# Press report May 2015

Alexis M. Vidal

PLOS | COMPUTATIONAL BIOLOGY

EDITORIAL

# Ten Simple Rules to Win a Nobel Prize

**Richard J. Roberts***

New England Biolabs, Ipswich, Massachusetts, United States of America

* roberts@neb.com

## 9. Always Be Nice to Swedish Scientists

Several laureates had their prize severely delayed by picking a fight with the wrong person, someone who was either already a Nobel Committee member or became one subsequent to the fight. Some individuals may even have lost out altogether, although one would need to search the archives (only available 50 years after the award) to find them. This is usually an easy rule to follow as in my experience the Swedes are very nice people, good scientists, easy to collaborate with, and extremely amiable drinking partners.

It is never too early to get started on this. Then, should your name magically appear on the candidates' list and you have to wait for it to reach the top, you may still be around to cash in. Peyton Rous had to wait from 1911 until 1966 for the Medicine Prize, just four years before his death.

## 2. Hope That Your Experiments Fail Occasionally

There are usually two main reasons why experiments fail. Very often, it is because you screwed up in the design by not thinking hard enough about it ahead of time. Perhaps more often, it is because you were not careful enough in mixing the reagents (I always ask students if they spat in the tube or, more recently, were texting when they were labeling their tubes). Sometimes, you are not careful enough in performing the analytics (did you put the thermometer in upside down, as I once witnessed from a medical student whose name now appears on my list of doctors who I won't allow to treat me even if I'm dying?). These problems

Table of Contents: *PLOS Computational Biology*: Ten Simple Rules

COVER
Image Credit: PLOS

Written by *PLoS Computational Biology* Editor-in-Chief Philip E. Bourne, sometimes with collaborators, the "Ten Simple Rules" provide a quick, concentrated guide for mastering some of the professional challenges research scientists face in their careers. New articles will be added to the Ten Simple Rules Collections as they are published.

Download the Ten Simple Rules Collection: Screen PDF | Large PDF

Download the Ten Simple Rules Collection in Chinese: PDF. Translated by members of the EpiMan Forum, coordinated by Qiguo Lian (**qglian [at] fudan.edu.cn**). *Please note that the translation is the work of the authors and PLoS is not responsible for any inaccuracies or additional content.*

**Ten Simple Rules for a Successful Cross-Disciplinary Collaboration**

**Ten Simple Rules for Finishing Your PhD**

**Ten Simple Rules for Approaching a New Job**

**Ten Simple Rules for Writing Research Papers**

**Ten Simple Rules for Writing a Literature Review**

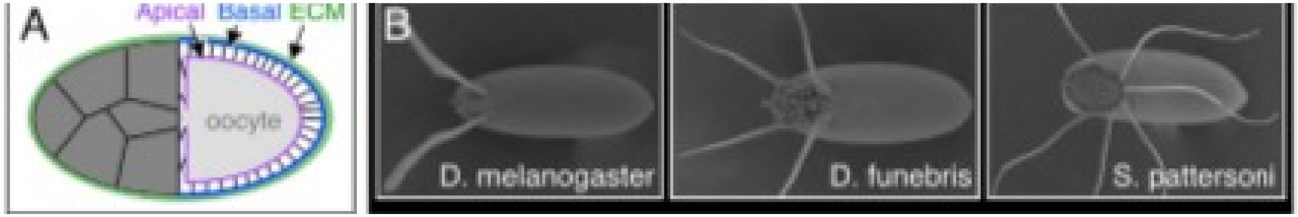
**Ten Simple Rules for Writing a PLOS Ten Simple Rules Article**

© 2015. Published by The Company of Biologists Ltd | Development (2015) 142, 1-7 doi:10.1242/dev.119404

