Title

Insulin/insulin-like growth factor signaling pathway promotes higher fat storage in *Drosophila*

females

Authors

Puja Biswas[1], Huaxu Yu[2], Lianna W. Wat[1,3], Colin J. Miller[1], Tao Huan[2], Elizabeth J.

Rideout[1,4, *]

Affiliations

[1] Department of Cellular and Physiological Sciences, Life Sciences Institute, The University

of British Columbia, Vancouver, Canada.

[2] Department of Chemistry, Faculty of Science, The University of British Columbia,

Vancouver, Canada.

[3] Present address: Department of Pathology, Stanford Diabetes Research Center, Stanford

Cardiovascular Institute, Stanford University School of Medicine, Stanford University

[4] Lead contact

* Correspondence: elizabeth.rideout@ubc.ca

Summary

In *Drosophila*, adult females store more fat than males. While the mechanisms that restrict

body fat in males are becoming clearer, less is known about how females achieve higher fat

storage. Here, we perform a detailed investigation of the mechanisms that promote higher

fat storage in females. We show greater intake of dietary sugar supports higher fat storage

due to female-biased remodeling of the fat body lipidome. Dietary sugar stimulates a female-

specific increase in *Drosophila* insulin-like peptide 3 (Dilp3), which acts together with greater

peripheral insulin sensitivity to augment insulin/insulin-like growth factor signaling pathway

(IIS) activity in adult females. Given that adult-specific IIS inhibition reduced the sex

difference in fat storage due to a female-biased decrease in body fat, our data reveal IIS as

a key determinant of female fat storage.

Keywords

Sex difference, body fat, triglyceride, insulin/insulin-like growth factor signaling pathway,

sugar, insulin sensitivity

Introduction

In *Drosophila*, as in other animals, triglyceride is the main stored form of fat[1]. The primary depot for stored fat in insects is called the fat body[1]; however, other cell types and organs in the body also have the capacity to synthesize and store triglyceride (*e.g.*, gut, oenocytes, neuron, glia, muscle, testis, ovary)[2-9]. While many factors influence the total amount of stored fat, one important determinant of body fat in flies is biological sex[5,9,10]. For example, *Drosophila* virgin females store more fat than males[5], a difference that is amplified post-mating[9,11]. Virgin female flies also break down fat more slowly than males after nutrient withdrawal[5]. These sex differences in body fat regulation are physiologically relevant for reproduction. In females, greater fat stores are needed to support the energetic demands of reproduction[9,12] and to survive long periods without food[5]. In males, restricting excess triglyceride accumulation is important to maintain fertility[8].

Over the past two decades, studies in *Drosophila* have played a key role in identifying many genes and pathways that contribute to whole-body fat storage. For example, loss-of-function mutations or RNAi-mediated knockdown of genes predicted to promote triglyceride synthesis lead to reduced fat storage in both individual cells and in the whole body[12-16]. In contrast, genetic inhibition of genes predicted to facilitate triglyceride breakdown cause a significant increase in fat storage at the cellular and organismal levels[17-19]. Gain- and loss-of-function experiments with genes predicted to regulate lipid droplet dynamics, a specialized organelle dedicated to triglyceride storage, similarly influence cellular and organismal fat stores[16,19-24]. Beyond these enzymes directly involved in triglyceride metabolism and lipid droplet biology, large-scale screening efforts have revealed many additional genes that influence *Drosophila* body fat[4,18,25-39].

In addition to the action of individual genes, a large body of literature has identified many hormones and peptides that influence whole-body fat storage[9,40-57]. In many cases, these hormones modulate whole-body fat storage via effects on cells that produce

adipokinetic hormone (Akh)[43-46,58] and *Drosophila* insulin-like peptides (Dilps)[30,43,45,59-62].

Akh and Dilps have opposing effects on whole-body fat storage[63]. Under conditions where

nutrients are plentiful, Dilps are released from the median neurosecretory cells in the

Drosophila brain into the hemolymph. Binding of the Dilps to the insulin receptor (InR) on

the fat body stimulates the insulin/insulin-like growth factor signaling pathway (IIS) to

promote fat storage[53]. When nutrients are scarce, Akh is released into the hemolymph from

the Akh-producing cells in the *corpora cardiaca*[46,64-67]. Akh binds to the Akh receptor (Akhr)

located in the fat body where it promotes fat breakdown[55-57]. While studies on specific genes

and hormones have advanced knowledge of the mechanisms underlying the regulation of

fat storage, most studies used single- or mixed-sex animal groups. As a result, we know

less about the mechanisms underlying sex differences in fat storage.

Recent studies have begun to close this knowledge gap. Both large-scale RNAseq

data and targeted gene expression studies reveal profound sex differences in expression of

genes known to influence cellular and whole-body fat storage[5,68,69]. For example, male flies

express higher mRNA levels of the *Drosophila* homolog of adipose triglyceride lipase called

brummer (*bmm*), an enzyme that limits triglyceride accumulation across most cell types[17].

This male-biased *bmm* expression is physiologically significant, as whole-body loss of *bmm*

abolishes the sex difference in fat storage via a male-biased increase in body fat[5]. A similar

male bias has also been reported in the production and secretion of Akh[10]. Specifically,

males produce and secrete more Akh than females under basal conditions, which prevents

fat accumulation to drive lower body fat in males[10]. A sex bias in two central lipolytic

pathways therefore plays a key role in establishing the sex difference in body fat by

restricting triglyceride accumulation in males. Yet, the mechanisms that allow increased fat

storage in females remain less clear, as females are largely unaffected by loss of *bmm* and

Akh[10].

In mated females, higher levels of steroid hormone ecdysone enhance body fat by

stimulating food intake[9]. Adult mated females also show higher mRNA levels of Dilp3[70],

where Dilp3 has been implicated in promoting fat storage[43,62]. Whether these mechanisms

also influence the sex difference in fat storage remains unclear. We therefore performed a

detailed analysis of adult virgin males and females to explore how females achieve a higher

level of fat storage. We found that virgin female flies normally consume more food than

males, and show that female fat storage is sensitive to changes in food quantity. In particular,

consumption of dietary sugar and not simply a greater number of calories explained this

higher fat storage in females. Unbiased lipidomic and metabolomic analysis of abdominal

carcasses from adult flies revealed dietary sugar caused a profoundly female-biased

metabolic remodeling of energy-storing cells including the fat body. Given that ecdysone did

not promote increased body fat in virgin females, we characterized sex differences in IIS,

the other key pathway that promotes fat storage. We identified a significant female bias in

Dilp3 mRNA levels and fat body insulin sensitivity, leading to increased IIS activity in the

female fat body. This sex bias in IIS was significant in promoting female fat storage, as

ablating the Dilp-producing cells in adults caused a female-specific reduction in body fat.

Together, these data identify IIS as a key pathway that promotes higher fat storage in adult

females.

Results

Dietary sugar promotes increased fat storage in adult females

To determine whether unmated females have higher food intake than males we used the

capillary feeder (CAFE) assay[71] to assess food consumption in 5-day-old *Drosophila* virgin

males and females. Five-day-old adult *Canton-S* (*CS*) females consumed significantly more

food per body weight over 24 hr than genotype-matched males (Figure 1A), a trend we

reproduced in 5-day-old *w[1118]* adults (p=0.0812; Figure S1A). Considering changes in food

intake affect body fat[26,47,72], this suggests higher food consumption may explain this

increased fat storage in females. Indeed, reducing nutrient content in the diet significantly

reduced body fat in *CS* females (Figure 1B). Because body fat in *CS* males was unaffected

by an identical food dilution (Figure 1B), the sex difference in body fat was reduced. We next

tested the contribution of specific diet components to higher fat storage in females. Given

that dietary sugar affects body fat in a mixed-sex population of *Drosophila*[73-77], we

transferred newly-eclosed *CS* and *w[1118]* flies to a diet lacking added sugar (0S) for 5 days[78].

In both *w[1118]* and *CS* strains, adult females transferred to the 0S diet had significantly less

body fat compared with genotype-matched flies kept on a widely-used lab diet with sugar

(1S; Figure 1C and S1B)[79]. Because the magnitude of the reduction in body fat was smaller

in *w[1118]* males (Figure 1C; sex:genotype interaction $p<0.0001$), with the same trend in *CS*

males (Figure S1B), the sex difference in fat storage was reduced.

The female-biased reduction in fat storage on 0S cannot be attributed to altered food

intake on the low-sugar diet, as food consumption was not different between flies kept on

the 0S diet compared with flies transferred to the 1S diet (Figure S1C). A decrease in

calories similarly cannot explain the effect of reduced sugar on body fat, as female flies

transferred to a reduced-calorie diet with sugar still had higher body fat than females kept

on the 0S diet (Figure 1D). Because neither sucrose nor D-glucose on their own were

sufficient to restore fat storage to the level observed in females maintained on the 1S diet

(Figure 1E), our data suggests it is the total amount of sugar rather than a specific sugar

that promotes increased fat storage in female flies. Indeed, providing females with more

sugar is sufficient to augment body fat even further (Figure 1F). Supporting a model in which

the nutritive value of sugar rather than sweet taste promotes increased female fat storage,

body fat was not higher in either male or female flies kept on the 0S diet containing a non-

nutritive but sweet-tasting sugar[80] (Figure S1D). Thus, our data suggest that higher food

intake, specifically increased consumption of dietary sugar, promotes higher fat storage in

females.

Female-biased effect of dietary sugar on metabolism

To assess how sex and dietary sugar affect the lipidome and metabolome of fat-storing

organs in *Drosophila*, we performed untargeted mass spectrometry (MS)-based lipidomic

profiling on abdominal carcasses isolated from adult male and female flies transferred to

either a 1S or 0S diet as adults. We detected 464 lipid species in total (Supplemental Table

S1). We first compared lipid abundance between males and females. We identified sex

differences in the abundance of 163 lipids in flies maintained on the 1S diet ($p<0.01$): 117

lipid species were significantly higher in females and 46 lipid species were significantly

higher in males (Figure 2A). Triglyceride was the lipid subclass showing the strongest female

bias, with 48/57 (86%) species significantly higher in females compared with males (Figure

2B). This supports increased stored fat in females. When we examined the chain length of

fatty acids in the triglyceride pool, we found that females had a greater percentage of

monounsaturated fatty acids such as myristoleic acid (C14:1), palmitoleic acid (C16:1), and

oleic acid (C18:1) in the triglyceride pool (Figure S2A). Females also showed a greater

percentage of most odd-chain fatty acids in the triglyceride pool (Figure S2A), with a similar

female bias in C28:2 (7/7). In males, there was a strong bias in levels of C24:1 (4/4) in the

triglyceride pool (Figure S2A). Beyond triglyceride, we also noted a significant female bias

in lipids such as acyl-carnitine (acyl-Car) (4/5), ceramide (Cer) (4/7), diacylglycerol (DG)

(6/9), phosphatidylcholine (PC) (16/25), ether-linked phosphatidylcholine (PC-O) (4/6),

phosphatidylethanolamine   (PE)   (17/20),   phosphatidylglycerol   (PG)   (3/3),

phosphatidylinositol (PI) (3/3), sterol-ester (SE) (4/4) and sterol (ST) (4/4) (Figure 2B). Lipids

with a significant male bias included lysophosphatidylcholine (LPC) (2/3) and ether-linked

triacylglycerol (TG-O) (12/13) (Figure 2B). As with lipids, there was a significant female bias

in many metabolites ($p<0.05$) (Figure 2C), including asparagine, glutamine, glutamic acid,

glucose-6-phosphate, ADP, propionylcarnitine, pantothenic acid, which together suggest a

female bias in glycolysis and the tricarboxylic acid (TCA) cycle. Thus, our data show that

biological sex is a key regulator of the lipidome and metabolome.

To determine how dietary sugar affects the lipidome and metabolome in each sex,

we compared these parameters in abdominal carcasses of flies transferred to the 1S or 0S

diets as adults. In females, we observed significant differences in levels of 218 lipids

between flies transferred to 1S compared with flies out on 0S ($p<0.01$). Specifically, dietary

sugar was associated with an increased abundance of 154 lipids and reduced abundance

of 64 lipids (Figure 2D). Triglyceride showed the largest sugar-dependent change in

abundance, where females maintained on 0S had significantly lower triglyceride abundance

than females kept on 1S (61/81) (Figure S2B-D), consistent with our triglyceride assay data.

Females maintained without sugar had a lower percentage of many fatty acids, such as

C16:1 and C18:1, in the triglyceride pool compared with females kept on the 1S diet (Figure

S2E). A similar reduction in the abundance of C28:2 in the triglyceride pool was also

observed in females maintained on 0S (Figure S2E). Broader effects of reduced dietary

sugar were also observed across many lipid subclasses in females: Acyl-Car (3/4), Cer (5/9),

DG (11/17), PC (29/33), PC-O (4/7), PE (25/27), PG (5/5) (Figure S2B). Lipids that were

significantly higher in abundance in females maintained on the 0S diet included PI species

(2/6) and TG-O (4/21) (Figure S2B). Because body size is fixed before the adult stage of

development[81], and the females are only fed 1S or 0S after eclosion, these diet-induced

alterations in lipid abundance cannot be explained by a sugar-dependent change in body

size. In males, only 27 lipid species were differentially regulated by dietary sugar: 17 lipids

were higher in abundance in flies maintained on a 1S diet whereas 10 lipids were lower in

abundance (Figure 2E and S2F). Lipids that were lower in abundance in males on the 0S

diet included PC (7/7), PC-O (2/3), triglyceride (4/6) (Figure S2G).

This female bias in sugar-induced changes in the fat body was reproduced in our

metabolomic data (Supplemental Table S1, Figure 2F): 38 metabolites showed a difference

in abundance in females maintained on the 0S diet whereas only 13 metabolites were

altered in males kept on 0S ($p<0.05$ threshold for both sexes) (Figure 2F). Metabolites that

were altered in females on the 0S diet indicate reduced glycolysis and TCA cycle

(asparagine, glutamine, glutamic acid, glucose-6-phosphate, ADP, nicotinamide,

propionylcarnitine, pantothenic acid) and lower oxidative stress (oxidized glutathione, tans-

4-hydroxy-L-proline, methioninesulfoxide, L-5-oxoproline (also known as pyroglutamic acid),

kynurenine) (Figure 2F). In males, metabolites that were altered suggest reduced glycolysis

on the 0S diet (nicotinamide, NAD, AMP) (Figure 2G). Dietary sugar therefore caused a

strongly female-biased remodeling of the lipidome and metabolome in abdominal carcasses.

While the reason for this profound female bias in changes to the lipidome and metabolome

in response to dietary sugar is unclear, males showed higher levels of sugar excretion on

the 1S diet (Figure 2H).

