

Sphingolipid metabolism affects the anticancer effect of cisplatin

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Abstract

Cisplatin, a DNA crosslinking agent, is widely used for the treatment of a variety of solid tumors. Numerous studies have demonstrated that sphingolipid metabolism, which acts as a target for cisplatin treatment, is a highly complex network that consists of sphingolipid signaling molecules and related catalytic enzymes. Ceramide (Cer), which is the central molecule of this network, has been established to induce apoptosis. However, another molecule, sphingosine-1-phosphate (S1P), exerts the opposite function, *i.e.*, serves as a regulator of pro-survival. Other sphingolipid molecules, including dihydroceramide, ceramide-1-phosphate, glucosylceramide (GluCer), and sphingosine (Sph), or sphingolipid catalytic enzymes such as Sph kinase (SphK), Cer synthase (CerS), and S1P lyase, have also attracted considerable attention, particularly Cer, GluCer, SphK, CerS, and S1P lyase, which have been implicated in cisplatin resistance. This review summarizes specific molecules involved in sphingolipid metabolism and related catalytic enzymes affecting the anticancer effect of cisplatin, particularly in relation to induction of apoptosis and drug resistance.

Key words: Apoptosis; Sphingolipid metabolism; Drug resistance; Cisplatin; Anticancer

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Core tip: Cisplatin classifies as a classical anticancer drug and DNA is identified as the most important target of cisplatin. However, increasing evidences have

testified that sphingolipid metabolism is associated with the anticancer effect of cisplatin. In this mini-review, we discussed sphingolipid signaling molecules and/or related enzymes affected the anticancer effect of cisplatin, particularly in cisplatin-induced cancer cell apoptosis and drug resistance. Targeting these sphingolipid molecules and enzymes might contribute to the development of novel anticancer strategies or to increase the sensitivity of currently used drugs.

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INTRODUCTION

The mechanisms underlying the anticancer effect of cisplatin (cis-diamminedichloroplatinum) have been extensively investigated by researchers since the discovery of its activity in 1969^[1]. It is well known that DNA is the most important target of cisplatin in a variety of cancers, especially ovarian cancer, colorectal cancer, bladder cancer, testicular cancer, head and neck cancer, and lung cancer. DNA adducts of cisplatin with covalent coordinate bonds results in DNA damage and subsequent failure to maintain normal replication and ultimately induced apoptosis^[2-5]. However, increasing evidences have testified that sphingolipid metabolism is associated with cancer therapies of cisplatin^[6-8]. Treatment with cisplatin in several cancer cells often results in the generation of ceramide (Cer), which has been involved in regulating the cell death response. For example, cisplatin activates acid sphingomyelinase (aSMase) and induces the production of Cer in cancer cells, which triggers a series cellular response, including redistribution of CD95 and cell apoptosis^[6]. In addition, sphingolipid molecules and relative enzymes have been implicated in regulating cisplatin sensitivity^[7,8]. In this review, we mainly discuss the molecules of sphingolipid metabolism and relative enzymes affecting the anticancer effect of cisplatin, particularly in the induction of apoptosis and drug resistance.

SPHINGOLIPID METABOLISM AFFECTS THE FATE OF CANCER CELLS

Sphingolipids are membrane lipids that are important constituents of eukaryotic cells. Sphingolipid metabolism is a highly complex network that is composed of various sphingolipid molecules and enzymes that have been identified as pivotal regulators of various cellular processes, including cell growth, migration, adhesion, apoptosis, cell arrest, senescence, autophagy, and drug resistance^[8-12]. Cer and sphingosine-1-phosphate (S1P) are the most essential sphingolipid molecules,

