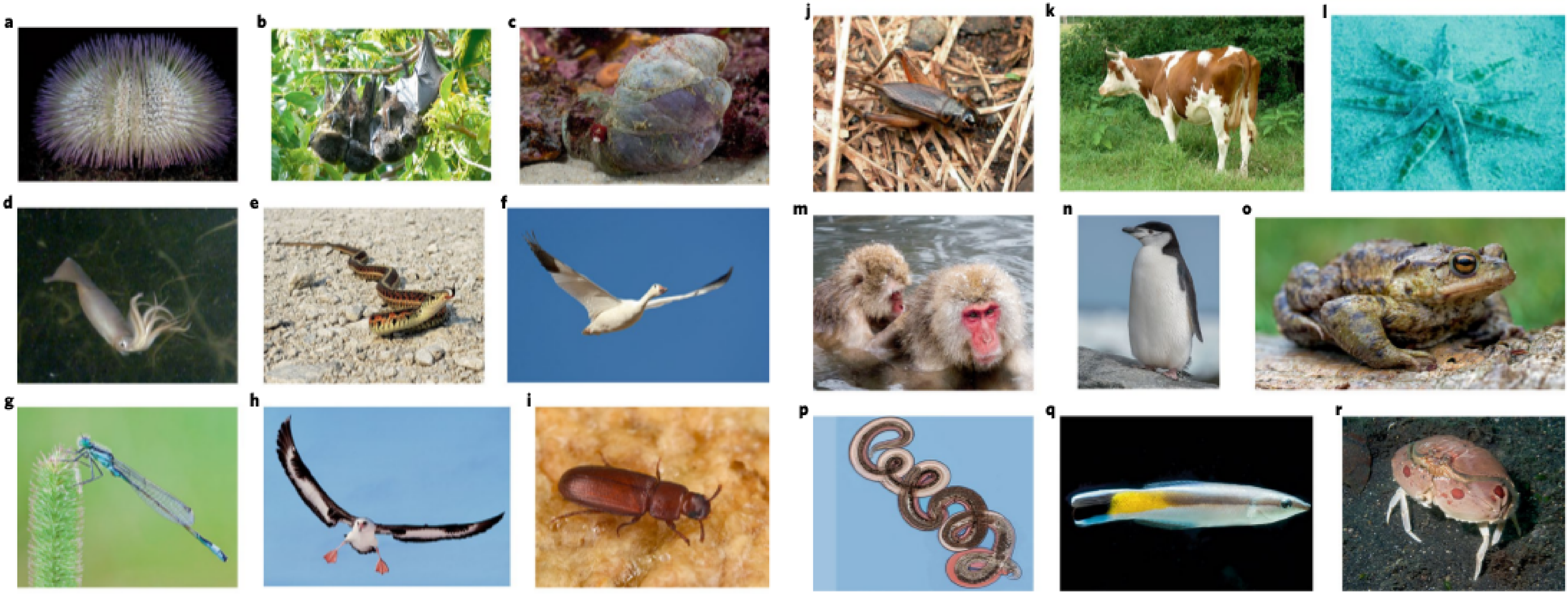
Press report – November 2019

Which character do these species share?

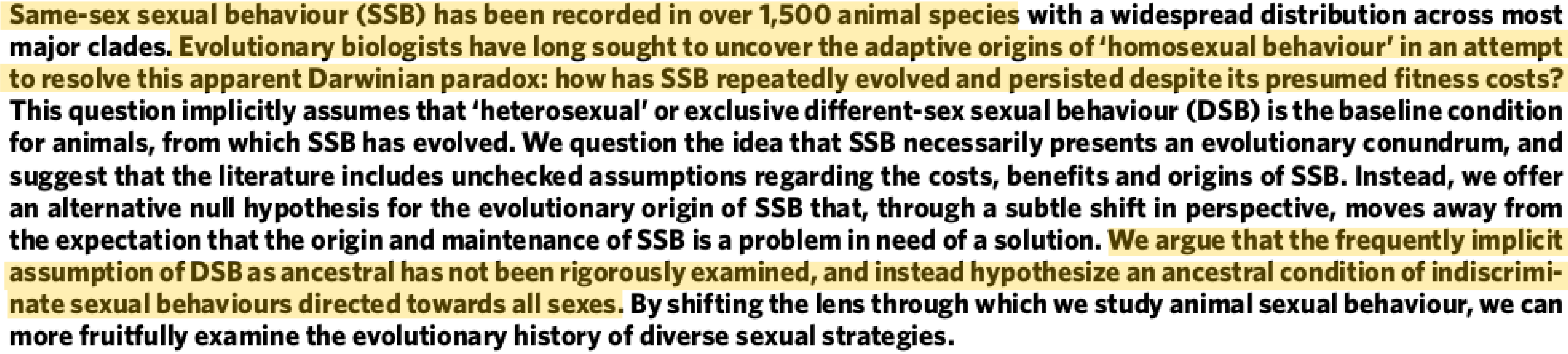


Bénédicte

Monk et al., 2019

An alternative hypothesis for the evolution of same-sex sexual behaviour in animals

J. D. Monk, E. Giglio, A. Kamath, M. R. Lambert and C. E. McDonough -
Nature Ecology & Evolution
doi: https://doi.org/10.1038/s41559-019-1019-7



Same-sex sexual behaviour (SSB) has been recorded in over 1,500 animal species with a widespread distribution across most major clades. Evolutionary biologists have long sought to uncover the adaptive origins of 'homosexual behaviour' in an attempt to resolve this apparent Darwinian paradox: how has SSB repeatedly evolved and persisted despite its presumed fitness costs? This question implicitly assumes that 'heterosexual' or exclusive different-sex sexual behaviour (DSB) is the baseline condition for animals, from which SSB has evolved. We question the idea that SSB necessarily presents an evolutionary conundrum, and suggest that the literature includes unchecked assumptions regarding the costs, benefits and origins of SSB. Instead, we offer an alternative null hypothesis for the evolutionary origin of SSB that, through a subtle shift in perspective, moves away from the expectation that the origin and maintenance of SSB is a problem in need of a solution. We argue that the frequently implicit assumption of DSB as ancestral has not been rigorously examined, and instead hypothesize an ancestral condition of indiscriminate sexual behaviours directed towards all sexes. By shifting the lens through which we study animal sexual behaviour, we can more fruitfully examine the evolutionary history of diverse sexual strategies.

