Transcriptional control of steroid biosynthesis genes in the Drosophila prothoracic gland by Ventral veins lacking and Knirps

Danielsen, Erik Thomas; Møller, Morten Erik; Dorry, Elad; Komura-Kawa, Tatsuya; Fujimoto, Yoshinori; Troelsen, Jesper; Herder, Rachel; O'Connor, Michael B.; Niwa, Ryusuke; Rewitz, Kim Furbo

Published in:
P L o S Genetics

DOI:
10.1371/journal.pgen.1004343

Publication date:
2014

Document Version
Publisher's PDF, also known as Version of record

Citation for published version (APA):
Transcriptional Control of Steroid Biosynthesis Genes in the *Drosophila* Prothoracic Gland by Ventral Veins Lacking and Knirps

E. Thomas Danielsen¹, Morten E. Moeller¹, Elad Dorry¹, Tatsuya Komura-Kawa², Yoshinori Fujimoto³, Jesper T. Troelsen⁴, Rachel Herder⁵, Michael B. O’Connor⁵, Ryusuke Niwa²,⁶, Kim F. Rewitz¹

¹Department of Biology, University of Copenhagen, Copenhagen, Denmark, ²Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki, Japan, ³Department of Chemistry and Materials Science, Tokyo Institute of Technology, Meguro, Tokyo, Japan, ⁴Department of Science, Systems and Models, Roskilde University, Roskilde, Denmark, ⁵Department of Genetics, Cell Biology and Development, University of Minnesota, Minneapolis, Minnesota, United States of America, ⁶PRESTO, JST, Kawaguchi, Saitama, Japan

Abstract

Specialized endocrine cells produce and release steroid hormones that govern development, metabolism and reproduction. In order to synthesize steroids, all the genes in the biosynthetic pathway must be coordinately turned on in steroidogenic cells. In *Drosophila*, the steroid producing endocrine cells are located in the prothoracic gland (PG) that releases the steroid hormone ecdysone. The transcriptional regulatory network that specifies the unique PG specific expression pattern of the ecdysone biosynthetic genes remains unknown. Here, we show that two transcription factors, the POU-domain Ventral veins lacking (Vvl) and the nuclear receptor Knirps (Kni), have essential roles in the PG during larval development. Vvl is highly expressed in the PG during embryogenesis and is enriched in the gland during larval development, suggesting that Vvl might function as a master transcriptional regulator in this tissue. Vvl and Kni bind to PG specific cis-regulatory elements that are required for expression of the ecdysone biosynthetic genes. Knock down of either *vvl* or *kni* in the PG results in a larval developmental arrest due to failure in ecdysone production. Furthermore, Vvl and Kni are also required for maintenance of TOR/S6K and prothoracicotropic hormone (PTTH) signaling in the PG, two major pathways that control ecdysone biosynthesis and PG cell growth. We also show that the transcriptional regulator, Molting defective (Mld), controls early biosynthetic pathway steps. Our data show that Vvl and Kni directly regulate ecdysone biosynthesis by transcriptional control of biosynthetic gene expression and indirectly by affecting PTTH and TOR/S6K signaling. This provides new insight into the regulatory network of transcription factors involved in the coordinated regulation of steroidogenic cell specific transcription, and identifies a new function of Vvl and Knirps in endocrine cells during post-embryonic development.

Introduction

Steroid hormones have a conserved role in the regulation of developmental transitions, growth, metabolism and reproduction in animals [1-3]. Specialized endocrine tissues with cell-type specific complements of enzymes that form biochemical pathways mediate the biosynthesis of steroids. In *Drosophila* larvae, the steroid biosynthetic enzymes are expressed in the prothoracic gland (PG), the endocrine tissue of insects and the major source of the steroid hormone ecdysone. The production of ecdysone in the PG is regulated by a checkpoint control system in response to external and internal signals [2]. These checkpoints allow the endocrine system to assess growth and nutrient status before activating the biochemical pathway that increases the release of ecdysone, which triggers developmental progression.

Despite the importance of the coordinated expression in endocrine cells of the steroidogenic enzymes, the PG specific transcriptional regulatory networks that underlie steroidogenic cell function remain unknown. The steroidogenic function of the PG cells is defined by the restricted expression of the genes involved in ecdysone biosynthesis that mediate the conversion of cholesterol to ecdysone. The components of the ecdysone biosynthetic pathway include the Rieske-domain protein Neverland (Nvl) [4,5], the short-chain dehydrogenase/reductase Shroud (Sro) [6] and the P450 enzymes Spook (Spo), Spookier (Spok), Phantom (Phim), Disembodied (Dib) and Shadow (Sad) [7–12] collectively referred to as the Halloween genes. Ecdysone produced by the PG is released into circulation and converted into the more active hormone, 20-hydroxycyecdosterone (20E), in peripheral tissues by the P450 enzyme, Shade (Shd) [13,14].
Steroid hormones play important roles in physiology and disease. These hormones are molecules produced and secreted by endocrine cells in the body and control sexual maturation, metabolism and reproduction. We found transcriptional regulators that underlie the specialized function of endocrine steroid-producing cells. In the steroid-producing cells of the fruit fly Drosophila, Ventral veins lacking (Vvl) and Knirps (Kni) turn on all the genes required for steroid production. When Vvl or Kni were inactivated in the cells where the hormone is made, the genes involved in steroid production were not activated. Because of this, the juvenile larvae failed to develop and undergo maturation to adulthood. Inactivation of Vvl and Kni also reduces endocrine cell growth by disturbing their response to growth promoting signals. Genetic variations in humans with the loss of a homolog of Vvl have been associated with disorders caused by insufficient steroid production. Together with the fact that Vvl is highly expressed in the steroid-producing cells of Drosophila, this suggests that Vvl may be a conserved master regulator of steroid production. Our findings provide insight into the network of factors that control endocrine cell function and steroid hormone levels that could have implication for human diseases.

Here, we report a novel role for Ventral veins lacking (Vvl) and Knirps (Kni) in regulating ecdysteroidogenesis in Drosophila. The cis-regulatory elements responsible for PG specific expression of spok, phm and dib contain conserved Vvl and Kni binding sites. Expression of vvl is high in the PG compared to the whole animal, while kni expression is less PG-specific. Knock down of vvl and kni in the PG results in larval developmental arrest due to impaired ecdysone production. We show that Vvl and Kni specifically regulate expression of all the ecdysone biosynthetic enzymes through functionally important regulatory sites. Furthermore, we find that Molting defective (Mld) specifically regulates enzymes that catalyze early steps in the ecdysone biosynthetic pathway. Our study identifies Vvl as a PG cell-specific transcription factor that underlies steroidogenic cell function. We conclude that Vvl and Kni are involved in the transcriptional regulatory network of the PG that coordinates expression of biosynthetic enzymes required for ecdysone production during Drosophila development.