followed by sphingosine (Sph), ceramide-1-phosphate (C1P), dihydroceramide, sphingomyelin (SM), and glycosphingolipids, of which glucosylceramide (GluCer), lactosylceramide, and galactosylceramide (GalCer) have been extensively studied in various sphingolipid metabolism pathways. Cer and S1P play opposite functions in the regulation of cell fate; the former is implicated in apoptosis^[10,13-16], senescence^[17,18], differentiation^[19,20], and autophagy^[11,21,22], whereas the latter promotes cell survival and proliferation, vasculogenesis, inflammation, and resistance to widely used drugs^[23-25]. In addition, Sph inhibits cell cycle progression and induces apoptosis^[26], whereas C1P and GluCer induce proliferation of cells and are associated with the development of resistance to cisplatin. As we all know, Cer is thought as the central in sphingolipid pathways (Figure 1), and is the precursor of several kinds of sphingolipid molecules, including SM, C1P, GluCer and GalCer. Cer and each of these sphingolipid molecules can be reversibly converted by the action of related enzymes. Cer is generated by multiple pathways, including the synthesis by *de novo*, the SM hydrolysis, or the Sph recycling^[11,27,28]. The main generated route is the *de novo* synthesis pathway, which takes place in the endoplasmic reticulum (ER). Cer is synthesized from palmitoyl-CoA and serine to form 3-ketodihydrosphingosine through the catalyst, serine palmitoyltransferase^[29,30]. Subsequently, the conversion of 3-ketodihydrosphingosine to sphinganine, which is condensed with fatty acyl-CoA by six specific dihydroceramide synthase (CerS 1-6) to form dihydroceramides of different lengths^[31], which is then catalyzed by dihydroceramide desaturase to generate Cer. In the hydrolysis of SM pathway, SM is catabolized to Cer through the action of the neutral or SMase, but not alkaline SMase, which is mainly due to the specific forms of phospholipase C^[32-35]. The catalysis of acidic and neutral SMases plays a pivotal role in apoptotic process and cell cycle arrest^[32,36]. Cer is generated *via* dephosphorylation of C1P by Cer-1-phosphate phosphatase. In addition, C1P can be recovered from the phosphorylation of Cer by ceramide kinase. Cer can also be formed *via* the degradation of the glycosphingolipids, GluCer and GalCer, which each contains a single sugar molecule linked to Cer^[37], and hydrolyzed by specific β -glucosidases and galactosidases, to yield Cer^[38]. Inversely, GluCer is generated by GluCer synthase (GCS) in the Golgi apparatus^[39].

Cer is degraded by ceramidases (CDase) to produce Sph, Sph is subsequently phosphorylated by two sphingosine kinase isoenzymes (SK-1 and SK-2) to produce S1P, which then is decomposed under the action of S1P lyase to produce ethanolamine phosphate and hexadecenal. This is the only exit pathway of this complex network. In addition, Sph and S1P can be recycled back to Cer by CerS or dephosphorylated back to Sph, respectively^[40].

Recent studies have identified the sphingolipid molecule Cer and enzymes CerS, SK, and S1P lyases as important targets for developing anticancer drugs and

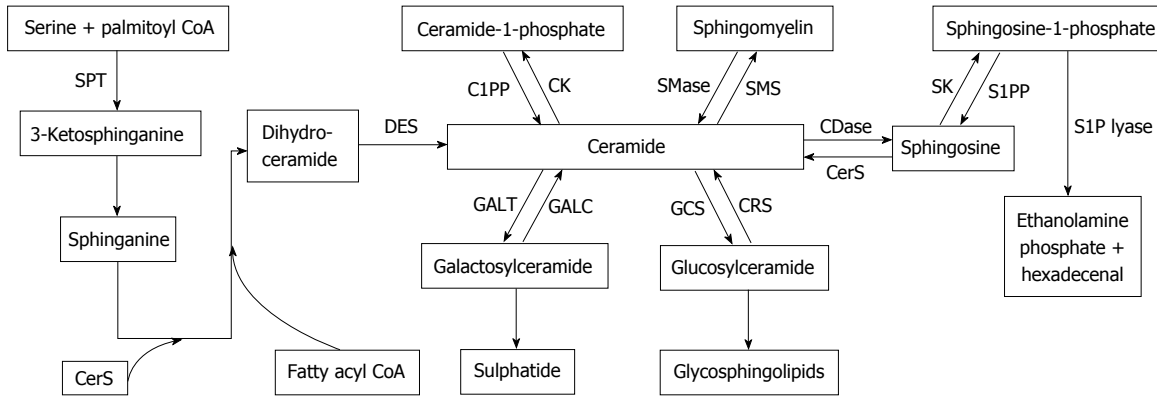


Figure 1 Sphingolipid metabolism pathways. Cer is the central in sphingolipid pathway, it is generated via multiple pathways, including the synthesis by *de novo*, the degradation of SM or the recycling of Sph; it is further metabolized and then produces many metabolites. Unidirectional arrows mean the generation of lipid molecules from one direction and bidirectional arrows mean mutual transformation between the two lipid molecules. SPT: Serine palmitoyl transferase; CerS: Ceramide synthase; DES: Dihydroceramide desaturase; C1PP: Ceramide-1-phosphate phosphatase; CK: Ceramide kinase; SMase: Sphingomyelinase; SMS: Sphingomyelin synthase; CDase: Ceramidase; SK: Sphingosine kinase; S1P: Sphingosine-1-phosphate; S1PP: S1P phosphatase; GALT: Galactosyltransferase; GALC: Galactosylceramidase; GCS: Glucosyl ceramide synthase; CRS: Cerebrosidase; Sph: Sphingosine.

