Press report April 2015
Virginie Orgogozo

Drosophila evolution

Tanaka, K. M., Hopfen, C., Herbert, M. R., Schlötterer, C., Stern, D. L., Masly, J. P., ... & Nunes, M. D. (2015). Genetic Architecture and Functional Characterization of Genes Underlying the Rapid Diversification of Male External Genitalia Between Drosophila simulans and Drosophila mauritiana. *Genetics*, *200*(1), 357-369.
Using QTL and introgression-based high-resolution mapping, we identified several small regions on chromosome arms 3L and 3R that contribute to differences in morphology of the claspers, posterior lobes, and anal plates exhibit striking differences between Drosophila mauritiana and D. simulans.

Sofía Lavista-LlanosCorresponding Author, Aleš Svatoš, Marco Kai, Thomas Riemensperger, Serge Birman, Marcus C Stensmyr, Bill S Hansson. Dopamine drives Drosophila sechellia adaptation to its toxic host. eLife 2014;3:e03785.
We analyzed the tight association of Drosophila sechellia to its sole host, the fruit of Morinda citrifolia, which is toxic to other members of the melanogaster species group. Molecular polymorphisms in the dopamine regulatory protein Catsup cause infertility in D. sechellia due to maternal arrest of oogenesis. In its natural host, the fruit compensates for the impaired maternal dopamine metabolism with the precursor l-DOPA, resuming oogenesis and stimulating egg production. l-DOPA present in morinda additionally increases the size of D. sechellia eggs, what in turn enhances early fitness. We argue that the need of l-DOPA for successful reproduction has driven D. sechellia to become an M. citrifolia obligate specialist. This study illustrates how an insect's dopaminergic system can sustain ecological adaptations by modulating ontogenesis and development.

Dworkin, I., & Jones, C. D. (2015). Evolutionary Genetics: You Are What You Evolve to Eat. *Current Biology*, *25*(8), R341-R344.
The evolution of host specialization can potentially limit future evolutionary opportunities. A new study now shows how Drosophila sechellia, specialized on the toxic Morinda fruit, has evolved new nutritional needs influencing its reproduction.

Turissini, D. A., Liu, G., David, J. R., & Matute, D. R. (2015). The evolution of reproductive isolation in the Drosophila yakuba complex of species. *Journal of Evolutionary Biology*. Alex, Isabelle, Olga

Eric M. Camino, John C. Butts, Alison Ordway, Jordan E. Vellky, Mark Rebeiz, Thomas M. Williams. The Evolutionary Origination and Diversification of a Dimorphic Gene Regulatory Network through Parallel Innovations in cis and trans. PLOS Genetics: published 02 Apr 2015 | info:doi/10.1371/journal.pgen.1005136
By elucidating how yellow and tan are connected to the web of abdominal trans-regulators, we discovered that the yellow and tan abdominal CREs are composed of distinct regulatory inputs that exhibit contrasting responses to the same Hox proteins and Hox cofactors. These results provide an example in which CRE origination underlies a recently evolved novel trait, and highlights how coordinated expression patterns can evolve in parallel through the generation of unique regulatory linkages.

Vicoso, B., Doris Bachtrog. Numerous Transitions of Sex Chromosomes in Diptera. PLOS Biology. Published: April 16, 2015. DOI: 10.1371/journal.pbio.1002078
We use whole-genome analysis in 37 fly species belonging to 22 different families of Diptera and

uncover tremendous hidden diversity in sex chromosome karyotypes among flies. We identify over a dozen different sex chromosome configurations, and the small dot chromosome is repeatedly used as the sex chromosome, which presumably reflects the ancestral karyotype of higher Diptera.

Ávila, V., Campos, J. L., & Charlesworth, B. (2015). The effects of sex-biased gene expression and X-linkage on rates of adaptive protein sequence evolution in Drosophila. *Biology Letters*, *11*(4), 20150117.

Evolution in other taxa

Reinhardt, K., Anthes, N., & Lange, R. (2014). Copulatory Wounding and Traumatic Insemination. *The Genetics and Biology of Sexual Conflict*. Cold Spring Harbor Laboratory Press.
Very nice review on traumatic mating. Alex Michael

O'Shaughnessy, K. L., Dahn, R. D., & Cohn, M. J. (2015). Molecular development of chondrichthyan claspers and the evolution of copulatory organs. *Nature communications*, *6*.
Our results suggest that the genetic circuit for male clasper development evolved an androgen regulatory input, which prolonged signalling activity and drove clasper skeletogenesis in male fins.

Nagasawa, M., Mitsui, S., En, S., Ohtani, N., Ohta, M., Sakuma, Y., ... & Kikusui, T. (2015). Oxytocin-gaze positive loop and the coevolution of human-dog bonds. *Science*, *348*(6232), 333-336.
MacLean, E. L., & Hare, B. (2015). Dogs hijack the human bonding pathway. *Science*, *348*(6232), 280-281.
Oxytocin facilitates social connections between humans and dogs.The human-dog bond is facilitated by the interaction of oxytocin feedback loops that emerged over the course of domestication.