Results

Regulatory regions of ecdysone biosynthesis genes contain conserved binding sites for Vvl and Kni

We analyzed the phm and dib PG specific regulatory elements for transcription factor binding sites. Our in silico search revealed conserved binding sites for the POU-domain transcription factor Vvl and the nuclear receptor Kni in the phm promoter and dib enhancer (Fig. 1A and S1). Analysis of the phm promoter identified one conserved Vvl site and four Kni sites of which three are highly conserved, indicating that they are important regulatory sites. In support of this, mutations disrupting the Vvl site and one of the conserved Kni sites eliminate PG specific GFP reporter expression [20]. In contrast, mutations in the non-conserved Kni binding sites do not reduce PG expression. The third intron dib enhancer also contains one Vvl site and two Kni sites, both in regions that have been conserved. We also identified a 300 bp PG specific promoter for spok, encoding an enzyme that acts at an early step in the ecdysone biosynthetic pathway [9]. This element located −331 to −32 bp upstream of translation start drives specific PG reporter GFP expression. This spok promoter contains three Vvl and three Kni binding sites, although these sites are less conserved compared to the Vvl and Kni sites identified in the phm and dib regulatory elements. Expression of spok has previously been reported to require Molting defective (Mld), a nuclear zinc finger protein [9]. Since the DNA binding sequence motif for Mld has not yet been characterized, we were unable to examine potential Mld binding sites in the spok promoter.

Vvl and Kni are expressed in the prothoracic gland

The observation of Vvl and Kni binding sites in the promoter/enhancer of the steroidogenic enzymes prompted us to verify if these transcription factors are expressed in the PG. We performed in situ hybridization on third instar larvae and observed an intense staining of vvl mRNA in the PG (Fig. 1B). Moreover, strong embryonic vvl expression is seen in the primordium of the PG from stage 13. Importantly, the appearance of vvl in the PG precedes that of the biosynthetic genes which are expressed by stage 15 in the PG primordium [11,12]. Although in situ expression of kni was undetectable in the PG of embryos, expression in the PG was observed at the L3 stage (Fig 1B). We also detected expression of vvl in nurse and follicle cells of adult female ovaries (Fig. S1).

Using specific antibodies, we also confirmed that Vvl and Kni are expressed in the PG and that these transcription factors localize in the nucleus (Fig. 1C). Although kni expression was not detected using in situ hybridization in the embryonic PG,
expression of Kni was found in the PG at the L2 stage (Fig. S1). Next, we quantified vvl and kni expression in the ring gland (an organ with by far the most of its volume constituted by PG cells) compared to the whole body in order to see if these transcription factors are enriched in the PG (Fig. 1D). As a control, we measured phm expression, which indeed is highly expressed in the PG compared to the whole animal and mld, encoding a factor with a specific role in the PG, but with a broader expression pattern.
Expression of vvl was highly enriched in the ring gland, like phm, while kni expression was less specific to this tissue similar to mild.

**PG loss of vvl and kni result in developmental arrest due to failure in ecdysone production**

Based on the potential regulatory role of Vvl and Kni, we next sought to determine if these transcription factors are required for PG expression of the genes involved in ecdysone biosynthesis. We used the PG specific phm-Gal4 (phm>) driver and observed that knock down of vvl in the PG using UAS-vvl-RNAi (vvl-RNAi) resulted in first instar (L1) arrest (Fig. 2A). Furthermore, RNAi mediated knock down of kni in the PG, by using phm> with a UAS-kni-RNAi (kni-RNAi), led to an L1 and second instar (L2) arrest phenotype. To exclude the contribution of off-target effects, we tested PG specific knock down of vvl and kni using other transgenic RNAi lines that target different regions of the vvl and kni mRNA and found that they produce similar phenotypes (Table S1). To support this, we also used the P0206-Gal4 (P0206>) driver that promotes weak expression in the PG cells [22]. When expression of vvl and kni was reduced using P0206>, development was arrested during later stages compared to when crossed with phm>.

Knock down of mld in the PG with phm> driven UAS-mld-RNAi (mld-RNAi) also resulted in L1 arrest (Fig. 2A) consistent with mutant analysis [9,21].

If kni and vvl are involved in specifying the gland during embryonic development, reducing their expression may cause a lack of PG cell differentiation. We used a phm>GFP to label and examine the morphology of the PG in L1 larvae 36 hours after egg lay (AEL). PG cell number and morphology of L1 larvae with reduced expression of vvl, kni or mld in the PG were indistinguishable from the phm> control (Fig. 2A). This demonstrates that knock down of these factors does not compromise PG cell fate specification and survival. The developmental arrest indicates that loss of vvl and kni in the PG impair the cellular production of ecdysone. We therefore investigated the ecdysone levels in L1 larvae 36 hours AEL by measuring E75B mRNA expression in the whole animal, which has been used as a readout for ecdysone levels [20,23]. Expression of E75B was significantly reduced in mid-first instar phm>vvl-RNAi and phm>mld-RNAi larvae compared to the control (Fig. 2B). This is consistent with the failure of phm>vvl-RNAi and phm>mld-RNAi larvae to molt to the L2 stage. A portion of larvae with knock down of kni in the PG undergoes the L1–L2 transition, suggesting that some of these animals can produce sufficient ecdysone for the L1–L2 molt. Consistent with this observation, knock down of kni in the PG did not lead to a significant reduction of E75B in the mid-first instar. To demonstrate that the observed phenotypes are a result of decreased ecdysone biosynthesis, we tested if ecdysone supplementation could rescue the developmental arrest. Indeed, animals with reduced expression of vvl, kni or mld in the PG were rescued by the addition of 20E to their food, showing that it is the lack of this hormone that is causing the arrest (Fig. 2A). To confirm this, we measured the ecdysteroid titer, which demonstrates that larvae with reduced expression of vvl, kni or mld in the PG have low levels of ecdysteroids 36 hours AEL compared to the control (Fig. 2C). Taken together, these results indicate that the transcription factors Vvl and Kni, like Mld, are required for ecdysone biosynthesis in the endocrine cells of PG during early larval development.

**Vvl and Kni are required for ecdysone production by regulating steroidogenic gene expression**

We next investigated if Vvl and Kni regulate the expression of the genes involved in ecdysone biosynthesis. phm>vvl-RNAi and
phm
kni-RNAi
larvae showed reduction in the expression of phm, dib and sad by the mid-first instar 36 hours AEL compared to the control (Fig. 3A). Knock down of vvl also reduced expression of sro and spok, catalyzing early steps in the pathway, as well as a reduction of phm, dib and sad mediating the last three steps in the biosynthetic pathway. Knock down of kni results in down-regulation of phm, dib and sad, while knock down of mld causes a specific down-regulation of sro and a moderate reduction of sro.

Expression was measured in mid-first instar larvae 36 hours AEL. Error bars indicate s.e.m. (n = 4). *P<0.05, **P<0.01, versus the phm>++ control. (B, C) Direct binding of Vvl or Kni to the regulatory sites in phm promoter indicated by electrophoretic mobility shift assay (EMSA). Nuclear extract was incubated with [γ-32P]ATP-labeled oligonucleotide sequences of phm promoter containing the vvl (B) or the kni sites (C) and resulted in shifted DNA-protein bands (lane 1). Competition assays were performed with unlabeled non-specific random oligonucleotide sequences (lane 2), the phm promoter containing the vvl or kni sites (lane 3), the phm promoter with mutated vvl or kni sites (lane 4), an oligonucleotide sequence with vvl or kni consensus motif sequence (lane 5), or with the consensus motif mutated (lane 6).