drug resistance. Glycosphingolipids also play important role in multidrug resistance^[15,41,42].

SPHINGOLIPID METABOLISM IN CISPLATIN-INDUCED CELL APOPTOSIS

Cisplatin induces apoptosis via the Cer-mediated mitochondria pathway

Although DNA is regarded as the main therapeutic target of cisplatin in various tumor cells, cisplatin induces apoptosis *via* signaling through plasma membrane lipid rafts that contain abundant sphingolipids, and these membrane lipid rafts are perhaps the targets of cisplatin-induced apoptosis^[43-45]. It has been reported that sphingolipids are the major components of lipid rafts, and sphingolipids act as pivotal roles in maintaining the structural integrity of cell membranes and in modulating apoptosis *via* gene regulation and signal transduction^[46]. In addition, an imbalance in sphingolipid levels results in apoptosis, which may be triggered by deviant intracellular apoptotic signaling^[47]. Thus, cisplatin-induced apoptosis is closely associated with sphingolipid metabolism. However, Cer, the central molecule of sphingolipids metabolism, is involved in cisplatin-induced apoptosis. The two main apoptotic pathways include the receptor-involved extrinsic pathway and the mitochondria-associated intrinsic pathway^[48]. The mechanism involved the Fas death receptor-mediated pathway that contributes to cisplatin-induced apoptosis will be discussed later. In the present section, we will talk about the Cer-played role in cisplatin-induced apoptosis in the mitochondria.

A central role in the intrinsic pathway of apoptosis is played by mitochondria. Stressors such as cisplatin, a chemotherapeutic agent, targets the mitochondria, resulting in the alteration of mitochondrial outer membrane permeabilization (MOMP) that promotes some proteins of mitochondria releasing from the intermembrane space into the cytosol. Then the caspase cascade

pathway is activated and cells die within minutes. Thus, MOMP is strictly regulated and is identified as an irreversible event^[49-51]. Early in 1993, Obeid *et al.*^[52] firstly illustrated that Cer is a potent apoptotic inducer. Subsequently, several studies have indicated that the increase in cellular Cer early in apoptosis is a common cellular response to cisplatin^[8,53,54]. Research has shown that Cer, coupled with downstream Cer metabolites that participate in apoptosis, can change the function of mitochondria and give rise to increase of MOMP^[49,50,55]. Accompanying the increase in cellular Cer levels, some proteins release from the mitochondrial intermembrane space to the cytoplasm, reactive oxygen species produce more in mitochondria, and the inner membrane potential of mitochondria is decreased^[56-58]. Suppressing mitochondrial function can inhibit apoptosis induced by Cer^[59]. In addition, the channels formation by Cer itself facilitates apoptosis in the mitochondrial membrane with elevated Cer levels^[60]. Therefore, Cer is regarded as a pro-apoptotic molecule. A study in C6 rat glioma cells revealed that cisplatin-induced apoptosis links to Cer production resulting from cisplatin-mediated neutral sphingomyelinase activation. After that, cytochrome C releases from mitochondrion to the cytosol, which is dependent upon the BCL-2 family and activation of caspases-9 and caspases-3^[55,61]. These post-mitochondrial events also intrinsically trigger apoptosis. Furthermore, Cers are generally synthesized from sphingoid bases, and very long (C24) or long (C16) fatty acid chains are added by specific Cer synthases. Cers containing different acyl chain lengths may affect susceptibility to cisplatin-induced apoptosis. During cisplatin-induced apoptosis, although intracellular Cer levels are not changed, C16 Cers are specifically elevated^[54,62]. In addition, the function of certain proteins involved in apoptosis, including cathepsin D, PKC- ζ , PP1, PP2A, and ceramide-activated protein kinase, were modulated by Cer. These indirect mechanisms may possibly contribute to the mechanism underlying Cer-mediated apoptosis

that is involved in the mitochondria pathway^[11].

