
Spingomyelin and Its Role in Cellular Signaling

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Abstract

Sphingolipid *de novo* biosynthesis is related with metabolic diseases. However, the mechanism is still not quite clear. Sphingolipids are ubiquitous and critical components of biological membranes. Their biosynthesis starts with soluble precursors in the endoplasmic reticulum and culminates in the Golgi complex and plasma membrane. The interaction of sphingomyelin, cholesterol, and glycosphingolipid drives the formation of plasma membrane rafts. Lipid rafts have been shown to be involved in cell signaling, lipid and protein sorting, and membrane trafficking. It is well known that toll-like receptors, class A and B scavenger receptors, and insulin receptor are located in lipid rafts. Sphingomyelin is also a reservoir for other sphingolipids. So, sphingomyelin has important impact in cell signaling through its structural role in lipid rafts or its catabolic intermediators, such as ceramide and glycosphingolipid. In this chapter, we will discuss both aspects.

Keywords

Sphingomyelin • Ceramide • Diacylglycerol • Sphingolipids • Sphingolipid biosynthesis • Lipid rafts • Cholesterol homeostasis

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1.1 Introduction

Although the discovery of sphingomyelin (SM) was reported more than a century ago, its role as a significant ‘bioactive lipid’ along with other members of the sphingolipid family have been recognized just couple of decades ago. Technological advances in lipid detection, analysis, and quantitation have played a key role in promoting the

development of the sphingolipid research field. There have been numerous studies establishing sphingolipids' multifunctional roles in the regulation of various cellular processes such as cell growth, death, senescence, adhesion, migration, inflammation, angiogenesis and intracellular trafficking [1, 2].

However, the concept that SM is involved in cellular signaling is relatively new. We believe that SM mediated cellular signaling can be broadly manifested in two ways:

- (i) SM metabolism resulting in the production of various interconvertible bioactive sphingolipids or derivatives such as ceramide, diacylglyceride, and sphingosine-1-phosphate. These bioactive lipids act on their specific targets within the cell and regulate various signal transduction pathways, thereby affecting cellular functions.
- (ii) SM-enriched lipid raft mediated cell signaling. The interaction of SM with cholesterol and glycosphingolipid is known to drive the

formation of plasma membrane microdomains called lipid rafts [3]. As much as 70 % of all cellular SM is found in these rafts [4, 5] and they have proven to be involved in cell signaling, lipid, and protein sorting, and membrane trafficking [3, 6, 7].

This review specifically aims at deciphering the role of SM as a bioactive lipid in cellular signaling through its metabolism and its contribution to lipid rafts.

1.2 Structure, Sub-cellular Localization, and Measurement of Sphingomyelin Levels

The SM molecule consists of two regions: a phosphorylcholine head group attached to a ceramide molecule (Fig. 1.1). The latter in turn is made up of a sphingosine backbone and a fatty acid (acyl chain). SM usually contains 16:0, 18:0, 22:0, 24:0, and 24:1 acyl chains but the most