Dietary sugar promotes sex differences in IIS regulation

Considering dietary sugar stimulates the production and secretion of Dilps from the insulin-

producing cells (IPC) in the brain[82-85], we tested if Dilp production, Dilp secretion, and IIS

activity differed between males and females maintained on 1S. We first measured mRNA

levels of IPC-derived *dilp2*, *dilp3* and *dilp5* in adult heads using quantitative real-time

polymerase chain reaction (qPCR). Female heads had higher mRNA levels of *dilp3* than

male heads (Figure 3A); no significant differences in mRNA levels of *dilp2* and *dilp5* were

found between the sexes (Figure 3B and 3C). To test whether dietary sugar caused the sex

difference in *dilp3* mRNA levels, we compared *dilp3* mRNA levels in males and females

transferred to either 1S or 0S diets as adults. Female flies transferred to 0S had significantly

lower *dilp3* mRNA levels than females kept on 1S (Figure 3D). Because there was no sugar-

dependent change in male *dilp3* levels, the sex difference in *dilp3* levels was eliminated

(Figure 3D; sex:diet interaction *p*=0.0128). Our data therefore suggest dietary sugar plays a

role in the female bias in *dilp3* mRNA levels. We next monitored Dilp secretion from the IPCs

in the brain by expressing a calcium-responsive chimeric transcription factor LexA-VP16-

NFAT (*UAS-LexA-VP16-NFAT* [called *UAS-CaLexA*]) specifically in these cells using *dilp2-*

GAL4 (full genotype *dilp2-GAL4>UAS-LexA-VP16-NFAT*). This chimeric transcription factor

drives expression of GFP in response to changes in cellular calcium levels, providing an

indirect readout for neuronal activity and consequently Dilp release[86]. On the 1S diet, there

was no significant difference in GFP expression between males and females in the IPC

(Figure 3E). This suggests Dilp release was equivalent between the sexes, confirming

results from a very recent study showing IPC activity does not differ between the sexes[87].

Given the female bias in *dilp3* mRNA levels, and the known role of *dilp3* in promoting

IIS activity, we next compared IIS activity in males and females. To assess IIS activity, we

measured mRNA from known transcriptional targets of Forkhead box, sub-group O (Foxo;

FBgn0038197) in male and female abdominal carcasses. When IIS activity is high, Foxo is

phosphorylated and repressed, leading to lower mRNA levels of its known target genes *InR*,

bmm, and *eukaryotic initiation factor 4E-binding protein* (*4E-BP*)[88-91]. In adult males and

females maintained on 1S, mRNA levels of Foxo target genes were significantly lower in

females than in males (Figure 3F). This suggests IIS activity is normally higher in females

than in males. Given that *Drosophila* female larvae are more insulin sensitive than male

larvae[78], a sex difference that also exists across many tissues in mammals[92,93], we also

compared insulin sensitivity between adult virgin males and females kept on 1S. Considering

female abdominal carcasses showed significant insulin-induced repression of Foxo target

genes (Figure 3G), a response we did not observe in males (Figure 3H), our data suggest

female abdominal carcasses are more insulin sensitive than males. Taken together, our data

show that dietary sugar promotes higher expression of *dilp3* in females. Increased *dilp3*,

combined with higher insulin sensitivity in females, likely contribute to elevated IIS activity in

females compared with males.

Females require IIS to maintain fat storage

Insulin is a potent lipogenic hormone in multiple animals including *Drosophila*[53,94-98].

Increased IIS activity in female abdominal carcasses may therefore explain their higher fat

storage. Because reduced IIS activity during development significantly impairs larval growth

and survival to adulthood[54,99-104], and increased IIS activity during development augments

body size[103-106], we needed a system to modulate IIS activity specifically in adults.

Unfortunately, existing systems for inducible gene expression have undesirable limitations

for studying sex differences in fat metabolism. The Gene Switch system[107,108] induces

transgene expression by feeding flies mifepristone, which has sex-specific effects on adult

physiology[109-111]. The AGES (Auxin-inducible Gene Expression System) uses auxin feeding

to induce transgene expression[112], which we and others recently showed affects feeding

and triglyceride metabolism in a sex-biased manner[113].

Another inducible system for gene expression, the temporal and regional gene

expression targeting (TARGET) system[114], normally requires long-term temperature shifts

at 29°C to inactivate temperature-sensitive repressor GAL80. Given that inactive GAL80

cannot repress GAL4, UAS transgene-mediated expression is initiated as long as the

animals are kept at 29°C. Unfortunately, 29°C is a temperature known to disrupt lipid

metabolism[115,116], making a long-term heat shock to induce transgene expression or RNAi-

mediated knockdown undesirable. To overcome this limitation, we reasoned that we could

deliver a brief 3 hr heat shock to newly-eclosed male and female flies to transiently express

proapoptotic gene *reaper* (*rpr*) specifically in the IPC (genotype: *dilp2-GAL4>UAS-rpr,tub-*

GAL80^ts). We expected this approach would ablate the IPC specifically in adults. Supporting

successful IPC ablation, mRNA levels of *dilp2, dilp3* and *dilp5* were significantly lower in

adult heads from female and male flies with a brief heat shock compared with genotype-

matched controls without heat shock (Figure 4A and 4B). Additional evidence supporting

effective IPC ablation was the extremely long lifespan of the IPC-ablated female and male

flies (Figure 4C and 4D)[117-122] and the reduced fertility in female flies (Figure 4E)[123]. IPC

ablation in male flies had no effect on fertility (Figure 4F).

Using this system to ablate the IPC, we tested whether increased IIS was required

for females to store more body fat than males. We found that triglyceride levels were

significantly lower in 5-day-old females with ablated IPCs (genotype *dilp2-GAL4>UAS-*

rpr,tub-GAL80^{ts}) than in control females (genotypes *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-*

rpr) (Figure 4G). In contrast, IPC ablation in males had no significant effect on body fat

(Figure 4G). We also found that females (genotype *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}*)

subjected to a brief heat shock had lower body fat compared with genotype-matched

females that were not heat-shocked (Figure 4H). While heat-shocked *dilp2-GAL4>UAS-*

rpr,tub-GAL80^{ts} males showed a modest decrease in body fat (Figure 4H), the magnitude of

the decrease was greater in females (sex:genotype interaction *p*=0.0258). The reduction in

female body fat was not explained by the brief heat shocks, as control females (genotype

dilp2-GAL4>w^{1118},tub-GAL80^{ts}) subjected to an identical heat shock showed no significant

effect on body fat (Figure 4I). The decrease in body fat was also not due to altered feeding

in animals with IPC ablation, as no significant differences in food consumption were present

in either females or males with IPC ablation compared with control flies (Figure 4J and 4K).

Supporting a specific role for IIS in maintaining higher fat storage in females, supplementing

the diet of virgin females with an ecdysteroid called 20-hydroxyecdysone (20HE) did not

promote fat storage in females (Figure S3A). Our data therefore reveal sex differences in

IIS regulation in adult flies, and demonstrate the importance of this regulation to the male-

female difference in fat storage.

Discussion

Our findings provide significant insight into the mechanisms by which adult females store more fat than males. This information is critical to our understanding of how sex differences in body fat are established and maintained, as past studies identified mechanisms that operate in males with little effect in females[5,10]. Based on our data, we propose a model in which higher consumption of dietary sugar in females leads to elevated *dilp3* mRNA levels, which act together with greater insulin sensitivity to promote higher IIS activity and body fat in females. Supporting this model, reduced sugar consumption or IPC ablation lessened the sex difference in fat storage by lowering body fat in females with little effect in males. This reveals previously unrecognized sex-specific IIS regulation in adult flies, and identifies IIS as a key pathway that supports increased fat storage in adult females.

One key advance of our study was to extend knowledge of how food intake affects physiology in unmated females. Past studies used mated females to show that greater food consumption supports the quality and quantity of eggs produced[9,124-131]. While greater total nutrient intake could explain these effects, specific macronutrients such as dietary protein play individual roles in supporting egg production, egg-laying, and postcopulatory behaviors in mated females[132-134]. Indeed, dietary protein is limiting for *Drosophila* egg production[135], where its biological importance is shown by the fact that mated females will adjust their food preferences to ensure adequate protein intake[133,136,137]. Dietary protein does not hold the same physiological value for unmated females, however, as virgin females do not adjust their preferences after protein restriction[137]. Instead, our data suggest that dietary sugar is a key macronutrient for virgin female physiology due to its effects on IIS activity and fat accumulation. Because IIS activity supports normal germline stem cell proliferation and maintenance in the ovary[54,123,135,138-141], and high levels of body fat are required for successful egg production[12], dietary sugar consumption likely helps to establish a supportive metabolic state prior to reproduction. Once mated, this role for dietary sugar becomes less

important, as reflected by the limited consumption of a sugar-rich diet in mated females compared with males[142]. Thus, our data suggests that higher food intake in both virgin and mated females provides macronutrients to fuel the specific needs that accompany particular life history stages (*e.g.* prior to mating or during egg production).

Another advance of our study was to reveal a profound sex difference in how dietary sugar affects metabolism in the fat body. In females, sugar caused profound remodeling of the lipidome and many changes in the metabolome. This sex difference was most apparent when examining triglyceride, the lipid sub-class that shows the most obvious sugar-dependent changes in female lipid abundance. However, females showed a sugar-dependent increase across many lipid sub-classes (*e.g.*, DG, PG, PE, Acyl-Car). Given that females have lower lipase activity than males[5], the presence of high diglyceride and triglyceride levels suggests increased lipid synthesis in females. Diglyceride is also a precursor for phospholipids such as PE and PC synthesis[1,143]. High levels of PE and PC in females maintained on 1S further support higher lipid synthesis in females, a possibility that will be important to test in future studies.

Other than this broad lipid accumulation in females kept on 1S, other interesting findings were that dietary sugar enhanced levels of a fatty acid precursor used for synthesis of female-specific pheromones (28:2) and odd-chain fatty acids in the triglyceride pool. Fatty acid 28:2 is the direct precursor for the synthesis of a cuticular hydrocarbon called 7,11-heptacosadiene, the major female pheromone that mediates female sexual attractiveness[144-146]. Thus, in addition to supporting IIS activity and fat accumulation in females, dietary sugar consumption may also ensure females emit an optimal pheromone profile. Indeed, sexual attractiveness is altered in females with abnormal levels of cuticular hydrocarbons[147]. Given that the gut microbiota help produce odd-chain fatty acids[148] and the microbe load is higher in adult female intestines than in males[149], our data suggest that the intestinal microbiome may provide precursors used for fat storage in females exposed

to dietary sugar. Thus, dietary sugar provides an array of physiological benefits for females

that likely optimize reproduction.

In males, there were few changes in lipids or metabolites due to changes in dietary

sugar. One notable finding from our comparison of differentially-regulated lipids between

males and females was that only one lipid subclass, TG-O, was more abundant in males

than in females. Ether-linked lipids such as TG-O are synthesized by a multi-step process

mediated by enzymes located both in the peroxisome and endoplasmic reticulum[150-152].

Higher levels of TG-O in males may indicate sugar-induced lipotoxicity in males, as a recent

study found high levels of TG-O were induced in male flies chronically fed a high-sugar

diet[153]. In that study, elevated TG-O levels were associated with metabolic dysfunction, as

genetically reducing production of ether-linked lipids in male flies reversed defects in glucose

levels, cardiac function, and insulin signaling caused by a high-sugar diet[153,154]. Future

studies will therefore need to examine ether-linked lipid synthesis in both sexes to determine

whether male-female differences exist in this process and its relationship to metabolic

dysfunction. Follow-up studies will also need to determine the ultimate reason that males

largely fail to adjust the lipidome in response to dietary sugar. Potential explanations

suggested by our data include insulin resistance, increased sugar excretion, and high lipase

and lipolytic pathway activity[5,10]. Published data suggest that greater carbohydrate

breakdown within the male gut to support spermatogenesis might also explain the female-

biased lipidomic response to dietary sugar[155].

Other key findings of our study include showing that dietary sugar promotes a female

bias in *dilp3* levels, and revealing a female bias in IIS activity within the adult fat body. This

extends knowledge from past studies on sex differences in IIS activity in third-instar larvae[103]

by showing this female bias in IIS activity is present in adults and is physiologically

significant. Given that elevated *dilp3* levels are known to promote body fat[43,62,156] and

prolong starvation resistance[61,157,158], the female bias in *dilp3* is significant for higher fat

accumulation in females. However, the mechanisms underlying the sex bias in *dilp3* levels

remain unclear. Because the IPCs do not directly sense sugar[85], dietary sugar likely does

not directly act on the IPCs to influence the sex difference in *dilp3* levels. Instead, future

studies will need to determine whether *dilp3*-regulatory factors identified in single- and

mixed-sex studies such as gut-derived neuropeptide F[43], octopamine[157], tachykinin[159],

leucokinin[61,160], adiponectin receptor[161], Allatostatin A[45], bursicon[62], drosulfakinin[158], and

potentially Akh and Limostatin[156,162,163], contribute to the sex difference in *dilp3* mRNA

levels. Indeed, sex differences in expression of multiple *dilp3*-regulatory factors have been

reported[10,164,165], where these factors have sex-specific effects on physiology[10,42-

46,61,62,156,157,159] and influence mating and/or reproductive behaviors[166-174].

Overall, our findings identify IIS as a major determinant of female fat storage, with

only minor effects on male body fat. This contrasts with males, where a set point of stored

fat is maintained by *bmm* and Akh, pathways with little effect on female body fat[5,10]. The

primary mechanisms that establish fat storage are therefore not identical between the sexes:

females sustain body fat primarily via the anabolic effects of insulin whereas body fat in

males is maintained by the lipolytic effects of *bmm* and Akh. Future studies will need to

determine whether the sex-biased effects of changing IIS and Akh on body fat are

reproduced in other aspects of physiology regulated by these pathways (*e.g.* locomotion,

lifespan, aggression, feeding, sleep)[64,122,123,126,175-179]. Future studies will also need to

determine whether the extensive crosstalk between IIS and Akh identified in single- and

mixed-sex studies in adults and larvae is shared between males and females[45,57,99,163,180].

Because IIS and Akh mediate responses to a variety of extrinsic and intrinsic cues, gaining

a better understanding of the interplay between these two major hormone pathways in males

and females will provide critical insights into how diverse cues are integrated to maintain

whole-body triglyceride homeostasis in each sex. Given that sex differences in sucrose-

induced changes to mammalian adipose tissue lipolysis, hepatic lipogenesis, and adipose

tissue gene expression broadly reproduce the effects we report in flies[181], the sex-biased

effects of IIS and Akh on body fat we observed have implications for our understanding of

sex differences in parallel hormone systems in mammals (*e.g.* insulin, glucagon) and the

sex-biased risk of diseases associated with these hormones[182-186].

Resource availability

Lead contact

Further information and requests for resources and reagents should be directed to and will

be fulfilled by the lead contact, Elizabeth J. Rideout (elizabeth.rideout@ubc.ca).

Materials availability

This study did not generate new unique reagents.

Data and code availability

• Fly lipidomic and metabolomic data are available in Supplemental Table S1.

• This paper does not report original code.

• Any additional information required to reanalyze the data reported in this paper is available

from the lead contact upon request.

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Author contributions

P. B. conceived studies, collected samples, conducted experiments, interpreted

experiments, wrote and edited the manuscript.

H. Y. performed lipidomic and metabolomic experiments.

L. W. W. conducted ecdysone experiment.

C. J. M. conducted brain dissection and IPC activity.

T. H. edited the manuscript and acquired funding for lipidomic and metabolomic analyses.

E. J. R. conceived studies, interpreted experiments, wrote and edited the manuscript,

acquired funding, and is the guarantor of this work.

Declaration of interests

442 The authors declare no competing interests.

Supplemental information

445 Table S1. Excel file containing raw data with calculations and primer list

446 Table S2. Excel file containing statistics for all data

 Figure legends

Figure 1. Dietary sugar promotes increased fat storage in adult females.