Cisplatin induces apoptosis through the Cer-mediated death receptor Fas pathway

Fas (also known as CD95) use the death domain that is important for protein-protein interaction inside the cell to recruit Fas-associated death domain (FADD), subsequently to recruit the proenzyme of caspase-8^[63]. It is necessary to recruit FADD (the adaptor protein) and procaspase-8 to the rafts of Fas ligation in order to initiate the signaling of Fas-mediated apoptosis, disrupting the integrity of rafts fails to initiate the Fas apoptotic signaling^[64,65]. Previous reports have manifested that the death receptor Fas is localized in lipid rafts constitutively or under stimulation state, the receptor clustering in lipid rafts is necessary to the cell death mediated by Fas^[66,67]. It has been reported that cisplatin causes the Fas clustering at the membrane of HT29 cancer cells derived from human colon, which in turn is inhibited by an inhibitor of aSMase, imipramine^[44]. Additionally, CD95 could contribute to cisplatin-induced HT29 cell apoptosis in which redistribution of CD95 played a key role; however, a cholesterol sequestering agent, nystatin through preventing aSMase translocation and Cer production, inhibits cisplatin-induced CD95 clustering and decreases cisplatin-induced HT29 apoptosis^[6]. Taking together, these results show that cisplatin triggers Fas redistribution into the plasma membrane rafts by activation of aSMase and induction of Cer production. Therefore, the contribution of Fas redistribution to cell apoptosis and cell death is clearly confirmed^[6,44]. Furthermore, it has been reported that apoptosis is easy to be induced by many kinds of factors, for example cisplatin, Fas, tumor necrosis factor-1, growth factor withdrawal, or hypoxia. Several of above apoptotic stimuli can regulate Cer production, that hints us Cer plays an important role in apoptotic process^[14]. In addition, the levels of Cer elevate in response to cisplatin, and the Cer increase by using inhibitors of enzymes that is responsible for metabolizing Cer or by overexpressing enzymes that account for Cer production leads to apoptosis^[68]. The formation of Fas capping that involves decoupling of Fas ligand and Fas receptor at the plasma membrane enriched sphingolipids especially sphingomyelin is one mechanism in Cer-mediated apoptosis^[69]. In other words, cells are resistant to mitochondria-involved apoptosis if they are not sensitive to Fas-mediated apoptotic signaling^[70], suggesting that cells will lose sensitivity to death signaling if their Cer-Fas pathway is disturbed. Therefore, Cer has a tight connection with apoptosis, the Fas death receptor pathway is one of the mechanisms in which cisplatin induces apoptosis.

Cisplatin-induced apoptosis through other pathways

Several other mechanisms are responsible for the induction of cisplatin-induced apoptosis. Perrotta *et al.*^[71] reported that cisplatin triggers the apoptosis of dendritic cells (DCs) through increased expression and activation

of aSMase, which could be inhibited by preconditioning DCs with nitric oxide donors. Further studies involving human colon cancer cells have shown that cells' acidification, which is depended on NHE1, appears early in the process of cisplatin-mediated apoptosis, subsequently leading to aSMase activation and fluidity elevation in cell membrane, which differs from cisplatin-induced DNA adduct formation^[72]. Furthermore, de-N-acetyl-lysoglycosphingolipid, a hydrolyzed product of ganglioside GM1, inhibits the growth of various tumor cell lines, which occurs in synergy with cisplatin^[73].

SPHINGOLIPID METABOLISM AFFECTS CISPLATIN RESISTANCE

Sphingolipid metabolism in Dictyostelium discoideum alters the sensitivity to cisplatin

