The effect of own, related (brother), and unrelated male AG secretion on sperm survival in the monandrous bumble bee and fungus-growing ant and the polyandrous honeybee and fungus-growing ants. Photos of males are given in the panels. (From Science 2010 327: 1506. Abstract No. 68 in this issue. Without Permission).
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39. Alternative Splicing Modulates Ubx Protein Function in *Drosophila melanogaster*
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40. Natural Variation in Odorant Recognition Among Odorant-Binding Proteins in *Drosophila melanogaster*
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61. Contribution of photoreceptor subtypes to spectral wavelength preference in Drosophila  
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67. **Colony fusion and worker reproduction after queen loss in army ants**
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70. **Olfactory signalling in vertebrates and insects: differences and commonalities**
*Nature Reviews Neuroscience* 11, 188-200 (March 2010)
Insect Behaviour

1. Knowing who’s who: nestmate recognition in the facultatively social carpenter bee, Xylocopa virginica

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When animals live in groups, the ability to discriminate group members from nonmembers allows individuals to adjust their behaviour in ways that enhance both individual and group fitness. In social insects, especially bees, this kind of recognition has mainly been studied with reference to colony-based social interactions, but they also interact in other kinds of group contexts. In the facultatively social carpenter bee, Xylocopa virginica, individuals of both sexes interact repeatedly, in such activities as cooperative brood raising by females, territorial competition by males, and matings near nest entrances. In light of these varied interactions, in which the ability to discriminate familiar from unfamiliar individuals might be advantageous, the aim of our study was to determine whether X. virginica adults are capable of nestmate recognition. Nestmates were defined operationally as bees that were caught at the same nest entrance after spending the night together, whereas non-nestmates were from different nests. We used circle tube assays of male–male, female–female and male–female dyads to compare rates of aggressive (pushing, biting and C-postures) and tolerant/cooperative (head-to-head touching and passing) behaviour in nestmates versus non-nestmates. In general, aggression occurred sooner and more frequently among non-nestmates than among nestmates, whereas tolerance was more common among nestmates. This indicates that male and female bees can recognize familiar individuals of both sexes and adjust their behaviour accordingly. Since tested individuals may have been nestmates for less than 24 h, this further suggests that both female and male bees may learn the identities of their nestmates quickly.


2. Plasticity in mating behaviour drives asymmetric reproductive interference in whiteflies

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Department of Entomology, Washington State University, USA
Department of Zoology, Miami University, USA

Reproductive interference between species with incomplete mate recognition can disrupt the process of mate acquisition. Accordingly, reproductive interference can reduce female and male fitness and lead to sexual exclusion. Here, we tested the hypothesis that flexible mating behaviours could mitigate the fitness-reducing effects of reproductive interference between reproductively incompatible biotypes of the haplodiploid whitefly Bemisia tabaci. We show that females of the globally distributed and invasive B biotype respond to reproductive interference from the Q biotype by increasing their acceptance of copulation attempts from B males. This behavioural plasticity increases the ability of B females to mate successfully and maintain a constant sex ratio in their offspring despite reproductive interference. In contrast, females of competing biotypes have invariant behaviour and produce fewer female offspring because of reproductive interference from the B biotype. Heuristic simulation models incorporating data on behavioural and life history traits of the B and Q biotypes obtained here, and published data on other biotypes, show that this plasticity in mating behaviour of B females could contribute to sexual exclusion of closely related biotypes. Our results demonstrate a powerful link...
between mating behaviour, reproductive interference and sexual exclusion, suggesting that variation in mating behaviour could determine the effects of reproductive interference and drive sexual exclusion among closely related species or among biotypes of a species.

**3. Assessment of oviposition site quality by aphidophagous hoverflies: reaction to conspecific larva**

Raki Almohamad, François J. Verheggen, Frédéric Francis, Georges Lognay and Eric Haubruge

Aphidophagous predators adapt their foraging behaviour to the presence of conspecific and heterospecific larvae. We studied the effect of the presence of conspecific larvae and their tracks on the oviposition site selection of an aphid-specific predator, *Episyrphus balteatus* DeGeer (Diptera: Syrphidae), in two-choice experiments using a leaf disc bioassay. Gas chromatography – mass spectrometry analysis was used to identify the volatile chemicals released from odour extracts of *E. balteatus* larval tracks. The behavioural effects of these volatile substances on hoverfly females were also evaluated. Our experiments demonstrated that *E. balteatus* females were deterred from ovipositing when presented with a *Vicia faba* leaf with aphids and conspecific larvae. The oviposition-deterring stimulus was also active when females were presented with a leaf that contained conspecific larval tracks. A mixture of chemical compounds was found in the volatile pattern of odour extracts of larval tracks. The main volatile chemicals were 3-methylbutanoic acid, 2-methylbutanoic acid, 2-methylpropanoic acid, 3-hydroxy-2-butanone, hexanoic acid and phenol. Females also laid significantly fewer eggs in response to odorant volatiles emitted from larval extracts. These results highlight that predatory hoverfly females avoid ovipositing in aphid colonies in which conspecific larvae or their tracks are already present, suggesting that this behaviour constitutes a strategy that enables females to optimize their oviposition site and reduce competition suffered by their offspring.

**4. Effects of queen mandibular pheromone on nestmate recognition in worker honeybees, *Apis mellifera***

Yongliang Fan, Freddie-Jeanne Richard, Nabila Rouf and Christina M. Grozinger

The ability to distinguish between members of a social group and unfamiliar individuals is a critical element of social behaviour. Social insects can differentiate between nestmates and non-nestmates via recognition cues, which in most species are cuticular hydrocarbons. Cuticular hydrocarbon patterns are altered by genotype and environmental conditions, but it is unclear whether colony social conditions can also affect nestmate interactions. Honeybee queens produce pheromones that regulate many aspects of worker behaviour, physiology and colony organization. A five-component blend, queen mandibular pheromone (QMP), produces many of the effects of a live queen. We found that QMP treatment alters how resident bees interact with intruder bees, based on standard nestmate recognition assays. However, QMP does not appear to alter the ability...
of bees to distinguish between nestmates and non-nestmates, or general aggression levels. Rather, QMP exposure significantly alters cuticular hydrocarbon patterns of worker bees, suggesting that QMP-treated nestmates are no longer recognized as nestmates by untreated bees, and vice versa. Thus, queen pheromone can have significant effects on nestmate recognition and interactions in honeybees, which may be important for colony cohesion.

http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6W9W-4Y6THYW-18&_user=108&_coverDate=03/31/2010&_rdoc=18&_fmt=high&_orig=browse&_snclid=196151117151112714114278118&_docanchor=&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=0ada5ca8bde43ded9479c08482086

**5. Synchronization of wing beat cycle of the desert locust, Schistocerca gregaria, by periodic light flashes**

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Studies on the generation of rhythmic motor patterns have shown that peripheral sensory input may contribute substantially to the rhythm generating network. A prominent example is the wing beat frequency of desert locusts, which can be entrained to rhythmic mechanosensory input, but also to the frequency of periodic light flashes. To further analyze the entrainment by light, tethered flying locusts were presented with periodic light flashes, while the position of the forewing was filmed. We show that entrainment of wing beat occurs both in the UV and green range of light. Animals maintained a characteristic phase relationship to the light stimulus with the most elevated wing position occurring at the end of the dark phase. Speed and time course of entrainment varied greatly and ranged from the duration of a single wing beat cycle to several seconds. To identify the visual system mediating entrainment, synchronization to UV light was tested after cutting the optic stalks to the optic lobes/compound eyes or the ocellar nerves. The results show that light entrainment of the locust flight pattern is largely and perhaps exclusively mediated via the fast ocellar pathway and may have a role to stabilize flight with respect to the horizon.

**Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology** Volume 196, Number 3 / March, 2010 199-211
http://www.springerlink.com/content/fr5727405k3784nv/

**Insect Biochemistry**

**6. The α-Glycerophosphate Cycle in Drosophila melanogaster V. Molecular Analysis of α-Glycerophosphate Dehydrogenase and α-Glycerophosphate Oxidase Mutants**

Amber Carmon, Jeff Chien, David Sullivan, and Ross MacIntyre

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Two enzymes, α-glycerophosphate dehydrogenase (GPDH-1) in the cytoplasm and α-glycerophosphate oxidase (GPO-1) in the mitochondrion cooperate in *Drosophila* flight muscles to generate the ATP needed for muscle contraction. Null mutants for either enzyme cannot fly. Here, we characterize 15 ethyl methane sulfonate (EMS)-induced mutants in GPDH-1 at the molecular level and assess their effects on structural and evolutionarily conserved domains of this enzyme. In addition, we molecularly characterize 3 EMS-induced GPO-1 mutants and excisions of a P element insertion in the GPO-1 gene. The latter represent the best candidate for null or amorphic mutants in this gene.


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The genome sequences of 12 Drosophila species contain 3 paralogs for glycerophosphate dehydrogenase (GPDH) and for the mitochondrial glycerophosphate oxidase (GPO). These 2 enzymes participate in the glycerophosphate cycle in the adult thoracic flight muscles. The flight muscle enzymes are encoded by gpdh-1 at 26A2 and gpo-1 at 52C8. In this paper, we show that the GPDH paralogs share the same evolutionarily conserved functional domains and most intron positions, whereas the GPO paralogs share only some of the functional domains of mitochondrial oxidoreductases. The GPO paralogs not expressed in the flight muscles essentially lack introns. GPDH paralogs encoded by gpdh-2 and gpdh-3 and the GPO paralogs encoded by gpo-2 and gpo-3 are expressed only in the testes. Gene trees for the GPDH and GPO paralogs indicate that the genes expressed in the flight muscles are evolving very slowly presumably under strong purifying selection whereas the paralogs expressed in the testes are evolving more rapidly. The concordance between species and gene trees, dN/dS ratios, phylogenetic analysis by maximum likelihood-based tests, and analyses of radical and conservative substitutions all indicate that the additional GPDH and GPO paralogs are also evolving under purifying selection.

http://jhered.oxfordjournals.org/cgi/content/abstract/101/2/225

Insect Biocontrol

8. Female-specific flightless phenotype for mosquito control

Guoliang Fu1,2, Rosemary S. Lees1,2, Derric Nimmo2,1, Diane Aw2,1, Li Jim2,1, Pam Gray2, Thomas U. Berendonk2, Helen White-Cooper1, Sarah Scaife2, Hoang Kim Phuc2, Osvaldo Marinotti2, Nijole Jasinskie2, Anthony A. James3,4,2, and Luke Alphey1,2,4,5 aajames@uci.edu or luke.alphey@oxitec.com

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Dengue and dengue hemorrhagic fever are increasing public health problems with an estimated 50–100 million new infections each year. Aedes aegypti is the major vector of dengue viruses in its range and control of this mosquito would reduce significantly human morbidity and mortality. Present mosquito control methods are not sufficiently effective and new approaches are needed urgently. A “sterile-male-release” strategy based on the release of mosquitoes carrying a conditional dominant lethal gene is an attractive new control methodology. Transgenic strains of Aedes aegypti were engineered to have a repressible female-specific flightless phenotype using either two separate transgenes or a single transgene, based on the use of a female-specific indirect flight muscle promoter from the Aedes aegypti Actin-4 gene. These strains eliminate the need for sterilization by irradiation, permit male-only release (“genetic sexing”), and enable the release of eggs instead of adults. Furthermore, these strains are expected to facilitate area-wide control or elimination of dengue if adopted as part of an integrated pest management strategy.

