marijuana and cannabis-based products. As of January 1, 2020, 33 states have legalized the sale of medical marijuana, with additional states considering similar legislation with possible enaction in the near future.

The primary psychoactive component of cannabis was identified as  $\Delta^9$ -tetrahydrocannabinol (THC) by Yechiel Gaoni and Raphael Mechoulam in the 1960s [1, 2]. While hundreds of bioactive molecules have been identified in cannabis thus far [3], THC recapitulates many of the pharmacological properties attributed to marijuana in both rodent models and in humans [4, 5]. Subsequent

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worldwide efforts were aimed at the discovery of both synthetic and semi-synthetic cannabinoids capable of producing cannabinoid-like effects in vivo for the eventual development of patentable drugs with verifiable therapeutic value. While many hundreds of cannabinoid compounds were created in subsequent years, the pharmacological properties of these compounds often retained or exacerbated psychoactive effects when compared with THC [6], and thus many of these early cannabinoid-mimetics were not heavily pursued in clinical trials. Alternatively, synthetic cannabinoids began to reemerge as a recreational alternative to traditional cannabis in convenience stores and online marketplaces during the mid-2000s under pseudonyms such as "Spice" and "K2". Synthetic cannabinoids were generally consumed by inhalation via cigarettes containing herbal substances along with these synthetic molecules to obtain euphoric, anxiolytic, and antidepressantlike effects. Whereas traditional cannabis products generally have been considered safe across a wide dose range, numerous case reports illustrate that synthetic cannabinoids produce deleterious effects including paranoia, tachycardia, panic, convulsions, psychosis, visual/auditory hallucinations, vomiting, and seizures [6].

Thus far, two cannabinoid-based therapeutics have obtained FDA approval: Marinol® (dronabinol or THC) and Cesamet® (nabilone), a synthetic cannabinoid [7, 8], for the treatment of chemotherapy-induced nausea and emesis. Marinol also has been indicated as an appetite stimulant to treat cachexia in AIDS patients. A third medication, formulated with equivalent concentrations of THC and cannabidiol (CBD) known as Sativex<sup>®</sup>, has been approved in several countries outside the United States for the relief of spasticity in multiple sclerosis (MS) patients [9]. While the widespread use of medical marijuana suggests potential therapeutic value for a number of diseases, psychoactive effects and addictive potential of cannabinoids with chronic usage may limit widespread use in clinical practice. Additionally, their CNS effects complicate interpretation of efficacy in clinical trials as patients can easily determine whether or not they are receiving the drug or a placebo. Thus, substantial efforts are directed toward evaluating alternative targets in the cannabinoid signaling pathway for the development of safe and effective therapeutics.

# 8.2 Selective Modulation of Cannabinoid Receptors

While significant adverse effects and lack of efficacy have hampered the development of cannabinoid receptor antagonists for clinical use [10–14], these compounds served as important tools for the discovery of endogenous cannabinoid receptors 1 ( $CB_1$ ) and 2 ( $CB_2$ ) and their classification as G protein-coupled receptors [15]. Binding studies conducted using radiolabeled versions of potent synthetic cannabinoids such as CP-55,940 revealed high-affinity cannabinoid-specific binding sites via radioactive displacement by THC or other synthetic cannabinoids [16, 17]. Subsequent efforts harnessed these approaches to discover  $CB_1$  [18, 19] and  $CB_2$  receptors [20], respectively. Both CB<sub>1</sub> and CB<sub>2</sub> receptors couple to  $G\alpha_{i/o}$  proteins to inhibit adenylate cyclase activity and reduce production of cyclic AMP [21, 22]. While CB<sub>1</sub> receptors are enriched in neuronal synapses (where they inhibit neurotransmitter release),  $CB_2$  is strongly expressed in immune cells and glia [23-25]. Many of the psychoactive effects of THC and other cannabinoids can be attributed to actions on the  $CB_1$  receptor [26], yet mounting evidence paints a more complex picture of the cell-type specific expression patterns of cannabinoid receptors in vivo.

Following the discovery of endogenously expressed cannabinoid receptors, investigators raced to develop the first potent and selective  $CB_1$  and  $CB_2$  receptor modulators. From the many compounds identified, SR141716A (rimonabant) represents the most well-characterized drug in this class [27]. Subsequently, it was demonstrated that  $CB_1$ -selective rimonabant blocks acute cannabinoid-induced tetrad behaviors in mice [27], alters dopamine release in rats [28, 29], precipitates withdrawal in THC-dependent rats [30–32], and inhibits long-term potentiation in rodent brain slices [33, 34]. It has been shown in multi-

ple preclinical models of nociception that rimonabant exacerbates hyperalgesia [35-37] and attenuates cannabinoid-induced analgesic effects [35, 37] suggesting an opportunity for newer generation therapeutics that modify endocannabinoid signaling in the treatment of chronic pain. Rimonabant approved in 2006 as an antiobesity medication in Europe (Acomplia, Zimulti), but was later associated with increased incidence of severe adverse psychiatric consequences during Phase III clinical trials to examine its efficacy as an obesity treatment and smoking cessation therapy [38, 39]. As a result, rimonabant did not garner FDA approval in the United States, and was subsequently pulled from the market worldwide in 2008.

The localization of CB<sub>2</sub> primarily in immune cells with limited expression in neurons may underlie its implication in several diseases with an inflammatory component including neurodegenerative and autoimmune diseases [40–42]. While a suite of  $CB_2$  agonists have been synthesized to date, a collaborative effort between multiple academic and industry laboratories identified substantial differences in their mechanisms of action, pharmacokinetic properties, and off-target effects in vivo [43]. Based on their collective findings on a wide range of compounds, this research team recommends using HU910, HU308, or JWH133 as potent and in vivo active agonists of the CB<sub>2</sub> receptor for subsequent drug discovery efforts of clinically useful CB<sub>2</sub>-based therapeutics. This endeavor has proven to be more challenging than initially expected, as only a few synthetic CB<sub>2</sub> agonists have reached trials clinical (GW842166X, CP-55,940, S-777469, and JTE-907), with none completing phase II for chronic pain indications [42]. Currently, the CB<sub>2</sub> agonist JBT-101 is undergoing Phase II testing for efficacy in autoimmune diseases including systemic lupus erythematosus (NCT03093402) and diffuse scleroderma, where has shown some beneficial effects it (NCT02465437).

# 8.3 Two Primary Endogenous Cannabinoids: Anandamide and 2-Arachidonoylglycerol

Nearly 30 years ago, two derivatives of arachidonic acid were identified as the endogenous cannabinoid receptor ligands. Anandamide (AEA) was the first endocannabinoid (eCB) to be discovered [44], closely followed by identification of a second endogenous molecule, 2-arachido noylglycerol (2-AG), signaling via  $CB_1$  and  $CB_2$ receptors [45, 46]. AEA and 2-AG retain an arachidonoyl moiety that imparts a significant amount of their bioactivity. While endocannabinoidrelated lipids generated from other fatty acids substrates, including palmitoylethanolamide [47] and oleoylethanolamide [48] have described as eCBs, these molecules do not interact with cannabinoid receptors [49, 50]. Thus, AEA and 2-AG are still viewed as the primary endogenous mediators of cannabinoid signaling.

Historically, evidence for an eCB mechanism in vivo was determined indirectly using cannabinoid receptor antagonists, without certainty of the identity of the signaling molecule(s). Most studies quantified eCB content primarily by lipid extraction and purification from bulk tissue, followed by subsequent analysis with liquid chromatography coupled with mass spectrometry. Several excellent articles outline this process [51–54]. However, there is significant debate regarding the physiological range of eCB concentrations in various regions, as there is considerable variability in estimates of brain AEA and 2-AG content. Notably, a significant pool of 2-AG serves as an intracellular substrate for triacylglycerol formation in energy metabolism and may not participate in cannabinoid signaling [55]. An alternate approach utilizing *in vivo* microdialysis samples of interstitial, signalingcompetent eCBs from awake, behaving animals with exquisite sensitivity [55, 56]. Using this method, basal interstitial AEA and 2-AG in the brain are estimated at low to mid-nanomolar levels, physiologically relevant concentrations for activating cannabinoid receptors in vivo [55, 57].

# 8.4 Selective Inhibitor Development Using Activity-Based Protein Profiling (ABPP)

Drug selectivity presented a major challenge in early efforts in the discovery of drug candidates that modulate endocannabinoid metabolism. Initial pharmacology studies suggested that these enzymes were not rate-limiting, and thus nearcomplete inhibition is required to produce therapeutic effects [58–61]. Moreover, many of these enzymes utilized the same mechanism of action (serine hydrolase), so compounds used at doses needed for complete inhibition were more likely to exhibit off-target effects. Thus, it was particularly challenging to develop inhibitors for the serine hydrolases, a class of over 200 enzymes with a wide range of biological functions [62]. For example, partial inhibition of acetylcholinesterase by donepezil can improve cognitive function in patients with Alzheimer's disease [63]. However, acetylcholinesterase knockout mice typically do not survive to adulthood [64], and complete inhibition by non-selective nerve agents such as Sarin produce lethal neurotoxicity [65]. Given the large number of unannotated serine hydrolases in the human body [62], it is plausible that inhibition of additional off-target serine hydrolases may have similar safety and toxicity issues. Thus, the development of a safe and effective therapeutic targeting endocannabinoid metabolism requires substantial preclinical pharmacokinetic and pharmacodynamic validation prior to entering clinical trials.

The use of activity-based protein profiling (ABPP) approaches has greatly facilitated the development of many of the selective inhibitors currently used in academic research and clinical trials [66]. While non-selective serine hydrolase inhibitors such as organophosphates would raise safety concerns as chronically administered therapeutics, their broad-spectrum capacity to covalently capture a wide range of endogenous serine hydrolases render them an excellent tool for evaluating potency and selectivity of potential drug candidates *in vivo*. The first broad-spectrum fluorophosphonate probes contained a rhodamine or biotin tag [67], which allowed any serine hydro-

lases captured by these probes to be visualized by in-gel fluorescence or identified using mass spectrometry. In competition experiments, any serine hydrolase inhibited by a drug would fail to be captured by the fluorophosphonate probe under those treatment conditions and the corresponding fluorescence or mass spectra would be diminished. In addition to broad-spectrum probes that capture high abundance serine hydrolases, a number of more selective ABPP probes have been synthesized for discovery of inhibitors for difficult targets, such as diacylglycerol lipases [59, 68–71], with procedural details outlined in several excellent reviews [71, 72]. It follows that potential drug-like molecules can be modified to contain alkyne moieties which have minimal effect on their selectivity but allow their direct targets to then be bound by an azide-functionalized rhodamine or biotin using click chemistry techniques. Collectively, this approach can provide an in vivo readout of both potency and selectivity while significantly facilitating the identification of off-targets for novel inhibitors.

These techniques have been employed to great effect in the development of a selective fatty acid amide hydrolase (FAAH) inhibitor by Pfizer. Systemic delivery of the initial lead compound (PF-3845) exhibits minimal serine hydrolase offtarget effects in both brain and liver tissue at doses that abolish FAAH activity [58]. Moreover, an alkyne-functionalized PF-3845 provides direct evidence for the selectivity of this compound, as minimal off-target binding was identified. While minor modifications of the lead compound were made to improve efficacy and reduce interactions with liver cytochrome P450s (CYPs) that cause unwanted drug-drug interactions [73], the final candidate to enter clinical trials (PF-04457845) is based on the chemotype PF-3845, retaining the selectivity profile of the original lead compound [74].

# 8.5 Targeting Endocannabinoid Degradation

Increasing endogenous cannabinoid signaling represents an alternative therapeutic approach to using cannabinoid receptor agonists such as THC. By inhibiting the natural breakdown of endogenous AEA and/or 2-AG, this approach would ideally recapitulate some of the beneficial therapeutic effects of cannabinoids while reducing undesirable side effects. In support of this approach, Long and colleagues used a combination of chemical inhibitors and genetic approaches to show that inhibiting all of the primary endodegradative enzymes (FAAH, cannabinoid MGLL, ABHD6) in mice produces similar cannabinoid-appropriate responding in a drug discrimination test to THC [75]. Importantly, selective inhibition of either AEA or 2-AG degradation failed to recapitulate THC-like responsivity. This study provides clear support for the therapeutic viability of selective inhibition of specific endocannabinoid pathways with potential for reduced side-effect profile. Accordingly, the following sections will evaluate current clinical and preclinical studies evaluating inhibitors fatty acid amide hydrolase (FAAH), monoacylglycerol lipase (MGLL), and  $\alpha/\beta$  hydrolase domain 6 (ABHD6).

Acid Fatty Amide Hydrolase (FAAH) Following the discovery of AEA as an endogenous ligand for the CB<sub>1</sub> receptor [44], the search began for the enzyme(s) regulating its metabolism. In 1996, the fatty acid amide hydrolase (FAAH) was identified as the primary enzyme responsible for AEA degradation [76, 77]. Perturbation of FAAH activity via genetic deletion or pharmacological inhibition markedly reduces AEA hydrolysis, thereby elevating AEA levels in multiple organ systems in rodents [78]. In addition to AEA, FAAH metabolizes a number of other fatty acid amide substrates such as oleoylethanolamine and palmitoylethanoamine [58, 73], resulting in a battery of  $CB_1$ -dependent and CB<sub>1</sub>-independent behavioral changes in rodents. These effects include, but are not limited to, decreased anxiety-like [79–81] and depression-like behaviors [82, 83], gastrointestinal function [84–88], altered expression of drug and alcohol withdrawal [89-93], as well as diminished inflammatory and neuropathic pain states [74, 94–97]. This substantial body of preclinical evidence inspired clinical development of FAAH inhibitors by several pharmaceutical

companies including PF-04457845 (Pfizer), JNJ-42165279 (Janssen), ASP3652 (Astellas), V158866 (Vernalis) and BIA 10-2474 (Bial). Likewise, FAAH inhibitors have been evaluated for treatment of several disease indications, including cannabis use disorder [98], fear mem-[99], Tourette ory extinction Syndrome (NCT02134080 - terminated for lack of funding), chronic pain due to spinal cord injury (NCT01748695), osteoarthritis [100], and prostatitis [101].

The most notable failure in FAAH drug development to date is BIA 10-2474, a potent and long-acting CNS-active inhibitor of FAAH which produced acute neurotoxicity in 5 patients, one of which resulted in death in the multiple ascending dose part of the study in Phase I [102]. The expression of severe adverse events had not yet been observed at such a late stage of a first-inhuman study [103]. It was later revealed that BIA 10-2474 inhibits several lipases that are not targeted by PF04457845, and produces substantial changes in lipid networks in human cortical neurons that may lead to metabolic dysregulation [104]. One of these off-targets is Aldehyde Dehydrogenase 2, which has been implicated in neuroprotection from oxidative stress-related damage [105]. While BIAL has since conducted a series of toxicity studies in animals [106], indepth analysis of the trial PK/PD parameters and study periods may help determine conclusively the drug and metabolite concentrations underlying these adverse events.

In contrast to BIA 10-2474, most clinical candidates were generally safe and well-tolerated [101, 107–109], and some report efficacy of FAAH inhibition in primary outcome measurements for reducing stress reactivity [99] and cannabis withdrawal symptoms [98]. However, PF-04457845 and ASP3652 failed to attenuate osteoarthritis or prostatitis pain, respectively [101, 110] despite considerable data demonstrating antihyperalgesic effects of FAAH inhibition in several preclinical models of chronic pain states. It has been hypothesized that premature termination of the osteoarthritis study due to lack of efficacy, while necessary, may have prevented the adequate assessment of contribution of nonresponders and placebo effects [110]. Furthermore, the human trial focused on assessment of affective measures of pain that generally were not evaluated in rodent models, with exception of one study reporting no effect of FAAH inhibition on osteoarthritis-induced burrowing behavior [111]. Thus, it may be advantageous to include spontaneous and functional output measures of pain-like behaviors (e.g., locomotor activity, grip force, nesting, sucrose preference) in preclinical studies in order to help inform selection of disease indication for clinical trials.

Monoacylglycerol Lipase (MGLL) The discovery of 2-AG as a bonafide endocannabinoid led to the search for enzymes regulating its metabolism in vivo. While FAAH was briefly considered a potential candidate, both chemical and genetic inhibition of FAAH failed to substan-2-AG tially elevate compared with AEA. Monoacylglycerol lipase was identified as the primary metabolic driver of cannabinergic 2-AG breakdown [112, 113], and genetic deletion of MGLL in mice confirmed these findings [114]. Genetic and pharmacological analyses demonstrate ubiquitous expression of MGLL across most tissues including brain, liver, kidney, lung, heart, muscle, intestines, and adipose tissue [60, 115, 116]. These mice exhibited decreased body weight as adults, hastened increased latency to inflammatory thermal hyperalgesia, and alterations in basal pain sensitivity [117]. Genetic inactivation of MGLL enhanced extinction and reversal learning [118] and facilitates anxietylike behavior [119], neurophysiological analyses reveals cannabinoid-dependent changes in excitatory and inhibitor synaptic plasticity in multiple brain regions in mice [119–121]. Accordingly, selective chemical inhibitors would be necessary to distinguish between role of 2-AG signaling in adults with the critical role of this pathway in neuronal development.

The early chemical inhibitors developed in academic labs suggested a prominent role for MGLL in 2-AG metabolism and neuronal signaling [122–127]. The first ABPP-validated selective murine MGLL inhibitor JZL-184 confirmed many of these findings, including enhancement of depolarization-induced 2-AG release and reduction of cannabinoid-sensitive pain states [128]. The development of JZL-184 greatly accelerated the evaluation of the molecular and behavioral role of MGLL in mice, with over 200 publications using this compound to date. A number of potential physiological roles have been discovered using JZL-184 including, but not limited to, drug withdrawal [91, 129, 130], pain states [131–133], stress [134, 135], immune function [136–138], cancer [139–141], gastrointestinal function [137, 142, 143], and neurodegeneration [144–147]. Importantly, chronic administration of JZL-184 produces CB<sub>1</sub> receptor desensitization and functional antagonism [148], suggesting that pharmacological tolerance of an MGLL inhibitor may produce a therapeutic profile more similar to a CB<sub>1</sub> antagonist than with cannabinoid-based therapeutics such as THC. However, limitations in JZL-184 pharmacology including partial inhibition of ABHD6 and FAAH during chronic dosing procedures [149] and limited efficacy in rats [60] have helped open the door for next-generation compounds that address these concerns [149-152]. Thus, future studies should validate the pharmacological selectivity of these compounds and dosing procedures for proper interpretation of results.

Recently, Abide Therapeutics discovered ABX-1431 Lundbeck, (acquired by and rebranded as Lu AG06466) as the potent first-inclass, orally bioavailable and selective inhibitor of MGLL, now under development for as a therapeutic for movement disorders, neurodegenerative diseases and pain [153]. A Phase I Experimental Hyperalgesia study of ABX-1431 may yield insight into its viability in this therapeutic space (NCT02929264), as this model is generally highly predictive of clinical success for Neuropathic Pain [154]. At present, this molecule is undergoing a Phase IIa trial for the treatment of Tourette syndrome (NCT03625453) and a Phase I trial for neuropathic pain (NCT03138421). Likewise, Pfizer has developed a selective covalent MGLL inhibitor [155] and a corresponding <sup>11</sup>C-PET tracer [156] for evaluating the pharmacokinetics of this compound as part of a Phase 1 clinical trial (NCT03100136). Additionally, both Takeda Pharmaceutical Co. [157] and Janssen Research [158] recently have developed noncovalent MGLL inhibitors that show preclinical viability for target engagement and increased 2-AG levels in CNS and peripheral tissue, but these candidates have not yet entered clinical trials.

 $\alpha/\beta$  Hydrolase Domain 6 (ABHD6) While MGLL drives the majority of 2-AG breakdown in vivo, emerging evidence suggests that other enzymes play a supportive role in this process. Initial studies using immortalized BV-2 microglial cells, which do not express MGLL, provide clear evidence of alternative 2-AG metabolism pathways [159]. While compensation by FAAH accounted for about half of the 2-AG metabolism, the use of selective inhibitors revealed that the remaining activity could be attributed to unknown enzyme(s). Using a functional proteomic approach, two additional serine hydrolases (ABHD6 and ABHD12) were identified as potential 2-AG metabolic enzymes [160]. Ultimately, the unknown 2-AG activity in BV-2 microglia was attributed to ABHD6, which regulates endocannabinergic signals to alter excitatory [161] and inhibitory [162] synapses in the brain.

Our understanding of the significance of ABHD6 in regulating endocannabinoid signaling and other lipid pathways has emerged from studies of targeted inactivation using genetic and chemical tools [163]. Constitutive deletion of ABHD6 reveals its critical role in energy metabolism [164, 165] but not in lysosomal storage disorders [166]. ABHD6 knockout mice are protected from high-fat diet-induced obesity [164] and displayed increased decreased body weight, increased energy expenditure, improved glucose tolerance and insulin sensitivity, and changes in white and brown adipose tissue composition [165]. Many of these metabolic effects can be recapitulated by antisense oligonucleotides or treatment with WWL70, the first chemical inhibitor designed to target ABHD6. Early studies using WWL70 implicate ABHD6 function in traumatic brain injury [167], obesity and type II diabetes [165, 168], seizure activity [169, 170], inflammation and pain [171, 172]. Selective blockade of ABHD6 with the newer generation inhibitor peripherally-restricted KT-203 decreases pancreatic cancer cell metastasis [173], while KT-182 modestly attenuates autoimmune demyelination [174, 175], in contrast with a previous study reporting significant reduction of clinical signs in the experimental autoimmune encephalitis model of Multiple Sclerosis with WWL70 [176]. At present, it is not clear if ABHD6 drives metabolic changes by enzymatic regulation of 2-AG signaling [177] or other lipid pathways [164]. Since ABHD6 exhibits promiscuity in its acceptance of lipid substrates [164], the process of determining the specific lipid mediators responsible for its effects presents a substantial challenge. Thus, studies utilizing inhibitors with off-target effects should be interpreted with caution for future drug development efforts.