An alternative hypothesis for the evolution of same-sex sexual behaviour in animals

J. D. Monk, E. Giglio, A. Kamath, M. R. Lambert and C. E. McDonough - Nature Ecology & Evolution
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« We note, however, that a population comprised entirely of exclusive [Same-sex Sexual Behavior] individuals would likely go extinct. »

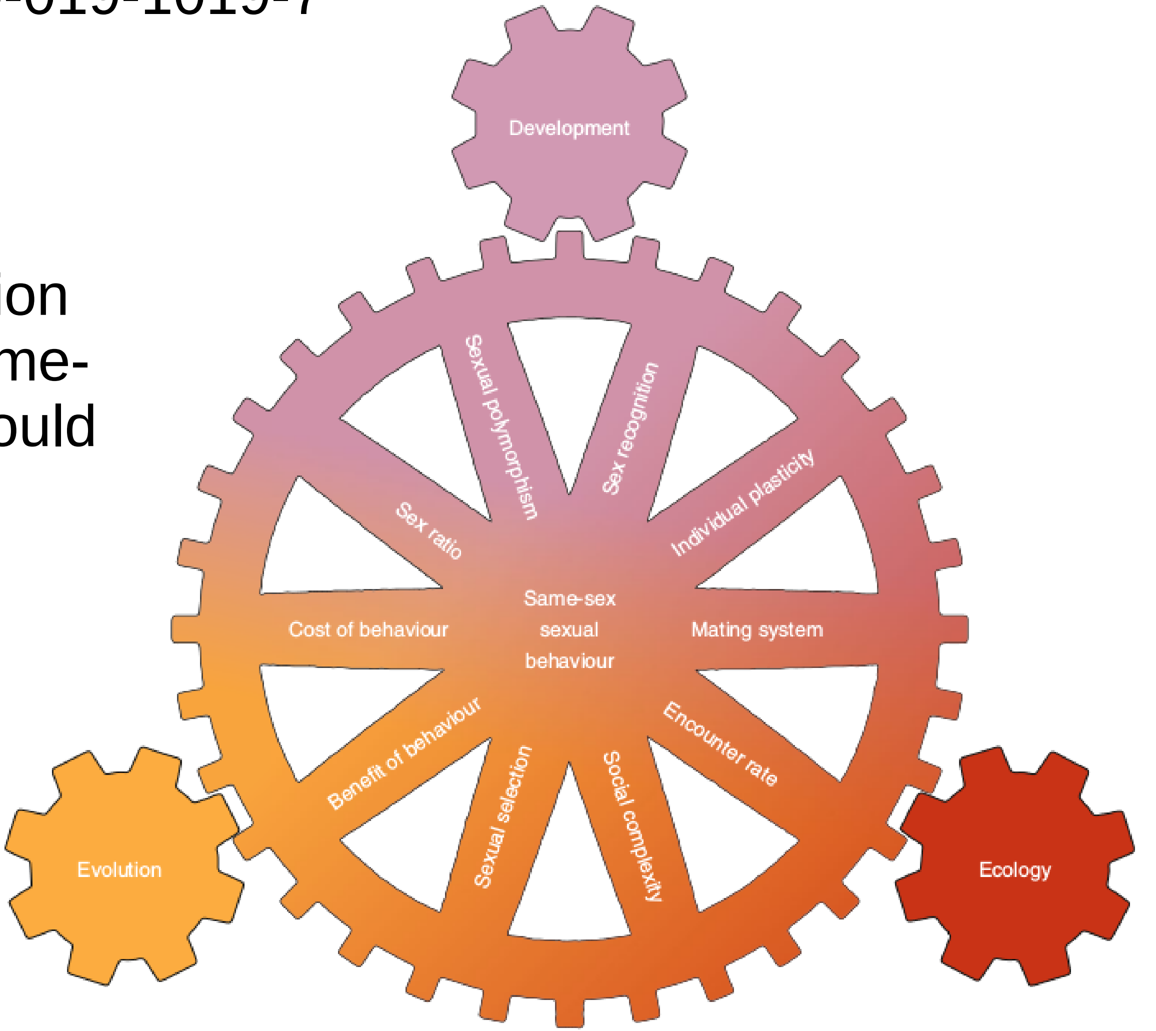
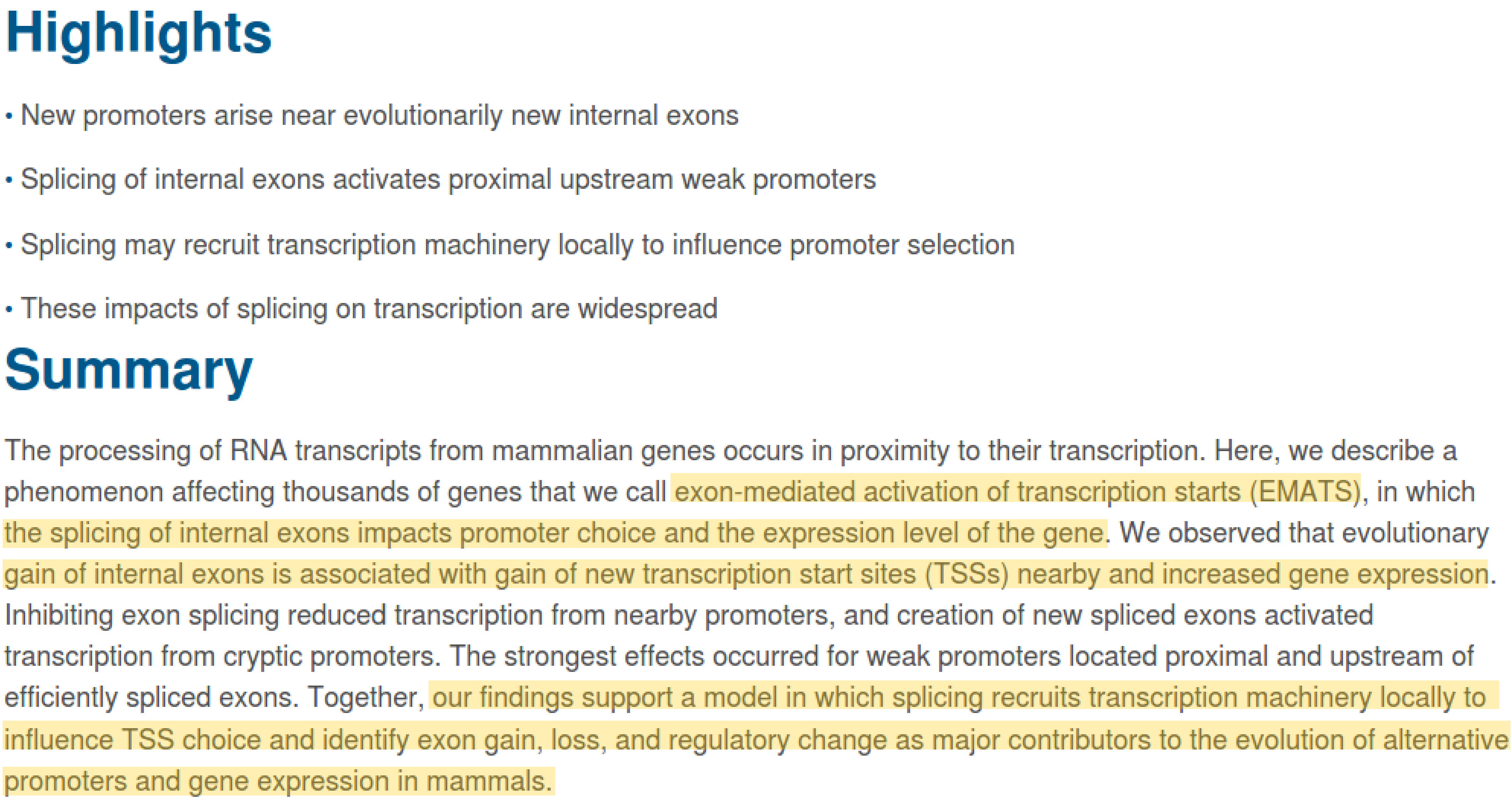


