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REVIEW

Roles of sphingolipids in *Drosophila* development and disease

Rachel Kraut

School of Biological Sciences, Nanyang Technological University, Singapore, Singapore

Abstract

The last 10 years have seen a rebirth of interest in lipid biology in the fields of *Drosophila* development and neurobiology, and sphingolipids have emerged as controlling many processes that have not previously been studied from the viewpoint of lipid biochemistry. Mutations in sphingolipid regulatory enzymes have been pinpointed as affecting cell survival and growth in tissues ranging from muscle to retina. Specification of cell types are also influenced by sphingolipid regulatory pathways, as genetic interactions of glycosphingolipid biosynthetic enzymes with many well-known signaling receptors such as Notch and epidermal growth factor receptor reveal. Furthermore, studies in flies are now uncovering unexpected roles of sphingolipids in controlling lipid storage and response

to nutrient availability. The sophisticated genetics of *Drosophila* is particularly well suited to uncover the roles of sphingolipid regulatory enzymes in development and metabolism, especially in light of conserved pathways that are present in both flies and mammals. The challenges that remain in the field of sphingolipid biology in *Drosophila* are to combine traditional developmental genetics with more analytical biochemical and biophysical methods, to quantify and localize the responses of these lipids to genetic and metabolic perturbations.

Keywords: development, *Drosophila*, genetics, metabolism, nervous system, sphingolipids.

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Time was, when the worst nightmare of every student of Drosophila development was to find out that a laboriously cloned gene turned out to encode, in the words of one PhD advisor, 'probably just a lipase!' How things have changed over the course of the last 20 years, as the role of lipases and everything else having to do with lipid metabolism has moved from the realm of so-called housekeeping genes to center stage in one of the most exciting and current aspects of developmental and cell biology. Part of the reason for this decades-long lapse in general appreciation for lipids and their role in developmental events was surely because of the fact that fewer tools existed then (and now) to be able to visualize particular lipids in the developing animal, and to study their effects on morphological processes. With the low-hanging fruit of obvious embryonic phenotypes having been plucked the earliest, these difficult-to-analyze mutations in lipidmodulatory genes largely began to emerge only later.

This review focuses on work over the last decade that discovered novel roles of the sphingolipids, and how they feature in the development and health of the fly. With respect to sphingolipid biology, effects on normal embryonic and pupal development are only part of the news. Lipid regulation of such phenomena as energy household, lifespan,

and degenerative processes that afflict adult animals were only recently made accessible by new screening and quantitative methods to detect these phenotypes. Now that these approaches have become routine, regulatory functions of sphingolipids in metabolic homeostasis are revealing themselves. Also coming of age is the part that lipids, in

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Address correspondence and reprint requests to Rachel Kraut, School of Biological Sciences, Nanyang Technological University, Singapore, 60 Nanyang Drive, Singapore 637551, Singapore.

E-mail: rskraut@ntu.edu.sg

Abbreviations used: CIP, ceramide-1-phosphate; Dacer, *Drosophila* alkaline ceramidase; EGF-R, epidermal growth factor receptor; ERK, extracellular signal-related kinase; GalNAc, *N*-acetylgalactosamine; GalNAc-T, *N*-acetylgalactosaminyl transferase; GlcNAc, *N*-acetylglucosamine; GlcT-1, glucosylceramide transferase-1; JNK, c-jun N-terminal kinase; MAPK, mitogen-activated protein kinase; nCDase, neutral ceramidase; NPC, Niemann–Pick type C disease; PE, phosphoethanolamine; PI3K, phosphinositide-3-kinase; PLC, phospholipase C; S1P, sphingosine-1-phosphate; SBD, sphingolipid-binding domain peptide; SMase, sphingomyelinase; SMS, sphingomyelin synthase; spt, serine-palmitoyl transferase; SREBP, serum response element binding protein; TAG, triacylglycerol; TGFα, transforming growth factor α.

particular sphingolipids and sterols, may have in the development of progressive neurodegenerative disorders. We will discuss both the peculiarities of *Drosophila* sphingolipids and the commonalities with mammals that make the fly a good model in which to study nervous system development, degeneration, and metabolic disorders where sphingolipids and sphingolipid-regulated mechanisms figure prominently.

Fly-specific structures and species

Studying the functions of sphingolipid metabolic enzymes in *Drosophila* has an obvious genetic advantage in that flies usually have many fewer gene candidates for a particular enzymatic step, making analysis of mutant phenotypes much more clear-cut (Acharya and Acharya 2005). In addition, over-expression or knockout of a given gene in *Drosophila*, even in a tissue-specific way and in any desired combination, is experimentally straightforward – a matter of weeks or months of work, not years. On top of this, since *Drosophila* larvae are very reliable and consistent eating machines, nutrient conditions, or drugs that might alter sphingolipid metabolism are very easy to administer to flies in the larval stage, simply by adding agents to the food (Adachi-Yamada *et al.* 1999; Mair *et al.* 2005; Ye *et al.* 2007; Vargas *et al.* 2010).

Many of the major sphingolipid biosynthetic and processing enzymes have known orthologs in *Drosophila*, including all the ones required for the production of sphingosine and ceramide, as well as those involved in generating metabolites of and breaking down these sphingolipids, e.g. ceramide kinase and different ceramidases (CDase; Adachi-Yamada

et al. 1999; Acharya et al. 2003; Gorski et al. 2003; Fyrst et al. 2004; Herr et al. 2004; Rohrbough et al. 2004; Acharya and Acharya 2005; Bauer et al. 2009). Sphingosine-metabolizing enzymes, such as the sphingosine kinases, which generate the important signaling molecule sphingosine-1-phosphate (S1P), and S1P-lyase which breaks it down, have interesting developmental defects when absent, and these are discussed further below. A comprehensive review on sphingolipid-metabolizing enzymes in the fly, and information on the suspected or known orthologs is available (Acharya and Acharya 2005). There are important differences in lipid structure, however, the length of the sphingoid base product of serine-palmitoyl transferase (spt) in Drosophila being much shorter, generally containing only 12 carbons derived from laurate instead of the 16 carbons from palmitate as in mammals. This gives a sphingoid base alkyl chain of C14 instead of C18, whereas the fatty acyl chain, which is attached by an amide linkage to the sphingoid base, is quite long, with C20 being the major species (Fyrst et al. 2004; Acharya and Acharya 2005; Fig. 1). Shorter chain length may have the advantage of not solidifying at the preferred fly body temperature of $\sim 25^{\circ}$ C (Holthuis et al. 2001).