PNAS March 9, 2010 vol. 107 no. 10 4550-4554
http://www.pnas.org/content/107/10/4550.abstract?etoc
9. Drosophila Parkin requires PINK1 for mitochondrial translocation and ubiquitinates Mitofusin

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Loss of the E3 ubiquitin ligase Parkin causes early onset Parkinson's disease, a neurodegenerative disorder of unknown etiology. Parkin has been linked to multiple cellular processes including protein degradation, mitochondrial homeostasis, and autophagy; however, its precise role in pathogenesis is unclear. Recent evidence suggests that Parkin is recruited to damaged mitochondria, possibly affecting mitochondrial fission and/or fusion, to mediate their autophagic turnover. The precise mechanism of recruitment and the ubiquitination target are unclear. Here we show in Drosophila cells that PINK1 is required to recruit Parkin to dysfunctional mitochondria and promote their degradation. Furthermore, PINK1 and Parkin mediate the ubiquitination of the profusion factor Mfn on the outer surface of mitochondria. Loss of Drosophila PINK1 or parkin causes an increase in Mfn abundance in vivo and concomitant elongation of mitochondria. These findings provide a molecular mechanism by which the PINK1/Parkin pathway affects mitochondrial fission/fusion as suggested by previous genetic interaction studies. We hypothesize that Mfn ubiquitination may provide a mechanism by which terminally damaged mitochondria are labeled and sequestered for degradation by autophagy.

PNAS March 16, 2010 vol. 107 no. 11 5018-5023
http://www.pnas.org/content/107/11/5018.abstract?etoc

10. A Peroxidase/Dual Oxidase System Modulates Midgut Epithelial Immunity in Anopheles gambiae

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Extracellular matrices in diverse biological systems are cross-linked by dityrosine covalent bonds catalyzed by the peroxidase/oxidase system. We show that a peroxidase, secreted by the Anopheles gambiae midgut, and dual oxidase form a dityrosine network that decreases gut permeability to immune elicitors. This network protects the microbiota by preventing activation of epithelial immunity. It also provides a suitable environment for malaria parasites to develop within the midgut lumen without inducing nitric oxide synthase expression. Disruption of this barrier results in strong and effective pathogen-specific immune responses.

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http://www.sciencemag.org/cgi/content/abstract/327/5973/1644?sa_campaign=Email/toc/26-March-2010/10.1126/science.1184008

11. Egg attachment of the asparagus beetle Crioceris asparagi to the crystalline waxy surface of Asparagus officinalis

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Plant surfaces covered with crystalline epicuticular waxes are known to be anti-adhesive, hardly wettable and preventing insect attachment. But there are insects that are capable of gluing their eggs to these surfaces by means of proteinaceous secretions. In this study, we analysed the bonding region between the eggs of *Crioceris asparagi* and the plant surface of *Asparagus officinalis* using light and cryo-scanning electron microscopy. The wettability of the plant surface by egg secretion was compared with that by Aqua Millipore water, aqueous sugar solution and chicken egg white. Furthermore, the force required to remove *C. asparagi* eggs from the plant surface was measured, in order to evaluate the egg's bonding strength. Mean pull-off force was 14.7 mN, which is about 8650 times higher than the egg weight. Egg glue was observed spreading over the wax crystal arrays on the plant cladophyll and wetting them. Similar wetting behaviour on the *A. officinalis* surface was observed for chicken egg white. Our results support the hypothesis that the mechanism of insect egg adhesion on micro- and nanostructured hydrophobic plant surfaces is related to the proteinaceous nature of adhesive secretions of insect eggs. The secretion wets superhydrophobic surfaces and after solidifying builds up a composite, consisting of the solidified glue and wax crystals, at the interface between the egg and plant cuticle.

Proc. R. Soc. B 22 March 2010 vol. 277 no. 1683 895-903
http://rspb.royalsocietypublishing.org/content/277/1683/895.abstract

**Insect Chemoreception**

**12. Odorant reception in the malaria mosquito *Anopheles gambiae***

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The mosquito *Anopheles gambiae* is the major vector of malaria in sub-Saharan Africa. It locates its human hosts primarily through olfaction, but little is known about the molecular basis of this process. Here we functionally characterize the *Anopheles gambiae* odorant receptor (AgOr) repertoire. We identify receptors that respond strongly to components of human odour and that may act in the process of human recognition. Some of these receptors are narrowly tuned, and some salient odorants elicit strong responses from only one or a few receptors, suggesting a central role for specific transmission channels in human host-seeking behaviour. This analysis of the *Anopheles gambiae* receptors permits a comparison with the corresponding *Drosophila melanogaster* odorant receptor repertoire. We find that odorants are differentially encoded by the two species in ways consistent with their ecological needs. Our analysis of the *Anopheles gambiae* repertoire identifies receptors that may be useful targets for controlling the transmission of malaria.

http://www.nature.com/nature/journal/v464/n7285/abs/nature08834.html?lang=en

**13. Molecular basis of odor coding in the malaria vector mosquito *Anopheles gambiae***

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A systematic functional analysis across much of the conventional *Anopheles gambiae* odorant receptor (AgOR) repertoire was carried out in *Xenopus* oocytes using two-electrode, voltage-clamp electrophysiology. The resulting data indicate that each AgOR manifests a distinct odor-response profile and tuning breadth. The large diversity of tuning responses ranges from AgORs that are responsive to a single or small number of odorants (specialists) to more broadly tuned receptors (generalists). Several AgORs were identified that respond robustly to a range of human volatiles that may play a critical role in anopheline host selection. AgOR responses were analyzed further by constructing a multidimensional odor space representing the relationships between odorants and AgOR responses. Within this space, the distance between odorants is related to both chemical class and concentration and may correlate with olfactory discrimination. This study provides a comprehensive overview of olfactory coding mechanisms of *An. gambiae* that ultimately may aid in fostering the design and development of olfactory-based strategies for reducing the transmission of malaria and other mosquito-borne diseases.

PNAS March 2, 2010 vol. 107 no. 9 4418-4423
http://www.pnas.org/content/107/9/4418.abstract

**Insect Development**

**14. MAPK Substrate Competition Integrates Patterning Signals in the *Drosophila* Embryo**

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**Highlights** Spatial pattern of MAPK signaling in the early *Drosophila* embryo exhibits AP asymmetry. Bcd is a competitive inhibitor of MAPK-mediated downregulation of Cic. Hunchback is a new substrate of MAPK in the embryo. MAPK substrate competition is a new mechanism for patterning signal integration

**Summary** Terminal regions of the *Drosophila* embryo are patterned by the localized activation of the mitogen-activated protein kinase (MAPK) pathway [1]. This depends on the MAPK-mediated downregulation of Capicua (Cic), a repressor of the terminal gap genes [2,3,2,3]. We establish that downregulation of Cic is antagonized by the anterior patterning morphogen Bicoid (Bcd). We demonstrate that this effect does not depend on transcriptional activity of Bcd and provide evidence suggesting that Bcd, a direct substrate of MAPK, decreases the availability of MAPK for its other substrates, such as Cic. Based on the quantitative analysis of MAPK signaling in multiple mutants, we propose that MAPK substrate competition coordinates the actions of the anterior and terminal patterning systems. In addition, we identify Hunchback as a novel target of MAPK phosphorylation that can account for the previously described genetic interaction between the posterior and terminal systems [4]. Thus, a common enzyme-substrate competition mechanism can integrate the actions of the anterior, posterior, and terminal patterning signals. Substrate competition can be a general signal integration strategy in networks where enzymes, such as MAPK, interact with their multiple regulators and targets [5,6,7,8,9,10].

Current Biology, *Volume 20, Issue 5*, 446-451, 18 February 2010
http://www.cell.com/current-biology/abstract/S0960-9822(10)00058-8

**15. Retinoids Regulate a Developmental Checkpoint for Tissue Regeneration in *Drosophila***

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**Highlights** Irradiation of *Drosophila* larvae or damage to their imaginal discs delays pupariation. This delay operates like a checkpoint mechanism and allows for regenerative growth. Synthesis of the peptide PTTH, which promotes ecdysone release, is delayed. Retinoids function in the pathway that links tissue damage to developmental delay

**Summary** Damage to *Drosophila* imaginal discs elicits a robust regenerative response from the surviving tissue [1,2,3,4]. However, as in other organisms, developmental progression and differentiation can restrict the regenerative capacity of *Drosophila* tissues. Experiments in *Drosophila* and other holometabolous insects have demonstrated that either damage to imaginal tissues [5,6,5,6] or transplantation of a damaged imaginal disc [7,8,7,8] delays the onset of metamorphosis. Therefore, in *Drosophila* there appears to be a mechanism that senses tissue damage and extends the larval phase to coordinate tissue regeneration with the overall developmental program of the organism. However, how such a pathway functions remains unknown. Here we demonstrate that a developmental checkpoint extends larval growth after imaginal disc damage by inhibiting the transcription of the gene encoding PTTH, a neuropeptide that promotes the release of the steroid hormone ecdysone. Using a genetic screen, we identify a previously unsuspected role for retinoid biosynthesis in regulating PTTH expression and delaying development in response to tissue damage. Retinoid signaling plays an important but poorly defined role in several vertebrate regeneration models [9,10,11]. Our findings demonstrate that retinoid biosynthesis in *Drosophila* is important for the maintenance of a condition that is permissive for regenerative growth.

Current Biology, *Volume 20, Issue 5*, 458-463, 04 March 2010
http://www.cell.com/current-biology/abstract/S0960-9822(10)00080-1

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**16. Prioritization of Competing Damage and Developmental Signals by Migrating Macrophages in the *Drosophila* Embryo**

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**Highlights** The immediate damage signal that attracts hemocytes to wounds is H$_2$O$_2$. In the early embryo, hemocytes are refractile to wounds and prioritize guidance cues. Apoptotic signals override developmental cues even during the wound refractile period.

**Summary** The function of immune cells is critically dependent on their capacity to respond to a complex series of navigational cues that enable them to home to various organ sites in the body or to respond to inflammatory cues such as those released at sites of tissue damage. From early embryonic stages, immune cells are faced with a barrage of signals that will not all be directing the cell to do the same thing. Here we use the *Drosophila* embryo to investigate how hemocytes (*Drosophila* macrophages), are able to prioritize key guidance signals and ignore others so that they are not pulled every which way. We identify the immediate wound attractant signal as H$_2$O$_2$ and investigate how *Drosophila* macrophages respond to competing guidance cues—those emanating from a wound—versus standard developmental guidance cues, as well as those signals drawing cells toward neighboring dying cells. We reveal a hierarchy of responsiveness to attractant cues that varies over time and we identify why there is a wound refractile period early in embryonic development when macrophages cannot be distracted from their developmental migratory pathway to a site of tissue damage.

Current Biology, *Volume 20, Issue 5*, 464-470, 25 February 2010
http://www.cell.com/current-biology/abstract/S0960-9822(10)00090-4
17. Differential requirement of Salvador-Warts-Hippo pathway members for organ size control in Drosophila melanogaster

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The Salvador-Warts-Hippo (SWH) pathway contains multiple growth-inhibitory proteins that control organ size during development by limiting activity of the Yorkie oncoprotein. Increasing evidence indicates that these growth inhibitors act in a complex network upstream of Yorkie. This complexity is emphasised by the distinct phenotypes of tissue lacking different SWH pathway genes. For example, eye tissue lacking the core SWH pathway components salvador, warts or hippo is highly overgrown and resistant to developmental apoptosis, whereas tissue lacking fat or expanded is not. Here we explore the relative contribution of SWH pathway proteins to organ size control by determining their temporal activity profile throughout Drosophila melanogaster eye development. We show that eye tissue lacking fat, expanded or discs overgrown displays elevated Yorkie activity during the larval growth phase of development, but not in the pupal eye when apoptosis ensues. Fat and Expanded do possess Yorkie-repressive activity in the pupal eye, but loss of fat or expanded at this stage of development can be compensated for by Merlin. Fat appears to repress Yorkie independently of Dachs in the pupal eye, which would contrast with the mode of action of Fat during larval development. Fat is more likely to restrict Yorkie activity in the pupal eye together with Expanded, given that pupal eye tissue lacking both these genes resembles that of tissue lacking either gene. This study highlights the complexity employed by different SWH pathway proteins to control organ size at different stages of development.