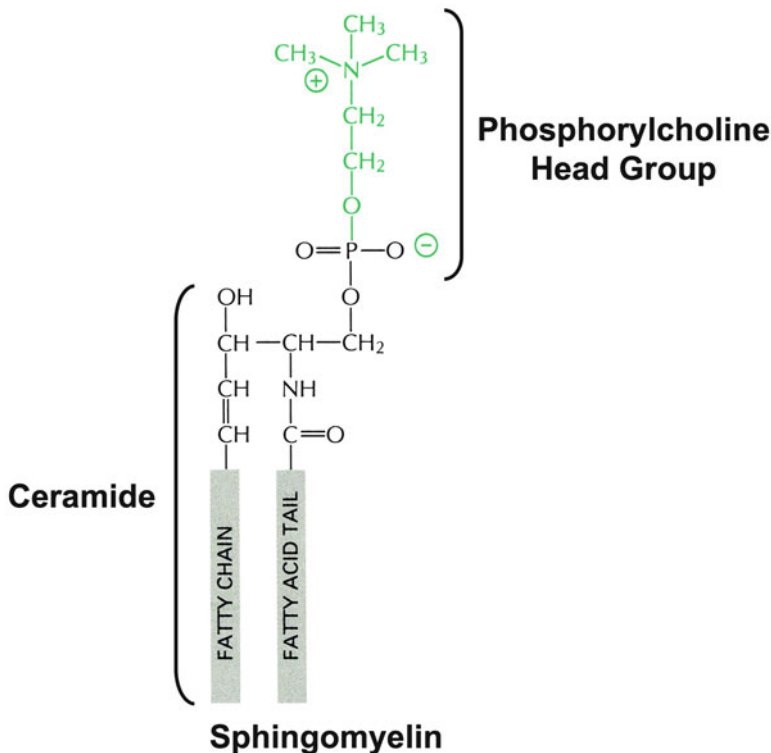


Fig. 1.1 Molecular structure of sphingomyelin

abundant SM species found in mammalian tissues are 16:0 [8]. Whether or not the differing acyl chain lengths in SMs dictate unique functions or important biophysical distinctions has not yet been established.

SM is the most abundant sphingolipid in mammalian cells and the majority of the cellular SM is located in the outer leaflet of plasma membranes [5, 9]. SM is indispensable for mammalian cell viability, as evidenced by the inability of mammalian cells to survive in culture, when they are unable to produce SM [10].

SM levels can be measured by the following methods: (i) enzyme-based assay: tissue homogenates can be incubated with bacterial sphingomyelinase, alkaline phosphatase, choline oxidase, peroxidase, N-ethyl-N-(2-hydroxy-3-sulfopropyl)-3,5-dimethoxyaniline, and 4-aminoantipyrine for 45 min. This results in a product with blue color, whose intensity is proportional to the SM present in the tissue sample, and can be measured at an optimal absorption of 595 nm [11]; (ii) liquid chromatography tandem mass spectrometry (LC/MS/MS); and, (iii) lysenin-mediated cell lysis assay. Lysenin is a SM-specific cytotoxin, which recognizes SM only when it forms aggregates or microdomains and eventually leads to cell lysis [12]. Based on the lysenin-mediated cell lysis intensity, plasma membrane SM levels can be indirectly evaluated. More SM on the plasma membrane can cause high cell mortality [12, 13].

1.3 Sphingomyelin Metabolism-Mediated Cell Signaling

1.3.1 De Novo Sphingomyelin Synthesis

SM biosynthesis initiates in the endoplasmic reticulum (ER), utilizing non-sphingolipid hydrophilic precursor molecules, serine, and palmitoyl-CoA (Fig. 1.2). The condensation of L-serine and palmitoyl-CoA to form 3-ketodihydrosphingosine is facilitated by ER membrane associated serine palmitoyltransferase (SPT). The next step in the sphingolipid biosynthesis is the reduction of 3-ketodihydrosphingosine

to dihydrosphingosine by a reductase. N-acylation of the dihydrosphingosine gives rise to dihydroceramide, a product that is still relatively hydrophilic. Conversion of dihydroceramide to ceramide is facilitated by ceramide synthases and involves a desaturation step. Ceramides are hydrophobic and therefore become membrane associated. The majority of ceramides are transported from ER to the Golgi by ceramide transport protein (CERT), and the rest are converted to ceramide phosphoethanolamine (CPE). In the Golgi apparatus, ceramides are further converted to sphingomyelin by the sphingomyelin synthase (SMS) [14, 15], to glucosylceramide by the glucosylceramide synthase and, then, to more complex sphingolipids such as glucosylceramide and hematoside (GM3) by their respective synthases (Fig. 1.2). These products are then transported to plasma membrane, the major cellular reservoir for these lipids. SM and other sphingolipids may reach to the blood circulation through lipoprotein secretion or lipid efflux (Fig. 1.2).

1.3.2 Sphingomyelin and Its Related Bioactive Lipids

Sphingomyelin synthase (SMS), utilizing ceramide and phosphatidylcholine as its two substrates to produce SM and diacylglyceride, sits at the crossroads of bioactive lipid synthesis (Fig. 1.3). SM can also be hydrolyzed by sphingomyelinase (SMase) to yield ceramide and choline phosphate. The resulting ceramide can be further converted into sphingosine and sphingosine-1-phosphate (Fig. 1.3). Potentially, manipulating SMS and SMase could influence these bioactive lipid levels, thus influencing cell biological functions.

1.3.2.1 Sphingomyelinase-Mediated Ceramide Production

Twenty years ago, it had been disclosed that SMase-mediated SM hydrolysis (SM cycle) is a novel pathway of transmembrane signal transduction. In response to extracellular agonists, membrane SM can be hydrolyzed by SMase to yield ceramide and choline phosphate [16–20].