In spite of the differences in structure of fly sphingolipids, and the lower abundance of sterols in fly membranes, sphingolipid- and sterol-rich microdomains have been documented by several authors in *Drosophila* cells and tissues (Rietveld *et al.* 1999; Karpen *et al.* 2001; Zhai *et al.* 2004; Hebbar *et al.* 2008), and the raft-associated adaptor proteins reggie/flotillins are expressed in flies (Stuermer *et al.* 2001; Hoehne *et al.* 2005). So-called 'detergent resistant membranes' can be isolated from fly cell membranes, and the lipid

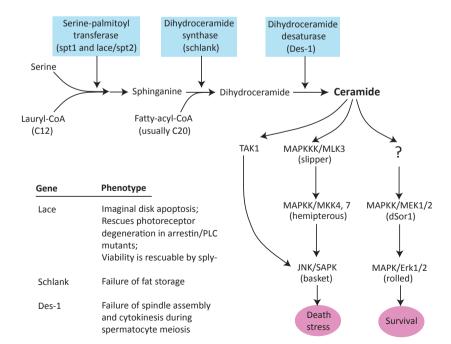


Fig. 1 Ceramide biosynthesis in *Drosophila*. In each figure, enzyme names and the corresponding fly homologs (in parentheses) are boxed in blue; physiological effects of the given pathways are circled in purple. Mutant phenotypes of the given genes and genetic interactions are listed in the tables at the bottom of the figures.

content of these membranes roughly corresponds to what would be expected if as in mammals, these domains contain sphingolipids and sterol. Moreover, detergent resistant membranes from fly membranes co-segregate with markers thought to associate with ordered sphingolipid-containing domains (Zhai et al. 2004; Hebbar et al. 2008). Sterol depletion by methyl- β -cyclodextrin results in $\sim 50\%$ reduction in sterol levels in cultured Drosophila cells, and also changes the distribution of markers, such as flotillin and sphingolipid-binding domain peptide (SBD; Hebbar et al. 2008; Steinert et al. 2008). Sterol was also required for translocation of the InaD-containing phototransduction machinery in fly photoreceptors (Sanxaridis et al. 2007), and certain neurotransmitter receptors and ion channels likewise appear to be activated by raft domains (Eroglu et al. 2003; Gasque et al. 2005). Depletion of sterols or prevention of sphingolipid biosynthesis using the fungal antibiotic Fumonisin B1 prevents recognition of fly neuronal cells by the SBD peptide, suggesting that Fumonisin B1 may be able to inhibit production of sphingolipids in Drosophila in a functionally analogous way to its inhibition of dihydroceramide synthase in mammalian cells (Merrill et al. 1996; Hebbar et al. 2008).

Sphingolipid metabolizing enzymes in fly

Even though flies appear to make negligible amounts of sphingomyelin, there are several orthologs of sphingomyelin synthases (SMSs) in the fly genome (Huitema et al. 2004; Tafesse et al. 2006), that are candidate enzymes for the synthesis of the much more abundant species, phosphoethanolamine ceramide (PE-ceramide). Sphingomyelin synthase candidate orthologs were identified in Drosophila by virtue of their domain similarity to yeast AUR1 which synthesizes the yeast equivalent of sphingomyelin, inositol-phosphorylceramide (Dickson 1998), and the presence of conserved domains found in lipid phosphate phosphatases (Huitema et al. 2004). A recent study determined that one of these synthases, SMSr (sphingomyelin synthase 1-related) can synthesize PE-ceramide, but does not do this in vivo. In fact, it functions in mammalian and fly cells as a sensor and regulator of ceramide homeostasis, which prevents accumulation of ceramide in the endoplasmic reticulum. In the absence of this protein, ceramide builds up and leads to fragmentation of Golgi stacks (Vacaru et al. 2009). The more likely candidate for the actual PE-ceramide generating enzyme is evidently one of the other three SMS homologous genes.

A dihydroceramide desaturase was identified in flies, and named Des-1 because of its degenerative spermatocyte phenotype (Basu and Li 1998). In spermatocytes, Des-1 has a role in spindle assembly and meiosis, and seems to associate strongly with mitochondria and with the contractile ring during division, suggesting that the production of

ceramide might be important somehow in anchoring cytoskeletal elements. This is reminiscent of the more recent observations by Bieberich's group that ceramides are present in and required for the formation of cytoskeleton-dependent structures like cilia and tight junctions in epithelia (Wang et al. 2009a,b).

Other sphingolipid biosynthetic and processing enzymes have been identified in the fly, including ceramide transfer protein, which as in mammals is required to move ceramide from the site of its synthesis in the endoplasmic reticulum to the Golgi, where it is further processed to glycosphingolipids and, in the case of flies, PE ceramide instead of phosphocholine-ceramide (sphingomyelin). Ceramide transfer protein mutations in the fly, as might be expected given the membrane-gelling properties of ceramide, result in phenotypes related to altered fluidity of membranes, including heightened sensitivity to oxidative stress and premature aging (Rao *et al.* 2007; Goñi and Alonso 2009). This outcome has interesting implications for the use of flies to study the role of ceramide in age-related diseases, such as neurodegeneration and type II diabetes.