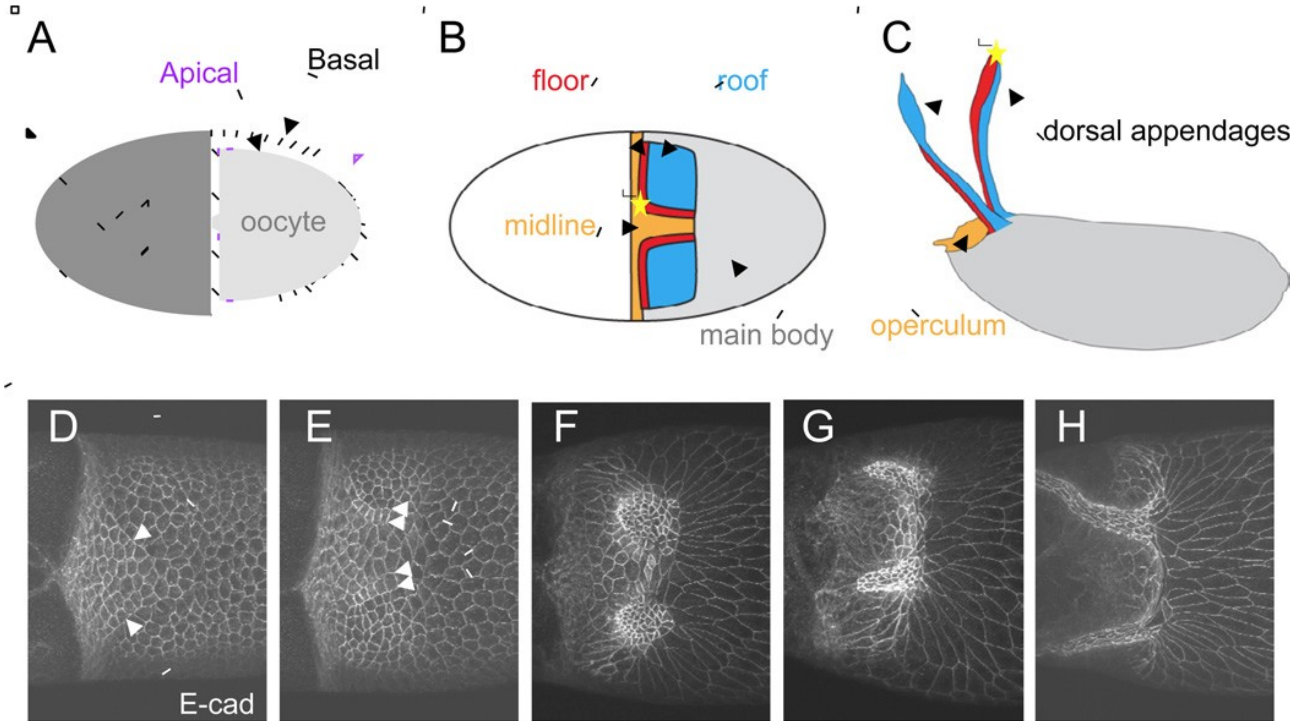
RESEARCH REPORT

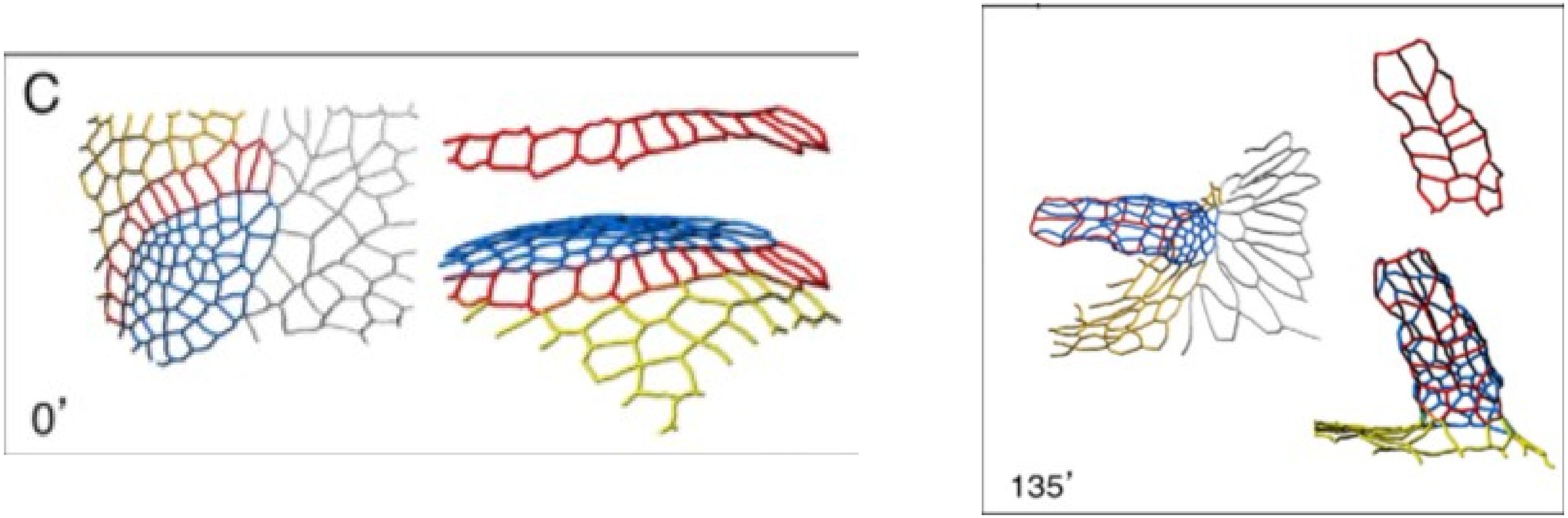
# Diversity of epithelial morphogenesis during eggshell formation in drosophilids

**Miriam Osterfield[1,*], Trudi Schüpbach[2], Eric Wieschaus[2] and Stanislav Y. Shvartsman[1,3]**

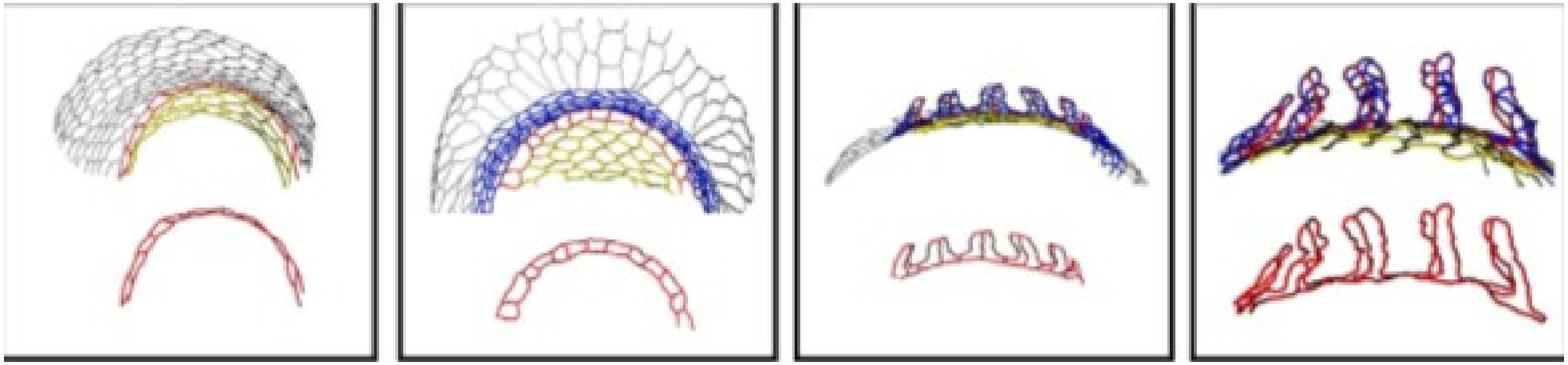


## Dorsal appendages of eggshells





D. melanogaster



S. pattersoni

The appendage floor in Drosophila melanogaster is formed through spatially ordered neighbor exchanges,

The same structure in Scaptodrosophila pattersoni is formed through extreme changes in cell shape, whereas Drosophila funebris appears to display a combination of both cellular mechanisms.

