

Community: Journal table of contents highlights

****published between 1st and last day of **JUNE**** (in print *and* early access). **Finish it by July 7th**.**

Please add everything as nested bullet-points.

CTRL-K for links

CTRL-SHIFT-V paste w/o format

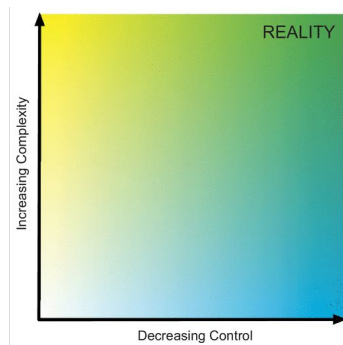
Look at the table of content duties [here](#) (github)

- [Am Nat](#)

- [Species Pool Functional Diversity Plays a Hidden Role in Generating \$\beta\$ -Diversity](#)

The authors modelled empirical patterns in invertebrate communities from 570 streams in 52 watersheds & found that functional diversity can play an important role in driving β -diversity; however, within guilds the nature of interspecific interactions and species pool size complicated the relationship.

- [Models on the Runway: How Do We Make Replicas of the World?](#)



- [Bioinformatics](#)

- [Cell](#)

- [Current Biology](#)

- [The Maternal Effect Gene Wds Controls Wolbachia Titer in Nasonia](#) Funkhouser-Jones et al. <https://doi.org/10.1016/j.cub.2018.04.010>. Some wasp species have more bacteria than others. They compared Wolbachia communities between closely-related wasp species, identified a gene associated with bacteria abundance from mother to offsprings. Positive selection drives the evolution of this gene in certain wasp lineages.
- [The Mutation Rate and the Age of the Sex Chromosomes in Silene latifolia](#) Krasovec et al. DOI: <https://doi.org/10.1016/j.cub.2018.04.069>. Degeneration of Y-chromosome in plants is not well understood. They resequenced the genome of a white campion plant (short and long reads), found mutations between parent and offsprings, calculated mutation rate, estimated the age of both sex chromosomes (6 and 11 mya), inferred that many Y-linked genes are not functional.
- [Supergene Evolution Triggered by the Introgression of a Chromosomal Inversion](#) Jay et al. Doi: <https://doi.org/10.1016/j.cub.2018.04.072>. How come a chromosomal inversion is found in 2 distant Heliconius species? They tested for presence of introgression after first evolution of supergene (phylogenetic analysis, ABBA-BABA, divergence analysis), ruling out incomplete lineage sorting. Thorough study.

- [eLife](#)

- [Striking circadian neuron diversity and cycling of *Drosophila* alternative splicing](https://doi.org/10.7554/eLife.35618) Wang et al. DOI: <https://doi.org/10.7554/eLife.35618>. Regulatory mechanisms behind circadian rhythm, in particular alternative splicing, are not well understood. They dissected subgroups of neuron areas of the fly brain, sequenced pre-mRNA, analysed with their new tool (de novo annotation of alternative splicing profiles) and did a gene ontology search.
- [Current CRISPR gene drive systems are likely to be highly invasive in wild populations](https://doi.org/10.7554/eLife.33423) Noble et al. DOI: <https://doi.org/10.7554/eLife.33423>. What will happen to the wild population if one lab releases 15 CRISPR-loaded individuals? They model different scenarios (structured population, inbreeding level, family size, etc) and show that the current CRISPR technology will have major impacts on all population levels.
- [Shearing in flow environment promotes evolution of social behavior in microbial populations](https://doi.org/10.7554/eLife.34862) Uppal & Vurdal DOI: <https://doi.org/10.7554/eLife.34862>. Evolution of altruistic behaviours is not well understood, especially in the case of assortment (different environments lead to evolution of cheaters and cooperators). They focus on microorganism communities, modelling flowing environments. They found that large shear rate cause the individuals to change their grouping, and by doing so limit opportunities for cheaters.

- **Evolution**

- [A global analysis of selection at the avian MHC](#): Here, we analyze a global dataset of avian MHC class I and class II sequences (ca. 11,000 sequences from over 250 species) to gain insight into the processes that govern macroevolution of MHC genes in birds. Non-passerines showed stronger selection at MHC class II, which is primarily involved in recognition of extracellular pathogens, while passerines showed stronger selection at MHC class I, which is involved in recognition of intracellular pathogens. Positions of positively selected amino-acid residues showed marked discrepancies with peptide-binding residues (PBRs) of human MHC molecules, suggesting that using a human classification of PBRs to assess selection patterns at the avian MHC may be unjustified. Finally, our analysis provided evidence that indel mutations can make a substantial contribution to adaptive variation at the avian MHC.

