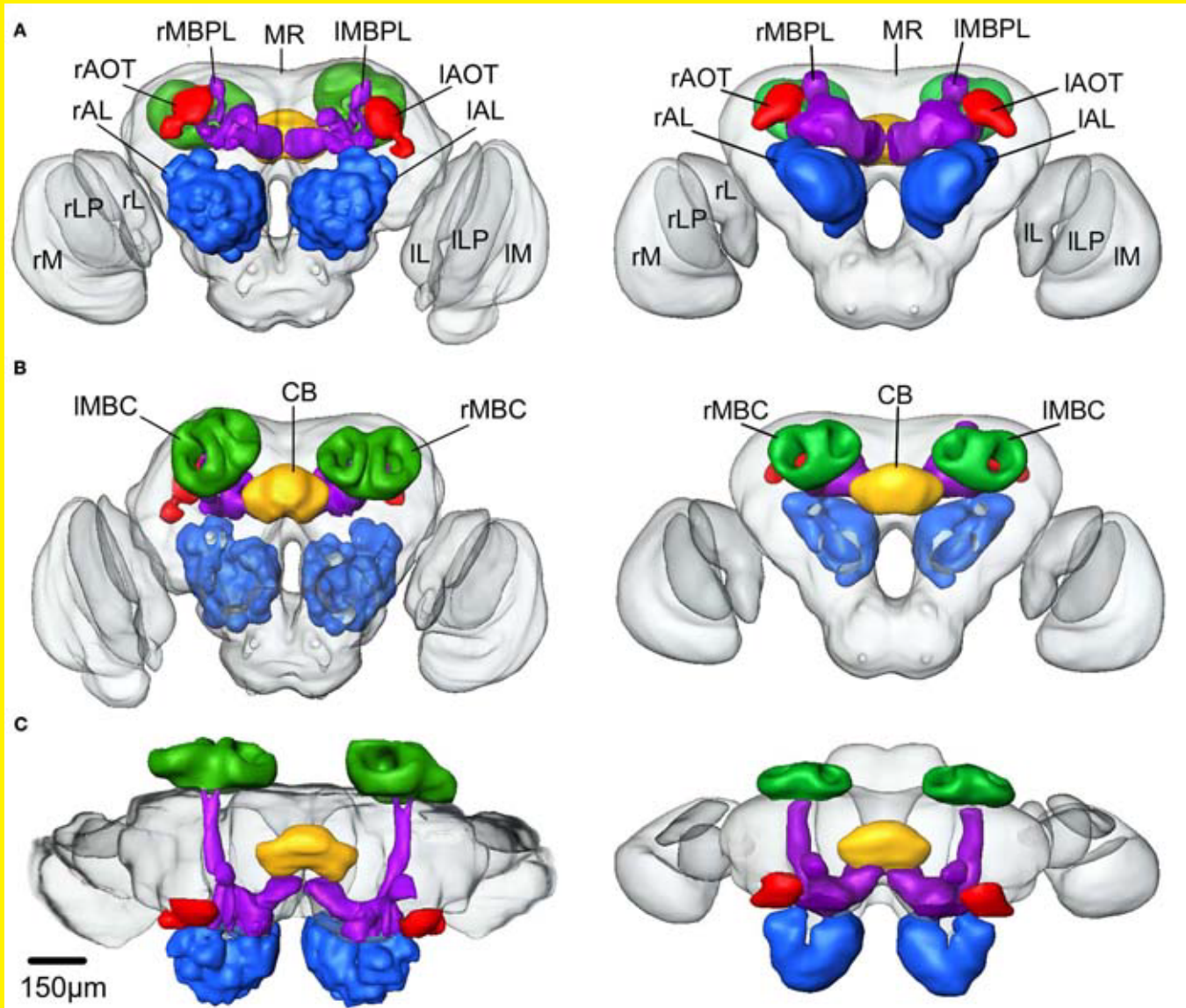


Insect Frontiers



Standard Brain of the helitohine moth. Midbrain region (MR), right mushroom body calyces (rMBC), right mushroom body peduncle and lobes (rMBPL), central body (CB), right anterior optic tubercle (rAOT), right antennal lobe (rAL), right medulla (rM), right lobula plate (rLP), right lobula (rL), left mushroom body calyces (IMBC), left mushroom body peduncle and lobes (IMBPL), left anterior optic tubercle (IAOT), left antennal lobe (IAL), left medulla (IM), left lobula plate (ILP), left lobula (IL) (From Front. Syst. Neurosci. 3:14. doi:10.3389/neuro.06.014.2009. Abstract No. 63 in this issue. OA article).

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Insect Behaviour

1. Illness-induced anorexia may reduce trade-offs between digestion and immune function

Shelley A. Adamo^a, Amy Bartlett^a, Jeffrey Le^a, Nora Spencer^a and Kenneth Sullivan^a

^a Department of Psychology and Neuroscience, Dalhousie University, Canada

Animals from across the animal kingdom decrease feeding during an infection. Superficially this response seems maladaptive because the decline in food intake occurs at the same time as immune activation increases energy expenditure. However, illness-induced anorexia could be beneficial by decreasing trade-offs between the immune system and digestion. For example, in insects (i.e. crickets) there is a trade-off between lipid transport and immune function. We predicted that increasing the need for lipid transport (e.g. when digesting a high fat meal) would reduce immune function. After consuming a high fat meal, crickets (*Gryllus texensis*) showed an increase in haemolymph lipid concentration. Crickets also showed a decrease in resistance to bacterial infection (*Serratia marcescens*). After an immune challenge, crickets not only ate less, they also preferred foods containing less fat. This occurred whether the target food was an ecologically valid food item (dead cricket), natural foods (e.g. lettuce and ground meat) or an artificial diet containing different amounts of lipid. Therefore, the change in feeding behaviour after an immune challenge is consistent with the need to reduce lipid transport in order to maximize immune function. Illness-induced anorexia may be one method by which animals can bias physiological pathways towards enhanced immune function. Some behaviours may be adaptive because they can bias the direction of physiological trade-offs.

[Animal Behaviour Volume 79, Issue 1](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMTFMH-7&_user=10&_coverDate=01%2F31%2F2010&_rdoc=3&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=72dc667bcb0691dd1161af0c105b6607), January 2010, Pages 3-10

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2. Extreme cost of male riding behaviour for juvenile females of the Zeus bug

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^b Animal Ecology, Department of Ecology and Evolution, University of Uppsala, Sweden

Precopulatory male mate guarding is predicted to occur close to the female's fertile period. However, in many species mate guarding commences when females are juveniles and may be several moults from sexual maturity. Such behaviour is inconsistent with the above prediction. In the Zeus bug, *Phoreticovelia disparata*, sexual size dimorphism is very pronounced and adult males commence riding on the backs of juvenile fourth-instar females. Males derive direct benefits from this association but the fitness consequences of precopulatory male riding behaviour for females are unknown. We investigated the effect of male presence during juvenile development for female Zeus bugs. We found a dramatic cost of male riding for females allocated a mate from the fourth instar: they were less likely to survive to adulthood and had substantially reduced adult longevity. These costs were significantly reduced for females allocated a mate during their fifth instar or as adults. We found no evidence that male presence affected female development time, adult size, body shape or the number of melanized dorsal scars present on their abdomen. Our study indicates that adult females and older juvenile females (fifth instar) are adapted to bear the costs imposed by riding males but that sexual conflict is likely to be intense between males and fourth-instar females. We suggest that the Zeus bug mating system originates from both sexes striving to make the best of a bad job: males ride immature females in the absence of unguarded adult females and females permit riding males as a form of convenience polyandry.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 11-16

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3. (*E*)-Methylgeranate, a chemical signal of juvenile hormone titre and its role in the partner recognition system of burying beetles

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^b Behavior, Ecology, Evolution and Systematics Section, School of Biological Sciences, Illinois State University, USA

In recent years, studies have shown that animals can communicate their physiological state or condition by means of chemical signals. However, as the chemicals involved in the condition-dependent signals have rarely been identified, evolutionary mechanisms that ensure their reliability are not well understood. We identified a volatile chemical signal that may serve as a reliable indicator of hormonal state in burying beetles, and is involved in their partner recognition system. Burying beetles reproducing on carcasses are able to distinguish between their breeding partners and infanticidal conspecifics. This discrimination depends on breeding status, which is positively linked to juvenile hormone III (JH III) titre. Breeding *Nicrophorus vespilloides* beetles, in contrast to nonbreeding ones, emitted considerable amounts of (*E*)-methylgeranate. The amount of emitted (*E*)-methylgeranate was positively correlated with juvenile hormone titres known from other burying beetle studies. Moreover, our behavioural experiments showed that dummies treated with methylgeranate induced tolerant behaviour, whereas control dummies were treated aggressively. The fact that (*E*)-methylgeranate and JH III share a conspicuous structural similarity and the same biosynthetic pathway may explain how the reliability of the signal for JH titre is ensured. We discuss the implications of our results in the light of theoretical work on the evolution of chemical communication, particularly on the origin of chemical signals.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 17-24

[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMTFMH-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=5&_fmt=high&_orig=browse&_srch=doc-infor%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume\)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=75783a495468260b1c2eaf9763d2bfb](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMTFMH-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=5&_fmt=high&_orig=browse&_srch=doc-infor%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=75783a495468260b1c2eaf9763d2bfb)

4. Recruiter or recruit: who boosts the recruitment in starved nests in mass foraging ants?

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^b Unit of Social Ecology, Université Libre de Bruxelles, Belgium

In social insects, each behavioural group holds information that may be crucial for the colony's functioning and regulation. We investigated which behavioural group plays the key role in the regulation of recruitment and how it manages to tune the foraging effort according to the level of starvation in the colony. We focused on recruiters and recruits: Recruiters hold information concerning the characteristics of the food source whereas domestics and potential recruits may be better informed about the colony's needs because of the constant contact that they have with their recruits and/or larvae. We imposed different starvation levels on nest-workers and recruiters and observed their interactions. The level of starvation did not alter the behaviour of the recruiters. However, we observed a change in the recruits' response to the recruiter's signal if the starvation level increased. This induced more recruits and thus more workers foraging in starved colonies. In nonstarved colonies, recruits did not respond to the recruitment signal and no recruitment occurred. Our results suggest that the recruits' response is the major key to the regulation of the recruitment process. This study has deciphered how individuals

assess the colony's needs and integrate all the information to build up an optimal food exploitation strategy adjusted to starvation.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 31-35

[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMTFMH-2&_user=10&_coverDate=01%2F31%2F2010&_rdoc=7&_fmt=high&_orig=browse&_srch=doc-info\(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume\)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=47adbc487df454ba37e4972a7ce2a30c](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMTFMH-2&_user=10&_coverDate=01%2F31%2F2010&_rdoc=7&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=47adbc487df454ba37e4972a7ce2a30c)

5. Crickets groom to avoid lethal parasitoids

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Hosts that are infected by parasitoids pay the ultimate cost: death. Here we investigate whether hosts can combat the lethal effects of parasitoids by enhancing their grooming behaviour and removing the parasitoids before they have a chance to enter the host's body. Many field cricket species are stalked and parasitized by gravid females of the parasitoid fly *Ormia ochracea*. Female parasitoids lay live first-instar larvae (planidia) on and around the cricket. Planidia burrow into the cricket host where they feed and grow. Because parasitism invariably results in host death, there should be strong selection for crickets to avoid being parasitized. We investigated whether field-caught Texas field crickets, *Gryllus texensis*, groom to avoid parasitism by *O. ochracea*. We quantified grooming behaviour of crickets when they were in the same area as *O. ochracea* adults or larvae (proximity avoidance), and following contact between the cricket and *O. ochracea* adults or larvae (contact avoidance). Crickets did not adjust grooming behaviour when in close proximity to adult gravid female *O. ochracea*, nor did they avoid planidia-laden grass. Crickets did, however, substantially increase their grooming activity when placed in an arena filled with planidia-laden grass. Furthermore, crickets that groomed more were much less likely to succumb to parasitoid infestation, compared to crickets that groomed less. Our findings suggest that grooming in *G. texensis* may function as a strong defence against parasitism by *O. ochracea*.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 51-56

[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XM6NFX-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=10&_fmt=high&_orig=browse&_srch=doc-info\(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume\)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=f3d904aaedb896aab3fc57fdc24aeb40](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XM6NFX-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=10&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=f3d904aaedb896aab3fc57fdc24aeb40)

6. Reproductive hierarchies and status discrimination in orphaned colonies of *Pachycondyla apicalis* ants

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In group-living animals where dominance hierarchies occur, aggression can be reduced if individuals are able to recognize each other. To do this, and to adapt their behaviour suitably when faced with a rival, individuals may rely on two nonmutually exclusive recognition means: they could recognize group members individually and/or their social status. Within insect societies, although conflicts over reproduction resulting in hierarchy establishment are widespread, relatively little is known about the cognitive abilities involved in the regulation of agonistic interactions. We tested whether low-ranking workers of *Pachycondyla apicalis* ants are able to discriminate each other individually and/or if they can discriminate the status of their nestmates. We found no evidence of individual discrimination among subordinates whereas they were able to discriminate their nestmates on the basis of their social and reproductive status. Such a skill may allow them to regulate worker reproduction in queenright colonies efficiently. By considering the structure of the hierarchy and the nature of the dominance relationships in *P. apicalis* societies, we discuss the existence of a more accurate recognition system among the high-ranking workers.