# Gain of *cis*-regulatory activities underlies novel domains of *wingless* gene expression in *Drosophila*

**Shigeyuki Koshikawa[a,b,c], Matt W. Giorgianni[a,b], Kathy Vaccaro[a,b], Victoria A. Kassner[a,b], John H. Yoder[d], Thomas Werner[e], and Sean B. Carroll[a,b,1]**

[a]Laboratory of Molecular Biology, University of Wisconsin, Madison, WI 53706; [b]Howard Hughes Medical Institute, University of Wisconsin, Madison, WI 53706; [c]The Hakubi Center for Advanced Research and Graduate School of Science, Kyoto University, Kyoto 606-8502, Japan; [d]Department of Biological Sciences, University of Alabama, Tuscaloosa, AL 35487; and [e]Department of Biological Sciences, Michigan Technological University, Houghton, MI 49931

Contributed by Sean B. Carroll, May 10, 2015 (sent for review April 2, 2015; reviewed by Michael Eisen and Gregory A. Wray)

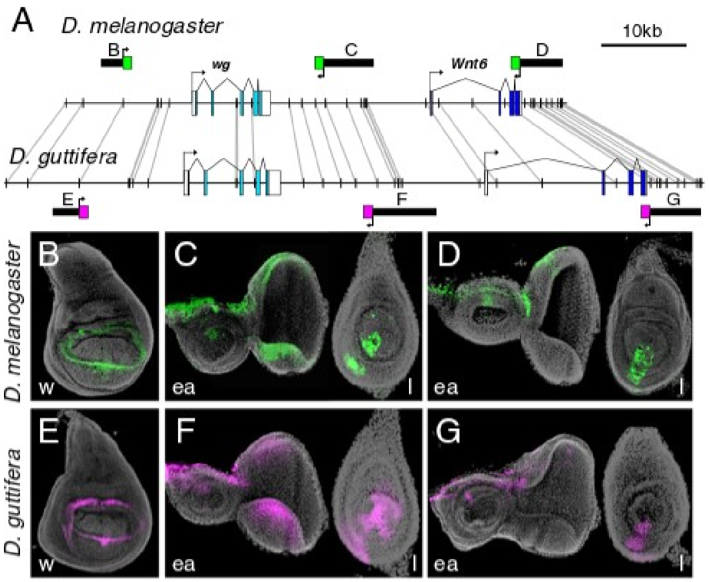


**Fig. 2.** Conserved *wg cis*-regulatory elements control similar gene-expression patterns in *Drosophila* imaginal discs. (*A*) Schematic of enhancers plotted on the *wg* locus of *D. melanogaster* and *D. guttifera*. Solid vertical lines connected by gray lines represent sequences longer than 40 bp with 100% nucleotide conservation between species. (*B–D*) *D. melanogaster* third-instar imaginal discs showing reporter expression with *D. melanogaster* enhancer fragments (EGFP, green). (*E–G*) *D. guttifera* third-instar imaginal discs showing very similar reporter expression patterns driven by orthologous *D. guttifera* enhancer fragments (DsRed, magenta). All discs are oriented with anterior to the left and dorsal on top. ea, eye-antennal disc; l, leg disc; w, wing disc. (Magnification: *B–G*, 200×.)