(A) Food consumption per unit of body weight was significantly higher in 5-day-old adult

Canton-S (CS) females than males (p=0.0072; Student's t-test); n=8 biological replicates.

(B) Whole-body triglyceride levels were significantly lower in 5-day-old *CS* females

maintained on a diet with reduced nutrients (20% of normal nutrient content) compared with

females kept on our normal diet (100% diet; p<0.0001). No change in whole-body

triglyceride was observed in male flies (p>0.9999; sex:diet interaction p<0.0001). Two-way

ANOVA followed by Bonferroni post-hoc test; n=16 biological replicates.

(C) Whole-body triglyceride levels were significantly higher in 5-day-old adult w^{1118} females

and males maintained on the 1S diet compared with sex-matched flies kept on the 0S diet

(Females: p<0.0001; Males: p=0.0195). The magnitude of the decrease in body fat was

greater in females than in males (sex:diet interaction p<0.0001).Two-way ANOVA followed

by Bonferroni post-hoc test; n=16 biological replicates.

(D) Whole-body triglyceride levels were significantly higher in 5-day-old adult w^{1118} females

maintained on sugar-containing diet with reduced calories (1S-LC) compared with females

kept on the 0S diet (same calorie content as 1S-LC) (p=0.0032); no significant change in

body fat was observed in males (p=0.3715; sex:diet interaction p=0.0019). Two-way ANOVA

followed by Bonferroni post-hoc test; n=8 biological replicates.

(E) Whole-body triglyceride levels were not significantly different between 5-day-old adult

w^{1118} females maintained on the 0S diet and sex-matched flies kept on the 0S diet with either

added sucrose or D-glucose diet (females: p=0.9998 (sucrose), p=0.7532 (D-glucose). One-

way ANOVA followed by Tukey HSD test; n=8 biological replicates.

(F) Whole-body triglyceride levels were significantly higher in 5-day-old adult w^{1118} females

maintained on our lab diet with 30% added sugar (HSD) compared with females kept on the

1S diet (p=0.0015; Student's t-test). n=8 biological replicates.

All data plotted as mean ± SEM. ns indicates not significant with p>0.05; * p<0.05, ** p<0.01,

*** p<0.001, **** p<0.0001.

See also figure S1.

Figure 2. Female-biased effect of dietary sugar on metabolism.

(A) Volcano plot of differentially-regulated lipid species between 5-day-old adult female and

male w^{1118} fat bodies in 1S diet (colored dots represent p<0.01; Student's t-test).

(B) Proportion of species in each lipid subclass with a sex bias in abundance on the 1S diet

(p<0.01; Student's t-test). Numbers on histograms indicate the number of lipid species with

differential abundance.

(C) Sex bias of all metabolites with differential abundance between female and male fat

bodies in 1S diet (p<0.05; Student's t-test).

(D) Volcano plot of lipid species that are differentially-regulated between females maintained

on either the 1S or the 0S diet (colored dots represent p<0.01; Student's t-test).

(E) Volcano plot of lipid species that are differentially-regulated between males maintained

on either the 1S or the 0S diet (colored dots represent p<0.01; Student's t-test).

(F) Volcano plot of metabolites that are differentially-regulated between females maintained

on either the 1S or the 0S diet (colored dots represent p<0.05; Student's t-test).

(G) Volcano plot of metabolites that are differentially-regulated between males maintained

on either the 1S or the 0S diet (colored dots represent p<0.05; Student's t-test).

(H) Glucose levels in the excreta of 6-day-old adult w^{1118} males were higher than females

(p=0.0461, Student's t-test); n=4-6 biological replicates. Data plotted as mean ± SEM. *

p<0.05

TG: triglyceride; TG-O: ether-linked TG; DG: diglyceride; PI: phosphatidylinositol; PC:

phosphatidylcholine; PC-O: ether-linked PC; ST: sterol; LPC: lyso-PC; PG:

phosphatidylglycerol; PS: phosphatidylserine; PE: phosphatidylethanolamine; PE-O or PE-

P: ether-linked PE; NAE: N-acetylethanolamine; Cer: Ceramide; Acyl-Car: acyl-carnitine;

SE: sterol ester; Hex-Cer: hexosyl-ceramide.

See also figure S2.

Figure 3. Dietary sugar promotes sex differences in IIS regulation.

(A) mRNA levels of IPC-derived *dilp3* in heads were significantly higher in 5-day-old w^{1118}

females compared with males (p<0.0001; Student's t-test); n=7 biological replicates.

(B, C) mRNA levels of IPC-derived *dilp2* (B) and *dilp5* (C) in heads were not significantly

different between 5-day-old w^{1118} males and females (p=0.1282, Mann-Whitney test (*dilp2*);

p=0.5753, Student's t-test (*dilp5*)); n=7 biological replicates.

(D) mRNA levels of IPC-derived *dilp3* in heads were significantly lower in females

maintained on the 0S diet compared to females kept on the 1S diet (p<0.0001). There was

no sugar-dependent change in *dilp3* mRNA in males (p=0.4809; sex:diet interaction

p=0.0128). Two-way ANOVA followed by Bonferroni post-hoc test; n=7 biological replicates.

Note: *dilp3* mRNA levels in 1S diet were replotted from Figure 3A as these data were

collected in the same experiment.

(E) Quantification of GFP intensity produced by expression of *UAS-CaLexA* in the IPCs

(*dilp2-GAL4>UAS-CaLexA,UAS-mRFP*), normalized to RFP levels. Normalized GFP

intensity was not significantly different between females and males in 1S diet (p=0.4782;

Mann-Whitney test); n=15-23 animals.

(F) mRNA levels of Foxo target genes (*InR, bmm,* and *4E-BP*) in fat bodies were significantly

higher in 5-day-old w^{1118} males compared to females in 1S diet (p=0.0240; Mann-Whitney

test); n=7 biological replicates.

(G) mRNA levels of Foxo target genes (*InR, bmm*, and *4E-BP*) in 5-day-old w^{1118} female fat

bodies were significantly reduced after stimulation with 1 µM insulin compared with fat

bodies lacking insulin stimulation (p<0.0001; Student's *t*-test); n=6 biological replicates.

(H) mRNA levels of Foxo target genes *(InR, bmm,* and *4E-BP*) in 5-day-old w^{1118} male fat

bodies were not significantly different between unstimulated and insulin-stimulated

conditions (p=0.5841; Mann-Whitney test); n=6 biological replicates.

All data plotted as mean ± SEM. ns indicates not significant with p>0.05; * p<0.05, ** p<0.01,

*** p<0.001, **** p<0.0001.

Figure 4. Females require IIS to maintain fat storage.

(A, B) mRNA levels of IPC-derived *dilp2, dilp3, dilp5* in heads were significantly lower in both

female (A; p<0.0001, Student's *t*-test) and male (B; p=0.0016, Mann-Whitney test) *dilp2-*

GAL4>UAS-rpr,tub-GAL80^{ts} flies with heat shock at 29°C compared to sex-matched flies

reared in room temperature; n=4-6 biological replicates.

(C) Lifespan was significantly longer in *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* females compared

with *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* controls (p<0.0001 and p<0.0001,

respectively; Log-rank test); n=100-213 females.

(D) Lifespan was significantly longer in *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* males compared with *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* controls ($p<0.0001$ and $p<0.0001$, respectively; Log-rank test); n=100-148 males.

(E) The number of eggs laid by females in the first 24-hour period post-mating that developed into pupae was significantly lower in *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* females compared with *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* controls ($p<0.0001$ and $p<0.0001$, respectively; one-way ANOVA followed by Tukey HSD). The number of eggs laid by females in the first 24-hour period post-mating that developed into pupae produced by females in the second (48 hr) and third (72 hr) 24-hour periods after mating was not significantly different between *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* females and *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* controls ([48 hours] $p=0.5486$ and $p=0.3327$; [72 hours] $p=0.4374$ and $p=0.0142$; Kruskal-Wallis test followed by Dunn's test). Total eggs laid by females in the entire 72-hour period post-mating that developed into pupae produced was significantly lower in *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* females compared with *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* controls ($p=0.0116$ and $p<0.0001$, respectively; one-way ANOVA followed by Tukey's HSD); n=30 females.

(F) The number of eggs laid by females mated to either *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* males or control *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* males that developed into pupae over the first (24 hr), second (48 hr), and third (72 hr) 24-hour periods after mating was not significantly different ([24 hours] $p=0.0032$ and $p=0.7420$; [48 hours] $p=0.0598$ and $p=0.7339$; [72 hours] $p=0.0812$ and $p=0.7902$; one-way ANOVA followed by Tukey's HSD). The total number of eggs laid by females over a 72-hr period after mating with either *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* males or control *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* males that developed into pupae was not significantly different ($p=0.0011$ and $p=0.9980$, respectively; one-way ANOVA followed by Tukey's HSD). n=22-30 males.

(G) Whole-body triglyceride levels were significantly lower in *dilp2-GAL4>UAS-rpr,tub-*

GAL80^{ts} females compared with *dilp2-GAL4>+,tub-GAL80^{ts}* and *+>UAS-rpr* control females

($p<0.0001$ and $p<0.0001$, respectively). Whole-body triglyceride levels were not significantly

different between *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* males and *dilp2-GAL4>+,tub-GAL80^{ts}*

and *+>UAS-rpr* control males ($p=0.9397$ and $p=0.0022$, respectively) (sex:genotype

interaction $p=0.0002$). Two-way ANOVA followed by Bonferroni post-hoc test; n=8 biological

replicates.

(H) Whole-body triglyceride levels were significantly lower in female *dilp2-GAL4>UAS-*

rpr,tub-GAL80^{ts} after heat shock compared with genotype-matched females without heat

shock ($p<0.0001$). A modest reduction in whole-body triglyceride levels was also observed

in males ($p=0.0156$); however, the magnitude of the decrease was smaller than in females

(sex:genotype interaction $p=0.0258$). Two-way ANOVA followed by Bonferroni post-hoc test;

n=16 biological replicates.

(I) Whole-body triglyceride levels were not significantly different between *dilp2-*

GAL4>w^{1118},tub-GAL80^{ts} females that received a heat shock compared with *dilp2-*

GAL4>w^{1118},tub-GAL80^{ts} females that received no heat shock ($p=0.7266$; Student's *t*-test);

n=8 biological replicates.

(J, K) Food consumption was not significantly different in either females (J) or males (K)

between *dilp2-GAL4>UAS-rpr,tub-GAL80^{ts}* flies and *dilp2-GAL4>+,tub-GAL80^{ts}* or *+>UAS-*

rpr controls (females: $p=0.9999$ [GAL4 control] and $p=0.9318$ [UAS control]; males:

$p=0.6516$ [GAL4 control] and $p=0.0628$ [UAS control]). One-way ANOVA followed by Tukey

HSD; n=8-9 biological replicates.

All data in (A, B, E-J) plotted as mean ± SEM. ns indicates not significant with $p>0.05$, *

$p<0.05$, ** $p<0.01$, *** $p<0.001$, **** $p<0.0001$.

See also figure S3.

Materials and methods

Fly strains

The following fly strains from the Bloomington *Drosophila* Stock Center were used: *Canton-S (CS)* (#64349), *w1118* (#3605), *dilp2-GAL4* (IPCs) (#37516), *UAS-reaper (rpr)* (#5823), *UAS-CaLexA* (*UAS-LexA-VP16-NFAT*) (#66542), *tubP-GAL80[ts]* (#7018). We obtained *UAS-mRFP* as a kind gift from Dr Douglas Allan at The University of British Columbia.

Fly husbandry

The recipe for our regular lab diet (1S) is as follows: 20.5 g/L sucrose, 70.9 g/L D-glucose, 48.5 g/L cornmeal, 45.3 g/L yeast, 4.55 g/L agar, 0.5g CaCl2•2H2O, 0.5 g MgSO4•7H2O, 11.77 mL acid mix (propionic acid/phosphoric acid). To make 1 L of 20% food, 800 mL 0.7% agar was mixed with 200 mL of 1S food. The low-sugar diet (0S) was made by leaving out sucrose and D-glucose from the 1S diet. The 1S diet was calorie-matched to 0S (1S-low calorie) by removing 8.6 g/L cornmeal from the 1S diet. For diets with sugar added back, either 20.5 g/L sucrose (0S+sucrose), 70 g/L D-glucose (0S+D-glucose), or 62.5 g/L L-glucose (0S+L-glucose; Biosynth, MG05247) were added to 0S. To make 30% high sugar diet, 300 g/L extra sucrose was added to the 1S diet in line with published work [187,188]. For ecdysone-supplemented food, 0.5 mg/mL of 20-hydroxyecdysone (20-HE) in ethanol was added to the food (abcam, ab142425). For control food, the same ethanol volume without 20-HE was added to the food. For all experiments, we allowed female flies to lay eggs on grape juice agar plates for 12 hr. At 24 hr after egg laying, 50 larvae were picked into vials containing 10 mL food and reared at 22°C. Males and females were distinguished by the presence of sex combs late in the pupal period and placed into single-sex vials to eclose. After eclosion, adult flies were maintained at a density of twenty flies per vial in single-sex groups. Unless otherwise stated, all experiments used 5- to 7-day-old virgin flies.

Adult weight

616 Groups of 10 flies were placed in preweighed 1.5 ml tubes (Diamed Lab Supplies,

617 DIATEC610-2550) and weighed on an analytical balance (Mettler-Toledo, ME104).

Capillary feeder (CAFE) assay

One biological replicate consisted of measurements from one group of 10 flies. Flies were

placed into a specialized 15 ml conical vial with access to two capillary tubes, as previously

described[80]. Briefly, capillary tubes were filled with fly food media containing nutrients

equivalent to the 1S diet (20.5 g/L sucrose, 70.9 g/L D-glucose, 45.3 g/L yeast extract in

water) or 0S diet (45.3 g/L yeast extract in water). To prevent evaporation, approximately

0.5 µl of mineral oil was added to the top of each capillary tube. The vials were placed into

fitted holes in the lid of a large plastic container. To maintain high humidity throughout the

experiment, a shallow layer of water was poured into the base of the container. The

meniscus of the fly food media was marked before the start of the experiment and again

after 24 hr. The distance between the marks was used to quantify the volume of fly food

media that was consumed by the 10 flies (1 mm=0.15 µl). To account for sex differences in

body size, the volume of fly food consumed was normalized to the weight of individual flies.

Whole-body triglyceride measurements

One biological replicate consisted of five flies. Flies were collected in a 1.5 ml tube and

homogenized in 200-350 µl of 0.1% Tween (Amresco, 0777-1L) in 1X phosphate-buffered

saline (PBS; Sigma-Aldrich, P5493) using 50 µl of glass beads (Sigma-Aldrich, Z250473)

agitated at 8 m/s for 5 s (OMNI International BeadRuptor 24). Triglyceride concentration was

measured using either Sigma kit (G7793, T2449, F6428) or Stanbio kit (FT7610, BD386a/d,

BD386b) according to the manufacturer's instructions and as described previously[4,5] with

the following modifications. For Sigma kit, 30 µl of homogenate was transferred in duplicate

to a 96-well plate and heat treated at 70°C for 10 min (Bio-Rad T100 Thermal Cycler).