Development March 1, 2010 137, 735-743.
http://dev.biologists.org/content/137/5/735.abstract

18. Echinoid regulates Flamingo endocytosis to control ommatidial rotation in the Drosophila eye

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Planar cell polarity (PCP) refers to a second polarity axis orthogonal to the apicobasal axis in the plane of the epithelium. The molecular link between apicobasal polarity and PCP is largely unknown. During Drosophila eye development, differentiated photoreceptors form clusters that rotate independently of the surrounding interommatidial cells (ICs). Here, we demonstrate that both Echinoid (Ed), an adherens junction-associated cell adhesion molecule, and Flamingo (Fmi), a PCP determinant, are endocytosed via a clathrin-mediated pathway in ICs. Interestingly, we found that Ed binds the AP-2 adaptor and is required for the internalization of Fmi into ICs. Loss of ed led to increased amounts of Fmi on the cell membrane of non-rotating ICs and also to the misrotation of photoreceptor clusters. Importantly, overexpression of fmi in ICs alone was sufficient to cause misrotation of the adjacent photoreceptor clusters. Together, we propose that Ed, when internalized by AP-2, undergoes co-endocytosis with, and thereby decreases, Fmi levels on non-rotating ICs to permit correct rotation of ommatidial clusters. Thus, co-endocytosis of Ed and Fmi provides a link between apicobasal polarity and PCP.

Development March 1, 2010 137, 745-754.
19. *lethal giant larvae* is required with the *par* genes for the early polarization of the *Drosophila* oocyte

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Most cell types in an organism show some degree of polarization, which relies on a surprisingly limited number of proteins. The underlying molecular mechanisms depend, however, on the cellular context. Mutual inhibitions between members of the Par genes are proposed to be sufficient to polarize the *C. elegans* one-cell zygote and the *Drosophila* oocyte during mid-oogenesis. By contrast, the Par genes interact with cellular junctions and associated complexes to polarize epithelial cells. The Par genes are also required at an early step of *Drosophila* oogenesis for the maintenance of the oocyte fate and its early polarization. Here we show that the Par genes are not sufficient to polarize the oocyte early and that the activity of the tumor-suppressor gene *lethal giant larvae* (*lgl*) is required for the posterior translocation of oocyte-specific proteins, including germline determinants. We also found that Lgl localizes asymmetrically within the oocyte and is excluded from the posterior pole. We further demonstrate that phosphorylation of Par-1, Par-3 (Bazooka) and Lgl is crucial to regulate their activity and localization in vivo and describe, for the first time, adherens junctions located around the ring canals, which link the oocyte to the other cells of the germline cyst. However, null mutations in the *DE-cadherin* gene, which encodes the main component of the zonula adherens, do not affect the early polarization of the oocyte. We conclude that, despite sharing many similarities with other model systems at the genetic and cellular levels, the polarization of the early oocyte relies on a specific subset of polarity proteins.

Development March 1, 2010 137, 815-824. http://dev.biologists.org/content/137/5/815.abstract

20. *giant* is a bona fide gap gene in the intermediate germ band insect, *Oncopeltus fasciatus*

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*Drosophila* undergoes a form of development termed long germ segmentation, where all segments are specified nearly simultaneously so that by the blastoderm stage, the entire body plan has been determined. This mode of segmentation is evolutionarily derived. Most insects undergo short or intermediate germ segmentation, where only anterior segments are specified early, and posterior segments are sequentially specified during germ band elongation. These embryological differences imply that anterior and posterior segments might rely upon different molecular mechanisms. In *Drosophila*, embryos mutant for *giant* show a gap in the anterior as well fusions of several abdominal segments. In *Tribolium*, a short germ beetle, *giant* is required for segmental identity, but not formation, in gnathal segments and also for segmentation of the entire abdomen. This raises the possibility that *giant* might not act as a gap gene in short and intermediate germ insects. *Oncopeltus fasciatus* is an intermediate germ insect that is an outgroup to the clade containing *Drosophila* and *Tribolium*. We cloned the *Oncopeltus* homolog of *giant* and determined its expression and function during segmentation. We find that *Oncopeltus giant* is a canonical gap gene in the maxillary and labial segments and also plays a gap-like role in the first four abdominal segments. Our results suggest that *giant* was a bona fide gap gene in the ancestor of these insects with this role being
lost in the lineage leading towards Tribolium. This highlights the conservation of anterior patterning and evolutionary plasticity of the genetic regulation controlling posterior segmentation, even in short and intermediate germ insects.

http://dev.biologists.org/content/137/5/835.abstract

21. Systematic genetic analysis of muscle morphology and function in Drosophila

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Systematic genetic approaches have provided deep insight into the molecular and cellular mechanisms that operate in simple unicellular organisms. For multicellular organisms, however, the pleiotropy of gene function has largely restricted such approaches to the study of early embryogenesis. With the availability of genome-wide transgenic RNA interference (RNAi) libraries in Drosophila1,2, it is now possible to perform a systematic genetic dissection of any cell or tissue type at any stage of the lifespan. Here we apply these methods to define the genetic basis for formation and function of the Drosophila muscle. We identify a role in muscle for 2,785 genes, many of which we assign to specific functions in the organization of muscles, myofibrils or sarcomeres. Many of these genes are phylogenetically conserved, including genes implicated in mammalian sarcomere organization and human muscle diseases.

http://www.nature.com/nature/journal/v464/n7286/abs/nature08799.html?lang=en

22. Sestrin as a Feedback Inhibitor of TOR That Prevents Age-Related Pathologies

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Sestrins are conserved proteins that accumulate in cells exposed to stress, potentiate adenosine monophosphate–activated protein kinase (AMPK), and inhibit activation of target of rapamycin (TOR). We show that the abundance of Drosophila sestrin (dSesn) is increased upon chronic TOR activation through accumulation of reactive oxygen species that cause activation of c-Jun amino-terminal kinase and transcription factor Forkhead box O (FoxO). Loss of dSesn resulted in age-associated pathologies including triglyceride accumulation, mitochondrial dysfunction, muscle degeneration, and cardiac malfunction, which were prevented by pharmacological activation of AMPK or inhibition of TOR. Hence, dSesn appears to be a negative feedback regulator of TOR that integrates metabolic and stress inputs and prevents pathologies caused by chronic TOR activation that may result from diminished autophagic clearance of damaged mitochondria, protein aggregates, or lipids.

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Insect Ecology

23. Insect overwintering in a changing climate

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Insects are highly successful animals inhabiting marine, freshwater and terrestrial habitats from the equator to the poles. As a group, insects have limited ability to regulate their body temperature and have thus required a range of strategies to support life in thermally stressful environments, including behavioural avoidance through migration and seasonal changes in cold tolerance. With respect to overwintering strategies, insects have traditionally been divided into two main groups: freeze tolerant and freeze avoiding, although this simple classification is underpinned by a complex of interacting processes, i.e. synthesis of ice nucleating agents, cryoprotectants, antifreeze proteins and changes in membrane lipid composition. Also, in temperate and colder climates, the overwintering ability of many species is closely linked to the diapause state, which often increases cold tolerance ahead of temperature-induced seasonal acclimatisation. Importantly, even though most species can invoke one or both of these responses, the majority of insects die from the effects of cold rather than freezing. Most studies on the effects of a changing climate on insects have focused on processes that occur predominantly in summer (development, reproduction) and on changes in distributions rather than winter survival per se. For species that routinely experience cold stress, a general hypothesis would be that predicted temperature increases of 1°C to 5°C over the next 50-100 years would increase winter survival in some climatic zones. However, this is unlikely to be a universal effect. Negative impacts may occur if climate warming leads to a reduction or loss of winter snow cover in polar and sub-polar areas, resulting in exposure to more severe air temperatures, increasing frequency of freeze—thaw cycles and risks of ice encasement. Likewise, whilst the dominant diapause-inducing cue (photoperiod) will be unaffected by global climate change, higher temperatures may modify normal rates of development, leading to a decoupling of synchrony between diapause-sensitive life-cycle stages and critical photoperiods for diapause induction. In terms of climate warming and potential heat stress, the most recent predictions of summer temperatures in Europe of 40°C or higher in 50-75 years, are close to the current upper lethal limit of some insects. Long-term data sets on insect distributions and the timing of annual migrations provide strong evidence for ‘positive’ responses to higher winter temperatures over timescales of the past 20-50 years in North America, Europe and Asia.

http://jeb.biologists.org/cgi/content/abstract/213/6/980?etoc

24. A multi-scale study of Orthoptera species richness and human population size controlling for sampling effort

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Recent large-scale studies have shown that biodiversity-rich regions also tend to be densely populated areas. The most obvious explanation is that biodiversity and human beings tend to match the distribution of energy availability, environmental stability...
and/or habitat heterogeneity. However, the species–people correlation can also be an artefact, as more populated regions could show more species because of a more thorough sampling. Few studies have tested this sampling bias hypothesis. Using a newly collated dataset, we studied whether Orthoptera species richness is related to human population size in Italy’s regions (average area 15,000 km$^2$) and provinces (2,900 km$^2$). As expected, the observed number of species increases significantly with increasing human population size for both grain sizes, although the proportion of variance explained is minimal at the provincial level. However, variations in observed Orthoptera species richness are primarily associated with the available number of records, which is in turn well correlated with human population size (at least at the regional level). Estimated Orthoptera species richness (Chao2 and Jackknife) also increases with human population size both for regions and provinces. Both for regions and provinces, this increase is not significant when controlling for variation in area and number of records. Our study confirms the hypothesis that broad-scale human population–biodiversity correlations can in some cases be artefactual. More systematic sampling of less studied taxa such as invertebrates is necessary to ascertain whether biogeographical patterns persist when sampling effort is kept constant or included in models.

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http://springerlink.com/content/t486x61284r20q7p/?p=63433513e7834703a325b7228162e0ed&pi=2

25. Molecular diagnosis of a previously unreported predator–prey association in coffee: *Karnyothrips flavipes* Jones (Thysanoptera: Phlaeothripidae) predation on the coffee berry borer

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The coffee berry borer, *Hypothenemus hampei*, is the most important pest of coffee throughout the world, causing losses estimated at US $500 million/year. The thrips *Karnyothrips flavipes* was observed for the first time feeding on immature stages of *H. hampei* in April 2008 from samples collected in the Kisii area of Western Kenya. Since the trophic interactions between *H. hampei* and *K. flavipes* are carried out entirely within the coffee berry, and because thrips feed by liquid ingestion, we used molecular gut-content analysis to confirm the potential role of *K. flavipes* as a predator of *H. hampei* in an organic coffee production system. Species-specific COI primers designed for *H. hampei* were shown to have a high degree of specificity for *H. hampei* DNA and did not produce any PCR product from DNA templates of the other insects associated with the coffee agroecosystems. In total, 3,327 *K. flavipes* emerged from 17,792 *H. hampei*-infested berries collected from the field between April and September 2008. Throughout the season, 8.3% of *K. flavipes* tested positive for *H. hampei* DNA, although at times this figure approached 50%. Prey availability was significantly correlated with prey consumption, thus indicating the potential impact on *H. hampei* populations.