7. Antipredatory properties of an animal architecture: how complex faecal cases thwart arthropod attack

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Animals create a wide variety of structures to deal with abiotic and biotic challenges. We evaluated an intriguing structure whose function has never been thoroughly tested. Specifically, we evaluated the hypothesis that the body-enclosing 'faecal case' created and lived in by the immature stages of *Neochlamisus* leaf beetles reduces their risk of predation. We especially focus on the case of *N. platani*, which is externally covered with host-plant trichomes, and includes a distinct trichome-filled chamber ('attic') in the case apex. Here, we separately evaluated the effects of case, trichomes and attic on each of several behavioural stages of predator attack using *N. platani* and *N. bimaculatus* larvae and pupae. Three generalist predators (crickets, soldier bugs and lynx spiders) that represent different feeding strategies were used in our individual-level repeated observation behavioural trials. Results strongly demonstrated that the faecal case itself greatly reduced predation risk for all combinations of beetle species, life history stage and predator. Additional evidence indicated that both trichomes and attics further and independently reduced predation risk. Variation in results among treatments was also informative. For example, the capacity of faecal case components to reduce predation sometimes varied markedly among predators and between larval versus pupal life stages. Patterns of predator behaviour provided no evidence that caseless larvae have alternative means of defence. This study further presents a rare example of the co-option of a physical plant defence (trichomes) by an herbivore.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 127-136

http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XMC05H-2&_user=10&_coverDate=01%2F31%2F2010&_rdoc=19&_fmt=high&_orig=browse&_srch=docinfo%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume%23&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=c1c6654ceb3ccf6da9dea4f0bd287369

8. Sexual harassment by males reduces female fecundity in the alfalfa leafcutting bee, *Megachile rotundata*

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Under sexual conflict, males evolve traits to increase their mating and reproductive success that impose costs on females. Females evolve counteradaptations to resist males and reduce those costs. Sexual harassment is a form of sexual conflict in which males make repeated, costly attempts to mate. Costs to female foraging or predation risk have been measured in several species, but quantitative measurements of direct fitness costs are rare. In the alfalfa leafcutting bee, *Megachile rotundata* (Fabricius; Hymenoptera: Megachilidae), males harass females, and females resist all mating attempts. We placed bees in large, outdoor cages with various male-biased sex ratios. Harassment rate, nest progression, offspring production, temperature, and food availability were measured daily for 7 days. Harassment rates were highest at intermediate sex ratios. Harassment reduced the number of foraging trips and increased the duration of foraging trips made by females. Females produced offspring at a slower rate when subjected to higher rates of harassment. This shows a direct link from sex ratio to harassment to female fitness under natural conditions. We also discuss an alternative explanation that female resistance is a mechanism for mate choice for high-quality males, which would require that indirect benefits accrue through either daughters or grandsons, because all sons in haplodiploid species arise from unfertilized eggs.

9. Female reproductive success is affected by selective male harassment in the damselfly *Ischnura senegalensis*

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In animals without any courtship behaviour, persistent mating attempts by males are frequently observed. Male harassment affects female reproductive success in the laboratory, but few studies have evaluated the costs of male harassment in the wild. In the damselfly *Ischnura senegalensis*, females exhibit colour dimorphism (andromorph and gynomorph), and the morph frequency varies between local populations. In two populations where gynomorphs were common, we found that males harassed more gynomorphs than andromorphs throughout their daily foraging and oviposition activity period. Gynomorphs excreted less faeces than andromorphs, indicating that preferential harassment of gynomorphs decreased their food intake. Gynomorphs also produced fewer eggs than andromorphs. As a result, gynomorphs laid 35% fewer eggs per day than andromorphs, suggesting that male harassment decreased their reproductive success.

[Animal Behaviour Volume 79, Issue 1](#), January 2010, Pages 211-216

[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XSV0N5-3&_user=10&_coverDate=01%2F31%2F2010&_rdoc=30&_fmt=high&_orig=browse&_srch=doc-info\(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume\)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=96eab399a7b673812975e5bb581dba9e](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4XSV0N5-3&_user=10&_coverDate=01%2F31%2F2010&_rdoc=30&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236693%232010%23999209998%231578136%23FLA%23display%23Volume)&_cdi=6693&_sort=d&_docanchor=&_ct=36&_acct=C00050221&_version=1&_urlVersion=0&_userid=10&md5=96eab399a7b673812975e5bb581dba9e)

10. Visual Targeting of Forelimbs in Ladder-Walking Locusts

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Accurate limb placement helps animals and robots to walk on substrates that are uneven or contain gaps. Visual information is important in controlling limb placement in walking mammals [1,2,3,4] but has received little attention in insects [5,6,7]. We investigated whether desert locusts walking along a horizontal ladder use vision to control limb placement. High-speed video analysis showed that locusts targeted their front legs to specific rungs in the absence of any previous contact, suggesting that visual information alone is sufficient for targeting single steps. Comparison between the proportions of missed steps before and after monocular occlusion showed that monocular visual information was used to place the ipsilateral but not the contralateral front leg. Accurate placement also depended upon mechanosensory inputs from the antennae and proprioceptive feedback from the ipsilateral but not the contralateral forelimb. Locusts also compensated for the loss of inputs to one eye by altering their stepping pattern. Changing the rung position after initiation of a step showed that targeting of the front leg depends on visual information acquired before but not during a step. The trajectory was only modified after missing the rung. Our data show that locusts walking in environments where footholds are limited use visual and mechanosensory information to place their front legs.

Current Biology, [Volume 20, Issue 1](#), 86-91, 2010

<http://www.cell.com/current-biology/abstract/S0960-9822%2809%2902080-6>

11. The moment before touchdown: landing manoeuvres of the honeybee *Apis mellifera*

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Although landing is a crucial part of insect flight, it has attracted relatively little study. Here, we investigate, for the first time, the final moments of a honeybee's (*Apis mellifera*) landing manoeuvre. Using high-speed video recordings, we analyse the behaviour of bees as they approach and land on surfaces of various orientations. The bees enter a stable hover phase, immediately prior to touchdown. We have quantified behaviour during this hover phase and examined whether it changes as the tilt of the landing surface is varied from horizontal (floor), through sloped (uphill) and vertical (wall), to inverted (ceiling). The bees hover at a remarkably constant distance from the surface, irrespective of its tilt. Body inclination increases progressively as the tilt of the surface is increased, and is accompanied by an elevation of the antennae. The tight correlation between the tilt of the surface, and the orientation of the body and the antennae, indicates that the bee's visual system is capable of inferring the tilt of the surface, and pointing the antennae toward it. Touchdown is initiated by extending the appendage closest to the surface, namely, the hind legs when landing on horizontal or sloping surfaces, and the front legs or antennae when landing on vertical surfaces. Touchdown on inverted surfaces is most likely triggered by a mechanosensory signal from the antennae. Evidently, bees use a landing strategy that is flexibly tailored to the varying topography of the terrain.

Journal of Experimental Biology 213, 262-270 (2010)

<http://jeb.biologists.org/cgi/content/abstract/213/2/262>

Insect Biocontrol

12. Host-seeking behavior and parasitism by *Spathius agrili* Yang (Hymenoptera: Braconidae), a parasitoid of the emerald ash borer

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Spathius agrili Yang (Hymenoptera: Braconidae) is a newly described and important idiobiont ectoparasitoid of the emerald ash borer (EAB) that has excellent potential as a biological control agent against EAB populations in the USA. In order to understand the ecological factors involved in the search and discovery of concealed hosts by *S. agrili*, we investigated the behavioral responses of adult female wasps to potential semiochemicals from host plants, hosts, and host frass as well as to vibration signals from host feeding and movement. Using a bioassay, we showed that *S. agrili* first finds the host's habitats by detecting the volatile compounds emitted by ash. In the second phase of host location and acceptance, the parasitoids detect the mechanical vibrations produced by host feeding and movement under the surface of the bark and then probe to find the EAB larvae. Contact chemicals seem to play little or no role in short-range host finding. Female wasps avoided laying eggs on EAB larvae already parasitized and thus paralyzed.

We hypothesized that female wasps were not attracted to these larvae due to their lack of feeding or movement. While an induced paralysis in the host is instrumental in avoiding superparasitism, we cannot rule out that *S. agrili* females also use an oviposition pheromone to deter conspecific females. Together, these results suggest that vibration and olfactory cues play significant roles in distinct phases of *S. agrili* host habitat and host location behaviors.

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[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6WBP-4X97CYF-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=5&_fmt=high&_orig=browse&_srch=doc-info\(%23toc%236716%232010%23999479998%231565121%23FLA%23display%23Volume\)&_cdi=6716&_sort=d&_docanchor=&_ct=13&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=4f913dcd1b5bc2d73018fc0cc1ec9bba](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6WBP-4X97CYF-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=5&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236716%232010%23999479998%231565121%23FLA%23display%23Volume)&_cdi=6716&_sort=d&_docanchor=&_ct=13&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=4f913dcd1b5bc2d73018fc0cc1ec9bba)

13. Effects of six sugars on the longevity, fecundity and nutrient reserves of *Microplitis mediator*

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Parasitoid adults can directly feed on floral nectar and honeydew containing monosaccharides and disaccharides. Oligosaccharides such as maltose, melezitose and raffinose are also found in honeydew but are rare in floral nectar. The effects of six different sugar resources on the longevity, fecundity and nutrient reserves of *Microplitis mediator*, a larval endoparasitoid in the cotton bollworm *Helicoverpa armigera* (Hübner) were determined in our laboratory. The results showed that both food and sex affected longevity of this wasp. Females and males of *M. mediator* fed with 1 M sucrose solution survived longer than controls fed with water (5.7- and 3.7-fold longer, respectively). When provided with sucrose, glucose or fructose solutions, the parasitoid generated 3.6- to 3.7-fold more offspring than controls, and 60–75% of these progenies were produced during the first 5 days. When separately given fructose, sucrose or glucose, this wasp accumulated fructose and total sugar at the highest level, which means a high sugar levels might lead to prolonging longevity and more offspring in *M. mediator*. In addition, compared with organisms fed galactose or raffinose, *M. mediator* fed sucrose or fructose accumulated high glycogen levels. Furthermore, in *M. mediator*, the lipid content declined with the advancing age. Females showed the slowest lipid metabolic rates when fed with sucrose, glucose, fructose, mannose and galactose solutions versus when fed with raffinose and control. In addition, only sucrose had a significant effect on lipid levels in males nearing the end of life.

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[http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6WBP-4X66S4B-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=9&_fmt=high&_orig=browse&_srch=doc-info\(%23toc%236716%232010%23999479998%231565121%23FLA%23display%23Volume\)&_cdi=6716&_sort=d&_docanchor=&_ct=13&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=55de1b23f133d75d4738b329a0a364b3](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6WBP-4X66S4B-1&_user=10&_coverDate=01%2F31%2F2010&_rdoc=9&_fmt=high&_orig=browse&_srch=doc-info(%23toc%236716%232010%23999479998%231565121%23FLA%23display%23Volume)&_cdi=6716&_sort=d&_docanchor=&_ct=13&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=55de1b23f133d75d4738b329a0a364b3)

Insect Cell Biology

14. The nuclear cofactor DOR regulates autophagy in mammalian and *Drosophila* cells

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The regulation of autophagy in metazoans is only partly understood, and there is a need to identify the proteins that control this process. The diabetes- and obesity-regulated gene (DOR), a recently reported nuclear cofactor of thyroid hormone receptors, is expressed abundantly in metabolically active tissues such as muscle. Here, we show that DOR shuttles between the nucleus and the cytoplasm, depending on cellular stress conditions, and re-localizes to autophagosomes on autophagy activation. We demonstrate that DOR interacts physically with autophagic proteins Golgi-associated ATPase enhancer of 16 kDa (GATE16) and microtubule-associated protein 1A/1B-light chain 3. Gain-of-function and loss-of-function studies indicate that DOR stimulates autophagosome formation and accelerates the degradation of stable proteins. CG11347, the DOR *Drosophila* homologue, has been predicted to interact with the *Drosophila* Atg8 homologues, which suggests functional conservation in autophagy. Flies lacking CG11347 show reduced autophagy in the fat body during pupal development. All together, our data indicate that DOR regulates autophagosome formation and protein degradation in mammalian and *Drosophila* cells.

EMBO reports (2009) 11, 37 - 44

<http://www.nature.com/embor/journal/v11/n1/abs/embor2009242.html>

15. An actomyosin-based barrier inhibits cell mixing at compartmental boundaries in *Drosophila* embryos

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Partitioning tissues into compartments that do not intermix is essential for the correct morphogenesis of animal embryos and organs^{1, 2, 3}. Several hypotheses have been proposed to explain compartmental cell sorting, mainly differential adhesion^{1, 2, 3, 4, 5, 6, 7, 8, 9}, but also regulation of the cytoskeleton^{10, 11} or of cell proliferation^{10, 12}. Nevertheless, the molecular and cellular mechanisms that keep cells apart at boundaries remain unclear. Here we demonstrate, in early *Drosophila melanogaster* embryos, that actomyosin-based barriers stop cells from invading neighbouring compartments. Our analysis shows that cells can transiently invade neighbouring compartments, especially when they divide, but are then pushed back into their compartment of origin. Actomyosin cytoskeletal components are enriched at compartmental boundaries, forming cable-like structures when the epidermis is mitotically active. When MyoII (non-muscle myosin II) function is inhibited, including locally at the cable by chromophore-assisted laser inactivation (CALI)^{13, 14}, in live embryos, dividing cells are no longer pushed back, leading to compartmental cell mixing. We propose that local regulation of actomyosin contractibility, rather than differential adhesion, is the primary mechanism sorting cells at compartmental boundaries.