Life, death, and sphingolipids

One of the first sphingolipid metabolic enzymes to be described in Drosophila, and its loss of function phenotype studied was serine palmitoyl transferase (spt), the enzyme that is responsible for the rate-limiting step in de novo sphingolipid biosynthesis. A mutant in the spt2 subunit, known as lace, was identified because it suppressed hyperactivation in the growth-mediating mitogen-activated protein kinase (MAPK)/extracellular signal-related kinase (ERK) pathway, achieved by over-expressing the fly MAPK and MAPKK orthologs rolled and dSor1 (Adachi-Yamada et al. 1999; Fig. 1). Spt2/lace mutants showed abnormal development and ectopic apoptosis in imaginal discs triggered by cjun N-terminal kinase (JNK) activity (basket in flies), and these effects were rescued by increased signaling through the opposing MAPKK survival pathway. These interactions imply that ceramide or its metabolites might suppress a suppressor of the MAPK/ERK survival pathway such that removal of spt would reduce dSor1 and rolled hyperactivation. A candidate for this might be the transforming growth factor β (TGFβ)-activated kinase 1 homolog TAK1, which is activated by ceramide and regulates both the JNK pathway in flies (Takatsu et al. 2000) and the MAPK/ERK pathway (Sharma and Shi 1999; Zhang and Dong 2007). Alternatively, a sphingolipid metabolite might activate the presumptive ras/raf initiator of this pathway (Raabe 2000), such that removing spt would turn down signaling. Interestingly, the lethality of *lace* was rescued by feeding sphingosine during larval growth, but not by feeding sphingomyelin or ceramide, suggesting that sphingosine or an immediate metabolite may activate the MAP kinase kinase kinase \rightarrow MAPK/ERK kinase (dSor1) → Erk (rolled) survival pathway. A second MAPKKK upstream of death-mediating JNK, the mixedlineage kinase (dMLK) was found to be controlled by ceramide in Drosophila S2 cells (Sathyanarayana et al. 2002). Thus, the one product of sphingolipid metabolism, sphingosine, or more likely its metabolite S1P, mediates survival and prevents apoptosis, whereas the other, ceramide, induces death (Spiegel and Milstien 2002; Fyrst and Saba 2010). Presumably, since the activities of sphingosine and S1P have extremely different consequences for cell survival (Hannun and Obeid 2002), and the concentrations of these molecules differs greatly in the cell, the conversion by sphingosine kinases must be highly regulated. Likewise the single CDase step that converts ceramide to sphingosine must be tightly controlled. Indeed, other ceramide conversion pathways also rescue cell survival, e.g. to glycosylated ceramides by the glucosylceramide synthase GlcT-1, and the *N*-acetylgalactosamine-transferase (GalNAc-T) GlcT-1 over-expression prevents induction of apoptosis by reaper and grim, and RNAi knockouts in GlcT-1 result in widespread embryonic cell death (Kohyama-Koganeya et al. 2004). Likewise, α4GT1 was shown to be an inhibitor of apoptosis in the eye (Protzer et al. 2009).

Another case in which the balance of sphingolipid metabolites regulates cell growth versus death during development was revealed by the loss of S1P-lyase in *sply* mutants. Sply, unlike most other sphingolipid metabolic enzymes, irreversibly removes sphingolipids from circulation by converting S1P to 2-dodecenal and PE, so mutants accumulate huge excesses in both S1P and unphosphorylated sphingoid base metabolites (Herr *et al.* 2003; Fyrst and Saba

2010; Fig. 2). sply animals showed severely abnormal flight muscles and excessive apoptosis in reproductive organs, which could be suppressed by mutation in pro-apoptotic genes reaper and hid (Herr et al. 2003; Phan et al. 2007). This suggested that although there is an overabundance of sphingosine in mutants, the death knell in sply may be dealt ultimately by ceramide, since reaper expression can lead to the production of ceramide (Bose et al. 1998). Reduction in lace (spt2) strongly reduced sply sphingosine/S1P accumulation, as well as its muscle phenotype. Conversely, sply mutations also rescued viability in the lace mutants, supporting the idea that lace apoptosis and lethality may be primarily brought about by a loss of sphingosine or S1P, whereas sply defects presumably arise from excess sphingosine or S1P. Mutations in sphingosine kinases, of which there are two in Drosophila, Sphk1 and Sphk2, should clear up the ambiguity in the effects of these two metabolites, since they should only accumulate sphingosine, but lack S1P. Sphk2 mutants in fact impair flight and reduce fecundity, but do not resemble sply mutants in which the ovaries and testes degenerate. Rather, Sphk2 mutants retain eggs (Herr et al. 2004). Thus, it would appear that accumulation of sphingosine alone cannot explain the defects in sply.

With regard to sorting out the roles of the phosphorylated and non-phosphorylated sphingoid base metabolites, it will also be interesting to find out whether the lipid phosphate phosphatases wunen and wunen2 (Zhang et al. 1997; Starz-Gaiano et al. 2001), among whose targets may be S1P and/or ceramide-1-phosphate (C1P), exhibit similar growth or apoptotic defects to the sply mutants described earlier, which result in excesses of both sphingosine and S1P (Herr et al.

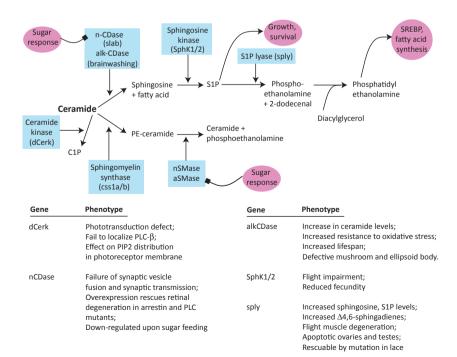


Fig. 2 Biosynthetic pathways of ceramide metabolites sphingosine-1-phosphate (S1P) and phosphoethanolamine (PE)-ceramide, and sphingolipid catabolism via S1P lyase. SREBP, serum response element binding protein activation.

2003). So far, these genes, which are expressed in the nervous system, are known to affect migration of embryonic germ cells by controlling the release of a repellent; notably, the expression of these genes can not only repel the germ cells, but also kill them (Hanyu-Nakamura *et al.* 2004; Sano *et al.* 2005). It is very likely that the *wunen* genes have other functions in the nervous system, since they were also identified in a screen for genes that when over-expressed in the nervous system lead to altered patterns of neuromuscular connectivity (Kraut *et al.* 2001). This finding, along with a subsequent report that S1P affects axon guidance in the visual system of Xenopus (Strochlic *et al.* 2008), may point to S1P as being at least one target of the wunens.