Although cisplatin is an extremely effective drug that induces apoptosis in cancer cells, the efficacy of cisplatin treatment in some types of cancer is often impeded by drug resistance^[74]. Therefore, intrinsic and acquired resistance to cisplatin is a vital problem when using this drug clinically. The mechanisms underlying cisplatin resistance^[74-77] include some classical drug resistance mechanisms such as the decrease in the concentration of intracellular cisplatin, inactivation of the drug, increase in DNA repair, and reduction in apoptotic response. However, some resistance related genes including cyclooxygenase-2, heat shock proteins, or other cell signaling pathways and molecules also play some roles in the resistance to cisplatin. Additionally, cell membrane fluidity and lipids are also associated with cisplatin resistance^[78]. To investigate the underlying molecular basis of resistance to cisplatin, Alexander *et al.*^[79] used *Dictyostelium discoideum* (*D. discoideum*) as an excellent eukaryotic model for studying the mechanisms underlying cisplatin drug sensitivity^[79-82]. Genome sequencing of *D. discoideum* has shown that various genes and pathways are highly homologous to those in human cells^[79,83]. Because the pathway of sphingolipid metabolism is highly conserved between humans and *D. discoideum*^[79], mutations in sphingolipid metabolism-related genes confer cisplatin resistance in both species^[78]. The role of some of the enzymes in sphingolipid metabolism (S1P lyase and SK) in the regulation of cisplatin resistance has been investigated by establishing a *D. discoideum* model^[78,79,84]. S1P lyase (sglA) is highly conserved in humans and this enzyme accounts for the final metabolism in the sphingolipid pathway^[85]. Although the sphingolipid metabolism pathway has been extensively investigated in mammalian cells, no previous studies have indicated the relationship between this pathway and cisplatin resistance prior to 2000. SglA was found for the first time to modulate sensitivity to anticancer drug cisplatin in *D. discoideum*^[84]. Sphingolipids are involved in regulating cell fate, and the ratio of Cer and S1P levels could be used to determine whether cells enter the pathway of cell death or survival^[86-89]. Various

stimuli, including γ -irradiation and anticancer drugs, have also been reported to lead Cer increase and/or to decrease S1P, which is a bioactive sphingolipid that plays a central role in apoptosis inhibition, pro-survival, or cell movement^[23] in cancer cells. These effects are reversed with decreased Cer or increased S1P, which results in cell survival and proliferation. Therefore, we hypothesized that deletion of the S1P lyase increases resistance to cisplatin, whereas overexpression of this enzyme yields the opposite effect. The reports that the S1P lyase null (*sglA^Δ*) and overexpressing cells (*sglA^{OE}*) displayed decreased or increased sensitivity to cisplatin, respectively, have thoroughly proven the above hypotheses in *D. discoideum*^[7,90,91].

Two other enzymes associated with the direct regulation of the production of S1P in *D. discoideum* include the *sgkA* and *sgkB* sphingosine kinases that produce S1P from sphingosine and ATP. We thought that reducing sphingosine kinase expression leads cells are more sensitive to cisplatin, whereas over-expressing this enzyme results in resistance to this drug. *D. discoideum* *sgkA* and *B* genes mutants were generated, which harbored disrupted single or double sphingosine kinases or overexpressed the *sgkA* gene. Single or double disruption of the sphingosine kinases resulted in a reduction of growth rates, whereas overexpressing mutants presented elevated growth rates. Furthermore, these two enzymes showed a capacity to modulate sensitivity to cisplatin. The null mutants of sphingosine kinase appeared elevated sensitivity to cisplatin, whereas overexpression of *SgkA* in these mutants would rescue this effect. The addition of S1P or using N, N-dimethylsphingosine, a sphingosine kinase inhibitor^[92], counteracts these effects^[90]. The effects of sensitivity of the null or *sgkA*-overexpressing mutants were similar to those of another platinum-based drug, carboplatin. Taken together, these findings in *D. discoideum* allowed us to conclude that modulation of cisplatin sensitivity can be achieved through the regulation of related enzymes of sphingolipid metabolism.

Sphingolipid metabolism enhances cisplatin sensitivity in mammalian cells

Based on the above results, considerable attention has been paid to study cisplatin resistance and related mechanisms in mammalian cells. The results of studies on the mechanism underlying the resistance to cisplatin on *D. discoideum* should be confirmed in mammalian cells. Researchers have investigated the effect of overexpressing or deleting S1P lyase on cisplatin sensitivity in mammalian cells. The overexpression of S1P lyase in both human lung cancer (A549) and human embryonic kidney 293 cells resulted in an increase in cisplatin sensitivity, whereas the opposite effects were obtained with the disruption of S1P lyase^[93]. The role of sphingosine kinases (*SphK1* and *SphK2*, which are the equivalent of the *SgkA* and *SgkB* on *D. discoideum*, respectively) affecting cisplatin resistance was also examined in mammalian cells. Although

these human isoenzymes generate the same product, S1P possesses different functions in cells^[94-96]. Thus, *SphK1* and *SphK2* also had different effects on cisplatin sensitivity. Increasing the expression of *SphK1* reduced cisplatin sensitivity, whereas *SphK2* generated cells that with higher cisplatin sensitivity^[8]. The deletion or overexpression of S1P lyase or *SphKs* affects the generation of S1P, indicating that the regulation of S1P is one of the mechanisms underlying cisplatin resistance.