Nature Cell Biology 12, 60 - 65 (2010)

<http://www.nature.com/ncb/journal/v12/n1/abs/ncb2005.html?lang=en>

16. Dynein light chain 1 is required for autophagy, protein clearance, and cell death in *Drosophila*

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Autophagy is a catabolic pathway that is important for turnover of long-lived proteins and organelles, and has been implicated in cell survival, tumor progression, protection from infection, neurodegeneration, and cell death. Autophagy and caspases are required for type II autophagic cell death of *Drosophila* larval salivary glands during development, but the mechanisms that regulate these degradation pathways are not understood. We conducted a forward genetic screen for genes that are required for salivary gland cell death, and here we describe the identification of *Drosophila dynein light chain 1 (ddlc1)* as a gene that is required for type II cell death. Autophagy is attenuated in *ddlc1* mutants, but caspases are active in these cells. *ddlc1* mutant salivary glands develop large fibrillar protein inclusions that stain positive for amyloid-specific dyes and ubiquitin. Ectopic expression of Atg1 is sufficient to induce autophagy, clear protein inclusions, and rescue degradation of *ddlc1* mutant salivary glands. Furthermore, *ddlc1* mutant larvae have decreased motility, and mutations in *ddlc1* enhance the impairment of motility that is observed in a *Drosophila* model of neurodegenerative disease. Significantly, this decrease in larval motility is associated with decreased clearance of protein with polyglutamine expansion, the accumulation of p62 in neurons and muscles, and fewer synaptic boutons. These results indicate that DDLC1 is required for protein clearance by autophagy that is associated with autophagic cell death and neurodegeneration.

PNAS January 12, 2010 vol. 107 no. 2 742-747

<http://www.pnas.org/content/107/2/742.abstract>

Insect Chemoecology

17. Eating chemically defended prey: alkaloid metabolism in an invasive ladybird predator of other ladybirds (Coleoptera: Coccinellidae)

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By comparison with studies of herbivore physiological adaptation to plant allelochemicals, work on predator physiological adaptation to potentially toxic prey has been very limited. Such studies are important in understanding how evolution could shape predator diets. An interesting question is the specificity of predator adaptation to prey allelochemicals, given that many predators consume diverse prey with different chemical defences. The ladybird *Harmonia axyridis*, an invasive species in America, Europe and Africa, is considered a significant predatory threat to native invertebrates, particularly other aphid-eating ladybirds of which it is a strong intraguild predator. Although ladybirds possess species-specific alkaloid defences, *H. axyridis* exhibits high tolerance for allospecific ladybird prey alkaloids. Nonetheless, it performs poorly on species with novel alkaloids not commonly occurring within its natural range. We examined alkaloid fate in *H. axyridis* larvae after consumption of two other ladybird species, one containing an alkaloid historically occurring within the predator's native range (isopropyleine) and one containing a novel alkaloid that does not (adaline). Our results indicate that *H. axyridis* rapidly chemically modifies the alkaloid to which it has been historically exposed to render it less harmful: this probably occurs outside of the gut. The novel, more toxic alkaloid persists in the body unchanged for longer. Our results suggest metabolic alkaloid specialisation, in spite

of the diversity of chemically defended prey that the predator consumes. Physiological adaptations appear to have made *H. axyridis* a successful predator of other ladybirds; however, limitations are imposed by its physiology when it eats prey with novel alkaloids.

Journal of Experimental Biology 213, 237-241 (2010)

<http://jeb.biologists.org/cgi/content/abstract/213/2/237>

Insect Chemical Senses

18. The Soluble Proteome of the *Drosophila* Antenna

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The olfactory system of *Drosophila melanogaster* is one of the best characterized chemosensory systems. Identification of proteins contained in the third antennal segment, the main olfactory organ, has previously relied primarily on immunohistochemistry, and although such studies and in situ hybridization studies are informative, they focus generally on one or few gene products at a time, and quantification is difficult. In addition, purification of native proteins from the antenna is challenging because it is small and encased in a hard cuticle. Here, we describe a simple method for the large-scale detection of soluble proteins from the *Drosophila* antenna by chromatographic separation of tryptic peptides followed by tandem mass spectrometry with femtomole detection sensitivities. Examination of the identities of these proteins indicates that they originate both from the extracellular perilymph and from the cytoplasm of disrupted cells. We identified enzymes involved with intermediary metabolism, proteins associated with regulation of gene expression, nucleic acid metabolism and protein metabolism, proteins associated with microtubular transport, 8 odorant-binding proteins, protective enzymes associated with antibacterial defense and defense against oxidative damage, cuticular proteins, and proteins of unknown function, which represented about one-third of all soluble proteins. The procedure described here opens the way for precise quantification of any target protein in the *Drosophila* antenna and should be readily applicable to antennae from other insects.

Chemical Senses 2010 35(1):21-30

<http://chemse.oxfordjournals.org/cgi/content/abstract/35/1/21>

Insect Development

19. *Drosophila* Genome-wide Obesity Screen Reveals Hedgehog as a Determinant of Brown versus White Adipose Cell Fate

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Whole-genome RNAi screen for obesity genes in adult *Drosophila* yields many candidates
Tissue-specific screening in flies reveals hedgehog as a fat-specific regulator
Mice with fat-specific activation of hedgehog signaling lack white but not brown fat
Mechanistically, hedgehog transcriptionally targets key adipogenic factors

Over 1 billion people are estimated to be overweight, placing them at risk for diabetes, cardiovascular disease, and cancer. We performed a systems-level genetic dissection of adiposity regulation using genome-wide RNAi screening in adult *Drosophila*. As a follow-up, the resulting ~500 candidate obesity genes were functionally classified using muscle-, oenocyte-, fat-body-, and neuronal-specific knockdown in vivo and revealed hedgehog signaling as the top-scoring fat-body-specific pathway. To extrapolate these findings into mammals, we generated fat-specific hedgehog-activation mutant mice. Intriguingly, these mice displayed near total loss of white, but not brown, fat compartments. Mechanistically, activation of hedgehog signaling irreversibly blocked differentiation of white adipocytes through direct, coordinate modulation of early adipogenic factors. These findings identify a role for hedgehog signaling in white/brown adipocyte determination and link in vivo RNAi-based scanning of the *Drosophila* genome to regulation of adipocyte cell fate in mammals.

Cell, [Volume 140, Issue 1](#), 148-160, 8 January 2010

<http://www.cell.com/abstract/S0092-8674%2809%2901591-8>

20.Epithelial Polarity Proteins Regulate *Drosophila* Tracheal Tube Size in Parallel to the Luminal Matrix Pathway

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Regulation of epithelial tube size is critical for organ function. However, the mechanisms of tube size control remain poorly understood. In the *Drosophila* trachea, tube dimensions are regulated by a luminal extracellular matrix (ECM) [1,2,3,4]. ECM organization requires apical (luminal) secretion of the protein Vermiform (Verm), which depends on the basolateral septate junction (SJ) [5,6]. Here, we show that apical and basolateral epithelial polarity proteins interact to control tracheal tube size independently of the Verm pathway. Mutations in *yurt* (*yrt*) and *scribble* (*scrib*), which encode SJ-associated polarity proteins [7,8], cause an expansion of tracheal tubes but do not disrupt Verm secretion. Reducing activity of the apical polarity protein Crumbs (Crb) suppresses the length defects in *yrt* but not *scrib* mutants, suggesting that Yrt acts by negatively regulating Crb. Conversely, Crb overexpression increases tracheal tube dimensions. Reducing *crb* dosage also rescues tracheal size defects caused by mutations in *coracle* (*cora*), which encodes an SJ-associated polarity protein [8,9]. In addition, *crb* mutations suppress *cora* length defects without restoring Verm secretion. Together, these data indicate that Yrt, Cora, Crb, and Scrib operate independently of the Verm pathway. Our data support a model in which Cora and Yrt act through Crb to regulate epithelial tube size.

Current Biology, [Volume 20, Issue 1](#), 55-61, 2010

<http://www.cell.com/current-biology/abstract/S0960-9822%2809%2901992-7>

21. Sec24-Dependent Secretion Drives Cell-Autonomous Expansion of Tracheal Tubes in *Drosophila*

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Highlights Secretion drives local expansion of tracheal tubes despite high mobility of secreted proteins in the lumen. Individual cells autonomously adjust epithelial tube diameter and length. Cell-intrinsic program, rather than extrinsic cues, controls tracheal tube dimensions

Epithelial tubes in developing organs, such as mammalian lungs and insect tracheae, need to expand their initially narrow lumina to attain their final, functional dimensions [1]. Despite its critical role for organ function, the cellular mechanism of tube expansion remains unclear. Tracheal tube expansion in *Drosophila* involves apical secretion and deposition of a luminal matrix [2,3,4,5], but the mechanistic role of secretion and the nature of forces involved in the process were not previously clear. Here we address the roles of cell-intrinsic and extrinsic processes in tracheal tube expansion. We identify mutations in the *sec24* gene *stenosis*, encoding a cargo-binding subunit of the COPII complex [6,7,8]. Via genetic-mosaic analyses, we show that *stenosis*-dependent secretion drives tube expansion in a cell-autonomous fashion. Strikingly, single cells autonomously adjust both tube diameter and length by implementing a sequence of events including apical membrane growth, cell flattening, and taenidial cuticle formation. Known luminal components are not required for this process. Thus, a cell-intrinsic program, rather than nonautonomous extrinsic cues, controls the dimensions of tracheal tubes. These results indicate a critical role of membrane-associated proteins in the process and imply a mechanism that coordinates autonomous behaviors of individual cells within epithelial structures.

Current Biology, [Volume 20, Issue 1](#), 62-68, 2010

<http://www.cell.com/current-biology/abstract/S0960-9822%2809%2902079-X>

22. The *Drosophila* nuclear receptors DHR3 and β FTZ-F1 control overlapping developmental responses in late embryos

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Studies of the onset of metamorphosis have identified an ecdysone-triggered transcriptional cascade that consists of the sequential expression of the transcription-factor-encoding genes *DHR3*, *β FTZ-F1*, *E74A* and *E75A*. Although the regulatory interactions between these genes have been well characterized by genetic and molecular studies over the past 20 years, their developmental functions have remained more poorly understood. In addition, a transcriptional sequence similar to that observed in prepupae is repeated before each developmental transition in the life cycle, including mid-embryogenesis and the larval molts. Whether the regulatory interactions between *DHR3*, *β FTZ-F1*, *E74A* and *E75A* at these earlier stages are similar to those defined at the onset of metamorphosis, however, is unknown. In this study, we turn to embryonic development to address these two issues. We show that mid-embryonic expression of *DHR3* and *β FTZ-F1* is part of a 20-hydroxyecdysone (20E)-triggered transcriptional cascade similar to that seen in mid-prepupae, directing maximal expression of *E74A* and *E75A* during late embryogenesis. In addition, *DHR3* and *β FTZ-F1* exert overlapping developmental functions at the end of embryogenesis. Both genes are required for tracheal air filling, whereas *DHR3* is required for ventral nerve cord condensation and *β FTZ-F1* is required for proper maturation of the cuticular denticles. Rescue experiments support these observations, indicating that *DHR3* has essential functions independent

from those of β FTZ-F1. *DHR3* and β FTZ-F1 also contribute to overlapping transcriptional responses during embryogenesis. Taken together, these studies define the lethal phenotypes of *DHR3* and β FTZ-F1 mutants, and provide evidence for functional bifurcation in the 20E-responsive transcriptional cascade.

Development 137, 123-131 January 1, 2010.

<http://dev.biologists.org/content/137/1/123.abstract>

23. *Drosophila* growth cones: A genetically tractable platform for the analysis of axonal growth dynamics

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The formation of neuronal networks, during development and regeneration, requires outgrowth of axons along reproducible paths toward their appropriate postsynaptic target cells. Axonal extension occurs at growth cones (GCs) at the tips of axons. GC advance and navigation requires the activity of their cytoskeletal networks, comprising filamentous actin (F-actin) in lamellipodia and filopodia as well as dynamic microtubules (MTs) emanating from bundles of the axonal core. The molecular mechanisms governing these two cytoskeletal networks, their cross-talk, and their response to extracellular signaling cues are only partially understood, hindering our conceptual understanding of how regulated changes in GC behavior are controlled. Here, we introduce *Drosophila* GCs as a suitable model to address these mechanisms. Morphological and cytoskeletal readouts of *Drosophila* GCs are similar to those of other models, including mammals, as demonstrated here for MT and F-actin dynamics, axonal growth rates, filopodial structure and motility, organizational principles of MT networks, and subcellular marker localization. Therefore, we expect fundamental insights gained in *Drosophila* to be translatable into vertebrate biology. The advantage of the *Drosophila* model over others is its enormous amenability to combinatorial genetics as a powerful strategy to address the complexity of regulatory networks governing axonal growth. Thus, using pharmacological and genetic manipulations, we demonstrate a role of the actin cytoskeleton in a specific form of MT organization (loop formation), known to regulate GC pausing behavior. We demonstrate these events to be mediated by the actin-MT linking factor Short stop, thus identifying an essential molecular player in this context.