Recently, the same group as cited earlier (Fyrst et al. 2009) detected a novel species of sphingolipid that was present during Drosophila development, namely sphingadienes having two double bonds (designated $\Delta^{4,6}$) instead of the usual one (Δ^4) in the sphingoid base. These were also strongly over-expressed in sply mutants, and similarly to the previously characterized Δ^4 monounsaturated sphingoid bases in sply, were brought back toward normal levels by introduction of a lace (spt2) mutation (Fyrst et al. 2008). Interestingly, sphingadienes were shown to be powerful anti-growth agents and suppressors of tumor cell proliferation via their suppression of Akt kinase; conversely, they were inducers of apoptosis accompanied by caspase activation and poly ADP-ribose polymerase cleavage. At the same time, sphingadienes localized with autophagosomal markers, and induced autophagy, which when dysregulated can also lead to cell death (Fyrst et al. 2009; Pattingre et al. 2009b). Thus, it was postulated that the overabundance of $\Delta^{4,6}$ sphingadienes and corresponding $\Delta^{4,6}$ ceramides were responsible for the muscle degeneration in the sply mutants; indeed these compounds were able to decrease cell proliferation when added to cultured wing disc cells, and were extremely enriched (28×) in mutants in exactly the muscles that were most susceptible (Fyrst and Saba 2008).

Ceramidase, sphingomyelinase, and nutrient metabolism

In mammals, sphingolipid balance has a central role in controlling nutrient utilization and growth (Unger 2003; Holland *et al.* 2007). In particular, the breakdown of sphingomyelin at the plasma membrane by neutral and acid sphingomyelinases (Bartke and Hannun 2009), which produces ceramide, has powerful effects on the storage versus export of cholesterol (Slotte and Bierman 1988; Ridgway 2000), on glucose uptake (Summers *et al.* 1998; Al-Makdissy *et al.* 2003; Liu *et al.* 2004), and on the storage of fats in the form of triacylglycerols (TAG; Deevska *et al.* 2009). Sphingolipids are also activators of serum response element binding protein (SREBP) signaling,

which controls biosynthesis of fats and cholesterol in mammals (Scheek *et al.* 1997; Horton *et al.* 2002; Worgall 2008). Feeding rodents with saturated fat, as found in lard, or with pure palmitate supplemented in the food leads to drastic changes in fat metabolism and insulin resistance, owing to conversion of the fatty acid to sphingolipid (Holland *et al.* 2007). The key metabolite doing the damage is thought to be ceramide, through its repressive effects on protein kinase B/Akt and insulin downstream signaling, since these effects can be mitigated by blocking spt activity with myriocin.

Starting in the 1970s, experiments were done with feeding different high-fat diets, including palmitate, soy, and beef to flies (Driver and Cosopodiotis 1979; Ye et al. 2007). The high-palmitate diet led to shortened lifespan, suggesting possible involvement with insulin-like growth factor/ phosphinositide-3-kinase (PI3K) signaling that is known to control longevity in flies (Britton et al. 2002). Since palmitate in flies also feeds into the sphingolipid biosynthetic pathway, whose immediate effects would be to increase levels of ceramide, one might expect the PI3K signaling to be suppressed, as in the Summers model (Dobrosotskaya et al. 2002; Holland and Summers 2008) where ceramide activates protein phosphatase 2A thereby dephosphorylating and down-regulating protein kinase B/Akt (Dobrowsky and Hannun 1992). It is clearly established that suppression of insulin-like growth factor/PI3K signaling extends lifespan (Broughton and Partridge 2009), but it is possible that very high doses of saturated fat and/or ceramide, as an acute stress and apoptotic signal, might also introduce other toxic or senescence-promoting signals (like sphingosine) that tip the balance toward decrepitude rather than long life (Hannun and Obeid 2008). High saturated fat diets may also be inflammatory and result in oxidative stress in flies, since fatinduced shortening of lifespan in flies was suppressible by the anti-oxidant Acai fruit (Sun et al. 2010). Acai not only increased transcription of stress-response detoxification genes, but in a fat-fed background, it also strongly lowered the levels of phosphoenolpyruvate carboxykinase, the first committed step in gluconeogenesis.

In flies, it is not known whether a sphingolipid-dependent pathway similar to that identified in rodents interferes with insulin signaling and could lead to a diabetic phenotype. However, it is intriguing that changes in sphingolipid metabolic genes were part of the transcriptional response to sugar feeding (but not starvation) of larvae in a study done by the Pankratz lab (Zinke et al. 2002). This microarray study identified an acid Sphingomyelinase (aSMase; CG15533) and a neutral CDase (nCDase/slab, CG1471) both as being down-regulated after sugar feeding, whereas fatty acid synthesis was up-regulated. This result would imply that the products of SMase and CDase, namely ceramide and sphingosine, may have some role in down-regulating fatty acid synthesis, and should be avoided if the desired

metabolic response is increased glucose and fatty acid storage.