 $\alpha/\beta$  Hydrolase Domain 12 (ABHD12) Since its discovery as a serine hydrolase with in vitro 2-AG metabolic activity [160], the physiological role of ABHD12 has remained poorly understood. Loss-of-function mutations in ABHD12 cause the rare neurodegenerative disorder PHARC (polyneuropathy, hearing loss, retinosis pigmentosa, and cataract) in humans [178–182], which is phenocopied in ABHD12 knockout mice [178]. While ABHD12 knockout mice have increased levels of 2-AG in multiple brain regions [183], the primary function of this enzyme in *vivo* is likely a lysophosphatidylserine lipase. Indeed, both genetic deletion [178, 184] and selective inhibition [184, 185] of ABHD12 generate substantially elevated levels of very long chain lysophosphatidylserine levels in vivo [186]. ABHD12 and downstream target lysophosphatidylserine receptors are coexpressed in glia and in immune cells, and treatment of macrophages with the selective ABHD12 inhibitor DO264 exacerbated immune responsivity [178, 184,

187]. Although acute chemical inactivation of ABHD12 did not produce the severe behavioral deficits found in knockout mice [184, 187], it is presently unclear if the PHARC phenotype would emerge following chronic, long-term drug treatment. Given its restricted contribution to endocannabinoid signaling and potential role in neuroprotection, ABHD12 may offer limited opportunity for therapeutic development when compared with other targets in the endocannabinoid metabolic pathway.

### 8.6 Targeting Endocannabinoid Biosynthesis

Due to concerns regarding safety and tolerability with cannabinoid receptor antagonism, efforts have emerged to selectively decrease cannabinoid signaling as an alternative therapeutic approach. While CB<sub>1</sub> receptor antagonists or inverse agonists such as rimonabant and taranabant demonstrated efficacy in the treatment of obesity, type II diabetes and nicotine dependence [188–192], serious adverse psychiatric consequences significantly limit clinical utility [10–14], ultimately precluding their approval by the FDA. Instead, by inhibiting the natural production of endogenous AEA and/or 2-AG, targetendocannabinoid ing biosynthesis might recapitulate some of the beneficial therapeutic effects of receptor antagonists while mitigating undesirable side effects.

The FDA-approved drug Orlistat (tetrahydrolipstatin, sold over-the-counter as Alli<sup>®</sup>) indicated for the treatment of obesity was designed as a pancreatic and gastric lipase inhibitor [193, 194], but nonetheless has a number of potential offtarget effects including inhibition of the two diacylglycerol lipases  $\alpha$  (DAGL $\alpha$ ) and  $\beta$  (DAGL $\beta$ ) that generate 2-AG *in vivo*. Unlike rimonabant, Orlistat does not produce serious psychiatric events, suggesting that inhibition of endocannabinoid biosynthesis may represent a viable alternative to CB<sub>1</sub> receptor antagonists. While the study of endocannabinoid biosynthetic pathways and the subsequent discovery of corresponding selective chemical inhibitors is in its nascent stage, a number of recent advances have bolstered this field and may yield unique candidates for future drug development. Several selective ABPP probes have been developed to facilitate inhibitor development against DAGLs and other potential endocannabinoid biosynthases, including some based on the tetrahydrolipstatin structure [195]. Accordingly, the following sections will evaluate current clinical and preclinical studies evaluating inhibitors of DAGL $\alpha$  and  $\beta$ phosphatidylethanolamine  $(DAGL\beta,$ n-acyl phospholipase D (NAPE-PLD), and other enzymes involved in endocannabinoid biosynthesis.

**Diacylglycerol Lipase**  $\alpha$  (DAGL $\alpha$ ) The endogenous biosynthesis of signaling competent 2-AG is driven by the enzymes diacylglycerol lipase  $\alpha$ (DAGL $\alpha$ ) and diacylglycerol lipase  $\beta$  (DAGL $\beta$ ). While both of these serine hydrolases convert diacylglycerol into 2-AG, they exhibit unique cellular and tissue specific expression. Specifically, DAGL $\alpha$  is predominantly expressed in neuronal tissue [196] and DAGL $\alpha$  knockout mice exhibit approximately 80% lower levels of 2-AG in the brain and spinal cord, compared with a 50% reduction of 2-AG in liver and adipose tissue [197, 198]. Within the central nervous system, neurons contain the predominant amount of DAGL $\alpha$  as compared with glial cells [196, 199– 201]. In addition, many of the metabolic and behavioral phenotypes found in CB<sub>1</sub> receptor knockout mice are recapitulated by genetic deletion of DAGLa. Mice with genetic inactivation of either  $CB_1$  or  $DAGL\alpha$  both exhibit signs of enhanced metabolic function including lower body weight and decreased body fat, as well as reduced fasting insulin release and blood lipid levels [197, 202]. However, both genotypes also showed signs of psychiatric dysfunction including less marble-burying and shorter latencies in the forced swim test [202–204]. DAGL $\alpha$  mice also exhibited increased mortality beginning around 8-10 weeks of age [202]. Mounting evidence indicates that DAGL $\alpha$  plays a critical role in neuronal developmental processes [205-210], suggesting that psychiatric behavioral phenotypes may results from neurodevelopmental deficiencies as opposed to the direct signaling actions of DAGL $\alpha$ . Collectively, these findings highlight the necessity for rigorous behavioral evaluation of a selective DAGL $\alpha$  inhibitor prior to initiation of clinical development.

Early DAGL $\alpha$  inhibitors such as tetrahydrolipstatin were utilized mainly in electrophysiological studies, yet the recent development of in vivo-active diacylglycerol lipase inhibitors has offered important insight into the consequences of global chemical inactivation of these enzymes [211]. Ogasawara and colleagues created a suite of CNS-active covalent inhibitors of diacylglycerol lipases, most notably DO34 and DH376 [61]. Compared with DH376, DO34 exhibits enhanced selectivity for DAGL $\alpha$ , however both compounds block DAGLa and DAGLB following systemic administration and are blood-brain barrier permeable. Despite their off-target effects, each molecule targets a unique group of serine hydrolases. Importantly, DO53 blocks all spurious targets of DO34 while sparing DAGL $\alpha$  and DAGL $\beta$ , thus serving as a critical negative control compound for in vivo pharmacology studies. Furthermore, Baggelaar et al. report LEI105 as a reversible inhibitor of diacylglycerol lipases, with potent inactivation of DAGL $\alpha$  and DAGL $\beta$ and minimal cross-reactivity with other endocannabinoid metabolic enzymes in mice [69]. Surprisingly, intracerebroventricular administration in rats of the DAGLβ inhibitor KT172 (originally validated in mice) actually reduces activity of DAGL $\alpha$  (~80%) and DAGL $\beta$  (~50%) in the brain [162], suggesting this approach as a potential alternative to rimonabant antagonism of  $CB_1$ for smoking cessation. While the selectivity of these compounds generally has been evaluated against the human and mouse orthologs, there is precedent for species-specific selectivity when targeting enzymes in the eCB pathway [60]. Thus, optimization is needed in order to fully validate effects of these compounds in rats for behavioral studies and in multiple species for future clinical development.

**Diacylglycerol Lipase**  $\beta$  (DAGL $\beta$ ) With the initial cloning in 2003 of DAGL $\alpha$  and DAGL $\beta$ 

[196], it was demonstrated that DAGL expression pattern shifts from axonal tracts to dendritic fields, consistent with later reports that DAGL activity is required for synaptic plasticity [125, 126, 212, 213], axonal growth and guidance [214], adult neurogenesis [215, 216] and oligodendrocyte differentiation [217]. Several studies suggest that while DAGL $\alpha$  is the predominant 2-AG synthesizing enzyme for endocannabinoidmediated modulation of neurotransmission in adults [197, 198, 218], DAGL<sub>β</sub> is more abundantly expressed in the developing CNS [196, 219]. DAGL $\beta$  contributes to depolarizationinduced suppression of excitation in early postnatal hippocampal autaptic neurons [209] and neurite outgrowth in culture models [208]. Outside of the CNS, DAGL $\beta$  is widely expressed in multiple sites including white blood cells [220], liver [197] and adipose tissue [221], where it may be correlated with serum high-density lipoprotein cholesterol levels. Most notably, while LPS-induced eCB-eicosanoid crosstalk is dependent on DAGL $\beta$  in microglia [201], macrophages [59] and dendritic cells [222]. These observations indicate a crucial role for DAGL $\beta$  in immune function and inflammation, consistent with the implication of this enzyme in pathologies associated with alcoholic fatty liver disease [223], Alzheimer's disease [224] as well as inflammatory, neuropathic and post-surgical pain [225–227].

The development of in vivo-active DAGLB inhibitors has facilitated significantly our understanding of the role of this enzyme. Systemic administration of currently available blood-brain barrier-permeable DAGL $\beta$  inhibitors exhibit cross-reactivity with both DAGL $\alpha$  and DAGL $\beta$ [211], however Hsu and colleagues have developed peripherally-restricted inhibitors KT109 and KT172, which exhibit ~60-fold selectivity for DAGL $\beta$  versus DAGL $\alpha$  in mice [59]. To account for its limited off-target effects on ABHD6 and to determine DAGLβ-specific biology, the negative control compound KT195 was utilized as a selective ABHD6 inhibitor. Acute treatment with KT109 or KT172 reveals a role for DAGL $\beta$  in 2-AG metabolism, as well as in downstream eicosanoid production and inflammatory signaling in peripheral macrophages [59]. Delivery of liposome-encapsulated KT109 produces macrophage-specific targeted inhibition of DAGL $\beta$ , with no apparent activity of other tissues *in vivo* [228]. This mode of administration substantially enhances anti-nociceptive potency of KT109 compared with traditional systemic treatment, thereby demonstrating potential for DAGL $\beta$  as a novel druggable target with potential indications in inflammatory diseases.

N-Acyl Phosphatidylethanolamine Phospholipase D (NAPE-PLD) While multiple enzymatic pathways have been implicated in the endogenous biosynthesis of AEA, none has been definitively nominated as the "AEA synthase" to date. The initial evaluation of n-acyl phosphatidylethanolamine phospholipase D (NAPE-PLD) as a zinc hydrolase capable of producing n-acylethanolamines (including AEA) offered the first example of a potential anandamide synthase [229]. Consistent with this purported role of NAPE-PLD in vivo, overexpression of this enzyme in mammalian culture systems increases AEA and other n-acylethanolamines [230]. However, while NAPE-PLD knockout mice express lower levels of saturated and monounsaturated n-acylethanolamines, reduction of AEA is inconsistent between reports [231–233].

Recent studies utilizing global and spatiotemporal genetic inactivation of NAPE-PLD have attempted to elucidate the physiological role of this enzyme. Mice expressing a constitutive knockout of NAPE-PLD exhibit no changes in body mass composition or glucose tolerance on a normal chow diet, yet inactivation of NAPE-PLD selectively in either adipose [234] or intestinal tissue [235] leads to an exaggerated obese phenotype on a high-fat diet. Spatio-temporal deletion of NAPE-PLD produces significant decreases in AEA and other n-acylethanolamines in the targeted tissues and alters the composition of gut microbiota in these animals [234, 235]. NAPE-PLD may limit development of obesity through non-cannabinergic pathways, as other

n-acylethanolamines such as oleoylethanolamine produce robust anorexic effects [48] through multiple receptors including GPR119 [236] and PPAR $\alpha$  [237]. However, it should be noted that given the potential for compensatory lipid metabolic pathways in constitutive knockout models, selective chemical inhibitors are critical in order to clarify the function of NAPE-PLD in activitydependent AEA signaling. Unfortunately, potent CNS-active inhibitors are currently not available as existing compounds lack the necessary pharmacological properties to inhibit NAPE-PLD in vivo [230, 238, 239]. Future work will evaluate if these metabolic changes can be recapitulated and treated using pharmacological tools and subsequently translated into a potential therapeutic for obesity.

**Other Potential Anandamide Biosynthetic** Enzymes In addition to NAPE-PLD, multiple enzymatic pathways leading to the biosynthesis of n-acylethanolamines, a family of lipid species that includes AEA, have been discovered. However, current evidence highlights several obstacles to therapeutic drug discovery in this arena. For example, the serine hydrolase ABHD4 can act in concert with glycerophosphodiesterase GDE1 to produce anandamide and other n-acylethanolamines in vitro [240], however levels of AEA in brain tissue are unaltered in GDE1 knockout mice [241]. Likewise, ABHD4 regulates multiple lipid classes, and genetic inactivation of this enzyme elicits comparatively greater changes in lysophosphatidylserine levels [242]. An additional pathway for AEA production utilizing sequential activity of phospholipase C and tyrosine phosphatases such as lymphoid-specific tyrosine phosphatase (PTPN22) was discovered in macrophages [243, 244]. However, targeting either phospholipases C or PTPN22 alone is expected to exert substantial non-cannabinergic effects, as these enzymes are broadly involved in lipid metabolism and in responsiveness of B and T cells, respectively. Collectively, research on AEA biosynthesis suggests that multiple redundant pathways likely exist in vivo [241, 244], as illustrated by biological compensation when one of these enzymes is inactivated. It follows that the physiological source(s) of AEA and thus the therapeutic utility of inhibitors for these enzymes remain to be fully elucidated.

# 8.7 The Interaction Between Endocannabinoids and Eicosanoid Production

Precursors for Eicosanoid Production The primary focus of research on endocannabinoid metabolism centers on changes in 2-AG signaling via cannabinoid receptors. However, recent work has uncovered an important role for prostaglandins and other arachidonic acid metabolites that are derived from endocannabinoid precursors. Although it was previously thought that prostaglandins arise mainly from actions of cytosolic phospholipase A<sub>2</sub>, genetic inactivation of this enzyme exerts only minimal effect on arachidonic acid levels in the brain [245]. Instead, metabolic breakdown of 2-AG by MGLL supplies arachidonic acid for production of proinflammatory prostaglandins by cyclooxygenases during neuroinflammation [138]. Both genetic and chemical inactivation of MGLL attenuate lipopolysaccharide-induced cytokine release and protect against neurodegeneration of dopamine neurons through a CB<sub>1</sub>-independent mechanism of reduced prostaglandin synthesis. Accordingly, MGLL activity liberates prostaglandins in the brain to facilitate neurodegeneration in mouse models of Alzheimer's disease [246–248], while deletion or pharmacological inhibition of MGLL facilitates cannabinoid receptor-independent blunting of disease progression [246]. MGLLdependent prostaglandins also mediate the fever response in mice, as genetic or pharmacological inactivation of MGLL blunts LPS-induced elevations in body temperature without altering core body temperature in control mice [249, 250].

Upstream of MGLL, DAGL $\alpha$  and DAGL $\beta$ both contribute to release of arachidonic acid [197, 201] and subsequent production of prostaglandins [201], with a prominent role of DAGL $\alpha$ in the brain [59, 197, 201] and DAGL $\beta$  in microglia and other immune cells [59, 201], respectively. For example, inhibition of DAGLβ following injury decreases local PGE<sub>2</sub> production and attenuates chronic pain-like behaviors in mouse models of neuropathic and inflammatory pain [225]. Furthermore, targeted delivery of the DAGL $\beta$  inhibitor KT-109 using liposomes produces 80% inactivation in macrophages without altering activity in other tissues such as brain and heart, and reduces LPS-induced allodynia [228], thus providing more direct evidence for peripheral immune DAGL $\beta$  in the inflammatory response. Alternatively, pharmacological or genetic inactivation of DAGLa abrogates production of prostaglandins in brain tissue, blocks central LPS-induced prostaglandin release and blunts the fever response in these mice [225]. While the role of eCBs in prostaglandin signaling has become clear, our understanding of their contribution(s) to other eicosanoid pathways remains limited, and future studies will establish potential links with lipoxygenases and cytochrome P450s.

Eicosanoid-Like 2-AG Metabolites Endocannabinoids also may interact directly with cyclooxygenases as substrates to produce prostaglandin-like compounds with unique biological effects [251]. While the (S)-enantiomers of nonsteroidal anti-inflammatory drugs (NSAID<sub>s</sub>) such as ibuprofen and naproxen inhibit cyclooxygenase to prevent the formation of proinflammatory prostaglandins [252], the (R)-enantiomers of these compounds accomplish only minimal inhibition of enzymatic activity against arachidonic acid substrate. However, (R)-NSAIDs attenuate cyclooxygenase-dependent activity with AEA and 2-AG, thereby acting as potent substrateselective inhibitors of this class of lipid signals [253]. Importantly, (R)-NSAIDS exhibit antihyperalgesic activity in models of neuropathic pain that is superior to that of traditionally prescribed (S)-NSAID<sub>s</sub> [254, 255]. Furthermore, levels of endogenous prostaglandin E<sub>2</sub> glycerol ester are elevated in the carrageenan model of inflammatory pain, contributing to thermal hyperalgesia that is not fully reversed by prostaglandin receptor antagonists [256]. Accordingly, prostaglandin

 $E_2$  glycerol ester functions as an agonist for the g-protein coupled receptor  $P_2Y_6$ , with almost four orders of magnitude more potency than the proto-typical agonist uridine diphosphate [257]. In a model of colon inflammation, prostaglandin  $D_2$  glycerol ester derived from 2-AG, but not related metabolites arising from arachidonic acid or AEA, reduced dextran sulfate sodium-induced colitis in mice and are blocked by antagonists of traditional prostaglandin receptors,  $DP_1$  and PPARy [258].

**Eicosanoid-Like** Anandamide Metabo**lites** While serving only a limited role in colon inflammation, prostaglandin D<sub>2</sub> ethanolamine induces skin cancer apoptosis independent of the putative DP receptors, but the precise mechanism remains unclear [259]. Perhaps the most wellestablished endogenous prostamide, prostaglandin  $F_2\alpha$  ethanolamine exerts minimal activity through the prostaglandin  $F_{2\alpha}$  receptor and instead likely acts through an FP receptor variant [260]. A structural analogue of prostaglandin  $F_{2\alpha}$ ethanolamine, Bimatoprost is an FDA-approved drug marketed under the name Lumigan® (Allergan) for reducing intraocular pressure as a treatment for glaucoma [261], and a sustainedrelease formulation of Bimatoprost is currently undergoing testing in Phase I/II clinical trials [262]. Patients reported longer and fuller eyelashes during administration of Bimatoprost, so the drug was repurposed as Latisse® and received FDA approval for the treatment of eyelash hypotrichosis [263] In contrast, an antagonist of the prostamide  $F_{2\alpha}$  receptor AGN211336 reduces inflammatory pain in mice [264]. Substrateselective inhibitors affect a number of different pathologies in mice including stress and anxietylike behaviors (23912944), and future research likely will uncover additional biological roles for these lipids as signaling molecules.

While it has become clear that cyclooxygenases utilize 2-AG and AEA as substrates, research investigating the biological activity of corresponding lipoxygenase and cytochrome P450 enzymes on these lipid species is limited [251] and future studies will help clarify their role(s) in endocannabinoid biology. Collectively, these results suggest a number of novel potential therapeutic avenues for endocannabinoid metabolism inhibitors.

### 8.8 Conclusions and Future Directions

Considerable efforts have been concentrated on targeting endocannabinoid biosynthetic and degradative enzymes as alternatives to CB1-receptorbased therapeutics that can produce serious adverse effects associated with a number of failures in clinical trials. In general, potent and selective inhibitors of FAAH or MGLL that are devoid of off-target effects have demonstrated safety and tolerability in human volunteers. These drug candidates could be met with success in the treatment of neurological diseases and pain if caution is exercised in interpreting preclinical data as well as selection of clinical indication and output measures. Small molecule inhibitors of other eCB enzymes remain in the preclinical discovery stage, but current research suggests some potential druggable targets. DAGLa serves an important physiological role in metabolism and brain function, yet its temporal inhibition may improve smoking cessation. Chemical inactivation of DAGL<sup>β</sup> by liposome-mediated delivery of a peripherally-restricted inhibitor reduces inflammation and pain-like behaviors in mice. DAGL inhibitors undoubtedly will benefit from further chemical optimization in order to improve both selectivity and brain-barrier permeability for CNS indications. In addition, future studies elucidating pathways of anandamide synthesis and exploring substrate-specific inhibitors of cyclooxygenases, lipoxygenases and cytochrome P450s may yield additional promising targets for drug discovery in the cannabinoid therapeutic space.

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9

Drugging the Phosphoinositide 3-Kinase (PI3K) and Phosphatidylinositol 4-Kinase (PI4K) Family of Enzymes for Treatment of Cancer, Immune Disorders, and Viral/Parasitic Infections

Jacob A. McPhail and John E. Burke

#### Abstract

The lipid kinases that generate the lipid signalling phosphoinositides have been established as fundamental signalling enzymes that control numerous aspects of how cells respond to their extracellular environment. In addition, they play critical roles in regulating membrane trafficking and lipid transport within the cell. The class I phosphoinositide kinases which generate the critical lipid signal PIP<sub>3</sub> are hyperactivated in numerous human pathologies including cancer, overgrowth syndromes, and primary immunodeficiencies. The type III phosphatidylinositol 4-kinase beta isoform (PI4KB), which are evolutionarily similar to the class I PI3Ks, have been found to be essential host factors mediating the replication of numerous devastating pathogenic viruses. Finally, targeting the parasite variant of PI4KB has been established as one of the most promising strategies for the development of anti-malarial and anticryptosporidium strategies. Therefore, the development of targeted isoform selective inhibitors for these enzymes are of paramount importance. The first generation of PI3K inhibitors have recently been clinically approved for a number of different cancers, highlighting their therapeutic value. This review will examine the history of the class I PI3Ks, and the type III PI4Ks, their relevance to human disease, and the structural basis for their regulation and inhibition by potent and selective inhibitors.