Developmental Neurobiology Volume 70 Issue 1, Pages 58 – 71 2010

<http://www3.interscience.wiley.com/journal/123188795/abstract>

24. Genetic and biochemical definition of the Hedgehog receptor

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Although the transporter-like protein Patched (Ptc) is genetically implicated in reception of the extracellular Hedgehog (Hh) protein signal, a clear definition of the Hh receptor is complicated by the existence of additional Hh-binding proteins and, in *Drosophila*, by the lack of physical evidence for direct binding of Hh to Ptc. Here we show that activity of Ihog (Interference hedgehog), or of its close relative Boi (Brother of Ihog), is absolutely required for Hh biological response and for sequestration of the Hh protein to limit long-range signaling. We demonstrate that Ihog interacts directly with Ptc, is required for presentation of Ptc on the cell surface, and that Ihog and Ptc are both required for high-affinity Hh binding. On the basis of their joint roles in ligand binding, signal transduction,

and receptor trafficking, we conclude that Ihog and Ptc together constitute the *Drosophila* Hh receptor.

Genes & Dev. 2010. 24: 57-71

<http://genesdev.cshlp.org/content/24/1/57.abstract>

25. Multifunctional factor ENY2 is associated with the THO complex and promotes its recruitment onto nascent mRNA

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Metazoan E(y)2/ENY2 is a multifunctional protein important for transcription activation and mRNA export, being a component of SAGA/TFTC and the mRNA export complex AMEX. Here, we show that ENY2 in *Drosophila* is also stably associated with THO, the complex involved in mRNP biogenesis. The ENY2–THO complex is required for normal *Drosophila* development, functioning independently on SAGA and AMEX. ENY2 and THO arrive on the transcribed region of the *hsp70* gene after its activation, and ENY2 plays an important role in THO recruitment. ENY2 and THO show no direct association with elongating RNA polymerase II. Recruitment of ENY2 and THO occurs by their loading onto nascent mRNA, apparently immediately after its synthesis, while the AMEX component Xmas-2 is loaded onto mRNA at a later stage. Knockdown of either ENY2 or THO, but not SAGA or AMEX, affects the processing of the transcript's 3' end. Thus, ENY2, as a shared subunit of several protein complexes governing the sequential steps of gene expression, plays an important role in the coordination of these steps.

Genes & Dev. 2010. 24: 86-96

<http://genesdev.cshlp.org/content/24/1/86.abstract>

26. A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in *Drosophila* embryogenesis

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Cytoplasmic polyadenylation is a widespread mechanism to regulate mRNA translation that requires two sequences in the 3' untranslated region (UTR) of vertebrate substrates: the polyadenylation hexanucleotide, and the cytoplasmic polyadenylation element (CPE). Using a cell-free *Drosophila* system, we show that these signals are not relevant for *Toll* polyadenylation but, instead, a "polyadenylation region" (PR) is necessary. Competition experiments indicate that PR-mediated polyadenylation is required for viability and is mechanistically distinct from the CPE/hexanucleotide-mediated process. These data indicate that *Toll* mRNA is polyadenylated by a noncanonical mechanism, and suggest that a novel machinery functions for cytoplasmic polyadenylation during *Drosophila* embryogenesis.

Genes & Dev. 2010. 24: 129-134

<http://genesdev.cshlp.org/content/24/2/129.abstract?etoc>

27. A Transient Niche Regulates the Specification of *Drosophila* Intestinal Stem Cells

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Stem cell niches are locations where stem cells reside and self-renew. Although studies have shown how niches maintain stem cell fate during tissue homeostasis, less is known about their roles in establishing stem cells. The adult *Drosophila* midgut is maintained by intestinal stem cells (ISCs); however, how they are established is unknown. Here, we show that an ISC progenitor generates a niche cell via Notch signaling. This niche uses the bone morphogenetic protein 2/4 homolog, decapentaplegic, to allow progenitors to divide in an undifferentiated state and subsequently breaks down and dies, resulting in the specification of ISCs in the adult midgut. Our results demonstrate a paradigm for stem cell–niche biology, where progenitors generate transient niches that determine stem cell fate and may give insights into stem cell specification in other tissues.

Science 8 January 2010:Vol. 327. no. 5962, pp. 210 – 213

http://www.sciencemag.org/cgi/content/abstract/327/5962/210?sa_campaign=Email/toc/8-January-2010/10.1126/science.1181958

Insect Ecology

28. Seasonal variation in the trophic structure of a spatial prey subsidy linking aquatic and terrestrial food webs: adult aquatic insects

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Research over the past decade has established spatial resource subsidies as important determinants of food web dynamics. However, most empirical studies have considered the role of subsidies only in terms of magnitude, ignoring an important property of subsidies that may affect their impact in recipient food webs: the trophic structure of the subsidy relative to in situ resources. This may be especially important when subsidies are composed of organisms, as opposed to nutrient subsidies, because the trophic position of subsidy organisms may differ from in situ prey. I explored the relative magnitude and trophic structure of a cross-habitat prey subsidy, adult aquatic insects, in terrestrial habitats along three streams in the south-central United States. Overall, adult aquatic insects contributed more than one-third of potential insect prey abundance and biomass to the terrestrial habitat. This contribution peaked along a permanent spring stream, reaching as high as 94% of abundance and 86% of biomass in winter. Trophic structure of adult aquatic and terrestrial insects differed. Nearly all adult aquatic insects were non-consumers as adults, whereas all but one taxon of terrestrial insects were consumers. Such a difference created a strong relationship between the relative contribution of the prey subsidy and the trophic structure of the prey assemblage: as the proportion of adult aquatic insects increased, the proportion of consumers in the prey assemblage declined. Specific effects varied seasonally and with distance from the stream as the taxonomic composition of the subsidy changed, but general patterns were consistent. These findings show that adult aquatic insect subsidies to riparian food webs not only elevate prey availability, but also alter the trophic structure of the entire winged insect prey assemblage.

Oikos Volume 119 Issue 1, Pages 170 – 178 2010

<http://www3.interscience.wiley.com/journal/122684147/abstract>

29. Clarity on Honey Bee Collapse?

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Over the past few years, the media have frequently reported deaths of honey bee (*Apis mellifera* L.) colonies in the United States, Europe, and Japan. Most reports express opinions but little hard science. A recent historical survey (1) pointed out that extensive colony losses are not unusual and have occurred repeatedly over many centuries and locations. Concern for honey bees in the United States has been magnified by their vital role in agriculture. The California almond industry alone is worth \$2 billion annually and relies on over 1 million honey bee hives for cross-pollination. So what is killing honey bee colonies worldwide, and what are the implications for agriculture?

Science 8 January 2010: Vol. 327. no. 5962, pp. 152 - 153

http://www.sciencemag.org/cgi/content/summary/327/5962/152?sa_campaign=Email/to/c/8-January-2010/10.1126/science.1185563

Insect Evolution

30.EVOLUTION OF MIMICRY PATTERNS IN *METRIORRHYNCHUS* (COLEOPTERA: LYCIDAE): THE HISTORY OF DISPERSAL AND SPECIATION IN SOUTHEAST ASIA

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The concept of Müllerian mimicry suggests convergent evolution to an intermediate pattern and does not predict polymorphism in mimicry rings. We examined the evolution of mimicry patterns and the order of divergence of various factors, including the role of aposematic patterns in speciation, in a clade of net-winged beetles with a robust phylogeny that suggests that they dispersed from the Australian to Asian plate. We found strong evidence for the evolution of mimicry via advergence in *Metriorrhynchus* because older patterns are represented in the Oriental region within more than 100 species of lycids from several lineages. Advergence was likely the cause of the observed intraspecific polymorphism in contrast to the predicted universal monomorphism. Polymorphism was found in populations of two species in Sumatra and Borneo and in populations fine-tuned to subtle variants in various habitats. The advergence is likely to be based on the small population sizes of immigrants. The differences in population sizes result in much higher benefits for dispersing species than native populations. Speciation was triggered by the divergence in aposematic coloration, and the genetic differences accumulated slowly during incomplete isolation. We assumed that the differentiation in genitalia through sexual selection ultimately reinforced speciation initiated by the shift between mimicry patterns.

[Evolution](#) Volume 64 Issue 1, 2010 Pages 39 - 52

<http://www3.interscience.wiley.com/journal/122539848/abstract>

31.OPTIMAL DEFENSIVE COLORATION STRATEGIES DURING THE GROWTH PERIOD OF PREY

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Defensive coloration that reduces the risk of predation is considered to be widespread in animals. Many closely related species adopt differing coloration strategies during the life cycle, including crypsis, conspicuousness, and ontogenic change between the two coloration types. Here, we use a dynamic state-dependent approach to use ecological and intrinsic factors to predict the proportion of the developmental period of immature animals that should be spent as cryptic or conspicuous, and when conspicuous coloration should be reliably associated with investment in defenses. The model predicts that animals should change color more than once during development only in specific

circumstances. In contrast, change from crypsis to conspicuous can occur over a range of conditions related to the frequency of detection by predators, but may also depend on the opportunity costs of crypsis and the effect of size on the deterrent effect of conspicuous coloration. We also report the results of a survey of coloration strategies in lepidopteron larvae, and note a qualitative agreement with the predictions of our model in the relationship between body size and coloration strategy. Our results provide explanations for several widespread antipredator coloration phenomena in prey animals, and provide a comprehensive predictive framework for the types of coloration strategies that are employed in nature.

[Evolution](#) Volume 64 Issue 1, 2010 Pages 53 - 67
<http://www3.interscience.wiley.com/journal/122539849/abstract>

32. DIET QUALITY AFFECTS WARNING COLORATION INDIRECTLY: EXCRETION COSTS IN A GENERALIST HERBIVORE

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Aposematic herbivores are under selection pressure from their host plants and predators. Although many aposematic herbivores exploit plant toxins in their own secondary defense, dealing with these harmful compounds might underlay costs. We studied whether the allocation of energy to detoxification and/or sequestration of host plant defense chemicals trades off with warning signal expression. We used a generalist aposematic herbivore *Parasemia plantaginis* (Arctiidae), whose adults and larvae show extensive phenotypic and genetic variation in coloration. We reared larvae from selection lines for small and large larval warning signals on *Plantago lanceolata* with either low or high concentration of iridoid glycosides (IGs). Larvae disposed of IGs effectively; their body IG content was low irrespective of their diet. Detoxification was costly as individuals reared on the high IG diet produced fewer offspring. The IG concentration of the diet did not affect larval coloration (no trade-off) but the wings of females were lighter orange (vs. dark red) when reared on the high IG diet. Thus, the difference in plant secondary chemicals did not induce variation in the chemical defense efficacy of aposematic individuals but caused variation in reproductive output and warning signals of females.

[Evolution](#) Volume 64 Issue 1, 2010 Pages 68 - 78
<http://www3.interscience.wiley.com/journal/122526545/abstract>

33. UNEXPLAINED SPLIT SEX RATIOS IN THE NEOTROPICAL PLANT-ANT, *ALLOMERUS OCTOARTICULATUS* VAR. *DEMERARAE* (MYRMICINAE): A TEST OF HYPOTHESES

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We investigated sex allocation in the Neotropical ant *Allomerus octoarticulatus* var. *demerarae*. Because *Allomerus* is a plant symbiont, we could make geographically extensive collections of complete colonies and of foundresses in saplings, allowing us to estimate not only population- and colony-level sex allocation but also colony resource levels and the relatednesses of competing ant foundresses. This species exhibits a strongly split sex ratio, with 80% of mature colonies producing ≥90% of one sex or the other. Our genetic analyses (DNA microsatellites) reveal that *Allomerus* has a breeding

system characterized by almost complete monogyny and a low frequency of polyandry. Contrary to theoretical explanations, we find no difference in worker relatedness asymmetries between female- and male-specialist colonies. Furthermore, no clear link was found between colony sex allocation and life history traits such as the number of mates per queen, or colony size, resource level, or fecundity. We also failed to find significant support for male production by workers, infection by *Wolbachia*, local resource competition, or local mate competition. We are left with the possibility that *Allomerus* exhibits split sex ratios because of the evolution of alternative biasing strategies in queens or workers, as recently proposed in the literature.

[Evolution](#) Volume 64 Issue 1, 2010 Pages 126 - 141
<http://www3.interscience.wiley.com/journal/122574050/abstract>

34.SIMULATING RANGE EXPANSION: MALE SPECIES RECOGNITION AND LOSS OF PREMATING ISOLATION IN DAMSELFLIES

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Prolonged periods of allopatry might result in loss of the ability to discriminate against other formerly sympatric species, and can lead to heterospecific matings and hybridization upon secondary contact. Loss of premating isolation during prolonged allopatry can operate in the opposite direction of reinforcement, but has until now been little explored. We investigated how premating isolation between two closely related damselfly species, *Calopteryx splendens* and *C. virgo*, might be affected by the expected future northward range expansion of *C. splendens* into the allopatric zone of *C. virgo* in northern Scandinavia. We simulated the expected secondary contact by presenting *C. splendens* females to *C. virgo* males in the northern allopatric populations in Finland. Premating isolation toward *C. splendens* in northern allopatric populations was compared to sympatric populations in southern Finland and southern Sweden. Male courtship responses of *C. virgo* toward conspecific females showed limited geographic variation, however, courtship attempts toward heterospecific *C. splendens* females increased significantly from sympatry to allopatry. Our results suggest that allopatric *C. virgo* males have partly lost their ability to discriminate against heterospecific females. Reduced premating isolation in allopatry might lead to increased heterospecific matings between taxa that are currently expanding and shifting their ranges in response to climate change.