Along the same lines, several exciting new studies clearly point to ceramide as playing a regulatory role in fat storage in flies. A fly homolog of the longevity assurance genes, a family of six mammalian dihydroceramide synthases responsible for the synthesis of the various chain-length ceramides (Pewzner-Jung et al. 2006), was identified by virtue of its abnormally thin larval phenotype in mutants. This gene, schlank (meaning slender in German), seems to be the functional homolog of the lass genes in the fly, since only one other homolog was found, and it does not rescue the schlank fat storage defect (Bauer et al. 2009). schlank mutants fail to bulk up during larval development, because of their suppression of fat storage in the form of triacylglycerides (TAGs), of which they have strongly reduced levels. This matched the up-regulation in schlank- animals of the TAG lipase encoded by brummer (Grönke et al. 2005), which is turned on by starvation conditions, and the TAG lipase3 gene, an indicator of the starvation response (Zinke et al. 1999; Fuss et al. 2006). Thus, one of the normal functions of ceramide synthesis by schlank is to participate in the accumulation of fat stores, and in keeping with this, overexpression of schlank gives somewhat higher levels of di- and triglycerides, fatty acids, and increased transcription of both SREBP and fatty acid synthase (Bauer et al. 2009). These results are perhaps consistent with the findings of Zinke et al., where the response to sugar feeding would be to decrease nCDase levels, if ceramides are required to convert sugars into fats via fatty acid synthase and SREBP. Interestingly, sply mutants in mice, similarly to schlank in flies, have reduced adiposity, although they show increased lipid storage in the serum and liver, suggesting that the causative metabolite that leads to such a pathology could be excess sphingosine or sphinganine (see Figs 1 and 2) rather than strictly loss of ceramide (Bektas et al. 2010). However, a fat storage defect in sply flies was not noted.

Ceramide: death molecule or savior?

Interesting insight into the effects of ceramide on developmental maturation as well as oxidative stress and lifespan was provided by a recent paper that analyzed Drosophila alkaline CDase (Dacer) mutants (Yang et al. 2010). This CDase was previously identified as brainwashing, which affects the mushroom and ellipsoid bodies in the brain (Boquet et al. 2000). First, the current authors showed that Dacer does indeed have alkaline CDase activity, and that ceramide levels increase in mutants. Dacer mutants also significantly increased the activity of an enzyme that is required for the production of juvenile hormone, an epoxide that is required for larval growth and prevention of metamorphosis (Postlethwait 1974). Larval developmental time in Dacer mutants was accordingly lengthened by about 50% compared with wild type. In contrast to dCert mutants, which fail to transport ceramide to the plasma membrane (discussed earlier; Rao et al. 2007), loss of Dacer led to an increase in stress resistance. Interestingly, and similarly to yeast that are deficient in alkaline CDase, it also lengthened lifespan substantially (Powers et al. 2006; Yang et al. 2010). The interpretation of this study is complex, since excess ceramide is generally associated with increased apoptosis and deleterious effects, including shortened lifespan (see above; Kohyama-Koganeya et al. 2004; Hannun and Obeid 2008), whereas in this case an increase appears to be beneficial. Perhaps ceramide, as a stress-response coordinator and activator in the MAP kinase kinase kinase \rightarrow JNK pathway (Ruvolo 2003; Fig. 1), is acting to mobilize defenses against acute stress (Hannun and Obeid 2002).

Although the relationships between sphingolipids and nutrient storage, oxidative stress, and lifespan in flies are as yet far from clear, the ability to manipulate at will the genetic background in these animals should allow one to determine definitively which sphingolipid metabolites are responsible for modulating these pathways.

Ceramide metabolites and neuronal function

A study carried out by Acharya et al. (2003) suggested that eliminating ceramide could be protective under certain circumstances, in this case in the background of arrestin and phospholipase C β (PLC; norpA) mutations that lead to photoreceptor degeneration in the fly eye (Acharya et al. 2003). Lowered ceramide levels were achieved by targeted over-expression of the nCDase in the eye, as well as by introducing the lace (spt2) mutation, which decreases de novo synthesis of ceramide (Adachi-Yamada et al. 1999). In both cases, the measured decrease in ceramide levels clearly rescued the degenerative phenotype, which is brought about by hyperstable arrestin-rhodopsin complexes and an accumulation of defective rhabdomeric membranes (Alloway et al. 2000; Kiselev et al. 2000). Both of these genetic backgrounds seemed to exert their effect through a dynamindependent process, suggesting that active endocytosis is particularly important in maintaining the health of neurons, especially photoreceptors. A later study using mutants in the same nCDase (Acharya et al. 2008), which themselves showed photoreceptor apoptosis, came out with the surprising result that the effect of CDase on photoreceptor neurons is non-cell autonomous, and is able to act from as far away as the fat body.

Possibly related to the findings above on the effects of CDase on membrane dynamics and turnover, the group of Broadie et al. found that it is also important for synaptic function of the neuromuscular junction in Drosophila (Rohrbough et al. 2004). Slab (slugabed) mutants in the same nCDase gene that was studied by Acharya et al., although they did not show increased apoptosis in the

nervous system, had impaired pre-synaptic neuronal transmission and faulty synaptic vesicle fusion, as well as a shortage of fusion-ready vesicles.

The Broadie laboratory's findings with slab corroborate the reported role of sphingosine, the product of CDase, in exocytic vesicle fusion events, as suggested initially by genetic studies in yeast, where mutants in the synaptobrevin ortholog snc are rescuable by over-expressing the dihydrosphingosine phosphate lyase DPL1 (Grote et al. 2000), or by combining with certain mutations in ELO genes that are responsible for the elongation of very long chain fatty acids from which ceramides are synthesized (David et al. 1998). Darios et al. (2009) recently demonstrated how this works using an *in vitro* system that identified sphingosine as the key lipid: sphingosine allows the release of the v-SNARE (vesicular-soluble n-ethylmaleimide sensitive factor attachment protein receptor) synaptobrevin from association with phospholipids in the synaptic vesicular membrane such that SNARE fusion complexes can be formed with syntaxin/ SNAP-25 (synaptosomal-associated protein 25) (reviewed in Verhage and van Meer 2009). Ceramides probably affect synaptic growth and morphology as well, by dint of their activation of autophagy (Pattingre et al. 2009a). Autophagy was reported to promote expansion of the larval neuromuscular junction, and this was mediated once again through MAPK pathway members wallenda (a fly MAPKKK) and basket (JNK; Collins et al. 2006; Shen and Ganetzky 2009).