### Keywords

Phosphoinositides · Phosphatidylinositol · PI3K · p110 · p85 · PIK3CA · PIK3R1 · PI4K · PI4KB · PI4KA · Oncogenes · Cancer · Malaria · Cryptosporidiosis · Enteroviruses

### 9.1 Phosphoinositide Kinases and Their Role in Signalling/ Human Disease

### 9.1.1 Phosphoinositides

Phosphoinositides are essential membrane signalling molecules that regulate a multitude of cellular processes, from membrane identity

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and compartmentalization to growth and cell division. While they represent a small percentage of total cellular lipid composition, their correct spatiotemporal location in a cell is an essential mechanism maintaining organelle identify and membrane trafficking [1, 2]. All phosphoinositides are generated from phosphatidylinositol (PI), and the inositol headgroup can be phosphorylated at the hydroxyls present at the D3, D4 and D5 positions, generating a total of seven different phosphoinositides: phosphatidylinositol 3-phosphate (PI3P), phosphatidylinositol 4-phosphate (PI4P), phosphatidylinositol 5-phosphate (PI5P), phosphatidylinositol 3,4-bisphosphate (PI(3,4)  $P_2$ ), phosphatidylinositol 3,5-bisphosphate  $(PI(3,5)P_2)$ , phosphatidylinositol 4,5-bisphosphate  $(PI(4,5)P_2)$  and phosphatidylinositol 3,4,5-triphosphate (PIP<sub>3</sub>). While numerous lipid kinases and phosphatases regulate the location and concentration of these phosphoinositide pools, this chapter will focus on the most clinically promising targets: the class I phosphoinositide 3-kinases (PI3Ks) which function downstream of cell surface receptors at the plasma membrane and are critically involved in cancer, and phosphatidylinositol 4-kinase type III beta (PI4KB), which functions at the Golgi, is involved in viral infection, and is a major target for treatment of parasitic infections (Fig. 9.1a).

### 9.1.2 Class | PI3Ks

The class I PI3Ks are the enzymes that mediate the phosphorylation of  $PI(3,4,5)P_3$  from the substrate  $PI(4,5)P_2$ . They were originally discovered as oncoproteins derived from viral proteins associated with an unknown lipid kinase activity [3, 4]. It was quite rapidly determined that the generation of PIP<sub>3</sub> was critical in growth factor signalling [5, 6], and in immune cell regulation [7]. One of the most important discoveries was on the key role of PI3Ks in regulating signalling downstream of the insulin receptor [8, 9]. Excellent reviews recently have described the history of the discovery of the PI3K field, and readers are suggested to consult these for full details [1, 10].

The class I PI3Ks are divided into three distinct classes based upon their regulatory binding partners and lipid substrate specificity. Only the class I PI3Ks can generate PIP<sub>3</sub> from PI(4,5)P<sub>2</sub> at the plasma membrane in vivo [11]. These enzymes are major components of intracellular signalling networks downstream of receptor tyrosine kinases (RTKs) and G-protein coupled receptors (GPCRs) [12, 13]. Upon activation, the generation of PIP<sub>3</sub> by class I PI3Ks drives the recruitment of PIP<sub>3</sub> effectors to the plasma membrane, including protein kinases (i.e. PDK1, AKT) [14], and regulators of Ras superfamily GTPases, with signal cascades downstream of these effectors playing key roles in cell proliferation, growth, survival and tumorigenesis [12, 13, 15]. Class I enzymes form heterodimers with regulatory subunits, and are further subdivided into the class IA PI3Ks ( $p110\alpha$ ,  $p110\beta$ ,  $p110\delta$ ) which can bind any of five different p85 like regulatory subunits (p85a, p55a, p50a, p85β, and p55 $\gamma$ ), and the class IB PI3Ks (p110 $\gamma$ ) which bind either a p84 or p101 regulatory subunit. The p110 subunits will be referred to by their gene names, PIK3CA (p110 $\alpha$ ), PIK3CB (p110 $\beta$ ), PIK3CD (p110 $\delta$ ), and PIK3CG (p110 $\gamma$ ) for the remainder of this review. Both PIK3CA and PIK3CB are ubiquitously expressed, with PIK3CA primarily responsible for insulin signalling [16], and PIK3CB playing key roles in platelet function and blood clotting [17]. The PIK3CG and PIK3CD isoforms are primarily expressed in immune cells and are important in lymphocyte activation, mast cell degranulation and leukocyte chemotaxis [18–23].

The first insight into the structural basis of regulation of these kinases was from the crystal structure of class IB PIK3CG, which revealed marked homology with protein kinases [24]. The kinase domain (also referred to as the catalytic domain) exhibits a bi-lobal organization consisting of an N-terminal-lobe and C-terminal lobe that form a cleft for ATP-binding and the machinery to facilitate phosphorylation of the PI head-group (Fig. 9.1b) [24, 25]. This kinase domain packs against a helical domain, a conserved feature of all PI3Ks and type III PI4Ks [26–30]. The kinase hinge region, located at the cleft between the two lobes, is a key feature of the ATP binding



A Cellular Localization of the druggable class I PI3Ks and PI4KB B Conserved Catalytic Structure of class I PI3Ks and PI4KB

Fig. 9.1 (a) Cellular localizations of druggable class I PI3Ks and PI4KB. Class I PI3Ks are activated downstream of activated cell surface receptors, driving PIP<sub>3</sub> production at the plasma membrane. PI4KB generates PI4P from PI at the Golgi. (b) Conserved catalytic structure of class I PI3Ks and PI4KB. The kinase domain consists of a well conserved N-terminal lobe and C-terminal lobe which fold to form the active site. The kinase domain packs against the helical domain, a conserved feature of all PI3K's and class III PI4K's; PDB: 1E8X. (c) Schematic of the class I PI3Ks/PI4KB ATP-binding pocket. Key features of ATP binding include hydrogen bonds between the kinase hinge region and adenine moiety, accommodation of the nucleoside by hydrophobic regions, and charged interactions between ATP phosphates and lysine in the kinase P-loop. (d) Domain architecture of class IA PI3Ks

pocket and makes key hydrogen bonds with the adenine moiety of ATP. The nucleoside is further accommodated by hydrophobic regions and

(p110α,β,δ refer to PIK3CA, PIK3CB, PIK3CD) include a canonical helical and bi-lobal kinase domain, lipid binding domain (C2), Ras-binding domain (RBD) and an adaptor binding domain (ABD) which drives obligate hetero-dimerization with the p85, p55 or p50 regulatory subunits. Inhibitory contact sites between regulatory subunit SH2 domains and p110 are shown as colored lines. Class IB PI3K (p110γ refers to PIK3CG) associates with p84 and p101 regulatory subunits. (e) Domain architecture of the smaller PI4KB lacks the ABD, RBD and C2 domains of class I PI3Ks, and contains a long, disordered linker region within the N-lobe of the kinase domain. Solid arrows and dashed arrows indicate interactions with key regulatory PI4KB binding partners, and putative activators, respectively

charged interactions between ATP phosphates and lysine(s) in the kinase P-loop (Fig. 9.1c). Phosphorylation of the inositol headgroup is catalyzed by the DRH motif in the catalytic loop and is facilitated by a magnesium-dependent interaction of  $\beta$  and  $\gamma$  phosphates with the DFG motif in the activation loop [31]. The very C-terminus of class I PI3Ks, class III PI3Ks, and type III PI4Ks is critical for membrane binding and kinase activity on lipid membranes and is thought to be critial in binding PI substrate [28, 32].

The structures of the class IA PI3K catalytic subunits (PIK3CA, PIK3CB and PIK3CD) have revealed they are composed of an N-terminal adaptor binding domain (ABD), a Ras binding domain (RBD), a membrane-binding C2 domain (C2), a helical domain, and a C-terminal kinase domain with a bi-lobal architecture (N-lobe and C-lobe; Fig. 9.1d) [26, 27, 29]. Class IA PI3K catalytic p110 subunits associate with one of the p85a, p85b, p55a, p55y or p50a regulatory subunits, with binding driven through an extremely tight interaction between the ABD domain of the catalytic subunit and the iSH2 coiled coil domain of the regulatory subunit [33]. This interaction with the regulatory subunit plays three key roles for the p110 subunit: it stabilizes the p110 subunit, inhibits p110 activity, and allows for activation by phosphorylated receptors and their adaptors [34, 35]. The SH2 domains present in the regulatory subunits inhibit p110 kinase activity through transient inhibitory interactions, with these interactions disrupted by phosphorylated pYXXM motifs in receptors and their adaptors [33, 36, 37]. Class IB PI3K (PIK3CG) interacts with either a p84 [38] or p101 [39] regulatory subunit, which play important roles in the activation of PIK3CG activation downstream of Ras GTPases and GPCR  $G\beta\gamma$  subunits [40, 41] (Fig. 9.1d). The class I PI3Ks can all be activated downstream of Ras superfamily GTPases, with PIK3CA, PIK3CD, and PIK3CG activated by Ras family GTPases [42, 43], and PIK3CB activated by Rho family GTPases [44].

#### 9.1.3 PI4KB

PI4KB is one of four distinct PI4Ks that generate PI4P from PI in humans. The focus of this chapter will be on the type III PI4KB isoform (also

frequently referred to as PI4KIIIβ) which is primarily found at the Golgi and Trans-Golgi Network (TGN) [45–47]. This enzyme was originally identified in yeast (Pik1) [48], with the mammalian variant identified in the late 1990s through its sensitivity to the PI3K inhibitor wortmannin [49, 50]. PI4KB is essential for proper Golgi formation and function, and plays important roles in mediating membrane trafficking, cytokinesis and lipid transport [51-53]. The activity of PI4KB is hijacked by a number of pathogenic viruses, with this playing a critical role in mediating intracellular viral replication [54–56]. Finally targeting the parasite variant of PI4KB is an extremely promising approach for the eradication of multiple human pathogens, including plasmodium and cryptosporidium, which are the causative agents of malaria and cryptosporidiosis [57–60].

PI4KB makes a large fraction of the pool of Golgi PI4P, which is recognized by the oxysterolbinding-protein (OSBP), four-phosphate-adaptor protein (FAPP), ceramide transfer protein (CERT), GOLPH3, and other protein modules important for Golgi stability and lipid transport [61–64]. In addition to generating PI4P, PI4KB has key non-catalytic roles, including recruiting a pool of PI4KB associated Rab11 to the TGN [51, 65] The activity of PI4KB at the Golgi is regulated by a variety of direct binding partners (Fig. 9.1e), including the Golgi protein Acyl CoA binding domain containing 3 (ACBD3) [55, 66, 67], the protein c10orf76 [54, 68], and 14-3-3 proteins mediated by PKD phosphorylation of PI4KB [69–71]. In addition, there are a number of proteins that do not form direct interactions, including the GTPase Arf1 [52], and the PI transfer proteins (PITPs, Sec14 in yeast) [72, 73], which activate PI4KB activity by still unknown mechanisms.

Structural analysis of PI4KB revealed that it has a very similar overall architecture to the class I PI3Ks in respect to the helical and kinase domains [28], with the main difference being an additional extension of the N-lobe of the kinase domain including a longer disordered N-lobe kinase linker (Fig. 9.1e). PI4KB is primarily recruited to the Golgi through an interaction between a disorder-order transition of the N-terminus of PI4KB with the Q domain of ACBD3 [66, 67]. Phosphorylation of PI4KB at Ser294 drives binding of 14-3-3 proteins, which stabilizes PI4KB and increases Golgi PI4P levels through a not fully understood mechanism [69–71]. Multiple viruses manipulate PI4KB-dependent PI4P levels via specifically hijacking these regulatory PI4KB interacting proteins to mediate their intracellular replication [66, 74–79].

# 9.2 Phosphoinositide Kinases as Drug Targets

### 9.2.1 Class | PI3Ks

The class IA PI3Ks are frequently misregulated in numerous devastating human diseases. The most well-established link to disease is the frequent occurrence of activating somatic point mutations in PIK3CA [80], with it being one of the most frequently mutated oncogenes in all human cancers. The PIK3R1 regulatory subunit encoding p85 $\alpha$  is also mutated in a variety of human tumors, with these majority of these mutations resulting in increased PI3K activity [81, 82]. In addition to this frequent involvement in cancer, activating mutations in PIK3CA also lead to overgrowth disorders [83, 84]. Activating mutations in PIK3CD and PIK3R1 are causative of a primary immunodeficiency disease known as activated PI3K delta syndrome (APDS), also known as p110 delta activating mutation causing senescent T cells, lymphadenopathy, and immunodeficiency (PASLI) syndrome [85–91]. An important recent discovery has been that targeting PI3Ks both in the tumor and the tumor microenvironment appears to be a powerful strategy to generate an anti-tumor response. Inhibiting the PIK3CD isoform in T reg cells blocks tumor induced immune tolerance, leading to a potent anti-tumor immune response [92]. Inhibiting PIK3CG in myeloid cells can generate a similar anti-tumor immune response [93, 94], with PIK3CG also being an excellent target in multiple inflammatory diseases [95, 96]. In studies in

mice, it has been shown that PI3K inhibition leads to increased insulin signalling, and decreasing insulin levels either through diet or pharmacological intervention dramatically increased PI3K inhibitor anti-tumor efficiency [97]. A summary of the roles of PI3Ks in tumors and the tumor microenvironment are shown in (Fig. 9.2a). Finally, highlighting the important role of maintaining proper levels of PI3K activity in human health, inactivating mutations in PIK3R1 that disrupt signalling downstream of the insulin receptor lead to SHORT syndrome, a developmental disorder characterised by short stature, hyperextensibility of joints and/or hernias, ocular depression, Rieger anomaly, and delays of tooth eruption [98–100].

Due to their key signaling roles and implications in cancer, primary immunodeficencies, and overgrowth disorders [101] the class I PI3Ks have been a major focus of medical chemistry efforts, which have resulted in several clinically approved therapeutics. The PI3K portion of this chapter will focus on inhibition of class I PI3K's in treatment of cancer, overgrowth disorders, and primary immunodeficiencies. The specific focus of this section will be on the structure/function study of class I PI3K inhibitors, and the advantages of developing isoform specific inhibitors.

A table summarising some of the class I PI3K inhibitors currently in the clinic or clincal trials is shown in Table 9.1. The structure activity relationship (SAR) of both pan-class I PI3K inhibitors [102] and isoform-specific class I PI3K inhibitors [103] have been extensively reviewed recently, therefore this review will focus on a selection of inhibitors that are FDA-approved or in clinical trials, particularily those in which the structural basis of inhibition has been well defined.

**Pan-PI3K Inhibitors** The majority of the first generation of class I PI3Ks were pan specific PI3K inhibitors that were able to inhibit all of the PIK3CA, PIK3CB, PIK3CD, and PIK3CG. Many pan-PI3K inhibitors are also able to inhibit the protein kinase mTOR, which is structurally similar to PI3Ks. Bayer's Aliqopa<sup>TM</sup> (copanlisib, BAY 80-6946) was approved for relapsed follicu-



**Fig. 9.2** (a) Class I PI3Ks are key signalling molecules involved in cancer growth, survival and progression. PIK3CA is ubiquitously expressed in all cell types and functions as a key driver of cancer growth and metastasis, while PIK3CD and PIK3CG are mainly expressed in immune cells that modulate the tumour environment. (b) Active site of PIK3CG bound to the Pan-PI3K, FDA-approved inhibitor copanlisib (PDB: 5G2N). (c) Active site of PIK3CA bound to the PIK3CA-specific, FDA-approved inhibitor alpelisib (PDB: 4JPS). (d) Active site

lar lymphoma in 2017. While copanlisib predominantly inhibits PIK3CA and PIK3CD in the sub-nanomolar range, it still potently inhibits PIK3CB and PIK3CG in the low nanomolar range, and to a lesser extent mTOR, thus is considered a pan-PI3K selective inhibitor (Table 9.1) [104]. Characteristic of most kinase inhibitors, copanlisib forms the critical hydrogen bond to the hinge V882 (PIK3CG numbering) backbone amide with its imidazoline group, while the aminopyrimidine group fills the affinity pocket (a well conserved class I PI3K feature lined by Y867, I879, I963 and D841 in PIK3CG), forming hydrogen bonds with K833, D836, D841 and a pi-stacking interaction with D964 of the DFG motif (Fig. 9.2b) [105].

of human PIK3CA bound to the PIK3CA-specific, covalent inhibitor CNX-1351 (PDB:3ZIM). (e) Active site of human PIK3CD bound to the PIK3CD-specific, FDAapproved inhibitor Idelalisib (PDB: 4XE0). Arrow indicates outward shift of M752 in presence of idelalisib. Key hydrogen bonds indicated as blue dotted lines; N-lobe colored red, C-lobe colored yellow; water molecules involved in hydrogen-bond networks indicated as blue spheres

Additional pan-PI3K compounds from Adlai Noryte/Novartis (buparlisib) and Genentech (pictilisib) both recently entered phase II-phase III clinical trials for hormone-receptor positive, human epidermal growth factor receptor 2 (HER2)-negative breast cancer (Table 9.1) [106, 107]. Both compounds form a hydrogen bond with the hinge V882 and additional hydrogen bonds within the affinity pocket, while pictilisib also forms a hydrogen bond with K802 and the backbone amide of A805. Interestingly, buparlisib was identified to have an off-target effect as a tubulin inhibitor, with its antiproliferative activity possibly due to microtubule-dependent binding [108]. The compound bimiralisib, which shares a very similar molecular structure to buparlisib, has been designed with the replacement of a single carbon atom in the core of bupar-

-								
	Inhibitor	Trail phase	$IC_{50}$ (nM)					
Target			<b>PIK3CA</b>	<b>PIK3CB</b>	PIK3CG	PIK3CD	mTOR	Company (reference)
Pan-class I	Buparlisib (BKM120)	III	52	166	262	116	4600	Adlai Noryte, Novartis [106]
Pan-class I	Pictilisib (GDC-0941)	Π	3	33	75	3	580	Genentech [107]
Pan-class I & mTOR	Bimiralisib (PQR309)	Π	33	661	708	451	89	PIQUR [109]
Pan-class I	Aliqopa <sup>TM</sup> (Copanlisib, BAY 80–6946)	FDA approved	0.5	3.7	6.4	0.7	45	Bayer [104]
PIK3CA	Piqray <sup>®</sup> (Alpelisib, BYL719)	FDA approved	5	1200	250	290	>9100	Novartis [113]
PIK3CG	IPI-549	Π	3200	3500	16	8400	N.D.	Infinity Pharmaceuticals [125]
PIK3CG & PIK3CD	Copiktra® (Duvelisib, IPI-145)	FDA approved	1600	85	27	2.5	N.D.	Verastem Oncology & Infinity Pharmaceuticals [124]
PIK3CD	Zydelig (Idelalisib, CAL-101)	FDA approved	820	565	89	2.5	N.D.	Gilead [118]
PIK3CD	Leniolisib (CDZ173)	III	244	424	2230	11	N.D.	Novartis [122]

 Table 9.1
 Representative class I PI3K inhibitors in advanced clinical trials

N.D. not determined

lisib that leads to disruption of microtubule binding [109], with this molecule also currently in clinical trials. The major issue with the majority of pan-PI3K inhibitors has been dose limiting toxicity [13, 110], with intensive efforts focused on the development of isoform selective inhibitors.

**PIK3CA Specific Inhibitors** Novartis' Piqray<sup>®</sup> (alpelisib, BYL719) was approved for HER2negative, PI3KCA mutated breast cancer in 2019 [111]. Alpelisib represents the first FDAapproved PIK3CA-specific inhibitor, and continues to show promise in clinical trials for various other types of cancer. Intriguingly, this compound also showed promise in the treatment of PIK3CA dependent overgrowth conditions [112]. Apelisib potently inhibits PIK3CA with an IC<sub>50</sub> of 50 nM, and displays a greater than 50-fold selectivity over other PI3K isoforms (Table 9.1) [113]. Apelisib satisfies the hinge hydrogen bond in which the thiazole nitrogen and 2-NH group form hydrogen bonds with the backbone amide and carbonyl of V851 (Fig. 9.2c). The pyrimidine moiety sits in the less solvent accessible affinity pocket which includes residues Y836, K802 and D933. The pyridine nitrogen atom is part of a hydrogen-bond network involving three water molecules and the side chains of residues Y836, D810, D933 and K802. One of the fluorine atoms of the trifluoromethyl group also makes a putative hydrogen bond with K802. The basis for PIK3CA specificity resides in the donor-acceptor interactions between alpelisib with the PIK3CA side chain Q859. Residue Q859 is unique to PIK3CA (D, N and K in PIK3CB, PIK3CD and PIK3CG respectively) with the other isoforms unable to form this particular set of hydrogen bonds, revealing the likely molecular mechanism of selectivity. Additional PI3K inhibitors of different chemotypes [114-116], also take advantage of the unique Q859 in PIK3CA to drive specificity. Another mechanism to target PIK3CA in an isoform specific manner, has been in the use of covalent inhibitors that modify C862, another residue unique to PIK3CA (L, L and Q in PIK3CB, PIK3CD and PIK3CG, respectively) to drive specificity. CNX-1351 potently inhibits PIK3CA ( $IC_{50} = 6.8$  nM) with >20-fold selectivity over other class I PI3Ks due to hydrogen bonds between the hinge V851 amide backbone, the Y836 side chain, D810 side chain, and a covalent modification of PIK3CA C862 (Fig. 9.2d) [117].

PIK3CD & PIK3G Specific Inhibitors While PIK3CA and PIK3CB are ubiquitously expressed, PIK3CD and PIK3CG are expressed in immune cells. Both PIK3CD and PIK3CG play key roles in the immune-suppressive tumor microenvironment [92, 93]. Gilead's Zydelig<sup>®</sup> (idelalisib, CAL-101) was the first PI3K inhibitor to successfully progress through clinical trials, gaining FDA approval in 2014. Idelalisib specifically and potently targets PIK3CD over other class I PI3Ks, and was approved for relapsed follicular lymphoma (FL), chronic lymphocytic leukemia (CLL) and small lymphocytic lymphoma (SLL) (Table 9.1) [118, 119]. The purine group of idelalisib forms hydrogen bonds with backbone amide of hinge V828, the backbone carbonyl of E826, and a water-mediated hydrogen bond network involving the D911 sidechain. Idelalisib is a propeller-shaped inhibitor, a shape previously utilized to gain PIK3CD selectivity [16, 29]. In an apo state, M752 of the PIK3CD P-loop packs "in" against Y760, however binding of idelalisib and other propeller inhibitors pushes M752 "out", forming a hydrophobic specificity pocket [120]. While these two residues are conserved throughout class I PI3Ks, differences in P-loop residues and native hydrogen bond networks involving the tryptophan residues are thought to make the opening of this pocket more energetically unfavorable for PIK3CA, PIK3CB. Additionally, the phenyl group of idelalisib packs against the side chains of a wall capped by N836, which is unique to PIK3CD (Q859, D856 and K890 in PIK3CA, PIK3CB and PIK3CG, respectively). Studies on another propeller-shaped series has suggested modifications at this position can affect potency and selectivity of propeller compounds [121]. The PIK3CD selective inhibitor leniolisib (CDZ173; Table 9.1) exploits a different molecular mechanism to mediate PIK3CD selectivity, with a acetylpiperazine group from the inhibitor forming a pistacking interaction with W760 in PIK3CD, with this corresponding interaction not possible with W780 in PIK3CA [122]. This inhibitor has shown initial promise for the treatment of APDS patients [123].

