




Press Report

July 2019

Flora Borne

Female Genetic Contributions to Sperm Competition in *Drosophila melanogaster*

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remain elusive. Here, we functionally tested 26 candidate genes implicated via a GWAS for their contribution to the female's role in sperm competition, measured as changes in the relative success of the first male to mate (P1). Of these 26 candidates, we identified eight genes that affect P1 when knocked down in females, and showed that five of them do so when knocked down in the female nervous system. In particular, *Rim* knockdown in sensory *pickpocket* (*ppk*)⁺ neurons lowered P1, confirming previously published results, and a novel candidate, *caup*, lowered P1 when knocked down in octopaminergic *Tdc2*⁺ neurons. These results demonstrate that specific neurons in the female's nervous system play a functional role in sperm competition and expand our understanding of the genetic, neuronal, and mechanistic basis of female responses to multiple matings. We propose that these neurons in females are used to sense, and integrate, signals from courtship or ejaculates, to modulate sperm competition outcome accordingly.

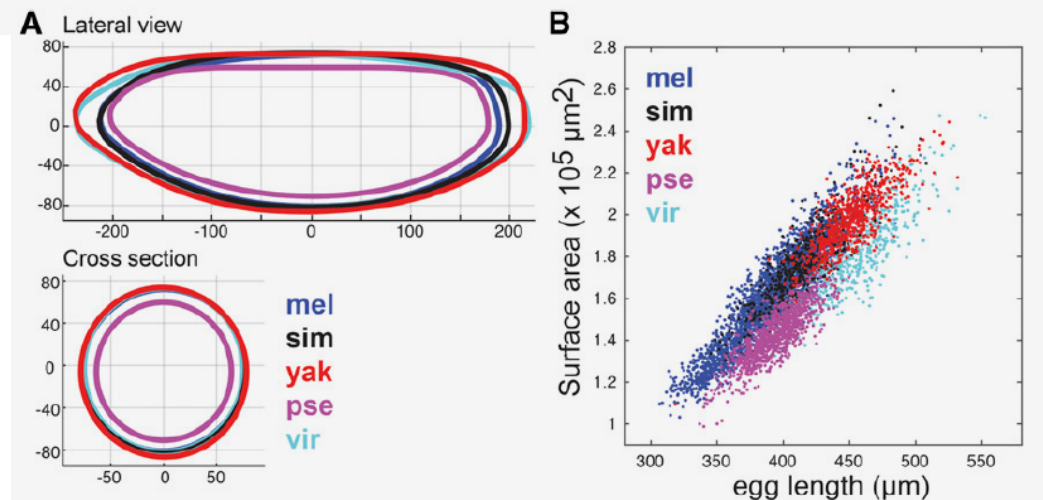
Quantitative Comparison of the Anterior-Posterior Patterning System in the Embryos of Five *Drosophila* Species

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ABSTRACT Complex spatiotemporal gene expression patterns direct the development of the fertilized egg into an adult animal. Comparisons across species show that, in spite of changes in the underlying regulatory DNA sequence, developmental programs can be maintained across millions of years of evolution. Reciprocally, changes in gene expression can be used to generate morphological novelty. Distinguishing between changes in regulatory DNA that lead to changes in gene expression and those that do not is therefore a central goal of evolutionary developmental biology. Quantitative, spatially-resolved measurements of developmental gene expression patterns play a crucial role in this goal, enabling the detection of subtle phenotypic differences between species and the development of computational models that link the sequence of regulatory DNA to expression patterns. Here we report the generation of two atlases of cellular resolution gene expression measurements for the primary anterior-posterior patterning genes in *Drosophila simulans* and *Drosophila virilis*. By combining these data sets with existing atlases for three other *Drosophila* species, we detect subtle differences in the gene expression patterns and dynamics driving the highly conserved axis patterning system and delineate inter-species differences in the embryonic morphology. These data sets will be a resource for future modeling studies of the evolution of developmental gene regulatory networks.