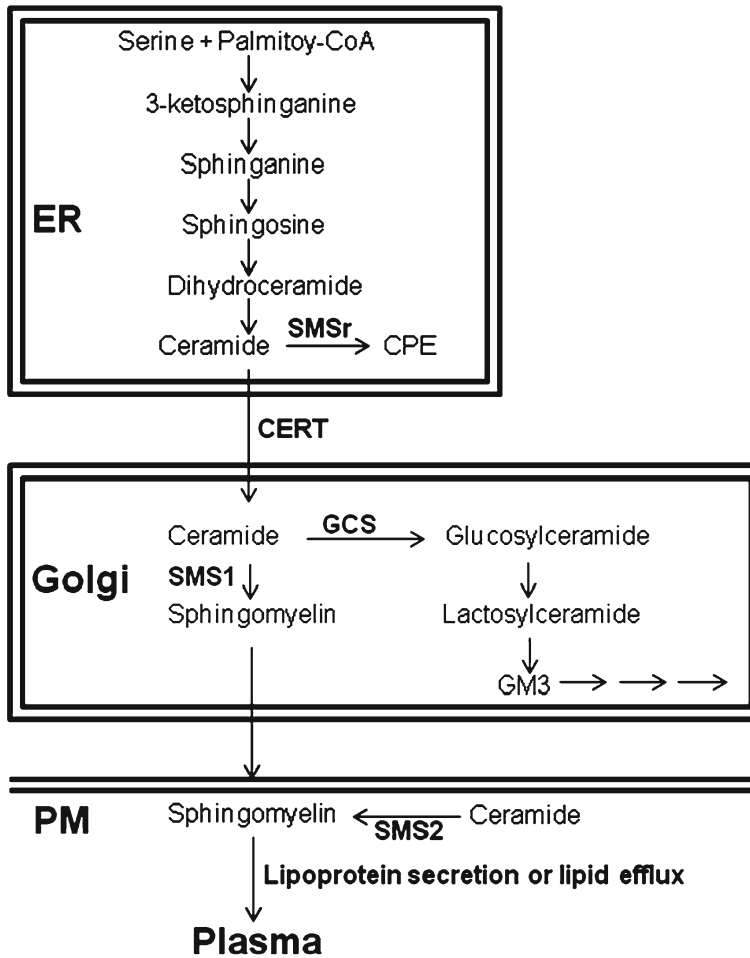


Fig. 1.2 Scheme of sphingomyelin biosynthesis. *SMS* 1 and 2, sphingomyelin synthase 1 and 2; *SMSr*, sphingomyelin synthase related protein; *GCS* glucosylceramide

synthase, *CPE* ceramide phosphoethanolamine synthase, *CERT* ceramide trafficking protein, *GM3* hematocide, *ER* endoplasmic reticulum, *PM* plasma membrane

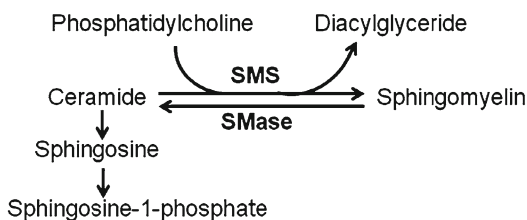


Fig. 1.3 SMS and SMase-related bioactive lipid productions. *SMS* sphingomyelin synthase, *SMase* sphingomyelinase

So far, five type of SMases have been reported and they are classified based on their optimal pH and metal ion dependence activity [21]. They are lysosomal acid SMase, secreted

zinc-dependent acid SMase, magnesium-dependent neutral SMase, magnesium-independent neutral SMase, and alkaline SMase. Multiple reviews have summarized the current knowledge about these SMases, from an overview of structure and catalysis to specific properties, roles, and regulation of these enzymes in physiological and pathological contexts [22–24].

Ceramide is a product of SMase reaction (Fig. 1.3) and has been identified as a second messenger, mediating the effects of cell growth, cell differentiation, and apoptosis. Hannun and Obeid [25] have recently summarized a large body of information with regards to metabolism, structure, and function of ceramides.