Fig. 3 | Ecological, evolutionary and developmental factors may influence the expression of SSB

Exon-Mediated Activation of Transcription Starts

A. Fiszbein, K. S. Krick, B. E. Begg, C. B. Burge - Cell
doi: https://doi.org/10.1016/j.cell.2019.11.002



Highlights

- New promoters arise near evolutionarily new internal exons
- Splicing of internal exons activates proximal upstream weak promoters
- Splicing may recruit transcription machinery locally to influence promoter selection
- These impacts of splicing on transcription are widespread

Summary

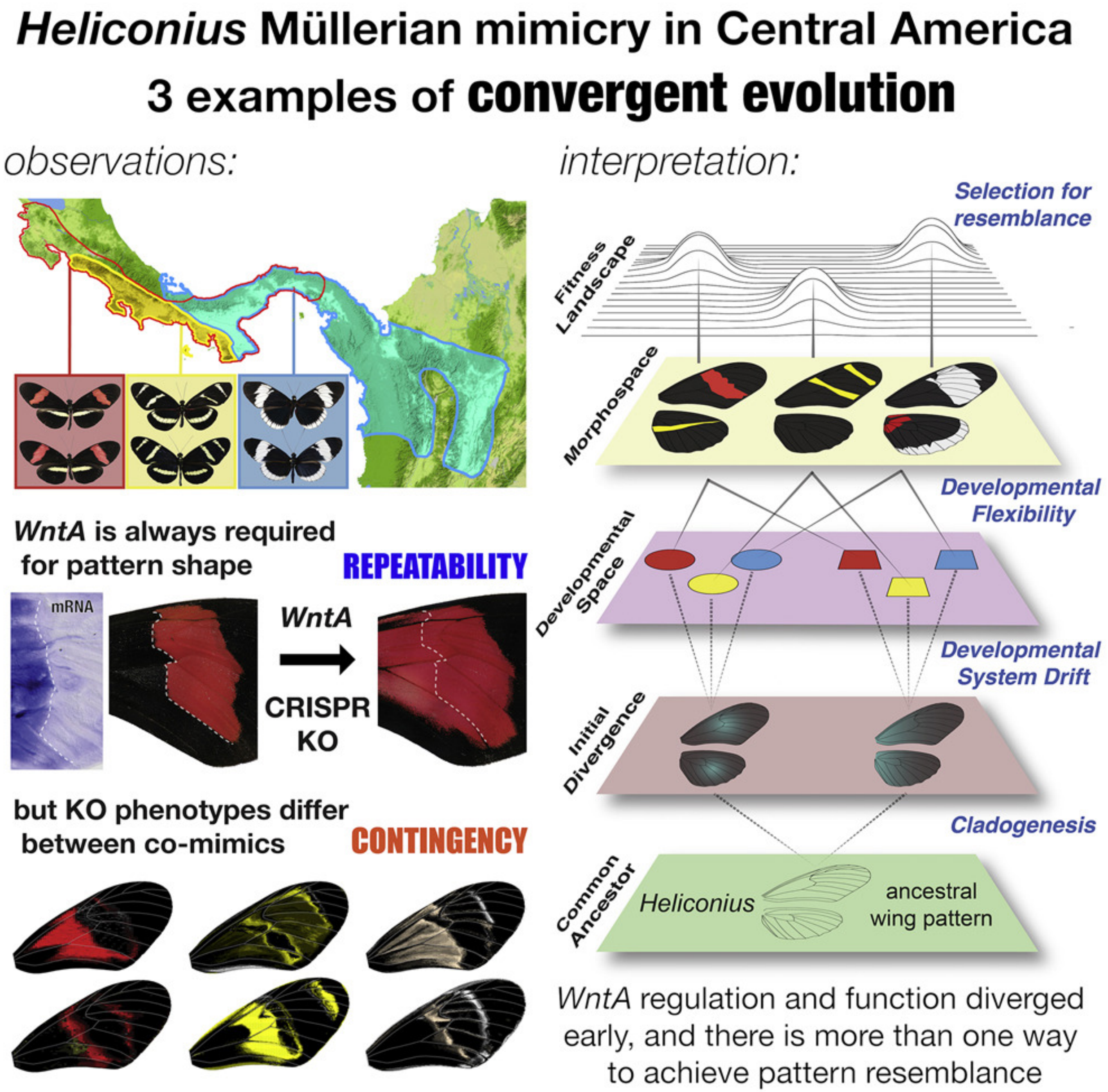
The processing of RNA transcripts from mammalian genes occurs in proximity to their transcription. Here, we describe a phenomenon affecting thousands of genes that we call exon-mediated activation of transcription starts (EMATS), in which the splicing of internal exons impacts promoter choice and the expression level of the gene. We observed that evolutionary gain of internal exons is associated with gain of new transcription start sites (TSSs) nearby and increased gene expression. Inhibiting exon splicing reduced transcription from nearby promoters, and creation of new spliced exons activated transcription from cryptic promoters. The strongest effects occurred for weak promoters located proximal and upstream of efficiently spliced exons. Together, our findings support a model in which splicing recruits transcription machinery locally to influence TSS choice and identify exon gain, loss, and regulatory change as major contributors to the evolution of alternative promoters and gene expression in mammals.