doi:10.1371/journal.pgen.1004343.g003

Figure 3. vvl, kni and mld are required for the expression of genes in the ecdysone biosynthetic pathway. (A) Knock down of vvl, kni and mld in the PG reduces expression of genes in the steroidogenic pathway. vvl knock down results in a down-regulation of spok and sro, catalyzing early steps in the pathway, as well as a reduction of phm, dib and sad mediating the last three steps in the biosynthetic pathway. Knock down of kni results in down-regulation of phm, dib and sad, while knock down of mld causes a specific down-regulation of sro and a moderate reduction of sro. Expression was measured in mid-first instar larvae 36 hours AEL. Error bars indicate s.e.m. (n = 4). *P<0.05, **P<0.01, versus the phm>++ control. (B, C) Direct binding of Vvl or Kni to the regulatory sites in phm promoter indicated by electrophoretic mobility shift assay (EMSA). Nuclear extract was incubated with [γ-32P]ATP-labeled oligonucleotide sequences of phm promoter containing the vvl (B) or the kni sites (C) and resulted in shifted DNA-protein bands (lane 1). Competition assays were performed with unlabeled non-specific random oligonucleotide sequences (lane 2), the phm promoter containing the vvl or kni sites (lane 3), the phm promoter with mutated vvl or kni sites (lane 4), an oligonucleotide sequence with vvl or kni consensus motif sequence (lane 5), or with the consensus motif mutated (lane 6).

doi:10.1371/journal.pgen.1004343.g003

phm>++RNAi larvae showed reduction in the expression of phm, dib and sad by the mid-first instar 36 hours AEL compared to the control [Fig. 3A]. Knock down of vvl also reduced expression of sro and spok, encoding enzymes believed to work in early steps in the pathway known as the black box [4,5,9]. However, expression of nvd, encoding a PG specific gene involved in the first step in the biosynthetic pathway, was not significantly reduced in the mid-first instar by knock down of vvl or kni in the PG. This further supports the notion that the PG is specified normally during embryogenesis. Previous studies have indicated that mld mutants have reduced ecdysone levels because of a specific lack of spok expression [9,21].

Our knock down results involving mld-RNAi in the PG support that Mld is required specifically for the expression of spok, but not for the later acting products of phm, dib and sad.

The binding sites of these factors in the PG specific regulatory elements indicate that Vvl and Kni are involved in a transcriptional network necessary for co-expression of the biosynthetic enzymes. We therefore sought to establish if Vvl and Kni can bind directly to the PG specific regulatory elements by performing a DNA/protein binding assay. For this purpose, we performed...
electrophoretic mobility shift assays (EMSAs) with the conserved sites in the phm promoter since the functional importance of these sites has been confirmed [20]. Radiolabeled DNA oligonucleotide sequences that contained the conserved vvl or kni binding sites in the phm promoter required for PG expression (Fig. 1A) formed DNA/protein complexes with nuclear cell extract (Fig. 3B and C). These complexes were outcompeted by unlabeled oligonucleotide sequences containing consensus vvl or kni sites and by the unlabeled phm oligonucleotides containing the vvl or kni site, but not by the unlabeled phm oligonucleotides with mutated vvl or kni binding sites or by an unspecific oligonucleotide sequence. This finding demonstrates that the vvl and kni sites are required for

Figure 4. vvl, kni and mld have a specific role in regulating ecdysone biosynthesis in the L3 stage. (A) Expression of steroidogenic genes in ring glands from wild type (phm-GFP) larvae increases little from early (72 hours AEL) to mid (96 hours AEL) third instar, but rises dramatically in the late (120 hours AEL) third instar. vvl expression exhibits a minor increase in the late third instar, while mld, kni and especially Br-Z4 show a strong increase (n = 4). (B) Expression in the ring gland from larvae with knock down of vvl, kni or mld during the L3 stage two days after temperature induced activation of the RNAi with the Gal80ts:phm> driver 96 hours AEL. Expression of all the steroidogenic genes were significantly reduced in animals with reduces vvl or kni expression. Knock down of mld results in a dramatic reduction in expression of vvl and spok that mediate two early steps in the biosynthesis of ecdysone (n = 4). (C) Quantified level of Phm protein in brain-ring gland complexes (BRGCs) from L3 larvae two days after temperature induced RNAi (96 hours AEL) normalized to Tubulin levels determined by immunoblotting (top panel) (n = 3). (D) Ecdysteroid levels determined by ELISA in L3 larvae with reduced PG expression of vvl, kni or mld two days after temperature induced activation of the RNAi effect (96 hours AEL) (n = 4). Error bars indicate s.e.m. *, **, *** P < 0.05, < 0.01, < 0.001, versus the Gal80ts:phm> control.
doi:10.1371/journal.pgen.1004343.g004
formation of the DNA/protein complex and supports that Vvl and Kni regulate transcription of the genes involved in ecdysone biosynthesis by direct binding to their promoters and enhancers.

Vvl and kni are required to maintain expression of the biosynthetic genes during late larval development

The data indicate that Vvl and Kni are critical for the steroidogenic activity of the PG during early post-embryonic development. Later during larval development the up-regulation of ecdysone biosynthetic genes and the growth of the gland are required to produce the high-level ecdysone pulse that triggers metamorphosis. To investigate the role of Vvl and Kni during later stages of postembryonic development, we analyzed their expression in third instar (L3) larval ring glands from early (72 hours AEL), mid (96 hours AEL) and late (120 hours AEL) L3 larvae. In wild type larvae, expression of the steroidogenic genes showed no or little increase from the early to mid L3, but a dramatic up-regulation in the late L3 (Fig. 4A), coinciding with the high-level ecdysone peak that triggers pupariation 120 hours AEL [20]. While the expression of vvl showed only a minor increase during the L3 stage, a stronger up-regulation of kni and mld was observed. Compared to both vvl, kni and mld, expression of Br-\(
\text{\(\Delta 4\)}\) was highly up-regulated in the late L3 consistent with its role in the temporal up-regulation of the biosynthetic genes important for the high-level ecdysone pulse 120 hours AEL that triggers pupariation [24]. Considering the tissue-specificity and that vvl expression in the PG shows little relation with the ecdysone titer, it seems likely that Vvl is important for the spatial control of ecdysone biosynthetic gene expression in the PG, but not for the temporal regulation during development. On the other hand, kni expression is less PG specific, but show more correlation with the ecdysone titer during L3.

To determine whether Vvl and Kni are only required to set the initial expression of the biosynthetic enzymes during embryonic and early larval development or also to maintain PG expression during late larval stages, we used tub-Gal80\(\text{ts}\);phm-Gal4 (Gal80\(\text{ts}\);phm) to conditionally induce the UAS-RNAi effect. Gal80\(\text{ts}\);phm-vvl-RNAi and Gal80\(\text{ts}\);phm-kni-RNAi larvae develop normally at 18°C and were shifted to 29°C to induce the RNAi at different times during larval stages. Development of most Gal80\(\text{ts}\);phm-vvl-RNAi, Gal80\(\text{ts}\);phm-kni-RNAi and Gal80\(\text{ts}\);phm-mld-RNAi larvae was arrested in L3 when larvae were shifted to 29°C 120 hours AEL or earlier, while larvae that were shifted 144 hours AEL or later pupariated normally (Fig. S2). Because development is slowed down at 18°C, 120 hours AEL is corresponding to the late L2 stage under these conditions [25]. Thus, inducing RNAi in late L2 or earlier causes developmental arrest in L3, suggesting that it prevents the production of the high-level ecdysone pulse in late L3 that triggers metamorphosis.