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http://springerlink.com/content/h084lp6572887824/?p=63433513e7834703a325b7228162e0ed&pi=5
26. Discovery of mycangia and the associated xylose-fermenting yeasts in stag beetles (Coleoptera: Lucanidae)

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Most wood-feeding insects need an association with microbes to utilize wood as food, and some have special organs to store and convey the microbes. We report here the discovery of the microbe-storage organ (mycangium) in stag beetles (Coleoptera: Lucanidae), which develop in decayed wood. The mycangium, which was discovered in the abdomen, is present in all adult females of 22 lucanid species examined in this study, but absent in adult males. By contrast, adult insects of both sexes of selected Passalidae, Geotrupidae, and Scarabaeidae, which are related to Lucanidae, lacked mycangia similar to those of the lucanid species. Yeast-like microbes were isolated from the mycangium of five lucanid species. DNA sequence analyses indicate that the microbes are closely related to the xylose-fermenting yeasts Pichia stipitis, Pichia segobiensis, or Pichia sp. known from the gut of a passalid species.

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http://springerlink.com/content/e26334114816w585/?p=63433513e7834703a325b7228162e0ed&pi=7

27. The alternative Pharaoh approach: stingless bees mummify beetle parasites alive

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Workers from social insect colonies use different defence strategies to combat invaders. Nevertheless, some parasitic species are able to bypass colony defences. In particular, some beetle nest invaders cannot be killed or removed by workers of social bees, thus creating the need for alternative social defence strategies to ensure colony survival. Here we show, using diagnostic radioentomology, that stingless bee workers (Trigona carbonaria) immediately mummify invading adult small hive beetles (Aethina tumida) alive by coating them with a mixture of resin, wax and mud, thereby preventing severe damage to the colony. In sharp contrast to the responses of honeybee and bumblebee colonies, the rapid live mummification strategy of T. carbonaria effectively prevents beetle advancements and removes their ability to reproduce. The convergent evolution of mummification in stingless bees and encapsulation in honeybees is another striking example of co-evolution between insect societies and their parasites.

Naturwissenschaften Volume 97, Number 3 / March, 2010 319-323
http://springerlink.com/content/v6n2t6516770t455/?p=63433513e7834703a325b7228162e0ed&pi=8

28. Activation of the immune system promotes insect dispersal in the wild
Dispersal has important ecological and evolutionary consequences but is a poorly understood behaviour. We experimentally tested whether activation of the immune system affects dispersal in male damselflies, *Calopteryx virgo*, from three natural populations. We show that males that contained an experimentally inserted artificial pathogen, a nylon monofilament implant, had higher dispersal rates and flew further than control males, but not further than sham manipulated males. Our data suggest that dispersal may reduce the risk of further infections if immune system activation indicates high parasite infection risk in the present habitat. We, thus, suggest that parasites may play an important role in the evolution of host dispersal.

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http://www.springerlink.com/content/r8130rv516q75179/

29. Developmental plasticity and reduced susceptibility to natural enemies following host plant defoliation in a specialized herbivore

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Host-specific phytophagous insects that are short lived and reliant on ephemeral plant tissues provide an excellent system in which to investigate the consequences of disruption in the timing of resource availability on consumer populations and their subsequent interactions with higher trophic levels. The specialist herbivore, *Belonocnema treatae* (Hymenoptera: Cynipidae) induces galls on only newly flushed leaves of live oak, *Quercus fusiformis*. In central Texas (USA) episodic defoliation of the host creates variation in the timing of resource availability and results in heterogeneous populations of *B. treatae* that initiate development at different times. We manipulated the timing of leaf flush in live oak via artificial defoliation to test the hypothesis that a 6- to 8-week delay in the availability of resources alters the timing of this gall former’s life cycle events, performance and survivorship on its host, and susceptibility to natural enemies. *B. treatae* exhibits plasticity in development time, as the interval from egg to emergence was significantly reduced when gallers oviposited into the delayed leaf flush. As a consequence, the phenologies of gall maturation and adult emergence remain synchronized in spite of variation in the timing of resource availability. Per capita gall production and gall-former performance are not significantly affected by the timing of resource availability. The timing of resource availability and natural enemies interact, however, to produce strong effects on survivorship: when exposed to natural enemies, *B. treatae* developing in galls initiated by delayed oviposition exhibited an order-of-magnitude increase in survivorship. Developmental plasticity allows this gall former to circumvent disruptions in resource availability, maintain synchrony of life cycle events, and results in reduced vulnerability to natural enemies following defoliation of the host plant.

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http://www.springerlink.com/content/hq3l741731u83186/?p=261931e4e29e467f976c594e432fd0718&pi=13

30. Natural enemy diversity reduces temporal variability in wasp but not bee parasitism

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Biodiversity may enhance and stabilise ecosystem functioning, but little evidence exists for diversity–function relationships involving multitrophic interactions in real landscapes. In multitrophic communities diversity may vary at different trophic levels, with either synergistic or antagonistic effects on ecosystem functioning. Intensification of land-use systems is often found to reduce diversity, which in turn may lead to reduced associated ecological functions in natural food webs, such as host-parasite interactions. In this study we investigated the relationship between the number of natural enemy and host species and the mean rate and temporal variability of parasitism (inverse of stability), along an intensification gradient of coffee agroforests in Ecuador. We used standardised trap nests for bees and wasps and their natural enemies in 14 agroforests, and evaluated these monthly over a period of 17 months. We found that parasitism rates of wasps and bees increased with increasing number of enemy species and decreased with increasing number of host species. Temporal variability in parasitism rates decreased with increasing number of enemy species and increased with temporal variability in enemy species richness; however, these effects were restricted to wasp hosts. Intensification of agroforests did not significantly affect species richness of hosts or enemies or their relation to parasitism and its temporal variability. We conclude that high enemy diversity may enhance parasitism rates and that high host diversity may provide resistance against consumption. Furthermore, we show that a diverse and stable enemy community may also have a stabilizing effect on parasitism rates. However, these effects may be host-guild specific, as these relations were restricted to wasps.

Oecologia Volume 162, Number 3 / March, 2010 755-762
http://www.springerlink.com/content/v11n730q75hp6444/?p=251a9eb802594531a39fde9e0bab39edd&pi=20

31. Repeated stress exposure results in a survival–reproduction trade-off in Drosophila melanogaster
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While insect cold tolerance has been well studied, the vast majority of work has focused on the effects of a single cold exposure. However, many abiotic environmental stresses, including temperature, fluctuate within an organism's lifespan. Given that organisms may trade-off survival at the cost of future reproduction, we investigated the effects of multiple cold exposures on survival and fertility in the model organism Drosophila melanogaster. We found that multiple cold exposures significantly decreased mortality compared with the same length of exposure in a single sustained bout, but significantly decreased fecundity (as measured by $r$, the intrinsic rate of increase) as well, owing to a shift in sex ratio. This change was reflected in a long-term decrease in glycogen stores in multiply exposed flies, while a brief effect on triglyceride stores was observed, suggesting flies are reallocating energy stores. Given that many environments are not static, this trade-off indicates that investigating the effects of repeated stress exposure is important for understanding and predicting physiological responses in the wild.

Proc. R. Soc. B 22 March 2010 vol. 277 no. 1683 963-969
http://rspb.royalsocietypublishing.org/content/277/1683/963.abstract

Insect Evolution

32. Adaptation to desiccation fails to generate pre- and postmating isolation in replicate Drosophila melanogaster laboratory populations
Many laboratory speciation experiments have raised allopatric populations in different environments to determine whether reproductive isolation evolves as a byproduct of adaptation (a form of ecological speciation). Few, however, have addressed the evolution of both pre- and postmating isolation or investigated the conditions affecting the process. We present results of an evolution experiment in which 12 lines of *Drosophila melanogaster* were derived from a common population and then independently evolved for more than 57 generations under alternative selection treatments. Six "desiccation" populations had access to food and water removed during a period of their adult lives generating strong desiccation selection, and six "starvation" populations had access to food but not water removed for the same period, generating a mild starvation stress. Substantial divergence of cuticular hydrocarbons occurred between the desiccation and starvation populations, key traits that have been implicated in sexual isolation in *Drosophila*. Despite this divergence, there was no detectable premating isolation between desiccation and starvation populations and postmating isolation was asymmetrical: the fitness of F1 hybrids was reduced in the desiccation but not the starvation environment. This asymmetry was likely caused by the absence of divergent selection: adaptation to desiccation appears to have come at no cost to performance in the starvation environment. Novel environments are thought to promote the evolution of reproductive isolation. Understanding the conditions that favor or hamper this remains a key challenge for speciation research.

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http://www3.interscience.wiley.com/journal/122638315/abstract

33.FEATURE THEORY AND THE TWO-STEP HYPOTHESIS OF MÜLLERIAN MIMICRY EVOLUTION

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The two-step hypothesis of Müllerian mimicry evolution states that mimicry starts with a major mutational leap between adaptive peaks, followed by gradual fine-tuning. The hypothesis was suggested to solve the problem of apostatic selection producing a valley between adaptive peaks, and appears reasonable for a one-dimensional phenotype. Extending the hypothesis to the realistic scenario of multidimensional phenotypes controlled by multiple genetic loci can be problematic, because it is unlikely that major mutational leaps occur simultaneously in several traits. Here we consider the implications of predator psychology on the evolutionary process. According to feature theory, single prey traits may be used by predators as features to classify prey into discrete categories. A mutational leap in such a trait could initiate mimicry evolution. We conducted individual-based evolutionary simulations in which virtual predators both categorize prey according to features and generalize over total appearances. We found that an initial mutational leap toward feature similarity in one dimension facilitates mimicry evolution of multidimensional traits. We suggest that feature-based predator categorization together with predator generalization over total appearances solves the problem of applying the two-step hypothesis to complex phenotypes, and provides a basis for a theory of the evolution of mimicry rings.

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http://www3.interscience.wiley.com/journal/122613653/abstract

34.Multiple aquatic invasions by an endemic, terrestrial Hawaiian moth radiation
Insects are the most diverse form of life on the planet, dominating both terrestrial and freshwater ecosystems, yet no species has a life stage able to breathe, feed, and develop either continually submerged or without access to water. Such truly amphibious insects are unrecorded. In mountain streams across the Hawaiian Islands, some caterpillars in the endemic moth genus *Hyposmocoma* are truly amphibious. These larvae can breathe and feed indefinitely both above and below the water’s surface and can mature completely submerged or dry. Remarkably, a molecular phylogeny based on 2,243 bp from both nuclear (elongation factor 1α and carbomoylphosphate synthase) and mitochondrial (cytochrome oxidase I) genes representing 216 individuals and 89 species of *Hyposmocoma* reveals that this amphibious lifestyle is an example of parallel evolution and has arisen from strictly terrestrial clades at least three separate times in the genus starting more than 6 million years ago, before the current high islands existed. No other terrestrial genus of animals has sponsored so many independent aquatic invasions, and no other insects are able to remain active indefinitely above and below water. Why and how *Hyposmocoma*, an overwhelmingly terrestrial group, repeatedly evolved unprecedented aquatic species is unclear, although there are many other evolutionary anomalies across the Hawaiian archipelago. The uniqueness of the community assemblages of Hawaii’s isolated biota is likely critical in generating such evolutionary novelty because this amphibious ecology is unknown anywhere else.

PNAS March 30, 2010 vol. 107 no. 13 5903-5906
http://www.pnas.org/content/107/13/5903.abstract?etoc

**Insect Genetics**

35.A Neo-Sex Chromosome That Drives Postzygotic Sex Determination in the Hessian Fly (*Mayetiola destructor*)

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Two nonoverlapping autosomal inversions defined unusual neo-sex chromosomes in the Hessian fly (*Mayetiola destructor*). Like other neo-sex chromosomes, these were normally heterozygous, present only in one sex, and suppressed recombination around a sex-determining master switch. Their unusual properties originated from the anomalous Hessian fly sex determination system in which postzygotic chromosome elimination is used to establish the sex-determining karyotypes. This system permitted the evolution of a master switch (*Chromosome maintenance, Cm*) that acts maternally. All of the offspring of females that carry *Cm*-associated neo-sex chromosomes attain a female-determining somatic karyotype and develop as females. Thus, the chromosomes act as maternal effect neo-W’s, or W-prime (W’) chromosomes, where ZW’ females mate with ZZ males to engender female-producing (ZW’) and male-producing (ZZ) females in equal numbers. Genetic mapping and physical mapping identified the inversions. Their distribution was determined in nine populations. Experimental matings established the association of the inversions with *Cm* and measured their recombination suppression. The inversions are the functional equivalent of the sciarid X-prime chromosomes. We speculate that W’ chromosomes exist in a variety of species that produce unisexual broods.