- **GBE**

- [Conserved Noncoding Elements Influence the Transposable Element Landscape in *Drosophila*](#)
They combine comparative and population genomic data in *Drosophila melanogaster* to show that the abundance of transposable element insertions in intronic and intergenic conserved noncoding elements (CNEs) is reduced relative to random expectation, supporting the idea that selective constraints on CNEs eliminate a proportion of TE insertions in noncoding regions. They can provide evidence that selective constraints on CNEs contribute to shaping the landscape of TE insertion in eukaryotic genomes, and provide further evidence that CNEs are indeed functionally constrained and not simply mutational cold spots.
- [Horizontal Gene Acquisitions Contributed to Genome Expansion in Insect-Symbiotic *Spiroplasma clarkii*](#)
They investigated the molecular evolution events that led to the genome expansion of the bacterium *Spiroplasma clarkii*, by determining its complete genome sequence and inferring the evolutionary origin of each protein-coding gene based on the phylogenetic distribution of homologs. They identified a high number of *S. clarkii* specific protein-coding genes (some related to carbohydrate transport and metabolism) suggesting that these acquired genes contributed to the expansion of both genome size and metabolic capability.
- [Evolution of Gustatory Receptor Gene Family Provides Insights into Adaptation to Diverse Host Plants in Nymphalid Butterflies](#)
They analyzed the evolutionary dynamics of GRs in four closely related butterfly species to test whether host range expansion is associated with the increase in the repertoire size of

GRs. Their results suggest that frequent gene duplications in GRs, which might be involved in the detection of plant secondary metabolites, were associated with host range expansion.

- **Genome Biol**

- [A major locus controls local adaptation and adaptive life history variation in a perennial plant](#)
Wang et al. <https://doi.org/10.1186/s13059-018-1444-y>. They asked how the aspen tree adapts to temperature gradient in Sweden. They sequenced 94 genomes and found one locus associated with local adaptation (timing of bud set). They also checked in a greenhouse the effect of genetic provenance and confirmed that the gene had different expression patterns depending on the local environment.
- [Diversification and independent domestication of Asian and European pears](#)
- [CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness](#)
- [Post-translational buffering leads to convergent protein expression levels between primates](#)

- **Genome Res**

- [Allele-specific control of replication timing and genome organization during development](#)
- [RNA editing in nascent RNA affects pre-mRNA splicing](#)

- **Insectes Sociaux**

- **Journal of Evolutionary Biology**

- [The role of epistatic interactions underpinning resistance to parasitic Varroa mites in haploid honey bee \(*Apis mellifera*\) drones](#)
They investigated the importance of epistatic interactions in the expression of parasite resistance in a haploid host by performing QTL analysis. They found three previously unidentified loci on three different chromosomes. Two of those loci interact epistatically with the third locus. Also identified 16 genes that might play a role in parasite resistance.
- [Patterns of reproductive isolation in a haplodiploid – strong post-mating, prezygotic barriers among three forms of a social spider mite](#)
They tested whether intensity of reproductive isolation increases with genetic distance and whether biogeographic patterns (allopatry/parapatry) affect the evolution of prezygotic reproductive barriers in a social spider mite (three recently diverged forms). Their results show that the three forms are reproductively isolated, despite the absence of premating barriers, and that the post-mating, prezygotic component contributes most to reproductive isolation.
- [RAD-seq linkage mapping and patterns of segregation distortion in sedges: meiosis as a driver of karyotypic evolution in organisms with holocentric chromosomes](#)
RAD-seq was performed for individuals from F1 and F2 generations. They identified 32 linkage groups of which three exhibit more loci under segregation distortion than expected by chance. This finding implicates meiotic drive in the segregation of chromosome variants, suggesting that selection of chromosome variants in meiosis may contribute to the establishment and fixation of chromosome variants in *Carex*, which is renowned for high chromosomal and species diversity.

- **MBE**

- [Phylogenomic evidence overturns current conceptions of social evolution in wasps \(*Vespidae*\)](#)
- [Consequences of Asexuality in Natural Populations: Insights from Stick Insects](#): Predicted consequences of the loss of recombination include a reduced effectiveness of selection, changes in the amount of neutral polymorphisms segregating in populations, and an arrest of GC-biased gene conversion. We identify the consequences of asexuality using de novo transcriptomes of five independently derived, obligately asexual lineages of stick insects, and their sexual sister-species. We find strong evidence for higher rates of deleterious mutation accumulation, lower levels of segregating polymorphisms and arrested GC-biased

gene conversion in asexuals as compared with sexuals. Taken together, our study conclusively shows that predicted consequences of genome evolution under asexuality can indeed be found in natural populations.

- [Distinct Patterns of Selection in Selenium-Dependent Genes between Land and Aquatic Vertebrates](#): we compared the evolutionary forces acting on the coding sequences of selenoprotein genes and genes that regulate Se between vertebrate clades and between the Se-dependent genes and their paralogs with Cys. We find that the strength of natural selection in genes that use or regulate Se is distinct between land vertebrates and teleost fishes and more variable than in the Cys paralogs, particularly in genes involved in the preferential supply of Se to some organs and the tissue-specific expression of selenoproteins.
- [The evolution of caste-biasing symbionts in the social hymenoptera](#): The separation of individuals into reproductive and worker castes is the defining feature of insect societies. However, caste determination is itself a complex phenomenon, dependent on interacting genetic and environmental factors. We argue that there are in fact three distinct evolutionary scenarios in which maternally transmitted symbionts might be selected to influence the process of caste determination in a social hymenopteran host. Each of these scenarios generate testable predictions which we outline here. Given the increasing recognition of the complexity and multi-faceted nature of caste determination in social insects, we argue that maternally transmitted symbionts should also be considered as possible factors influencing the development of social hymenopterans.