[Evolution](#) Volume 64 Issue 1, 2010 Pages 242 - 252
<http://www3.interscience.wiley.com/journal/122539851/abstract>

35.EPISTASIS MODIFIES THE DOMINANCE OF LOCI CAUSING HYBRID MALE STERILITY IN THE *DROSOPHILA PSEUDOOBSCURA* SPECIES GROUP

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Speciation, the evolution of reproductive isolation between populations, serves as the driving force for generating biodiversity. Postzygotic barriers to gene flow, such as F_1 hybrid sterility and inviability, play important roles in the establishment and maintenance of biological species. F_1 hybrid incompatibilities in taxa that obey Haldane's rule, the observation that the heterogametic sex suffers greater hybrid fitness problems than the homogametic sex, are thought to often result from interactions between recessive-acting X-linked loci and dominant-acting autosomal loci. Because they play such prominent roles in producing hybrid incompatibilities, we examine the dominance and nature of epistasis between alleles derived from *Drosophila persimilis* that confer hybrid male sterility in the genetic background of its sister species, *D. pseudoobscura bogotana*. We

show that epistasis elevates the apparent dominance of individually recessive-acting QTL such that they can contribute to F_1 hybrid sterility. These results have important implications for assumptions underlying theoretical models of hybrid incompatibilities and may offer a possible explanation for why, to date, identification of dominant-acting autosomal "speciation genes" has been challenging.

Evolution Volume 64 Issue 1, 2010 Pages 253 - 260
<http://www3.interscience.wiley.com/journal/122553151/abstract>

36. SEXUALLY MONOMORPHIC MATING PREFERENCES CONTRIBUTE TO PREMATING ISOLATION BASED ON SONG IN EUROPEAN GREEN LACEWINGS

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When species are in intermediate stages of divergence, complicated patterns of reproductive isolation can arise among males and females of the incipient species. The *Chrysoperla carnea* group of green lacewings (Neuroptera: Chrysopidae) has recently experienced rapid speciation. They possess sexually monomorphic mating signals that were assumed to be important in mate recognition. Our objective was to compare patterns of reproductive isolation among five European species within the species complex as well as sex differences in mating strategies that contribute to those patterns. The species were in fact reproductively isolated based on mating signals. In addition, different species showed different degrees of responsiveness to conspecific signals, and those species that responded more frequently to conspecific signals were less discriminating against heterospecific signals. This suggests differences in mating strategies among species that may be related to population densities and heterospecific encounter rates. Sexual dimorphism in mating preference was apparent only in *C. agilis*, whose males were more responsive to all signals and less discriminating against heterospecific signals compared to females. Thus high variance in male quality may be characteristic of *C. agilis*, but not the remaining four species, whose male versus female mating strategies were similar.

Evolution Volume 64 Issue 1, 2010 Pages 261 - 270
<http://www3.interscience.wiley.com/journal/122574054/abstract>

37. *Wolbachia* as a bacteriocyte-associated nutritional mutualist

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Many insects are dependent on bacterial symbionts that provide essential nutrients (ex. aphid-*Buchnera* and tsetse-*Wigglesworthia* associations), wherein the symbionts are harbored in specific cells called bacteriocytes that constitute a symbiotic organ bacteriome. Facultative and parasitic bacterial symbionts like *Wolbachia* have been regarded as evolutionarily distinct from such obligate nutritional mutualists. However, we discovered that, in the bedbug *Cimex lectularius*, *Wolbachia* resides in a bacteriome and appears to be an obligate nutritional mutualist. Two bacterial symbionts, a *Wolbachia* strain and an unnamed γ -proteobacterium, were identified from different strains of the bedbug. The *Wolbachia* symbiont was detected from all of the insects examined whereas the γ -proteobacterium was found in a part of them. The *Wolbachia* symbiont was specifically localized in the bacteriomes and vertically transmitted via the somatic stem cell niche of germaria to oocytes, infecting the incipient symbiotic organ at an early stage of the embryogenesis. Elimination of the *Wolbachia* symbiont resulted in retarded growth and sterility of the host insect. These deficiencies were rescued by oral supplementation of B vitamins, confirming the essential nutritional role of the symbiont for the host. The

estimated genome size of the *Wolbachia* symbiont was around 1.3 Mb, which was almost equivalent to the genome sizes of parasitic *Wolbachia* strains of other insects. These results indicate that bacteriocyte-associated nutritional mutualism can evolve from facultative and prevalent microbial associates like *Wolbachia*, highlighting a previously unknown aspect of the parasitism-mutualism evolutionary continuum.

PNAS **January 12, 2010** vol. 107 no. 2 **769-774**

<http://www.pnas.org/content/107/2/769.abstract>

Insect Genome

38. Widespread Transcriptional Autosomal Dosage Compensation in *Drosophila* Correlates with Gene Expression Level

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Little is known about dosage compensation in autosomal genes. Transcription-level compensation of deletions and other loss-of-function mutations may be a mechanism of dominance of wild-type alleles, a ubiquitous phenomenon whose nature has been a subject of a long debate. We measured gene expression in two isogenic *Drosophila* lines heterozygous for long deletions and compared our results with previously published gene expression data in a line heterozygous for a long duplication. We find that a majority of genes are at least partially compensated at transcription, both for $1/2$ -fold dosage (in heterozygotes for deletions) and for 1.5-fold dosage (in heterozygotes for a duplication). The degree of compensation does not vary among functional classes of genes. Compensation for deletions is stronger for highly expressed genes. In contrast, the degree of compensation for duplications is stronger for weakly expressed genes. Thus, partial transcriptional compensation appears to be based on regulatory mechanisms that insure high transcription levels of some genes and low transcription levels of other genes, instead of precise maintenance of a particular homeostatic expression level. Given the ubiquity of transcriptional compensation, dominance of wild-type alleles may be at least partially caused by of the regulation at transcription level.

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<http://gbe.oxfordjournals.org/cgi/content/abstract/2010/0/44>

39. Functional and Evolutionary Insights from the Genomes of Three Parasitoid *Nasonia* Species

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We report here genome sequences and comparative analyses of three closely related parasitoid wasps: *Nasonia vitripennis*, *N. giraulti*, and *N. longicornis*. Parasitoids are important regulators of arthropod populations, including major agricultural pests and disease vectors, and *Nasonia* is an emerging genetic model, particularly for evolutionary and developmental genetics. Key findings include the identification of a functional DNA methylation tool kit; hymenopteran-specific genes including diverse venoms; lateral gene transfers among Pox viruses, *Wolbachia*, and *Nasonia*; and the rapid evolution of genes involved in nuclear-mitochondrial interactions that are implicated in speciation. Newly developed genome resources advance *Nasonia* for genetic research, accelerate mapping and cloning of quantitative trait loci, and will ultimately provide tools and knowledge for further increasing the utility of parasitoids as pest insect-control agents.

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http://www.sciencemag.org/cgi/content/abstract/327/5963/343?sa_campaign=Email/toc/15-January-2010/10.1126/science.1178028

40. Genetic Screen in *Drosophila melanogaster* Uncovers a Novel Set of Genes Required for Embryonic Epithelial Repair

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The wound healing response is an essential mechanism to maintain the integrity of epithelia and protect all organisms from the surrounding milieu. In the "purse-string" mechanism of wound closure, an injured epithelial sheet cinches its hole closed via an intercellular contractile actomyosin cable. This process is conserved across species and utilized by both embryonic as well as adult tissues, but remains poorly understood at the cellular level. In an effort to identify new players involved in purse-string wound closure we developed a wounding strategy suitable for screening large numbers of *Drosophila* embryos. Using this methodology, we observe wound healing defects in *Jun-related antigen* (encoding DJUN) and *scab* (encoding *Drosophila* α PS3 integrin) mutants and performed a forward genetics screen on the basis of insertional mutagenesis by transposons that led to the identification of 30 lethal insertional mutants with defects in embryonic epithelia repair. One of the mutants identified is an insertion in the *karst* locus, which encodes *Drosophila* β_{Heavy} -spectrin. We show β_{Heavy} -spectrin (β_{H}) localization to the wound edges where it presumably exerts an essential function to bring the wound to normal closure.

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<http://www.genetics.org/cgi/content/abstract/184/1/129>

41. *Drosophila* Translational Elongation Factor-1 γ Is Modified in Response to DOA Kinase Activity and Is Essential for Cellular Viability

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Drosophila translational elongation factor-1 γ (EF1 γ) interacts in the yeast two-hybrid system with DOA, the LAMMER protein kinase of *Drosophila*. Analysis of mutant *EF1 γ* alleles reveals that the locus encodes a structurally conserved protein essential for both organismal and cellular survival. Although no genetic interactions were detected in combinations with mutations in *EF1 α* , an *EF1 γ* allele enhanced mutant phenotypes of *Doa* alleles. A predicted LAMMER kinase phosphorylation site conserved near the C terminus of all EF1 γ orthologs is a phosphorylation site *in vitro* for both *Drosophila* DOA and tobacco PK12 LAMMER kinases. EF1 γ protein derived from *Doa* mutant flies migrates with altered mobility on SDS gels, consistent with it being an *in vivo* substrate of DOA kinase. However, the aberrant mobility appears to be due to a secondary protein modification, since the mobility of EF1 γ protein obtained from wild-type *Drosophila* is unaltered following treatment with several nonspecific phosphatases. Expression of a construct expressing a serine-to-alanine substitution in the LAMMER kinase phosphorylation site into the fly germline rescued null *EF1 γ* alleles but at reduced efficiency compared to a wild-type construct. Our data suggest that EF1 γ functions in vital cellular processes in addition to translational elongation and is a LAMMER kinase substrate *in vivo*.

42. Molecular Characterization of the Key Switch *F* Provides a Basis for Understanding the Rapid Divergence of the Sex-Determining Pathway in the Housefly

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The housefly, *Musca domestica*, is an excellent model system to study the diversification of the pathway that specifies the sexual fate. A number of different mechanisms have been described in the housefly, which reflects in part the broad diversity of sex-determining strategies used in insects. In this study we present the molecular identification and characterization of *F*, which acts as the master switch in the housefly pathway. We provide evidence that *F* corresponds to the *transformer* ortholog in *Musca* (*Mdtra*), which, as a result of alternative processing, expresses functional products only in individuals committed to the female fate. We demonstrate that, once activated, a self-sustaining feedback loop will maintain the female-promoting functions of *Mdtra*. Absence of *Mdtra* transcripts in eggs of *Arrhenogenic* (*Ag*) mutant females suggests that maternally deployed *Mdtra* activity initiates this self-sustaining loop in the zygote. When an *M* factor is paternally transmitted to the zygote, the establishment of the loop is prevented at an early stage before cellularization and splicing of *Mdtra* shifts irreversibly to the male nonproductive mode. On the basis of the analysis of two mutant alleles we can explain the different sex-determining systems in the housefly largely as deviations at the level of *Mdtra* regulation. This plasticity in the housefly pathway may provide a suitable framework to understand the evolution of sex-determining mechanisms in other insect species. For instance, while sex determination in a close relative, the tsetse fly *Glossina morsitans*, differs at the level of the instructive signal, we find that its *tra* ortholog, *Gmtra*, is regulated in a mode similar to that of *Mdtra*.

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<http://www.genetics.org/cgi/content/abstract/184/1/155>

43. Seizure Sensitivity Is Ameliorated by Targeted Expression of K⁺-Cl⁻ Cotransporter Function in the Mushroom Body of the Drosophila Brain

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The *kcc^{DHS1}* allele of *kazachoc* (*kcc*) was identified as a seizure-enhancer mutation exacerbating the bang-sensitive (BS) paralytic behavioral phenotypes of several seizure-sensitive *Drosophila* mutants. On their own, young *kcc^{DHS1}* flies also display seizure-like behavior and demonstrate a reduced threshold for seizures induced by electroconvulsive shock. The product of *kcc* shows substantial homology to KCC2, the mammalian neuronal K⁺-Cl⁻ cotransporter. The *kcc^{DHS1}* allele is a hypomorph, and its seizure-like phenotype reflects reduced expression of the *kcc* gene. We report here that *kcc* functions as a K⁺-Cl⁻ cotransporter when expressed heterologously in *Xenopus laevis* oocytes: under hypotonic conditions that induce oocyte swelling, oocytes that express *Drosophila kcc* display robust ion transport activity observed as a Cl⁻-dependent uptake of the K⁺ congener ⁸⁶Rb⁺. Ectopic, spatially restricted expression of a UAS-*kcc*⁺ transgene was used to determine

where cotransporter function is required in order to rescue the *kcc^{DHS1}* BS paralytic phenotype. Interestingly, phenotypic rescue is largely accounted for by targeted, circumscribed expression in the mushroom bodies (MBs) and the ellipsoid body (EB) of the central complex. Intriguingly, we observed that MB induction of *kcc⁺* functioned as a general seizure suppressor in *Drosophila*. *Drosophila* MBs have generated considerable interest especially for their role as the neural substrate for olfactory learning and memory; they have not been previously implicated in seizure susceptibility. We show that *kcc^{DHS1}* seizure sensitivity in MB neurons acts via a weakening of chemical synaptic inhibition by GABAergic transmission and suggest that this is due to disruption of intracellular Cl⁻ gradients in MB neurons.

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<http://www.genetics.org/cgi/content/abstract/184/1/171>

44. The Retinal Determination Gene *eyes absent* Is Regulated by the EGF Receptor Pathway Throughout Development in *Drosophila*

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Members of the Eyes absent (Eya) protein family play important roles in tissue specification and patterning by serving as both transcriptional activators and protein tyrosine phosphatases. These activities are often carried out in the context of complexes containing members of the Six and/or Dach families of DNA binding proteins. *eyes absent*, the founding member of the Eya family is expressed dynamically within several embryonic, larval, and adult tissues of the fruit fly, *Drosophila melanogaster*. Loss-of-function mutations are known to result in disruptions of the embryonic head and central nervous system as well as the adult brain and visual system, including the compound eyes. In an effort to understand how *eya* is regulated during development, we have carried out a genetic screen designed to identify genes that lie upstream of *eya* and govern its expression. We have identified a large number of putative regulators, including members of several signaling pathways. Of particular interest is the identification of both *yan/anterior open* and *pointed*, two members of the EGF Receptor (EGFR) signaling cascade. The EGFR pathway is known to regulate the activity of Eya through phosphorylation via MAPK. Our findings suggest that this pathway is also used to influence *eya* transcriptional levels. Together these mechanisms provide a route for greater precision in regulating a factor that is critical for the formation of a wide range of diverse tissues.