Genetics, Vol. 184, 769-777, March 2010
http://www.genetics.org/cgi/content/abstract/184/3/769?etoc
36. Simple Y-Autosomal Incompatibilities Cause Hybrid Male Sterility in Reciprocal Crosses Between Drosophila virilis and D. americana

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Postzygotic reproductive isolation evolves when hybrid incompatibilities accumulate between diverging populations. Here, I examine the genetic basis of hybrid male sterility between two species of Drosophila, Drosophila virilis and D. americana. From these analyses, I reach several conclusions. First, neither species carries any autosomal dominant hybrid male sterility alleles: reciprocal F₁ hybrid males are perfectly fertile. Second, later generation (backcross and F₂) hybrid male sterility between D. virilis and D. americana is not polygenic. In fact, I identified only three genetically independent incompatibilities that cause hybrid male sterility. Remarkably, each of these incompatibilities involves the Y chromosome. In one direction of the cross, the D. americana Y is incompatible with recessive D. virilis alleles at loci on chromosomes 2 and 5. In the other direction, the D. virilis Y chromosome causes hybrid male sterility in combination with recessive D. americana alleles at a single QTL on chromosome 5. Finally, in contrast with findings from other Drosophila species pairs, the X chromosome has only a modest effect on hybrid male sterility between D. virilis and D. americana.

Genetics, Vol. 184, 779-787, March 2010
http://www.genetics.org/cgi/content/abstract/184/3/779?etoc

37. Drosophila Raf's N Terminus Contains a Novel Conserved Region and Can Contribute to Torso RTK Signaling

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Drosophila Raf (DRaf) contains an extended N terminus, in addition to three conserved regions (CR1–CR3); however, the function(s) of this N-terminal segment remains elusive. In this article, a novel region within Draf's N terminus that is conserved in BRaf proteins of vertebrates was identified and termed conserved region N-terminal (CRN). We show that the N-terminal segment can play a positive role(s) in the Torso receptor tyrosine kinase pathway in vivo, and its contribution to signaling appears to be dependent on the activity of Torso receptor, suggesting this N-terminal segment can function in signal transmission. Circular dichroism analysis indicates that DRaf's N terminus (amino acids 1–117) including CRN (amino acids 19–77) is folded in vitro and has a high content of helical secondary structure as predicted by proteomics tools. In yeast two-hybrid assays, stronger interactions between DRaf's Ras binding domain (RBD) and the small GTPase Ras1, as well as Rap1, were observed when CRN and RBD sequences were linked. Together, our studies suggest that DRaf's extended N terminus may assist in its association with the upstream activators (Ras1 and Rap1) through a CRN-mediated mechanism(s) in vivo.

Genetics, Vol. 184, 717-729, March 2010
http://www.genetics.org/cgi/content/abstract/184/3/717?etoc

38. The Chromatin-Remodeling Protein Osa Interacts With CyclinE in Drosophila Eye Imaginal Discs

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Coordinating cell proliferation and differentiation is essential during organogenesis. In Drosophila, the photoreceptor, pigment, and support cells of the eye are specified in an orchestrated wave as the morphogenetic furrow passes across the eye imaginal disc. Cells anterior of the furrow are not yet differentiated and remain mitotically active, while most cells in the furrow arrest at G1 and adopt specific ommatidial fates. We used microarray expression analysis to monitor changes in transcription at the furrow and identified genes whose expression correlates with either proliferation or fate specification. Some of these are members of the Polycomb and Trithorax families that encode epigenetic regulators. Osa is one; it associates with components of the Drosophila SWI/SNF chromatin-remodeling complex. Our studies of this Trithorax factor in eye development implicate Osa as a regulator of the cell cycle: Osa overexpression caused a small-eye phenotype, a reduced number of M- and S-phase cells in eye imaginal discs, and a delay in morphogenetic furrow progression. In addition, we present evidence that Osa interacts genetically and biochemically with CyclinE. Our results suggest a dual mechanism of Osa function in transcriptional regulation and cell cycle control.

39. Alternative Splicing Modulates Ubx Protein Function in Drosophila melanogaster

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The Drosophila Hox gene Ultrabithorax (Ubx) produces a family of protein isoforms through alternative splicing. Isoforms differ from one another by the presence of optional segments—encoded by individual exons—that modify the distance between the homeodomain and a cofactor-interaction module termed the "YPWM" motif. To investigate the functional implications of Ubx alternative splicing, here we analyze the in vivo effects of the individual Ubx isoforms on the activation of a natural Ubx molecular target, the decapentaplegic (dpp) gene, within the embryonic mesoderm. These experiments show that the Ubx isoforms differ in their abilities to activate dpp in mesodermal tissues during embryogenesis. Furthermore, using a Ubx mutant that reduces the full Ubx protein repertoire to just one single isoform, we obtain specific anomalies affecting the patterning of anterior abdominal muscles, demonstrating that Ubx isoforms are not functionally interchangeable during embryonic mesoderm development. Finally, a series of experiments in vitro reveals that Ubx isoforms also vary in their capacity to bind DNA in presence of the cofactor Extradenticle (Exd). Altogether, our results indicate that the structural changes produced by alternative splicing have functional implications for Ubx protein function in vivo and in vitro. Since other Hox genes also produce splicing isoforms affecting similar protein domains, we suggest that alternative splicing may represent an underestimated regulatory system modulating Hox gene specificity during fly development.
Chemical recognition is essential for survival and reproduction. Adaptive evolution has resulted in diverse chemoreceptor families, in which polymorphisms contribute to individual variation in chemosensation. To gain insights into the genetic determinants of individual variation in odorant recognition, we measured olfactory responses to two structurally similar odorants in a population of wild-derived inbred lines of Drosophila melanogaster. Odorant-binding proteins (OBPs) are the first components of the insect olfactory system to encounter odorants. Previously four single-nucleotide polymorphisms (SNPs) in the Obp99 group were associated with variation in olfactory responses to benzaldehyde. Here, we identify six different SNPs that are associated with variation in responses to a structurally similar odorant, acetophenone, in the same Obp genes. Five SNPs are in coding regions of Obp99b and Obp99d and one SNP is in the 3'-untranslated region of Obp99a (A610G). We found that the 610G allele is associated with higher response scores to acetophenone than the 610A allele, but with lower expression of Obp99a, suggesting that binding of acetophenone to Obp99a might limit rather than facilitate access to odorant receptors. Our results show that overlapping sets of OBPs contribute to odorant recognition for structurally similar odorants, but that different SNPs are associated with odorant-specific individual variation. Thus, dual olfactory recognition where OBPs regulate odorant access to receptors may enhance olfactory discrimination.

The non-LTR retrotransposons forming Drosophila telomeres constitute a robust mechanism for telomere maintenance, one which has persisted since before separation of the extant Drosophila species. These elements in D. melanogaster differ from nontelomeric retrotransposons in ways that give insight into general telomere biology. Here, we analyze telomere-specific retrotransposons from D. virilis, separated from D. melanogaster by 40 to 60 million years, to evaluate the evolutionary divergence of their telomeric traits. The telomeric retrotransposon Het-A from D. melanogaster has an unusual promoter near its 3’ terminus that drives not the element in which it resides, but the adjacent downstream element in a head-to-tail array. An obvious benefit of this promoter is that it adds nonessential sequence to the 5’ end of each transcript, which is reverse transcribed and added to the chromosome. Because the 5’ end of each newly transposed element forms the end of the chromosome until another element transposes onto it, this nonessential sequence can buffer erosion of sequence essential for Het-A. Surprisingly, we have now found that Het-A in D. virilis has a promoter typical of non-LTR retrotransposons. This promoter adds no buffering sequence; nevertheless, the complete 5’ end of the element persists in telomere arrays, necessitating a more precise processing of the extreme end of the telomere in D. virilis.
Population dynamics and rapid spread of Cardinium, a bacterial endosymbiont causing cytoplasmic incompatibility in Encarsia pergandiella (Hymenoptera: Aphelinidae)

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Cytoplasmic incompatibility (CI) is a common phenotype of maternally inherited bacterial symbionts of arthropods; in its simplest expression, uninfected females produce few or no viable progeny when mated to infected males. Infected females thus experience a reproductive advantage relative to that of uninfected females, with the potential for the symbiont to spread rapidly. CI population dynamics are predicted to depend primarily on the strength of incompatibility, the fitness cost of the infection and how faithfully symbionts are inherited. Although the bacterial symbiont lineage Wolbachia has been most identified with the CI phenotype, an unrelated bacterium, Cardinium may also cause CI. In the first examination of population dynamics of CI-inducing Cardinium, we used population cages of the parasitic wasp Encarsia pergandiella (Hymenoptera: Aphelinidae) with varying initial infection frequencies to test a model of invasion. Cardinium was found to spread rapidly in all populations, even in cases where the initial infection frequency was well below the predicted invasion threshold frequency. The discrepancy between the modeled and actual results is best explained by weaker CI than measured in the lab and a cryptic fitness benefit to the infection.

Heredity (2010) 104, 239–246
http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009130a.html

The cys-loop ligand-gated ion channel gene superfamily of the parasitoid wasp, Nasonia vitripennis

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Members of the cys-loop ligand-gated ion channel (cysLGIC) superfamily mediate chemical neurotransmission and are studied extensively as potential targets of drugs used to treat neurological disorders, such as Alzheimer’s disease. Insect cys-loop LGICs also have central roles in the nervous system and are targets of highly successful insecticides. Here, we describe the cysLGIC superfamily of the parasitoid wasp, Nasonia vitripennis, which is emerging as a highly useful model organism and is deployed as a biological control of insect pests. The wasp superfamily consists of 26 genes, which is the largest insect cysLGIC superfamily characterized, whereas Drosophila melanogaster, Apis mellifera and Tribolium castaneum have 23, 21 and 24, respectively. As with Apis, Drosophila and Tribolium, Nasonia possesses ion channels predicted to be gated by acetylcholine, γ-amino butyric acid, glutamate and histamine, as well as orthologues of the Drosophila pH-sensitive chloride channel (pHCl), CG8916 and CG12344. Similar to other insects, wasp cysLGIC diversity is broadened by alternative splicing and RNA A-to-I editing, which may also serve to generate species-specific receptor isoforms. These findings on N. vitripennis enhance our understanding of cysLGIC functional genomics and provide a useful basis for the study of their function in the wasp model, as well as for the development of improved insecticides that spare a major beneficial insect species.

Heredity (2010) 104, 247–259
http://www.nature.com/hdy/journal/v104/n3/abs/hdy200997a.html
44. Evolution of sex-specific wing shape at the widerwing locus in four species of Nasonia

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How do morphological differences between species evolve at the genetic level? This study investigates the genetic basis of recent divergence in male wing size between species of the model parasitoid wasp Nasonia. The forewings of flightless Nasonia vitripennis males are 2.3 times smaller than males of their flighted sister species N. giraulti. We describe a major genetic contributor to this difference: the sex-specific widerwing (wdw) locus, which we have backcrossed from N. giraulti into N. vitripennis and mapped to an 0.9 megabase region of chromosome 1. This introgression of wdw from large-winged N. giraulti into small-winged N. vitripennis increases male but not female forewing width by 30% through wing region-specific size changes. Indirect evidence suggests that cell number changes across the wing explain the majority of the wdw wing-size difference, whereas changes in cell size are important in the center of the wing. Introgressing the same locus from the other species in the genus, N. longicornis and N. oneida, into N. vitripennis produces intermediate and large male wing sizes. To our knowledge, this is the first study to introgress a morphological quantitative trait locus (QTL) from multiple species into a common genetic background. Epistatic interactions between wdw and other QTL are also identified by introgressing wdw from N. vitripennis into N. giraulti. The main findings are (1) the changes at wdw have sex- and region-specific effects and could, therefore, be regulatory, (2) the wdw locus seems to be a co-regulator of cell size and cell number, and (3) the wdw locus has evolved different wing width effects in three species.