- **[Mol Ecol](#)**

- [Positive selection on sociobiological traits in invasive fire ants](#)
- [Meta-analysis of chromosome-scale crossover rate variation in eukaryotes and its significance to evolutionary genomics](#)
- [Uncovering the drivers of host-associated microbiota with joint species distribution modelling](#)

- **[Myrmecological News](#)**

- **[Nature](#)**

- [A naturally occurring antiviral ribonucleotide encoded by the human genome](#)

- **[Nature Comms](#)**

- [Chemical warfare between leafcutter ant symbionts and a co-evolved pathogen](#)

- **[Nature Genetics](#)**

- **[Nature Methods](#)**

- **[Plos Biol](#)**

- [In search of a general theory of species' range evolution](#)
- [Vitellogenin-like A-associated shifts in social cue responsiveness regulate behavioral task specialization in an ant](#) Kohlmeier et al. <https://doi.org/10.1371/journal.pbio.2005747>. How does a worker switch tasks during her life? They sequenced RNA of full-bodied *Temnothorax longispinosus* and found an orthologue to honey bee Vitellogenin A. By knocking it down with RNAi, they found that workers switch from nursing larvae to caring for nestmates.
- [Haploid selection, sex ratio bias, and transitions between sex-determining systems](#) “both selection to equalise the sex ratio and the benefits of associating with haploid-selected alleles can drive transitions between sex-determining systems, leading to stronger or weaker sex linkage and increased or decreased sex ratio bias.” gametic competition and meiotic drive

- **[Plos Comp Biol](#)**

- [Removing contaminants from databases of draft genomes](#) Computational method for removing incorrect/erroneous sequences from existing DNA databases. Developed to

address contamination in databases specific to eukaryotic pathogens in humans.
DOI:10.1371/journal.pcbi.1006277

- **Plos Genet**

- [Within-patient mutation frequencies reveal fitness costs of CpG dinucleotides and drastic amino acid changes in HIV](#) Fitness cost of mutations in rapidly mutating HIV differ. Specifically this is interesting because they not only look at the standard non-synonymous vs synonymous mutations but the cost of G -> A vs A -> G. DOI:10.1371/journal.pgen.1007420
- [Human demographic history has amplified the effects of background selection across the genome](#): Utilizing a global sample of human whole-genome sequences from the Thousand Genomes Project and extensive simulations, we investigate how non-equilibrium demographic processes magnify and dampen the consequences of selection at linked sites across the human genome. The results show that non-equilibrium demography significantly alters the consequences of selection at linked sites and support the need for more work investigating the dynamic process of multiple evolutionary forces operating in concert.

- **PNAS**

- **Proc B**

- [Insect societies fight back: the evolution of defensive traits against social parasites](#)
- [Lower bumblebee colony reproductive success in agricultural compared with urban environments](#)

- **Science**

- [Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis](#)
- [The dynamics of gene expression in vertebrate embryogenesis at single-cell resolution](#)
- [Single-cell mapping of gene expression landscapes and lineage in the zebrafish embryo](#)

- **TREE**

- **Trends in Genetics**

- [The Third Revolution in Sequencing Technology](#). A review of the methods and research produced by long read sequencing. Of special interest for PRIYAM and EMELINE. DOI:10.1016/j.tig.2018.05.008
- [Genetic Network Complexity Shapes Background-Dependent Phenotypic Expression](#). Single SNPs explaining phenotypes are a wild assumption (who'd have guessed?), the genetic environment of any given mutation makes its effects unpredictable. The authors give some theoretical framework to this idea. DOI: 10.1016/j.tig.2018.05.006
- [Transcribing Centromeres: Noncoding RNAs and Kinetochore Assembly](#). Some transcribed elements of the centromeres appear to be functional, more specifically, they would help the attachment to the spindle. DOI: 10.1016/j.tig.2018.05.001

- **BioRxiv**

- [Aequatus: An open-source homology browser](#). "... provides an in-depth view of gene structure across gene families ... It relies on pre-calculated alignment and gene feature information typically held in, but not limited to, the Ensembl Compara and Core databases ..." (see their Figure 2)

[1]. **Other papers/tools that you feel someone should have seen:**

- Scientific Reports: [Molecular chaperoning helps safeguarding mitochondrial integrity and motor functions in the Sahara silver ant *Cataglyphis bombycina*](#) (Serge Aron)
- Animal Behaviour: [Ant nurse workers exhibit behavioural and transcriptomic signatures of specialization on larval stage](#) (Tim Linksvayer)

- Genetics
- Heredity
- Aging
- Mol Cell Biol
- J Gerontol
- Methods in Ecology and Evolution
- Current Opinion in Insect Science
- Molecular Phylogenetics & Phylogenetic
- PeerJ