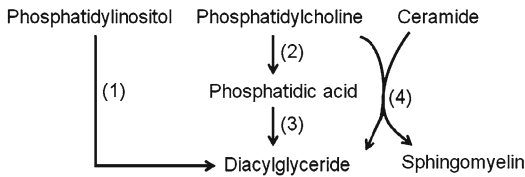


Fig. 1.4 Three pathways for diacylglyceride production. (1) phosphatidylinositol phospholipase C; (2) phosphatidylcholine phospholipase D; (3) phosphatidic acid phosphatase; (4) sphingomyelin synthase

1.3.2.2 Sphingomyelin Synthase-Mediated Diacylglycerol Production

There are three different pathways that can produce diacylglycerol [26] (Fig. 1.4). Many studies have clearly established the significant role of diacylglycerol in the regulation of fundamental cellular functions such as proliferation and apoptosis through the activation of protein kinase C [27–29]. However, we still do not know the importance of the diacylglycerol produced by the reaction catalyzed by SMS. This is because hydrolysis of membrane inositol phospholipids by phospholipase C, or hydrolysis of other membrane phospholipids, particularly choline phospholipids, by phospholipase D and phospholipase A2 can produce diacylglycerol that links extracellular signals to intracellular events through activation of protein kinase C [30]. However, it is conceivable that SMS activity-mediated diacylglycerol can potentially play an important role in maintaining cellular diacylglycerol pools [26].

1.4 Sphingomyelin as a Critical Component of Lipid Rafts in Mediating Signal Transduction

1.4.1 Sphingomyelin-Enriched Cell Membrane Lipid Rafts

Sphingolipids, including SM and glycosphingolipids, together with cholesterol, have been implicated in lateral microdomain or ‘lipid raft’ formation in biological membranes. These microdomains serve as signaling platforms and are involved in cellular processes, such as signal

transduction, membrane trafficking, and protein sorting [31, 32]. Other lipids found in raft structures include phosphatidylethanolamine, glycerophospholipids, phosphatidylserine, arachidonic acid, phosphatidylglucoside, ceramide, and lactylceramide [33, 34].

The formation of lipid rafts in biological membranes is driven by lipid–lipid interactions, which are largely dependent on the structure and biophysical properties of the lipid components. It is favored by the presence of long-chain saturated sphingolipids and phospholipids as well as by physiological proportions of cholesterol [35, 36]. There is strong evidence suggesting a preferential interaction between SM and cholesterol, stabilized by hydrogen bonding [37–39]. Infrared spectroscopic studies have also confirmed the presence of intermolecular hydrogen bonding between the amide group of SM and the 3-hydroxyl group of cholesterol [40]. The levels of cholesterol and SM in the plasma membrane are also tightly controlled [41, 42]. Greater lateral packing density in SM-containing membranes is known to be responsible for lowering the rate of spontaneous cholesterol transfer from SM-containing membranes [43]. Highly saturated glycosphingolipids are also capable of forming extensive hydrogen-bonding network with cholesterol and are therefore found in lipid rafts. However, in the presence of both SM and glycosphingolipids, cholesterol preferentially interacts with SM [44]. The rafts co-existing with the fluid matrix of the plasma membrane exist in the liquid-ordered phase [45, 46] due to its cholesterol content. Cholesterol promotes phase separation of saturated SMs [47] and SM needs cholesterol to be detergent-insoluble [45].

1.4.2 Lipid Rafts and Cell Signaling

Lipid rafts act as organizing centers for processes such as membrane trafficking and signal transduction [48, 49]. Cytoplasmic proteins that are covalently modified by saturated fatty acids (palmitoyl or myristoyl moieties) and cell surface proteins that are attached via a glycosyl phosphatidylinositol (GPI) anchor are highly concentrated within lipid rafts. Many proteins involved

in signal transduction, such as Src family kinases, G proteins, growth factor receptors, mitogen-activated protein kinase (MAPK), and protein kinase C are predominantly found in lipid rafts [32]. In addition, lipid rafts are dynamic in nature, which tends to scaffold certain signaling molecules, while excluding others. By such spatial segregation, lipid rafts not only provide a favorable environment for intra-molecular cross talk but also aid to expedite the signal relay.

Due to their insolubility in nonionic detergents such as Triton X-100, lipid rafts have been frequently termed as ‘detergent resistant membranes’ (DRMs). In fact, subpopulations of rafts have been proposed, in part based on their size, constituents, and functional properties [50, 51]. Caveolae are a subset of rafts and are considered to be 50–100 nm flask-like invaginations of the plasma membrane. Rafts and caveolae are dynamic entities, forming and dissipating in response to various external stimuli [52]. Upon stimulation, they internalize and serve a clathrin (coated pit)-independent mechanism of endocytosis of plasma membrane constituents. Raft/caveolae-mediated endocytosis is reported to facilitate transportation of entities to other cellular regions and across the cell (transcytosis) [53–55].