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45. Control of Wing Size and Proportions by *Drosophila* Myc

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Generation of an organ of appropriate size and shape requires mechanisms that coordinate growth and patterning, but how this is achieved is not understood. Here we examine the role of the growth regulator dMyc in this process during *Drosophila* wing imaginal disc development. We find that dMyc is expressed in a dynamic pattern that correlates with fate specification of different regions of the wing disc, leading us to hypothesize that dMyc expression in each region directs its growth. Consistent with this view, clonal analysis of growth in each region demonstrated distinct temporal requirements for dMyc that match its expression. Surprisingly, however, experiments in which dMyc expression is manipulated reveal that the endogenous pattern has only a minor influence on wing shape. Indeed, when dMyc function is completely lacking in the

wing disc over most of its development, the discs grow slowly and are small in size but appear morphologically normal. Our experiments indicate, therefore, that rather than directly influence differential growth in the wing disc, the pattern of dMyc expression augments growth directed by other regulators. Overall, however, an appropriate level of dMyc expression in the wing disc is necessary for each region to achieve a proportionately correct size.

Genetics, Vol. 184, 199-211, January 2010

<http://www.genetics.org/cgi/content/abstract/184/1/199>

46. Recurrent Selection on the Winters *sex-ratio* Genes in *Drosophila simulans*

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Selfish genes, such as meiotic drive elements, propagate themselves through a population without increasing the fitness of host organisms. X-linked (or Y-linked) meiotic drive elements reduce the transmission of the Y (X) chromosome and skew progeny and population sex ratios, leading to intense conflict among genomic compartments. *Drosophila simulans* is unusual in having a least three distinct systems of X chromosome meiotic drive. Here, we characterize naturally occurring genetic variation at the Winters *sex-ratio* driver (*Distorter on the X* or *Dox*), its progenitor gene (*Mother of Dox* or *MDox*), and its suppressor gene (*Not Much Yang* or *Nmy*), which have been previously mapped and characterized. We survey three North American populations as well as 13 globally distributed strains and present molecular polymorphism data at the three loci. We find that all three genes show signatures of selection in North America, judging from levels of polymorphism and skews in the site-frequency spectrum. These signatures likely result from the biased transmission of the driver and selection on the suppressor for the maintenance of equal sex ratios. Coalescent modeling indicates that the timing of selection is more recent than the age of the alleles, suggesting that the driver and suppressor are coevolving under an evolutionary "arms race." None of the Winters *sex-ratio* genes are fixed in *D. simulans*, and at all loci we find ancestral alleles, which lack the gene insertions and exhibit high levels of nucleotide polymorphism compared to the derived alleles. In addition, we find several "null" alleles that have mutations on the derived *Dox* background, which result in loss of drive function. We discuss the possible causes of the maintenance of presence-absence polymorphism in the Winters *sex-ratio* genes.

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<http://www.genetics.org/cgi/content/abstract/184/1/253>

Insect Heredity

47. Rapid evolution of *Wolbachia* density in insecticide resistant *Culex pipiens*

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The maternally inherited symbiotic *Wolbachia* have been previously shown to have much greater densities in insecticide-resistant *Culex pipiens* mosquitoes than in insecticide-susceptible individuals. These high densities were shown to be at least partially responsible for the costs related to insecticide resistance in this species. We report here the rapid evolution, on the order of 50 generations, of bacterial densities both in

laboratory and field populations. Along with other recently published studies, this report shows that *Wolbachia*-host interactions are very dynamic.

Heredity (2010) 104, 15–19

<http://www.nature.com/hdy/journal/v104/n1/abs/hdy2009100a.html>

48. Response to selection and realized heritability of sperm length in the yellow dung fly (*Scathophaga stercoraria*)

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Sperm length shows considerable phenotypic variation both inter- and intra-specifically, but a general explanation for this variation is lacking. In addition, our understanding of the genetic variation underlying sperm length variation is also limited because there have been few studies on the genetics of sperm size. One factor that could explain the variation in sperm length is that length influences sperm competitiveness, and there is some evidence for this. However, in yellow dung flies (*Scathophaga stercoraria*), microevolutionary responses to experimental variation at levels of sperm competition indicate that sperm length does not influence sperm competitiveness, although this lack of response may simply indicate sperm length lacks evolutionary potential (that is, it is constrained in some way), in spite of evidence that sperm length is heritable. Here we report on a laboratory study, in which we artificially selected upwards and downwards on sperm length in *S. stercoraria*. We found that sperm length significantly diverged after four generations of selection, but the response to selection was asymmetrical: upward selection generated a rapid response, but downward did not. We estimated the realized heritability of sperm length to be approximately 50%, which is consistent with previous sire-son estimates. We also assessed the fertility of males from upward and downward lines and found they did not differ. Results are discussed in the context of sperm competition.

Heredity (2010) 104, 61–66

<http://www.nature.com/hdy/journal/v104/n1/abs/hdy200993a.html>

49. Proteomic characterization of a temperature-sensitive conditional lethal in *Drosophila melanogaster*

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Genetic variation that is expressed only under specific environmental conditions can contribute to additional adverse effects of inbreeding if environmental conditions change. We present a proteomic characterization of a conditional lethal found in an inbred line of *Drosophila melanogaster*. The lethal effect is apparent as a large increase in early mortality at the restrictive temperature (29 °C) as opposed to normal survival at the permissive temperature (20 °C). The increased mortality in response to the restrictive temperature is probably caused by a single recessive major locus. A quantitative trait locus (QTL) region segregating variation affecting the lethal effect has been identified, allowing for a separation of primary/causal effects and secondary consequences in the proteome expression patterns observed. In this study, the proteomic response to the restrictive temperature in the lethal-line (L-line) was compared with the response in an inbred-control-line (IC-line) and an outbred-control-line (OC-line). Quantitative protein changes were detected using isobaric tags for relative and absolute quantitation (iTRAQ) two-dimensional liquid chromatography-tandem mass spectrometry. In all, 45 proteins

were found to be significantly differently regulated in response to the restrictive temperature in the L-line as compared with the IC-line. No proteins were significantly differently regulated between the IC-line and the OC-line, verifying that differential protein regulation was specific to a genetic defect in the L-line. Proteins associated with oxidative phosphorylation and mitochondria were significantly overrepresented within the list of differentially expressed proteins. Proteins related to muscle contraction were also found to be differentially expressed in the L-line in response to the restrictive temperature, supporting phenotypic observations of moribund muscle hyper-contraction.

Heredity (2010) 104, 125–134

<http://www.nature.com/hdy/journal/v104/n2/abs/hdy2009132a.html>

Insect Molecular Biology

50. Global Analysis of Short RNAs Reveals Widespread Promoter-Proximal Stalling and Arrest of Pol II in *Drosophila*

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Emerging evidence indicates that gene expression in higher organisms is regulated by RNA polymerase II stalling during early transcription elongation. To probe the mechanisms responsible for this regulation, we developed methods to isolate and characterize short RNAs derived from stalled RNA polymerase II in *Drosophila* cells. Significant levels of these short RNAs were generated from more than one-third of all genes, indicating that promoter-proximal stalling is a general feature of early polymerase elongation. Nucleotide composition of the initially transcribed sequence played an important role in promoting transcriptional stalling by rendering polymerase elongation complexes highly susceptible to backtracking and arrest. These results indicate that the intrinsic efficiency of early elongation can greatly affect gene expression.

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Insect Molecular Ecology

51. Cryptic differences in dispersal lead to differential sensitivity to habitat fragmentation in two bumblebee species

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Habitat loss has led to fragmentation of populations of many invertebrates, but social hymenopterans may be particularly sensitive to habitat fragmentation due to their low effective population sizes. The impacts of fragmentation depend strongly on dispersal abilities, but these are difficult to quantify. Here, we quantify and compare dispersal abilities of two bumblebee species, *Bombus muscorum* and *Bombus jonellus*, in a model island system. We use microsatellites to investigate population genetic structuring, dispersal and spatial patterns in genetic diversity. Populations of both species showed significant structuring, and isolation by distance, but this was markedly greater in *B. muscorum* ($\theta = 0.13$) than in *B. jonellus* ($\theta = 0.034$). This difference could reflect a higher effective population size in *B. jonellus* compared to *B. muscorum*, but this is not

consistent with the observed abundance of the two species. We argue that it is more likely that *B. jonellus* has a higher propensity to disperse than *B. muscorum*. This will influence their relative susceptibility to habitat fragmentation and may in part explain differential declines of mainland populations of these and other bumblebee species.

[Molecular Ecology](#) Volume 19 Issue 1, Pages 53 - 63
<http://www3.interscience.wiley.com/journal/123194211/abstract>

52. Genome scan in the mosquito *Aedes rusticus*: population structure and detection of positive selection after insecticide treatment

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Identification of genes involved in local adaptation is particularly challenging for species functioning as a network of interconnected populations undergoing frequent extinctions–recolonizations, because populations are submitted to contrasted evolutionary pressures. Using amplified fragment length polymorphism markers, population genetic structure of the mosquito *Aedes rusticus* was analysed in five geographical areas of the French Rhône-Alpes region. We included a number of sites that were treated with the bio-insecticide *Bacillus thuringiensis israelensis* (*Bti*) for more than 15 years. Analysis of molecular variance revealed that most of the genetic variability was found within populations (96%), with no significant variation among geographical areas, although variation among populations within areas (4%) was significant. The global genetic differentiation index F_{ST} was low (0.0366 ± 0.167). However, pairwise F_{ST} values were significant and no isolation-by-distance at the regional level was observed, suggesting a metapopulation structure in this species. *Bti*-treatment had no effect on genetic structure and on within-population genetic diversity. Potential signatures of positive selection associated with *Bti*-treatment were detected for five loci, even though toxicological bioassays performed on field-collected larvae showed no significant difference in mortality between *Bti*-treated and nontreated sites. The difficulty of detecting moderate resistance in field-collected larvae together with possible differential persistence of toxins in the environment may explain our inability to detect a toxicological response to *Bti* in treated sites. The evidence for positive selection occurring at several genomic regions suggests a first step towards *Bti* resistance in natural mosquito populations treated with this bio-insecticide. Furthermore, this signal was detectable using genomic tools before any toxicological evidence for resistance could be identified.

[Molecular Ecology](#) Volume 19 Issue 2, 2010 Pages 325 - 337
<http://www3.interscience.wiley.com/journal/123212880/abstract>

53. Association between *Wolbachia* and *Spiroplasma* within *Drosophila neotestacea*: an emerging symbiotic mutualism?

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Interspecific mutualism can evolve when specific lineages of different species tend to be associated with each other from one generation to the next. Different maternally transmitted endosymbionts occurring within the same cytoplasmic lineage fulfil this requirement. *Drosophila neotestacea* is infected with maternally transmitted *Wolbachia* and *Spiroplasma*, which are cotransmitted at high frequency in natural populations. Molecular phylogenetic evidence indicates that both endosymbionts have been present in *D. neotestacea* for considerable evolutionary periods. Thus, conditions are suitable for the evolution of mutualism between them. In support of this possibility, there is a significant positive association between *Wolbachia* and *Spiroplasma* infection in many

samples of *D. neotestacea* from natural populations. Theoretically, such a positive association can result from either mutualism between these endosymbionts or recent spread. Collections from present-day populations suggest that recent spread and mutualism have both operated to generate the positive association between *Wolbachia* and *Spiroplasma*. If selection acts on the combination of these two endosymbionts, they may be in the early stages of evolution of a more complex, cooperative association.

Molecular Ecology Volume 19 Issue 2, 2010 Pages 414 - 425
<http://www3.interscience.wiley.com/journal/123194223/abstract>

Insect Morphology

54. Morphological variation in the forelegs of the Hawaiian Drosophilidae. I. The AMC clade

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The Hawaiian Drosophilidae possess spectacular diversity in male foreleg modifications, many of which are unknown in other Diptera. The greatest diversity in foreleg morphology is in the *antopocerus*, *modified tarsus*, and *ciliated tarsus* clade (AMC Clade), a group of 95 species. The *modified tarsus* flies are divided into the *bristle*, *ciliated*, *split*, and *spoon tarsus* subgroups. The *bristle tarsus* species feature one or two rows of thickened setae on the basitarsus. The *split tarsus* species are characterized by only having four tarsal segments, in contrast to five tarsomeres in the remainder of Diptera. Based on comparisons of the apparent ground state of ventral setal rows across the Hawaiian *Drosophila*, we suggest that it is the second tarsal segment which has been lost. The *spoon tarsus* species are characterized by having the second tarsomere modified into a setae-filled, concave-shaped spoon. The *ciliated tarsus* species, all of which possess one or more elongate setae on the tarsus of males, are probably not monophyletic with respect to the *bristle tarsus* subgroup. The *antopocerus* flies are characterized by a long basitarsus, with extensive setation on the tibia and basitarsus of some species. The use of these foreleg modifications in courtship behavior has been previously described and it is suggested that they represent the results of sexual selection. The current work expands on previous morphological analyses, presenting a level of detail not previously possible without SEM images. The new characters revealed will figure prominently in future cladistic studies.