Verastem Oncology Infinity and Pharmaceuticals' Copiktra® (duvelisib, IPI-145) was approved for relapsed or refractory chronic lymphocytic leukemia/small lymphocytic lymphoma (CLL/SLL) in 2018. Duvelisib potently inhibits PIK3CG and PIK3CD in the lownanomolar range (Table 9.1) [124]. While no cocrystal structure is available, duvelisib is very similar in structure to idelalisib and likely exerts inhibition through a similar propeller mechanism. In terms of specific PIK3CG inhibition, IPI-549 maintains the same 8-Cl isoquinolinone core as duvelisib, but achieves greater than 200fold selectivity over PIK3CD and other class I isoforms (Table 9.1) [125]. The increase in potency is thought to be due to nonfavorable interactions between the alkyne moiety of IPI-549 and nonconserved residues adjacent to the specificity pocket such as PIK3CD T750 (PIK3CG K802). IPI-549 is currently in phase II clinical trials for several malignancies. Recently AstraZeneca has reported on a novel strategy to generate PIK3CG inhibitors that induce large allosteric conformational changes in PIK3CG, with these changes not possible in other class I PI3Ks [126].

# 9.2.2 PI4KB Inhibitors as Tool Compounds to Define the Role of PI4KB in Viral Infection

Picornaviruses hijack host PI4KB during infection to generate replication organelles which are essential for viral replication, and direct inhibition of PI4KB has been shown to disrupt viral infection progression [56]. Picornaviruses are nonenveloped, positive-sense, single-stranded RNA viruses that cause diverse human diseases including gastroenteritis, poliomyelitis, aseptic

meningitis, hand-foot-and-mouth disease, respiratory illness and acute flaccid paralysis, and particularily affect young children [127]. Viruses that have been shown to specifically manipulate PI4KB include Aichivirus. Poliovirus. Rhinovirus, Coxsackievirus, Enterovirus D68 and Enterovirus A71 [77]. These viruses hijack host PI4KB during infection to generate replication organelles, which are essential for viral replication (Fig. 9.3a). These replication organelles are abnormal, PI4P-enriched membranes upon which multiple specific lipids are enriched, along with recruitment of viral replication machinery (i.e. RNA polymerase, etc.) [74]. PI4KB recruitment to replication organelles appears to be dependent on viral 3A proteins [56]. Viral 3A proteins do not directly interact with PI4KB, instead they recruit PI4KB-regulatory proteins such as ACBD3 and the Arf1 GEF GBF1 (Fig. 9.3a) [55, 66, 76]. Specific enteroviruses have also shown a dependence on the PI4KBregulatory c10orf76 protein [128]. As infection progresses, the hijacking of PI4KB via regulatory proteins and subsequent redistribution of PI4P pools disrupts normal trafficking and eventually leads to collapse of the Golgi (Fig. 9.3a) [56, 129].

Pharmacologically or genetically inhibiting PI4KB prevents the formation of replication organelles and halts viral infection progression. When considering the potential value of PI4KB inhibitors as anti-viral therapeutics it is important to note that while these inhibitors are not generally cytotoxic and effectively disrupt viral replication, some PI4KB inhibitors have been shown to have immunosuppressive effects, specifically an antiproliferative effect on lymphocytes in mice [130, 131]. These currently are most useful as tool compounds for the study of the role of PI4KB in viral replication, with the discussion focused on the molecular mechanisms of inhibitor specificity.

**Potent and Selective PI4KB Inhibitors** The compound PIK-93 represents the original PI4KB "specific" inhibitor used extensively to study the cellular roles of PI4KB and its roles in viral replication [16]. While PIK93 is highly selective for



A Enteroviruses depend on hijacking human PI4KB to generate PI4P-enriched replication organelles upon which replication

**Fig. 9.3** (a) Human PI4KB is hijacked by enteroviruses to facilitate viral replication. The virus-encoded 3A protein indirectly hijacks PI4KB through its regulatory proteins and utilizes it to build PI4P-enriched replication organelles, upon which viral replication machinery assembles. PM = plasma membrane. (b) Active site of

PI4KB over PI4KA, it has a high cross reactivity for PIK3CG, PIK3CD and the class III PI3K vps34. Derivatives of PIK-93 were optimized to specifically decrease reactivity with the class I PI3Ks [132]. This led to the identification of compound 9, which takes advantage of the less sterically crowded pocket of PI4KB (Fig. 9.3b). Compound 9 makes two key hydrogen bonds between the thiazole and acetamide groups with the hinge V598 backbone amide and carbonyl. A hydrogen bond is also present between the sulfonamide group and K549. These hydrogen bonds are conserved with PIK93, yet the N-phenol sulfonamide para-hydroxyl group of compound 9 forms an additional hydrogen bond with the G660 carbonyl, which is important for the increased potency (PI4KB IC<sub>50</sub> 7 nM vs. 17 nM). The presence of this hydroxyl group also

human PI4KB bound to the anti-viral Compound 9 (PDB: 5EUQ). (c) Active site of human PI4KB bound to the antiviral MI356 (PDB: 5FBL). (d) Active site of human PI4KB bound to the immunosuppressant UCB9608 (PDB:6GL3). Key hydrogen bonds indicated as blue dotted lines; N-lobe colored red, C-lobe colored yellow

increases potency for PIK3CG and vps34, suggesting this hydrogen bond is conserved. The acetamide and methoxy substituent of compound 9 mediate selectivity, as the interacting residues in PI4KB (L383 and L663) are significantly bulkier in the class I PI3Ks.

The most potent human PI4KB inhibitor to date, MI356 (IC<sub>50</sub> = 0.98 nM) [133], is a derivatization of the amino heterocyclic core of T-00127-HEV1, an anti-enterovirus PI4KB inhibitor [134]. MI356 forms an extensive hydrogen bond network with the active site of PI4KB (Fig. 9.3c). Amines from the imidazole of the bicyclic core and the (2-acetamidoethyl)amino moiety of MI356 form hydrogen bonds with the hinge V598 backbone amide and carbonyl, respectively (Fig. 9.3c). The carbonyl of the (2-acetamidoethyl)amino group forms a hydro-

gen bond with hinge N600 amide, and a hydrogen bond is also present between the sulfonamide moiety and K549. The sulfonamide moiety also likely coordinates hydrogen bonds to the backbone of G660 and N661, however these were not modelled in the crystal structure due to low resolution. While MI356 exhibits remarkable selectivity over PI4KA (IC<sub>50</sub> 48  $\mu$ M), it has not been tested against class I PI3Ks, however the (2-acetamidoethyl)amino group would likely cause a steric clash, similar to the PIK93 derivatives discussed above. When considering potential value as a tool in cells, MI356 and similar derivatives with the (2-acetamidoethyl) amino moiety appear to be poorly permeable through cell membranes. However, compound 10, a derivative of the MI356 series, substitutes a 2-ethylpyridine moiety for the (2-acetamidoethyl) amino group and still displays potent inhibition of PI4KB (IC<sub>50</sub> = 6.1 nM) and great selectivity over class I PI3Ks (no IC<sub>50</sub> below 10  $\mu$ M), with improved cell penetration and anti-viral activity against HRV1 and HCV 1b ( $EC_{50} = 75$  and 29 nM, respectively).

The pyrazolopyrimidine UCB9608, a potent PI4KB inhibitor (IC<sub>50</sub> = 11 nM) was recently identified as a potent immunosuppressive agent capable of prolonging heterotopic allograft retention in mice [131]. The amino pyrimidine of UCB908 makes two hydrogen bonds with the backbone amide and carbonyl of PI4KB hinge V598 (Fig. 9.3d). There is no contact with K549 as seen in Compound 9 and MI356, however this residue appears to be coordinating a water molecule that may participate in a hydrogen bonding network. Another water molecule is present within hydrogen bonding range of the urea carbonyl and S618 side-chain. The urea NH and carbonyl of UCB9608 form hydrogen bonds with the G660 carbonyl and N375 side chain, respectively. The N375 interaction shifts the P-loop inwards, with the side-chain methylene of N375 and main-chain methylene of G660 available to make putative C – H/ $\pi$  interactions with the electron-rich aromatic ring of the UCB9608 urea group. UCB9608 displays greater than 1000-fold selectivity for PI4KB over class I and III PI3Ks, and 80-fold selectivity over class II PI3Ks.

Selectivity for PI4KB over PIK3CG is likely due to the lack of the N375 to hydrogen bond (A805 in PIK3CG) and potentially steric hindrance by PIK3CG D950 and T887 residues (G660 and S603 in PI4KB, respectively). Selectivity over vps34 may be due to the presence of D747 in place of G660, with steric hindrance again preventing hydrogen bonding with the backbone carbonyl.

### 9.2.3 PI4KB Inhibitors as Anti-parasitics

PI4K activity is required for successful replication of the malaria parasite, which encodes a larger variant of PI4KB [60]. Plasmodium falciparum and Plasmodium vivax cause the vast majority of malaria cases worldwide, which are transferred to humans through the bites of infected female Anopheles mosquitoes. The parasite first infects hepatocytes in the liver, then eventually progresses to a symptomatic erythrocyte infection in the bloodstream. Artemisininbased combination therapies have been recommended by the WHO since 2005, and have caused significant reductions in the global malaria burden and mortality - however, elimination of malaria has been threatened by the emergence of artemisinin resistance in P. falciparum across mainland Southeast Asia [135]. Complicating matters, P. vivax is able to persist in the liver for years after treatment before relapsing and reinitiating a blood stage infection [136]. Considering these challenges, to eradicate malaria, medicines are needed that cure the symptomatic asexual blood stage and clear the preceding liver stage that can cause relapses. *Plasmodium* PI4K inhibitors target all life stages of the parasite, in both mammalian hosts and the mosquito vector, kill drug-resistant parasites, and protect monkeys from malaria infection [60]. Inhibition of Plasmodium PI4K alters intracellular distribution of PI4P, which disrupts PI4P effector (including Rab11a) recruitment and regulation of transport vesicles destined for the ingressing plasma membrane, eventually causing failure of merozoite cytokinesis within asexual

blood stage schizonts (Fig. 9.4a). These parasite PI4K inhibitors also display potent activity against another related parasite, Cryptosporidium, which is a leading cause of death in the developing world. Inhibition of Cryptosporidium PI4K leads to potent reduction in intestinal infection of immunocompromised mice, and rapid resolution of diarrhea and dehydration in neonatal calves [57]. Finally, a third parasite, Trypanosoma brucei, the causative agent of African Sleeping Sickness Trypanosoma brucei, also depends on activity of its PI4K homolog for growth, proper Golgi formation and cytokinesis [137]. While parasite PI4K inhibitors have only recently entered clinical trials, preclinical studies have been very promising, and the need for their development is clear.

Plasmodium and Cryptosporidium PI4KB Inhibitors The Plasmodium PI4K Imidazopyrazines and quinoxaline inhibitors (examples KDU691 and BQR695) were found to be active against all liver and blood-stage forms of the parasite. Whole genome sequencing of parasites resistant to imidazopyrazines and BQR695 identified mutations in Plasmodium PI4K were conferring resistance. These compounds potently inhibited recombinant P. vivax PI4K, and disrupt cytokinesis in the parasite blood-stage schizont, when membranes are built up around multiple nuclei of developing daughter merozoites (Fig. 9.4a) [60]. KDU691 is a potent inhibitor of *Plasmodium* PI4K (IC<sub>50</sub> = 1.5 nM) with great selectivity over human PI4KB and class I PI3Ks (>1000-fold]). BQR695 is also a potent anti-malarial Plasmodium PI4K inhibitor  $(IC_{50} 3.5 \text{ nM})$  with sub-micromolar potency against human PI4KB (IC50 88 nM) and good selectivity other human over kinases. MMV390048, a 2-aminopyridine [138], another *Plasmodium* PI4K inhibitor ( $IC_{50} = 3.4 \text{ nM}$ ) [58], showed single dose cures of malaria in mice (PMID:22390538). MMV390048 also exhibits a prophylactic effect against malaria in monkeys, blocking all life cycle stages of the Plasmodium parasite and is currently in phase II clinical trials for the treatment of malaria. Additional plasmodium selective PI4K inhibitors have been discovered including BRD73842 ( $IC_{50} = 21 \text{ nM}$ ) [59], and the MMV390048 derivative UCT943  $(IC_{50} = 23 \text{ nM})$  [139]. In the absence of the Plasmodium PI4K structure, the structural basis for specificity of anti-malarial PI4K inhibitors over human PI4KB remains poorly defined. P. vivax PI4K (1528 residues) is much larger than the human PI4KB homolog (801 residues for human isoform 2) although the parasite variant maintains the canonical class I PI3K/class III PI4K helical and kinase domain (Fig. 9.4b). Crystallization and structure determination of human PI4KB is so far only possible through the removal of disordered regions throughout the protein that impede crystallization [28]. The larger Plasmodium PI4K homolog is predicted to have many additional such disordered regions, which have hindered efforts towards crystallization and structure determination. The structure of the anti-malarial BQR695 bound to human PI4KB provides limited insight into inhibition of Plasmodium PI4KB (Fig. 9.4c) [140]. BQR695 makes a key hydrogen bond in the human PI4KB active site between the central quinoxaline and V598 and another between the amino group off of the central quinoxaline and the A601 backbone carbonyl (Fig. 9.4c).

Comparing *P. vivax* PI4K to human PI4KB, a region of the *P. vivax* PI4K kinase domain spanning the C-terminal region of the N-lobe and entirety of the C-lobe (residues 1245–1525) is well conserved with the human PI4KB kinase domain (residues 520–801) with 43% of residues identical and 62% similar (Fig. 9.4d). While the C-lobe active site residues show good conservation, the N-terminal half of the *P. vivax* N-lobe and the N-lobe linker shows poor sequence similarity to human PI4KB, including a significantly divergent P-loop. These key differences are likely contributing to observed specificity observed for *Plasmodium* PI4KB, including of the PaKB.

*Cryptosporidium* PI4K was identified as a therapeutic target of pyrazolopyridines, including the previously mentioned KDU691 [57]. Pyrazolopyridine compounds inhibit recombinant *Cryptosporidum* PI4K (KDU-691  $IC_{50} = 25$  nM, KDU-731  $IC_{50} = 17$  nM) with


**Fig. 9.4** (a) The malaria parasite requires the function of *Plasmodium* PI4K and Rab11a for proper plasma membrane biogenesis and cytokinesis of daughter merozoites, which are disrupted upon treatment with small molecule PI4K inhibitors. PM = plasma membrane, PVM = parisitophorous vacuolar membrane. (b) Active site of human PI4KB bound to the human and *Plasmodium* inhibitor BQR695 (PDB: 5C4G). Key hydrogen bonds indicated as blue dotted lines; N-lobe colored red, C-lobe colored yel-

low. (c) Domain architecture of human PI4KB (89 kDa) and predicted architecture of related *P. vivax* (172 kDa) and *C. parvum* (128 kda) PI4Ks. (d) Alignment of wellconserved region of human (residues 520–801), *Plasmodium vivax* (1245–1525) and *Cryptosporidium Parvum* (830–114) PI4KB kinase domains, consisting of the C-term of the N-lobe and entire C-lobe. Alignment generated using clustal omega and Espript 3.0 [141] greater than 50-fold selectivity over human PI4KB. Considering the most urgent need for an effective cryptospiridiosis treatment is among children under two, KDU-731 was tested for numerous pharmacology safety parameters and represents an excellent preclinical candidate for the treatment of cryptospiridiosis - it displays low toxicity, no inhibition of any major forms of cytochrome P450, and > 20-fold selectivity over class I and III PI3Ks. An exciting prospect to consider is the potential to develop a parasite PI4K inhibitor that could be utilized to treat both malaria and cryptosporidiosis. However, like the Plasmodium homolog, the Cryptosporidium PI4K structure has yet to be determined and the structural basis for inhibitor specificity remains poorly defined. C. parvum PI4K is smaller than the P. vivax homolog, but shares greater homology in its active site with P. vivax PI4K (56% identical and 72% similar) than with the smaller human PI4KB (43% identical and 60% similar) in the conserved core of the kinase domain spanning the C-terminal region of the N-lobe and entirety of the C-lobe (Fig. 9.4d). Intriguingly, inhibitors exist that potently target human and Plasmodium PI4Ks, but not Cryptosporidium PI4K (BQR695). Inhibitors also exist that target Plasmodium and Cryptosporidium PI4Ks, but not human PI4KB (KDU-691). This suggests there are both conserved and non-conserved features within each homolog, and highlights the need for structural insights into parasite PI4K enzymes in order to define the molecular basis of PI4K inhibitor specificity to aid anti-parasitic drug development.

# 9.3 Future Directions of Phosphoinositide Kinase Drug Discovery

Recent years has seen an explosion in the development of potent and selective small molecules targeting the class I PI3Ks and type III PI4KBs. The class I PI3K inhibitors are now quite advanced in the clinic, with multiple being approved for treatment of blood cancers. There have been a number of failed trials of PI3K inhibitors in solid tumors, with many complications from dose-limiting toxicity. The development of potent and isoform selective compounds allows for the tailoring of therapy to target PI3K both in the tumor and the tumor microenvironment. In addition, new data on the role of insulin feedback allows for the design of specific metabolic strategies to combine with PI3K inhibition. Overall there are myriad exciting new combination therapies for which PI3K inhibition may be useful in cancer therapy. PI3K inhibitors are also finding use in the treatment of other PI3K related diseases, including immunodeficiencies and overgrowth syndromes. Exciting times are ahead for the application of PI3K inhibitors in the clinic.

Inhibitors for PI4KB were originally designed as potential anti-viral therapeutics, but it is likely that there will be numerous problems in the development of these compounds in the clinic. However, additional work revealing the mechanisms by which viruses manipulate PI4KB signalling may reveal novel drug targets that can be disrupted without the side effects that come with PI4KB inhibition. The most exciting application of PI4KB inhibitors is in the treatment of devastating parasitic infections, including malaria and cryptosporidiosis. Limiting the development of these compounds is any structural information on these enzymes that could guide medicinal chemistry efforts. Continued study on this approach will hopefully lead to the next generation of parasite PI4K inhibitors that hopefully will be effective, single-dose cures.

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# Druggable Lipid GPCRs: Past, Present, and Prospects

10

Hirotaka Mizuno and Yasuyuki Kihara

#### Abstract

G protein-coupled receptors (GPCRs) have seven transmembrane spanning domains and comprise the largest superfamily with ~800 receptors in humans. GPCRs are attractive targets for drug discovery because they transduce intracellular signaling in response to endogenous ligands via heterotrimeric G proteins or arrestins, resulting in a wide variety of physiological and pathophysiological responses. The endogenous ligands for GPCRs are highly chemically diverse and include ions, biogenic amines, nucleotides, peptides, and lipids. In this review, we follow the KonMari method to better understand druggable lipid GPCRs. First, we have a comprehensive *tidy*ing up of lipid GPCRs including receptors for prostanoids, leukotrienes, specialized proresolving mediators (SPMs), lysophospholipids. sphingosine 1-phosphate (S1P). cannabinoids, platelet-activating factor (PAF), free fatty acids (FFAs), and sterols. This tidying up consolidates 46 lipid GPCRs and declutters several perplexing lipid GPCRs. Then, we further *tidy up* the lipid GPCR-directed drugs

Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA, USA e-mail: kihara-yasuyuki@umin.net from the literature and databases, which identified 24 clinical drugs targeting 16 unique lipid GPCRs available in the market and 44 drugs under evaluation in more than 100 clinical trials as of 2019. Finally, we introduce drug designs for GPCRs that spark joy, such as positive or negative allosteric modulators (PAM or NAM), biased agonism, functional antagonism like fingolimod, and monoclonal antibodies (MAbs). These strategic drug designs may increase the efficacy and specificity of drugs and reduce side effects. Technological advances will help to discover more endogenous lipid ligands from the vast number of remaining orphan GPCRs and will also lead to the development novel lipid GPCR drugs to treat various diseases.