Ceramide metabolites have further functions in photoreceptors beyond maintaining membrane turnover and preventing degeneration. Dasgupta et al. (2009) showed that the product of ceramide kinase, C1P, is involved in phototransduction by PLC activity, and alters the balance and distribution of phosphatidylinositol-4,5-bisphosphate at the membrane. Ceramide kinase (dcerk) mutants, which lack C1P but have more ceramide, fail to localize PLC to membranes. PLC thus degrades, resulting in an excess of phosphatidylinositol-4,5-bisphosphate (PIP2) (Fig. 2). This work stands out in that it is one of the few that combines genetic methods with biophysical tests - in this case, fluorescence image correlation spectroscopy on supported lipid bilayers – to try to relate the behaviors of sphingolipids in membranes with their physiological functions in a biological process like phototransduction. This is an approach that will surely reap insight into the interplay between the interesting membrane properties of sphingolipids and their effects on signaling and developmental events.

Glycosphingolipids in development and the nervous system

Arthropod glycosphingolipids have been known for many years (Wiegandt 1992), but their composition specifically in *Drosophila* was only determined recently by Seppo *et al.* (2000) and Wandall *et al.* (2003, 2005) using TLC. Fly

glycosphingolipids are quite different from their mammalian counterparts in that the core disaccharide consists of Man^{β1–4}Glc^{β1}-Cer, aka mactosyl-ceramide, instead of Gal^{β1–4}Glc^{β1}-Cer in mammals (Seppo and Tiemeyer 2000; Fig. 3). There are 12 major species of glycosphingolipid, none of which are sialylated as in mammals, but many containing one or two PE-substituted-GlcNAc(Seppo *et al.* 2000). Glycosphingolipids can be very long in flies, the longest species having 10 sugar residues (GlcNAc, GalNAc, galactose, or a terminal glucuronic acid) in a linear chain.

The first evidence that glycosphingolipids have major effects on well-known developmental pathways in flies came from the identification of two mutants, called egghead and brainiac, so named because they had embryonic neuronal hypertrophy phenotypes similar to *Notch* mutants (Goode et al. 1992). In addition to Notch-like phenotypes, egghead and brainiac led to identical defects in polarity and adhesion of oocyte follicular epithelial cells, which was proposed to arise from an interaction with epidermal growth factor receptor (EGF-R), the receptor mediating a back-and-forth signaling between the developing oocyte and the surrounding follicle cells (Goode et al. 1996a,b; Nilson and Schupbach 1999). Egghead and brainiac turned out to encode the glycosyl transferases responsible for sequential addition of the second and third sugar residues, mannose and GlcNAc, that form the core of all Drosophila glycosphingolipids, and whose products in insect cells were determined by TLC, mass spectrometry, and NMR in vitro (Müller et al. 2002; Schwientek et al. 2002; Wandall et al. 2003) and in vivo (Wandall et al. 2005). Interestingly, the blockage of the core mactosyl-ceramide and the resultant phenotype in egghead animals could be fully rescued by introducing a transgene for the human galactosyltransferase enzyme, which makes lactosyl ceramide (Wandall et al. 2005). Apparently, flies can function perfectly well with the mammalian lactosyl core instead of their own mannose-containing core.

Enzymes that catalyze further steps in more complex glycosphingolipids have also been identified, among them the \beta 4-N-GalNAc transferases A and B, which in the case of transferase A (GalNAc-T A) mutants alone, had neuromuscular innervation and coordination defects (Haines and Irvine 2005; Haines and Stewart 2007). Unlike the egghead and brainiac deficiencies in core glycolipids, flies seem to be able to do without these GalNAc-ylated complex glycolipids for most essential functions, as the β4GalNAc-TA, B double mutants are viable and fertile (Haines and Irvine 2005; Stolz et al. 2008). The group of Cohen, however, not only confirmed the results of Haines et al. that transferase A displays un-coordination and abnormal climbing behavior, but that the other transferase mutant β4GalNAc-TB showed ventralized ovarian follicles similar to egghead, brainiac, and EGF-R knockouts (Chen et al. 2007), and moreover that both of these phenotypes interacted genetically with egghead and brainiac. Further, it was shown that the transferase acts

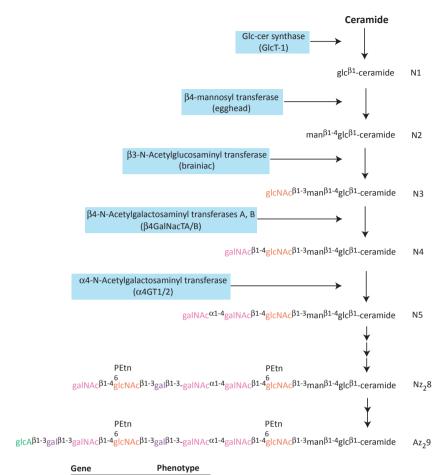


Fig. 3 Glycosphingolipid biosynthesis in *Drosophila*. Notation with N = number of sugar residues in the neutral core, and z = number of phosphoethanolamine (PEtn) substituted N-acetylglucosamine (GlcNAc) residues, is according to Seppo *et al.* (2000). Shorter variants with fewer sugars (colored) also exist, but are not shown.

GlcT-1	Apoptosis in embryo; overexpression suppresses apoptosis induced by reaper and grim
Egghead/ brainiac	Notch-like neuronal hypertrophy; Defective EGF-R signaling in oocyte (ventralized follicle cells)
β4GalNacTA/B	(A) Defective neuromuscular junction innervation and coordination;(B) Similar to egghead/brainiac defective oocyte
α4GT1/2	Overexpression suppresses Mindbomb Notch-like phenotype and inhibits apoptosis in eye disk (no phenotype alone)

in the oocyte, which produces $TGF\alpha$ -like ligand *gurken* and secretes it to the follicle cells, leading to the speculation that N4 or higher order glycosphingolipids might be involved in the secretion or distribution of the $TGF\alpha$ -like signal, or interact with its EGF-R receptor (Chen *et al.* 2007). In fact, a follow-up study by the same group demonstrated that glycosphingolipid is required for the distribution of the *gurken* ligand gradient, but not for its secretion or for EGF-R activity *per se* (Pizette *et al.* 2009).