Interplay between Developmental Flexibility and Determinism in the Evolution of Mimetic Heliconius Wing Patterns

C. Concha, R. Wallbank, J. Hanly, J. Fenner, L. Livraghi, E. Santiago Rivera, D. Paulo, C. Arias, M. Vargas, M. Sanjeev, C. Morrison, D. Tian, P. Aguirre, S. Ferrara, J. Foley, C. Pardo-Diaz, C. Salazar, M. Linares, D. Massardo, B. Counterman, M. Scott, C. Jiggins, R. Papa, A. Martin, W. McMillan

doi: https://doi.org/10.1016/j.cub.2019.10.010

Interplay between Developmental Flexibility and Determinism in the Evolution of Mimetic Heliconius Wing Patterns



***Heliconius* Müllerian mimicry in Central America**

3 examples of convergent evolution

WntA is always required for pattern shape

but KO phenotypes differ between co-mimics

WntA regulation and function diverged early, and there is more than one way to achieve pattern resemblance

Interplay between Developmental Flexibility and Determinism in the Evolution of Mimetic Heliconius Wing Patterns

C. Concha, R. Wallbank, J. Hanly, J. Fenner, L. Livraghi, E. Santiago Rivera, D. Paulo, C. Arias, M. Vargas, M. Sanjeev, C. Morrison, D. Tian, P. Aguirre, S. Ferrara, J. Foley, C. Pardo-Diaz, C. Salazar, M. Linares, D. Massardo, B. Counterman, M. Scott, C. Jiggins, R. Papa, A. Martin, W. McMillan

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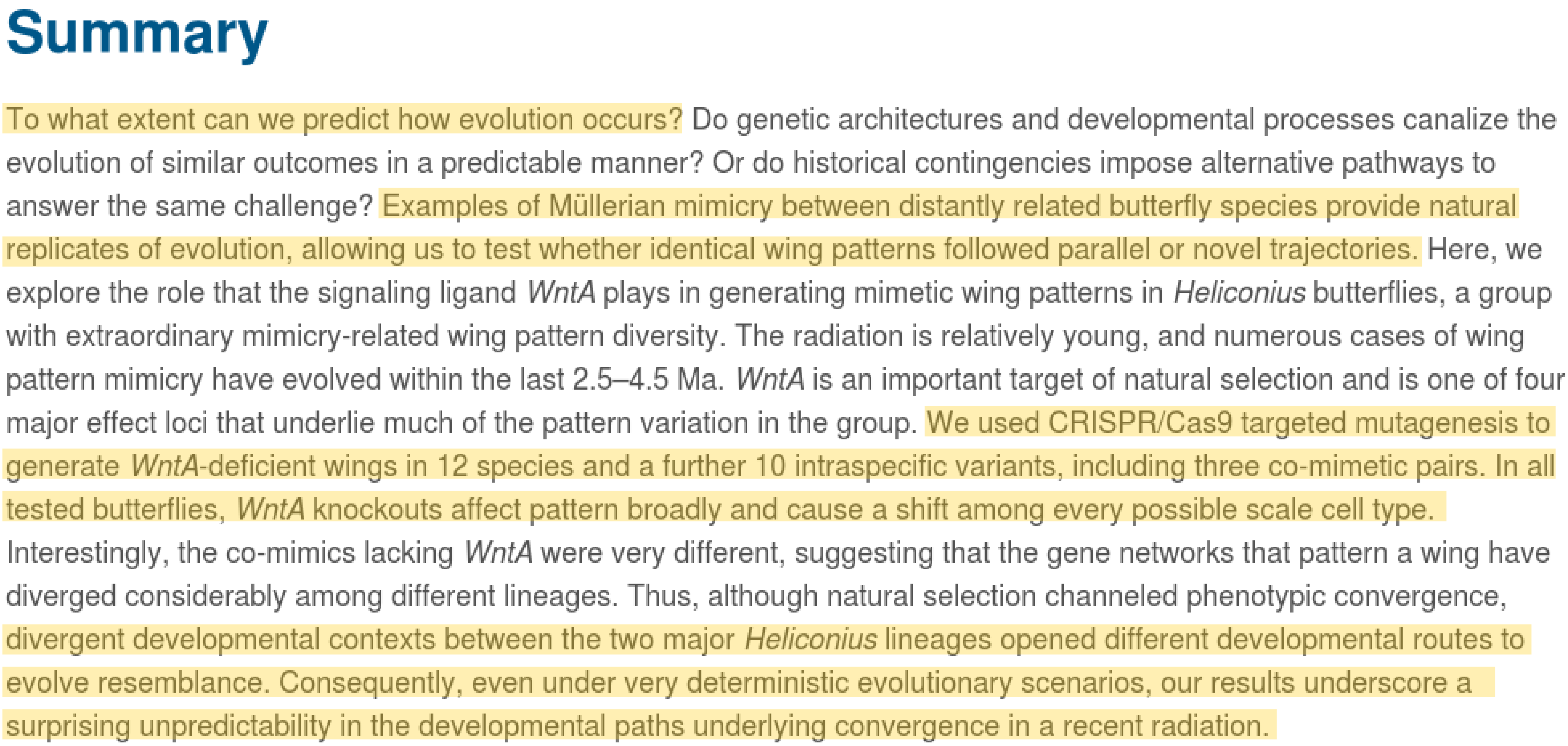

Summary

To what extent can we predict how evolution occurs? Do genetic architectures and developmental processes canalize the evolution of similar outcomes in a predictable manner? Or do historical contingencies impose alternative pathways to answer the same challenge? Examples of Müllerian mimicry between distantly related butterfly species provide natural replicates of evolution, allowing us to test whether identical wing patterns followed parallel or novel trajectories. Here, we explore the role that the signaling ligand *WntA* plays in generating mimetic wing patterns in *Heliconius* butterflies, a group with extraordinary mimicry-related wing pattern diversity. The radiation is relatively young, and numerous cases of wing pattern mimicry have evolved within the last 2.5–4.5 Ma. *WntA* is an important target of natural selection and is one of four major effect loci that underlie much of the pattern variation in the group. We used CRISPR/Cas9 targeted mutagenesis to generate *WntA*-deficient wings in 12 species and a further 10 intraspecific variants, including three co-mimetic pairs. In all tested butterflies, *WntA* knockouts affect pattern broadly and cause a shift among every possible scale cell type. Interestingly, the co-mimics lacking *WntA* were very different, suggesting that the gene networks that pattern a wing have diverged considerably among different lineages. Thus, although natural selection channeled phenotypic convergence, divergent developmental contexts between the two major *Heliconius* lineages opened different developmental routes to evolve resemblance. Consequently, even under very deterministic evolutionary scenarios, our results underscore a surprising unpredictability in the developmental paths underlying convergence in a recent radiation.