Membrane rafts and caveolae usually express specific proteins like flotillins and caveolins (Cavs) within their structure [56]. Cavs are structural proteins that provide an important, defining feature of caveolae and can be secreted into the extracellular space [57, 58]. Cavs are highly conserved among species and the three different isoforms of Cavs (Cav-1, -2, and -3) are differentially expressed in cells: Cav-3 is restricted to skeletal, cardiac, and smooth muscle, Cav-1 is more ubiquitously expressed, while expression of Cav-2 generally parallels that of Cav-1 [59]. Cavs also undergo covalent modifications like palmitoylation and phosphorylation [57–61]. It is known that insulin receptor (IR) is located in caveolae [62] and insulin receptor can interact with Cav1 [63]. In caveolae, the mobility of IR is increased by dissociation of the IR–Cav1 interaction [63]. It has been reported that SMS2 is able to regulate the dynamic structure of

SM-rich lipid microdomains on the plasma membrane [64, 65] and could modify protein function, such as that of CD36 or Cav 1 located in the lipid microdomains [64]. SMS2 gene knockout (KO) mice exhibited disrupted regulation of the lipid microdomains function, leading to a prevention of lipid droplet formations, fatty liver, obesity, and insulin resistance [64, 65].

1.4.3 Role of the Lipid Rafts in Inflammatory Signaling

Toll like receptors (TLRs) are critically involved in inflammatory responses [66, 67]. Lipid rafts appear to provide a platform for the interaction of TLRs with their ligands in cells [68–71].

Each one of TLRs has a unique extracellular domain that allows specific ligand recognition. The intracellular toll/interleukin-1 (IL-1) receptor (TIR) domain of TLRs shares high degree of homology, but there are enough differences to cause diversified functions mediated by different TLRs [66, 67, 72, 73]. Upon ligand-induced stimulation, the TIR domain of TLRs associates with the TIR domain of their respective adaptor molecules to initiate intracellular signaling. Myeloid differentiation primary response gene 88 (MyD88) is a common TLR adaptor used by all TLRs, except for TLR3 [73]. Upon stimulation with a specific ligand, the membrane-associated TLRs (such as TLR2 and TLR4, and other components of the TLR complex) are recruited into the lipid rafts [74, 75]. These rafts aid in the interaction of TLRs with their ligands in macrophages [68–71], initiating nuclear factor kappa-light-chain-enhancer of activated B cells (NF κ B) and MAP kinase activation and proinflammatory cytokine production, thus resulting into inflammatory responses.

Tumor necrosis factor alpha (TNF α) is one of the cytokines involved in systemic inflammation. TNF α can specifically bind to TNF receptors (TNFRs). It is known that lipid rafts play an essential role in TNFR1 clustering [76]. Upon contact with TNF α , TNF receptors form trimers and this binding causes a conformational change to occur in the receptor, leading to the dissociation of the

inhibitory protein silencer of death domain (SODD) from the intracellular death domain. This dissociation enables the adaptor protein TNFR type 1-associated DEATH domain protein (TRADD) to bind to the death domain, serving as a platform for subsequent protein binding. Following TRADD binding, three pathways can be initiated [77, 78]: (1) activation of NF κ B, (2) activation of MAPK pathways, and, (3) induction of cell death signaling.

Luberto et al. [79] found that D609, a nonspecific SMS inhibitor, blocks TNF α and phorbol ester-mediated NF κ B activation that was concomitant with decreased levels of SM and diacylglyceride. Moreover, this did not affect the generation of ceramide, suggesting SM and diacylglycerol, derived from SM synthesis, are involved in NF κ B activation. However, D609 is widely used to inhibit PC-phospholipase C (PLC) (Fig. 1.4), a well-known regulator of NF κ B activation via diacylglyceride-mediated signaling [80]. Thus, it remains unclear what pathway is inhibited by D609 in particular that causes a diminished NF κ B activation.