Since expression of the biosynthetic genes detected in L1 larvae with reduced expression of vvl and kni was measured on RNA extracted from whole animals (Fig. 3A), and normalized to RpL23 and Rpl32, ubiquitously expressed ribosomal housekeeping genes, it is possible that reduced PG cell growth could be responsible for the observed decrease in biosynthetic gene expression because of a reduced PG to whole animal size ratio. To exclude this possibility and to test whether Vvl and Kni are required to maintain PG specific expression of steroidogenic genes later during development, we analyzed expression in isolated ring glands from L3 larvae. We first confirmed the efficient reduction of vvl and kni mRNA levels compared to the control (Fig. S2). Additional analysis showed that expression of all of the steroidogenic enzymes was dramatically decreased in L3 ring glands in which vvl and kni were knocked down compared to the control (Fig. 4B). This demonstrates that the decreased expression of the ecdysone biosynthetic genes in vvl-RNAi and kni-RNAi animals is a consequence of a specific reduction in the transcription of steroidogenic genes, and not reduced glandular growth or a general reduction in transcription. Compared to vvl-RNAi and kni-RNAi, mld knock down had little or no influence on the
transcription of the genes encoding enzymes acting in late steps in the biosynthetic pathway. However, spok and nvd levels were strongly reduced in the ring glands of mld-RNAi larvae compared to the control, suggesting that these are direct targets of mld regulation. This indicates that Mld is involved in the transcriptional regulation of the enzymes mediating early biosynthetic conversions of cholesterol. The observation that mld-RNAi also regulates nvd expression may explain why spok overexpression in the PG is insufficient to rescue mld mutants [9].

To examine the influence of vvl and kni knock down on the biosynthetic enzyme level, we measured Phm protein levels in brain-ring gland complexes (BRGCs) using immunoblotting analysis. Consistent with the reduced mRNA levels, these results show that Phm protein levels are dramatically reduced in vvl-RNAi and kni-RNAi larvae compared with the control (Fig. 4C). To reinforce that knock down of vvl, kni or mld in the PG impairs ecdysone biosynthesis, we also measured the ecdysteroid levels in L3 larvae. Ecdysteroid levels were reduced in L3 larvae where RNAi mediated knock down of vvl, kni or mld in the PG had been induced in the L2 stage (Fig. 4D).

The developmental arrest by PG inactivation of vvl and kni can be rescued by ecdysone and 20E

Taken together, the data suggest that the coordinated expression of steridogenic enzymes in the PG requires Vvl and Kni function. To further corroborate our findings that Vvl and Kni are involved in co-regulating all components in the biosynthetic pathway, we examined whether supplementation of any 20E precursors to the larval growth medium was able to rescue the developmental arrest of vvl or kni RNAi larvae. When fed cholesterol, 7-dehydrocholesterol or 5b-ketodiol, most phm>vvl-RNAi and phm>kni-RNAi animals develop to small L2 larvae (Fig. 5A and B). Since phm>vvl-RNAi and phm>kni-RNAi arrest in L1 and L2 without supplementation, it appears that increasing the amount of substrate for ecdysone synthesis provides some compensation, but not complete rescue, when the pathway activity

Figure 6. vvl and kni knock down affects PG cell size and disturbs PTTH/Torso and insulin/TOR signaling. (A, B) PG (green) and nuclei (magenta: DAPI) show that the morphology of the gland is intact in L3 larvae with reduced expression of vvl, kni, or mld in the PG. PG cell and nucleus size of L3 larvae (measured as the diameter) are reduced when vvl and kni are knocked down (n = 11). RNAi was induced using the Gal80ts;phm++;96 hours AEL corresponding to the late L2 stage at 18 °C. The PG was analyzed after two days at 29 °C when control larvae are in the wandering stage. (C) Knock down of vvl and kni results in decreased expression of torso (tor), 4EBP and S6K in dissected ring glands containing the PG. Likewise, 4EBP and S6K are down regulated in ring glands of mld-RNAi animals that also exhibit reduced expression of the InR. Contrary, akt is increased in vvl-RNAi animals (n = 4). (D) Loss of vvl, kni or mld results in a strong increase of npc1a expression in the ring gland. In C and D, expression was measured in L3 larvae raised as described in A and B (n = 4). Error bars indicate s.e.m. *P<0.05, **P<0.01, ***P<0.001, versus the Gal80ts++;control.

doi:10.1371/journal.pgen.1004343.g006
is reduced. Supporting this notion, providing intermediates further downstream in the pathway gradually increased rescue of \( \text{phm} > \text{vvl-RNAi} \) and \( \text{phm} > \text{kni-RNAi} \) larvae to the L3 stage. In particular, 20E and its precursor ecdysone efficiently rescue \( \text{phm} > \text{vvl-RNAi} \) and \( \text{phm} > \text{kni-RNAi} \) larvae to the L3 stage (Fig. 5B).

We then tested whether increased availability of cholesterol substrate is sufficient to promote ecdysone biosynthesis. Indeed, supplementation with cholesterol increased E75E mRNA in wild type larvae and ecdysteroid levels in the control and in larvae grown on standard food (Fig. S3). Like rescue of the L1 arrest (Fig. 5B), cholesterol also provided minor rescue of the L3 developmental arrest observed when the RNAi effect was induced in the L2 stage (Table S2). Increasing cholesterol concentrations only provides minor rescue for loss of \( \text{vvl} \) and \( \text{kni} \). In contrast, we confirmed that it provides complete compensation for loss of \( \text{Niemann-Pick type C-1a (npc1a)} \) (Fig. S3), which reduces substrate delivery for ecdysone biosynthesis [26,27]. These results suggest that the hormone deficiency observed in \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) larvae is a result of impaired ecdysone pathway activity and not compromised cholesterol substrate delivery, like in \( \text{phm} > \text{npc1a-RNAi} \). Larvae. These findings overall indicate that silencing \( \text{phm} \) regulates genes involved in early steps in the pathway responsible for the conversion of cholesterol to the 5β-ketodiol, an intermediate downstream of the black box reaction(s).