The genomic footprint of sexual conflict

A. Sayadi, A. Martinez Barrio, E. Immonen, J. Dainat, D. Berger, C. Tellgren-Roth, B. Nystedt & G. Arnqvist, Nature ecology & evolution.
DOI : https://doi.org/10.1038/s41559-019-1041-9

Abstract

Genes with sex-biased expression show a number of unique properties and this has been seen as evidence for conflicting selection pressures in males and females, forming a genetic ‘tug-of-war’ between the sexes. However, we lack studies of taxa where an understanding of conflicting phenotypic selection in the sexes has been linked with studies of genomic signatures of sexual conflict. Here, we provide such a link. We used an insect where sexual conflict is unusually well understood, the seed beetle *Callosobruchus maculatus*, to test for molecular genetic signals of sexual conflict across genes with varying degrees of sex-bias in expression. We sequenced, assembled and annotated its genome and performed population resequencing of three divergent populations. Sex-biased genes showed increased levels of genetic diversity and bore a remarkably clear footprint of relaxed purifying selection. Yet, segregating genetic variation was also affected by balancing selection in weakly female-biased genes, while male-biased genes showed signs of overall purifying selection. Female-biased genes contributed disproportionally to shared polymorphism across populations, while male-biased genes, male seminal fluid protein genes and sex-linked genes did not. Genes showing genomic signatures consistent with sexual conflict generally matched life-history phenotypes known to experience sexually antagonistic selection in this species. Our results highlight metabolic and reproductive processes, confirming the key role of general life-history traits in sexual conflict.

Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies

E. Fowler, T. Bradley, S. Moxon, T. Chapman. Scientific reports.
DOI : https://doi.org/10.1038/s41598-019-51141-9

Mating → flash freezing at 3 h after start of mating in liquid N2 → RNA seq on abdomen or head and thorax

Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies

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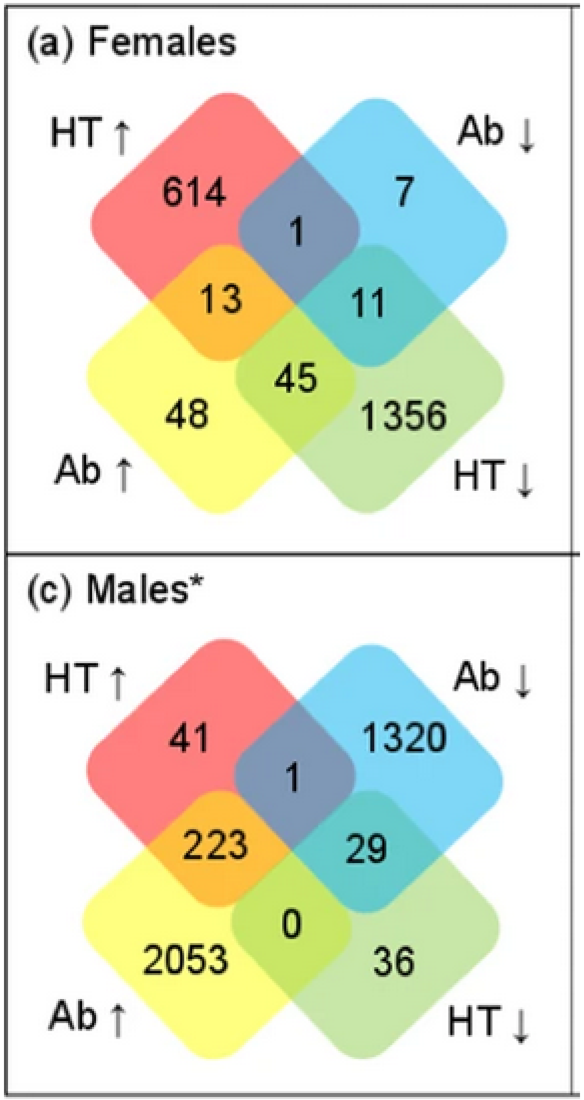
DOI : https://doi.org/10.1038/s41598-019-51141-9

Figure 2



Overlap of the identities of up- and downregulated genes in response to mating in the different transcriptomes. (a) Numbers of DE genes upregulated (↑), or downregulated (↓) in response to mating in female abdomen (Ab) or head-thorax (HT). (c) Numbers of DE genes upregulated, or downregulated in response to mating in male Ab or HT *DE calling based on a significance threshold of $p < 0.05$.