Cer is regarded as another sphingolipid metabolism-related molecule that influences cisplatin sensitivity. Based on the bioactivity of Cer, the alteration of Cer accumulation alters a cell's sensitivity to cisplatin. Although Cer can be produced from various sphingolipids, *de novo* synthesis has proven to be the ultimate source of Cer. Each of the six key dihydroceramide synthase (*CerS1* through *CerS6*) enzymes prefers a fatty acyl CoA with different chain length as a substrate to produce specific Cer molecules^[31,97]. Three of these enzymes have yet to be tested in terms of its capacity to regulate cisplatin sensitivity. Only expression of *CerS1* leads cell is more sensitive to the all tested drugs such as cisplatin, vincristine, doxorubicin, and carboplatin, accompanied by more p38 MAPK activation. Nevertheless, *CerS5* expression resulted in an increased sensitivity to vincristine and doxorubicin, whereas the overexpression of *CerS4* had not similar effect on all the above mentioned reagents. The effects of *CerS1* expression are implicated in its specific translocation from the ER to the Golgi apparatus, but not *CerS4* or *CerS5*, and are reversed by the expression of *SphK1*, but not *SphK2*.

It has been previously reported that overexpression of GCS efficiently leads GluCer formation from Cer in some cancer cells, including breast cancer cells and human ovarian carcinoma cells^[98-100]. Compared to sensitive cells, GluCer production is markedly higher in resistant cells^[99,101,102], which is accompanied by an increase in the expression of P-glycoprotein, a membrane efflux transporter and one of the most common alterations in resistant cells^[99,103,104], indicating that glucosylation of Cer is associated with drug resistance^[105]. GCS is associated with multidrug resistant cancers and elevates the expression of multidrug resistance protein 1 (MDR1). Previous studies have revealed that MDR1 expression is markedly inhibited by siRNA-mediated GCS deletion, which functions as a membrane translocase and reverses drug resistance^[98,99]. This finding indicates that the downregulation of GCS prevents the accumulation of glucosylceramide, which in turn increases sensitivity to anticancer drugs^[15,106]. However, this phenomenon has not been observed despite the downregulation of GCS expression using specific inhibitors^[107]. In addition, MDR1, as the major GluCer translocase, is required for the synthesis of neutral glycosphingolipids, but not for acid glycosphingolipids^[108]. The production of glycosphingolipids with α -hydroxy fatty acids and longer carbohydrate chains is markedly higher in the human ovarian carcinoma cisplatin-resistant KF28 cells (KFr13) and taxol-resistant KF28 cells (KF28TX) compared to

that of sensitive KF28 cells, suggesting that changes in the glycosphingolipid composition of cancer cells are associated with cisplatin resistance^[100]. Taken together, these results suggest that the molecules related to the sphingolipid metabolic pathway can be manipulated to a certain extent by regulating the expression of related enzymes to improve cisplatin sensitivity.

CONCLUSION

In conclusion, sphingolipid metabolism may play crucial roles in the induction of apoptosis and resistance of cisplatin. In particular, Cer is closely related to cisplatin-induced apoptosis and is considered a potential target for cancer therapeutics. To study the mechanisms underlying cisplatin resistance in sphingolipid metabolism pathways, *D. discoideum* was established as an excellent eukaryotic model. The results obtained from this model have been extensively translated to and validated in human cells. Thus far, sphingolipid molecules particularly S1P, GluCer, and related enzymes, particularly SphK, CerS, and S1P lyase have been implicated in cisplatin sensitivity. Tumor pathogenesis is considered as an intricate process; therefore, to fully understand the mechanisms underlying the use of cisplatin as an anticancer drug targeting the sphingolipid metabolism pathway, a variety of strategies should be utilized. Targeting these essential molecules of sphingolipid metabolism may contribute to the development of novel anticancer strategies or to increase the sensitivity of currently used drugs.

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