1.4.4 Role of Lipid Raft Sphingomyelin in Inflammatory Signaling

Studies from our laboratory [81] indicate that SMS2 knockdown in macrophages results in blockage of ligand-induced internalization as well as recruitment of TNFR1 to lipid rafts, suggesting a mechanism for the modulation of NF κ B activity by SMS2. On similar lines, lipopolysaccharide (LPS)-induced plasma membrane recruitment of TLR4-MD-2 (TLR4 co-receptor) complex is also diminished in SMS2-knockout macrophages. As a result, SMS2 deficiency attenuates both NF κ B and MAP kinase pathways, both of which are signaled via raft-associated TNFR1 and TLR4 along with their adaptor proteins. These findings strongly suggest the critical role of SMS2-synthesized SM for the normal function of TNFR1 and TLR4 on the plasma membrane following stimulation by their respective ligands (TNF α and LPS) [81].

We also created SMS1 knockout mice and found that SMS1 deficiency significantly decreased SM in plasma, liver, and macrophages but had only a marginal effect on ceramide levels [82]. Surprisingly, we found that SMS1 deficiency dramatically increased glucosylceramide and hematoside (GM3) levels in plasma, liver, and macrophages (4- to 12-fold), while SMS2 deficiency had no such effect. We evaluated total SMS activity in tissues and found that SMS1 deficiency causes 77 % reduction of SMS activity in macrophages [82], while SMS2 deficiency causes 70 % reduction of SMS activity in the liver [13], indicating SMS1 is the major SMS in macrophages, whereas SMS2 is predominant in the liver. We also found that SMS1 deficiency significantly attenuated TLR4-mediated NF κ B and MAP kinase activation after LPS treatment.

The content of SM in the plasma membrane can also be modulated by SPT, the first and rate-limiting enzyme of the sphingolipid biosynthetic pathway [83]. SPT deficiency in macrophages also results in lower plasma membrane SM content as evidenced by lysenin-sensitivity assays, making the cells more resistant to lysis when treated with lysenin [81, 84]. LPS treatment of SPT deficient macrophages results in lesser recruitment of TLR4-MD2 complex, thereby attenuating both NF κ B and MAP kinase activation. SPT deficient macrophages produce less TNF α and IL-6 *in vitro* when treated with LPS. SM supplementation experiments further prove that exogenous SM can enrich plasma membrane SM levels and can eventually restore the wild-type inflammatory phenotype in SPT deficient macrophages [128]. In general, SMS2 deficiency and SPT partial deficiency yield similar phenotypes, in terms of membrane SM levels, NF κ B and MAP kinase activation. Unlike SMS2 deficiency, SPT partial deficiency does not change ceramide at the intracellular level or either in the plasma membrane or its lipid rafts. Thus, ceramide levels may have negligible role in mediating inflammatory signaling [128]. A reduction of plasma membrane SM levels are closely related to inflammation [81, 82].

1.4.5 Role of Lipid Raft Sphingomyelin Content in Cholesterol Homeostasis

Reverse cholesterol transport (RCT) is a multi-step process resulting in the net movement of cholesterol from peripheral tissues back to the liver via the plasma [85] and it plays a major role in cholesterol homeostasis. The first and most crucial step of RCT is cholesterol efflux from peripheral tissues, such as macrophages [85].

Foam cell formation due to excessive accumulation of cholesterol by macrophages is a pathological hallmark of atherosclerosis [86]. Macrophage scavenger receptor class A is implicated in the deposition of cholesterol in arterial walls during atherogenesis, through receptor-mediated endocytosis of modified low-density lipoproteins [87]. A member of scavenger receptor class B, CD36, is also involved in macrophage foam cell formation [88]. However, macrophages cannot limit the uptake of cholesterol, and therefore depend on cholesterol efflux pathways for preventing their transformation into foam cells. Several ATP-binding cassette (ABC) transporters, including ABCA1 [89] and ABCG1 [90], as well as scavenger receptor class B1 (SR-B1) [90], facilitate the efflux of cholesterol from macrophages.

In macrophages, ABCA1 exports cholesterol and phospholipids to lipid-free apolipoproteins, while ABCG1 and SR-B1 export cholesterol to phospholipid-containing acceptors [90]. ABCA1-dependent cholesterol efflux requires aid from membrane lipid rafts [91, 92], while ABCG1 is mainly found intracellularly in the basal state, with little cell surface presentation. Under stimulation, for example by liver X receptor agonist treatment, ABCG1 redistributes itself to the plasma membrane, and increases cholesterol mass efflux to HDL [93]. ABCA1 and ABCG1 are known to cooperate in cholesterol efflux [90]. SR-B1 also facilitates cholesterol efflux from macrophages [94]. ABCA1, ABCG1, and SR-B1 are located in the plasma membrane, and exist either in rafts (SR-B1) [95, 96], or associated with the redistribution of lipids in the plasma

membrane (ABCA1 and ABCG1) [90, 97]. It is, therefore, conceivable that fundamental changes in SM and glycosphingolipid levels of the plasma membrane can influence the functions of these proteins and alter cholesterol efflux [98, 99].