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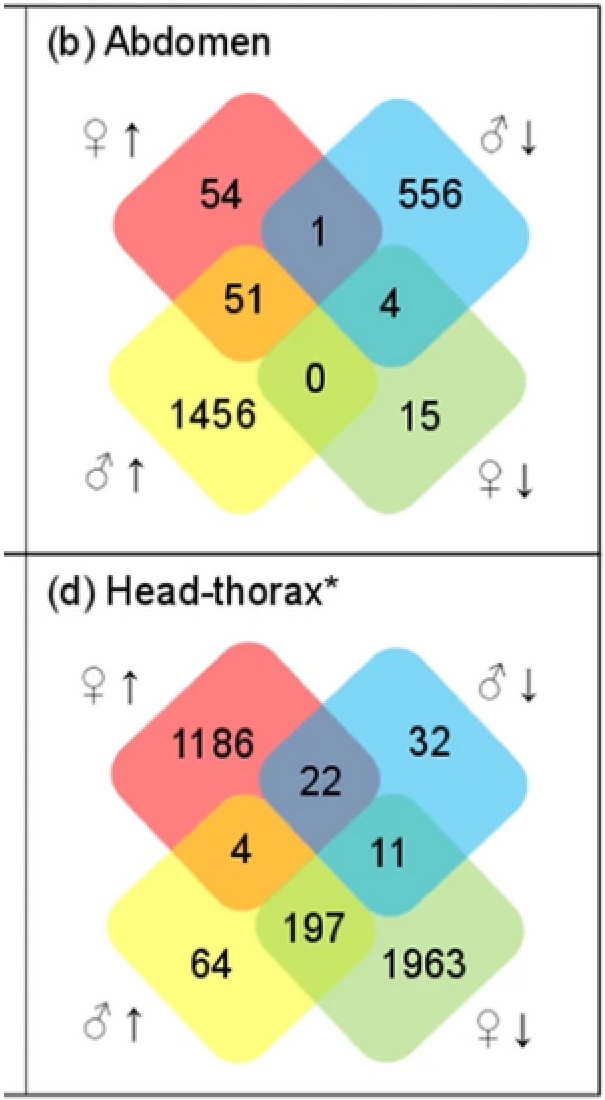
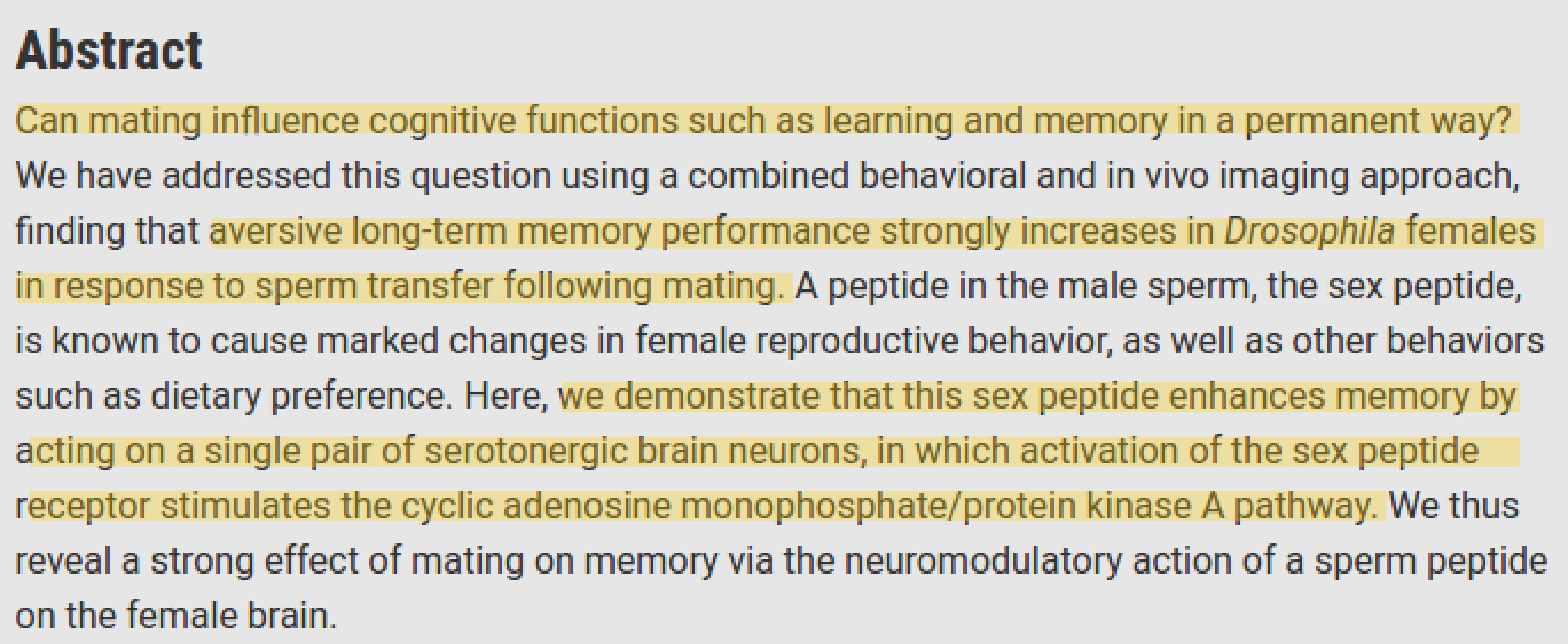


(b) Numbers of DE genes up- or downregulated in female or male Ab tissues. (d) Numbers of DE genes upregulated, or downregulated in response to mating in female (♀) or male (♂) HT tissue. *DE calling based on a significance threshold of $p < 0.05$.

A sperm peptide enhances long-term memory in female Drosophila

L. Scheunemann, A. Lampin-Saint-Amaux, J. Schor and T. Preat*, Sciences advances.
DOI : https://doi.org/10.1126/sciadv.aax3432



