

## ISSUE HIGHLIGHTS

GENETICS, Vol. 195, NOVEMBER 2013, Copyright © 2013

### High resolution mapping of complex traits with a four-parent advanced intercross yeast population, pp. 1141–1155

Francisco A. Cubillos, Leopold Parts, Francisco Salinas, Anders Bergström, Eugenio Scovacricchi, Amin Zia, Christopher J. R. Illingworth, Ville Mustonen, Sebastian Istedt, Jonas Warringer, Edward J. Louis, Richard Durbin, and Gianni Liti

This article describes a powerful resource for the highest resolution mapping of complex traits available in any organism. The authors developed a four parent, 12-generation mapping population of yeast they call SGRP-4X that retains the phenotypic diversity of the parental strains. It consists of over 10,000,000 individuals with fine-grained mosaic genomes in which nearly 70% of single nucleotide variation in yeasts segregates in small linkage blocks.

### Genetic studies of spectrin in the larval fat body of *Drosophila melanogaster*: evidence for a novel lipid uptake apparatus, pp. 871–881

Bianca Diaconeasa, G. Harper Mazock, Anthony P. Mahowald, and Ronald R. Dubreuil

Because oil and water don't mix, animals have evolved elegant strategies for moving dietary fat between tissues and in and out of cells. This article describes a novel mechanism that couples lipid uptake through the plasma membrane to lipid storage in cytoplasmic lipid droplets.

### Phylogenies of central element proteins reveal the dynamic evolutionary history of the mammalian synaptonemal complex: ancient and recent components, pp. 781–793

Johanna Fraune, Céline Brochier-Armanet, Manfred Alsheimer, and Ricardo Benavente

The synaptonemal complex (SC) is responsible for stable pairing of homologous chromosomes in meiotic prophase I. Although the tripartite structure of the SC is evolutionarily conserved, its characterized protein components in *Drosophila melanogaster*, *Caenorhabditis elegans*, and *Mus musculus* lack any detectable homology. But Fraune *et al.* now find homologues of the four central element proteins of mammals in various metazoan species, for two of them down to the basal-branching Cnidaria. The phylogenies suggest that the SC is ancient in Metazoa, but evolved dynamically during animal diversification.

### Exciting prospects for precise engineering of *Caenorhabditis elegans* genomes with CRISPR/Cas9, pp. 635–642

Christian Frøkjær-Jensen

The CRISPR-Cas9 nuclease has rapidly become the tool of choice for genome editing. This issue of *GENETICS* witnesses a significant advance for *Caenorhabditis elegans* genetics with five articles that describe its use to edit the worm genome. A commentary article highlights and contrasts the different protocols. Another article in this issue complements one published in the journal last month (see Lo *et al.*) describing application of this technology to *Drosophila*. The genetic playing field for model organisms has been leveled.

### Quantifying population genetic differentiation from next-generation sequencing data, pp. 979–992

Matteo Fumagalli, Filipe G. Vieira, Thorfinn Sand Korneliusen, Tyler Linderoth, Emilia Huerta-Sánchez, Anders Albrechtsen, and Rasmus Nielsen

Genetic inferences about populations from next-generation sequencing data can be problematic due to high error rates and low sequencing coverage. This article presents powerful and reliable tools for investigating population genetic variation on a large scale directly from high-throughput sequencing data, and demonstrates the high performance of these methods compared to classic approaches based on SNP and genotype calling.

### Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect, pp. 969–978

Elodie Gazave, Diana Chang, Andrew G. Clark, and Alon Keinan

Human populations experienced dramatic growth in recent millennia, causing them to carry an excess of recent, rare mutations. The authors of this article disentangled the effects of population growth and natural selection on the spectrum of deleterious mutations to show that individuals in growing populations carry a larger number of deleterious

alleles that are less harmful (on average) than in a population at equilibrium. These results shed new light on patterns of genetic variation in human populations.

### Rate of adaptation in sexuals and asexuals: a solvable model of the Fisher-Muller effect, pp. 941–955

Su-Chan Park and Joachim Krug

What use is sex? In the 1930s, Fisher and Muller argued that sex speeds up adaptation of large populations by allowing different beneficial mutations to combine into a single genome. These authors show that the Fisher-Muller mechanism can result in a two-fold increase of the rate of adaptation in large populations.

### Complex genetic effects on early vegetative development shape resource allocation differences between *Arabidopsis lyrata* populations, pp. 1087–1102

David L. Remington, Päivi H. Leinonen, Johanna Leppälä, and Outi Savolainen

How do organisms allocate limited resources among competing needs, such as growth vs. reproduction? These investigators mapped genes affecting growth vs. reproduction trade-offs in crosses between populations of *Arabidopsis lyrata* from quite different environments—North Carolina and Norway. Some chromosomal regions affected traits in both parental environments, but acted at different stages of development, leading to their contrasting effects on reproduction, growth, and survival in the two environments.

### Nutritional control of epigenetic processes in yeast and human cells, pp. 831–844

Meru J. Sadhu, Qiaoning Guan, Fei Li, Jade Sales-Lee, Anthony T. Iavarone, Ming C. Hammond, W. Zacheus Cande, and Jasper Rine

Nutritional deficiencies affect a significant number of the world's population. Nutritional status may affect chromatin modification, and the epigenetic nature of those modifications can result in long-lasting consequences. This article shows that folate deficiency disrupts histone methylation, from yeasts to humans. The authors suggest this is due to metabolic triage, whereby nutrient scarcity prompts prioritization of biological processes.

## This Month's Perspectives

### A perspective on micro-evo-devo: progress and potential, pp. 625–634

Maria D. S. Nunes, Saad Arif, Christian Schlötterer, and Alistair P. McGregor

Micro-evolutionary developmental biology (micro-evo-devo) combines evolutionary developmental biology (evo-devo) and population genetics to investigate the evolution of variation in form and function among populations. This article showcases micro-evo-devo studies to illustrate how this synthesis can shine a brighter light on how and why organismal diversity evolves than either field can do alone.

## This Month in the American Journal of Human Genetics

### Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries, Am. J. Hum. Genet. 93(5)

Meredith L. Carpenter, Jason D. Buenrostro, Cristina Valdiosera, Hannes Schroeder, Morten E. Allentoft, Martin Sikora, Morten Rasmussen, Simon Gravel, Sonia Guillén, Georgi Nekhrizov, Krasimir Leshtakov, Diana Dimitrova, Nikola Theodossiev, Davide Pettener, Donata Luiselli, Karla Sandoval, Andrés Moreno-Estrada, Yingrui Li, Jun Wang, M. Thomas P. Gilbert, Eske Willerslev, William J. Greenleaf, and Carlos D. Bustamante

Where did we come from? Nothing captures the imagination quite like this question. Recent technological advances, coupled with archaeological best practices, have made it possible to address this question in ways previously thought to be impossible. We now have full genome sequences of several ancient humans (and animals). However, for each high-quality specimen, there are numerous samples that, due to time and contamination, contain very low levels of endogenous DNA. Now, Carpenter *et al.* present a whole-genome capture-based method that should enable researchers to obtain high-quality sequence information from a variety of ancient sources. The low-cost associated with this method will make it possible to conduct population-level studies, which, one can imagine, could begin to provide unprecedented views into the life of times of early man (as well as his animal companions).