An α 1,4GalNAc-T in flies has also been identified (Protzer *et al.* 2009), in which a specific (but again, not lethal) interaction was discovered with Notch signaling, in a recent study by the Schweisguth group (Hamel *et al.*

2010). Here, Gal4-mediated over-expression of the α 1,4GalNAc-T gene was found to suppress the Notch-like phenotype of loss of function in *mindbomb* (*Mib1*), an E3 ubiquitin ligase that functions in Notch endocytosis and activation. The Notch ligand Serrate was also found to bind to glycosphingolipids, suggesting that glycosphingolipids act at multiple steps in the Notch signaling cascade. Although the disruption of α 1,4GalNAc-T by itself has no detectable phenotype, the interaction of its glycosphingolipid products with Notch possibly contribute to the more severe phenotypes of *egghead* and *brainiac*, which disrupt an earlier step in glycosphingolipid biosynthesis (Hamel *et al.* 2010).

On the subject of signaling receptors interacting with sphingolipid-rich domains, it is interesting to note that a study of olfactory receptor neurons in the moth Manduca was able to detect what appeared to be cholesterol-dependent membrane domains containing both glycosphingolipid, recognized by fluorescent lectins, and various signaling receptors including EGF-R and the cell-adhesion molecules FasII and neuroglian (Gibson et al. 2009). In humans and mice, the EGF-receptor (Puri et al. 2005; Lajoie et al. 2007) and insulin receptors are thought to be able to translocate into sphingolipid-rich domains where they are regulated by particular gangliosides, in both cases GM3 (Rebbaa et al. 1996; Yamashita et al. 2003; Kabayama et al. 2007). Taking a cue from mammalian cells, where glycosphingolipids are known in many cases to interact directly with cell surface receptors and regulate their lateral organization and signaling capability (Proia 2003; Lopez and Schnaar 2009), the above studies of fly glycosphingolipid biosynthesis mutants hint that the same is very likely to be true in Drosophila. As the previous examples of different glycosphingolipid deficiencies show, flies provide an excellent system in which to detect genetic interactions that will reveal the players involved.

Sphingolipids and cholesterol

The usefulness of *Drosophila* as a model for metabolic processes and diseases that involve cholesterol has been questioned because flies regulate sterols - the single most abundant structural component of mammalian membranes – completely differently from mammals. Flies are sterol auxotrophs, meaning that they do not synthesize their own sterols, but rather absorb them (primarily ergosterol) from their main food source, yeast. Fly membranes also contain considerably less sterol proportionately than mammalian membranes, being only $\sim 18\%$ versus $\sim 30\%$ (Rietveld et al. 1999; http://www.Cyberlipid.org). Unexpectedly, Drosophila cells in culture, like Schneider S2 cells, are able to survive and divide after sterol depletion (Gupta et al. 2009), casting serious doubt on any critical function of sterol in their basic physiology. By extension, sphingolipid biosynthesis and storage, which is known to be closely coupled with cholesterol (Guan et al. 2009), would be expected to be regulated differently from mammals, although very little is known about this at present.

Although many of the critical lipid metabolic enzymes are there, including hydroxymethylglutaryl (HMG)-CoA reductase, which synthesizes mevalonate, the precursor to cholesterol biosynthesis, the SREBP pathway that regulates cholesterol and lipid biosynthesis in mammals is not controlled by feedback through cholesterol concentration in the membrane (Dobrosotskaya *et al.* 2002). Moreover, and somewhat surprisingly, SREBP does not control hydroxymethylglutaryl (HMG)-CoA reductase, but rather the

synthesis of saturated fatty acids. Although most SREBP pathway components are present in the fly, its activity is instead regulated by the glycerol lipid phosphatidylethanolamine (PE), the major constituent of cell membranes in *Drosophila* (Jones *et al.* 1992; Rawson 2003). Sphingolipids also play a regulatory role in SREBP cleavage by controlling the availability of PE, since the ethanolamine group on this lipid can be donated indirectly by S1P (Herr *et al.* 2003). Notably, palmitate, but not sterols or other fatty acids, block cleavage of SREBP when added to *Drosophila* cultured cells, and this blockage is dependent on cycling through sphingolipids. Another possible source of PE would be cleavage of PE-ceramide by a SMase (Fig. 2).

Niemann-Pick models in the fly

Fly models of diseases that arise from aberrant cholesterol storage have come on the stage recently, with the analysis of mutants in the various orthologs of the genes responsible for the neurodegenerative disease Niemann-Pick type C, NPC-1 and NPC-2. These are important in considering the potential validity of fly models of sphingolipid storage diseases and neurodegeneration, because of the established interdependence of sterol and sphingolipid trafficking, degradation, and metabolism (Puri et al. 1999, 2003; Ridgway 2000) even in eukaryotes much less advanced than Drosophila (Guan et al. 2009). In the first of these NPC models, one of two fly homologs of NPC-1, dnpc1a, was mutated and this led to accumulated sterol throughout the body and developmental arrest in first instar larvae. Dnpc1a mutants could be fully rescued by feeding with the sterol precursors of the ecdysone molting hormone, suggesting that the main problem was that sterol was being sequestered in aberrant compartments and unable to be released for ecdysone production (Huang et al. 2005; Fluegel et al. 2006). Of the eight NPC-2 genes in Drosophila, Dnpc2a was the most conserved with human NPC-2, and mutants looked similar to Dnpc1a in their aberrant punctate accumulation of sterol in some tissues, including brain (Huang et al. 2007).