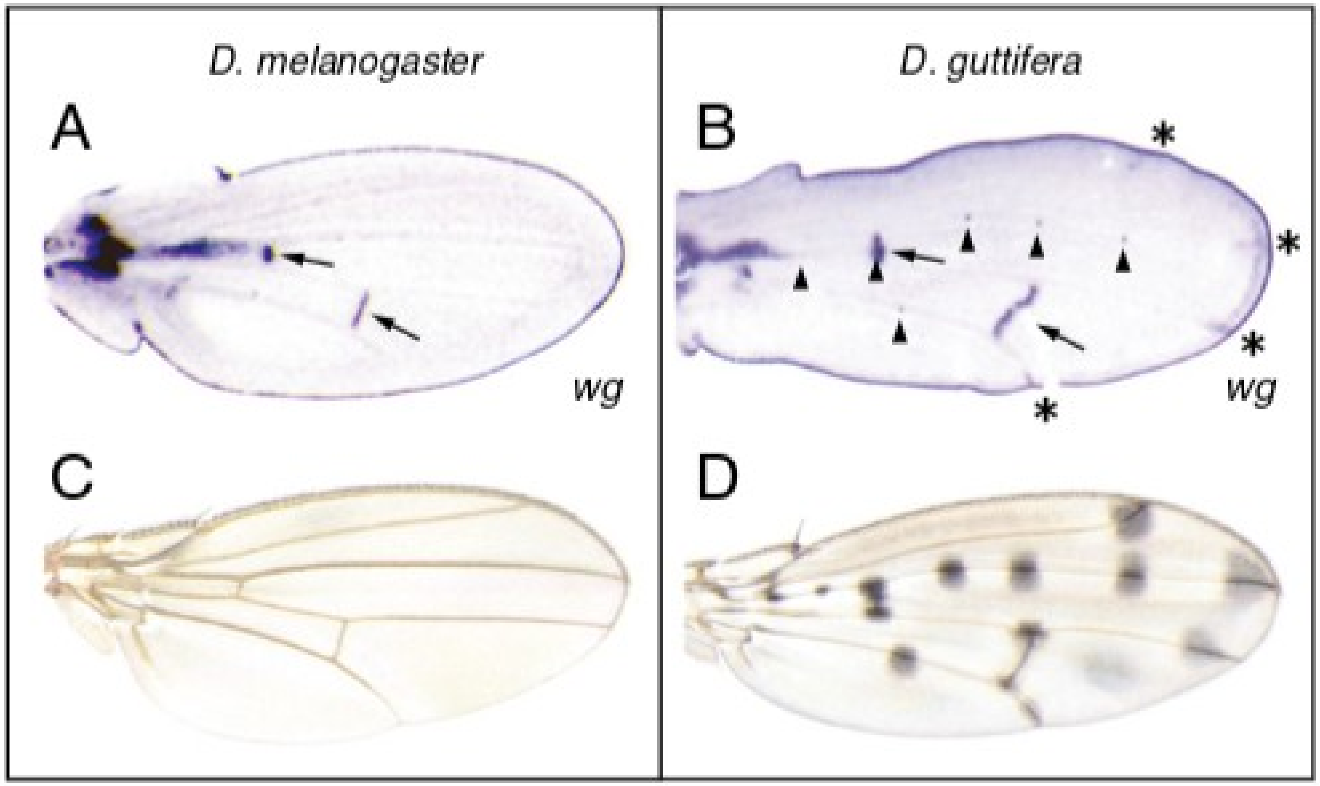
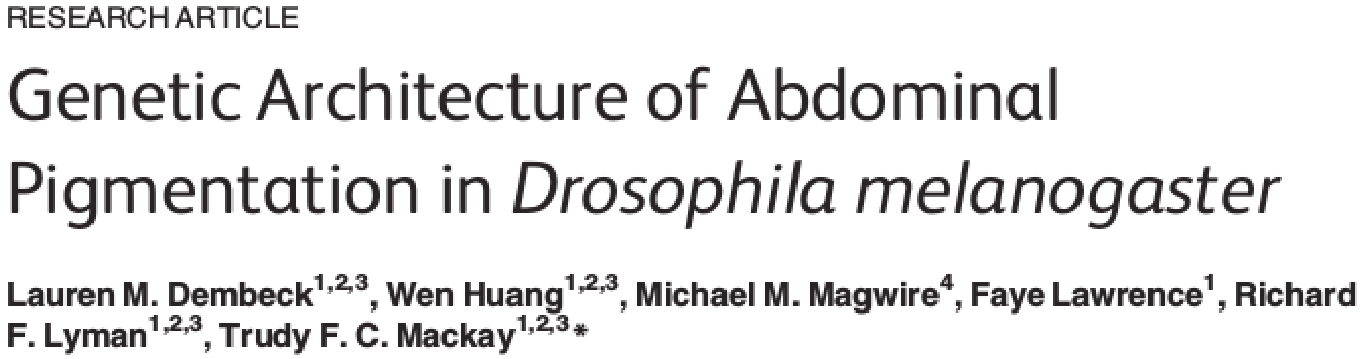