KEYWORDS

gene expression
Drosophila
embryo
gene regulatory
network
evo-devo



Sexual signals of fish species mimic the spatial statistics of their habitat: evidence for processing bias in animal signal evolution

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humans find certain visual stimuli, like works of art, more appealing than others¹⁶. A number of studies have found that humans prefer, and find more pleasurable, images that are more efficiently processed^{17–19}. In parallel, other studies have shown that visual art has fractal-like statistics similar to natural scenes, whereas less aesthetic images, such as those of laboratory objects (i.e. spectrometers, lab benches, etc...) do not. Psychologists hypothesize that people prefer art with the spatial statistics of natural scenes because our brains have evolved to efficiently process them^{20–24}. Results from cognitive psychology therefore suggest a processing bias rooted in the reward (pleasure) of efficient information processing^{5,25}. Renoult & Mendelson hypothesize that this processing bias is not limited to humans, predicting that other animals should also prefer the fractal-like statistics of their habitats, and that this preference could help explain the evolution and diversification of complex animal signal patterns⁵.

disregarding potential variation between habitats. However, other studies have shown that habitats can differ significantly in spatial statistics, and specifically in the statistics that measure visual redundancies^{26,27}. Such studies quantify the intuitive: an image of the forest understory, with highly repeating vertical contrast (trees), will have different spatial statistics than an image of a desert, or a beach. Thus, organisms occupying habitats with different spatial redundancies are predicted to have environment-dependent differences in visual processing. In keeping with a hypothesis of sensory drive, these processing differences could lead to environment-dependent differences in pattern preferences, with the most efficiently processed (and thus preferred) environments being those inhabited by a given perceiver or by its ancestors. A hypothesis of signal diversification based on processing bias therefore predicts that the spatial statistics of complex visual signals whose function is attraction, as in courtship, will match those of the local habitat⁵. Here, we test that prediction in a diverse genus of freshwater fish with complex visual courtship signals.

Sexual signals of fish species mimic the spatial statistics of their habitat: evidence for processing bias in animal signal evolution

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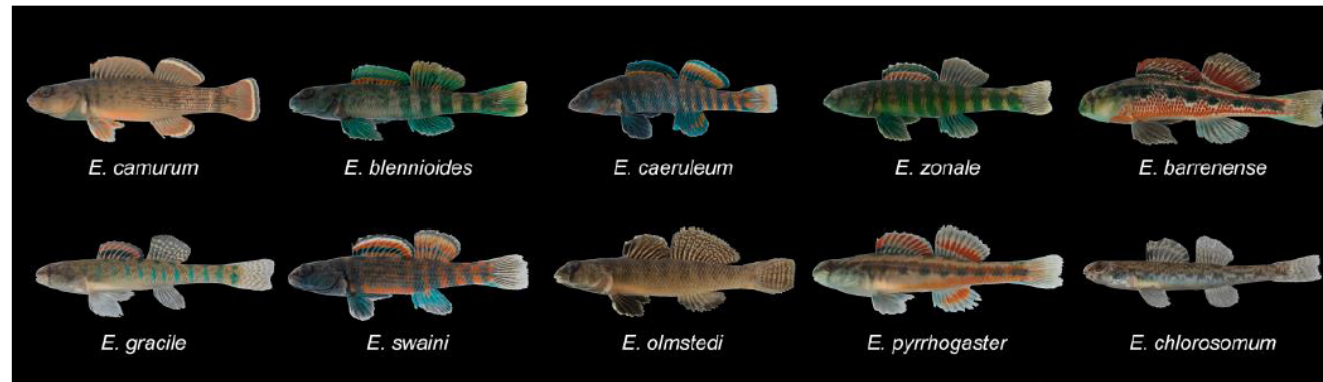


Figure 1. Example images for males of each species included in this study.

In this study, we investigated for the first time whether differences in environmental visual statistics correlate with observable differences in the visual statistics of sexually selected phenotypes. We captured

environment in which they evolve³. Our results support this prediction. We have shown that the habitats occupied by different darter species have different visual statistics, measured as the distribution of luminance contrast across different spatial frequencies (i.e., Fourier slope). We also found a significant correlation between the Fourier slope of a species' habitat and that of male nuptial patterns. Our results are therefore consistent with a hypothesis of sensory drive that incorporates efficient information processing in receivers as a driving force in preference and signal evolution⁵.