Journal of Morphology Volume 271 Issue 1, Pages 86 - 103
<http://www3.interscience.wiley.com/journal/122580731/abstract>

Insect Neuroethology

55. Behavioural state affects motion-sensitive neurones in the fly visual system

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The strength of stimulus-induced responses at the neuronal and the behavioural level often depends on the internal state of an animal. Within pathways processing sensory information and eventually controlling behavioural responses, such gain changes can originate at several sites. Using motion-sensitive lobula plate tangential cells (LPTCs) of blowflies, we address whether and in which way information processing changes for two different states of motor activity. We distinguish between the two states on the basis of haltere movements. Halteres are the evolutionarily transformed hindwings of flies. They

oscillate when the animals walk or fly. LPTCs mediate, amongst other behaviours, head optomotor responses. These are either of large or small amplitude depending on the state of motor activity. Here we find that LPTC responses also depend on the motor activity of flies. In particular, LPTC responses are enhanced when halteres oscillate. Nevertheless, the response changes of LPTCs do not account for the corresponding large gain changes of head movements. Moreover, haltere activity itself does not change the activity of LPTCs. Instead, we propose that a central signal associated with motor activity changes the gain of head optomotor responses and the response properties of LPTCs.

Journal of Experimental Biology 213, 331-338 (2010)

<http://jeb.biologists.org/cgi/content/abstract/213/2/331>

Insect Neuroscience

56.The Shaping of Male Courtship Posture by Lateralized Gustatory Inputs to Male-Specific Interneurons

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Highlights

Inactivation of the *Gr32a* or *Obp57d* gene impairs male courtship posture
 The gustatory inputs from a foreleg tarsus make the wing display unilateral
Gr32a neurons likely have connections with *fru*-expressing mAL interneurons
 Lateral inhibition between the left and right mALs may induce lateralized outputs

Background Unilateral wing vibration to generate "love songs" is a hallmark of male courtship posture in *Drosophila melanogaster*. In contrast, males of some other *Drosophila* species extend both wings simultaneously during courtship. Thus, the patterns of wing movement vary among species and are under stringent genetic control, although there are few variations among individuals within a single species. These observations prompted the postulation that the proper wing display by courting males of *D. melanogaster* does not require sensory inputs.

Results Here we show that when males of *D. melanogaster* are deprived of gustatory inputs mediated by the sensory neurons expressing the taste receptor gene *Gr32a*, a close relative to the pheromone receptor gene *Gr68a*, they often fail to perform unilateral wing extension during courtship because they become unable to keep a wing in the resting position while extending another wing. The tarsal amputation of a foreleg, but not other legs, increased the occurrence of simultaneous wing extension, indicating that *Gr32a*-expressing cells in this structure are involved in the regulation of courting posture. A similar simultaneous wing extension was also observed in males in which the putative pheromone-binding protein gene *Obp57d* was inactivated. The axons of *Gr32a*-expressing cells project to the subesophageal ganglion, where their terminals unilaterally contact mAL, which are male-specific *fruitless (fru)*-expressing interneurons that have bilateral branches.

Conclusions Our observations strongly suggest that gustatory pheromone inputs ensure the correct laterality of wing vibration that conforms to the species-specific behavioral pattern

Current Biology, [Volume 20, Issue 1](#), 1-8, 2010

<http://www.cell.com/current-biology/abstract/S0960-9822%2809%2902053-3#Summary>

57.Lineage-specific effects of Notch/Numb signaling in post-embryonic development of the *Drosophila* brain

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Numb can antagonize Notch signaling to diversify the fates of sister cells. We report here that paired sister cells acquire different fates in all three *Drosophila* neuronal lineages that make diverse types of antennal lobe projection neurons (PNs). Only one in each pair of postmitotic neurons survives into the adult stage in both anterodorsal (ad) and ventral (v) PN lineages. Notably, Notch signaling specifies the PN fate in the vPN lineage but promotes programmed cell death in the missing siblings in the adPN lineage. In addition, Notch/Numb-mediated binary sibling fates underlie the production of PNs and local interneurons from common precursors in the IAL lineage. Furthermore, Numb is needed in the lateral but not adPN or vPN lineages to prevent the appearance of ectopic neuroblasts and to ensure proper self-renewal of neural progenitors. These lineage-specific outputs of Notch/Numb signaling show that a universal mechanism of binary fate decision can be utilized to govern diverse neural sibling differentiations.

Development 137, 43-51. January 1, 2010

<http://dev.biologists.org/content/137/1/43.abstract>

58. Role of Notch signaling in establishing the hemilineages of secondary neurons in *Drosophila melanogaster*

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The secondary neurons generated in the thoracic central nervous system of *Drosophila* arise from a hemisegmental set of 25 neuronal stem cells, the neuroblasts (NBs). Each NB undergoes repeated asymmetric divisions to produce a series of smaller ganglion mother cells (GMCs), which typically divide once to form two daughter neurons. We find that the two daughters of the GMC consistently have distinct fates. Using both loss-of-function and gain-of-function approaches, we examined the role of Notch signaling in establishing neuronal fates within all of the thoracic secondary lineages. In all cases, the 'A' (Notch^{ON}) sibling assumes one fate and the 'B' (Notch^{OFF}) sibling assumes another, and this relationship holds throughout the neurogenic period, resulting in two major neuronal classes: the A and B hemilineages. Apparent monotypic lineages typically result from the death of one sibling throughout the lineage, resulting in a single, surviving hemilineage. Projection neurons are predominantly from the B hemilineages, whereas local interneurons are typically from A hemilineages. Although sibling fate is dependent on Notch signaling, it is not necessarily dependent on *numb*, a gene classically involved in biasing Notch activation. When Numb was removed at the start of larval neurogenesis, both A and B hemilineages were still generated, but by the start of the third larval instar, the removal of Numb resulted in all neurons assuming the A fate. The need for Numb to direct Notch signaling correlated with a decrease in NB cell cycle time and may be a means for coping with multiple sibling pairs simultaneously undergoing fate decisions.

Development 137, 53-61 January 1, 2010.

<http://dev.biologists.org/content/137/1/53.abstract>

59. Neural correlates of odor learning in the honeybee antennal lobe

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Extracellular spiking activity and local field potentials (LFP) were recorded via tetrodes at the output of the antennal lobe (AL) in the honeybee brain during olfactory conditioning. Odors induce reliable rate responses that consist of either phasic-tonic responses, or complex responses with odor-specific profiles. In addition, odors evoke consistent responses of LFP oscillations in the 50-Hz band during the phasic ON-response to odor stimulation, and variable LFP responses at other frequency bands during the sustained response. A principal component analysis of the ensemble activity during differential conditioning consistently indicates the largest changes in response to the learned odor (conditioned stimulus; CS+). Relative LFP power increases for CS+ in the 15–40-Hz frequency band during the sustained response, and decreases for frequencies above 45 Hz. To quantify the relationship between these population responses given by the ensemble spiking activity and LFP, we show that for CS+ the learning-related changes in the degree of the phase-locked spiking activity correlate with the power changes in the corresponding frequency bands. Our results indicate associative plasticity in the AL of the bee leading to both enhancement and decrease of neuronal response rates. LFP power changes and the correlated changes in the locking between spikes and LFP at different frequencies observed for the learned odor serve as further evidence for a learning-induced restructuring of temporal ensemble representations.

[European Journal of Neuroscience 2010 Volume 31 Issue 1, Pages 119 – 133
http://www3.interscience.wiley.com/journal/123221213/abstract?CRETRY=1&SRETRY=0](http://www3.interscience.wiley.com/journal/123221213/abstract?CRETRY=1&SRETRY=0)

60.3D standard brain of the red flour beetle *Tribolium castaneum*: a tool to study metamorphic development and adult plasticity

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The red flour beetle *Tribolium castaneum* is emerging as a further standard insect model beside *Drosophila*. Its genome is fully sequenced and it is susceptible for genetic manipulations including RNA-interference. We use this beetle to study adult brain development and plasticity primarily with respect to the olfactory system. In the current study, we provide 3D standard brain atlases of freshly eclosed adult female and male beetles (A0). The atlases include eight paired and three unpaired neuropils including antennal lobes, optic lobe neuropils, mushroom body calyces and pedunculi, and central complex. For each of the two standard brains, we averaged brain areas of 20 individual brains. Additionally, we characterized eight selected olfactory glomeruli from 10 A0 female and male beetles respectively, which we could unequivocally recognize from individual to individual owing to their size and typical position in the antennal lobes. In summary, comparison of the averaged neuropil volumes revealed no sexual dimorphism in any of the reconstructed neuropils in A0 *Tribolium* brains. Both, the female and male 3D standard brain are also used for interspecies comparisons, and, very importantly, will serve as future volumetric references after genetical manipulation especially regarding metamorphic development and adult plasticity.

Front. Syst. Neurosci. doi:10.3389/neuro.06.003.2010
<http://frontiersin.org/neuroscience/systemsneuroscience/paper/10.3389/neuro.06/003.2010/>

61.The locust standard brain: a 3D standard of the central complex as a platform for neural network analysis

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Many insects use the pattern of polarized light in the sky for spatial orientation and navigation. We have investigated the polarization vision system in the desert locust. To create a common platform for anatomical studies on polarization vision pathways, Kurylas et al. (2008) have generated a three-dimensional (3D) standard brain from confocal microscopy image stacks of 10 male brains, using two different standardization methods, the Iterative Shape Averaging (ISA) procedure and the Virtual Insect Brain (VIB) protocol. Comparison of both standardization methods showed that the VIB standard is ideal for comparative volume analysis of neuropils, whereas the ISA standard is the method of choice to analyze the morphology and connectivity of neurons. The central complex is a key processing stage for polarization information in the locust brain. To investigate neuronal connections between diverse central-complex neurons, we generated a higher-resolution standard atlas of the central complex and surrounding areas, using the ISA method based on brain sections from 20 individual central complexes. To explore the usefulness of this atlas, two central-complex neurons, a polarization-sensitive columnar neuron (type CPU1a) and a tangential neuron that is activated during flight, the giant-fan shaped (GFS) neuron, were reconstructed three-dimensionally from brain sections. To examine whether the GFS neuron is a candidate to contribute to synaptic input to the CPU1a neuron, we registered both neurons into the standardized central complex. Visualization of both neurons revealed a potential connection of the CPU1a and GFS neurons in layer II of the upper division of the central body.

Front. Syst. Neurosci. **3**:21. doi:10.3389/neuro.06.021.2009

<http://frontiersin.org/neuroscience/systemsneuroscience/paper/10.3389/neuro.06/021.2009/>

62.Vibration-processing interneurons in the honeybee brain

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The afferents of the Johnston's organ (JO) in the honeybee brain send their axons to three distinct areas, the dorsal lobe, the dorsal subesophageal ganglion (DL-dSEG), and the posterior protocerebral lobe (PPL), suggesting that vibratory signals detected by the JO are processed differentially in these primary sensory centers. The morphological and physiological characteristics of interneurons arborizing in these areas were studied by intracellular recording and staining. DL-Int-1 and DL-Int-2 have dense arborizations in the DL-dSEG and respond to vibratory stimulation applied to the JO in either tonic excitatory, on-off-phasic excitatory, or tonic inhibitory patterns. PPL-D-1 has dense arborizations in the PPL, sends axons into the ventral nerve cord (VNC), and responds to vibratory stimulation and olfactory stimulation simultaneously applied to the antennae in long-lasting excitatory pattern. These results show that there are at least two parallel pathways for vibration processing through the DL-dSEG and the PPL. In this study, Honeybee Standard Brain was used as the common reference, and the morphology of two types of interneurons (DL-Int-1 and DL-Int-2) and JO afferents was merged into the standard brain based on the boundary of several neuropiles, greatly supporting the understanding of the spatial relationship between these identified neurons and JO afferents. The visualization of the region where the JO afferents are closely appositioned to these DL interneurons demonstrated the difference in putative synaptic regions between the JO afferents and these DL interneurons (DL-Int-1 and DL-Int-2) in the DL. The neural circuits related to the vibration-processing interneurons are discussed.

