GENETICS, Vol. 216, October 2020, Copyright © 2020

How much does N_e vary among species?, pp. 559–572

Nicolas Galtier and Marjolaine Rousselle

The population frequency of polymorphic alleles varies in time. This variation has a stochastic component, mainly determined by the size of the considered population, N_e: genetic drift. The intensity of drift in natural populations is difficult to measure experimentally. Indirect estimates based on genetic diversity have revealed surprisingly weak contrasts among species. Here, Galtier and Rousselle approach genetic drift via its impact on the load of deleterious mutations. Their analysis of site frequency spectra in coding sequences from >50 species of animals uncovers a ratio of 1000 of N_e among species, instead of 100 in previous studies.

A dCas9-based system identifies a central role for Ctf19 in kinetochore-derived suppression of meiotic recombination, pp. 395–408

Lisa-Marie Kuhl, Vasso Makrantoni, Sarah Recknagel, Animish N. Vaze, Adele L. Marston, and Gerben Vader

A dCas9-based system is developed to query the regulation of kinetochore-driven meiotic recombinational control.

Meiotic double-strand break processing and crossover patterning are regulated in a sex-specific manner by BRCA1-BARD1 in *Caenorhabditis elegans*, pp. 359–380

Qianyan Li, Sara Hariri, and JoAnne Engebrecht

Sperm and oocyte production are differentially regulated to ensure genetic information is accurately passed down from one generation to the next. To provide insight into sex-specific regulation of meiosis for gamete production, Li, Hariri, and Engebrecht analyzed the role of the tumor suppressor BRCA1-BARD1 complex in *Caenorhabditis elegans* male meiosis. They show that the complex functions in spermatogenesis at two different levels: regulating early meiotic recombination intermediate processing to promote homologous recombination and altering crossover patterning. These roles are distinct from those previously reported in female meiosis, suggesting that this complex is regulated in a sex-specific manner to optimize sperm and oocyte production.

An opaque cell-specific expression program of secreted proteases and transporters allows cell-type cooperation in *Candida albicans*, pp. 409–430

Matthew B. Lohse, Lucas R. Brenes, Naomi Ziv, Michael B. Winter, Charles S. Craik, and Alexander D. Johnson

The opportunistic human fungal pathogen *Candida albicans* switches between two distinct, heritable cell types named "white" and "opaque." Lohse *et al.* show that opaque cells, in response to proteins as the sole nitrogen source, up-regulate a specialized program, including specific secreted aspartyl proteases and peptide transporters. They demonstrate that, in mixed cultures, opaque cells enable white cells to respond and proliferate more efficiently under these conditions. These observations suggest that white-opaque switching creates mixtures of cells where the population characteristics, which derive from a single genome, reflect the contributions of two distinct cell types.

Experimental evolution of *Bacillus subtilis* reveals the evolutionary dynamics of horizontal gene transfer and suggests adaptive and neutral effects, pp. 543–558

Shai Slomka, Itamar Françoise, Gil Hornung, Omer Asraf, Tammy Biniashvili, Yitzhak Pilpel, and Orna Dahan

In this work, Slomka *et al.* have evolved the naturally competent *B. subtilis* in the lab, in the presence or absence of foreign genomic DNA. They examine the effects of foreign DNA acquisition on the growth improvement of the evolving bacteria and on their genomes. They show that extensive acquisition of DNA from close strains occurs, often in bursts, and introduces multitudes of single nucleotide variations that propagate in the population under selection. They show a connection between the integration of the foreign DNA and fitness improvement, highlighting the role of horizontal gene transfer in bacterial adaptation.

A conserved role for vezatin proteins in cargo-specific regulation of retrograde axonal transport, pp. 431–446

Michael A. Spinner, Katherine Pinter, Catherine M. Drerup, and Tory G. Herman

Vertebrate Vezatin is associated with the regulation of cell-cell junctions. A distantly-related *Aspergillus* protein, VezA, promotes dynein-dependent transport of endosomes within hyphae, but there has been no evidence that animal Vezatins do something similar. In a forward genetic screen for mutations that disrupt axon terminal morphology, Spinner *et al.* identified a mutation in a *Drosophila* gene that they found to be an ortholog of vertebrate *vezatin*. Using both fixed and live imaging first in *Drosophila* and then in zebrafish, they show that *vezatin* in both species is required for the retrograde axonal transport of endosomes, a process critical for neuronal function.

Variation among biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence across *Aspergillus* species, pp. 481–498

Jacob L. Steenwyk, Matthew E. Mead, Sonja L. Knowles, Huzefa A. Raja, Christopher D. Roberts, Oliver Bader, Jos Houbraken, Gustavo H. Goldman, Nicholas H. Oberlies, and Antonis Rokas

Aspergillus fumigatus is a major fungal pathogen of humans but its two closest relatives, *Aspergillus fischeri* and *Aspergillus oerlinghausenensis*, are not. Steenwyk *et al.* examined whether *A. fumigatus* secondary metabolites, some of which are known genetic determinants of *A. fumigatus* virulence, and the metabolic pathways that produce them, are conserved in *A. oerlinghausenensis* and *A. fischeri*. They found that the nonpathogenic relatives of *A. fumigatus* produce some, but not all, secondary metabolites thought to contribute to the success of *A. fumigatus* in causing human disease and that these similarities and differences were reflected in the underlying metabolic pathways involved in their biosynthesis.