Standard curve was prepared using glycerol standard (Sigma, G7793) for concentrations of

0 mg/ml, 0.125 mg/ml, 0.25 mg/ml, 0.5 mg/ml, 1 mg/ml, and 2 mg/ml. After heat treatment,

30 µl of each concentration of standard solution was transferred to the same 96-well plate

in duplicate. 30 µl of triglyceride reagent (Sigma, T2449) was added to 1 set of

samples/standard solutions and 0.1% Tween in 1x PBS was added to the other set of

samples/standard solutions. After 40 min incubation at 37°C, the 96-well plate was

centrifuged at 3800 rpm for 3 min at 4°C (VWR® Benchtop General Purpose Centrifuges,

10830-744) to precipitate cellular debris. 7.5 µl of supernatant was transferred to a 384-well

plate-reader plate and 25 µl of free glycerol reagent (Sigma, F6428) was added to each well.

Plate was incubated at 37°C for 5 min then absorbance was read at 540 nm (Thermo

Scientific – Multiskan FC Microplate Photometer). For Stanbio kit, 10 µl of either

homogenate or triglyceride standard (FT7610) was added to the 190 µl of activated

triglyceride reagent (Enzymatic Triglyceride Reagent, BD386a/d; Triglyceride Activator, Cat.

No. BD386b) in the 96-well plate. After 15 min incubation at room temperature, the

absorbance was read at 540 nm. Triglyceride concentration was used to calculate percent

body fat.

Lipidomics and metabolomics

Sample preparation

Abdominal carcasses were isolated from 5-day-old male and female w^{1118} flies maintained

on the 1S or 0S diet after eclosion. One biological replicate consisted of 30 abdominal

carcasses dissected from 5- to 7-day-old adult males and females; a total of 9 biological

replicates were collected for each sex and condition. After dissection, each carcass was

snap-frozen on dry ice in a 2 mL screw-cap microcentrifuge tube (Thermo Fisher Scientific,

Waltham, MA) and stored at –80°C until further processing. For a dual-phase extraction,

samples were homogenized with a Mini-Beadbeater-24 (Biospec Products, Bartlesville,

United States) at 3800 rpm. A total of 333 µl 90% MeOH was added and two 15 sec

homogenization cycles were performed with a 1 min rest on dry ice in between. The

homogenized solution was mixed with 1000 µl of methyl tert-butyl ether and shaken for 5

min. To induce the phase separation, 317 µl of water was added. After mixing, the solution

rested at room temperature for 10 min and then the two-layer solution was centrifuged at

14,000 rpm for 15 min at 4°C. For LC-MS analysis, the clear upper and lower layers were

separated into new vials, dried in a SpeedVac at 20°C, and reconstituted in 70 µl of

acetonitrile and isopropanol (1:1, v/v) and 70 µl of acetonitrile and water (1:1, v/v) mixed

solvent, respectively. A method blank sample was also prepared following the same protocol

but without *Drosophila* abdomens.

LC-MS/MS experiment

For metabolomics, hydrophilic interaction chromatography (HILIC) separation was

performed on a SeQuant ZIC-HILIC column (50 mm × 2.1 mm, 5 µm, 200 Å) with an elution

time of 8 min. Mobile phase A was 5% acetonitrile in water with 10 mM ammonium acetate

(Thermo Fisher Scientific) with pH = 9.8, adjusted by ammonium hydroxide (MilliporeSigma),

and mobile phase B was 5% water in acetonitrile with no buffer. The LC elution gradient was

optimized using the BAGO software[189] as follows: 0 min, 10% A; 1 min, 10% A; 2 min, 20%

A; 5 min, 20% A; 6 min, 45% A; 7 min, 95% A; 8 min, 95% A. For lipidomics, reversed phase

(RP) separation was achieved on a Waters UPLC Acquity BEH C18 Column (1.0 mm ×100

mm, 1.7 µm, 130 Å, Milford, MA, USA) with an elution time of 25 min. Mobile phase A was

acetonitrile and water (6:4, v/v) with 2 mM ammonium formate (pH = 4.8, adjusted by formic

acid), and mobile phase B was isopropanol and acetonitrile (9:1, v/v). LC elution gradient

was optimized using the BAGO software as follows: 0 min, 5% B; 1 min, 5% B; 4 min, 35%

B; 7 min, 40% B; 10 min, 50% B; 13 min, 55% B; 16 min, 55% B; 19 min, 75% B; 22 min,

75% B; 25 min, 95% B.

The MS was operated in electrospray ionization (ESI) positive mode. The ESI source

conditions were set as follows: dry gas temperature, 220°C; dry gas flow, 7 L/min; nebulizer

gas pressure, 1.6 bar; capillary voltage, 4500 V for positive mode. The MS1 analysis was

conducted using following parameters: mass range, 70-1000 m/z; spectrum type: centroid,

calculated using maximum intensity; absolute intensity threshold: 250. Data-dependent

MS/MS analysis parameters: collision energy: 16-30 eV; cycle time: 3 s; spectra rate: 4 Hz

when intensity < 10^4 and 12 Hz when intensity > 10^5, linearly increased from 10^4 to 10^5.

External calibration was applied using sodium formate to ensure the m/z accuracy before

sample analysis.

Data processing

The raw MS data were converted to ABF format in Reifycs Abf Converter (ver. 4.0.0). The

converted data were processed in MS-DIAL (ver. 4.90) for feature extraction, feature

alignment, and compound identification. The data processing parameters in MS-DIAL were

set as follows: MS1 tolerance, 0.01 Da; MS/MS tolerance, 0.05 Da; mass slice width, 0.05

Da; smoothing method, linear weighted moving average; smoothing level, 3 scans; minimum

peak width, 5 scans. Compound identification was achieved using NIST 20 for metabolomics

and the internal library within MS-DIAL for lipidomics. Post-acquisition sample normalization

was performed using the *MAFFIN* R package[190] to ensure fair quantitative comparison.

Excrement glucose assay

One biological replicate consists of 30 female flies or 60 male flies. Flies were fed with 1S

diet containing 5% blue dye (FD&C Blue no.1, Ward's Science, 470300-996) for 3.5 hr, and

subsequently transferred into a 1.5 mL tube for excrement collection at room temperature.

After 6 hr in the 1.5 mL tube, flies were discarded and 100 µL of 1x PBS was added to each

tube; tubes were vortexed to dissolve and pool all the blue-stained excrement deposited in

the tube. For blue dye measurement, 10 µL of the excrement was added to 10 µL of 1x PBS

in 384-well plate and absorbance was measured at 630 nm (Thermo Scientific – Multiskan

FC Microplate Photometer). The rest of the excreta (90 µL) was added to 110 µL of Glucose

Reagent (Sigma-Aldrich, GAHK20) in 96-well plate and incubated overnight at 37 °C for

measurement of glucose levels at 340 nm (Tecan Austria GmbH-Tecan Spark). Glucose

content in the excrement was normalized with blue dye to account for sex differences in

excreta volume, and to account for the number of flies that deposited the excreta[191].

RNA extraction, cDNA synthesis, and Quantitative real-time PCR (qPCR)

One biological replicate consisted of 10 adult heads or 15 adult fat bodies. Samples were

homogenized in 500 µl of Trizol (Thermo Fisher Scientific; 15596018) and precipitated using

isopropanol and 75% ethanol to extract RNA. Pelleted RNA was resuspended using 20-30

µl of molecular biology grade water (Corning, 46-000-CV) and stored at -80°C until use.

Each experiment contained 4-7 biological replicates per sex, per genotype, and per diet;

each experiment was repeated twice.

For cDNA synthesis, an equal amount of RNA per reaction was DNase-treated and

reverse transcribed according to manufacturer's instructions using the QuantiTect Reverse

Transcription Kit (Qiagen, 205314). Relative mRNA transcript levels were quantified using

qPCR as described previously[5]. Data were normalized to the average fold change of *Actin5C*

and *β-tubulin*. For a full primer list, refer to Supplemental Table S1.

IPC activity measurement

To isolate the Dilp-producing cells (IPC), individual flies were removed from food and

anesthetized briefly with CO_2. Brains were dissected in cold 1× PBS. Samples were fixed in

4% paraformaldehyde (Electron Microscopy Science 15710) for 40 min, followed by two

washes in cold 1× PBS. Samples were incubated with Hoechst (Sigma-Aldrich, 33342) at a

concentration of 1:1000 for 30 min and mounted in 75% (w/v) sucrose solution. Images were

captured using a LSI3-Leica SP5 laser scanning confocal microscope and processed using

Fiji (ImageJ;[192]). To quantify IPC activity we used IPC-specific GAL4 driver *dilp2-GAL4*[99] to

drive expression of both *UAS-mRFP* and *UAS-CaLexA* (*UAS-LexA-VP16-NFAT*)[86]. GFP

intensity in each IPC cluster was quantified by measuring the sum of pixel intensity within

the region of interest for both GFP and RFP. GFP was normalized to RFP that was co-

expressed in the APC to account for inter-individual and/or sex differences in GAL4-driven

transgene expression (ImageJ;[192]).

Insulin sensitivity test

To measure insulin sensitivity, we adapted a published protocol[77]. Briefly, abdominal

carcasses were isolated from 5-day-old adult flies; one biological replicate consisted of 15

abdominal carcasses. The carcasses were placed in a dish with ice-cold Schneider's

Drosophila solution (21720024, Thermo Scientific) for 30 min. After this initial incubation,

Schneider's media was replaced with 2 mL of fresh Schneider's *Drosophila* solution or fresh

Schneider's *Drosophila* solution with recombinant human insulin (final concentration 1 μM;

I2643, Sigma-Aldrich) and incubated at room temperature for 30 min. After stimulation,

carcasses were collected in a tube, snap-frozen, and used for RNA isolation and qPCR

analysis.

Lifespan

After eclosion, unmated male and female flies were transferred to new vials of fresh food

every 2–3 days until no living flies remained in the vial. Deaths were recorded when the flies

were transferred to fresh food.

Female fecundity

One 5-day-old virgin female was placed with a group of three 5-day-old virgin *CS* males for 1 hr. After a 1 hr mating period, the males were removed and the females were allowed to lay eggs. Females were transferred into new vials for egg-laying every 24 hr; the total number of pupae in each vial was counted several days later.

Male fertility

One singly-housed 5-day-old virgin male was placed with a group of three 5-day-old virgin *CS* females and allowed to interact for 1 hr. After the 1 hr mating period, the male was removed from the vial and the females were allowed to lay eggs. Females were transferred into new vials for egg-laying every 24 hr; the total number of pupae in each vial was counted several days later.

Statistical analysis

Statistical analyses and data presentation were completed using GraphPad Prism 9 (GraphPad Software, San Diego, CA, USA) (Supplemental Table S2). All data were tested for normality using the Shapiro-Wilk test. Normally-distributed data was subjected to parametric tests, including Student's *t*-test, one-way ANOVA followed by Tukey's HSD, and two-way ANOVA followed by Bonferroni post-hoc test as appropriate. For non-normally-distributed data we used Mann-Whitney test and Kruskal-Wallis test followed by Dunn's test. For all statistical analyses, differences were considered significant if the $p < 0.05$.

 Supplemental figure legends

Figure S1. Dietary sugar levels change body fat, but not food consumption, in adult

flies. Related to Figure 1.

(A) There was a trend toward higher food consumption in 5-day-old adult w^{1118} females

compared with age-matched males (p=0.0812; Student's t-test); n=11 biological replicates.

(B) Whole-body triglyceride levels were significantly lower in 5-day-old *CS* females

maintained on the 0S diet compared with females kept on the 1S diet (p=0.0181); no

significant change in body fat was observed in males (p=0.0582; sex:diet interaction

p=0.7239). Two-way ANOVA followed by Bonferroni post-hoc test; n=8 biological replicates.

(C) Food consumption was not significantly different between 5-day-old adult w^{1118} females

and males maintained on the 1S diet compared with sex-matched flies kept on the 0S diet

(females: p>0.9999; males: p>0.9999; sex:diet interaction p=0.5654). Two-way ANOVA

followed by Bonferroni post-hoc test; n=10-11 biological replicates. Note: food consumption

data in 1S diet was replotted from panel S1A as food intake data on 1S and 0S were

collected in the same series of experiments.

(D) Whole-body triglyceride levels were significantly lower in 5-day-old w^{1118} adult females

and males maintained on 0S with L-glucose diet compared with sex-matched flies kept on

the 1S diet (females: p<0.0001; males: p<0.0001); the magnitude of the decrease in body

fat was greater in females than in males (sex:diet interaction p=0.0029). Two-way ANOVA

followed by Bonferroni post-hoc test; n=8 biological replicates. Note: the 1S triglyceride data

was replotted from Figure 1E as they were part of the same large experiment.

All data plotted as mean ± SEM. ns indicates not significant with p>0.05; * p<0.05, ** p<0.01,

*** p<0.001, **** p<0.0001.

Figure S2. Sugar-induced changes in lipid species in the adult fat body. Related to

Figure 2.

(A) Sex bias of fatty acids in the triglyceride pool with significant differences in abundance

between female and male fat bodies in 1S diet ($p<0.01$; Student's t-test).

(B) Proportion of species in each lipid subclass that are differentially regulated between the

fat body of females maintained on the 1S and females kept on the 0S diet ($p<0.01$; Student's

t-test). Numbers on histograms indicate the number of species with differential abundance.

(C, D) Triglyceride species with significant changes in abundance between females

maintained on a 1S diet compared with females kept on the 0S diet ($p<0.01$; Student's t-

test); species organized by number of carbons C35-C48 (C) and C49-C62 (D).

(E) Fatty acids in the triglyceride pool with significant differences in abundance between

females maintained on either the 1S or the 0S diet ($p<0.01$; Student's t-test).

(F) Triglyceride species with significant changes in abundance between males maintained

on a 1S diet compared with males kept on the 0S diet ($p<0.01$; Student's t-test).

(G) Proportion of species in each lipid subclass that are significantly different in abundance

between the fat bodies of males raised on the 1S or the 0S diet ($p<0.01$; Student's t-test).

Numbers on histograms indicate the number of species with differential abundance.

TG: triglyceride; TG-O: ether-linked TG; DG: diglyceride; PC: phosphatidylcholine; PC-O:

ether-linked PC; PE: phosphatidylethanolamine; PG: phosphatidylglycerol; PI:

phosphatidylinositol;. Acyl-Car: acyl-carnitine; Cer: Ceramide.

Figure S3. Ecdysone feeding does not increase body fat in females. Related to Figure

4.

(A) Whole-body triglyceride levels were significantly lower in 5-day-old adult w^{1118} females

maintained on a diet supplemented with 0.5 mg/mL 20-HE compared with control females

(p=0.0067, Student's t-test); n=8 biological replicates.

Data plotted as mean ± SEM. ** p<0.01.