Front. Syst. Neurosci. doi:10.3389/neuro.06.019.2009

<http://frontiersin.org/neuroscience/systemsneuroscience/paper/10.3389/neuro.06/019.2009/>

63. Digital, three-dimensional average shaped atlas of the *heliiothis virescens* brain with integrated gustatory and olfactory neurons

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We use the moth *Heliothis virescens* as model organism for studying the neural network involved in chemosensory coding and learning. The constituent neurons are characterised by intracellular recordings combined with staining, resulting in a single neuron identified in each brain preparation. In order to spatially relate the neurons of different preparations a common brain framework was required. We here present an average shaped atlas of the moth brain. It is based on 11 female brain preparations, each stained with a fluorescent synaptic marker and scanned in confocal laser-scanning microscope. Brain neuropils of each preparation were manually reconstructed in the computer software AMIRA, followed by generating the atlas using the Iterative Shape Average Procedure. To demonstrate the application of the atlas we have registered two olfactory and two gustatory interneurons, as well as the axonal projections of gustatory receptor neurons into the atlas, visualising their spatial relationships. The olfactory interneurons, showing the typical morphology of inner-tract antennal lobe projection neurons, projected in the calyces of the mushroom body and laterally in the protocerebral lobe. The two gustatory interneurons, responding to sucrose and quinine respectively, projected in different areas of the brain. The wide projections of the quinine responding neuron included a lateral area adjacent to the projections of the olfactory interneurons. The sucrose responding neuron was confined to the suboesophageal ganglion with dendritic arborizations overlapping the axonal projections of the gustatory receptor neurons on the proboscis. By serving as a tool for the integration of neurons, the atlas offers visual access to the spatial relationship between the neurons in three dimensions, and thus facilitates the study of neuronal networks in the *Heliothis virescens* brain. The moth standard brain is accessible at http://www.nt.ntnu.no/users/kvello/H_virescens_standardbrain/

Front. Syst. Neurosci. **3**:14. doi:10.3389/neuro.06.014.2009

<http://frontiersin.org/neuroscience/systemsneuroscience/paper/10.3389/neuro.06/014.2009/>

64. Identification of an aggression-promoting pheromone and its receptor neurons in *Drosophila*

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Aggression is regulated by pheromones in many animal species^{1, 2, 3}. However, in no system have aggression pheromones, their cognate receptors and corresponding sensory neurons been identified. Here we show that 11-*cis*-vaccenyl acetate (cVA), a male-specific volatile pheromone, robustly promotes male-male aggression in the vinegar fly *Drosophila melanogaster*. The aggression-promoting effect of synthetic cVA requires olfactory sensory neurons (OSNs) expressing the receptor Or67d^{4, 5, 6}, as well as the receptor itself. Activation of Or67d-expressing OSNs, either by genetic manipulation of their excitability or by exposure to male pheromones in the absence of other classes of OSNs, is sufficient to promote aggression. High densities of male flies can promote aggression by the release of volatile cVA. In turn, cVA-promoted aggression can promote male fly dispersal from a food resource, in a manner dependent on Or67d-expressing OSNs. These data indicate that cVA may mediate negative-feedback control of male population density, through its effect on aggression. Identification of a pheromone-OSN

pair controlling aggression in a genetic organism opens the way to unravelling the neurobiology of this evolutionarily conserved behaviour.

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<http://www.nature.com/nature/journal/v463/n7278/abs/nature08678.html?lang=en>

65. Dissecting differential gene expression within the circadian neuronal circuit of *Drosophila*

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Behavioral circadian rhythms are controlled by a neuronal circuit consisting of diverse neuronal subgroups. To understand the molecular mechanisms underlying the roles of neuronal subgroups within the *Drosophila* circadian circuit, we used cell-type specific gene-expression profiling and identified a large number of genes specifically expressed in all clock neurons or in two important subgroups. Moreover, we identified and characterized two circadian genes, which are expressed specifically in subsets of clock cells and affect different aspects of rhythms. The transcription factor *Fer2* is expressed in ventral lateral neurons; it is required for the specification of lateral neurons and therefore their ability to drive locomotor rhythms. The *Drosophila melanogaster* homolog of the vertebrate circadian gene nocturnin is expressed in a subset of dorsal neurons and mediates the circadian light response. The approach should also enable the molecular dissection of many different *Drosophila* neuronal circuits.

Nature Neuroscience 13, 60 - 68 (2010)

<http://www.nature.com/neuro/journal/v13/n1/abs/nn.2451.html?lang=en>

Insect Pathology

66. Sigma viruses from three species of *Drosophila* form a major new clade in the rhabdovirus phylogeny

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The sigma virus (DMelSV), which is a natural pathogen of *Drosophila melanogaster*, is the only *Drosophila*-specific rhabdovirus that has been described. We have discovered two new rhabdoviruses, *D. obscura* and *D. affinis*, which we have named DObsSV and DAffSV, respectively. We sequenced the complete genomes of DObsSV and DMelSV, and the L gene from DAffSV. Combining these data with sequences from a wide range of other rhabdoviruses, we found that the three sigma viruses form a distinct clade which is a sister group to the Dimarhabdovirus supergroup, and the high levels of divergence between these viruses suggest that they deserve to be recognized as a new genus. Furthermore, our analysis produced the most robustly supported phylogeny of the *Rhabdoviridae* to date, allowing us to reconstruct the major transitions that have occurred during the evolution of the family. Our data suggest that the bias towards research into plants and vertebrates means that much of the diversity of rhabdoviruses has been missed, and rhabdoviruses may be common pathogens of insects.

Insect Pharmacology

67. Postembryonic development of centrally generated flight motor patterns in the hawkmoth, *Manduca sexta*

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This study analyses the maturation of centrally generated flight motor patterns during metamorphosis of *Manduca sexta*. Bath application of the octopamine agonist chlordimeform to the isolated central nervous system of adult moths reliably induces fictive flight patterns in wing depressor and elevator motoneurons. Pattern maturation is investigated by chlordimeform application at different developmental stages.

Chlordimeform also induces motor patterns in larval ganglia, which differ from fictive flight, indicating that in larvae and adults, octopamine affects different networks. First changes in motoneuron activity occur at the pupal stage P10. Rhythmic motor output is induced in depressor, but not in elevator motoneurons at P12. Adult-like fictive flight activity in motoneurons is observed at P16 and increases in speed and precision until emergence 2 days later. Pharmacological block of chloride channels with picrotoxin also induces fictive flight in adults, suggesting that the pattern-generating network can be activated by the removal of inhibition, and that proper network function does not rely on GABA_A receptors. Our results suggest that the flight pattern-generating network becomes gradually established between P12 and P16, and is further refined until adulthood. These findings are discussed in the context of known physiological and structural CNS development during *Manduca* metamorphosis.

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<http://www.springerlink.com/content/u26m41467j6703lj/>

68. Cellular mechanisms of acid secretion in the posterior midgut of the larval mosquito (*Aedes aegypti*)

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The gut contents of larval mosquitoes are alkalinized by the anterior midgut and reacidified by the posterior midgut. In the present study the cellular mechanisms of reacidification were studied in isolated, perfused posterior midgut by measuring the transepithelial voltage (V_{te}) and the rate of acid secretion as indicated by the color change of *m*-cresol purple during intervals of perfusion stop. The lumen-positive V_{te} and reacidification were significantly increased by serotonin ($0.2 \mu\text{mol l}^{-1}$). The V-type H⁺-ATPase inhibitor concanamycin A ($10 \mu\text{mol l}^{-1}$) on the luminal side inhibited acidification and decreased V_{te} . On the hemolymph side the carbonic anhydrase (CA) inhibitor acetazolamide (1 mmol l^{-1}) almost abolished V_{te} , but had no effect on acidification. Similarly, hemolymph-side DIDS (0.1 mmol l^{-1}), DPC (0.5 mmol l^{-1}), amiloride (1 mmol l^{-1}) and ouabain (2.5 mmol l^{-1}) significantly reduced V_{te} , whereas Ba²⁺ (5 mmol l^{-1}) was without effect. DPC and amiloride also reduced V_{te} when applied to the luminal side of the epithelium. Unilateral substitution of gluconate for Cl⁻ affected V_{te} in a way consistent with a greater permeability for Cl⁻ versus Na⁺. Cl⁻ replacement in the lumen decreased V_{te} , whereas replacement on the hemolymph side increased it. Bilateral replacement left the control voltage unaffected. Na⁺ replacement on either side of the tissue reduced V_{te} .

to different degrees. Omission of luminal amino acids was followed by a significant decrease in V_{te} . Except for concanamycin A, none of the above manipulations impaired acidification, indicating that acidification requires only the apical proton pump. However, the chemical source of secreted H^+ is still unknown and needs to be investigated.

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<http://jeb.biologists.org/cgi/content/abstract/213/2/295>

Insect Photoreception

69. Photoreceptor responses of fruitflies with normal and reduced arrestin content studied by simultaneous measurements of visual pigment fluorescence and ERG

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We have simultaneously measured the electroretinogram (ERG) and the metarhodopsin content via fluorescence in white-eyed, wild-type *Drosophila* and the arrestin2 hypomorphic mutant ($w^-; arr2^3$) at a range of stimulus wavelengths and intensities. Photoreceptor response amplitude and termination (transition between full repolarization and prolonged depolarizing afterpotential, PDA) were related to visual pigment conversions and arrestin concentration. The data were implemented in a kinetic model of the rhodopsin-arrestin cycle, allowing us to estimate the active metarhodopsin concentration as a function of effective light intensity and arrestin concentration. Arrestin reduction in the mutant modestly increased the light sensitivity and decreased the photoreceptor dynamic range. Compared to the wild type, in the mutant the transition between full repolarization and PDA occurred at a lower metarhodopsin fraction and was more abrupt. We developed a steady-state stochastic model to interpret the dependence of the PDA on effective light intensity and arrestin content and to help deduce the arrestin to rhodopsin ratio from the sensitivity and PDA data. The feasibility of different experimental methods for the estimation of arrestin content from ERG and PDA is discussed.

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<http://www.springerlink.com/content/4417v02211232720/>

Insect Vision

70. Requirement for an Enzymatic Visual Cycle in *Drosophila*

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Highlights ► A visual cycle exists outside of mammalian photoreceptor cells ► The *Drosophila* visual cycle prevents loss of rhodopsin during nutrient deprivation ► Impairment of the fly visual cycle causes retinal degeneration ► A human counterpart substitutes for a key enzyme in the fly visual cycle

Background The visual cycle is an enzymatic pathway employed in the vertebrate retina to regenerate the chromophore after its release from light-activated rhodopsin. However, a visual cycle is thought to be absent in invertebrates such as the fruit fly *Drosophila melanogaster*.

Results We demonstrate that an enzymatic visual cycle exists in flies for chromophore regeneration and requires a retinol dehydrogenase, PDH, in retinal pigment cells.

Absence of PDH resulted in progressive light-dependent loss of rhodopsin and retinal degeneration. These defects are suppressed by introduction of a mammalian dehydrogenase, RDH12, which is required in humans to prevent retinal degeneration. We demonstrate that a visual cycle is required in flies to sustain a visual response under nutrient deprivation conditions that preclude de novo production of the chromophore.

Conclusions Our results demonstrate that an enzymatic visual cycle exists and is required in flies for maintaining rhodopsin levels. These findings establish *Drosophila* as an animal model for studying the visual cycle and retinal diseases associated with chromophore regeneration.

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<http://www.cell.com/current-biology/abstract/S0960-9822%2809%2902146-0>

71. First evidence of fine colour discrimination ability in ants (Hymenoptera, Formicidae)

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In the present study, we report the first evidence that ants discriminate and learn perceptually close colour stimuli. Foragers of the ant species *Cataglyphis aenescens* and *Formica cunicularia* were trained in a Y-maze choice apparatus to monochromatic light stimuli of a constant intensity associated with a food reward. Two stimuli, with a mean wavelength of 40 nm perceptual distance, were chosen from the UV (340 nm vs 380 nm) and the green (510 nm vs 550 nm) range because these species are UV-green dichromats. Foragers were trained with two conditioning paradigms [absolute conditioning (AC) and differential conditioning (DC)]. In the UV range, *C. aenescens* foragers failed to discriminate when presented with a small colour difference in both training procedures. Foragers also failed in the green range when trained with AC but showed significant bias towards the rewarded stimulus when trained with DC. *Formica cunicularia* foragers achieved the task in the UV range when trained with DC only. In the green range, *F. cunicularia* foragers showed clear preference for the rewarded stimulus in both training conditioning procedures. Foragers never failed in choosing the rewarded stimulus in DC even when the intensity of the rewarded stimulus was reduced by one log unit. This clearly indicates that DC is of paramount importance to discriminate perceptually close colour stimuli.

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Insect Review

72. Ecological speciation in phytophagous insects

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Divergent natural selection has been shown to promote speciation in a wide range of taxa. For example, adaptation to different ecological environments, via divergent selection, can result in the evolution of reproductive incompatibility between populations. Phytophagous insects have been at the forefront of these investigations of 'ecological speciation' and it is clear that adaptation to different host plants can promote insect speciation. However, much remains unknown. For example, there is abundant variability in the extent to which divergent selection promotes speciation, the sources of divergent selection, the types of reproductive barriers involved, and the genetic basis of divergent adaptation. We review these factors here. Several findings emerge, including the observation that although

numerous different sources of divergent selection and reproductive isolation can be involved in insect speciation, their order of evolution and relative importance are poorly understood. Another finding is that the genetic basis of host preference and performance can involve loci of major effect and opposing dominance, factors which might facilitate speciation in the face of gene flow. In addition, we raise a number of other recent issues relating to phytophagous insect speciation, such as alternatives to ecological speciation, the geography of speciation, and the molecular signatures of speciation. Throughout, we aim to both synthesize what is known, as well as highlight areas where future work is especially needed.

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<http://www3.interscience.wiley.com/journal/122636830/abstract?CRETRY=1&SRETRY=0>

73. Sex differences in molecular neuroscience: from fruit flies to humans

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A plethora of discoveries relating to sex influences on brain function is rapidly moving this field into the spotlight for most areas of neuroscience. The domain of molecular or genetic neuroscience is no exception. The goal of this article is to highlight key developments concerning sex-based dimorphisms in molecular neuroscience, describe control mechanisms regulating these differences, address the implications of these dimorphisms for normal and abnormal brain function and discuss what these advances mean for future work in the field. The overriding conclusion is that, as for neuroscience in general, molecular neuroscience has to take into account potential sex influences that might modify signalling pathways.

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Insect Book Review

74. Far from simple: insect immune defences

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http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6VJ1-4X86F4F-5&_user=10&_coverDate=01%2F31%2F2010&_rdoc=1&_fmt=high&_orig=browse&_sort=d&_view=c&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=e261efea36ba51240ec612bee183086d

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