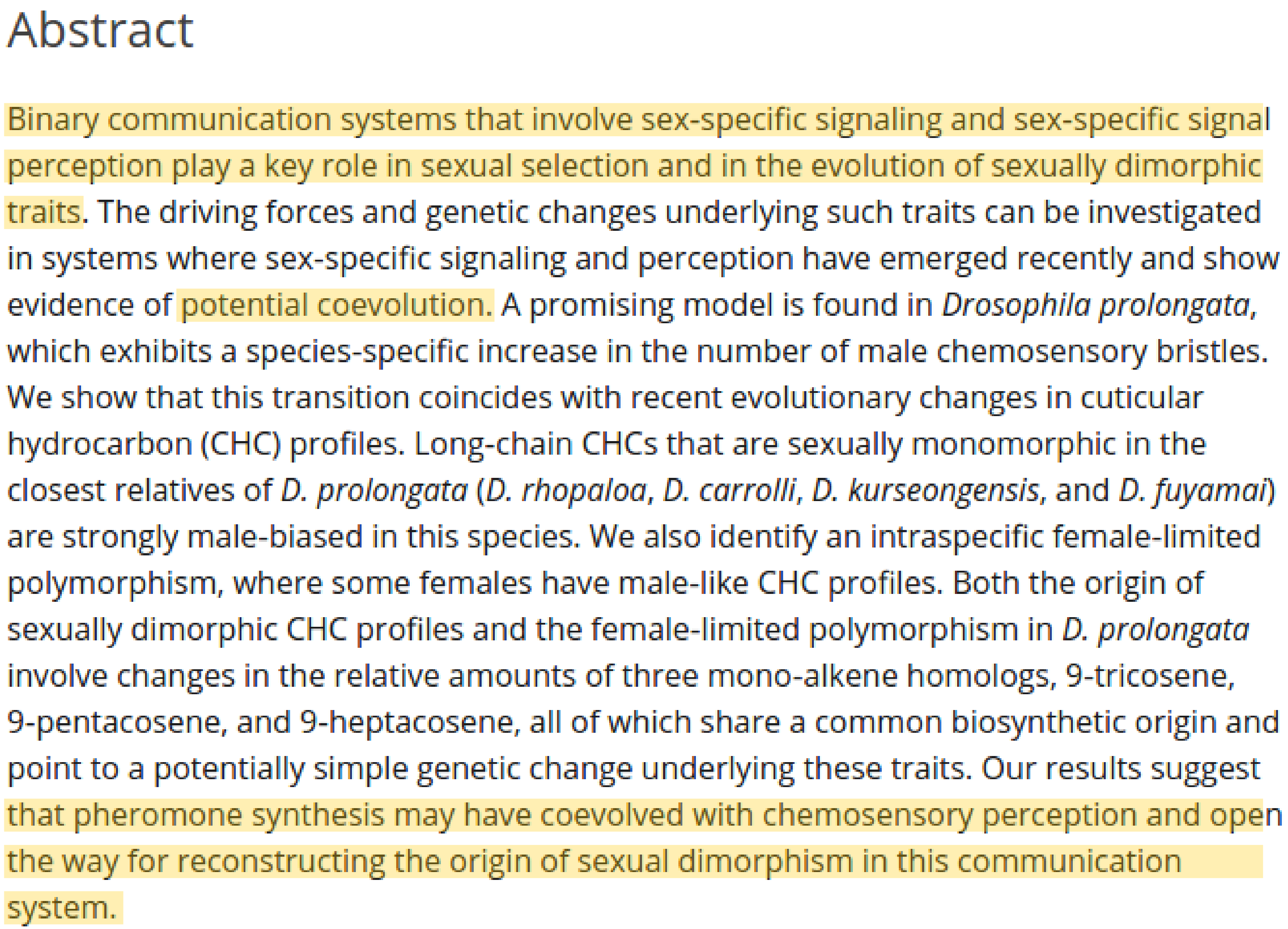
Abstract

Can mating influence cognitive functions such as learning and memory in a permanent way? We have addressed this question using a combined behavioral and in vivo imaging approach, finding that aversive long-term memory performance strongly increases in *Drosophila* females in response to sperm transfer following mating. A peptide in the male sperm, the sex peptide, is known to cause marked changes in female reproductive behavior, as well as other behaviors such as dietary preference. Here, we demonstrate that this sex peptide enhances memory by acting on a single pair of serotonergic brain neurons, in which activation of the sex peptide receptor stimulates the cyclic adenosine monophosphate/protein kinase A pathway. We thus reveal a strong effect of mating on memory via the neuromodulatory action of a sperm peptide on the female brain.

Evolution of sexually dimorphic pheromone profiles coincides with increased number of male-specific chemosensory organs in Drosophila prolongata

Y. Luo, Y. Zhang, J.-P. Farine, J.-F. Ferveur, S. Ramírez, A. Kopp, Ecology and Evolution.

DOI: https://doi.org/10.1002/ece3.5819



Abstract

Binary communication systems that involve sex-specific signaling and sex-specific signal perception play a key role in sexual selection and in the evolution of sexually dimorphic traits. The driving forces and genetic changes underlying such traits can be investigated in systems where sex-specific signaling and perception have emerged recently and show evidence of potential coevolution. A promising model is found in *Drosophila prolongata*, which exhibits a species-specific increase in the number of male chemosensory bristles. We show that this transition coincides with recent evolutionary changes in cuticular hydrocarbon (CHC) profiles. Long-chain CHCs that are sexually monomorphic in the closest relatives of *D. prolongata* (*D. rhopaloa*, *D. carrolli*, *D. kurseongensis*, and *D. fuyamai*) are strongly male-biased in this species. We also identify an intraspecific female-limited polymorphism, where some females have male-like CHC profiles. Both the origin of sexually dimorphic CHC profiles and the female-limited polymorphism in *D. prolongata* involve changes in the relative amounts of three mono-alkene homologs, 9-tricosene, 9-pentacosene, and 9-heptacosene, all of which share a common biosynthetic origin and point to a potentially simple genetic change underlying these traits. Our results suggest that pheromone synthesis may have coevolved with chemosensory perception and open the way for reconstructing the origin of sexual dimorphism in this communication system.

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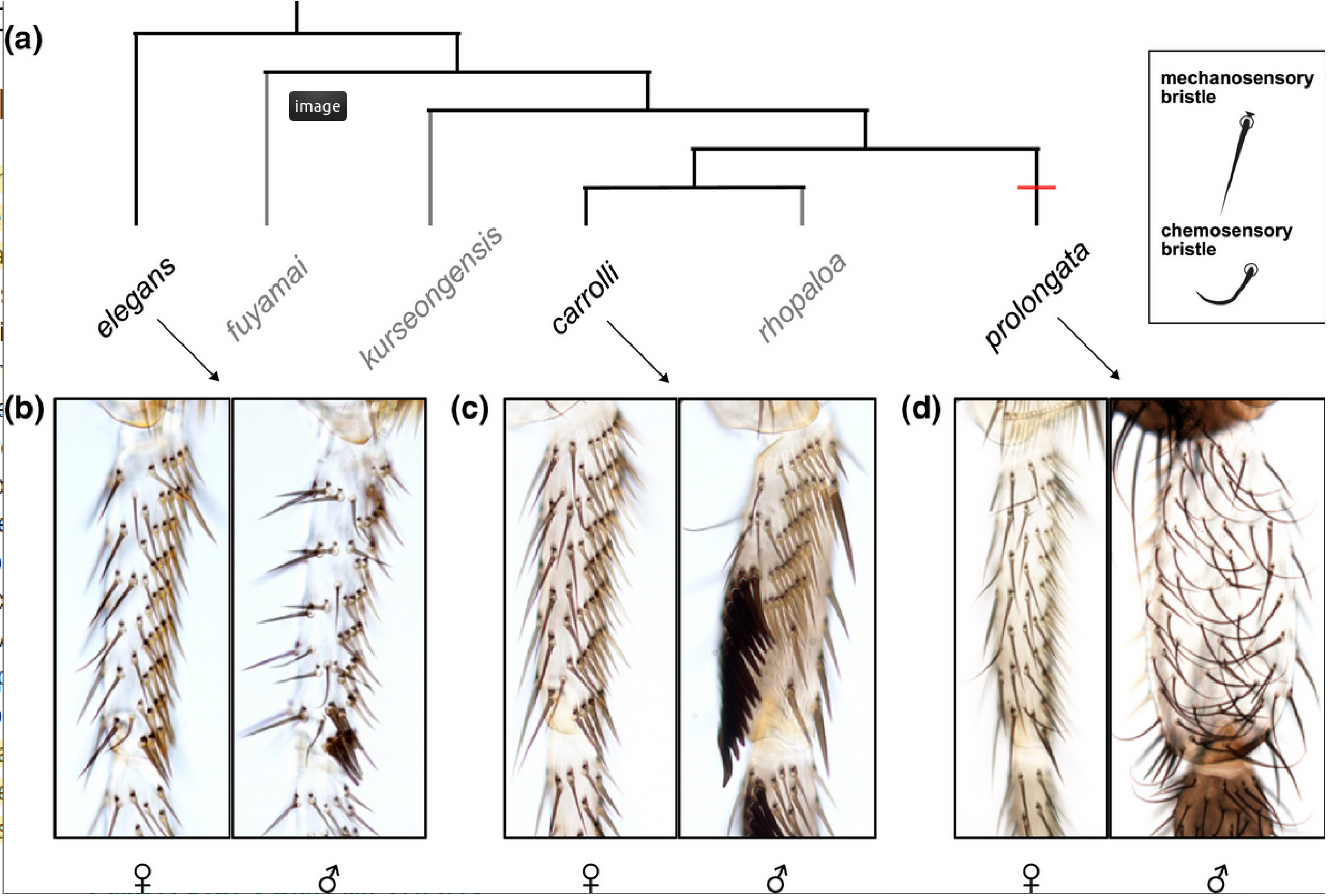