### Keywords

Lipid mediators · Bioactive lipids · Drug discovery · Mechanism of action

## 10.1 Introduction

G protein-coupled receptors (GPCRs) are the largest membrane receptor family in the human genome. Nearly 800 GPCRs have been identified in humans [1], about half of which are olfactory receptors [2], and the other half are classified into

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Fig. 10.1 A GPCR pyrogenetic tree

four major families including the Rhodopsin family (Class A), the Secretin and Adhesion family (Class B), the Glutamate family (Class C), and the Frizzled family (Class F) (Fig. 10.1). A list of GPCRs that includes their classification, structures, ligands, and other features is available in the Guide to Pharmacology, International Union of Basic and Clinical Pharmacology/ British Pharmacological Society (IUPHAR/BPS) [1, 3] and the GPCR database (GPCRdb) [4, 5]. GPCRs have seven transmembrane (TM) helices (TM1 ~ 7) that form an orthosteric ligand-binding pocket for small organic agonists, while some ligands such as glycoprotein hormones and glutamate bind to the amino terminus and extracellular domains [6]. Endogenous ligand binding to the orthosteric site causes a conformational change of the receptor that can interact with a heterotrimeric G protein (G $\alpha$ , G $\beta$  and G $\gamma$ ), which promotes the guanine nucleotide exchange (i.e., releasing guanosine diphosphate, GDP, and guanosine triphosphate, GTP) on the G $\alpha$  subunits. Thus, GPCRs act as guanine nucleotide exchange factors (GEF). GTP-bound G $\alpha$  dissociates from

Year	Event
1964	<i>The Nobel Prize in Physiology or Medicine (Bloch K and Lynen F)</i> for their discoveries concerning "the mechanism and regulation of the cholesterol and fatty acid metabolism."
1967	<i>The Nobel Prize in Physiology or Medicine (Wald G, Granit R, and Hartline H)</i> for their discoveries concerning "the primary physiological and chemical visual processes in the eye."
1970	<i>The Nobel Prize in Physiology or Medicine (von Euler U, Katz B, and Axelrod J)</i> for their discoveries concerning "the humoral transmitters in the nerve terminals and the mechanism for their storage, release and inactivation."
1982	<i>The Nobel Prize in Physiology or Medicine (Samuelsson BI, Bergstrom SK, and Vane JR)</i> for their discoveries concerning "prostaglandins and related biologically active substances."
1985	<i>The Nobel Prize in Physiology or Medicine (Brown MS and Goldstein JL)</i> for their discoveries concerning "the regulation of cholesterol metabolism."
1994	<i>The Nobel Prize in Physiology or Medicine (Gilman AG and Rodbell M)</i> for their "discovery of G-proteins and the role of these proteins in signal transduction in cells."
2004	<i>The Nobel Prize in Physiology or Medicine (Axel R and Buck LB)</i> for their "discoveries of odorant receptors and the organization of the olfactory system."
2012	The Nobel Prize in Chemistry (Lefkowitz RJ and Kobilka B) for "studies of G-protein-coupled receptors."

Table 10.1 Chronological table for the Nobel Prizes that are relevant to lipid or GPCR biology

 $G\beta\gamma$ , resulting in the activation of downstream signaling cascades including Ca<sup>2+</sup> mobilization, cyclic AMP (cAMP), Rho family of GTPase, mitogen-activated protein kinases (MAPKs), and others [7]. Distinct signaling mediated through arrestins requires receptor phosphorylation at the C-terminal tail by GPCR kinases (GRKs), which internalization. promotes receptor The mechanistic aspects of GPCRs have been thoroughly investigated particularly through a focus on adrenergic receptors or a rhodopsin, resulting in multiple Nobel Prize winners in the 120-years history of Nobel Prize (Table 10.1).

## 10.2 Tidying-Up of Lipid GPCR Histories

The GPCR history dates back to 1876 when the photosensitive pigment, "rhodopsin," was discovered by *Franz Boll* and isolated by *Wilhelm Kühne*. The requirement of covalent ligand retinal for physico-chemical processes of the "rhodopsin cycle" was discovered by *George Wald* who won the Nobel Prize in Physiology or Medicine (1967) and shared with *Ragnar Granit* and *Haldan Hartline*. In 1973, ATP-dependent cyclic nucleotide phosphodiesterase (PDE) was

reported to transduce visual signals through rhodopsin [8], while it was found that the coupling of rhodopsin to PDE is dependent on GTP [9]. The involvement of rhodopsin-coupled GTPase that mediates visual signals from rhodopsin to PDE was proposed in 1977 [10, 11] and confirmed by Fung B.K. et al. in 1981 [12]. It is now known as transducin which is a heterotrimeric GTPase composed of  $\alpha$ ,  $\beta$ , and  $\gamma$  subunits. The complete amino acid sequence of bovine rhodopsin was solved by Yuri Ovchinnikov in 1982 and Paul Hargrave in 1983, which highlighted the receptor containing 7 transmembrane domains (7TMs) [9]. In 1983, the gene encoding bovine rhodopsin was cloned by Jeremy Nathans and David Hogness [13]. Until then, only the structural features of rhodopsin had been studied. In 2000, Krzysztof Palczewski et al. solved the X-ray crystal structure of dark-adopted bovine rhodopsin as the first GPCR structure [14]. These studies, as well as the adrenergic receptors studied by Robert Lefkowitz and Brain Kobilka [15], opened up opportunities for understanding GPCR biology and GPCR-targeted drug discovery.

Rhodopsin is a photosensitive receptor requiring a lipophilic retinal in its orthosteric binding site, indicating that lipids could bind to the orthosteric site of other GPCRs. To date, the endoge-

Year	Events	Refs
1990	Cloning and identification of <b>CB</b> <sub>1</sub> / <i>CNR1</i>	[16]
	Cloning of EDG-1	[17]
1991	Cloning and identification of <b>PAFR</b> / <i>PTAFR</i>	[18]
	Cloning and identification of <b>TP</b> / <i>TBXA2R</i>	[19]
1992	Cloning and identification of <b>EP</b> <sub>3</sub> / <i>PTGER3</i>	[20]
	Discovery of AEA as endogenous ligand for <b>CB</b> <sub>1</sub>	[21]
1993	Cloning and identification of <b>EP</b> <sub>2</sub> / <i>PTGER2</i> and <b>EP</b> <sub>1</sub> / <i>PTGER1</i>	[22, 23]
	Cloning and identification of CB <sub>2</sub> /CNR2	[24]
	Cloning of <i>EDG-5</i> (also known as <i>AGR16</i> or <i>H218</i> )	[25, 26]
1994	Cloning and identification of <b>FP</b> / <i>PTGFR</i> , <b>IP</b> / <i>PTGIR</i> and <b>DP</b> <sub>1</sub> / <i>PTGDR</i>	[27– 32]
	Cloning and identification of ALX/ FPR2	[33]
1995	Discovery of 2-AG as endogenous ligand for <b>CB</b> <sub>1/2</sub>	[34, 35]
	Cloning of EDG-2	[36]
1996	Cloning and identification of <b>LPA<sub>1</sub>/LPAR1</b> (EDG-2, also known as VZG-1)	[37]
	Cloning of EDG-3	[38]
1997	Identification of <i>EDG-5</i> as <b>S1P</b> <sub>2</sub> / <i>S1PR2</i> and <i>EDG-3</i> as <b>S1P</b> <sub>3</sub> / <i>S1PR3</i>	[39]
	Cloning and identification of <b>BLT</b> <sub>1</sub> / <i>LTB4R</i>	[40]
1998	Identification of <i>EDG-1</i> as <b>S1P<sub>1</sub></b> / <i>S1PR1</i>	[41]
	Cloning and identification of LPA <sub>2</sub> /LPAR2 (EDG-4)	[42]
	Cloning of EDG-6	[43]
1999	Cloning and identification of CysLT <sub>1</sub> /CYSLTR1	[44]
	Cloning and identification of LPA <sub>3</sub> /LPAR3 (EDG-7)	[45]
	Cloning of CRTH2	[46]
2000	Identification of <i>EDG-6</i> as <b>S1P</b> <sub>4</sub> / <i>S1PR4</i>	[47, 48]
	(co	ntinued

 Table 10.2
 Chronological table for lipid GPCR identification

Table 10.2 (continued)

Year	Events	Refs
	Cloning and identification of <b>BLT</b> <sub>2</sub> / <i>LTB4R2</i>	[49]
	Cloning and identification of CysLT <sub>2</sub> /CYSLTR2	[50]
	Cloning and identification of <i>EDG-8</i> as <b>S1P</b> <sub>5</sub> / <i>S1PR5</i>	[51]
2001	Identification of <i>CRTH2</i> as <b>DP</b> <sub>2</sub> / <i>PTGDR2</i>	[52]
2002	Cloning and identification of <b>OXER</b> <sub>1</sub> / <i>OXER1</i> (GPR170)	[53– 55]
	Cloning and identification of <b>GPBA</b> (GPR131)	[56, 57]
2003	Identification of <i>P2RY9/GPR23</i> as <b>LPA</b> <sub>4</sub> /LPAR4	[58]
	Identification of GPR40, GPR43 and	[59-
	GPR41 as <b>FFA1</b> / <i>FFAR1</i> , <b>FFA2</b> / <i>FFAR2</i> , <b>FFA3</b> / <i>FFAR3</i> , respectively.	61]
2005	Discovery of RvE1 as an endogenous ligand for <b>ERV</b> <sub>1</sub> / <i>CMKLR1</i>	[62]
	Identification of <i>GPR120</i> as <b>FFA4</b> / FFAR4	[63]
	Identification of <i>GPR30</i> as <b>GPER</b> / <i>GPER</i>	[64]
2006	Identification of <i>GPR92</i> as <b>LPA</b> <sub>5</sub> / <i>LPAR5</i>	[65]
	Identification of <i>GPR34</i> as <b>lysoPS</b> <sub>1</sub>	[66]
2007	Identification of <i>GPR55</i> as <b>LPI</b> <sub>1</sub> / <i>LPIR1</i>	[67]
2008	Discovery of 12-HHT as an endogenous ligand for <b>BLT<sub>2</sub></b>	[68]
	Identification of <i>P2YR5</i> as <b>LPA</b> <sub>6</sub> /LPAR6	[69, 70]
2010	Discovery of RvD1 as an endogenous ligand for <b>DRV</b> <sub>1</sub> / <i>GPR32</i>	[71]
2011	Discovery of oxysterols as an endogenous ligand for <b>EBI</b> <sub>2</sub> / <i>GPR183</i>	[72]
	Discovery of 12-HETE as an endogenous ligand for 12-HETER/GPR31	[73]
2012	Identification of $P2YR10$ as <b>lysoPS</b> <sub>2</sub> , and $GPR174$ as <b>lysoPS</b> <sub>3</sub>	[74]
2013	Identification of <i>GPR99</i> as <b>CysLT</b> <sub>3</sub> /CYSLTR3	[75]
2015	Discovery of lysophosphatidylglucoside as another endogenous ligand for LPI <sub>1</sub> /LPIR1	[76]
	Discovery of RvD2 as an endogenous ligand for <b>DRV</b> <sub>2</sub> / <i>GPR18</i>	[77]

nous ligands for ~12% of ~400 non-olfactory GPCRs are lipophilic molecules which include eicosanoids (prostanoids and leukotrienes), lysophospholipids, sphingosine 1-phosphate (S1P), endocannabinoids, platelet-activating factors (PAF), free fatty acids (FFAs), sterols, and others. Tables 10.2 and 10.3 chronologically summarize the history of lipid GPCR identification and lipid GPCR structures, respectively.

Year	Events	Refs
2000	Dark-adopted bovine <b>rhodopsin</b> structure ( <i>the first GPCR</i>	[14]
2007	<b>β2AR</b> structure in complex with an inverse agonist (carazolol) and a monoclonal antibody (Mab5) against the native third intracellular loop of β2AR, or in complex with carazolol and T4 lysozyme (T4L) fusion in place of the third intracellular loop of β2AR ( <i>the second GPCR</i> <i>structure</i> )	[78]
2012	<b>S1P</b> <sub>1</sub> structure in complex with an antagonist (ML056) ( <i>the first lipid GPCR structure</i> ) PDB: 3V2W, 3V2Y	[79]
2014	<b>FFA1</b> structure in complex with agonists (TAK-875) PDB: 4PHU	[80]
2015	<b>LPA</b> <sub>1</sub> structure in complex with antagonists (ONO-9780307, ONO-9910539, and ONO-3080573) PDB: 4Z34, 4Z35, 4Z36	[81]
2016 ~ 17	<b>CB</b> <sub>1</sub> structure in complex with antagonists (AM6538, AM841, AM11542, and taranabant) PDB: 5TGZ, 5XR8, 5XRA, 5 U09	[82– 84]
2017	LPA <sub>6</sub> structure in the absence of any ligand PDB: 5XSZ	[85]
	<b>FFA1</b> structure in complex with agonists (MK-866 and AgoPAM AP8) PDB: 5TZR, 5TZY	[86]
2018	PAFR structure in complex with antagonists (SR 27417 and ABT491) PDB: 5ZKP, 5ZKQ	[87]

 Table
 10.3
 Chronological
 table
 for
 lipid
 GPCR

 structures

#### Table 10.3 (continued)

Year	Events	Refs
	<b>BLT</b> <sub>1</sub> structure in complex with an antagonist (BIIL260) PDB: 5X33	[88]
	<b>TP</b> structure in complex with antagonists (ramatroban and daltroban) PDB: 6IIU, 6IIV	[89]
	<b>DP</b> <sub>2</sub> structure in complex with antagonists (fevipiprant and CAY10471) PDB: 6D26, 6D27	[90]
2019	<b>EP</b> <sub>3</sub> structure in complex with an endogenous ligand (PGE <sub>2</sub> ) or an agonist (misoprostol) PDB: 6AK3, 6MQT	[91]
	<b>EP</b> <sub>4</sub> structure in complex with an antagonist (ONO-AE3-208) and Fab PDB: 5YHL, 5YWY, 5YF	[92]
	<b>CB</b> <sub>1</sub> structure in complex with an agonist (MDMB-Fubinaca) and Gi protein PDB: 6N4B	[93]
	<b>CB</b> <sub>2</sub> structure in complex with an agonist (AM10257) PDB: 5ZTY	[94]
	<b>CysLT</b> <sub>1</sub> structure in complex with antagonists (pranlukast and zafirlukast) PDB: 6RZ4, 6RZ5	[95]
	<b>CB</b> <sub>1</sub> structure in complex with an agonist (CP55940) and a NAM (ORG27596) PDB: 6KQI	[96]
	<b>CysLT</b> <sub>2</sub> structure in complex with antagonists (ONO-2570366, ONO-2770372, and ONO-2080365) PDB: 6RZ6, 6RZ7, 6RZ8, 6RZ9	[97]

(continued)

# 10.2.1 Prostanoid Receptors (TP, EP<sub>1,2,3,4</sub>, DP<sub>1,2</sub>, IP, FP)

Prostanoids are a class of eicosanoids including prostaglandins (PGs) and thromboxane (TX) [98]. Prostanoids are derived from arachidonic acid (AA) that is liberated from membrane phospholipids by phospholipases [99–101]. AA is metabolized into an unstable intermediate of

PGs, PGH<sub>2</sub>, by cyclooxygenase (COX-1/*PTGS1* and COX-2/*PTGS2*) [102]. PGH<sub>2</sub> is subsequently metabolized to PGs and TX by terminal enzymes. Here we introduce a brief history of prostanoid receptor identification [98, 101].

In 1934–1935, *Ulf von Euler* identified a lipophilic substance in semen that induces uterine contraction and named it PG which derives from prostate gland [103]. He also established the role

of norepinephrine as a neurotransmitter in 1945 and won the Nobel Prize in Physiology or Medicine in 1970 with Sir Bernard Katz and Julius Axelrod. Between 1957-1963, Sune K. Bergstrom isolated prostaglandins [104], and he won the Nobel Prize in Physiology or Medicine in 1982 shared with Bengt I. Samuelsson and John R. Vane (Table 10.1). In 1964, Sune K. Bergstrom and David van Dorp independently demonstrated the conversion of PGE<sub>2</sub> from AA [105, 106]. In 1968, E.J. Corey's group succeeded in the total synthesis of PGs [107, 108]. In 1975, B.I. Samuelsson's group discovered an unstable intermediate, TXA<sub>2</sub>, in the conversion of PGG<sub>2</sub> to TXB<sub>2</sub> [109]. In 1976, J.R. Vane and colleague identified an artery-derived unstable PG (prostacyclin/PGI<sub>2</sub>) that inhibits platelet aggregation [110], whose structure was also solved in the same year [111]. Osamu Hayaishi strongly suggested to Ono Pharmaceutical Co., Ltd., the development of PGs for clinical purposes which resulted in launching the program in 1966 on the basis of information provided by S.K. Bergstrom, B.I. Samuelsson, and E.J. Corey [112]. In 1974, Ono Pharmaceutical Co., Ltd. (Japan) placed the world's first PG product, PROSTARMON F Injection (dinoprost, a synthetic analogue of the naturally occurring  $PGF_{2\alpha}$ ) on the market as a labor-inducing drug. Since Ono then, Pharmaceutical Co., Ltd. has taken a lead in developing PG-related drugs including Prostarmon E<sup>TM</sup> (dinoprostone, a synthetic analogue of the naturally occurring  $PGE_2$ ) as an orally available labor-inducing drug in 1976, Prostandin<sup>TM</sup> (alprostadil, a synthetic analogue of the naturally occurring PGE<sub>1</sub>) for peripheral circulatory disorders in 1979, Preglandin<sup>™</sup> (gemeprost, a PGE<sub>1</sub> analog) for therapeutic abortion in mid-pregnancy in 1984, Ronok<sup>TM</sup> (ornoprostil, a PGE<sub>1</sub> derivative) for gastric ulcers in 1987, Cataclot<sup>TM</sup> (ozagrel, a TXA<sub>2</sub> synthase inhibitor) for injection for postoperative cerebral vaspospasm after subarachnoid hemorrhage surgery, Opalmon<sup>TM</sup> (limaprost, a PGE<sub>1</sub> derivative) for thromboangiitis obliterans in 1988, and Vega<sup>TM</sup> (ozagrel, a TXA<sub>2</sub> synthase inhibitor) for bronchial asthma in 1992. Other prostanoid receptor-targeted drugs were developed by many

pharmaceutical companies such as Doner® (beraprost, a synthetic analog of PGI<sub>2</sub>; Toray) for arterial occlusive disorders and pulmonary hypertension in 1992, Seratrodast (a TP antagonist; Takeda Pharmaceutical Co. Ltd.) for asthma, Flolan<sup>TM</sup> (epoprostenol, a synthetic analogue of PGI<sub>2</sub>; GlaxoSmithKline plc) for pulmonary hypertension in 1995, and Xalatan® (latanoprost, a PGF<sub>2α</sub> analog; Pfizer Inc.) for glaucoma in 1996.

In 1989, Shuh Narumiya's group solved partial amino-acid sequences of a human TX receptor (TP/TBXA2R) [113] using a TP-selective antagonist S-145 synthesized by Hitoshi Arita at Shionogi & Co., Ltd. [114]. Just a few weeks after the PAFR report in 1991 (see below), they succeeded in cloning the TBXA2R gene by screening a cDNA library of human megakaryocytic leukemia cells using an oligonucleotide probe design based on the amino-acid sequence [19]. PGE receptors had been pharmacologically subdivided into EP<sub>1</sub>, EP<sub>2</sub>, and EP<sub>3</sub>, which were cloned one after another by a Japanese group (Shuh Narumiya, Atsushi Ichikawa, Manabu Negishi, Yukihiko Sugimoto, et al.). In 1992, the first PGE receptor, EP<sub>3</sub>/PTGER3, was cloned from a mouse cDNA library by PCR based on the sequence of human TBXA2R [20]. In 1993, EP<sub>2</sub>/PTGER2 and EP<sub>1</sub>/PTGER1 were cloned by hybridization with the mouse EP<sub>3</sub> cDNA and TP cDNA, respectively [22, 23]. Subsequently, the PGF receptor (FP/PTGFR) was cloned in 1994 [27]. In the same year, PGI (prostacyclin) receptor (IP/PTGIR) was independently cloned by groups in Japan [28, 29] and Merck & Co. [30] using PCR and hybridization methods. PGD receptor  $(DP_1/PTGDR)$  was cloned by the Japanese group in 1994 [31] and by Merck's group in 1995 [32]. In 2001, a GPCR originally cloned as a type 2 helper T cell (Th2)-specific receptor (CRTH2, chemoattractant receptorhomologous molecule expressed on Th2 cells) was identified as the second PGD receptor  $(DP_2/PTGDR2)$  [52]. DP<sub>2</sub> has no significant homology in amino acid sequence with DP or all other PG receptors. Structures of TP [89], DP<sub>2</sub> [90], EP<sub>3</sub> [91], and EP<sub>4</sub> [92] were solved in complex with their antagonists.

## 10.2.2 Leukotriene, HETE, and Oxoeicosanoid Receptors (BLT<sub>1, 2</sub>, CysLT<sub>1,2,3</sub>, GPR31, GPR39, OXER<sub>1</sub>)

Leukotrienes (LTs) are also derived from AA by the action of 5-lipoxygenase (5-LOX/ALOX5). Lipoxygenases (12-LOX/ALOX12, 15-LOX/ALOX15, eLOX3/ALOXE3) produce hydroxyeicosatetraenoic acids (HETEs) that are further oxidized to oxoeicosanoids. 5-LOX metabolize AA to produce the intermediate metabolite, 5-hydroepoxy eicosatetoraenoic acid (5-HpETE), that are further metabolized to unstable LTA<sub>4</sub> and 5-HETE. LTA<sub>4</sub> is metabolized to LTB<sub>4</sub> by LTA<sub>4</sub> hydrolase and to cysteinyl LTs (cys-LTs, particularly LTC<sub>4</sub> by LTC<sub>4</sub> synthase). Here, we introduce the identification history of leukotriene and related lipid receptors.

 $LTB_4$  receptors (BLT<sub>1,2</sub>) – Leukotrienes ("leuko" = leukocytes, "trienes" = the three conjugated double bonds in the chemical structures) were introduced by *Bengt I. Samuelsson* [115] whose group identified a chemical structure of leukotriene  $B_4$  (LTB<sub>4</sub>: 5(S),12(R)-dihydroxy-6Z,8E,10E,14Z-eicosatetranoic acid) using <sup>14</sup>C-labeled arachidonic acid in 1979 [116]. After 18 years, the first  $LTB_4$  receptor  $(BLT_1/LTB4R)$ was cloned by Takehiko Yokomizo in Takao Shimizu's group by using a subtraction strategy between retinoic acid-differentiated vs. undifferentiated HL-60 cells [40]. In 2000, they also cloned the second, lower affinity LTB<sub>4</sub> receptor  $(BLT_2/LTB4R2)$  from the promotor region of LTB4R [117]. They also showed that hydrosxyeicosanoids (12-HETE and 15-HETE) could bind with  $BLT_2$  but not  $BLT_1$  [49]. Their continuing efforts result in the identification of a natural, high affinity ligand for BLT<sub>2</sub>, which is 12-HHT (12(S)-Hydroxyheptadeca-5Z,8E,10E-trienoic acid), an equimolar product of thromboxane synthase [68]. In 2018, the crystal structure of  $BLT_1$ in complex with the antagonist (BIIL260) was reported [88].