References:

1. Kühnlein, R.P. (2012). Lipid droplet-based storage fat metabolism in Drosophila: Thematic Review Series: Lipid Droplet Synthesis and Metabolism: from Yeast to Man. Journal of Lipid Research *53*, 1430–1436. https://doi.org/10.1194/jlr.R024299.
2. Kühnlein, R.P. (2011). The contribution of the *Drosophila* model to lipid droplet research. Progress in Lipid Research *50*, 348–356. https://doi.org/10.1016/j.plipres.2011.04.001.
3. Gutierrez, E., Wiggins, D., Fielding, B., and Gould, A.P. (2007). Specialized hepatocyte-like cells regulate Drosophila lipid metabolism. Nature *445*, 275–280. https://doi.org/10.1038/nature05382.
4. Sieber, M.H., and Thummel, C.S. (2009). The DHR96 Nuclear Receptor Controls Triacylglycerol Homeostasis in Drosophila. Cell Metabolism *10*, 481–490. https://doi.org/10.1016/j.cmet.2009.10.010.
5. Wat, L.W., Chao, C., Bartlett, R., Buchanan, J.L., Millington, J.W., Chih, H.J., Chowdhury, Z.S., Biswas, P., Huang, V., Shin, L.J., et al. (2020). A role for triglyceride lipase brummer in the regulation of sex differences in Drosophila fat storage and breakdown. PLOS Biology *18*, e3000595. https://doi.org/10.1371/journal.pbio.3000595.
6. Kis, V., Barti, B., Lippai, M., and Sass, M. (2015). Specialized Cortex Glial Cells Accumulate Lipid Droplets in Drosophila melanogaster. PLoS One *10*, e0131250. https://doi.org/10.1371/journal.pone.0131250.
7. Villanueva, J.E., Livelo, C., Trujillo, A.S., Chandran, S., Woodworth, B., Andrade, L., Le, H.D., Manor, U., Panda, S., and Melkani, G.C. (2019). Time-restricted feeding restores muscle function in Drosophila models of obesity and circadian-rhythm disruption. Nat Commun *10*, 2700. https://doi.org/10.1038/s41467-019-10563-9.
8. Chao, C.F., Pesch, Y.-Y., Yu, H., Wang, C., Aristizabal, M.J., Huan, T., Tanentzapf, G., and Rideout, E.J. (2024). An important role for triglyceride in regulating spermatogenesis. eLife *12*. https://doi.org/10.7554/eLife.87523.3.
9. Sieber, M.H., and Spradling, A.C. (2015). Steroid Signaling Establishes a Female Metabolic State and Regulates SREBP to Control Oocyte Lipid Accumulation. Current Biology *25*, 993–1004. https://doi.org/10.1016/j.cub.2015.02.019.
10. Wat, L.W., Chowdhury, Z.S., Millington, J.W., Biswas, P., and Rideout, E.J. (2021). Sex determination gene transformer regulates the male-female difference in Drosophila fat storage via the adipokinetic hormone pathway. eLife *10*, e72350. https://doi.org/10.7554/eLife.72350.
11. Schwasinger-Schmidt, T.E., Kachman, S.D., and Harshman, L.G. (2012). Evolution of starvation resistance in Drosophila melanogaster: measurement of direct and correlated responses to artificial selection. J Evol Biol *25*, 378–387. https://doi.org/10.1111/j.1420-9101.2011.02428.x.
12. Buszczak, M., Lu, X., Segraves, W.A., Chang, T.Y., and Cooley, L. (2002). Mutations in the midway Gene Disrupt a Drosophila Acyl Coenzyme A: Diacylglycerol Acyltransferase. Genetics *160*, 1511–1518. https://doi.org/10.1093/genetics/160.4.1511.
13. Wilfling, F., Wang, H., Haas, J.T., Krahmer, N., Gould, T.J., Uchida, A., Cheng, J.-X., Graham, M., Christiano, R., Fröhlich, F., et al. (2013). Triacylglycerol synthesis enzymes mediate lipid droplet growth by relocalizing from the ER to lipid droplets. Dev Cell *24*, 384–399. https://doi.org/10.1016/j.devcel.2013.01.013.
14. Bailey, A.P., Koster, G., Guillermier, C., Hirst, E.M.A., MacRae, J.I., Lechene, C.P., Postle, A.D., and Gould, A.P. (2015). Antioxidant Role for Lipid Droplets in a Stem Cell Niche of Drosophila. Cell *163*, 340–353. https://doi.org/10.1016/j.cell.2015.09.020.

15. Ugrankar, R., Liu, Y., Provaznik, J., Schmitt, S., and Lehmann, M. (2011). Lipin is a
central regulator of adipose tissue development and function in Drosophila
melanogaster. Mol Cell Biol *31*, 1646–1656. https://doi.org/10.1128/MCB.01335-10.
16. Beller, M., Bulankina, A.V., Hsiao, H.-H., Urlaub, H., Jäckle, H., and Kühnlein, R.P.
(2010). PERILIPIN-dependent control of lipid droplet structure and fat storage in
Drosophila. Cell Metab *12*, 521–532. https://doi.org/10.1016/j.cmet.2010.10.001.
17. Grönke, S., Mildner, A., Fellert, S., Tennagels, N., Petry, S., Müller, G., Jäckle, H.,
and Kühnlein, R.P. (2005). Brummer lipase is an evolutionary conserved fat storage
regulator in Drosophila. Cell Metabolism *1*, 323–330.
https://doi.org/10.1016/j.cmet.2005.04.003.
18. Palm, W., Sampaio, J.L., Brankatschk, M., Carvalho, M., Mahmoud, A., Shevchenko,
A., and Eaton, S. (2012). Lipoproteins in Drosophila melanogaster--assembly,
function, and influence on tissue lipid composition. PLoS Genet *8*, e1002828.
https://doi.org/10.1371/journal.pgen.1002828.
19. Bi, J., Xiang, Y., Chen, H., Liu, Z., Grönke, S., Kühnlein, R.P., and Huang, X. (2012).
Opposite and redundant roles of the two Drosophila perilipins in lipid mobilization. J
Cell Sci *125*, 3568–3577. https://doi.org/10.1242/jcs.101329.
20. Tian, Y., Bi, J., Shui, G., Liu, Z., Xiang, Y., Liu, Y., Wenk, M.R., Yang, H., and Huang,
X. (2011). Tissue-autonomous function of Drosophila seipin in preventing ectopic lipid
droplet formation. PLoS Genet *7*, e1001364.
https://doi.org/10.1371/journal.pgen.1001364.
21. Ding, L., Yang, X., Tian, H., Liang, J., Zhang, F., Wang, G., Wang, Y., Ding, M., Shui,
G., and Huang, X. (2018). Seipin regulates lipid homeostasis by ensuring calcium-
dependent mitochondrial metabolism. EMBO J *37*, e97572.
https://doi.org/10.15252/embj.201797572.
22. Teixeira, L., Rabouille, C., Rørth, P., Ephrussi, A., and Vanzo, N.F. (2003). Drosophila
Perilipin/ADRP homologue Lsd2 regulates lipid metabolism. Mech Dev *120*, 1071–
1081. https://doi.org/10.1016/s0925-4773(03)00158-8.
23. Grönke, S., Beller, M., Fellert, S., Ramakrishnan, H., Jäckle, H., and Kühnlein, R.P.
(2003). Control of fat storage by a Drosophila PAT domain protein. Curr Biol *13*, 603–
606. https://doi.org/10.1016/s0960-9822(03)00175-1.
24. Fauny, J.D., Silber, J., and Zider, A. (2005). Drosophila Lipid Storage Droplet 2 gene
(Lsd-2) is expressed and controls lipid storage in wing imaginal discs. Dev Dyn *232*,
725–732. https://doi.org/10.1002/dvdy.20277.
25. Pospisilik, J.A., Schramek, D., Schnidar, H., Cronin, S.J.F., Nehme, N.T., Zhang, X.,
Knauf, C., Cani, P.D., Aumayr, K., Todoric, J., et al. (2010). Drosophila Genome-wide
Obesity Screen Reveals Hedgehog as a Determinant of Brown versus White Adipose
Cell Fate. Cell *140*, 148–160. https://doi.org/10.1016/j.cell.2009.12.027.
26. Baumbach, J., Hummel, P., Bickmeyer, I., Kowalczyk, K.M., Frank, M., Knorr, K.,
Hildebrandt, A., Riedel, D., Jäckle, H., and Kühnlein, R.P. (2014). A Drosophila in vivo
screen identifies store-operated calcium entry as a key regulator of adiposity. Cell
Metab *19*, 331–343. https://doi.org/10.1016/j.cmet.2013.12.004.
27. Baranski, T.J., Kraja, A.T., Fink, J.L., Feitosa, M., Lenzini, P.A., Borecki, I.B., Liu, C.-
T., Cupples, L.A., North, K.E., and Province, M.A. (2018). A high throughput,
functional screen of human Body Mass Index GWAS loci using tissue-specific RNAi
Drosophila melanogaster crosses. PLoS Genet *14*, e1007222.
https://doi.org/10.1371/journal.pgen.1007222.
28. Kunte, A.S., Matthews, K.A., and Rawson, R.B. (2006). Fatty acid auxotrophy in
Drosophila larvae lacking SREBP. Cell Metab *3*, 439–448.
https://doi.org/10.1016/j.cmet.2006.04.011.
29. Teleman, A.A., Chen, Y.-W., and Cohen, S.M. (2005). 4E-BP functions as a metabolic
brake used under stress conditions but not during normal growth. Genes Dev *19*,

1844–1848. https://doi.org/10.1101/gad.341505.

30. Rajan, A., and Perrimon, N. (2012). Drosophila cytokine unpaired 2 regulates
physiological homeostasis by remotely controlling insulin secretion. Cell *151*, 123–
137. https://doi.org/10.1016/j.cell.2012.08.019.

31. Reis, T., Gilst, M.R.V., and Hariharan, I.K. (2010). A Buoyancy-Based Screen of
Drosophila Larvae for Fat-Storage Mutants Reveals a Role for Sir2 in Coupling Fat
Storage to Nutrient Availability. PLOS Genetics *6*, e1001206.
https://doi.org/10.1371/journal.pgen.1001206.

32. Tsuda-Sakurai, K., Seong, K.-H., Horiuchi, J., Aigaki, T., and Tsuda, M. (2015).
Identification of a novel role for Drosophila MESR4 in lipid metabolism. Genes to Cells
20, 358–365. https://doi.org/10.1111/gtc.12221.

33. Bennick, R.A., Nagengast, A.A., and DiAngelo, J.R. (2019). The SR proteins SF2 and
RBP1 regulate triglyceride storage in the fat body of *Drosophila*. Biochemical and
Biophysical Research Communications *516*, 928–933.
https://doi.org/10.1016/j.bbrc.2019.06.151.

34. Kishita, Y., Tsuda, M., and Aigaki, T. (2012). Impaired fatty acid oxidation in a
Drosophila model of mitochondrial trifunctional protein (MTP) deficiency. Biochem
Biophys Res Commun *419*, 344–349. https://doi.org/10.1016/j.bbrc.2012.02.026.

35. Palanker, L., Tennessen, J.M., Lam, G., and Thummel, C.S. (2009). Drosophila HNF4
Regulates Lipid Mobilization and β-Oxidation. Cell Metab *9*, 228–239.
https://doi.org/10.1016/j.cmet.2009.01.009.

36. Lee, S., Bao, H., Ishikawa, Z., Wang, W., and Lim, H.-Y. (2017). Cardiomyocyte
Regulation of Systemic Lipid Metabolism by the Apolipoprotein B-Containing
Lipoproteins in Drosophila. PLoS Genet *13*, e1006555.
https://doi.org/10.1371/journal.pgen.1006555.

37. Parra-Peralbo, E., and Culi, J. (2011). Drosophila lipophorin receptors mediate the
uptake of neutral lipids in oocytes and imaginal disc cells by an endocytosis-
independent mechanism. PLoS Genet *7*, e1001297.
https://doi.org/10.1371/journal.pgen.1001297.

38. Lim, H.-Y., Wang, W., Wessells, R.J., Ocorr, K., and Bodmer, R. (2011). Phospholipid
homeostasis regulates lipid metabolism and cardiac function through SREBP
signaling in Drosophila. Genes Dev *25*, 189–200.
https://doi.org/10.1101/gad.1992411.

39. Bauer, R., Voelzmann, A., Breiden, B., Schepers, U., Farwanah, H., Hahn, I., Eckardt,
F., Sandhoff, K., and Hoch, M. (2009). Schlank, a member of the ceramide synthase
family controls growth and body fat in Drosophila. EMBO J *28*, 3706–3716.
https://doi.org/10.1038/emboj.2009.305.

40. Li, Y., Hoffmann, J., Li, Y., Stephano, F., Bruchhaus, I., Fink, C., and Roeder, T.
(2016). Octopamine controls starvation resistance, life span and metabolic traits in
Drosophila. Sci Rep *6*, 35359. https://doi.org/10.1038/srep35359.

41. Neckameyer, W.S., Coleman, C.M., Eadie, S., and Goodwin, S.F. (2007).
Compartmentalization of neuronal and peripheral serotonin synthesis in Drosophila
melanogaster. Genes, Brain and Behavior *6*, 756–769. https://doi.org/10.1111/j.1601-
183X.2007.00307.x.

42. Malita, A., Kubrak, O., Koyama, T., Ahrentløv, N., Texada, M.J., Nagy, S., Halberg,
K.V., and Rewitz, K. (2022). A gut-derived hormone suppresses sugar appetite and
regulates food choice in Drosophila. Nat Metab *4*, 1532–1550.
https://doi.org/10.1038/s42255-022-00672-z.

43. Yoshinari, Y., Kosakamoto, H., Kamiyama, T., Hoshino, R., Matsuoka, R., Kondo, S.,
Tanimoto, H., Nakamura, A., Obata, F., and Niwa, R. (2021). The sugar-responsive
enteroendocrine neuropeptide F regulates lipid metabolism through glucagon-like and
insulin-like hormones in Drosophila melanogaster. Nat Commun *12*, 4818.

https://doi.org/10.1038/s41467-021-25146-w.

44. Scopelliti, A., Bauer, C., Yu, Y., Zhang, T., Kruspig, B., Murphy, D.J., Vidal, M.,
Maddocks, O.D.K., and Cordero, J.B. (2019). A Neuronal Relay Mediates a Nutrient
Responsive Gut/Fat Body Axis Regulating Energy Homeostasis in Adult Drosophila.
Cell Metab *29*, 269-284.e10. https://doi.org/10.1016/j.cmet.2018.09.021.

45. Hentze, J.L., Carlsson, M.A., Kondo, S., Nässel, D.R., and Rewitz, K.F. (2015). The
Neuropeptide Allatostatin A Regulates Metabolism and Feeding Decisions in
Drosophila. Sci Rep *5*, 11680. https://doi.org/10.1038/srep11680.

46. Kubrak, O., Koyama, T., Ahrentløv, N., Jensen, L., Malita, A., Naseem, M.T., Lassen,
M., Nagy, S., Texada, M.J., Halberg, K.V., et al. (2022). The gut hormone Allatostatin
C/Somatostatin regulates food intake and metabolic homeostasis under nutrient
stress. Nat Commun *13*, 692. https://doi.org/10.1038/s41467-022-28268-x.

47. Beshel, J., Dubnau, J., and Zhong, Y. (2017). A Leptin analog locally produced in the
brain acts via a conserved neural circuit to modulate obesity-linked behaviors in
Drosophila. Cell Metab *25*, 208–217. https://doi.org/10.1016/j.cmet.2016.12.013.

48. Yamamoto, R., Bai, H., Dolezal, A.G., Amdam, G., and Tatar, M. (2013). Juvenile
hormone regulation of Drosophila aging. BMC Biology *11*, 85.
https://doi.org/10.1186/1741-7007-11-85.