**Fig. 1.** Unique *wg* expression domains in *D. guttifera* pupal wings correlate with adult pigment spots. (*A*) *wg* expression pattern in the pupal wing of *D. melanogaster* visualized by in situ hybridization. *wg* is expressed in the developing crossveins and along the wing margin. (*B*) *wg* expression pattern in the pupal wing of *D. guttifera*. *wg* is expressed in the campaniform sensilla (arrowheads), crossveins (arrows), and longitudinal vein tips (asterisks), and along the entire wing margin. (*C*) Adult wing of *D. melanogaster*. (*D*) Adult wing of *D. guttifera*.

PLOS | GENETICS



RESEARCH ARTICLE

# Genetic Architecture of Abdominal Pigmentation in *Drosophila melanogaster*

**Lauren M. Dembeck**[1,2,3], **Wen Huang**[1,2,3], **Michael M. Magwire**[4], **Faye Lawrence**[1], **Richard F. Lyman**[1,2,3], **Trudy F. C. Mackay**[1,2,3]*

we assessed natural variation in female abdominal pigmentation in 175 sequenced inbred lines of the Drosophila melanogaster Genetic Reference Panel

We quantified the proportion of melanization on the two most posterior abdominal segments, tergites 5 and 6 (T5, T6).

We identified over 150 DNA variants associated with the proportion of melanization.

Mutational analyses and targeted RNAi-knockdown showed that 17 out of 28 (61%) novel candidate genes implicated by the genome-wide association study affected abdominal pigmentation. Several of these genes are involved in developmental and regulatory pathways, chitin production, cuticle structure, and vesicle formation and transport. These findings show that genetic variation may affect multiple steps in pathways involved in tergite development and melanization.

*ISSN 1062-3604, Russian Journal of Developmental Biology, 2015, Vol. 46, No. 3, pp. 99–110. © Pleiades Publishing, Inc., 2015.*
*Original Russian Text © T.A. Bukharina, D.P. Furman, 2015, published in Ontogenez, 2015, Vol. 46, No. 3, pp. 131–142.*

**REVIEWS**

# The Mechanisms Determining Bristle Pattern in *Drosophila melanogaster*[1]

**T. A. Bukharina[a] and D. P. Furman[a, b]**

[a] *Institute of Cytology and Genetics, Siberian Branch, Russian Academy of Sciences,*
*pr. Lavrent'eva 10, Novosibirsk, 630090 Russia*

[b] *Novosibirsk State University, ul. Pirogova 2, Novosibirsk, 630090 Russia*

*e-mail: bukharina@bionet.nsc.ru*

Received April 3, 2014; in final form, December 5, 2014

**Abstract**—Macrochaetes (large bristles) are arranged on the drosophila head and notum in a specific bristle pattern. The number and positions of the macrochaetes forming the pattern are important species-specific characteristics, which are determined by a strict positioning of the proneural clusters in the in the imaginal disc ectoderm in the third instar larvae and prepupae. In turn, the positioning of proneural clusters depends on the distribution of the so-called prepattern factors, responsible for the bristle prepatterning. The current concept identifies the prepattern factors with the transcription factors that initiate the local expression of the *achaete-scute* complex (*AS-C*) genes. Expression of these genes confined to certain regions of the ectoderm is the particular factor that determines the macrochaete pattern on the adult fly body. The review considers and systematizes the data on establishment of the prepatterning as the final stage in the functioning of hierarchically organized molecular genetic system resulting in the local expression of *AS-C* genes in the ectoderm of imaginal discs.

*Keywords*: drosophila, macrochaetes, prepattern, morphogenesis

**DOI:** 10.1134/S1062360415030029

# No evidence for external genital morphology affecting cryptic female choice and reproductive isolation in *Drosophila*

Hélène LeVasseur-Viens[1], Michal Polak[2], and Amanda J. Moehring[1,*]

we used a microdissection laser to alter the morphology of the external male genitalia in Drosophila.