Insect egg size and shape evolve with ecology but not developmental rate

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Over the course of evolution, organism size has diversified markedly. Changes in size are thought to have occurred because of developmental, morphological and/or ecological pressures. To perform phylogenetic tests of the potential effects of these pressures, here we generated a dataset of more than ten thousand descriptions of insect eggs, and combined these with genetic and life-history datasets. We show that, across eight orders of magnitude of variation in egg volume, the relationship between size and shape itself evolves, such that previously predicted global patterns of scaling do not adequately explain the diversity in egg shapes. We show that egg size is not correlated with developmental rate and that, for many insects, egg size is not correlated with adult body size. Instead, we find that the evolution of parasitoidism and aquatic oviposition help to explain the diversification in the size and shape of insect eggs. Our study suggests that where eggs are laid, rather than universal allometric constants, underlies the evolution of insect egg size and shape.

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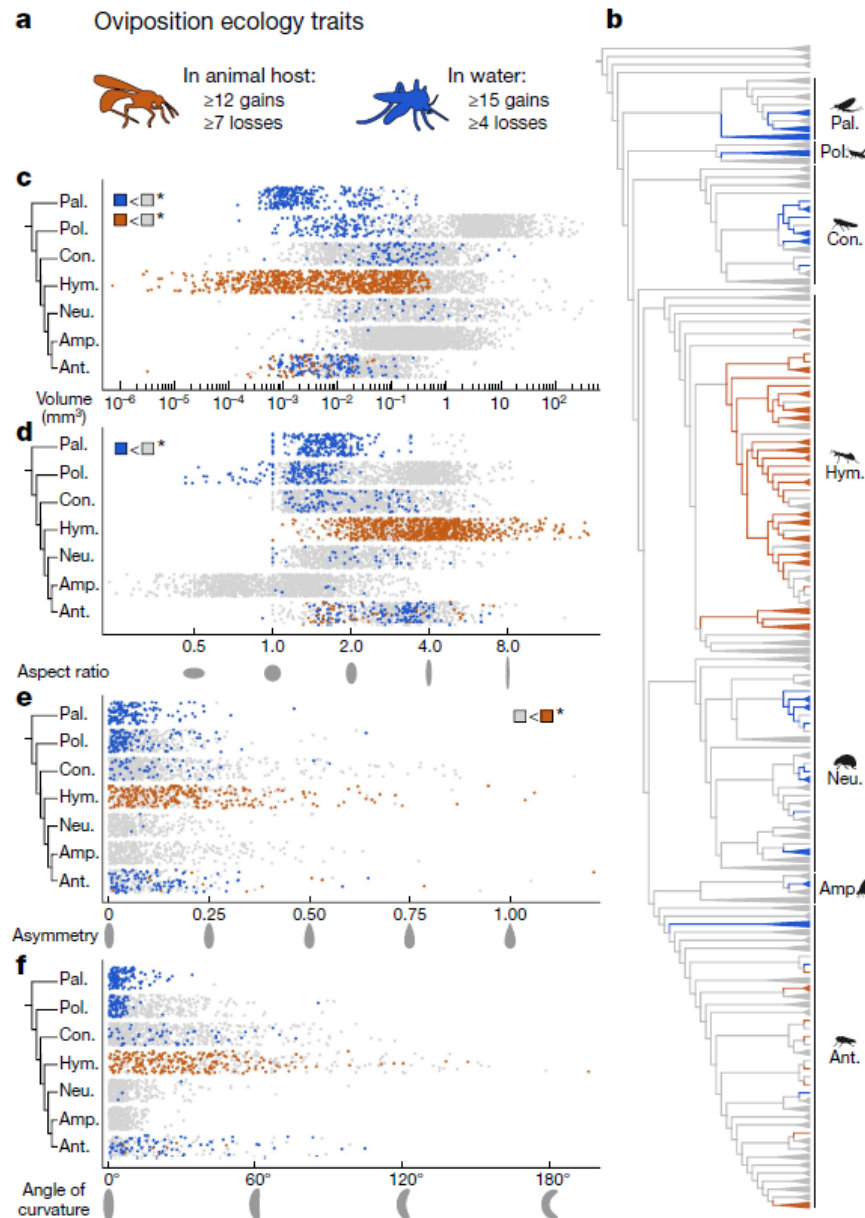
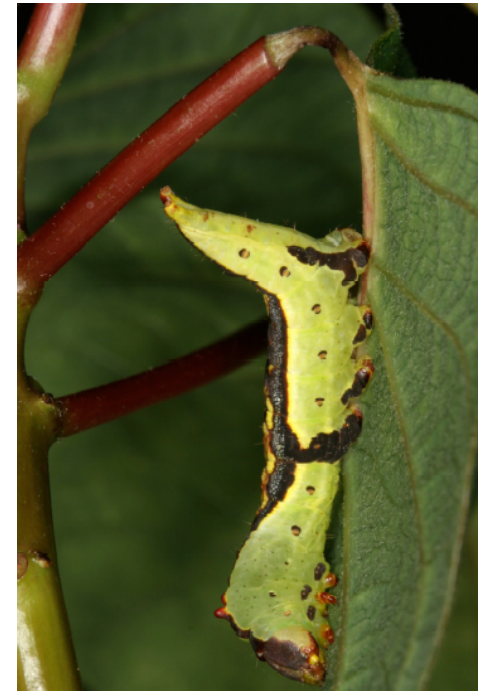