49. Kamoshida, Y., Fujiyama-Nakamura, S., Kimura, S., Suzuki, E., Lim, J., Shiozaki-
Sato, Y., Kato, S., and Takeyama, K.-I. (2012). Ecdysone receptor (EcR) suppresses
lipid accumulation in the Drosophila fat body via transcription control. Biochem
Biophys Res Commun *421*, 203–207. https://doi.org/10.1016/j.bbrc.2012.03.135.

50. Song, W., Veenstra, J.A., and Perrimon, N. (2014). Control of lipid metabolism by
tachykinin in Drosophila. Cell Rep *9*, 40–47.
https://doi.org/10.1016/j.celrep.2014.08.060.

51. Gera, J., Agard, M., Nave, H., Sajadi, F., Thorat, L., Kondo, S., Nässel, D.R., Paluzzi,
J.-P.V., and Zandawala, M. (2024). Anti-diuretic hormone ITP signals via a guanylate
cyclase receptor to modulate systemic homeostasis in Drosophila. eLife *13*.
https://doi.org/10.7554/eLife.97043.1.

52. Gáliková, M., and Klepsatel, P. (2022). Ion transport peptide regulates energy intake,
expenditure, and metabolic homeostasis in Drosophila. Genetics *222*, iyac150.
https://doi.org/10.1093/genetics/iyac150.

53. DiAngelo, J.R., and Birnbaum, M.J. (2009). Regulation of Fat Cell Mass by Insulin in
Drosophila melanogaster. Molecular and Cellular Biology *29*, 6341–6352.
https://doi.org/10.1128/MCB.00675-09.

54. Grönke, S., Clarke, D.-F., Broughton, S., Andrews, T.D., and Partridge, L. (2010).
Molecular evolution and functional characterization of Drosophila insulin-like peptides.
PLoS Genet *6*, e1000857. https://doi.org/10.1371/journal.pgen.1000857.

55. Grönke, S., Müller, G., Hirsch, J., Fellert, S., Andreou, A., Haase, T., Jäckle, H., and
Kühnlein, R.P. (2007). Dual lipolytic control of body fat storage and mobilization in
Drosophila. PLoS Biol *5*, e137. https://doi.org/10.1371/journal.pbio.0050137.

56. Bharucha, K.N., Tarr, P., and Zipursky, S.L. (2008). A glucagon-like endocrine
pathway in Drosophila modulates both lipid and carbohydrate homeostasis. J Exp Biol
211, 3103–3110. https://doi.org/10.1242/jeb.016451.

57. Gáliková, M., Diesner, M., Klepsatel, P., Hehlert, P., Xu, Y., Bickmeyer, I., Predel, R.,
and Kühnlein, R.P. (2015). Energy Homeostasis Control in Drosophila Adipokinetic
Hormone Mutants. Genetics *201*, 665–683.
https://doi.org/10.1534/genetics.115.178897.

58. Zhao, X., and Karpac, J. (2017). Muscle Directs Diurnal Energy Homeostasis through
a Myokine-Dependent Hormone Module in Drosophila. Curr Biol *27*, 1941-1955.e6.
https://doi.org/10.1016/j.cub.2017.06.004.

59. Kapan, N., Lushchak, O.V., Luo, J., and Nässel, D.R. (2012). Identified peptidergic

neurons in the Drosophila brain regulate insulin-producing cells, stress responses and
metabolism by coexpressed short neuropeptide F and corazonin. Cell Mol Life Sci *69*,
4051–4066. https://doi.org/10.1007/s00018-012-1097-z.

60. Luo, J., Becnel, J., Nichols, C.D., and Nässel, D.R. (2012). Insulin-producing cells in
the brain of adult Drosophila are regulated by the serotonin 5-HT1A receptor. Cell Mol
Life Sci *69*, 471–484. https://doi.org/10.1007/s00018-011-0789-0.

61. Zandawala, M., Yurgel, M.E., Texada, M.J., Liao, S., Rewitz, K.F., Keene, A.C., and
Nässel, D.R. (2018). Modulation of Drosophila post-feeding physiology and behavior
by the neuropeptide leucokinin. PLoS Genet *14*, e1007767.
https://doi.org/10.1371/journal.pgen.1007767.

62. Kubrak, O., Jørgensen, A.F., Koyama, T., Lassen, M., Nagy, S., Hald, J., Mazzoni,
G., Madsen, D., Hansen, J.B., Larsen, M.R., et al. (2024). LGR signaling mediates
muscle-adipose tissue crosstalk and protects against diet-induced insulin resistance.
Nat Commun *15*, 6126. https://doi.org/10.1038/s41467-024-50468-w.

63. Heier, C., and Kühnlein, R.P. (2018). Triacylglycerol Metabolism in Drosophila
melanogaster. Genetics *210*, 1163–1184.
https://doi.org/10.1534/genetics.118.301583.

64. Lee, G., and Park, J.H. (2004). Hemolymph sugar homeostasis and starvation-
induced hyperactivity affected by genetic manipulations of the adipokinetic hormone-
encoding gene in Drosophila melanogaster. Genetics *167*, 311–323.
https://doi.org/10.1534/genetics.167.1.311.

65. Noyes, B.E., Katz, F.N., and Schaffer, M.H. (1995). Identification and expression of
the Drosophila adipokinetic hormone gene. Mol Cell Endocrinol *109*, 133–141.
https://doi.org/10.1016/0303-7207(95)03492-p.

66. Mochanová, M., Tomčala, A., Svobodová, Z., and Kodrík, D. (2018). Role of
adipokinetic hormone during starvation in Drosophila. Comp Biochem Physiol B
Biochem Mol Biol *226*, 26–35. https://doi.org/10.1016/j.cbpb.2018.08.004.

67. He, Q., Du, J., Wei, L., and Zhao, Z. (2020). AKH-FOXO pathway regulates
starvation-induced sleep loss through remodeling of the small ventral lateral neuron
dorsal projections. PLoS Genet *16*, e1009181.
https://doi.org/10.1371/journal.pgen.1009181.

68. Li, H., Janssens, J., De Waegeneer, M., Kolluru, S.S., Davie, K., Gardeux, V.,
Saelens, W., David, F., Brbić, M., Spanier, K., et al. (2022). Fly Cell Atlas: a single-
nucleus transcriptomic atlas of the adult fruit fly. Science *375*, eabk2432.
https://doi.org/10.1126/science.abk2432.

69. Leader, D.P., Krause, S.A., Pandit, A., Davies, S.A., and Dow, J.A.T. (2018). FlyAtlas
2: a new version of the Drosophila melanogaster expression atlas with RNA-Seq,
miRNA-Seq and sex-specific data. Nucleic Acids Res *46*, D809–D815.
https://doi.org/10.1093/nar/gkx976.

70. De Groef, S., Ribeiro Lopes, M., Winant, M., Rosschaert, E., Wilms, T., Bolckmans,
L., Calevro, F., and Callaerts, P. (2024). Reference genes to study the sex-biased
expression of genes regulating Drosophila metabolism. Sci Rep *14*, 9518.
https://doi.org/10.1038/s41598-024-58863-5.

71. Ja, W.W., Carvalho, G.B., Mak, E.M., de la Rosa, N.N., Fang, A.Y., Liong, J.C.,
Brummel, T., and Benzer, S. (2007). Prandiology of Drosophila and the CAFE assay.
Proc Natl Acad Sci U S A *104*, 8253–8256. https://doi.org/10.1073/pnas.0702726104.

72. Al-Anzi, B., Sapin, V., Waters, C., Zinn, K., Wyman, R.J., and Benzer, S. (2009).
Obesity-Blocking Neurons in Drosophila. Neuron *63*, 329–341.
https://doi.org/10.1016/j.neuron.2009.07.021.

73. De Groef, S., Wilms, T., Balmand, S., Calevro, F., and Callaerts, P. (2021). Sexual
Dimorphism in Metabolic Responses to Western Diet in Drosophila melanogaster.
Biomolecules *12*, 33. https://doi.org/10.3390/biom12010033.

74. Musselman, L.P., Fink, J.L., and Baranski, T.J. (2019). Similar effects of high-fructose
and high-glucose feeding in a Drosophila model of obesity and diabetes. PLoS One
14, e0217096. https://doi.org/10.1371/journal.pone.0217096.

75. Rovenko, B.M., Perkhulyn, N.V., Gospodaryov, D.V., Sanz, A., Lushchak, O.V., and
Lushchak, V.I. (2015). High consumption of fructose rather than glucose promotes a
diet-induced obese phenotype in *Drosophila melanogaster*. Comparative
Biochemistry and Physiology Part A: Molecular & Integrative Physiology *180*, 75–85.
https://doi.org/10.1016/j.cbpa.2014.11.008.

76. Dam, E. van, Leeuwen, L.A.G. van, Santos, E. dos, James, J., Best, L., Lennicke, C.,
Vincent, A.J., Marinos, G., Foley, A., Buricova, M., et al. (2020). Sugar-Induced
Obesity and Insulin Resistance Are Uncoupled from Shortened Survival in Drosophila.
Cell Metabolism *31*, 710-725.e7. https://doi.org/10.1016/j.cmet.2020.02.016.

77. Musselman, L.P., Fink, J.L., Narzinski, K., Ramachandran, P.V., Sukumar
Hathiramani, S., Cagan, R.L., and Baranski, T.J. (2011). A high-sugar diet produces
obesity and insulin resistance in wild-type Drosophila. Disease Models & Mechanisms
4, 842–849. https://doi.org/10.1242/dmm.007948.

78. Millington, J.W., Biswas, P., Chao, C., Xia, Y.H., Wat, L.W., Brownrigg, G.P., Sun, Z.,
Basner-Collins, P.J., Klein Geltink, R.I., and Rideout, E.J. (2022). A low-sugar diet
enhances Drosophila body size in males and females via sex-specific mechanisms.
Development *149*, dev200491. https://doi.org/10.1242/dev.200491.

79. Lewis, E.B. (1960). A new standard food medium. Drosophila information service *34*,
1–55.

80. Stafford, J.W., Lynd, K.M., Jung, A.Y., and Gordon, M.D. (2012). Integration of Taste
and Calorie Sensing in Drosophila. J. Neurosci. *32*, 14767–14774.
https://doi.org/10.1523/JNEUROSCI.1887-12.2012.

81. Mirth, C.K., and Riddiford, L.M. (2007). Size assessment and growth control: how
adult size is determined in insects. Bioessays *29*, 344–355.
https://doi.org/10.1002/bies.20552.

82. Kréneisz, O., Chen, X., Fridell, Y.-W.C., and Mulkey, D.K. (2010). Glucose increases
activity and Ca2+ in insulin-producing cells of adult Drosophila. Neuroreport *21*,
1116–1120. https://doi.org/10.1097/WNR.0b013e3283409200.

83. Nässel, D.R., Liu, Y., and Luo, J. (2015). Insulin/IGF signaling and its regulation in
Drosophila. General and Comparative Endocrinology *221*, 255–266.
https://doi.org/10.1016/j.ygcen.2014.11.021.

84. Park, S., Alfa, R.W., Topper, S.M., Kim, G.E.S., Kockel, L., and Kim, S.K. (2014). A
Genetic Strategy to Measure Circulating Drosophila Insulin Reveals Genes
Regulating Insulin Production and Secretion. PLOS Genetics *10*, e1004555.
https://doi.org/10.1371/journal.pgen.1004555.

85. Oh, Y., Lai, J.S.-Y., Mills, H.J., Erdjument-Bromage, H., Giammarinaro, B., Saadipour,
K., Wang, J.G., Abu, F., Neubert, T.A., and Suh, G.S.B. (2019). A glucose-sensing
neuron pair regulates insulin and glucagon in Drosophila. Nature *574*, 559–564.
https://doi.org/10.1038/s41586-019-1675-4.

86. Masuyama, K., Zhang, Y., Rao, Y., and Wang, J.W. (2012). Mapping Neural Circuits
with Activity-Dependent Nuclear Import of a Transcription Factor. Journal of
Neurogenetics *26*, 89–102. https://doi.org/10.3109/01677063.2011.642910.

87. Bisen, R.S., Iqbal, F.M., Cascino-Milani, F., Bockemühl, T., and Ache, J.M. (2024).
Nutritional state-dependent modulation of Insulin-Producing Cells in Drosophila. eLife
13. https://doi.org/10.7554/eLife.98514.1.

88. Alic, N., Andrews, T.D., Giannakou, M.E., Papatheodorou, I., Slack, C., Hoddinott,
M.P., Cochemé, H.M., Schuster, E.F., Thornton, J.M., and Partridge, L. (2011).
Genome-wide dFOXO targets and topology of the transcriptomic response to stress
and insulin signalling. Molecular Systems Biology *7*, 502.

https://doi.org/10.1038/msb.2011.36.

89. Puig, O., and Tjian, R. (2005). Transcriptional feedback control of insulin receptor by
dFOXO/FOXO1. Genes Dev *19*, 2435–2446. https://doi.org/10.1101/gad.1340505.

90. Puig, O., Marr, M.T., Ruhf, M.L., and Tjian, R. (2003). Control of cell number by
Drosophila FOXO: downstream and feedback regulation of the insulin receptor
pathway. Genes Dev. *17*, 2006–2020. https://doi.org/10.1101/gad.1098703.

91. Zinke, I., Schütz, C.S., Katzenberger, J.D., Bauer, M., and Pankratz, M.J. (2002).
Nutrient control of gene expression in Drosophila: microarray analysis of starvation
and sugar-dependent response. The EMBO Journal *21*, 6162–6173.
https://doi.org/10.1093/emboj/cdf600.

92. Macotela, Y., Boucher, J., Tran, T.T., and Kahn, C.R. (2009). Sex and depot
differences in adipocyte insulin sensitivity and glucose metabolism. Diabetes *58*, 803–
812. https://doi.org/10.2337/db08-1054.

93. Geer, E.B., and Shen, W. (2009). Gender differences in insulin resistance, body
composition, and energy balance. Gend Med *6 Suppl 1*, 60–75.
https://doi.org/10.1016/j.genm.2009.02.002.

94. Engel, F.L., and White, J.E. (1960). Some Hormonal Influences on Fat Mobilization
from Adipose Tissue. The American Journal of Clinical Nutrition *8*, 691–704.
https://doi.org/10.1093/ajcn/8.5.691.

95. Zhao, J., Wu, Y., Rong, X., Zheng, C., and Guo, J. (2020). Anti-Lipolysis Induced by
Insulin in Diverse Pathophysiologic Conditions of Adipose Tissue. Diabetes Metab
Syndr Obes *13*, 1575–1585. https://doi.org/10.2147/DMSO.S250699.

96. Chakrabarti, P., Kim, J.Y., Singh, M., Shin, Y.-K., Kim, J., Kumbrink, J., Wu, Y., Lee,
M.-J., Kirsch, K.H., Fried, S.K., et al. (2013). Insulin Inhibits Lipolysis in Adipocytes via
the Evolutionarily Conserved mTORC1-Egr1-ATGL-Mediated Pathway. Mol Cell Biol
33, 3659–3666. https://doi.org/10.1128/MCB.01584-12.

97. Scherer, T., O'Hare, J., Diggs-Andrews, K., Schweiger, M., Cheng, B., Lindtner, C.,
Zielinski, E., Vempati, P., Su, K., Dighe, S., et al. (2011). Brain Insulin Controls
Adipose Tissue Lipolysis and Lipogenesis. Cell Metabolism *13*, 183–194.
https://doi.org/10.1016/j.cmet.2011.01.008.