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45. The genetic basis of interspecies host preference differences in the model parasitoid Nasonia

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The genetic basis of host preference has been investigated in only a few species. It is relevant to important questions in evolutionary biology, including sympatric speciation, generalist versus specialist adaptation, and parasite–host co-evolution. Here we show that a major locus strongly influences host preference in Nasonia. Nasonia are parasitic wasps that utilize fly pupae; Nasonia vitripennis is a generalist that parasitizes a diverse set of hosts, whereas Nasonia giraulti specializes in Protocalliphora (bird blowflies). In laboratory choice experiments using Protocalliphora and Sarcophaga (flesh flies), N. vitripennis shows a preference for Sarcophaga, whereas N. giraulti shows a preference for Protocalliphora. Through a series of interspecies crosses, we have introgressed a major locus affecting host preference from N. giraulti into N. vitripennis. The N. giraulti allele is dominant and greatly increases preference for Protocalliphora pupae in the introgression line relative to the recessive N. vitripennis allele. Through the utilization of a Nasonia genotyping microarray, we have identified the introgressed region as 16Mb of chromosome 4, although a more complete analysis is necessary to determine the exact genetic architecture of host preference in the genus. To our knowledge, this is the first introgression of the host preference of one parasitoid species into another, as well as one of the few cases of introgression of a behavioral gene between species.

Heredity (2010) 104, 270–277
http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009145a.html
46. Behavioral and genetic characteristics of a new species of Nasonia

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Nasonia (Hymenoptera: Pteromalidae) is a genus of parasitoid wasps, which is fast emerging as a model system for evolutionary, genetic, developmental and host–endosymbiont interaction studies. In this study, we report a new species, *Nasonia oneida*, distinguish its behavioral, genetic and morphological features, and characterize its pre-mating and post-mating isolation with the other *Nasonia* species. Phylogenetic analyses indicate that *N. oneida* is the sister species to *Nasonia giraulti* with its own uniquely distinct cuticular hydrocarbon profiles, behavioral characteristics and subtle morphological differences. An important characteristic of *N. oneida* is the strong mate discrimination shown by the females against all the other *Nasonia* species. A genetic analysis of this phenotype by interspecies hybridization indicates that this strong discriminating phenotype is recessive. A formal species description of *N. oneida* Raychoudhury & Desjardins is also provided.

Heredity (2010) 104, 278–288
http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009147a.html

47. Behavioral and spermatogenic hybrid male breakdown in Nasonia

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Several reproductive barriers exist within the *Nasonia* species complex, including allopatry, pre-mating behavioral isolation, postzygotic inviability and *Wolbachia*-induced cytoplasmic incompatibility. Here we show that hybrid males suffer two additional reproductive disadvantages, an inability to properly court females and decreased sperm production. Hybrid behavioral sterility, characterized by a reduced ability of hybrids to perform necessary courtship behaviors, occurs in hybrids between two species of *Nasonia*. Hybrid males produced in crosses between *N. vitripennis* and *N. giraulti* courted females at a reduced frequency (23–69%), compared with wild-type *N. vitripennis* and *N. giraulti* males (>93%). Reduced courtship frequency was not a simple function of inactivity among hybrids. A strong effect of cytoplasmic (mitochondrial) background was also found in *N. vitripennis* and *N. giraulti* crosses; F2 hybrids with *giraulti* cytoplasm showing reduced ability at most stages of courtship. Hybrids produced between a younger species pair, *N. giraulti* and *N. longicornis*, were behaviorally fertile. All males possessed motile sperm, but sperm production is greatly reduced in hybrids between the older species pair, *N. vitripennis* and *N. giraulti*. This effect on hybrid males, lowered sperm counts rather than nonfunctional sperm, is different from most described cases of hybrid male sterility, and may represent an earlier stage of hybrid sperm breakdown. The results add to previous studies of F2 hybrid inviability and behavioral sterility, and indicate that *Wolbachia*-induced hybrid incompatibility has arisen early in species divergence, relative to behavioral sterility and spermatogenic infertility.

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http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009152a.html

48. A comparison of recombination frequencies in intraspecific versus interspecific mapping populations of Nasonia

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A comparison of recombination frequencies in intraspecific versus interspecific mapping populations of *Nasonia*
We present the first intraspecific linkage map for *Nasonia vitripennis* based on molecular markers. The map consists of 36 new microsatellite markers, extracted from the *Nasonia* genome sequence, and spans 515 cM. The five inferred linkage groups correspond to the five chromosomes of *Nasonia*. Comparison of recombination frequencies of the marker intervals spread over the whole genome (*N* = 33 marker intervals) between the intraspecific *N. vitripennis* map and an interspecific *N. vitripennis × N. giraulti* map revealed a slightly higher (1.8%) recombination frequency in the intraspecific cross. We further considered an *N. vitripennis × N. longicornis* map with 29 microsatellite markers spanning 430 cM. Recombination frequencies in the two interspecific crosses differed neither between reciprocal crosses nor between mapping populations of embryos and adults. No major chromosomal rearrangements were found for the analyzed genomic segments. The observed differential F$_2$ hybrid male mortality has no significant effect on the genome-wide recombination frequency in *Nasonia*. We conclude that interspecific crosses between the different *Nasonia* species, a hallmark of *Nasonia* genetics, are generally suitable for mapping quantitative and qualitative trait loci for species differences.

http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009185a.html

### 49. Contrasting patterns of selective constraints in nuclear-encoded genes of the oxidative phosphorylation pathway in holometabolous insects and their possible role in hybrid breakdown in *Nasonia*

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The principal energy generating system in animals is the oxidative phosphorylation (OXPHOS) pathway, which depends on the tight interaction of nuclear- and mitochondrial-encoded genes to function properly. Mitochondrial genes accumulate substitutions more quickly than nuclear genes, yet the impact of selection on mitochondrial genes is significantly reduced relative to nuclear genes because of the non-recombining nature of the mitochondrial genome and its predicted smaller effective population size. It has therefore been hypothesized that the nuclear-encoded genes of the OXPHOS pathway are under strong selective pressure to compensate for the accumulation of deleterious nucleotide substitutions in mitochondrial-encoded OXPHOS genes, a process known as compensatory co-adaptation. We evaluated this hypothesis by analyzing nuclear-encoded OXPHOS genes for signatures of positive selection as well as evolutionary constraints at amino acid sites. We considered OXPHOS genes of six holometabolous insects and their orthologs from three *Nasonia* parasitoid wasps, the hybrids of which suffer from an increased mortality rate caused by cytonuclear genic incompatibilities. Although nuclear OXPHOS genes are typically highly conserved, we found significant evidence for elevated amino acid divergence in 4 of the 59 studied nuclear-encoded OXPHOS genes. We also found that three of these four genes, as well as six other OXPHOS genes, contain amino acid substitutions between *Nasonia* species at evolutionarily constrained sites. It is possible that these genes account for the reported incompatibility in *Nasonia* hybrids and their characterization may lead to a better understanding of the role of positive selection in the genetics of speciation.

50. Phylogeography of Nasonia vitripennis (Hymenoptera) indicates a mitochondrial–Wolbachia sweep in North America

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Here we report evidence of a mitochondrial–Wolbachia sweep in North American populations of the parasitoid wasp Nasonia vitripennis, a cosmopolitan species and emerging model organism for evolutionary and genetic studies. Analysis of the genetic variation of 89 N. vitripennis specimens from Europe and North America was performed using four types of genetic markers: a portion of the mitochondrial cytochrome oxidase I gene, nine polymorphic nuclear microsatellites, sequences from 11 single-copy nuclear markers and six Wolbachia genes. The results show that the European populations have a sevenfold higher mitochondrial sequence variation than North American populations, but similar levels of microsatellite and nuclear gene sequence variation. Variation in the North American mitochondria is extremely low (π = 0.31%), despite a highly elevated mutation rate (~35–40 times higher than the nuclear genes) in the mitochondria of Nasonia. The data are indicative of a mitochondrial sweep in the North American population, possibly due to Wolbachia infections that are maternally co-inherited with the mitochondria. Owing to similar levels of nuclear variation, the data could not resolve whether N. vitripennis originated in the New or the Old World.

http://www.nature.com/hdy/journal/v104/n3/abs/hdy2009160a.html

Insect Migration

51. A single wind-mediated mechanism explains high-altitude ‘non-goal oriented’ headings and layering of nocturnally migrating insects

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Studies made with both entomological and meteorological radars over the last 40 years have frequently reported the occurrence of insect layers, and that the individuals forming these layers often show a considerable degree of uniformity in their headings—behaviour known as ‘common orientation’. The environmental cues used by nocturnal migrants to select and maintain common headings, while flying in low illumination levels at great heights above the ground, and the adaptive benefits of this behaviour have long remained a mystery. Here we show how a wind-mediated mechanism accounts for the common orientation patterns of ‘medium-sized’ nocturnal insects. Our theory posits a mechanism by which migrants are able to align themselves with the direction of the flow using a turbulence cue, thus adding their air speed to the wind speed and significantly increasing their migration distance. Our mechanism also predicts that insects flying in the Northern Hemisphere will typically be offset to the right of the mean wind line when the atmosphere is stably stratified, with the Ekman spiral in full effect. We report on the first evidence for such offsets, and show that they have significant implications for the accurate prediction of the flight trajectories of migrating nocturnal insects.

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http://rspb.royalsocietypublishing.org/content/277/1682/765.abstract
52. Pickpocket Is a DEG/ENaC Protein Required for Mechanical Nociception in Drosophila Larvae

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**Highlights**
Builds upon previous findings that pickpocket expressing neurons are polymodal nociceptors. Shows that the Deg/ENaC Pickpocket is required for mechanical nociception. First evidence that Deg/ENaCs play a role in Drosophila mechanotransduction. Molecular pathways for mechanical nociception and thermal nociception are distinct.

**Summary**
Highly branched class IV multidendritic sensory neurons of the Drosophila larva function as polymodal nociceptors that are necessary for behavioral responses to noxious heat (＞39°C) or noxious mechanical (＞30 mN) stimuli. However, the molecular mechanisms that allow these cells to detect both heat and force are unknown. Here, we report that the pickpocket (ppk) gene, which encodes a Degenerin/Epithelial Sodium Channel (DEG/ENaC) subunit, is required for mechanical nociception but not thermal nociception in these sensory cells. Larvae mutant for pickpocket show greatly reduced nociception behaviors in response to harsh mechanical stimuli. However, pickpocket mutants display normal behavioral responses to gentle touch. Tissue-specific knockdown of pickpocket in nociceptors phenocopies the mechanical nociception impairment without causing defects in thermal nociception behavior. Finally, optogenetically triggered nociception behavior is unaffected by pickpocket RNAi, which indicates that ppk is not generally required for the excitability of the nociceptors. Interestingly, DEG/ENaCs are known to play a critical role in detecting gentle touch stimuli in Caenorhabditis elegans and have also been implicated in some aspects of harsh touch sensation in mammals. Our results suggest that neurons that detect harsh touch in Drosophila utilize similar mechanosensory molecules.