Fig. 4 | Shifts in oviposition ecology are associated with changes in egg morphology. **a**, Two modes of oviposition ecology: laying eggs within an animal host (orange; for example, parasitoid wasps), and in water (blue; for example, mosquitoes). Other oviposition substrates (for example, terrestrial or within plants) are shown in grey. **b**, Ancestral state reconstruction of oviposition mode reveals both evolved multiple times (see Supplementary Figs. 17, 18). **c–f**, The distribution of egg features, coloured by ecology. **c**, Volume (mm^3 ; shown on a log scale). **d**, Aspect ratio (unitless; shown on a log scale). **e**, Asymmetry (unitless). **f**, Angle of curvature (degrees). Asterisks indicate that the model that accounts for ecology fits the data better than a non-ecological model (Ornstein–Uhlenbeck model with multiple optima, $\Delta\text{AICc} > 2$, exact values are shown in Supplementary Tables 14–19).

A notodontid novelty: *Theroa zethus* caterpillars use behavior and anti-predator weaponry to disarm host plants

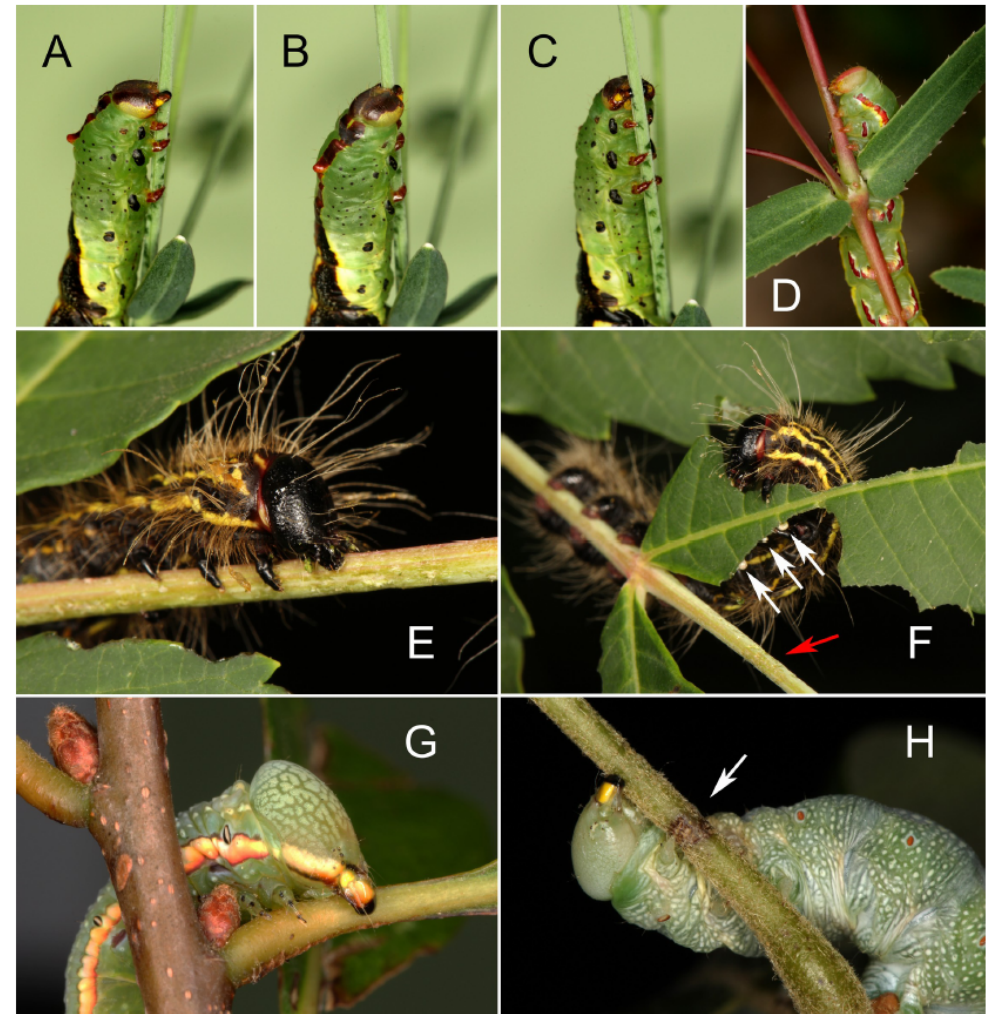
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Unlike most notodontids, *Theroa zethus* larvae feed on plants that emit copious latex when damaged. To determine how the larvae overcome this defense, we filmed final instars on poinsettia, *Euphorbia pulcherrima*, then simulated their behaviors and tested how the behaviors individually and combined affect latex exudation. Larvae initially scraped the stem, petiole, or midrib with their mandibles, then secreted acid from their ventral eversible gland (VEG) onto the abraded surface. Scraping facilitated acid penetration by disrupting the waxy cuticle. As the acid softened tissues, the larvae used their mandibles to compress the plant repeatedly, thereby rupturing the latex canals. Scraping, acid application, and compression created withered furrows that greatly diminished latex exudation distal to the furrows where the larvae invariably fed. The VEG in notodontids ordinarily serves to deter predators; when attacked, larvae spray acid aimed directly at the assailant. Using HPLC, we



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if VEG acids weaken walls. *Theroa zethus* is the only notodontid caterpillar known to use mandibular scraping and VEG acid to disable plant defenses. However, we document that mandibular constriction of petioles occurs also in other notodontids including species that feed on hardwood trees. This capability may represent a pre-adaptation that facilitated the host shift in the *Theroa* lineage onto latex-bearing plants by enabling larvae to deactivate laticifers with minimal latex contact.



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Protein interaction networks revealed by proteome coevolution

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Residue-residue coevolution has been observed across a number of protein-protein interfaces, but the extent of residue coevolution between protein families on the whole-proteome scale has not been systematically studied. We investigate coevolution between 5.4 million pairs of proteins in *Escherichia coli* and between 3.9 millions pairs in *Mycobacterium tuberculosis*. We find strong coevolution for binary complexes involved in metabolism and weaker coevolution for larger complexes playing roles in genetic information processing. We take advantage of this coevolution, in combination with structure modeling, to predict protein-protein interactions (PPIs) with an accuracy that benchmark studies suggest is considerably higher than that of proteome-wide two-hybrid and mass spectrometry screens. We identify hundreds of previously uncharacterized PPIs in *E. coli* and *M. tuberculosis* that both add components to known protein complexes and networks and establish the existence of new ones.