98. Krycer, J.R., Quek, L.-E., Francis, D., Zadoorian, A., Weiss, F.C., Cooke, K.C.,
Nelson, M.E., Diaz-Vegas, A., Humphrey, S.J., Scalzo, R., et al. (2020). Insulin
signaling requires glucose to promote lipid anabolism in adipocytes. Journal of
Biological Chemistry *295*, 13250–13266. https://doi.org/10.1074/jbc.RA120.014907.

99. Rulifson, E.J., Kim, S.K., and Nusse, R. (2002). Ablation of Insulin-Producing Neurons
in Flies: Growth and Diabetic Phenotypes. Science *296*, 1118–1120.
https://doi.org/10.1126/science.1070058.

100. Ikeya, T., Galic, M., Belawat, P., Nairz, K., and Hafen, E. (2002). Nutrient-dependent
expression of insulin-like peptides from neuroendocrine cells in the CNS contributes
to growth regulation in Drosophila. Curr Biol *12*, 1293–1300.
https://doi.org/10.1016/s0960-9822(02)01043-6.

101. Clancy, D.J., Gems, D., Harshman, L.G., Oldham, S., Stocker, H., Hafen, E., Leevers,
S.J., and Partridge, L. (2001). Extension of life-span by loss of CHICO, a Drosophila
insulin receptor substrate protein. Science *292*, 104–106.
https://doi.org/10.1126/science.1057991.

102. Brogiolo, W., Stocker, H., Ikeya, T., Rintelen, F., Fernandez, R., and Hafen, E. (2001).
An evolutionarily conserved function of the *Drosophila* insulin receptor and insulin-like
peptides in growth control. Current Biology *11*, 213–221.
https://doi.org/10.1016/S0960-9822(01)00068-9.

103. Rideout, E.J., Narsaiya, M.S., and Grewal, S.S. (2015). The Sex Determination Gene
transformer Regulates Male-Female Differences in Drosophila Body Size. PLOS
Genetics *11*, e1005683. https://doi.org/10.1371/journal.pgen.1005683.

104. Millington, J.W., Brownrigg, G.P., Basner-Collins, P.J., Sun, Z., and Rideout, E.J.
(2021). Genetic manipulation of insulin/insulin-like growth factor signaling pathway
activity has sex-biased effects on Drosophila body size. G3
Genes|Genomes|Genetics *11*, jkaa067. https://doi.org/10.1093/g3journal/jkaa067.
105. Grewal, S.S. (2009). Insulin/TOR signaling in growth and homeostasis: a view from
the fly world. Int J Biochem Cell Biol *41*, 1006–1010.
https://doi.org/10.1016/j.biocel.2008.10.010.
106. Teleman, A.A. (2009). Molecular mechanisms of metabolic regulation by insulin in
Drosophila. Biochem J *425*, 13–26. https://doi.org/10.1042/BJ20091181.
107. Osterwalder, T., Yoon, K.S., White, B.H., and Keshishian, H. (2001). A conditional
tissue-specific transgene expression system using inducible GAL4. Proc Natl Acad
Sci U S A *98*, 12596–12601. https://doi.org/10.1073/pnas.221303298.
108. Roman, G., Endo, K., Zong, L., and Davis, R.L. (2001). P{Switch}, a system for spatial
and temporal control of gene expression in Drosophila melanogaster. Proceedings of
the National Academy of Sciences *98*, 12602–12607.
https://doi.org/10.1073/pnas.221303998.
109. Poirier, L., Shane, A., Zheng, J., and Seroude, L. (2008). Characterization of the
Drosophila Gene-Switch system in aging studies: a cautionary tale. Aging Cell 7,
758–770. https://doi.org/10.1111/j.1474-9726.2008.00421.x.
110. Yamada, R., Deshpande, S.A., Keebaugh, E.S., Ehrlich, M.R., Soto Obando, A., and
Ja, W.W. (2017). Mifepristone Reduces Food Palatability and Affects Drosophila
Feeding and Lifespan. J Gerontol A Biol Sci Med Sci *72*, 173–180.
https://doi.org/10.1093/gerona/glw072.
111. Landis, G.N., Salomon, M.P., Keroles, D., Brookes, N., Sekimura, T., and Tower, J.
(2015). The progesterone antagonist mifepristone/RU486 blocks the negative effect
on life span caused by mating in female Drosophila. Aging (Albany NY) *7*, 53–69.
https://doi.org/10.18632/aging.100721.
112. McClure, C.D., Hassan, A., Aughey, G.N., Butt, K., Estacio-Gómez, A., Duggal, A.,
Ying Sia, C., Barber, A.F., and Southall, T.D. (2022). An auxin-inducible, GAL4-
compatible, gene expression system for Drosophila. Elife *11*, e67598.
https://doi.org/10.7554/eLife.67598.
113. Fleck, S.A., Biswas, P., DeWitt, E.D., Knuteson, R.L., Eisman, R.C., Nemkov, T.,
D'Alessandro, A., Tennessen, J.M., Rideout, E., and Weaver, L.N. (2024). Auxin
exposure disrupts feeding behavior and fatty acid metabolism in adult Drosophila.
eLife *12*, RP91953. https://doi.org/10.7554/eLife.91953.
114. McGuire, S.E., Le, P.T., Osborn, A.J., Matsumoto, K., and Davis, R.L. (2003).
Spatiotemporal rescue of memory dysfunction in Drosophila. Science *302*, 1765–
1768. https://doi.org/10.1126/science.1089035.
115. Klepsatel, P., Gáliková, M., Xu, Y., and Kühnlein, R.P. (2016). Thermal stress
depletes energy reserves in Drosophila. Sci Rep *6*, 33667.
https://doi.org/10.1038/srep33667.
116. Klepsatel, P., Wildridge, D., and Gáliková, M. (2019). Temperature induces changes
in Drosophila energy stores. Sci Rep *9*, 5239. https://doi.org/10.1038/s41598-019-
41754-5.
117. Kimura, K.D., Tissenbaum, H.A., Liu, Y., and Ruvkun, G. (1997). daf-2, an insulin
receptor-like gene that regulates longevity and diapause in Caenorhabditis elegans.
Science *277*, 942–946. https://doi.org/10.1126/science.277.5328.942.
118. Kenyon, C., Chang, J., Gensch, E., Rudner, A., and Tabtiang, R. (1993). A C. elegans
mutant that lives twice as long as wild type. Nature *366*, 461–464.
https://doi.org/10.1038/366461a0.
119. Partridge, L., Alic, N., Bjedov, I., and Piper, M.D.W. (2011). Ageing in Drosophila: The
role of the insulin/Igf and TOR signalling network. Exp Gerontol *46*, 376–381.

https://doi.org/10.1016/j.exger.2010.09.003.

120. Blüher, M., Kahn, B.B., and Kahn, C.R. (2003). Extended longevity in mice lacking the
insulin receptor in adipose tissue. Science *299*, 572–574.
https://doi.org/10.1126/science.1078223.

121. Fontana, L., Partridge, L., and Longo, V.D. (2010). Extending healthy life span--from
yeast to humans. Science *328*, 321–326. https://doi.org/10.1126/science.1172539.

122. Haselton, A., Sharmin, E., Schrader, J., Sah, M., Poon, P., and Fridell, Y.-W.C.
(2010). Partial ablation of adult Drosophila insulin-producing neurons modulates
glucose homeostasis and extends life span without insulin resistance. Cell Cycle *9*,
3063–3071. https://doi.org/10.4161/cc.9.15.12458.

123. Broughton, S.J., Piper, M.D.W., Ikeya, T., Bass, T.M., Jacobson, J., Driege, Y.,
Martinez, P., Hafen, E., Withers, D.J., Leevers, S.J., et al. (2005). Longer lifespan,
altered metabolism, and stress resistance in Drosophila from ablation of cells making
insulin-like ligands. Proc Natl Acad Sci U S A *102*, 3105–3110.
https://doi.org/10.1073/pnas.0405775102.

124. Carvalho, G.B., Kapahi, P., Anderson, D.J., and Benzer, S. (2006). Allocrine
Modulation of Feeding Behavior by the Sex Peptide of *Drosophila*. Current Biology
16, 692–696. https://doi.org/10.1016/j.cub.2006.02.064.

125. Hadjieconomou, D., King, G., Gaspar, P., Mineo, A., Blackie, L., Ameku, T., Studd,
C., de Mendoza, A., Diao, F., White, B.H., et al. (2020). Enteric neurons increase
maternal food intake during reproduction. Nature *587*, 455–459.
https://doi.org/10.1038/s41586-020-2866-8.

126. Cognigni, P., Bailey, A.P., and Miguel-Aliaga, I. (2011). Enteric Neurons and Systemic
Signals Couple Nutritional and Reproductive Status with Intestinal Homeostasis. Cell
Metab *13*, 92–104. https://doi.org/10.1016/j.cmet.2010.12.010.

127. Ja, W.W., Carvalho, G.B., Zid, B.M., Mak, E.M., Brummel, T., and Benzer, S. (2009).
Water- and nutrient-dependent effects of dietary restriction on Drosophila lifespan.
Proc Natl Acad Sci U S A *106*, 18633–18637.
https://doi.org/10.1073/pnas.0908016106.

128. Lee, K.P., Simpson, S.J., Clissold, F.J., Brooks, R., Ballard, J.W.O., Taylor, P.W.,
Soran, N., and Raubenheimer, D. (2008). Lifespan and reproduction in Drosophila:
New insights from nutritional geometry. Proc Natl Acad Sci U S A *105*, 2498–2503.
https://doi.org/10.1073/pnas.0710787105.

129. Chapman, T., and Partridge, L. (1996). Female fitness in Drosophila melanogaster:
an interaction between the effect of nutrition and of encounter rate with males. Proc
Biol Sci *263*, 755–759. https://doi.org/10.1098/rspb.1996.0113.

130. Barnes, A.I., Wigby, S., Boone, J.M., Partridge, L., and Chapman, T. (2008). Feeding,
fecundity and lifespan in female Drosophila melanogaster. Proc Biol Sci *275*, 1675–
1683. https://doi.org/10.1098/rspb.2008.0139.

131. Grandison, R.C., Piper, M.D.W., and Partridge, L. (2009). Amino-acid imbalance
explains extension of lifespan by dietary restriction in Drosophila. Nature *462*, 1061–
1064. https://doi.org/10.1038/nature08619.

132. Laturney, M., Sterne, G.R., and Scott, K. (2023). Mating activates neuroendocrine
pathways signaling hunger in Drosophila females. eLife *12*, e85117.
https://doi.org/10.7554/eLife.85117.

133. Strilbytska, O., Yurkevych, I., Semaniuk, U., Gospodaryov, D., Simpson, S.J., and
Lushchak, O. (2024). Life-History Trade-Offs in Drosophila: Flies Select a Diet to
Maximize Reproduction at the Expense of Lifespan. The Journals of Gerontology:
Series A *79*, glae057. https://doi.org/10.1093/gerona/glae057.

134. Lee, K.P., Kim, J.-S., and Min, K.-J. (2013). Sexual dimorphism in nutrient intake and
life span is mediated by mating in *Drosophila melanogaster*. Animal Behaviour *86*,
987–992. https://doi.org/10.1016/j.anbehav.2013.08.018.

135. Drummond-Barbosa, D., and Spradling, A.C. (2001). Stem cells and their progeny
respond to nutritional changes during Drosophila oogenesis. Dev Biol *231*, 265–278.
https://doi.org/10.1006/dbio.2000.0135.
136. Camus, M.F., Huang, C.-C., Reuter, M., and Fowler, K. (2018). Dietary choices are
influenced by genotype, mating status, and sex in Drosophila melanogaster. Ecology
and Evolution *8*, 5385–5393. https://doi.org/10.1002/ece3.4055.
137. Ribeiro, C., and Dickson, B.J. (2010). Sex peptide receptor and neuronal TOR/S6K
signaling modulate nutrient balancing in Drosophila. Curr Biol *20*, 1000–1005.
https://doi.org/10.1016/j.cub.2010.03.061.
138. Hsu, H.-J., and Drummond-Barbosa, D. (2009). Insulin levels control female germline
stem cell maintenance via the niche in Drosophila. Proceedings of the National
Academy of Sciences *106*, 1117–1121. https://doi.org/10.1073/pnas.0809144106.
139. Burn, K.M., Shimada, Y., Ayers, K., Lu, F., Hudson, A.M., and Cooley, L. (2015).
Somatic insulin signaling regulates a germline starvation response in Drosophila egg
chambers. Dev Biol *398*, 206–217. https://doi.org/10.1016/j.ydbio.2014.11.021.
140. LaFever, L., and Drummond-Barbosa, D. (2005). Direct control of germline stem cell
division and cyst growth by neural insulin in Drosophila. Science *309*, 1071–1073.
https://doi.org/10.1126/science.1111410.
141. Richard, D.S., Rybczynski, R., Wilson, T.G., Wang, Y., Wayne, M.L., Zhou, Y.,
Partridge, L., and Harshman, L.G. (2005). Insulin signaling is necessary for
vitellogenesis in Drosophila melanogaster independent of the roles of juvenile
hormone and ecdysteroids: female sterility of the chico1 insulin signaling mutation is
autonomous to the ovary. J Insect Physiol *51*, 455–464.
https://doi.org/10.1016/j.jinsphys.2004.12.013.
142. Chandegra, B., Tang, J.L.Y., Chi, H., and Alic, N. (2017). Sexually dimorphic effects
of dietary sugar on lifespan, feeding and starvation resistance in Drosophila. Aging
(Albany NY) *9*, 2521–2528. https://doi.org/10.18632/aging.101335.
143. Eichmann, T.O., and Lass, A. (2015). DAG tales: the multiple faces of
diacylglycerol—stereochemistry, metabolism, and signaling. Cell Mol Life Sci *72*,
3931–3952. https://doi.org/10.1007/s00018-015-1982-3.
144. Antony, C., and Jallon, J.-M. (1982). The chemical basis for sex recognition in
Drosophila melanogaster. Journal of Insect Physiology *28*, 873–880.
https://doi.org/10.1016/0022-1910(82)90101-9.
145. Jallon, J.M. (1984). A few chemical words exchanged by Drosophila during courtship
and mating. Behav Genet *14*, 441–478. https://doi.org/10.1007/BF01065444.
146. Fedina, T.Y., Kuo, T.-H., Dreisewerd, K., Dierick, H.A., Yew, J.Y., and Pletcher, S.D.
(2012). Dietary Effects on Cuticular Hydrocarbons and Sexual Attractiveness in
Drosophila. PLoS One *7*, e49799. https://doi.org/10.1371/journal.pone.0049799.
147. Wicker-Thomas, C., Garrido, D., Bontonou, G., Napal, L., Mazuras, N., Denis, B.,
Rubin, T., Parvy, J.-P., and Montagne, J. (2015). Flexible origin of
hydrocarbon/pheromone precursors in Drosophila melanogaster. J Lipid Res *56*,
2094–2101. https://doi.org/10.1194/jlr.M060368.
148. Scheitz, C.J.F., Guo, Y., Early, A.M., Harshman, L.G., and Clark, A.G. (2013).
Heritability and Inter-Population Differences in Lipid Profiles of Drosophila
melanogaster. PLOS ONE *8*, e72726. https://doi.org/10.1371/journal.pone.0072726.
149. Regan, J.C., Khericha, M., Dobson, A.J., Bolukbasi, E., Rattanavirotkul, N., and
Partridge, L. (2016). Sex difference in pathology of the ageing gut mediates the
greater response of female lifespan to dietary restriction. eLife *5*, e10956.
https://doi.org/10.7554/eLife.10956.
150. Faust, J.E., Manisundaram, A., Ivanova, P.T., Milne, S.B., Summerville, J.B., Brown,
H.A., Wangler, M., Stern, M., and McNew, J.A. (2014). Peroxisomes Are Required for
Lipid Metabolism and Muscle Function in Drosophila melanogaster. PLOS ONE *9*,

e100213. https://doi.org/10.1371/journal.pone.0100213.