Current Biology, Volume 20, Issue 5, 429-434, 18 February 2010

53. Spatial and temporal changes in genetic structure of greenhouse and field populations of cabbage looper, Trichoplusia ni

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Trichoplusia ni is a subtropical moth that migrates annually from southern California to southern British Columbia, Canada where it invades vegetable greenhouses and field crops. The heated greenhouse environment has altered the natural extinction–recolonization dynamics of T. ni populations, and allows year-round persistence in some locations. In addition, the extensive use of the biopesticide, Bacillus thuringiensis subspecies kurstaki (Bt) in some greenhouses has selected for resistance. Here we investigated the genetic structure of T. ni populations in British Columbia greenhouses and in field populations in California and British Columbia using amplified fragment length polymorphisms (AFLP) as related to patterns of Bt resistance. The majority of British Columbia field populations were similar to the California field populations, the potential source of migrants. However populations in two geographic areas with high concentrations of greenhouses showed local genetic differentiation. Some of these populations experienced severe bottlenecks over-winter and following Bt sprays.
Greenhouse populations showed a pattern of isolation by distance and a strong positive relationship between genetic differentiation and levels of Bt resistance. These patterns indicate that greenhouses that sometimes support year-round populations of T. ni and the ensuing strong bottlenecking effects following winter cleanups and Bt application cause genetic differentiation of T. ni populations. Long distance migrants to field populations contribute to genetic homogeneity of these.

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54. Changes in reproductive roles are associated with changes in gene expression in fire ant queens

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In species with social hierarchies, the death of dominant individuals typically upheaves the social hierarchy and provides an opportunity for subordinate individuals to become reproductives. Such a phenomenon occurs in the monogyne form of the fire ant, Solenopsis invicta, where colonies typically contain a single wingless reproductive queen, thousands of workers and hundreds of winged nonreproductive virgin queens. Upon the death of the mother queen, many virgin queens shed their wings and initiate reproductive development instead of departing on a mating flight. Workers progressively execute almost all of them over the following weeks. To identify the molecular changes that occur in virgin queens as they perceive the loss of their mother queen and begin to compete for reproductive dominance, we collected virgin queens before the loss of their mother queen, 6 h after orphaning and 24 h after orphaning. Their RNA was extracted and hybridized against microarrays to examine the expression levels of approximately 10 000 genes. We identified 297 genes that were consistently differentially expressed after orphaning. These include genes that are putatively involved in the signalling and onset of reproductive development, as well as genes underlying major physiological changes in the young queens.

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55. Geographic parthenogenesis and the common tea-tree stick insect of New Zealand

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Worldwide, parthenogenetic reproduction has evolved many times in the stick insects (Phasmatidae). Many parthenogenetic stick insects show the distribution pattern known as geographic parthenogenesis, in that they occupy habitats that are at higher altitude or latitude compared with their sexual relatives. Although it is often assumed that, in the short term, parthenogenetic populations will have a reproductive advantage over sexual populations; this is not necessarily the case. We present data on the distribution and evolutionary relationships of sexual and asexual populations of the New Zealand stick insect, Clitarchus hookeri. Males are common in the northern half of the species' range but rare or absent elsewhere, and we found that most C. hookeri from putative-parthenogenetic populations share a common ancestor. Female stick insects from bisexual populations of Clitarchus hookeri are capable of parthenogenetic reproduction, but those insects from putative-parthenogenetic populations produced few offspring via sexual reproduction when males were available. We found similar fertility (hatching success) in mated and virgin females. Mated females produce equal numbers of male and female offspring, with most hatching about 9–16 weeks after laying. In contrast, most
eggs from unmated females took longer to hatch (21–23 weeks), and most offspring were female. It appears that all C. hookeri females are capable of parthenogenetic reproduction, and thus could benefit from the numerical advantage this yields. Nevertheless, our phylogeographic evidence shows that the majority of all-female populations over a wide geographic area originate from a single loss of sexual reproduction.

56. Characterization of a hotspot for mimicry: assembly of a butterfly wing transcriptome to genomic sequence at the HmYb/Sb locus

The mimetic wing patterns of Heliconius butterflies are an excellent example of both adaptive radiation and convergent evolution. Alleles at the HmYb and HmSb loci control the presence/absence of hindwing bar and hindwing margin phenotypes respectively between divergent races of Heliconius melpomene, and also between sister species. Here, we used fine-scale linkage mapping to identify and sequence a BAC tilepath across the HmYb/Sb loci. We also generated transcriptome sequence data for two wing pattern forms of H. melpomene that differed in HmYb/Sb alleles using 454 sequencing technology. Custom scripts were used to process the sequence traces and generate transcriptome assemblies. Genomic sequence for the HmYb/Sb candidate region was annotated both using the MAKER pipeline and manually using transcriptome sequence reads. In total, 28 genes were identified in the HmYb/Sb candidate region, six of which have alternative splice forms. None of these are orthologues of genes previously identified as being expressed in butterfly wing pattern development, implying previously undescribed molecular mechanisms of pattern determination on Heliconius wings. The use of next-generation sequencing has therefore facilitated DNA annotation of a poorly characterized genome, and generated hypotheses regarding the identity of wing pattern at the HmYb/Sb loci.
assumption of considerable ongoing gene flow between M and S, these persistently divergent genomic islands were widely considered to be 'speciation islands'. In the course of microarray-based divergence mapping, we discovered a third centromere-associated island of divergence on chromosome 3, which was validated by targeted re-sequencing. To test for genetic association between the divergence islands on all three chromosomes, SNP-based assays were applied in four natural populations of M and S spanning West, Central and East Africa. Genotyping of 517 female M and S mosquitoes revealed nearly complete linkage disequilibrium between the centromeres of the three independently assorting chromosomes. These results suggest that despite the potential for inter-form gene flow through hybridization, actual (realized) gene flow between M and S may be substantially less than commonly assumed and may not explain most shared variation. Moreover, the possibility of very low gene flow calls into question whether diverged pericentromeric regions—characterized by reduced levels of variation and recombination—are in fact instrumental rather than merely incidental to the speciation process.

Molecular Ecology Volume 19 Issue s1, 2010 Pages 925 - 939
http://www3.interscience.wiley.com/journal/123276164/abstract

Insect Neuroscience

58. Phenotypic plasticity in number of glomeruli and sensory innervation of the antennal lobe in leaf-cutting ant workers (A. vollenweideri)

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In the leaf-cutting ant Atta vollenweideri, the worker caste exhibits a pronounced size-polymerorphism, and division of labor is dependent on worker size (alloethism). Behavior is largely guided by olfaction, and the olfactory system is highly developed. In a recent study, two different phenotypes of the antennal lobe of Atta vollenweideri workers were found: MG- and RG-phenotype (with/without a macroglomerulus). Here we ask whether the glomerular numbers are related to worker size. We found that the antennal lobes of small workers contain ~390 glomeruli (low-number; LN-phenotype), and in large workers we found a substantially higher number of ~440 glomeruli (high-number; HN-phenotype). All LN-phenotype workers and some small HN-phenotype workers do not possess an MG (LN-RG-phenotype and HN-RG-phenotype), and the remaining majority of HN-phenotype workers do possess an MG (HN-MG-phenotype). Using mass-staining of antennal olfactory receptor neurons we found that the sensory tracts divide the antennal lobe into six clusters of glomeruli (T1-T6). In LN-phenotype workers, ~50 glomeruli are missing in the T4-cluster. Selective staining of single sensilla and their associated receptor neurons revealed that T4-glomeruli are innervated by receptor neurons from the main type of olfactory sensilla, the Sensilla trichodea curvata. The other type of olfactory sensilla (Sensilla basiconica) exclusively innervates T6-glomeruli. Quantitative analyses of differently sized workers revealed that the volume of T6 glomeruli scales with the power of 2.54 to the number of Sensilla basiconica. The results suggest that developmental plasticity leading to antennal-lobe phenotypes promotes differences in olfactory-guided behavior and may underlie task specialization within ant colonies. © 2009 Wiley Periodicals, Inc.

http://www3.interscience.wiley.com/journal/123222113/abstract

59. Localization of a GABA transporter to glial cells in the developing and adult olfactory pathway of the moth Manduca sexta

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Glial cells have several critical roles in the developing and adult olfactory (antennal) lobe of the moth Manduca sexta. Early in development, glial cells occupy discrete regions of the developing olfactory pathway and processes of GABAergic neurons extend into some of these regions. Because GABA is known to have developmental effects in a variety of systems, we explored the possibility that the glial cells express a GABA transporter that could regulate GABA levels to which olfactory neurons and glial cells are exposed. By using an antibody raised against a characterized high-affinity M. sexta GABA transporter with high sequence homology to known mammalian GABA transporters (Mbungu et al. [1995] Arch. Biochem. Biophys. 318:489-497; Umesh and Gill [2002] J. Comp. Neurol. 448:388-398), we found that the GABA transporter is localized to subsets of centrally derived glial cells during metamorphic adult development. The transporter persists into adulthood in a subset of the neuropil-associated glial cells, but its distribution pattern as determined by light-and electron-microscopic-level immunocytochemistry indicates that it could not serve to regulate GABA concentration in the synaptic cleft. Instead, its role is more likely to regulate extracellular GABA levels within the glomerular neuropil. Expression in the sorting zone glial cells disappears after the period of olfactory receptor axon ingrowth, but may be important during ingrowth if GABA regulates axon growth. Glial cells take up GABA, and that uptake can be blocked by L-2,4-diaminobutyric acid (DABA). This is the first molecular evidence that the central glial cell population in this pathway is heterogeneous.

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http://www3.interscience.wiley.com/journal/122648775/abstract

60. Light-induced translocation of Drosophila visual Arrestin2 depends on Rac2

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Photoreceptor cells are remarkable in their ability to adjust their sensitivity to light over a wide range of intensities. Rapid termination of the photoresponse is achieved in part by shuttling proteins in and out of the light-transducing compartment of the photoreceptor cells. One protein that undergoes light-dependent translocation is the rhodopsin regulatory protein arrestin. However, the mechanisms coupling rhodopsin to arrestin movement are poorly understood. Here we show that light-dependent shuttling of the major arrestin in Drosophila photoreceptor cells, Arrestin2 (Arr2), occurs independently of known elements of the phototransduction cascade. Disruptions of the trimeric G protein, phospholipase Cβ, the TRP channel, or the Na+/Ca2+ exchanger did not influence Arr2 localization. Rather, we found that loss of the small GTPase Rac2 severely impaired Arr2 movement and prolonged the termination of the photoresponse. Our findings demonstrate that light-induced translocation of Arr2 occurs through a noncanonical rhodopsin/Rac2 pathway, which is distinct from the classical phototransduction cascade.

PNAS March 9, 2010 vol. 107 no. 10 4740-4745
http://www.pnas.org/content/107/10/4740.abstract

61. Contribution of photoreceptor subtypes to spectral wavelength preference in Drosophila

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The visual systems of most species contain photoreceptors with distinct spectral sensitivities that allow animals to distinguish lights by their spectral composition. In Drosophila, photoreceptors R1–R6 have the same spectral sensitivity throughout the eye and are responsible for motion detection. In contrast, photoreceptors R7 and R8 exhibit heterogeneity and are important for color vision. We investigated how photoreceptor types contribute to the attractiveness of light by blocking the function of certain subsets and by measuring differential phototaxis between spectrally different lights. In a “UV vs. blue” choice, flies with only R1–R6, as well as flies with only R7/R8 photoreceptors, preferred blue, suggesting a nonadditive interaction between the two major subsystems. Flies defective for UV-sensitive R7 function preferred blue, whereas flies defective for either type of R8 (blue- or green-sensitive) preferred UV. In a “blue vs. green” choice, flies defective for R8 (blue) preferred green, whereas those defective for R8 (green) preferred blue. Involvement of all photoreceptors [R1–R6, R7, R8 (blue), R8 (green)] distinguishes phototaxis from motion detection that is mediated exclusively by R1–R6.