We evaluate the effect of precision alterations to lobe morphology on both interspecific and intraspecific mating

We demonstrate experimentally that the male genital lobes do not affect copulation duration or cryptic female choice.

we demonstrate that the lobes are essential for copulation to occur.

slight alterations to the lobes significantly reduced copulatory success only in competitive environments (i.e., male competition).

NB : surgical control males : hairs from the genital region removed

Civetta and Gaudreau *BMC Evolutionary Biology* (2015) 15:75
DOI 10.1186/s12862-015-0355-8

BMC Evolutionary Biology

**RESEARCH ARTICLE** **Open Access**

# Hybrid male sterility between *Drosophila willistoni* species is caused by male failure to transfer sperm during copulation

Alberto Civetta* and Chelsea Gaudreau

## Abstract

**Background:** The biological concept of species stresses the importance of understanding what mechanisms maintain species reproductively isolated from each other. Often such mechanisms are divided into premating and postmating, with the latest being the result of either prezygotic or postzygotic isolation barriers. *Drosophila willistoni quechua* and *Drosophila willistoni willistoni* are two subspecies that experience reproductive isolation. When a *D. w. quechua* female is crossed with a *D. w. willistoni* male, the hybrid males ($F_{1QW}$) are unable to father progeny; however, the reciprocal cross produces fertile hybrids. Thus, the mechanism of isolation is unidirectional hybrid male sterility. However, the sterile $F_{1QW}$ males contain large amounts of motile sperm. Here we explore whether pre-copulatory or post-copulatory pre-zygotic mechanisms serve as major deterrents in the ability of $F_{1QW}$ males to father progeny.

**Results:** Comparisons of parental and hybrid males copulation durations showed no significant reduction in copulation duration of $F_{1QW}$ males. Interrupted copulations of the parental species confirmed that sperm transfer occurs before the minimum copulation duration registered for $F_{1QW}$ males. However, we found that when females mate with $F_{1QW}$ males, sperm is not present inside the female storage organs and that the lack of sperm in storage is due to failure to transfer sperm rather than spillage or active sperm dumping by females.

**Conclusions:** Sterility of $F_{1QW}$ hybrid males is primarily driven by their inability to transfer sperm during copulation.

**Keywords:** Hybrid male sterility, *Drosophila*, Speciation, Sperm transfer

eLIFE
elifesciences.org

FEATURE ARTICLE

THE NATURAL HISTORY OF MODEL ORGANISMS

# The secret lives of *Drosophila* flies

THE NATURAL HISTORY OF MODEL ORGANISMS

**Abstract** Flies of the genus *Drosophila*, and particularly those of the species *Drosophila melanogaster*, are best known as laboratory organisms. As with all model organisms, they were domesticated for empirical studies, but they also continue to exist as wild populations. Decades of research on these flies in the laboratory have produced astounding and important insights into basic biological processes, but we have only scratched the surface of what they have to offer as research organisms. An outstanding challenge now is to build on this knowledge and explore how natural history has shaped *D. melanogaster* in order to advance our understanding of biology more generally.