Key words:
Drosophila evolution, left right asymmetry, drosophila courtship, drosophila genitalia, genitalia evolution, drosophila morphogenesis, drosophila bristle, drosophila pachea, glue, bio adhesive, 3D printing

Journals:
Cell, Nature, Science, Plos, Current biology, PNAS, Development, Evolution, Evolution and Development, BioRxiv...

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Evolution

- Dichotomy of Dosage Compensation along the Neo Z Chromosome of the Monarch Butterfly
Gu et al. , Current biology. DOI : https://doi.org/10.1016/j.cub.2019.09.056

- **Exon-Mediated Activation of Transcription Starts**
Fiszbein et al., Cell. DOI : https://doi.org/10.1016/j.cell.2019.11.002

- **Interplay between Developmental Flexibility and Determinism in the Evolution of Mimetic Heliconius Wing Patterns**
Concha et al., Current biology. DOI : https://doi.org/10.1016/j.cub.2019.10.010

- **The genomic footprint of sexual conflict**
A. Sayadi, A. Martinez Barrio, E. Immonen, J. Dainat, D. Berger, C. Tellgren-Roth, B. Nystedt & G. Arnqvist, Nature ecology & evolution. DOI : https://doi.org/10.1038/s41559-019-1041-9

- Molecular and evolutionary dynamics of animal sex-chromosome turnover
Beatriz Vicoso, Nature ecology & evolution. DOI : https://doi.org/10.1038/s41559-019-1050-8

- **An alternative hypothesis for the evolution of same-sex sexual behaviour in animals**
Julia D. Monk, Erin Giglio, Ambika Kamath, Max R. Lambert & Caitlin E. McDonough . Nature ecology and evolution. DOI : https://doi.org/10.1038/s41559-019-1019-7

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- Beetle horns evolved from wing serial homologs
Y. Hu, D. M. Linz, A. P. Moczek, Science.
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- Genomic architecture and introgression shape a butterfly radiation
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- What does mitogenomics tell us about the evolutionary history of the *Drosophila buzzatii* cluster (repleta group)?
N. Moreyra et al., Plos One.
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DOI: https://doi.org/10.1073/pnas.1907068116

- Sexually antagonistic selection promotes genetic divergence between males and females in an ant
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DOI: https://doi.org/10.1073/pnas.1906568116

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Evolution

- **Evolution of sexually dimorphic pheromone profiles coincides with increased number of male-specific chemosensory organs in Drosophila prolongata**

  Y. Luo, Y. Zhang, J.-P. Farine, J.-F. Ferveur, S. Ramírez, A. Kopp, Ecology and Evolution.
  DOI: https://doi.org/10.1002/ece3.5819

- Strong and weak cross-sex correlations govern the quantitative-genetic architecture of social group choice in Drosophila melanogaster

  Adam P. Geiger and Julia B. Saltz, Evolution.
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- Environmental change and the evolution of genomes: Transposable elements (TEs) as translators of phenotypic plasticity into genotypic variability

  Sergio Pimpinelli and Lucia Piacentini, Functionnal ecology.
  DOI: https://doi.org/10.1111/1365-2435.13497

- Rapid divergent co-evolution of freshwater crab genitalia facilitates a burst of species diversification

  Fengxin YAO et al, Integrative zoology.
  DOI: https://doi.org/10.1111/1749-4877.12424

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- Complex evolutionary history of the Y chromosome in flies of the Drosophila obscura species group
Ryan Bracewell, Doris Bachtrog, BioRxiv
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-Inversions shape the divergence of Drosophila pseudoobscura and D. persimilis on multiple timescales
Katharine L Korunes, Carlos A Machado,Mohamed AF Noor, BioRxiv
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Press report – November 2019

Reproductive behavior in *Drosophila*

- **A sperm peptide enhances long-term memory in female *Drosophila***
  L. Scheunemann, A. Lampin-Saint-Amaux, J. Schor and T. Preat
  DOI : 10.1126/sciadv.aax3432

- **Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies**
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- First case of parthenogenesis in ladybirds (Coleoptera: Coccinellidae) suggests new mechanisms for the evolution of asexual reproduction
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- Male age affects female mating preference but not fitness in the monandrous moth Dendrolimus punctatus Walker (Lepidoptera: Lasiocampidae)
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Reproductive behavior in *Drosophila*

- Genotype-by-environment interactions for seminal fluid expression and sperm competitive ability
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- Molecular Evolution of the Sex Peptide Network in Drosophila
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Left-right asymmetry

- Emergence of a Bilaterally Symmetric Pattern from Chiral Components in the Planarian Epidermis
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Drosophila behavior

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- A conserved odorant binding protein is required for essential amino acid detection in Drosophila
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Press report – November 2019

Drosophila development

- Shaping the zebrafish myotome by intertissue friction and active stress
S. Tlili et al., PNAS.
DOI: https://doi.org/10.1073/pnas.1900819116

-Drosophila suzukii wing spot size is robust to developmental temperature
Ceferino Varón-González, Antoine Fraimout,Vincent Debat, BioRxiv
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C. Varón-González, A. Fraimout, A. Delapré, V. Debat, R. Cornette, BioRxiv
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Glue & bio adhesives

- Bound to get to the heart of a sticky problem
Eoin O’Cearbhaill, Science Translational Medicine. DOI: 10.1126/scitranslmed.aaz9755

- Linking energy loss in soft adhesion to surface roughness
S. Dalvi, et al., PNAS.
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- Mussel-Inspired Polymerization of Peptides: The Chemical Activation Route as Key to Broaden the Sequential Space of Artificial Mussel-Glue Proteins
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DOI: https://doi.org/10.1002/marc.201900431

Press report – November 2019

Tools

- Exploiting open source 3D printer architecture for laboratory robotics to automate high-throughput time-lapse imaging for analytical microbiology

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Shuai Zhan et al., Cell research. DOI : https://doi.org/10.1038/s41422-019-0252-6