PNAS March 23, 2010 vol. 107 no. 12 5634-5639
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Insect Neuroethology

62. Wide-field motion tuning in nocturnal hawkmoths

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Nocturnal hawkmoths are known for impressive visually guided behaviours in dim light, such as hovering while feeding from nectar-bearing flowers. This requires tight visual feedback to estimate and counter relative motion. Discrimination of low velocities, as required for stable hovering flight, is fundamentally limited by spatial resolution, yet in the evolution of eyes for nocturnal vision, maintenance of high spatial acuity compromises absolute sensitivity. To investigate these trade-offs, we compared responses of wide-field motion-sensitive neurons in three species of hawkmoth: Manduca sexta (a crepuscular hoverer), Deilephila elpenor (a fully nocturnal hoverer) and Acherontia atropos (a fully nocturnal hawkmoth that does not hover as it feeds uniquely from honey in bees’ nests). We show that despite smaller eyes, the motion pathway of D. elpenor is tuned to higher spatial frequencies and lower temporal frequencies than A. atropos, consistent with D. elpenor’s need to detect low velocities for hovering. Acherontia atropos, however, presumably evolved low-light sensitivity without sacrificing temporal acuity. Manduca sexta, active at higher light levels, is tuned to the highest spatial frequencies of the three and temporal frequencies comparable with A. atropos. This yields similar tuning to low velocities as in D. elpenor, but with the advantage of shorter neural delays in processing motion.

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http://rspb.royalsocietypublishing.org/content/277/1683/853.abstract

Insect Olfaction

63. Expression Analysis of the 3 G-Protein Subunits, G\(\alpha\), G\(\beta\), and G\(\gamma\), in the Olfactory Receptor Organs of Adult Drosophila melanogaster

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In many species, olfactory transduction is triggered by odorant molecules that interact with olfactory receptors coupled to heterotrimeric G-proteins. The role of G-protein-linked transduction in the olfaction of *Drosophila* is currently under study. Here, we supply a thorough description of the expression in the olfactory receptor organs (antennae and maxillary palps) of all known *Drosophila melanogaster* genes that encode for G-proteins. Using RT-polymerase chain reaction, we analyzed 6 Gα (Gαs, Gαi, Gαq, Gαo, Gαf, and *concertina*), 3 Gβ (Gβ5, Gβ13F, and Gβ67C), and 2 Gγ genes (Gγi and Gγ130A). We found that all Gα protein-encoding genes showed expression in both olfactory organs, but Gf mRNA was not detected in palps. Moreover, all the Gβ and Gγ genes are expressed in antennae and palps, except for Gβ76C. To gain insight into the hypothesis of different G-protein subunits mediating differential signaling in olfactory receptor neurons (ORNs), we performed immunohistochemical studies to observe the expression of several Gα and Gβ proteins. We found that Gs, Gi, Gq, and Gβ13F subunits displayed generalized expression in the antennal tissue, including ORNs support cells and glial cells. Finally, complete coexpression was found between Gi and Gq, which are mediators of the cyclic adenosine monophosphate and IP3 transduction cascades, respectively.

64. **Characterization of the Antennal Olfactory System of the Bed Bug (Cimex lectularius)**

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The common bed bug *Cimex lectularius* (Hemiptera; Cimicidae) is a temporary ectoparasite on humans that is currently reinvading the developed countries. Like other haematophagous arthropods, host seeking and orientation in *C. lectularius* is partially mediated by olfaction. In this study, we reconfirmed the distribution of the 44 olfactory sensilla and identified 3 different sensillum types located at the distal tip of *C. lectularius* antenna by external morphology mapping. Using a panel of relevant odorants previously reported to be bioactive in various haematophagous arthropods, we correlated the morphological mapping with an electrophysiological characterization of the olfactory receptor neurons housed in each specific sensillum. We found that all 9 grooved peg sensilla responded specifically in a dose-dependent manner to ammonia, whereas (E)-2-hexenal, (E)-2-octenal, dimethyl trisulfide, 6-methyl-5-hepten-2-one, α-pinene, indole, and ethyl butyrate evoked dose-dependent responses within the 6 smooth peg sensilla. Based on the pattern of response to the tested compounds, we were able to separate the 6 smooth peg sensilla of the bed bug into 3 distinct functional classes. We compare our results with previous electrophysiological recordings made with these compounds on other haematophagous arthropods.

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http://chemse.oxfordjournals.org/cgi/content/abstract/35/3/195

65. **Perfusion with cAMP analogue affects pheromone-sensitive trichoid sensilla of the hawkmoth Manduca sexta in a time-dependent manner**

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Octopamine causes time-dependent disadaptation of pheromone-sensitive olfactory receptor neurons (ORNs) of Manduca sexta. Because the majority of insect octopamine receptors are positively coupled to adenyl cyclases we examined whether cyclic adenosine monophosphate (cAMP) mimics octopamine-dependent modulation of pheromone transduction in a time-dependent manner. Long-term tip recordings of single trichoid sensilla of Manduca sexta were performed during three zeitgeber times (ZTs, ZT 0=lights on), while stimulating the sensilla with two doses of the main pheromone component bombykal in a non-adapting protocol. The membrane-permeable cAMP analogue 8bcAMP increased the normalized sensillar potential amplitude in a time- and bombykal dose-dependent way. At the higher bombykal dose only, the applied 8bcAMP antagonized an endogenous decrease in the mean sensillar potential amplitude at ZT 1-4 and ZT 8-11 when ORNs were adapted but not at ZT 22-1, when ORNs were sensitized. In contrast to octopamine, 8bcAMP did not consistently affect the initial pheromone-dependent action potential frequency, the phasic/tonic response pattern, or the time-dependent shift to lower mean action potential frequencies at ZT 8-11. Furthermore, 8bcAMP increased the spontaneous action potential frequency time dependently, but differently from octopamine. In conclusion, our results show that cAMP only partly mimics the octopamine-dependent disadaptation of olfactory receptor neurons during photophase, apparently due to another missing octopamine-dependent synergistic factor such as defined intracellular calcium levels.

http://jeb.biologists.org/cgi/content/abstract/213/5/842

Insect Pathology

66.Mixed genotype transmission bodies and virions contribute to the maintenance of diversity in an insect virus

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An insect nucleopolyhedrovirus naturally survives as a mixture of at least nine genotypes. Infection by multiple genotypes results in the production of virus occlusion bodies (OBs) with greater pathogenicity than those of any genotype alone. We tested the hypothesis that each OB contains a genotypically diverse population of virions. Few insects died following inoculation with an experimental two-genotype mixture at a dose of one OB per insect, but a high proportion of multiple infections were observed (50%), which differed significantly from the frequencies predicted by a non-associated transmission model in which genotypes are segregated into distinct OBs. By contrast, insects that consumed multiple OBs experienced higher mortality and infection frequencies did not differ significantly from those of the non-associated model. Inoculation with genotypically complex wild-type OBs indicated that genotypes tend to be transmitted in association, rather than as independent entities, irrespective of dose. To examine the hypothesis that virions may themselves be genotypically heterogeneous, cell culture plaques derived from individual virions were analysed to reveal that one-third of virions was of mixed genotype, irrespective of the genotypic composition of the OBs. We conclude that co-occlusion of genotypically distinct virions in each OB is an adaptive mechanism that favours the maintenance of virus diversity during insect-to-insect transmission.

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67. Colony fusion and worker reproduction after queen loss in army ants

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Theory predicts that altruism is only evolutionarily stable if it is preferentially directed towards relatives, so that any such behaviour towards seemingly unrelated individuals requires scrutiny. Queenless army ant colonies, which have anecdotally been reported to fuse with queenright foreign colonies, are such an enigmatic case. Here we combine experimental queen removal with population genetics and cuticular chemistry analyses to show that colonies of the African army ant Dorylus molestus frequently merge with neighbouring colonies after queen loss. Merging colonies often have no direct co-ancestry, but are on average probably distantly related because of overall population viscosity. The alternative of male production by orphaned workers appears to be so inefficient that residual inclusive fitness of orphaned workers might be maximized by indiscriminately merging with neighbouring colonies after queen loss. Merging colonies often have no direct co-ancestry, but are on average probably distantly related because of overall population viscosity. The alternative of male production by orphaned workers appears to be so inefficient that residual inclusive fitness of orphaned workers might be maximized by indiscriminately merging with neighbouring colonies after queen loss. We show that worker chemical recognition profiles remain similar after queen loss, but rapidly change into a mixed colony Gestalt odour after fusion, consistent with indiscriminate acceptance of alien workers that are no longer aggressive. We hypothesize that colony fusion after queen loss might be more widespread, especially in spatially structured populations of social insects where worker reproduction is not profitable.

Proc. R. Soc. B 7 March 2010 vol. 277 no. 1682 755-763
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68. Seminal Fluid Mediates Ejaculate Competition in Social Insects

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Queens of ants and bees normally obtain a lifetime supply of sperm on a single day of sexual activity, and sperm competition is expected to occur in lineages where queens receive sperm from multiple males. We compared singly mated (monandrous) and multiply mated (polyandrous) sister groups of ants and bees and show that seminal fluid of polyandrous species has a more positive effect on the survival of a male’s own sperm than on other males’ sperm. This difference was not observed in the monandrous species, suggesting that incapacitation of competing sperm may have independently evolved in both bees and ants. In Atta leafcutter ants, the negative effect of the seminal fluid of other males was negated by secretion from the queen sperm-storage organ, suggesting that queens may control ejaculate competition after sperm storage.

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http://www.sciencemag.org/cgi/content/abstract/327/5972/1506?sa_campaign=Email/toc/19-March-2010/10.1126/science.1184709

Insect Review

69. A meta-analysis of insect pest behavioral manipulation with plant volatiles

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Many insect pests utilize plant volatiles for host location and untangling the mechanisms of this process can provide tools for pest management. Numerous experimental results have been published on the effect of plant volatiles on insect pests. We used a meta-analysis to summarize this knowledge and to look for patterns. Our goal was to identify herbivore and plant traits that might explain the herbivores' behavioral response to plant volatiles in field applications. We scored a total of 374 unique plant volatile-insect herbivore interactions obtained from 34 published studies investigating 50 herbivore pest species. Attractants had a significant effect on insect herbivore abundance but repellents did not; this latter result could be a result of the comparatively small number of field studies that tested plant volatiles as repellents (3%). Females were significantly more attracted to plant volatile baits than males. The diet breadth of herbivores was independent of a behavioral response to plant volatiles, but more case studies show effects of volatiles on chewers, followed by wood-borers and sap-feeders. There are more demonstrations of attraction to plant volatiles in Lepidoptera than in Thysanoptera. The method of plant volatile application had a significant effect on herbivore abundance and increasing the number of chemicals in individual baits attracted more herbivores. The magnitude of the response of herbivores to plant volatiles in forest and agricultural habitats was similar. We explore consistent patterns and highlight areas needing research in using plant volatiles to manage insect pests.

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70. Olfactory signalling in vertebrates and insects: differences and commonalities

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Vertebrates and insects have evolved complex repertoires of chemosensory receptors to detect and distinguish odours. With a few exceptions, vertebrate chemosensory receptors belong to the family of G protein-coupled receptors that initiate a cascade of cellular signalling events and thereby electrically excite the neuron. Insect receptors, which are structurally and genetically unrelated to vertebrate receptors, are a complex of two distinct molecules that serves both as a receptor for the odorant and as an ion channel that is gated by binding of the odorant. Metabotropic signalling in vertebrates provides a rich panoply of positive and negative regulation, whereas ionotropic signalling in insects enhances processing speed.

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