**PTTH and insulin/TOR signaling in the PG is disturbed by loss of **\( \text{vvl} \) **and** \( \text{kni} \)

Our data demonstrate that \( \text{Vvl} \) and \( \text{Kni} \) are specifically involved in transcriptional regulation of ecdysone biosynthetic components. However, when we analyzed the morphology of PG cells with reduced expression of \( \text{vvl} \) and \( \text{kni} \), we found a mild decrease in PG cell size (Fig. 6A and B), indicating that knock down of these transcription factors also influence cellular growth. The major pathways that are thought to control PG cell growth are the PTTH and the insulin/TOR pathways [22,28–32]. Therefore, we investigated the possibility that \( \text{Vvl} \) and \( \text{Kni} \) affect PG cell growth and ecdysone synthesis indirectly by interfering with PTTH and/or insulin/TOR signaling. The neuropeptide, PTTH promotes PG growth and ecdysone synthesis through activation of its receptor Torso, a receptor tyrosine kinase (RTK) expressed specifically in the PG [33]. Activation of the insulin receptor (InR), another RTK, in the PG also regulates cell growth and stimulates ecdysone synthesis in response to circulating insulin levels. Although crosstalk between systemic insulin mediated growth regulation and TOR signaling might occur, the TOR pathway cell-autonomously regulates growth in response to cellular nutrient levels [34]. We therefore investigated whether PTTH and insulin/TOR signaling in the gland is affected by knock down of \( \text{vvl} \) and \( \text{kni} \). Analysis of \( \text{torno} \) transcript levels revealed that, while \( \text{mld-RNAi} \) larvae have normal \( \text{torno} \) mRNA levels, expression of the PTTH receptor is reduced in ring glands from L3 \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) larvae (Fig. 6C). Consistent with down-regulation of the PTTH receptor, we found reduced levels of phosphorylated ERK, an indicator of MAPK activity and PTTH signaling [33], in BRGCs from \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) larvae (Fig. S4). However, unlike the biosynthetic enzymes (Fig. 3), expression of \( \text{torno} \) was not reduced in L1 \( \text{phm} > \text{vvl-RNAi} \) larvae 36 hours AEL (Fig. S4), indicating that \( \text{torno} \) expression is initiated normally despite the loss of \( \text{vvl} \) in the PG. When examining the expression of the InR and components mediating insulin signaling, we found reduced expression in \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) animals of \( \text{4EBP} \) that encodes a negative growth regulator depressed by activation of the insulin pathway. Further, levels of \( \text{akt} \), which encodes a serine/threonine kinase of the insulin signaling pathway [35], were increased, while levels of InR were decreased in \( \text{vvl-RNAi} \) larvae. Increased insulin signaling is generally associated with decreased expression of both \( \text{4EBP} \) and \( \text{InR} \) [36,37]. These results imply that loss of \( \text{vvl} \) and \( \text{kni} \) increases insulin signaling. The most likely explanation for increased insulin signaling in PG of animals with reduced \( \text{vvl} \) and \( \text{kni} \) expression is the low ecdysone levels, which cause a general increase of insulin release from the brain [29]. Thus, the disturbance of insulin signaling in the PG of \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) animals seems unlikely to account for the PG cell growth reduction. However, we observed a strong transcriptional reduction of the S6 kinase (S6K), an important positive growth regulator downstream of TOR. This suggests that the combined reduction of both PTTH/Torso and TOR/S6K signaling in the PG contributes to the negative influence of \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) on PG cell growth and ecdysone synthesis.

**Knock down of **\( \text{vvl} \) **and** \( \text{kni} **affects** \( \text{Npc1a} **involved in cholesterol trafficking**

Finally, we investigated whether loss of \( \text{vvl} \) and \( \text{kni} \) in the PG affects cholesterol substrate delivery for ecdysone synthesis. Surprisingly, we found that, whereas the biosynthetic genes show a strong decrease, \( \text{npc1a} \) exhibits a dramatic increase in the gland of \( \text{vvl-RNAi} \), \( \text{kni-RNAi} \) and \( \text{mld-RNAi} \) larvae (Fig. 6D). This finding indicates that up-regulation of \( \text{npc1a} \) in the PG of \( \text{vvl-RNAi} \), \( \text{kni-RNAi} \) and \( \text{mld-RNAi} \) larvae reflect a compensatory feedback regulation to maintain cholesterol homeostasis and/or increase substrate delivery to promote steroidogenesis. Down-regulation of biosynthetic activity in \( \text{vvl-RNAi} \), \( \text{kni-RNAi} \) and \( \text{mld-RNAi} \) larvae reduces cholesterol flux through the ecdysone pathway and may lead to intracellular redistribution of cholesterol to maintain homeostasis through feedback regulation. We therefore explored the possibility that \( \text{npc1a} \), which is required for normal cholesterol distribution and availability for steroid synthesis, is controlled by feedback regulation of cholesterol. Expression of \( \text{npc1a} \) is repressed by cholesterol in wild type larvae (Fig. 5A), indicating that \( \text{npc1a} \) is feedback regulated. Recently, we showed that ecdysone biosynthesis is controlled by feedback circuits in the PG [20]. We therefore also examined whether ecdysone signaling in the gland is affected by knock down \( \text{vvl} \), \( \text{kni} \) or \( \text{mld} \). To test this, we measured mRNA levels of the ecdysone receptor (EcR) ring glands isolated from L3 larvae where \( \text{vvl-RNAi} \), \( \text{kni-RNAi} \) or \( \text{mld-RNAi} \) had been induced in the PG during L2. Transcript levels of \( \text{EcR} \) were not affected in ring glands from \( \text{vvl-RNAi} \) and \( \text{kni-RNAi} \) larvae (Fig. S4), indicating that the responsiveness of the PG to ecdysone is not reduced. Taken together, these results suggest alterations of cholesterol uptake and trafficking in the PG when flow through the biosynthetic pathway is impaired.
Discussion

*Drosophila* developmental progression is dictated by tightly regulated ecdysone pulses released from the PG. Like any cell specialized for steroid biosynthesis, the PG expresses a set of enzymes that mediate steps in the conversion of cholesterol into steroids. The tissue-specific expression of these enzymes is key to the specialization of the cells that endows the PG with the competence to produce ecdysone. The transcriptional control mechanism underlying such regulation is likely orchestrated by a regulatory network of transcription factors. Here, we identify two transcription factors Vvl and Kni that are required for the expression of the biosynthetic enzymes in the ecdysone producing PG cells. Vvl is a POU domain transcription factor which has multiple important functions during *Drosophila* development. Mutations in *vvl* cause embryonic lethality with defects in the development of the trachea and the nervous system [38–41]. Moreover, Vvl is required for wing vein development and is involved in innate immunity by regulation of the expression of antimicrobial peptides [42,43]. We show that Vvl is expressed in the PG during late embryogenesis and in the larval stages. One important characteristic of Vvl is that it maintains its own expression by autoregulation [44]. Once activated, Vvl maintains its expression and likely also the expression of the ecdysone biosynthetic genes in the PG. Knock down of *vvl* in the PG reduces the expression of all genes in the biosynthetic pathway, showing that Vvl is required for maintaining expression of all pathway components. Together with the high expression of Vvl in the gland, this suggests that Vvl is a master transcriptional regulator involved in specifying the genetic program that dictates PG cell identity including its tissue-specific expression of steroidogenic enzymes. It is interesting to note that human chromosome 6 deletions that affect POU3F2, a homolog of Vvl, have been associated with hypogonadotropic hypogonadism and adrenal insufficiency [45,46], making it possible that Vvl is a conserved regulator of steroid biosynthesis.

The gap gene *kni* is known for its role in embryonic segmentation patterning and development of the trachea and wing vein [47–51] similar to *vvl*. Kni is a nuclear receptor with a zinc-finger motif that is unlikely to be ligand activated since it lacks a ligand-binding domain. Our data show that Kni is required for expression of the genes involved in ecdysone biosynthesis in the PG, suggesting that Kni functions as an activator in this situation. Although Kni is generally considered a short-range repressor [52], it is required to activate hairy expression in stripe 6 during embryogenesis [53]. Thus, Kni may act either as a repressor or as an activator in a context-dependent manner. In mammals, nuclear receptors are also key regulators of steroidogenic target genes encoding P450 enzymes [54–56].

Although Vvl and Kni specifically control genes in the steroidogenic pathway, other targets of these factors could also be important for ecdysone synthesis in the PG. During development the continuous growth of the PG cells and endoreplication of DNA is important to scale its hormone production to the capacity required for developmental progression. We found that both *vvl* and *kni* mutants differentiate the embryonic cuticle [42,60], unlike the ecdysone deficient mutants that are unable to produce the embryonic ecdysone peak [11,59]. In adult females, the ovaries are believed to be the source of ecdysone consistent with expression of the ecdysone biosynthetic genes in the nurse and/or follicle cells [11–13]. In adult females, we find that *vvl* is expressed in both nurse and follicle cells, suggesting that Vvl may be involved in regulating expression of the ecdysone biosynthetic genes in the adult stage.