*Cys-LT receptors* (CysLT<sub>1,2,3</sub>) – In 1938, *Wilhelm Feldberg* and *Charles Kellaway* reported a slow and sustained contraction of smooth muscles by substances produced after antigen challenge [118]. In 1959, K. Frank Austen and Walter Brocklehurst termed them as a slow-reacting substance of anaphylaxis (SRS-A) that is separated from the activity of histamine [119]. In 1973, Fisons Ltd. (currently Sanofi) developed an SRS-A antagonist (FPL 55712) [120]. In 1979, Robert Murphy, Sven Hammarström, and Bengt I. Samuelsson identified the SRS-A as a cysteinecontaining derivative of 5-hydroxy-7,9,11,14icosatetraenoic acid (leukotriene C) [121]. In the following year, E.J. Corey's group established a full structure of the SRS-A as 5(S)-hydroxy-6(R)-glutathionyl-7,9-trans-11,14-ciseicosatetraenoic acid, and named LTC<sub>4</sub> [122]. Finally, three bioactive cys-LTs (LTC<sub>4</sub>, LTD<sub>4</sub>, and  $LTE_4$ ) were found to constitute SRS-A [122]. Pharmacological studies of FPL 55712, which showed selectivity against LTD<sub>4</sub> and LTE<sub>4</sub> as compared to LTC<sub>4</sub> [123, 124], predicted at least 2 cys-LT receptors existed in mammalian tissues [125]. SRS-A antagonists, particularly inhibiting the actions of  $LTD_4$ , were expected to be potent anti-asthmatic drugs. Before the cloning of the cys-LT receptors, three drugs were clinically applied to treat asthma. Ono Pharmaceutical Co., Ltd. launched a program in 1981 to develop cys-LT receptor antagonists for clinical application. Pranlukast (ONO-1078) was developed from a lead compound in 1985 [126, 127], entered a phase I clinical trial in 1986, and placed on the market as Onon<sup>TM</sup> in 1995 in Japan for the first time in the world. In 1996, zafirulukast (Accolate<sup>TM</sup>, AstraZeneca) was approved by the Food and Drug Administration (FDA) in the United States (US), followed by montelukast (Singulair®, Merck & Co.) approval in 1998. In 1999, Jilly F. Evans and colleagues identified the first cys-LT receptor, CysLT<sub>1</sub>/CYSLTR1 from an expressed sequence tag (EST) entry (GenBank) based on the identity to BLT<sub>1</sub> [44]. CysLT<sub>1</sub> shows a preference for LTD<sub>4</sub> whose action is inhibited by anti-asthmatic drugs. In 2000, they also cloned CysLT<sub>2</sub>/CYSLTR2 that binds to cys-LTs  $(LTC_4 = LTD_4 > > LTE_4)$  [50]. GPR99 was originally described as an orphan GPCR with homology to the P2Y subfamily [128], whose ligand 2-oxoglutarate was reported in 2004 [129]. Although its affinity was in the high micromolar range, a committee for Receptor Nomenclature and Drug Classification (NC-IUPHAR) pairs GPR99 and 2-oxoglutarate and named GPR99 as OXGR1 with its close family GPR91 as succinate receptor, SUCNR1 [130]. However, in 2013, Yoshihide Kanaoka and K. Frank Austen identified GPR99 as the third cys-LT receptor that shows preference for LTE<sub>4</sub> with an affinity in the low nanomolar range [75]. They also showed that LTE<sub>4</sub>-induced vascular leakage was prevented in **GPR99-deficient** mice. indicating that CysLT<sub>3</sub>/CYSLTR3 is an appropriate nomenclature for GPR99. In 2019, the crystal structure of CysLT<sub>1</sub> in complex with the antagonists (zafirlukast and pranlukast) [95] and the crystal structure of CysLT2 in complex with the antagonists (ONO-2570366, ONO-2770372, and ONO-2080365) were reported [97].

HETE receptor (12-HETER/GPR31, **GPR39**) – Kenneth V. Honn's group studied how 12-HETE regulates PC3 prostate cancer cell survival, growth, and angiogenesis [131–133]. PC3 cells showed binding with radiolabeled 12-HETE, suggesting its specific receptor existed. In 2011, they screened the binding efficacy of membrane fractions to 16 candidate GPCRs transfected CHO cells, which identified GPR31 as a 12-HETE receptor (12-HETER) [73]. GPR31 showed specific binding with 12(S)-HETE, while its enantiomer, 12(R)-HETE, did not show any binding. In 2018, Alkayed N.J. et al. reported that GPR39 is activated by 15-HETE, which is inhibited by 14,15-epoxyeicosatrienoate (14,15-EET) [134]. GPR39 belonging to the ghrelin receptor family was proposed to be activated by a peptide derived from the ghrelin precursor, obestatin [135], and it was controversial [136]. Later, *Holst* B. et al. reported that zinc ions induce GPR39 signaling including IP and cAMP accumulation [137]. Alkayed N.J. et al. showed zinc ion potentiates the effect of 15-HETE on Ca<sup>2+</sup> mobilization. Since no specific binding between 15-HETE vs. GPR39 has been provided, further studies are needed to confirm this binding partner.

*Oxoeicosanoid receptor* (OXER<sub>1</sub>/GPR170) – In 1992, 5-hydroxyeicosanoid dehydrogenase was found to metabolize 5-HETE to the oxidized form, 5-oxo-ETE [138]. Soon after, the potent chemoattractant activity of 5-oxo-ETE was reported in many kinds of leukocytes [139]. Between 2002 and 2003, three independent groups identified the 5-oxo-ETE receptor (OXER<sub>1</sub>/OXER1) [53–55]. Tatsuya Haga's group identified 50 GPCR candidate genes in 2002 [140]. Among them, GPCR48 was characterized as a 5-oxo-ETE receptor through screening of ~1000 natural and synthetic compounds in a GTP- $\gamma$ S binding assay using a GPCR48-G $\alpha_{i1}$ fusion protein [55]. A group of Tanabe Seiyaku Co., Ltd. identified the TG1019 gene by querying a BLAST database with a consensus sequence for the peptide ligand GPCR [53]. They screened a natural bioactive compound library and found 5-oxo-ETE as a ligand for TG1019. Novartis cloned the same gene (named R527) and identified the ligand from an ~2000 agonist library using a Ca<sup>2+</sup> assay in HEK293 cells stably expressing R527 and  $G\alpha_{16}$  [54].

# 10.2.3 Specialized Pro-Resolving Mediator (SPM) Receptors (ALX, DRV<sub>1,2</sub>, ERV<sub>1</sub>)

SPMs are a new class of lipid mediators derived from polyunsaturated fatty acids (PUFA) by the action of LOs, COXs, and cytochrome P450 monooxygenase enzymes. SPMs (lipoxins, resolvins, protectins/neuroprotectins, maresins) orchestrate the resolution of inflammation [141– 145]. There are many excellent reviews available by *Charles Serhan* [145–151].

*Lipoxin receptor* (ALX/FPR2) – Lipoxins (LXA<sub>4</sub> and LXB<sub>4</sub>), discovered by *Charles Serhan*, *Mats Hamberg*, and *Bengt I. Samuelsson* in 1984, are AA metabolites containing three hydroxy residues and four double bonds [147]. In 1994, based on the observation that LXA<sub>4</sub> exhibited a specific binding in human neutrophils and differentiated HL-60 cells, *Charles Serhan's* group cloned a HL-60-derived cDNA encoding a GPCR (*ALX/FPR2*) that displayed a high homology to the N-Formylmethionine-leucylphenylalanine (FMLP) receptor (FRP1) [33],

which was previously cloned as an FRP1 homolog in 1992 [152–154]. ALX/FRP2 overexpression in CHO cells showed a specific binding to LXA<sub>4</sub>, GTP hydrolysis, and AA release [33]. Although contradictory results about LXA<sub>4</sub>-ALX/FPR2 pairing have been reported, LXA<sub>4</sub>dependent pro-resolving effects were not observed in *Fpr2/Fpr3* double-knockout mice [139, 155].

Resolvin (ERV1/CMKLR1, receptors DRV1/GPR32, DRV2/GPR18) – Resolvins (E-, D- and T-series) are metabolites of  $\omega$ -3 PUFA (EPA, eicosapentaenoic acid and DHA, docosahexaenoic acid) and n-3 DPA (docosapentaenoic acid), respectively [146]. In 2005, Makoto Arita in Charles Serhan's group screened 10 GPCRs closely related to ALX by luciferase assay, resulting in the identification of ChemR23 (CMKLR1, chemokine like receptor 1) as a resolvin E1 (RvE1) receptor [62]. ChemR23 was originally identified as a receptor for a chemoattractant, chemerin, in 2003 [156]. Arita M. et al. also reported the specific ERV<sub>1</sub>/ChemR23 binding of RvE1 to  $(Kd = \sim 11 \text{ nM})$  and the inhibitory effects of RvE1 on dendritic cell functions [62]. In 2010, Charles Serhan's group showed a specific binding of resolvin D1 (RvD1) on the membrane fraction of human leukocytes [71]. Screening of 8 GPCRs by luciferase assay, and further validation by  $\beta$ -arrestin assay, identified that RvD1 directly acts at DRV1/GPR32 and ALX. In 2015, Nan Chiang in Charles Serhan's group identified GPR18 as resolvin D2 (RvD2) receptors by screening 77 orphan GPCRs with a  $\beta$ -arrestin assay [77]. They showed specific binding of RvD2 to DRV2/GPR18 (Kd =  $\sim 10$  nM). Furthermore, RvD2 limited infection-induced polymorphonuclear cell infiltration, which was lost in GPR18-deficient mice [77]. N-arachidonylglycine was originally reported as the endogenous ligand for GPR18 in 2006 [157]. Other groups proposed that N-palmitoylglycine or cannabinoids could activate GPR18 [158, 159]. However, β-arrestin or TGF-a shedding assay did not support these results [74, 160], and constitutive activity of GPR18 was reported [161].

## 10.2.4 Lysophospholipid Receptors (LPA<sub>1,2,3,4,5,6</sub>, lysoPS<sub>1,2,2L,3</sub>, GPR55/LPI<sub>1</sub>)

Lysophospholipids, such as lysophosphatidic acid (LPA, 1 or 2-acyl-sn-glycero-3-phosphate), lysophosphatidylserine (lysoPS), lysophosphatidylinositol (LPI), and lysophosphatidylcholine (LPC), are phospholipids in which one acyl chain is replaced with a hydroxy group. Here we provide a brief history of lysophospholipid receptors.

LPA receptors (LPA<sub>1,2,3,4,5,6</sub>) – Biological activity of LPA was reported in the early 1960s. Tokumura A. et al. first isolated LPA from soybeans in 1978 [162]. In 1989, Wouter H. Moolenaar's group proposed the involvement of G proteins in LPA-induced cell proliferation [163]. In 1996, Jerold Chun's group reported the first LPA receptor (LPA<sub>1</sub>/LPAR1) [37]. His group cloned cDNAs in neocortical cell lines by using primers for the 2nd and 7th transmembrane domains (TM II and TM VII) of known GPCR sequences. One of the cDNAs was uniquely expressed in the embryonic neuroproliferative layer of the cerebral cortex, which was originally ventricular zone gene-1 named (VZG-1).Overexpression of VZG-1 induced cell rounding in the presence of a heat-stable serum factor – LPA. VZG-1 was identical to the endothelium differentiation gene (EDG-2) cloned in 1995 [36] based on the sequence similarity with edg-1 cloned by Timothy Hla and Thomas Maciag in 1990 [17], which is now known as sphingosine 1-phosphate (S1P) receptor 1 (S1P<sub>1</sub>/S1PR1). The binding affinity (K<sub>D</sub>) of 1-oleoyl-LPA to LPA<sub>1</sub> was estimated as subnanomolar range [164]. In 1998, Edward J. Goetzl's group cloned EDG-4 from the EST entry (GenBank) based on the identity of EDG-2/VZG-1 [42] and characterized it as LPA<sub>2</sub>/LPAR2. In 1999, Junken Aoki in Keizo Inoue's group cloned EDG-7 from cDNAs of human Jurkat cells by using primer pairs for TM II and TM VI of *EDG-2* and *EDG-4*, which was characterized as LPA<sub>3</sub>/LPAR3 [45]. In 2003, Takao Shimizu's group screened a bioactive lipid library in orphan GPCR-expressing cells, resulting in deorphanization of P2RY5/GPR23 as the fourth LPA receptor (LPA<sub>4</sub>/LPAR4) that is structurally distinct from the EDG family of LPA receptors [58]. In 2006, Jerold Chun's group identified GPR92 as LPA5/LPAR5 through an unbiased screen of LPA-dependent cytoskeletal changes in cDNA library transfected cells [65]. In 2008, genetic and mutation screening of hypotrichosis simplex identified homozygous truncating mutations in P2RY5 which was proposed as a sixth LPA receptor [69, 70]. In the following year, Keisuke Yanagida in Takao Shimizu's group confirmed P2RY5 as LPA<sub>6</sub>/LPAR6 that couples to  $G\alpha_{12/13}$  with preferential binding to 2-acyl-LPA [165]. In 2015, the structure of LPA<sub>1</sub> in complex with antagonists (ONO-9780307, ONO-9910539, and ONO-3080573) was reported [81]. In 2017, LPA<sub>6</sub> structure was solved in the absence of any ligands [85].

LysoPS receptors (LysoPS<sub>1,2,2L,3</sub>) - In 2006, researchers of Takeda Pharmaceutical Co., Ltd. reported that GPR34 is a receptor for lysoPS that inhibits forskolin-induced cAMP accumulation and induces degranulation in mast cells [66]. In 2012, Junken Aoki's group confirmed that GPR34 is a lysoPS receptor with a ligand preference to 2-acyl-LysoPS [166]. In 2012, Asuka Inoue in Junken Aoki's group developed a TGF-a shedding assay that identified three additional lysoPS receptors: P2RY10, A630033H20, and GPR174 [74]. They proposed that GPR34, P2RY10, A630033H20, and GPR174 be designated as LPS<sub>1</sub>, LPS<sub>2</sub>, LPS<sub>2L</sub>, and LPS<sub>3</sub>, respectively [167]. However, to avoid confusion with lipopolysaccharide which is commonly referred to and widely used as "LPS; lipopolysaccharide," we used lysoPS1, lysoPS2, lysoPS2L, and lysoPS3 in the IUPHAR review [168].

LPI receptor (GPR55/LPI<sub>1</sub>) – GPR55 was identified from the EST database and cloned in 1999 [169]. In 2007, GlaxoSmithKline and AstraZeneca independently proposed that GPR55 as the third cannabinoid receptor [170–172]. GlaxoSmithKline showed GPR55 binds to an abnormal cannabidiol (Abn-CBD), a synthetic regioisomer of cannabidiol, using a GTP- $\gamma$ S assay, while GPR55-deficiency in mice did not alter Abn-CBD-induced lowering of mean arterial pressure in wild-type mice [171]. AstraZeneca showed a direct binding of endocannabinoids,  $\Delta^9$ -THC, and synthetic cannabinoids like CP55940 through a GTP- $\gamma$ S assay [172]. In the same year, Oka S. et al. reported that LPI induces ERK phosphorylation and intracellular Ca<sup>2+</sup> mobilization via GPR55 [67]. They also found that 2-arachidonoyl-LPI had greater activity in ERK phosphorylation than other LPI species [173]. In 2009, an assay that detects  $\beta$ -arrestin recruitment to the ligand-binding GPCR confirmed an agonistic activity of a CB1 antagonist/ inverse agonist, AM251 [160]. A TGF- $\alpha$  shedding assay revealed that LPI signaling through GPR55 preferably coupled with  $G\alpha_{13}$  rather than  $G\alpha_{12}$  [74]. In 2015, a TGF- $\alpha$  shedding assay revealed lysophosphatidylglucoside as an endogenous ligand for GPR55, which showed a tenfold lower  $EC_{50}$  than LPI [76].

# 10.2.5 Sphingosine 1-Phosphate Receptors (S1P<sub>1,2,3,4,5</sub>)

In 1991, Sarah Spiegel's group first reported that S1P induces cellular proliferation and intracellular Ca<sup>2+</sup> mobilization [174]. In 1990, *Timothy Hla* and Thomas Maciag cloned a gene, EDG-1, from human endothelial cells by differential hybridization between quiescent vs. differentiated endothelium [17, 175], which contains seven transmembrane domains with structural similarities to GPCRs. In 1993-94, two groups independently cloned a gene encoding GPCR (AGR16 or H218), later termed EDG-5 [25, 26], and currently known as S1P<sub>2</sub>/S1PR2. In 1996, EDG-3 was cloned by PCR with degenerate primers designed from  $CB_1$  sequences [38], which is now designated as S1P<sub>3</sub>/S1PR3. In 1997, Edward J. Goetzl's group revealed that S1P induces intracellular signaling via EDG-5 and EDG-3 [39]. In 1998, Timothy Hla's group identified that a heatstable serum-borne lipid, S1P, induced cell-cell aggregates in EDG-1 overexpressing cells, bound to EDG-1 with high affinity (Kd =  $\sim 8$  nM), and induced receptor internalization [41]. EDG-1 was designated as  $S1P_1/S1PR1$ . In the same year,

EDG-6 was cloned from in vitro differentiated dendritic cells by PCR [43]. In 2000, two groups including Kirin Brewery Co., Ltd. and Sarah Spiegel independently reported EDG-6 as the fourth S1P receptor  $(S1P_4/S1PR4)$  [47, 48]. Also, Kevin R. Lynch's group cloned EDG-8 and characterized it as S1P receptor (S1P<sub>5</sub>/S1PR5) by a binding assay and cAMP accumulation [51]. In 2012, S1P<sub>1</sub> structure in complex with an antagonist (ML056) was reported as the first lipid GPCR structure [79]. One of the most important drug discovery contributions from the sphingolipid biology field was the development of fingolimod (Gilenya®, Novartis International AG) for relapsing-remitting multiple sclerosis (MS). We have reviewed S1P receptor modulators including fingolimod and siponimod (Mayzent®, Novartis International AG) [176–179].

#### 10.2.6 Cannabinoid Receptors (CB<sub>1,2</sub>)

or marijuana (Cannabis sativa, Cannabis Cannabis *indica*, and *Cannabis* ruderalis), belonging to the Cannabaceae family of the Plantae Kingdom, is one of the oldest cultivated plants in Asia and it was grown for industrial (as hemp), medicinal, recreational, and ritual purposes since the third millennium BCE (Before the Common Era). The Greek historian Herodotus recorded cannabis usage in his book, "The Histories" in the 5th BCE, which is the oldest reported record regarding the practice of smoking or inhaling cannabis fumes [180]. A recent study scientifically verified evidence for psychoactive compound-containing cannabis smoking in western China beginning at least 2500 years The world's oldest Chinese ago [181]. Pharmacopeia "Shennong Ben Ts'ao King" described the use of cannabis achenes (seeds) as a laxative for over 1800 years [182]. In 1899, Thomas Wood and colleagues first isolated cannabinol (CBN), a metabolite of tetrahydrocannabinol (THC). In 1940, the full structure of CBN and its total synthesis was reported by two independent groups in United Kingdom (Lord Alexander R. Todd, who won the Nobel Prize in Chemistry in 1957) [183], and in USA (Roger Adams) [184]. In 1961, to combat drug abuse (cannabis, heroin, opium, cocaine, etc.), the United Nations drew up a treaty, "Single Convention on Narcotic Drugs," [185] making these drugs illegal. Several countries (Netherlands, Spain, Canada, and several states in the USA) have more recently legalized the recreational use of marijuana. In 1964, Yechiel Gaoni and Raphael Mechoulam isolated and defined the full structure of  $\Delta^9$ -THC from hashish (a resin of cannabis) [186]. Since then, the pharmacological actions of cannabis components have been investigated thoroughly [187]. In 1990, a research group in the National Institute of Mental Health, USA, cloned a first cannabinoid receptor  $(CB_1)$  from a rat cerebral cortex cDNA library using an oligonucleotide probe derived from the sequence of bovine substance-K receptor [16]. The major psychoactive cannabinoid in marijuana ( $\Delta^9$ -THC) and its synthetic analogue (CP 55940) inhibited forskolin-stimulated cAMP accumulation in CHO-K1 cells stably expressing rat CB<sub>1</sub>. However, endogenous ligands remained unknown until 1992 when William Devane and Raphael Mechoulam discovered the anandamide (N-arachidonoyl-ethanolamine, AEA) as a lipophilic endogenous ligand (endocannabinoid) for  $CB_1/CNR1$  [21], although cannabinoids are highly hydrophilic molecules. Munro S. et al. identified the peripheral cannabinoid receptor, CB<sub>2</sub>/CNR2, using a cDNA library of human leukemic cell line HL60 in 1993, which showed a displacement of the radioactive chemical compound by  $\Delta^9$ -THC as well as AEA [24]. Another endocannabinoid, 2-arachidonoyl-glycerol (2-AG), was independently reported by Mechoulam R. et al. and Sugiura T. et al. in 1995 [34, 35]. CB<sub>1</sub> structure was solved in complex with antagonists (AM6538 [82], AM841, AM11542 [83], and taranabant [84] in 2016-2017, MDMB-Fubinaca with  $G\alpha_i$  protein in 2019 [93]), and CB<sub>2</sub> in complex with an antagonist (AM10257) in 2019 [94]. Most recently, the CB<sub>1</sub> structure in complex with a negative allosteric modulator, ORG27569, and an agonist, CP55940, was reported [96].