Orzack, S. H., Stubblefield, J. W., Akmaev, V. R., Colls, P., Munné, S., Scholl, T., ... & Zuckerman, J. E. (2015). The human sex ratio from conception to birth. *Proceedings of the National Academy of Sciences*, *112*(16), E2102-E2111.
We describe the trajectory of the human sex ratio from conception to birth by analyzing data from (i) 3- to 6-d-old embryos, (ii) induced abortions, (iii) chorionic villus sampling, (iv) amniocentesis, and (v) fetal deaths and live births. Our estimate of the sex ratio at conception is 0.5 (proportion male), which contradicts the common claim that the sex ratio at conception is male- biased. The sex ratio may decrease in the first week or so after conception (due to excess male mortality); it then increases for at least 10–15 wk (due to excess female mortality), levels off after ∼20 wk, and declines slowly from 28 to 35 wk (due to excess male mortality). In conclusion: unbiased sex ratio at conception and total female mortality during pregnancy exceeds total male mortality.

Montes, C., Cardona, A., Jaramillo, C., Pardo, A., Silva, J. C., Valencia, V., ... & Niño, H. (2015). Middle Miocene closure of the Central American Seaway. *Science*, *348*(6231), 226-229.
The ocean gateway that once separated South America from North America disappeared 10 million years earlier than previously thought. Michael

Undheim, E. A., Hamilton, B. R., Kurniawan, N. D., Bowlay, G., Cribb, B. W., Merritt, D. J., ... & Venter, D. J. (2015). Production and packaging of a biological arsenal: Evolution of centipede venoms under morphological constraint. Proceedings of the National Academy of Sciences, 112(13), 4026-4031.
A nice example of a morphological constraint acting on venom protein evolution. Alexis MV

Harrison, P. W., Wright, A. E., Zimmer, F., Dean, R., Montgomery, S. H., Pointer, M. A., & Mank, J.

E. (2015). Sexual selection drives evolution and rapid turnover of male gene expression. Proceedings of the National Academy of Sciences, 112(14), 4393-4398.
Using a phylogenetically controlled analysis of birds that exhibit diverse levels of sexual selection, we show a rapid turnover in sex-biased gene expression primarily through evolution of male expression levels and that the degree of sexual selection predicts the proportion of male-biased genes but does not account for rates of coding sequence evolution.

Seike, T., Nakamura, T., & Shimoda, C. (2015). Molecular coevolution of a sex pheromone and its receptor triggers reproductive isolation in Schizosaccharomyces pombe. *Proceedings of the National Academy of Sciences*, *112*(14), 4405-4410.
This paper shows that novel reproductive populations of Schizosaccharomyces pombe, which are reproductively isolated from the WT population, can be created by genetically altering the primary structure of a mating pheromone and its receptor. Based on the biological concept of species, this reproductive group should be regarded as a new species. This is the first report, to our knowledge, of the artificial creation of a new species of any living organism in the history of evolutional research.

Alvarado, S., Rajakumar, R., Abouheif, E., & Szyf, M. (2015). Epigenetic variation in the Egfr gene generates quantitative variation in a complex trait in ants. *Nature communications*, *6*.

Genomics, population genetics, mutation rate

Russell B. Corbett-Detig, Daniel L. Hartl, Timothy B. Sackton. Natural Selection Constrains Neutral Diversity across A Wide Range of Species. PLOS Biology: published 10 Apr 2015 | info:doi/10.1371/journal.pbio.1002112
Under the assumptions of the neutral model of molecular evolution, the amount of variation present in a population should be directly proportional to the size of the population. However, this prediction does not tally with real-life observations: levels of genetic diversity are found to be substantially more uniform, even among species with widely differing population sizes, than expected. Because natural selection—which removes genetically linked neutral variation—is more efficient in larger populations, selection on novel mutations offers a potential reconciliation of this paradox. In this work, we align and jointly analyze whole genome genetic variation data from a wide variety of species. Using this dataset and population genetic models of the impact of selection on neutral variation, we test the prediction that selection will disproportionally remove neutral variation in species with large population sizes. We show that genomic signature of natural selection is pervasive across most species, and that the amount of linked neutral variation removed by selection correlates with proxies for population size. We propose that pervasive natural selection constrains neutral diversity and provides an explanation for why neutral diversity does not scale as expected with population size.

Kennedy, S. R., Schultz, E. M., Chappell, T. M., Kohrn, B., Knowels, G. M., & Herr, A. J. (2015). Volatility of Mutator Phenotypes at Single Cell Resolution. PLoS Genetics. 10.1371/journal.pgen.1005151
Our study utilizes a novel way of measuring mutation rates of individual cell divisions to show that mutator cells can adopt one of two mutation rates that differ tenfold in magnitude.