Interestingly, we observed that loss of *vvl* and *kni* mutants differentiate the embryonic cuticle [42,60], unlike the ecdysone deficient mutants that are unable to produce the embryonic ecdysone peak [11,59]. In adult females, the ovaries are believed to be the source of ecdysone consistent with expression of the ecdysone biosynthetic genes in the nurse and/or follicle cells [11–13]. In adult females, we find that *vvl* is expressed in both nurse and follicle cells, suggesting that Vvl may be involved in regulating expression of the ecdysone biosynthetic genes in the adult stage.

Our data show that Vvl and Kni are required in the PG during post-embryonic development to maintain PG specific expression of the ecdysone biosynthetic genes. During embryogenesis, *vvl* expression appears in the PG primordium by stage 13, after the embryonic ecdysone pulse (stage 8–12 [12]) that is required for morphogenesis and differentiation of the embryo. During early embryonic development where the PG primordium is not yet formed, the spatial expression patterns of *kni* and *vvl* (Fig. 1B) are different from the biosynthetic genes essential for the embryonic ecdysone pulse [8,9,11,12,59]. This suggests that Vvl and Kni regulate the biosynthetic genes in the PG, but not during early embryonic development. Consistent with this notion, *vvl* and *kni* mutants differentiate the embryonic cuticle [42,60], unlike the ecdysone deficient mutants that are unable to produce the embryonic ecdysone peak [11,59]. In adult females, the ovaries are believed to be the source of ecdysone consistent with expression of the ecdysone biosynthetic genes in the nurse and/or follicle cells [11–13]. In adult females, we find that *vvl* is expressed in both nurse and follicle cells, suggesting that Vvl may be involved in regulating expression of the ecdysone biosynthetic genes in the adult stage.
transport within the cells. Normally cholesterol is taken up as low density lipoproteins (LDLs) and trafficked within endosomes to the lysosomes where hydrolysis releases free cholesterol that is delivered to the plasma membrane and endoplasmic reticulum (ER) [61] where the first step in the conversion of cholesterol to ecdysone likely takes place. Why is npc1a up-regulated in the PG when ecdysone synthesis and pathway activity is impaired? It seems unlikely that Vvl, Kni and Mld are all involved in repression of npc1a. The block of flux through the biosynthetic pathway in the PG of vvl-RNAi, kni-RNAi and midl-RNAi animals may change intracellular cholesterol pools in the gland and affect feedback regulation to maintain cholesterol homeostasis. Our results indicate that npc1a is regulated by cholesterol suggesting that the up-regulation of npc1a may be part of a feedback regulatory response to changes in cellular cholesterol levels. This may indicate a compensatory mechanism to redistribute cholesterol by increasing storage of cholesterol esters and/or efflux to reduce free cholesterol levels when ecdysone biosynthesis is blocked. Moreover, npc1a is regulated by Br [27], a factor induced by EcR in the PG [20], implying that npc1a may also be regulated by ecdysone feedback. Our study shows that cholesterol availability is an important parameter for ecdysone biosynthesis. Interactions between cholesterol and ecdysone feedback mechanisms may therefore be important for coordinating the supply cholesterol with the rate of steroidogenesis.

A key aspect of steroidogenesis is regulating the tissue-specific expression of the biosynthetic enzymes. We have shown here that the transcription factors, Vvl and Kni, are required for the coordinated expression of ecdysone biosynthetic genes in the PG. The transcriptional activation by Vvl and Kni is likely mediated by direct binding to cis-regulatory elements responsible for PG specific expression. This identifies an important new role for Vvl and Kni during post-embryonic development in the gene regulatory network of the steroid hormone producing cells in *Drosophila*.

**Materials and Methods**

**Drosophila strains and husbandry**

The following *Drosophila* strains were used in this study: w1118, UAS-vvl-RNAi (#110729), UAS-kni-RNAi (#29880), UAS-midl-RNAi (#101867) and UAS-npc1a-RNAi (#103540) from the Vienna Drosophila RNAi Center (VDRC); UAS-vvl-RNAi (26228), UAS-kni-RNAi (#34705), tub-Gal800 and UAS-CD8-GFP (UAS-GFP) from the Bloomington Drosophila Stock Center (BDSL); phm2-Gal4 (phm-Gal4) [9] and P9206-Gal4 [29]. A transgenic line phm-291-4B (phm-GFP) with a 69 bp phm promoter in a pH-stinger GFP reporter vector generated in [20] was used to collect ring glands by dissection for analyzing the development expression profile in the gland. Flies were raised on standard cornmeal food under a 12:12 hour light:dark cycle. For experiments involving staged or timed larvae, flies were allowed to lay eggs at 25°C for 2-4 hours on apple juice agar plates supplemented with yeast paste in a humidified chamber. After 24 hours, 25 L1 larvae were collected and transferred to vials containing standard food. For experiments using tub-Gal800, eggs deposited at 25°C were immediately transferred to 18°C and 25 larvae were transferred to vials containing food 48 hours later. Images of phenotypes were transferred to 18

**Electrophoretic mobility shift assay (EMSA)**

EMSA was carried out as previously described [20]. DNA oligonucleotide sequences (Table S3) were designed to cover Vvl and Kni binding sites in the phm promoter based on in silico analysis using Transfac and Jaspar databases. Oligos containing Vvl (Vvl-wt) or Kni (Kni-wt) consensus binding sites and oligos with mutations that disrupt the Vvl (Vvl-mut) or Kni (Kni-mut) binding sites were adapted from [62,63]. The complementary oligonucleotides were annealed and labeled at the 5′-end labeling by [γ32P]ATP (Perkin Elmer) using T4 polynucleotide kinase (Fermentas) and purified using Microspin G-25 columns (GE Healthcare). The EMSA reaction was performed on ice by mixing Drosophila S2 cell nuclear extracts (Active Motif), dialysis buffer (25 mM Heps pH 7.6, 40 mM KCl, 0.1 mM EDTA, 10% glycerol), gelshift buffer (25 mM Tris-HCl pH 7.5, 5 mM MgCl2, 60 mM KCl, 0.5 mM EDTA, 5% Ficoll 400, 2.5% glycerol, 1 mM DTT and protease inhibitors) and poly(dI-dC) (Invitrogen). The reaction mixture was supplemented and incubated with 25-50-fold molar excess of unlabeled competitor nucleotides before adding the radiolabeled probe. After incubation the mixture was supplemented with gelshift loading buffer and run on a 5% non-denaturing polyacrylamide gel and dried on a slab gel dryer (Savant) followed by exposure onto a phosphorimager screen. The image was acquired using a Storm 840 scanner (Molecular Dynamics) and processed with ImageQuant software version 5.2.

**Immunostaining**

Tissue dissections were performed in PBS followed by fixation in 4% formaldehyde for 20 minutes at room temperature. For this study, the following primary antibodies were: mouse anti-GFP 1:200 (Clontech, #632380); rabbit anti-Phm 1:200 [18]; rat anti-Kni 1:1000 [64] and rat anti-Vvl 1:1000 [65]. Tissues were incubated over night with primary antibodies at 4°C. Fluorescent conjugated secondary antibodies used were goat anti-mouse Alexa Fluor 488 (A11001, Invitrogen), goat anti-rabbit Alexa Fluor 555 (A21429, Invitrogen) and goat anti-rat Alexa Fluor 555 (A21434, Invitrogen). Secondary antibodies were diluted 1:200 and incubated for two hours at room temperature. DAPI was used in 1:500 for nuclei staining. Confocal images were captured using Zeiss LSM 710 laser scanning microscope and processed using ImageJ (NIH). Images of mid-first instar PG morphology were obtained by confocal imaging of live L1 larvae (36 hours AEL) mounted in 80% glycerol.