## 10.2.7 Platelet-Activating Factor (PAF) Receptor (PAFR)

PAF was first proposed in 1972 by Jacques Benveniste, which induced histamine release from platelets [188]. In 1979, the chemical structure of PAF was determined as 1-O-alkyl-2-acetyl-snglyceryl-3-phosphorylcholine by Donald Hanahan [189]. PAF is produced from LPC by the action of acetyltransferase which was cloned by Hideo Shindou in Takao Shimizu's group in 2007 [190]. PAF-dependent phospholipase C activation through G proteins implied the presence of a receptor for PAF [191]. In 1991, Takao Shimizu's group discovered PAFR/PTAFR through functional cloning using electrophysiological detection in Xenopus laevis oocytes that expressed a guinea-pig lung cDNA library [18]. PAFR was identified as a GPCR with 7TM. Given the fact that no endogenous ligands were known when  $CB_1$  was cloned, PAFR is among the first to be a cloned lipid GPCR. A dual histamine H1 receptor and PAFR antagonist, rupatadine (Rupall<sup>™</sup>, Pediapharm Inc.), has been on the market in Canada since 2017. The crystal structure of human PAFR in complex with antagonists (SR 27417 and ABT491) was reported in 2018 [87].

## 10.2.8 Free Fatty Acid (FFA) Receptors (FFA1,2,3,4)

*Sawzdargo M.* et al. identified a group of intronless genes (FFA1/*GPR40*, FFA3/*GPR41*, *GPR42* and FFA2/*GPR43*) located in tandem at human chromosome 19q13.1 [192]. In 2003, Takeda Pharmaceutical Co., Ltd. and GlaxoSmithKline independently reported that FFAs are the endogenous ligands for an orphan GPR40 [59, 60]. Takeda Pharmaceutical Co., Ltd. screened over 1000 chemical compounds on CHO cells transiently expressing GPR40 in intracellular Ca<sup>2+</sup> mobilization, resulting in the identification of long-chain FFAs [60]. They also showed that FFAs amplify glucose-stimulated insulin secre-

tion (GSIS) from pancreatic  $\beta$  cells through FFA1/GPR40. Takeda Pharmaceutical Co., Ltd. synthesized a GPR40-selective ago-allosteric agonist, TAK-875 (fasiglifam), as a novel glucose-dependent insulin secretagogues [193], which acts as an ago-allosteric modulator of GPR40 [194]. Clinical trials of fasiglifam in type 2 diabetes showed positive results on reducing glycated hemoglobin HbA1c with minimum risk of hypoglycemia [195], while its development was terminated due to concerns about liver safety [196]. GlaxoSmithKline applied the same strategy in HEK293 cells with an agonist library of ~1500 known and putative natural GPCRs [59]. They also identified GPR41 and GPR43 as additional FFA receptors [61]. A pheromone pathwayresponsive FUS1-lacZ reporter assay in yeast (Saccharomyces cerevisiae) expressing GPR43 was used to screen the compound library, which identified several compounds containing acetate counterions activated by GPR43. Further investigation demonstrated that short chain carboxylic acids activate not only GPR43 but also GPR41. Although GPR42 lacked responses against carboxylate ligands, a single amino acid mutation (W174R) in GPR42 restored responses to propionate. GPR42 still remains as Class A orphan GPCR. In 2003, a database search in the human genome revealed seven evolutionarily conserved Class A GPCRs including GPR120 [197]. In 2005, Gozoh Tsujimoto's group screened over 1000 chemical compounds in HEK293 cells stably expressing FFA4/GPR120-enhanced green fluorescent protein (EGFP) and assessed receptor internalization with a high content screening system [63]. They identified that long-chain FFAs induced intracellular Ca<sup>2+</sup> signals, ERK phos-FFA4/GPR120-expressing phorylation in HEK293 cells, and glucagon-like peptide-1 (GLP-1) secretion in intestinal endocrine cells. FFA receptor-targeted drug discovery was summarized in a recent review [198]. FFA1 structure was solved in complex with agonists (TAK-875, MK-8666, and AgoPAM AP8), which revealed two distinct allosteric binding sites [80, 86].

## 10.2.9 Sterol Lipid GPCRs (GPER, GPBA, MRGPRX4, EBI2)

To date, three receptors in Class A GPCRs have been proposed as sterol lipid receptors as follows:

Estrogen receptor (GPER/GPR30) -The biological functions of estrogen have been wellstudied, particularly in the female reproductive system. Many actions of estrogen are mediated via the nuclear estrogen receptors (ER) from which the first ER $\alpha$  was cloned [199, 200] after 30 years following the first evidence of ER presented by Elwood V. Jensen in the 1950s [201]. Subsequently, the second nuclear ER (ER $\beta$ ) was cloned in 1985. In the late 1960s, Clara M. Szego showed that acute estrogen exposure increased uterine cAMP production [202], which was inhibited by glucocorticoids and  $\beta$  blockers [203, 204]. She also reported estrogen receptors in plasma membrane fractions and partial purification of the receptor [205]. In 2005 GPR30, that was cloned from an orphan GPCR in 1997, was identified as the third and the first transmembrane ER by Eric R. Prossnitz [64]. They showed that GPR30 was uniquely localized to the endoplasmic reticulum.  $17\beta$  estradiol binds to the receptor  $(K_i = 6.6 \text{ nM})$  and transduces intracellular Ca<sup>2+</sup>  $(EC_{50} = 0.5 \text{ nM})$  and phosphatidylinositol 3,4,5-trisphosphate (PIP<sub>3</sub>) signaling via GPR30. Data supporting the pairing between estrogen vs. GPR30 led to its designation as a G proteincoupled estrogen receptor (GPER) by the IUPHAR in 2007 [206].

*Bile acid receptor* (GPBA/GPR131, MRGPRX4) – Bile acids are mixtures of amphipathic steroid acids that are produced by the liver, stored in the gallbladder, and their homeostasis is controlled by enterohepatic circulation [207]. Bile acids facilitate digestion and absorption of lipids as digestive surfactants. In 1999, the farnesoid X receptor (FXR) was identified as a nuclear bile acid receptor that controls bile acid synthesis [208]. In 2002–2003, Banyu Pharmaceutical Co., Ltd. and Takeda Chemical Industries, Ltd., independently reported that bile acids increase intracellular cAMP levels via a GPCR, BG37 [56] or TGR5 [57], both now known as G protein-coupled bile acid receptor (GPBA). GPBA plays roles in the control of glucose homeostasis, inflammation, etc. [209]. In 2019, an additional bile acid receptor was reported by two independent groups [210, 211]. Both groups identified that bile acids elicited Ca2+ signals in neurons via MRGPRX4  $(EC_{50} = \sim 5 \mu M)$ . They proposed that bile acidsinduced itch in humans (cholestatic itch) is independent from histamine and GPBA, and dependent on MRGPRX4. These suggest that MRGPRX4 seems to be the second bile acid receptor. In addition to bile acids, the same group also reported that MRGPRX4 is a receptor for a heme metabolite, bilirubin, that is another major component of bile, which showed an EC<sub>50</sub> value of 61.9  $\mu$ M as determined by a Ca<sup>2+</sup> assay [212].

Oxysterol receptor (EBI2/GPR183)- In 2009, Jason G. Cyster's group reported that Epstein-Barr virus-induced gene 2 (EBI2, also known as GPR183) mediates B cell segregation between the outer and center follicle [213], while its endogenous ligand has not been determined. EBI2 was originally cloned from Burkitt's lymphoma cells, which are mainly expressed in B cells [214]. In 2011, EBI2 was identified as a receptor for oxysterol  $(7\alpha, 25$ dihydroxycholesterol,  $7\alpha$ ,25-OHC) [72]. Oxysterols induce intracellular Ca2+ mobilization via EBI2 with EC<sub>50</sub> values in a range of 2 nM to  $3 \,\mu\text{M}$  depending on the oxysterol species [72].

## 10.2.10 Perplexing Lipid GPCRs (GPR3, GPR6, GPR12, GPR35, GPR63, GPR84, GPR87, GPR119)

About ~25% of the Class A Rhodopsin family of GPCRs remain as orphan GPCRs whose endogenous ligands have not been determined. Lipid ligands for some of these receptors have been proposed, but additional studies are needed to confirm or reject the proposed ligand-receptor pairs.

GPR3, GPR6, GPR12, GPR63 - In 1993, GPR3 was cloned as GPCR21 by Saeki Y. et al. from a mouse brain cDNA library [215]. They also isolated GPR12 (GPCR01) [215] whose rat homolog was cloned in 1991 [216]. Human GPR3, GPR6, and GPR12 were isolated between 1994 and 1995 by three independent groups [217-219]. In 2002, Evi Kostenis's group reported that GPR3, GPR6, and GPR12 showed constitutive activation of adenylate cyclase in the presence of serum, while the constitutive activity was reduced by removing lipids by charcoal stripping [220]. They screened 200 bioactive lipids which resulted in the identification of S1P and dihydrosphingosine 1-phosphate (DHS1P) as ligands for these receptors. In the same year, H. Chica Schaller's group identified sphingosylphosphorylcholine (SPC) as a high-affinity ligand for GPR12 by  $Ca^{2+}$ signaling examining and GIRK (G-protein-gated inwardly rectifying  $K^+$ channel)-mediated inward currents in Xenopus oocytes [221]. They also reported S1P to be a high-affinity ligand for GPR6 [222]. However, other groups were not able to confirm these observations, which were not reproduced by  $\beta$ -arrestin assay [160]. In 2007, cannabidiol (CBD) was reported as an inverse agonist for GPR3 and GPR6 [223, 224]. In 2003, Evi Kostenis's group reported that S1P and dioleoylphosphatidic acid are low affinity ligands for GPR63 [225], but again the  $\beta$ -arrestin assay did not support this observation [160].

*GPR35* – In 2006, Kynurenic acid, a metabolite of L-tryptophan, was first reported as a ligand for GPR35 by screening of ~300 biochemical intermediates using an aequorin assay [226]. In 2010, *Oka S. et.al.* reported that 2-acyl-LPA activates intracellular Ca<sup>2+</sup> mobilization via GPR35 [227]. In 2012, a group in Corning Inc. reported the agonist activity of tyrosine metabolites [228]. Several surrogate ligands for GPR35 like zaprinast have been reported [229]. Controversy still remains about the endogenous ligand for GPR35.

GPR84, GPR87 – In 2001, GPR84, along with GPR86, GPR87, GPR90, and GPR91, was discovered by EST data mining [230]. Amgen Inc. reported medium chain fatty acids as ligands for GPR84 in 2006 [231]. Independent studies also supported the results by  $\beta$ -arrestin, cAMP, and Ca<sup>2+</sup> assays [229] or TGF- $\alpha$  shedding assay [74]. However, hydroxy fatty acids and 6-noctylaminouracil were proposed to activate GPR84 potently as compared to fatty acids [232]. In 2007, GPR87 was proposed as an LPA receptor [233], where the GPR87-G $\alpha_{16}$  fusion protein in CHO cells was used to determine the Ca<sup>2+</sup> mobilization (EC<sub>50</sub> =  $\sim$ 36 nM). Another group demonstrated the responses of GPR87 to 100 µM LPA by  $\beta$ -arrestin assay [234].

GPR119 – GPR119 was identified as one of ~60 novel GPCRs in 2002 [140]. In 2005, Yamanouchi Pharmaceutical Co. Ltd. (currently Astellas Pharma Inc.) reported GPR119 as a novel endogenous receptor for LPC, LPE, and LPI that induces insulin secretion from pancreatic  $\beta$ -cells [235]. In 2006, based on the homology between cannabinoid receptors vs. GPR119, Prosidion Limited/OSI Pharmaceuticals tested a series of cannabinoids and fatty-acid ethanolamides using a yeast fluorescent reporter assay, resulting in the identification of oleoylethanolamide as a ligand for GPR119 [236]. This was reproduced by a TGF- $\alpha$  shedding assay [74]. Then, in 2010, Arena Pharmaceuticals Inc. proposed that N-oleoyldopamine enhances glucose homeostasis via activation of GPR119-G $\alpha_s$  signaling [237]. Another group reported that 2-oleoyl glycerol and other 2-monoacylglycerols induces cAMP accumulation in GPR119expressing COS-7 cells [238]. Many pharmaceutical companies have tried to deorphanize GPR119 since receptor signaling is an attractive target for the treatment of type 2 diabetes and obesity [239]. However, all the identified ligands showed lower potency than other lipid-GPCR pairs, implying the existence of a real, natural ligand for GPR119.

# 10.2.11 Lipid GPCRs Belonging to the Class B2 Adhesion Family (ADGRB1, ADGRF1)

Among 33 Adhesion family GPCRs [240], two receptors have been proposed to bind with lipids as follows:

ADGRB1/BAI1 – ADGRB1/BAI1 was originally cloned as a p53-regulated gene in brain in 1997 [241]. In 2007, ADGRB1/BAI1 was discovered to be interacting with ELMO1 (engulfment and cell motility 1) [242] which promotes internalization of apoptotic cell corpses [243, 244]. Because thrombospondin type 1 repeats on the N-terminal of ADGRB1/BAI1 that binds with phosphatidylserine [242], it is proposed to be one of the receptors for the eat me signal exposed on apoptotic cells like Tim-4, Stabilin-2, CD300f, and RAGE [245].

ADGRF1/GPR110 - GPR110, and 7 other closely related GPCRs, were identified from the human genome database by hidden Markov models [246]. All contained a GPCR proteolytic site (GPS) domain in their N-termini [240]. In 2016, Lee J.W. et al. reported that ADGRF1/GPR110 is the receptor for N-docosahexaenoylethanolamine (they call it synaptamide) that binds to an extracellular N-terminus of ADGRF1/GPR110 [247]. The synaptamide-induced bioactivity via the receptor works in a cAMP-dependent manner [247]. Since only one group has reported this ligandreceptor interaction, further studies are needed to confirm this pairing.

## 10.3 Tidying-Up of Drugs Targeting Lipid GPCRs

GPCRs are attractive targets for drug discovery. According to a review by *Hauser A.S.* et al. in 2007 [248], the FDA approved 475 drugs (~34% of all FDA-approved drugs) targeting 108 unique GPCRs (~27% of non-olfactory GPCRs), which account for ~27% of the global market share of therapeutic drugs [248]. Most of the approved GPCR drugs (~77%) target opioid and amino-**GPCRs** (dopamine, acetylcholine, genic 5-hydroxytryptamine, histamine, adrenaline) [248]. Approved drugs targeting lipid GPCRs (Table 10.4) are curated from the GPCRdb [4, 5], while some drugs were omitted because they seem to be mistakenly registered in the DrugBank database [249]. Several lipid GPCRs have been crystalized with approved drugs, including EP<sub>3</sub> with misoprostol, TP with ramatroban, and  $CysLT_1$  with pranlukast (Fig. 10.2). There are 24 approved clinical drugs targeting pharmacologically well-characterized lipid GPCRs, of which 16 drugs are agonists for prostanoid or cannabinoid receptors (Table 10.4). The remaining 8 drugs are antagonists for TP, CysLT<sub>1</sub>, PAFR, and S1P<sub>1</sub>. For example, alprostadil is the pharmaceutical name of PGE<sub>1</sub> that was derived from dihomo-y-linolenic acid. Alprostadil (Caverject<sup>TM</sup>, Pfizer, approved in 1981; Muse<sup>TM</sup>, Meda Pharmaceuticals, approved in 1996) is used to treat erectile dysfunction in adult males. The mechanism of action (MOA) of alprostadil is similar but different from phosphodiesterase 5 (PDE5) inhibitors (sildenafil, Viagra®; avanafil, Stendra®; tadalafil, Cialis®; vardenafil, Levitra® or Staxyn®) that increase cGMP levels in smooth muscle. On the other hand, activation of the  $PGE_1$ receptor by alprostadil increases cAMP in smooth muscle cells, resulting in relaxation and penile erection formation. Considering the rank order of affinity of PGE<sub>1</sub> for the EPs  $(EP_3 = EP_4 > EP_2 > EP_1 = IP [252])$  and the receptor expression pattern, this efficacy might be mediated by  $EP_4$ .

The most recent (as of 2019) FDA-approved lipid GPCR drug is siponimod (Mayzent®, Novartis International AG) for the treatment of secondary progressive multiple sclerosis (SPMS) [253]. Siponimod, as well as fingolimod, functionally antagonize S1P<sub>1</sub> on lymphocytes, resulting in the sequestration of pathogenic lymphocytes in the peripheral lymphoid organs [254]. A major difference between siponimod vs.

Drugs	Types	Targets	MOA	Indications
Alprostadil (PGE <sub>1</sub> )	Small	$EP_1, EP_2,$	Agonist	Sexual dysfunction
	molecule	$EP_3, EP_4$	U U	
Misoprostol (PGE <sub>1</sub>	Small	$EP_3, EP_2^a$	Agonist	Anti-ulcer
analogue)	molecule	5, 2	0	
Dinoprostone (PGE <sub>2</sub> )	Small	<b>EP</b> <sub>1</sub> , <b>EP</b> <sub>2</sub> ,	Agonist	Abortifacient
	molecule	$EP_3, EP_4$		
Grapiprant	Small	EP.	Antagonist	Osteoarthritis (for dogs)
Grapiprani	molecule	L. 4	7 intugoinist	
Rimatoprost (PGF)	Prodrug	FP	Agonist	Antiglaucomic
analogue)	Trourug		rigomot	1 mughaconne
Carbonrost (PGF-	Small	FP	Agonist	Abortifacient
analogue)	molecule	II .	Agomst	Abortifacient
Latanonrost (PCF	Small	FD	Agonist	Antiglaucomic
analogue)	molecule	11	Agomst	Antigradeonne
Tafluprost (PCE	Small	FD	Agonist	Paduca intraccular pressure
analogua)	molecule	r i	Agomst	Reduce intraocular pressure
Transprost (DCE	Small	ED	Agonist	Antigloucomia
$(FGF_{2\alpha})$	moloculo	ГГ	Agoinst	Antigiauconnic
	Guall	TD	A	And:
Seratroaast	Small	IP	Antagonist	Anti-astimatic
	molecule	TD DD		A
Kamatroban	Small	$TP, DP_2$	Antagonist	Anti-allergic
	molecule	m		
$Epoprostenol (PGI_2)$	Small	IP	Agonist	Antihypertensive, platelet aggregation
	molecule	-	· · ·	inhibitor
$Iloprost (PGI_2 analogue)$	Small	IP	Agonist	Antihypertensive
	molecule			
Treprostinil (PGI <sub>2</sub>	Small	IP	Agonist	Antihypertensive
analogue)	molecule			
Selexipag	Small	IP	Agonist	Pulmonary arterial hypertension
	molecule			
Montelukast	Small	CysLT <sub>1</sub>	Antagonist	Anti-asthmatic
	molecule			
Pranlukast	Small	CysLT <sub>1</sub>	Antagonist	Anti-asthmatic
	molecule			
Zafirlukast	Small	CysLT <sub>1</sub>	Antagonist	Anti-asthmatic
	molecule			-
Fingolimod (Sphingosine	Prodrug	$S1P_1, S1P_3^a,$	Functional	Relapsing remitting multiple sclerosis
analogue)		$S1P_4^{a}, S1P_5^{a}$	antagonist	
Siponimod	Small	<b>S1P</b> <sub>1</sub> , <b>S1P</b> <sub>5</sub> <sup>a</sup>	Functional	Secondary progressive multiple
	molecule		antagonist	sclerosis
Dronabinol	Small	$CB_1, CB_2^a$	Agonist	Analgesics, appetite stimulant,
(Tetrahydrocannabinol)	molecule			antiemetics
Nabilone	Small	$CB_1, CB_2$	Agonist	Antiemetics
	molecule			
Cannabidiol	Plant	$CB_1, CB_2$	Agonist	Seizures associated with Lennox-
	extract			Gastaut syndrome or Dravet syndrome
	Small			
	molecule			
Rupatadine	Small	PAFR	Antagonist	Anti-allergic
	molecule			
Icosapent	Small	FFA1 <sup>a</sup>	Agonist	Hypertriglyceridemia
	molecule			

 Table 10.4
 Approved lipid GPCR drugs

<sup>a</sup>Secondary target



**Fig. 10.2** Lipid GPCR structures. Receptors are shown as cartoon representations and ligands are represented as spherical molecules. Surface representations in pink are binding pockets that were estimated using the HOLLOW program [250] with a spherical constraint, followed by manual extraction based on the existence of chemical

fingolimod is a receptor selectivity that siponimod selectively binds to  $S1P_1$  and  $S1P_5$  [255], while fingolimod binds to  $S1P_1$ ,  $S1P_3$ ,  $S1P_4$ , and  $S1P_5$ . Moreover, fingolimod is a pro-drug that requires *in vivo* phosphorylation by sphingosine kinases to bind with S1P receptors. There are many excellent reviews written by front-line researchers available [176, 177, 179, 256–259].