SM is also known as a cholesterol-binding molecule and there by plays an important role in cholesterol efflux. There are two possible SM-mediated cholesterol efflux mechanisms. Firstly, SM is involved in the recruitment of efflux-related transporters to the plasma membrane [94]. Indeed, SM-deficient cells enhance apoA-I-dependent cholesterol efflux by ABCA1 [98, 99]. This is further supported by SMS2 deficient and SPT partial deficient macrophage studies, where decrease of SM levels in macrophage plasma membrane increases both ABCA1 and ABCG1 protein levels on macrophage surfaces, thereby increasing cholesterol efflux *in vitro* and *in vivo* [100, 128]. Although ABCA1 is known to be located in a non-raft region, its levels influence lipid raft composition [101]. Overexpression of ABCA1 [97] and treatment of cells with high-density lipoprotein (HDL) or apoA-I [102, 103] disrupts or depletes raft domains, inhibiting raft-dependent signaling. This indicates a possible interaction between ABCA1 and raft-containing lipids.

Secondly, SM is also critical for cholesterol sequestration in the plasma membrane. It is known that lysosomal SMase is involved in cholesterol transport from lysosomes to the plasma membrane [98]. Because SM avidly binds cholesterol [104], SMase deficiency inhibits macrophage cholesterol efflux through promoting cholesterol sequestration by SM. Thus, SPT deficiency, leading to reduced plasma membrane SM levels, produces the inverse effect of SMase deficiency with reference to macrophage cholesterol efflux. SPT deficiency, therefore, aids in cholesterol efflux by inducing less cholesterol sequestration in the macrophage plasma membrane [128]. This is further supported by the finding that exogenously added SM significantly diminishes cholesterol efflux mediated by ABCA1 [99], suggesting that the increase of SM content in the plasma membrane prevents cholesterol efflux.

1.4.6 The Effect of Macrophage Lipid Raft Sphingomyelin Levels on Cholesterol Efflux and Inflammation

It is known that macrophage cholesterol efflux and inflammation are inversely related to each other. Yvan-Charvet et al. reported that macrophage ABCA1 and ABCG1 deficiencies increase free cholesterol accumulation and increase cell signaling via TLRs [105]. Zhu et al. reported that macrophage ABCA1 reduces MyD88-dependent TLR trafficking to lipid rafts by reduction of lipid raft cholesterol [106]. In addition, ABCA1 expression decreases cellular plasma membrane rigidity by reducing formation of tightly packed lipid rafts [97]. Therefore, more cholesterol efflux is related to less inflammation in macrophages. A recent report indicated that IL-6 markedly induced ABCA1 expression and enhanced ABCA1-mediated cholesterol efflux from human macrophages to apoA-I [107]. We found that SPT partial deficient macrophages have significantly lower SM levels in plasma membrane lipid rafts. This reduction not only impaired inflammatory responses triggered by TLR4 and its downstream NF κ B and MAPK pathways, but also enhanced reverse cholesterol transport mediated by ABC transporters [128]. Our findings in this study clearly provided the evidence that plasma membrane SM levels are also critical for the inverse relationship between macrophage cholesterol efflux and inflammation.

1.4.7 Significance of Lipid Raft Sphingomyelin in Insulin Sensitivity

1.4.7.1 A Question from SPT Inhibition Studies

A previous study has indicated that treatment with myriocin, a potent SPT inhibitor and an immune suppressor, effectively ameliorates glucocorticoid-, saturated fat-, and obesity-induced insulin resistance [108]. Insulin resistance is a pathological condition where the insulin becomes less effective at lowering blood sugars. The authors attributed that effect to the reduction of

ceramide in tissues, but they did not evaluate SM levels, especially in the plasma membrane. We and others have noted that myriocin treatment not only reduces ceramide, but also SM and glycosphingolipid levels [109–111]. This arises a fundamental question from the SPT inhibition studies: which sphingolipid in particular, ceramide, or SM, is responsible for causing the insulin resistance?