**Feeding experiment with steroids and precursors**

Preparation and synthesis of 3β,14x-Dihydroxy-5β-cholest-7-en-6-one (5β-ketiodiol) and 3β,14x,25-Trihydroxy-5β-cholest-7-en-6-one (5β-ketotriol) were previously described [8]. For the steroid feeding rescue experiment, 30 mg of dry yeast was mixed with 57 μl H2O and 3 μl ethanol or supplemented with 3 μl of the following sterols dissolved in ethanol: 20E (Sigma; 450 μg), ecdysone (Sigma; 100 μg), cholesterol (Sigma; 45 μg), 7-dehydroydrosterol (Sigma; 200 μg), 5β-ketodiol (450 μg), or 5β-ketotriol (280 μg). Thirty larvae were transferred to the yeast plate on an apple juice agar plate and allowed to develop in a hummid chamber at 25°C. The phenotype of the larvae was scored at day 5 prior to pupariation of w1118 control for rescue to the L3 stage. For other experiments with cholesterol supplementation of the food, standard cornmeal was supplied with cholesterol (Sigma) dissolved in ethanol to a final concentration of 40 μg/ml.

**Transcriptional Regulation of Steroid Biosynthesis**

Transcriptional Regulation of Steroid Biosynthesis
In situ hybridization

Digoxigenin (DIG)-labeled antisense RNA probes were synthesized using DIG RNA labeling mix (Roche) and T3 (Fermentas), T7 (Fermentas) or SP6 (Roche) RNA polymerase according to the manufacturer’s instructions. For the bni probe, an EST clone GH19318 [66] was used as a templates. For the vvl probe, a portion of vvl gene was amplified by PCR with cDNA derived from w1118 larvae and the following primers: vvl_PA_CDS_F (5’-ATGCGCGGACCTGTACATGAC-3’) and vvl_PA_CDS_R (5’-CTAGTGCGGCGCAAATGATGC-3’). For the mld probe, a portion of mld gene was amplified by PCR with the plasmid mld-pUAST [21]; a gift from S. M. Cohen and the following primers: mld_CDS_1_F (5’-ATGCGGTTGCCCACCGAAGAAGCAAGC-3’) and mld_CDS_1_R (5’-CTAGTGAAGTTGTACATGAC-3’). PCR products containing the vvl and mld fragments were subcloned into Smal-digested pBluescript II SK(–) and pCRII-Blunt-TOPO (Invitrogen), respectively, and then used as the templates for synthesizing RNA probes. Fixation, hybridization and detection were performed as previously described [8,67].

Quantitative RT-PCR

For gene expression experiments using the animals, 30 L1 larvae or 4 L3 larvae were used for each replicate. For analysis of ring gland expression, 10–15 ring glands were dissected in PBS and directly transferred to RNA lysis buffer. RNA was extracted using the RNeasy mini kit (Qiagen) according to the manufacturer’s instructions. RNA was quantified using a NanoDrop (Thermo Scientific) and the integrity was assessed using agarose gel electrophoresis. Total RNA was used for cDNA synthesis with the SuperScript III First-Strand Synthesis kit (Invitrogen). Primers were designed using the Primer3 software [68] (Table S4). Relative gene expression was analyzed using a Mx3000P qPCR System (Agilent Technologies) with the Quantitect SYBR Green PCR Kit (Qiagen) according to the manufacturer’s instructions as described [10,33,69]. All reactions were subjected to 95°C for 10 min, followed by 45 cycles of 95°C for 15 sec, 60°C for 15 sec and 72°C for 15 sec. Dissociation curve analysis was applied to all reactions to ensure the presence of single specific PCR product. Non-reverse transcribed template controls and non-template controls were included to check for background and potential genomic contamination. No product was observed in these reactions. Efficiencies were calculated for each primer pair from standard curves generated from serial dilutions of a mix of cDNA from all control samples. PCR efficiencies were always close to 100%, which was therefore used as the standard in all calculations. Expression of target genes was normalized to reference gene, RpI23 and RpI32. We confirmed that these reference [32,33,70–74] are stably expressed across tissues and experimental conditions, by comparing RpI23 and RpI32 mRNA levels in cDNA synthesized from equal amounts of RNA extracted from different tissues and developmental stages (Fig. S2). Reference gene stability determined using qBASE Plus (Biogazelle NV, Zwijnaarde, Belgium) was within the recommended limits (M = 0.274 and CV = 0.095). For definition of these stability factors see [75].

Ecdysteroid measurements

For ecdysteroid measurements, ecdysteroids were extracted from whole animals as described [24]. Briefly, whole larvae were rinsed in water and stored at −80°C. Samples were homogenized in 0.5 ml methanol and the supernatant was collected following centrifugation at 14,000 g. The remaining tissue was re-extracted first in 0.5 ml methanol then in 0.5 ml ethanol. The pooled supernatants were evaporated using a SpeedVac and redissolved in ELISA buffer (1 M phosphate solution, 1% BSA, 4 M sodium chloride and 10 mM EDTA). ELISA was performed according to the manufacturer’s instructions using a commercial ELISA kit (ACE Enzyme Immunoassay, Cayman Chemical) that detects ecdysones and 20-hydroxyecdysone with the same affinity [76]. Standard curves were generated using 20E (Sigma). Absorbance was measured at 405 nm on a plate reader, ELx800 (BioTek) using the Gen5 software (BioTek).

Western blotting

Four brain-ring gland complexes were dissected in cold PBS and transferred to 20 µl Laemmli Sample Buffer (Bio-Rad) supplemented with 2-mercaptoethanol. Samples were boiled for 5 minutes, centrifuged at 14,000 g and 10 µl supernatant were loaded on a 4–20% polyacrylamide gradient gel (Bio-Rad) followed by transfer onto a PVDF membrane (Millipore). Primary antibodies used were; mouse anti-α-tubulin, 1:5,000 (T9026, Sigma Aldrich), rabbit anti-Phm, 1:1,000 [18] and rabbit anti-phospho-ERK, 1:1,000 (9101, Cell Signaling Technology). Secondary antibodies were goat anti-mouse IRDye 680RD, 1:10,000 (926-68070, LI-COR) and goat anti-rabbit IRDye 800CW, 1:1,000 (926-32211, LI-COR). The blot was scanned on an Odyssey Fc (LI-COR) and the software, Image Studio for Odyssey Fc, was used for image processing and protein quantification.

Statistics

The statistical differences between data sets were calculated using two-tailed Student’s t-test and error bars represent standard error of the mean (s.e.m.).