Lipid GPCR drugs currently tested in clinical trials are curated mainly from the GPCRdb [4, 5]. Among them, drugs deposited in clinicaltrials.

compounds. The volume (Å<sup>3</sup>), sphericity ( $\psi$ : a measure of how much the volume resembles a sphere;  $\psi = 1.0$  is an exact sphere), and effective radius ( $r_{eff}$ : a radius of a sphere with the same surface area to volume ratio) of these binding pockets are also provided, which were analyzed using the <sup>3</sup>V program [251]

gov are summarized in Table 10.5. Although the list may be inexhaustive, we found more than 100 trials testing 44 drugs targeting 19 lipid GPCRs. Many drugs are in Phase 3 clinical trials including DP<sub>2</sub> antagonists for asthma, IP agonists for pulmonary arterial hypertension (PAH), FP and EP<sub>2</sub> agonists for glaucoma and ocular hypertension, and S1P receptor modulators for MS, Cohn's disease, ulcerative colitis, etc. Also, 11 approved drugs are being tested for new or other indications such as alprostadil for cardiovascular

Table 10.	5 Lipid GPCR drugs in clin	vical trials as of	October 2019			
Target	Drugs	MOA	NCT number	Indications	Phase	Sponsor
EP1	Alprostadil	Agonist		Congenital heart disease, acute kidney injury, respiratory distress syndrome, etc.	1~4	Multiple sponsors
	ONO-8539	Antagonist	NCT01705275 NCT00876421	Glaucoma/ocular hypertension Overactive bladder	1° 2°	Ono Pharmaceutical Ono Pharmaceutical
EP <sub>2</sub>	DE-117	Agonist	NCT03697811 NCT03691649	Glaucoma/ocular hypertension Glaucoma/ocular hypertension	Зr Эг	Santen Santen
$\mathrm{EP}_4$	Grapiprant (ARY-007)	Antagonist	NCT03691662 NCT03696212 NCT03658772	Glaucoma/ocular hypertension Non-small cell lung cancer Microsatellite stable colorectal cancer	$3^r$ $1 \sim 2^r$ 1	Santen Arrys Therapuetics, etc. Arrys Therapuetics. etc
đĐ	PDC31	Antagonist	NCT01250587	Dysmenorrhea	1c 2c	PDC Biotech GmbH
	Latanoprostene BUNUD (BOL-303259-X, NCX116)	Agonist	NCT01749904 NCT01749930 NCT01895972	Glaucoma/ocular hypertension Glaucoma/ocular hypertension Glaucoma/ocular hypertension	ň ñ ň	Bausch & Lomb Incorporated Bausch & Lomb Incorporated Mount Sinai
			NCT03949244	Glaucoma	, <sub>1</sub> 4	Multiple sponsors
FP/EP <sub>3</sub>	Latanoprost Bimatoprost	Agonist Agonist		Glaucoma Glaucoma/ocular hypertension	2 ~ 4 2 ~ 4 4 4	Allergan Multiple sponsors
	ONO-9054	Agonist	NCT02083289	Glaucoma/ocular hypertension	3°	Ono Pharmaceutical
dI	Ifetroban (BMS180291)	Antagonist	NCT02682511 NCT03028350	Scleroderma Asthma, aspirin-induced	2r 2	Cumberland Pharmaceuticals Cumberland Pharmaceuticals
			NCT02216357 NCT01436500	Aspirin exacerbated respiratory disease (AERD) Hepatorenal syndrome	ъъ	Cumberland Pharmaceuticals Cumberland Pharmaceuticals
			NCT02802228	Portal hypertension/liver cirrhosis	5.5	Cumberland Pharmaceuticals
			NCT03694249 NCT03326063	Breast cancer Nasal polyps, asthma	5 5	Cumberland Pharmaceuticals Brigham and Women's Hospital
IP	Ralinepag	Agonist	NCT02279160	Pulmonary arterial hypertension (PAH)	2°	Arena Pharmaceuticals
	(APD811)		NCT02279745	PAH	$3^{a}$	United Therapeutics
			NCT03626688	PAH	<u>ب</u> ب	United Therapeutics
	Iloprost Selexipag	Agonist Agonist		Pulmonary hypertension Pulmonary hypertension	$1 \sim 4$ $1 \sim 4$	Multiple sponsors Actelion

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$\mathrm{DP}_2$	Fevipiprant	Antagonist	NCT03681093	Asthma	3r	Novartis
	(QAW U39)		NC103629249	Asthma	3	Novartis
	Setipiprant	Antagonist	NCT02781311	Alopecia	2°	Allergan
	(ACT-129968)	)	NCT01225315	A sthma	30	Idorsia Pharm
			NCT01484119	Alleroic rhinitis	ů Š	Idorsia Pharm.
	ADC3680	Antaconict	NCT01730027	Acthma	°C	Dulmagen Theraneutice
			17000/101010		1 6	
	0C459	Antagonist	NC102660489	Asthma/rhinovirus	7.	Chiesi Farmaceutici S.p.A.
	(OC000459)		NCT02002208	Eosinophilic asthma	5	Chiesi Farmaceutici S.p.A.
			NCT02560610	Atopic dermatitis	2°	Chiesi Farmaceutici S.p.A.
	ACT-774312	Antagonist	NCT03688555	Nasal polyposis	2r	Idorsia Pharm.
	ATX2417	Antagonist	NCT02316912	Asthma	1c	Chiesi Farmaceutici S.p.A.
	ARRY-502	Antagonist	NCT01561690	Asthma	2°	Array BioPharm
CysLT <sub>1</sub>	Montelukast	Antagonist	NCT03402503	Alzheimer's disease	2r	IntelGenx
		)	NCT03991988	Alzheimer's disease	2r	Emory Univ.
			NCT03545997	Sleen annea	$2^{\mathrm{r}}$	Universitaire de Grenoble
			NCT03109288	Multiple sclerosis	$1 \sim 2^{r}$	NIAID
LPA	`SAR100842	Antagonist	NCT01651143	Systemic sclerosis	2°	Sanofi
	BMS-986020	Antagonist	NCT01766817	Idiopathic pulmonary fibrosis	2°	Bristol-Myers Squibb
		)	NCT02588625	Scleroderma	2°	Bristol-Myers Squibb
	<sup>18</sup> F-BMS-986327	PET ligand	NCT04069143	Idiopathic pulmonary fibrosis	1 <sup>n</sup>	Bristol-Myers Squibb
S1P <sub>1</sub>	Fingolimod			Multiple sclerosis	3~4	Multiple sponsors
	(FTY720)		NCT03943498	Chemotherapy-induced peripheral	1r	Mavo Clinic and NCI
	×		NCT04088630	neuropathy. etc.	1.	Wake Forest University
			NCT03941743	Intracerebral hemorrhage (IHC)	1r	Mayo Clinic and NCI
	Sinonimod		NCT03623243	Breast carcinoma		Novartis
	(BAF312)		NCT03338998	Multiple sclerosis	5 C	Novartis
	Ozanimod		NCT02576717	Hemorrhagic stroke IHC	a c	Celtene
	(RPC1063)		NCT03440385	Multinle colerocie	5 6	Celtene
			NCT02435922	Crohn's disease	n tr	Celgene
	Domesimod		NCT02007177	Thornetive contractions	2 2	Actalion
			NCT02727072	Multino colorocio	2a	A stalion
	(M00071-174)		NCT01002376	Multiple selectors	n c	
			NICTOR DOLOG		1 -	Tereston Disconstruction
			CC77886010N	Multiple scierosis	Γ,	Janssen Fnarmaceuucais
	Cenerimod		NCT03742037	In patients receiving Propranolol	2r	Idorsia Pharmaceuticals
	Etrasimod		NCT03945188	Systemic lupus erythematosus	Э.	Arena Pharmaceuticals
	(APD334)		NCT03996369	Ulcerative colitis	$3^{\rm n}$	Arena Pharmaceuticals
			NCT03950232	Ulcerative colitis	$3^{\mathrm{n}}$	Arena Pharmaceuticals
	Amiselimod		NCT02389790	Ulcerative colitis	2°	Mitsubishi Tanabe Pharma
	(MT1303)		NCT01890655	Crohn's disease	5	Mitsubishi Tanabe Pharma
			NCT01987843	Multiple sclerosis	2°	Mitsubishi Tanabe Pharma
				Plaque psoriasis		
						(continued)

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Table 10.5	5 (continued)					
Target	Drugs	MOA	NCT number	Indications	Phase	Sponsor
CB <sub>1</sub> /	Cannabidiol	Agonist		Pain, epilepsy, Rett syndrome, anxiety	3 ma	Multiple sponsors
${ m CB}_2$	Dronabinol	Agonist		Pain, trichotillomania, PTSD, schizophrenia	3 ma	Multiple sponsors
	Cannabidivarin	Agonist	NCT03202303	Autism spectrum disorder (ASD)	2r	GW Research Ltd
	(GWP420006)	1	NCT03848481	Prader-Willi syndrome	$2^{\mathrm{n}}$	Montefiore Medical Center
	Nabilone	Agonist	NCT03251326	PTSD	$1 \sim 2^{c}$	NIDA
		1	NCT03773796	Parkinson's disease	Зг	Medical University Innsbruck
	RYI-018	MAb	NCT03261739	Nonalcoholic fatty liver disease	1c	Bird Rock Bio
$CB_2$	Lenabasum	Agonist	NCT03398837	Diffuse cutaneous systemic sclerosis	3ª	Corbus Pharmaceuticals
	(JBT-101)	1	NCT03813160	Dermatomyositis	Зг	Corbus Pharmaceuticals
			NCT03451045	Cystic fibrosis	2 <sup>r</sup>	Corbus Pharmaceuticals
PAFR	Rupatadine	Antagonist	NCT03770923	Rheumatoid arthritis	3 <sup>r</sup>	Sherief Abd-Elsalam, etc
ALX?	BLXA4-ME	Agonist?	NCT02342691	Gingival inflammation	$1 \sim 2^{a}$	NIDCR
	(lipoxin analog)					
ERV1?	RX-10045	Agonist?	NCT01675570	Dry eye syndrome	2°	C.T. Development America
$BLT_1$ ?	(Resolvin E <sub>1</sub> analog)		NCT01639846	Allergic conjunctivitis	2°	C.T. Development America
			NCT02329743	Inflammation/pain//cataract	2°	A.T. Resolve SARL
			NCT00799552	Dry eye syndrome	2°	Resolvyx Pharmaceuticals
DRV1?	Resolvin $D_1$	Agonist?	NCT03483311	Psoriasis		Cairo Univ.
GPR84	GLGP1205	Antagonist	NCT02337608	Ulcerative colitis	2°	Galapagos NV
			NCT03725852	Idiopathic pulmonary fibrosis	2 <sup>r</sup>	Galapagos NV
GPR84/	PBI-4050	Antagonist/	NCT03184584	Alström syndrome	$2^{\mathrm{a}}$	ProMetic Biosciences
FFA1		Agonist	NCT02538536	Idiopathic pulmonary fibrosis	2°	<b>ProMetic Biosciences</b>
			NCT02562573	Type 2 diabetes, metabolic syndrome	2°	ProMetic Biosciences
			NCT02955888	Cystic fibrosis	2t	<b>ProMetic Biosciences</b>
	PBI-4547	Antagonist/ Agonist	NCT04068259		1 r	ProMetic Biosciences
			-			

Bold italic drugs are approved drugs. "active, "completed, "not yet recruiting, "recruiting, 'terminated

diseases, montelukast for Alzheimer's disease and MS, fingolimod for neuropathy, intracerebral hemorrhage (IHC), and carcinoma, and rupatadine for arthritis (Table 10.5). Grapiprant is an orally bioavailable  $EP_4$  antagonist [260], which was approved by the FDA's Center for Veterinary Medicine for control of pain and inflammation in with canines associated osteoarthritis (Galliprant®, Aratana Therapeutics). Since PGE<sub>2</sub>-EP<sub>2</sub>/EP<sub>4</sub> signaling suppresses cytotoxic T lymphocyte survival and function [260, 261], a combination therapy of the anti-PD-1 (programmed cell death protein 1) antibody and an EP<sub>4</sub> antagonist was proposed as a treatment for cancer and chronic viral infections. Thus, the clinical trials for galliprant aim to treat patients with non-small cell lung cancer in combination with anti-PD-1 antibodies.

## 10.4 Lipid GPCR Drugs that Spark Joy!

In this section, some key concepts of GPCR pharmacology (allosteric modulation, biased agonism, and functional antagonism) are introduced as the next generation modes of drug action for lipid GPCR drug discovery. Also, monoclonal antibodies are introduced as promising biological drugs that could modulate lipid GPCR functions with higher selectivity than small molecules.

#### 10.4.1 Allosteric Modulators

According to the definition by IUPHAR [262], allosterism is a modification of the orthosteric ligand-induced protein's properties by another ligand that binds to the spatially distinct site (allosteric site). Allosteric modulators that increase or decrease the affinity and/or efficacy of orthosteric ligands are defined as positive or negative allosteric modulators (PAMs or NAMs), respectively. An allosteric ligand that does not alter the action of the orthosteric ligand is called a neutral allosteric ligand (NAL) or silent allosteric modulator (SAM). Allosteric agonists increase the protein activity independently of orthosteric ligand binding, whereas allosteric inverse agonists reduce it.

As of 2019, 34,371 allosteric drugs targeting GPCRs, which is 42% of total modulator entries, have been deposited in the Allosteric Database (ASD) [263]. About 1% (369 drugs) are under clinical development. ASD displayed 4 approved allosteric modulators targeting GPCRs including cinacalcet (PAM for calcium-sensing receptor), ticagrelor (reversible allosteric antagonist for P2Y12), and niclosamide (PAM for neuropeptide Y4 receptor). Ivermectin is listed in the ASD as an approved PAM for the  $GABA_B$  receptor. However, because it is reported as a modulator for the  $GABA_A$  receptor [264], it might be mistakenly deposited in the database. ASD listed 18 drugs targeting lipid GPCRs including CysLT<sub>1</sub>,  $CB_1$ ,  $CB_2$ , and FFA1.

The Protein Data Bank (PDB) is the archive of structural data of biological macromolecules including crystal structures of GPCRs in complex with allosteric ligands [265]. Allosteric sites for Class A GPCRs are widely distributed. For example, the M2 muscarinic acetylcholine receptor showed a binding of its allosteric modulator, LY2119629, on the extracellular vestibule just above the orthosteric agonist [266]. On the other hand, a NAM (Compound-15) for  $\beta 2$  adrenergic receptor ( $\beta$ 2AR) binds to a pocket located on the cytoplasmic side, which is similar to the allosteric site of CC chemokine receptors (CCR2 and CCR9) [267]. In 2018, the  $BLT_1$  structure was solved in complex with an antagonist BIIL260 [88], which revealed that benzamidine moiety within the BIIL260 mimics the entire sodium ion-centered water cluster. Benzamidine serves as a NAM for  $BLT_1$  by interacting with highly conserved amino acids (D66<sup>2.50</sup>, S106<sup>3.39</sup>, and S2777.46) in Class A GPCRs (Fig. 10.3). The NAM activity of benzamidine was also proved in the  $\beta_1$  adrenergic receptor, which provides a rational for developing novel inverse agonists specific for each GPCR.



**Fig. 10.3** Allosteric sites of lipid GPCRs. Receptors are shown in cartoon and/or surface representation. Ligands are represented as stick or spherical molecules. Surface representation of  $BLT_1$  in green is a binding pocket

Crystal structures of FFA1 and CB1 in combination with allosteric modulators showed extrahelical allosteric sites in the inner leaflet of the plasma membrane. TAK-875 (also known as fasiglifam) was developed for the treatment of type 2 diabetes [198]. TAK-875 activates  $G\alpha_{q}$ signaling via FFA1/GPR40 in pancreatic  $\beta$ -cells, which enhances insulin secretion in a glucosedependent manner and improves glucose homeostasis [198]. It was first reported as a selective partial agonist of FFA1 [268], while further studies characterized TAK-875 as an ago-allosteric modulator [194]. Crystal structure revealed that TAK-875 binds to FFA1 between TM3 and TM4, and the extracellular loop 2 (ECL2) forms the roof of the binding cavity. Another allosteric modulator, MK-8666, also binds to the same binding cavity. An additional allosteric site for AgoPAM AP8 was identified on the TM3/4/5 interface (Fig. 10.3), where there is a binding site for allosteric modulators for complement 5a receptor (C5AR), avacopan, and NDT9513727. On the other hand, a NAM of CB<sub>1</sub>, ORG27569, binds at the TM2/3/4 interface (Fig. 10.3). ORG27569 enhances CB<sub>1</sub> agonist binding and inhibits  $G\alpha_i$  signaling. Allosteric modulation of  $CB_1$  signaling is a novel approach to manipulate the endocannabinoid system for therapeutic benefits including neuropsychiatric, behavioral, neuroendocrine, and immunological disorders [269].

## 10.4.2 Biased Agonism and Functional Antagonism

Ligand selectively that activates one pathway over another is referred to as "biased agonism." GPCR biased agonism is separated into G protein-biased and  $\beta$ -arrestin-biased agonists. For example, among 16 clinically relevant  $\beta$ -adrenergic receptor antagonists, carvedilol is uniquely reported as a  $\beta$ -arrestin-biased agonist because it shows inverse efficacy for stimulating G $\alpha_s$  signaling and activation of  $\beta$ -arrestinmediated receptor internalization and MAPK phosphorylation [270]. GPCR drug discovery focusing on biased agonism is well documented in several reviews [271–274].

Biased agonists for some lipid GPCRs have been reported. For example, ONO Pharmaceutical Co. Ltd. reported EP<sub>2</sub>-selective G protein-biased agonists, which activate cAMP signaling without affecting  $\beta$ -arrestin recruitment [275, 276]. Takeda Pharmaceutical Co. Ltd. reported five  $G\alpha_q$ -biased NAMs for LPA<sub>1</sub>, LQ1-5 [277], that did not show any antagonistic activity for  $G\alpha_i$  signaling and  $\beta$ -arrestin recruitment, while LPA-induced Ca<sup>2+</sup> mobilization was blocked by these compounds. In 2015, Hla's group proposed that high density lipoprotein (HDL)-bound S1P acts as a biased agonist for S1P<sub>1</sub> [278]. About 65% of plasma S1P is carried by an apolipoprotein M (ApoM) positive subfraction of HDL and the remaining ~35% of plasma S1P binds to albumin [279]. ApoM<sup>+</sup>HDLbound S1P attenuates TNF- $\alpha$ -induced endothelial inflammatory responses via selective recruitment of  $\beta$ -arrestin 2 on the cell surface. On the other hand, albumin-bound S1P triggers greater G $\alpha_i$  activation and induces more receptor endocytosis than ApoM<sup>+</sup>HDL-bound S1P, suggesting that distinct bound forms of S1P induce opposite biological effects. Biased agonists are promising drugs that selectively target pathogenic or therapeutic signaling pathways while avoiding side effects.

Functional antagonism is classically considered as physiological antagonism or indirect antagonism [280]. An example of physiological antagonism is the action of glucagon (increased blood glucose levels) that physiologically antagonize insulin-induced hypoglycemia via a Class B GPCR, glucagon receptor (GCGR). Indirect antagonism is defined as an inhibition of agonist actions by blockade of intermediate signaling molecules (e.g., protein kinase A inhibitors block agonist-induced  $\beta$  adrenergic receptor). The FDA-approved MS drug, fingolimod (FTY720), is also proposed as a functional antagonist [176]. However, because it shares the  $S1P_1$  orthosteric site with S1P, this "functional antagonism" is distinct from physiological/indirect antagonism. Phosphorylated fingolimod (fingolimod-p) initially activates  $S1P_1$  as an agonist, followed by inducing sustained receptor internalization, which results in desensitization to the endogenous agonist, S1P. This mechanism of action may have merits and demerits as compared to a pure antagonist like NIBR-0213 [281]. Fingolimod causes bradycardia through G protein-coupled inwardly rectifypotassium channel (GIRK) ing on cardiomyocytes, while NIBR-0213 has no effect on GIRK but induces pulmonary vascular leakage. The discovery of fingolimod as a functional antagonist may signal a new trend in lipid GPCR drug discovery.

## 10.4.3 GPCR-Directed Monoclonal Antibodies (MAbs)

The pharmaceutical market for therapeutic MAbs has been exponentially growing since the CD3specific MAb, muromonab (Orthoclone OKT3, Janssen-Cilag) was approved by the FDA in 1986 [282]. In 2018, the FDA approved the first GPCRtargeted MAb drug, erenumab (Aimovig®, Amgen) that inhibits the calcitonin gene-related peptide (CGRP) receptor, for the treatment of migraine [283]. CGRP is a neuropeptide that modulates nociceptive signals within the trigeminovascular system and plays a key role in migraine. The MOA of erenumab blocks the binding of CGRP to its receptor. In the same year, MAbs that neutralize circulating CGRP peptides were also approved by the FDA for migraine prevention (fremanezumab, Ajoby®, Teva Pharmaceutical Industries Ltd.; and galcanezumab, Emgality®, Eli Lilly and Company).

In 2018, mogamulizumab (Libtayo®, Kyowa Hakko Kirin) was also approved by the FDA for the treatment of cutaneous T cell lymphoma [284]. The proposed MOA of mogamulizumab is that it binds to CC-chemokine receptor 4 (CCR4) on cancer cells, which induces antibodydependent cellular cytotoxicity. Other GPCRtargeted antibodies have been developed and tested in clinical trials including the CCR5 antibody (leronlimab or PRO 140, CytoDyn Inc.) for acquired immune deficiency syndrome/human immunodeficiency virus (AIDS/HIV) and solid tumors, and the CX3C chemokine receptor 1 (CX3CR1) nanobody (BI 655088, Ablynx/ Boehringer Ingelheim) for renal failure.

Among lipid GPCRs,  $CB_1$  is an attractive and validated target for treating nonalcoholic steatohepatitis (NASH) and metabolic disorders [285]. Because small-molecule  $CB_1$  inhibitors cause psychotropic effects,  $CB_1$ -directed MAbs that do not pass through the blood-brain barrier have superior specificity and selectivity over small molecules. The  $CB_1$ -directed MAb, RYI-018 (Nimacimab, Bird Rock Bio), is currently being developed for the treatment of fibrotic, metabolic, and inflammatory diseases.

The EP<sub>4</sub> crystal structure was solved with antagonist ONO-AE3-208 and an antibody Fab001 [92]. The antibody developed by NB Health Laboratory Co. Ltd. inhibits PGE<sub>2</sub>dependent cAMP production by binding to the extracellular loops (ECLs) of EP<sub>4</sub>, indicating the NAM activity of the antibody. Considering the problems with small molecules targeting EP<sub>4</sub> that include selectivity and off-target effects, the antibody seems to be promising for the treatment of chronic inflammation such as colitis, asthma, and chronic obstructive pulmonary disease (COPD).

#### 10.5 Conclusions

In summary, this review provides an overview of lipid GPCR histories, lipid GPCR drugs that were approved or are in clinical trials, and key concepts driving the next generation of GPCR pharmacology. In the nearly 30 years of lipid GPCR history from the cloning of the first lipid GPCRs, 46 lipid GPCRs have been identified and characterized, in which 14 receptors have been crystalized. Only 5% of the 475 FDA-approved GPCR drugs target lipid GPCRs, while 44 drugs targeting 19 lipid GPCRs have been tested in more than 100 clinical trials. Accumulating knowledge about the physiological and pathophysiological functions of bioactive lipids will enable development of more lipid GPCR drugs for diseases including neurological, neuropsychiatric, metabolic, cardiovascular, allergic, immune diseases, and many others.

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