Since NPC in humans is severely neurodegenerative, presumably owing to a backup of cholesterol in degradative compartments of neurons, and resultant malfunctioning of endolysosomal trafficking (Vance et al. 2005), it was hoped that NPC models in *Drosophila* would show parallels to the disease, even though flies are sterol auxotrophs. In fact, alteration of cholesterol metabolism and storage was documented in another neurodegenerative mutant called *löchrig* (German for full of holes, referring to the brain degeneration in mutants), which corresponds to the gamma subunit of AMP-kinase (Tschäpe et al. 2002). It is interesting that a degenerative phenotype was accompanied by these changes in fat metabolism, but the degeneration was not shown to be actually caused by the increase in free cholesterol. The first clear indication that sterols in the fly may indeed play a part

in the metabolic health of neurons, instead of being just a precursor to ecdysone hormone and a comparatively minor structural component of membranes, was that certain mutant combinations of Dnpc2 and mutants in Dnpc1a led to not only sterol accumulation but also to other defects, such as lipofuscin-like membrane whorls and axonal accumulations of synaptotagmin, as well as shortened lifespan and neurodegeneration, which was rescuable in a cell-autonomous way (Huang et al. 2007; Phillips et al. 2008).

It was not established in these NPC models whether sphingolipid metabolism and trafficking were also affected, but this is certainly not far-fetched, given the situation in yeast and humans (Puri et al. 1999; Simons and Gruenberg 2000; Guan et al. 2009). A convincing case has been made that the defect in NPC-1 disease in humans is traceable to a primary accumulation of sphingosine in acidic compartments, which depletes lysosomal calcium and as a result ultimately leads to storage of other sphingolipids and cholesterol in endolysosomal compartments (Lloyd-Evans et al. 2008).

The observation that Drosophila appear to recapitulate neurodegenerative features of NPC disease, in spite of having a very different mode of sterol metabolism from humans, makes one optimistic that flies could also present a viable model for the numerous sphingolipid storage diseases that share a common cell biology and pathology with NPC. That sphingolipid misregulation can indeed lead to neurodegenerative defects in *Drosophila* was suggested by studies of the gene spinster, whose zebrafish ortholog Spns2 was deduced to be a S1P transporter, based on its phenocopying the defect of the S1P-receptor mutation in heart development (Kupperman et al. 2000; Kawahara et al. 2009). Although a S1Preceptor has not been identified in flies, spinster mutants accumulate multilamellar lipofuscin granules in the nervous system, and undergo some neuronal degeneration preceded by a defect in programmed cell death (Nakano et al. 2001; Dermaut et al. 2005). Intriguingly, loss of the Spinster protein (also called Benchwarmer), which is a late endolysosomal 12-pass transmembrane protein very distantly related to sugar transporters, also leads to enlargement of late endolysosomal compartments at synaptic termini and in oocytes in Drosophila (Sweeney and Davis 2002; Dermaut et al. 2005), where purportedly carbohydrate accumulation recognizable by the periodic acid Schiff stain occurs (Dermaut et al. 2005). Given the link to sphingolipid transporters, and the lysosomal accumulation of lipofuscinlike material in *spinster*, the question that springs to mind is whether the carbohydrate accumulation seen in these animals may actually arise from non-degraded glycolipids. If this is the case, spinster mutants would serve as an excellent model for lysosomal sphingolipid storage diseases, such as the gangliosidoses (Kolter and Sandhoff 2005).

Of potential relevance to these models, recent studies using sphingolipid tracers in Drosophila cultured neurons showed that increasing or decreasing the levels of sterols in the cells altered the trafficking behavior of a fluorescently tagged glycosphingolipid (boron-dipyrromethene [BODIPY]lactosyl-ceramide; Hortsch et al. 2010) and a raft- and sphingolipid-interacting peptide, the SBD (Hebbar et al. 2008; Steinert et al. 2008), in ways that would suggest that cellular sterol content controls a toggle switch between biosynthetic versus degradative pathways, as is the case in mammalian cells (Puri et al. 2001; Choudhury et al. 2004; Zhang et al. 2009). These studies provide support for the validity of fly models of lipid storage diseases that arise from sphingolipid and/or sterol accumulation, such as NPC, the gangliosidoses, and the lipofuscinoses, since it appears that the trafficking and storage mechanisms of sphingolipids are similar. More such cell biological analyses in primary cells from mutants and drug-fed or nutrient-controlled animals should enable a quite precise analysis of changes in sphingolipid trafficking and accumulation under different conditions that might affect lipid metabolism. This type of study would be facilitated by the development and validation of more sphingolipid-recognizing labels in fly cells as well as the application of high resolution imaging methods.

Conclusion

In Drosophila as much as in other systems, one of the major obstacles to analyzing the interplay between sphingolipids and the response to nutrients, or the response of sphingolipids to pathological conditions like diabetes and neurodegeneration, is the intrinsically self-correcting property of metabolism. Feedback loops and compensatory mechanisms, often coming from multiple enzymes whose activity can result in the same product (Merrill and Sandhoff 2010), may obscure fluctuations in levels of sphingolipids such that at steady state, they cannot be detected. Since the analysis of phenotypes and metabolites is generally done after extensive developmental time and averaged over many samples, it is difficult to determine the immediate responses to certain conditions or treatments. This probably results in acute changes in the representation of different sphingolipid species being masked by compensatory responses in the animal's physiology. In flies, this problem could be solved by analyzing lipids in genetic backgrounds that may reduce compensatory pathways (see, e.g., Breslow et al. 2010), and in animals that over-express sphingolipid metabolic enzymes in a spatially and temporally controlled manner.

In spite of differences from humans in both the variety of sphingolipid species present in the fly, and its means of regulating the sterol content of its membranes, it is obvious that sphingolipids are just as critical to developmental and metabolic processes in the fly as they are in mammals. With the growing popularity of Drosophila as a model for metabolic diseases, such as obesity and diabetes (Baker and Thummel 2007; Al-Anzi et al. 2009), more studies have

appeared that model these pathologies in the fly as a surprisingly good parallel to their human counterparts. Given the similarities, sphingolipids will also surely play a role in fly models of other diseases with a metabolic component, such as neurodegeneration. Importantly, novel visualization tools, as well as traditional and high accuracy mass spectrometry-based lipid analytic studies are showing that the nuts and bolts of sphingolipid cell biology and physiology are conserved. This by itself is a major advance, since with this knowledge one can now begin to combine very sophisticated fly genetics with analytical and pharmacological methods that are standard in lipid biochemistry, but not yet commonplace among Drosophilists.

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