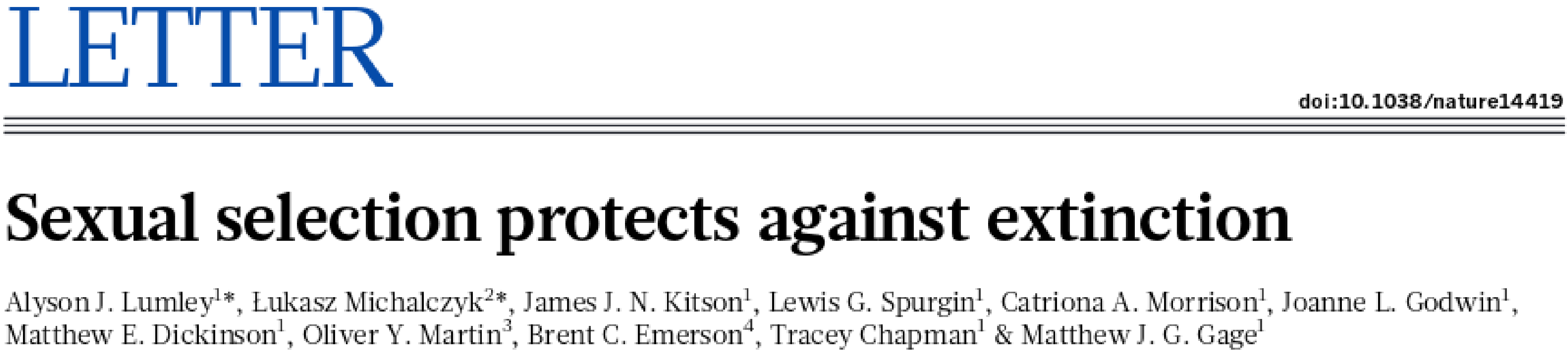
DOI: 10.7554/eLife.06793.001

**THERESE ANN MARKOW***

## Box 1. Outstanding questions about the natural history of *Drosophila*

- Why can some *Drosophila* species feed and breed in certain resources while other species cannot?
- Why can some *Drosophila* species tolerate extreme environmental conditions while others cannot?
- What accounts for the particular microbial communities found inside the guts of *D. melanogaster* and of other species?
- What accounts for the astounding variability in the reproductive biology of *Drosophila* species?

DOI: 10.7554/eLife.06793.005


LETTER

doi:10.1038/nature14419

# Sexual selection protects against extinction

Alyson J. Lumley[1]*, Łukasz Michalczyk[2]*, James J. N. Kitson[1], Lewis G. Spurgin[1], Catriona A. Morrison[1], Joanne L. Godwin[1], Matthew E. Dickinson[1], Oliver Y. Martin[3], Brent C. Emerson[4], Tracey Chapman[1] & Matthew J. G. Gage[1]

It has been theorized that sex costs could be countered if sex allows sexual selection to clear the universal fitness constraint of mutation load

After evolving replicate populations of the flour beetle Tribolium castaneum for 6 to 7 years under conditions that differed solely in the strengths of sexual selection, we revealed mutation load using inbreeding. Lineages from populations that had previously experienced strong sexual selection were resilient to extinction and maintained fitness under inbreeding, with some families continuing to survive after 20 generations of sib × sib mating. By contrast, lineages derived from populations that experienced weak or non-existent sexual selection showed rapid fitness declines under inbreeding, and all were extinct after generation 10.

TOPIC PAGE

# Inferring Horizontal Gene Transfer

Matt Ravenhall, Nives Škunca, Florent Lassalle, Christophe Dessimoz

Published: May 28, 2015 • DOI: 10.1371/journal.pcbi.1004095 • Featured in PLOS Collections

| 4 Saves | 0 Citations |
|---|---|
| 613 Views | 51 Shares |

## Abstract

Horizontal or Lateral Gene Transfer (HGT or LGT) is the transmission of portions of genomic DNA between organisms through a process decoupled from vertical inheritance. In the presence of HGT events, different fragments of the genome are the result of different evolutionary histories. This can therefore complicate the investigations of evolutionary relatedness of lineages and species. Also, as HGT can bring into genomes radically different genotypes from distant lineages, or even new genes bearing new functions, it is a major source of phenotypic innovation and a mechanism of niche adaptation. For example, of particular relevance to human health is the lateral transfer of antibiotic resistance and pathogenicity determinants, leading to the emergence of pathogenic lineages [1]. Computational identification of HGT events relies upon the investigation of sequence composition or evolutionary history of genes. Sequence composition-based ("parametric") methods search for deviations from the genomic average, whereas evolutionary history-based (" phylogenetic") approaches identify genes whose evolutionary history significantly differs from that of the host species. The evaluation and benchmarking of HGT inference methods typically rely upon simulated genomes, for which the true history is known. On real data, different methods tend to infer different HGT events, and as a result it can be difficult to ascertain all but simple and clear-cut HGT events.