1.4.7.2 Ceramide and Insulin Resistance

There are two considerations linking ceramide and insulin resistance. Firstly, ceramide blocks the translocation of Akt/Protein Kinase B (PKB) to the plasma membrane [112]. It has also been reported that ceramide inactivation of Akt/PKB requires the atypical PKC isoform PKC ζ [113, 114]. Secondly, ceramide may impair the action of insulin by facilitating signaling pathways initiated by inflammatory cytokines, such as TNF α and IL-6, which are known to impair insulin signaling [115, 116]. However, it has also been reported that various glycosphingolipid synthase inhibitors augment insulin-stimulated phosphorylation of the insulin receptor, as well as Akt/PKB and/or mammalian target of rapamycin phosphorylation, in the skeletal muscle [117] and liver [117, 118] of obese rodents, without altering ceramide levels. While ceramide accumulates in some insulin-resistant models [119, 120], it fails to do so in lipid-infused animals. In fact, the relative increase of ceramide in obese rodents and humans is rather quite small [121, 122]. Moreover, it is not known whether muscle ceramide content is a major factor in muscle insulin sensitivity. Adams et al. demonstrated that ceramide content is increased in skeletal muscle from obese, insulin-resistant humans [121], while Skovbro et al. found that human skeletal muscle ceramide content is not a major factor in muscle insulin sensitivity [123]. In general, the role of cellular ceramide in insulin resistance is controversial. Therefore more studies need to be done in this field to establish this relationship.

1.4.7.3 Lipid Rafts and Insulin Resistance

Insulin resistance, abdominal obesity, dyslipidemia coupled with high blood pressure, and a

proinflammatory state are common disorders associated with type 2 diabetes and atherosclerosis [124]. An important question is how these interrelated risk factors could be mechanistically coupled in a physiological situation. Considering a simple scenario, lipid raft disruption could affect insulin signaling. It has been suggested that lipid rafts play an important role in the pathogenesis of insulin resistance [125]. Indeed, disruption of caveolae in cultured cells by cholesterol extraction with β -cyclodextrin results in progressive inhibition of tyrosine phosphorylation of insulin receptor substrate 1, as well as reduced activation of glucose transport in response to insulin [126].

Glycosphingolipids are also known to be structurally and functionally important components in the lipid rafts [127]. Pharmacological inhibition of glycosphingolipid synthesis markedly improves insulin sensitivity in rodent models of insulin resistance [118]. Deficiency of GM3 ganglioside (a key glycosphingolipid in the rafts) is also known to enhance insulin receptor tyrosine phosphorylation [62]. Moreover, GM3 could dissociate insulin receptor/Cav-1 complex, thus causing insulin receptor dysfunctionality [63]. Since SM is also one of the major components within lipid rafts, it is conceivable that diminishing SM in the plasma membrane could have a similar impact on insulin signaling.

1.4.7.4 Reducing Plasma Membrane Sphingomyelin Increases Insulin Sensitivity

We utilized two models: SPT partial deficient mice and SMS2 knockout mice for the insulin sensitivity study [65]. We found that: (i) both SPT partial and SMS2 complete deficiency enhances insulin sensitivity; (ii) both deficiencies decrease plasma membrane SM levels, which contribute to the enhancement of insulin sensitivity; (iii) SPT deficiency decreases ceramide, while SMS2 deficiency increases it, therefore, ceramide is probably not the regulator of insulin sensitivity; (iv) there, they were no significant changes of glucosylceramide and GM3 levels in tissues or even cell plasma membrane, so they might not play a significant role in insulin

sensitivity in the above models; and finally, (v) this leads us to conclude that SPT or SMS2 inhibition is a promising pharmacological approach for the treatment of insulin resistance and metabolic syndrome.

1.5 Conclusions

The role of SM as a signaling molecule other than its membrane structural properties is recently being recognized in greater depth. And only a few of these important functions have been highlighted in this chapter, however, the scope of SM as a bioactive lipid mediator is enormous. Therefore, it is indeed essential to study and understand how SM is synthesized and degraded via its complex metabolic network. This would further shed light on this enigmatic molecule and its noteworthy roles in physiological processes. On the other hand, accumulating evidence showed that dynamic modification of SM in lipid rafts on cell plasma membrane controls development of obesity, insulin resistance, fatty liver, inflammation, and atherosclerosis. It is important to investigate the relationship between SM and other lipids, and between SM and functional proteins, such as insulin receptor, CD36, TLRs, and so on, in the lipid rafts.

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