Gudbjartsson, D. F., Helgason, H., Gudjonsson, S. A., Zink, F., Oddson, A., Gylfason, A., ... & Stefansson, K. (2015). Large-scale whole-genome sequencing of the Icelandic population. *Nature genetics*.
Kari Stefansson and colleagues report the whole-genome sequencing of 2,636 individuals from Iceland to a median of 20[times] coverage, providing a valuable genomic resource

for this population isolate. They characterize patterns of genetic variation and population structure and demonstrate the usefulness of this resource for genetic discovery for several disease phenotypes.

Helgason, A., Einarsson, A. W., Guðmundsdóttir, V. B., Sigurðsson, Á., Gunnarsdóttir, E. D., Jagadeesan, A., ... & Stefánsson, K. (2015). The Y-chromosome point mutation rate in humans. *Nature genetics*.
Agnar Helgason and colleagues report the point mutation rate for the male-specific euchromatic sequence of the Y chromosome based on 753 Icelandic males. They find that the non-recombining portions of the Y chromosome mutate at a faster rate than palindromic regions, suggesting that gene conversion acts to correct mutations in palindromic sequences.

Strope, P. K., Skelly, D. A., Kozmin, S. G., Mahadevan, G., Stone, E. A., Magwene, P. M., ... & McCusker, J. H. (2015). The 100-genomes strains, an S. cerevisiae resource that illuminates its natural phenotypic and genotypic variation and emergence as an opportunistic pathogen. *Genome research*, *25*(5), 762-774.

MicroRNA
Lauressergues, D., Couzigou, J. M., San Clemente, H., Martinez, Y., Dunand, C., Bécard, G., & Combier, J. P. (2015). Primary transcripts of microRNAs encode regulatory peptides. *Nature*.
Plant primary microRNA (miRNA) transcripts (pri-miRNAs) are not just a source of miRNAs but can also encode regulatory peptides (miPEPs) that enhance the accumulation, and so the effect, of the corresponding mature miRNAs—an observation that may have agronomical applications.

Hoffman, Y., & Pilpel, Y. (2015). MicroRNAs silence the noisy genome. *Science*, *348*(6230), 41-42.
Living organisms have imperfections. For aexample, although all the cells within an organ are genetically identical, the concentrations of many of their proteins can be “noisy”. Evolution may have selected for a dampening service for genes whose noise may have otherwise been too high.

Schmiedel, J. M., Klemm, S. L., Zheng, Y., Sahay, A., Blüthgen, N., Marks, D. S., & van Oudenaarden, A. (2015). MicroRNA control of protein expression noise. Science, 348(6230), 128-132.
Theoretical and experimental analyses show that microRNAs can reduce fluctuations in gene expression.

Symbiosis
Kiers, E. T., & West, S. A. (2015). Evolving new organisms via symbiosis. Science, 348(6233), 392-394.
Nice review.

Cancer evolution
Gundem, G., Van Loo, P., Kremeyer, B., Alexandrov, L. B., Tubio, J. M., Papaemmanuil, E., ... & Bova, G. S. (2015). The evolutionary history of lethal metastatic prostate cancer. *Nature*.
The subclonal composition of human prostate tumours and their metastases has been mapped by whole-genome sequencing, thus establishing the evolutionary trees behind the development and spread of these cancers; an important observation was that metastases could be re-seeded multiple times, and spread from one tumour to another was frequently seen.

Experimental evolution
Lind, P. A., Farr, A. D., & Rainey, P. B. (2015). Experimental evolution reveals hidden diversity in evolutionary pathways. *eLife*, *4*, e07074.

Amazing findings
Aldrich, John C., and Keith A. Maggert. "Transgenerational Inheritance of Diet-Induced Genome Rearrangements in Drosophila." (2015) PloS Genetics: e1005148.
We show that altering the nutritional medium of Drosophila cultures, emulating dietary largess in the wild, increases expression of the high copy-number ribosomal RNA genes and results in rDNA instability and loss. The reduction in gene copy number occurs both in somatic and germ cells, such that altered copy numbers are transmitted to the next generation.

Methods
Gantz, V. M., & Bier, E. (2015). The mutagenic chain reaction: A method for converting heterozygous to homozygous mutations. *Science*, *348*(6233), 442-444.
An organism with a single recessive loss-of-function allele will typically have a wild-type phenotype while individuals homozygous for two copies of the allele will display a mutant phenotype. Here, we develop a method that we refer to as the mutagenic chain reaction (MCR), which is based on the CRISPR/Cas9 genome editing system for generating autocatalytic mutations to generate homozygous loss-of-function mutations. We demonstrate in Drosophila that MCR mutations efficiently spread from their chromosome of origin to the homologous chromosome thereby converting heterozygous mutations to homozygosity in the vast majority of somatic and germline cells. MCR technology should have broad applications in diverse organisms.