151. Lodhi, I.J., and Semenkovich, C.F. (2014). Peroxisomes: a Nexus for Lipid Metabolism and Cellular Signaling. Cell Metab *19*, 380–392. https://doi.org/10.1016/j.cmet.2014.01.002.

152. Pridie, C., Ueda, K., and Simmonds, A.J. (2020). Rosy Beginnings: Studying Peroxisomes in Drosophila. Front. Cell Dev. Biol. *8*. https://doi.org/10.3389/fcell.2020.00835.

153. Tuthill, B.F., Searcy, L.A., Yost, R.A., and Musselman, L.P. (2020). Tissue-specific analysis of lipid species in Drosophila during overnutrition by UHPLC-MS/MS and MALDI-MSI [S]. Journal of Lipid Research *61*, 275–290. https://doi.org/10.1194/jlr.RA119000198.

154. Santoro, C., O'Toole, A., Finsel, P., Alvi, A., and Musselman, L.P. (2022). Reducing ether lipids improves Drosophila overnutrition-associated pathophysiology phenotypes via a switch from lipid storage to beta-oxidation. Sci Rep *12*, 13021. https://doi.org/10.1038/s41598-022-16870-4.

155. Hudry, B., de Goeij, E., Mineo, A., Gaspar, P., Hadjieconomou, D., Studd, C., Mokochinski, J.B., Kramer, H.B., Plaçais, P.-Y., Preat, T., et al. (2019). Sex Differences in Intestinal Carbohydrate Metabolism Promote Food Intake and Sperm Maturation. Cell *178*, 901-918.e16. https://doi.org/10.1016/j.cell.2019.07.029.

156. Alfa, R.W., Park, S., Skelly, K.-R., Poffenberger, G., Jain, N., Gu, X., Kockel, L., Wang, J., Liu, Y., Powers, A.C., et al. (2015). Suppression of Insulin Production and Secretion by a Decretin Hormone. Cell Metab *21*, 323–333. https://doi.org/10.1016/j.cmet.2015.01.006.

157. Luo, J., Lushchak, O.V., Goergen, P., Williams, M.J., and Nässel, D.R. (2014). Drosophila Insulin-Producing Cells Are Differentially Modulated by Serotonin and Octopamine Receptors and Affect Social Behavior. PLOS ONE *9*, e99732. https://doi.org/10.1371/journal.pone.0099732.

158. Söderberg, J.A.E., Carlsson, M.A., and Nässel, D.R. (2012). Insulin-Producing Cells in the Drosophila Brain also Express Satiety-Inducing Cholecystokinin-Like Peptide, Drosulfakinin. Front Endocrinol (Lausanne) *3*, 109. https://doi.org/10.3389/fendo.2012.00109.

159. Birse, R.T., Söderberg, J.A.E., Luo, J., Winther, Å.M.E., and Nässel, D.R. (2011). Regulation of insulin-producing cells in the adult Drosophila brain via the tachykinin peptide receptor DTKR. Journal of Experimental Biology *214*, 4201–4208. https://doi.org/10.1242/jeb.062091.

160. Yurgel, M.E., Kakad, P., Zandawala, M., Nässel, D.R., Godenschwege, T.A., and Keene, A.C. (2019). A single pair of leucokinin neurons are modulated by feeding state and regulate sleep–metabolism interactions. PLoS Biol *17*, e2006409. https://doi.org/10.1371/journal.pbio.2006409.

161. Kwak, S.-J., Hong, S.-H., Bajracharya, R., Yang, S.-Y., Lee, K.-S., and Yu, K. (2013). Drosophila Adiponectin Receptor in Insulin Producing Cells Regulates Glucose and Lipid Metabolism by Controlling Insulin Secretion. PLOS ONE *8*, e68641. https://doi.org/10.1371/journal.pone.0068641.

162. Buch, S., Melcher, C., Bauer, M., Katzenberger, J., and Pankratz, M.J. (2008). Opposing Effects of Dietary Protein and Sugar Regulate a Transcriptional Target of Drosophila Insulin-like Peptide Signaling. Cell Metabolism *7*, 321–332. https://doi.org/10.1016/j.cmet.2008.02.012.

163. Kim, J., and Neufeld, T.P. (2015). Dietary sugar promotes systemic TOR activation in Drosophila through AKH-dependent selective secretion of Dilp3. Nat Commun *6*, 6846. https://doi.org/10.1038/ncomms7846.

164. Hudry, B., Khadayate, S., and Miguel-Aliaga, I. (2016). The sexual identity of adult intestinal stem cells controls organ size and plasticity. Nature *530*, 344–348.

1411 https://doi.org/10.1038/nature16953.

165. Lee, G., Bahn, J.H., and Park, J.H. (2006). Sex- and clock-controlled expression of the neuropeptide F gene in Drosophila. Proceedings of the National Academy of Sciences *103*, 12580–12585. https://doi.org/10.1073/pnas.0601171103.

166. Asahina, K., Watanabe, K., Duistermars, B.J., Hoopfer, E., González, C.R., Eyjólfsdóttir, E.A., Perona, P., and Anderson, D.J. (2014). Tachykinin-expressing neurons control male-specific aggressive arousal in Drosophila. Cell *156*, 221–235. https://doi.org/10.1016/j.cell.2013.11.045.

167. Shankar, S., Chua, J.Y., Tan, K.J., Calvert, M.E.K., Weng, R., Ng, W.C., Mori, K., and Yew, J.Y. (2015). The neuropeptide tachykinin is essential for pheromone detection in a gustatory neural circuit. Elife *4*, e06914. https://doi.org/10.7554/eLife.06914.

168. Kim, W.J., Jan, L.Y., and Jan, Y.N. (2013). A PDF/NPF neuropeptide signaling circuitry of male Drosophila melanogaster controls rival-induced prolonged mating. Neuron *80*, 1190–1205. https://doi.org/10.1016/j.neuron.2013.09.034.

169. Liu, C., Zhang, B., Zhang, L., Yang, T., Zhang, Z., Gao, Z., and Zhang, W. (2020). A neural circuit encoding mating states tunes defensive behavior in Drosophila. Nat Commun *11*, 3962. https://doi.org/10.1038/s41467-020-17771-8.

170. Lebreton, S., Mansourian, S., Bigarreau, J., and Dekker, T. (2016). The Adipokinetic Hormone Receptor Modulates Sexual Behavior, Pheromone Perception and Pheromone Production in a Sex-Specific and Starvation-Dependent Manner in Drosophila melanogaster. Front. Ecol. Evol. *3*. https://doi.org/10.3389/fevo.2015.00151.

171. Rezával, C., Nojima, T., Neville, M.C., Lin, A.C., and Goodwin, S.F. (2014). Sexually dimorphic octopaminergic neurons modulate female postmating behaviors in Drosophila. Curr Biol *24*, 725–730. https://doi.org/10.1016/j.cub.2013.12.051.

172. Wang, T., Jing, B., Deng, B., Shi, K., Li, J., Ma, B., Wu, F., and Zhou, C. (2022). Drosulfakinin signaling modulates female sexual receptivity in Drosophila. Elife *11*, e76025. https://doi.org/10.7554/eLife.76025.

173. Ameku, T., Yoshinari, Y., Texada, M.J., Kondo, S., Amezawa, K., Yoshizaki, G., Shimada-Niwa, Y., and Niwa, R. (2018). Midgut-derived neuropeptide F controls germline stem cell proliferation in a mating-dependent manner. PLOS Biology *16*, e2005004. https://doi.org/10.1371/journal.pbio.2005004.

174. Zhang, C., Daubnerova, I., Jang, Y.-H., Kondo, S., Žitňan, D., and Kim, Y.-J. (2021). The neuropeptide allatostatin C from clock-associated DN1p neurons generates the circadian rhythm for oogenesis. Proc Natl Acad Sci U S A *118*, e2016878118. https://doi.org/10.1073/pnas.2016878118.

175. Lin, W.-S., Yeh, S.-R., Fan, S.-Z., Chen, L.-Y., Yen, J.-H., Fu, T.-F., Wu, M.-S., and Wang, P.-Y. (2018). Insulin signaling in female Drosophila links diet and sexual attractiveness. The FASEB Journal *32*, 3870–3877. https://doi.org/10.1096/fsb2fj201800067r.

176. Kuo, T.-H., Fedina, T.Y., Hansen, I., Dreisewerd, K., Dierick, H.A., Yew, J.Y., and Pletcher, S.D. (2012). Insulin Signaling Mediates Sexual Attractiveness in Drosophila. PLoS Genet *8*, e1002684. https://doi.org/10.1371/journal.pgen.1002684.

177. Cong, X., Wang, H., Liu, Z., He, C., An, C., and Zhao, Z. (2015). Regulation of Sleep by Insulin-like Peptide System in Drosophila melanogaster. Sleep *38*, 1075–1083. https://doi.org/10.5665/sleep.4816.

178. Isabel, G., Martin, J.-R., Chidami, S., Veenstra, J.A., and Rosay, P. (2005). AKH-producing neuroendocrine cell ablation decreases trehalose and induces behavioral changes in Drosophila. Am J Physiol Regul Integr Comp Physiol *288*, R531-538. https://doi.org/10.1152/ajpregu.00158.2004.

179. Bednářová, A., Tomčala, A., Mochanová, M., Kodrík, D., and Krishnan, N. (2018). Disruption of Adipokinetic Hormone Mediated Energy Homeostasis Has Subtle

Effects on Physiology, Behavior and Lipid Status During Aging in Drosophila. Front Physiol *9*, 949. https://doi.org/10.3389/fphys.2018.00949.

180. Post, S., Liao, S., Yamamoto, R., Veenstra, J.A., Nässel, D.R., and Tatar, M. (2019). Drosophila insulin-like peptide dilp1 increases lifespan and glucagon-like Akh expression epistatic to dilp2. Aging Cell *18*, e12863. https://doi.org/10.1111/acel.12863.

181. Stephenson, E.J., Stayton, A.S., Sethuraman, A., Rao, P.K., Meyer, A., Gomes, C.K., Mulcahy, M.C., McAllan, L., Puchowicz, M.A., Pierre, J.F., et al. (2022). Chronic intake of high dietary sucrose induces sexually dimorphic metabolic adaptations in mouse liver and adipose tissue. Nat Commun *13*, 6062. https://doi.org/10.1038/s41467-022-33840-6.

182. Mauvais-Jarvis, F., Merz, N.B., Barnes, P.J., Brinton, R.D., Carrero, J.-J., DeMeo, D.L., Vries, G.J.D., Epperson, C.N., Govindan, R., Klein, S.L., et al. (2020). Sex and gender: modifiers of health, disease, and medicine. The Lancet *396*, 565–582. https://doi.org/10.1016/S0140-6736(20)31561-0.

183. Mauvais-Jarvis, F. (2015). Sex differences in metabolic homeostasis, diabetes, and obesity. Biol Sex Differ *6*, 14. https://doi.org/10.1186/s13293-015-0033-y.

184. Chella Krishnan, K., Mehrabian, M., and Lusis, A.J. (2018). Sex differences in metabolism and cardiometabolic disorders. Curr Opin Lipidol *29*, 404–410. https://doi.org/10.1097/MOL.0000000000000536.

185. Tramunt, B., Smati, S., Grandgeorge, N., Lenfant, F., Arnal, J.-F., Montagner, A., and Gourdy, P. (2020). Sex differences in metabolic regulation and diabetes susceptibility. Diabetologia *63*, 453–461. https://doi.org/10.1007/s00125-019-05040-3.

186. Strack, C., Behrens, G., Sag, S., Mohr, M., Zeller, J., Lahmann, C., Hubauer, U., Loew, T., Maier, L., Fischer, M., et al. (2022). Gender differences in cardiometabolic health and disease in a cross-sectional observational obesity study. Biology of Sex Differences *13*, 8. https://doi.org/10.1186/s13293-022-00416-4.

187. May, C.E., Vaziri, A., Lin, Y.Q., Grushko, O., Khabiri, M., Wang, Q.-P., Holme, K.J., Pletcher, S.D., Freddolino, P.L., Neely, G.G., et al. (2019). High Dietary Sugar Reshapes Sweet Taste to Promote Feeding Behavior in Drosophila melanogaster. Cell Reports *27*, 1675-1685.e7. https://doi.org/10.1016/j.celrep.2019.04.027.

188. Nunes, R.D., and Drummond-Barbosa, D. (2023). A high-sugar diet, but not obesity, reduces female fertility in Drosophila melanogaster. Development *150*, dev201769. https://doi.org/10.1242/dev.201769.

189. Yu, H., Biswas, P., Rideout, E., Cao, Y., and Huan, T. (2023). Bayesian optimization of separation gradients to maximize the performance of untargeted LC-MS. Preprint at bioRxiv, https://doi.org/10.1101/2023.09.08.556930 https://doi.org/10.1101/2023.09.08.556930.

190. Yu, H., and Huan, T. (2022). MAFFIN: metabolomics sample normalization using maximal density fold change with high-quality metabolic features and corrected signal intensities. Bioinformatics *38*, 3429–3437. https://doi.org/10.1093/bioinformatics/btac355.

191. Li, Y., Wang, W., and Lim, H.-Y. (2021). Drosophila Solute Carrier 5A5 Regulates Systemic Glucose Homeostasis by Mediating Glucose Absorption in the Midgut. International Journal of Molecular Sciences *22*, 12424. https://doi.org/10.3390/ijms222212424.

192. Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., Preibisch, S., Rueden, C., Saalfeld, S., Schmid, B., et al. (2012). Fiji: an open-source platform for biological-image analysis. Nat Methods *9*, 676–682. https://doi.org/10.1038/nmeth.2019.

Figure 1

Figure 2

Figure 3

A *dilp3* mRNA levels in head

B *dilp2* mRNA levels in head

C *dilp5* mRNA levels in head

D *dilp3* mRNA levels in head

E Insulin secretion from IPCs

F Insulin activity in abdominal carcass

G Peripheral Insulin Sensitivity

H Peripheral Insulin Sensitivity

Figure 4

Supplemental Figure 1

A   **Food consumption**

B   **Triglyceride Levels**

C   **Food consumption**

D   **Triglyceride Levels**

Supplemental Figure 2

A Sex-differences in significant esterified FAs in TG in 1S

B Proportion of significant lipid species in female w^{1118} fat body

C Identity of TG 35-TG 48 with significant changes in females in 1S

D Identity of TG 49-TG 62 with significant changes in females in 1S

E Significant esterified FAs in TG in female in 1S and 0S

F Identity of TG with significant changes in males in 1S

G Proportion of significant lipid species in male w^{1118} fat body

Supplemental Figure 3