Supporting Information

Figure S1 PG-specific cis-regulatory elements of spok, pbn and dbh, immunostaining and in situ hybridization. (A) Vvl and Kni binding sites are indicated on the promoter and enhancer sequences. (B) Immunostaining of the PG from an L2 larva with antibodies against Kni (magenta) and Phm (green). Scale bars, 25 µm. (C) Staining with an antisense mld probe indicates expression of mld in the ring gland PG cells of L3 larvae (b’), but no staining was observed in the embryonic PG (a’). (D) In situ hybridization of adult female ovaries with antisense probes for vvl indicate strong staining in the nurse cells and weaker staining in the follicle cells. (TIF)

Figure S2 Effect of inducing the RNAi at different times during development, RNAi knock down efficiency and reference gene stability. RNAi mediated knock down of vvl, kni or mld was induced at different times using (A) tubGal80’-phm-Gal4 (Gal80’-phm>) or (B) tubGal80’-phm-Gal4,UAS-GFP (Gal80’-phm>GFP) by shifting larvae from 18°C to 29°C at the indicated times. (A) Inducing the RNAi effect until 120 hours AEL at 18°C blocks pupariation, while shifting larvae 144 hours and later has little influence on pupariation. This indicates that inducing knock down by Gal80’-phm> of vvl, kni and mld as late as 120 hours AEL reduces ecdysone biosynthesis and prevents formation of the high level pulse that triggers pupariation. (B) The effect is strongest when inducing the RNAi 96 hours AEL with the Gal80’-phm>GFP driver including GFP. To facilitate analysis of the ring gland, we chose to use Gal80’-phm>GFP that labels the PG by expression of GFP (for simplicity hereafter referred to as Gal80’-phm>) for all further experiments. (C) Knock down efficiency of vvl, kni and mld in the PG. When the RNAi was induced in the PG 96 hours AEL, expression of vvl and kni was reduced to 20 or 10 percent, respectively.
respectively, in dissected ring glands two days later, at the time when the control larvae were in the wandering stage. Expression of \( mld \) was reduced to 50 percent at this time. Black bars are the control (\( Gal\beta\delta^{+}\text{phm}^{+} \)) and gray bars show the indicated RNAi animals \(( n = 5) \). * \( P < 0.05 \), ** \( P < 0.001 \), versus the \( Gal\beta\delta^{+}\text{phm}^{+} \) control. (D) Stability of reference gene expression in different stages and tissues. Expression of the reference genes \( RpL32 \) and \( RpL32 \) in first instar (L1) and third instar (L3) whole larvae shows that these reference genes are stably expressed in the different developmental stages analyzed. Comparison of \( RpL32 \) and \( RpL32 \) relative quantities in the ring gland (prothoracic gland) of L3 larvae and whole L3 larvae shows stable expression of these genes. Error bars indicate s.e.m. (TIF)

**Figure S3** Effect of a high-cholesterol diet on ecdysteroid levels. (A) Effect of substrate concentrations on ecdysone biosynthesis was determined by measuring the transcription of \( E75B \), as a proxy for ecdysone levels. Expression of \( E75B \) was determined in wild type \(( u^{111B} \) ) late L3 larvae 120 hours AEL, grown either on standard food \((-) \) or a high-cholesterol diet \((+) \). Elevated \( E75B \) expression in L3 larvae grown in the presence of cholesterol indicates that the amount of ecdysone produced depends on the supply of substrates \(( n = 4) \). * \( P < 0.05 \), ** \( P < 0.001 \), versus the control grown on standard food. (B) RNAi was induced in larvae 96 hours AEL by switching larvae from 18°C to 29°C and ecdysteroid levels were analyzed 36 hours later when control \(( Gal\beta\delta^{+}\text{phm}^{+} \) ) larvae raised on high cholesterol exhibited wandering behavior, while animals raised on a standard diet were still in the pre-wandering stage. Ecdysteroids are increased in larvae raised on a high-cholesterol diet compared to standard food conditions, consistent with the accelerated development, indicated by the wandering behavior normally associated with the high-level ecdysone peak \(( u^{29} \) ) late L3 larvae 120 hours AEL, grown either on standard food \(( u^{111B} \) ) or a high-cholesterol diet \(( u^{29} \) ). Elevated ecdysone levels were measured in wild type \(( u^{29} \) ), \( phm^{+} \) and \( phm \) animals, with impaired delivery of cholesterol-metabolizing enzyme. J Biol Chem 286: 25756–25762. (C) The PM must take up cholesterol from circulation to support ecdysone synthesis, a process that requires the function of \( Npc1a \) \(( u^{29} \) ) \( phm^{+} \) \( npc1a \) animals, with impaired delivery of cholesterol for ecdysone biosynthesis, arrest development in L1 when grown on a standard diet, but develop normally when cholesterol is increased by dietary supplementation. Error bars indicate s.e.m. (TIF)

**Figure S4** Effect of loss of \( vvl \) and \( kni \) on PITH and ecdysone signaling and cholesterol feedback regulation of \( npc1a \). (A) Quantitation of phosphorylated ERK (p-ERK) levels in brain-ganglion complexes (BRGCs) from L3 animals determined by immunoblotting with an antibody specific for p-ERK. RNAi was induced 96 hours AEL by switching larvae from 18°C to 29°C and p-ERK levels were measured in BRGCs two days later, p-ERK levels were normalized to Tubulin. * \( P < 0.01 \), versus the \( Gal\beta\delta^{+}\text{phm}^{+} \) control. (B) Expression of \( torso \) was analyzed 36 hours AEL in mid-first instar larvae. (C) mRNA levels of \( npc1a \) were measured in wild type \(( u^{111B} \) ) L3 larvae 120 hours AEL, grown either on standard food \((-) \) or on a high-cholesterol diet \((+) \). Expression of \( npc1a \) was repressed by cholesterol \(( n = 4) \). ** \( P < 0.01 \), versus the control grown on standard food. (D) Expression of \( EcR \) in ring glands from L3 larvae two days after temperature induced activation of \( vvl\) RNAi, \( kni\) RNAi or \( mid\) RNAi in the PG by switching larvae 96 hours AEL from 18°C to 29°C \(( n = 5) \). * \( P < 0.01 \), versus the \( Gal\beta\delta^{+}\text{phm}^{+} \) control. Error bars indicate s.e.m. (TIF)

**Table S1** Phenotypes with different RNAi lines using the strong \( phm^{+} \) and weaker \( P0206^{+} \) PG drivers. Crosses using the weak \( P0206^{+} \) were raised at 29°C to enhance the activity of the Gal4/UAS system. Note that the \( vvl\) RNAi \#110723 and the \( kni\) RNAi \#34705 lines were used for all experiments unless otherwise stated. VDRC (Vienna Drosophila RNAi Center), BDSC (Bloomington Drosophila Stock Center).

**Table S2** Development of \( vvl\) RNAi, \( kni\) RNAi and \( mid\) RNAi larvae grown on a normal diet or on a high cholesterol diet. RNAi was induced 96 hours AEL by switching L2 larvae from 18°C to 29°C.

**Table S3** List of oligos used for EMSA. Mutations introduced are underlined.

**Table S4** List of primers used for qPCR. *Primers were adapted from [32].

**Acknowledgments**

We thank Thomas Gregor and Makoto Sato for Vvl and Kni antibodies, Stephen M. Cohen and Hideki Yoshiida for providing us with plasmids and Yota Hirano for a technical assistance. For use of confocal microscopy, we acknowledge the Core Facility for Integrated Microscopy, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark.

**Author Contributions**

Conceived and designed the experiments: ETD MEM YF RH MBO RN KFR. Performed the experiments: ETD MEM YTJ RH MBO RN KFR. Analyzed the data: ETD MEM ET TKK YF JTT RH MBO RN KFR. Contributed reagents/materials/analysis tools: YF JTT MBO RN KFR. Wrote the paper: ETD MEM ET TKK RH MBO RN KFR.

**References**

Transcriptional Regulation of Steroid Biosynthesis


