Do molecular markers inform about pleiotropy?, pp. 23–29
Daniel Gianola, Gustavo de los Campos, Miguel A. Toro, Hugo Naya, Chris-Carolin Schön, and Daniel Sorensen

Whole-genome regression methods have recently been extended to joint analysis of multiple traits, for investigation of mechanisms—such as pleiotropy—that cause trait associations. Gianola et al. show that a genomic correlation derived from molecular markers cannot always be interpreted as a genetic correlation. Without knowledge of linkage disequilibrium relationships between trait loci, and between trait loci and markers, speculating about genetic correlation and pleiotropy using genomic data is conjectural.

Genetics of rapid and extreme size evolution in island mice, pp. 213–228

Organisms on islands often evolve unusual body sizes. Little is known about the genetic basis of this intriguing pattern. Gray et al. demonstrate that Gough Island house mice—which are among the largest wild house mice in the world—rapidly evolved their exceptional size through a large number of genetic changes with individually modest effects. These results reveal that size evolution in nature is genetically complex, even when extreme changes happen on a short time scale.

Transgenerational effects of early life starvation on growth, reproduction, and stress resistance in Caenorhabditis elegans, pp. 201–212
Meghan A. Jobson, James M. Jordan, Moses A. Sandrof, Jonathan D. Hibshman, Ashley L. Lennox, and Ryan Baugh

It has been suggested that malnutrition early in life prompts organisms to adjust their physiology in anticipation of adverse conditions in the future. This hypothetical alteration would benefit the individual in famine conditions but may predispose them to disease if food becomes abundant. Jobson et al. used C. elegans to investigate how starvation during early life affects growth, reproduction, and stress resistance later in life and in future generations. Though the exposed generation suffers detrimental effects, the progeny and grandprogeny of starved larvae were more resistant to starvation and heat. This suggests epigenetic inheritance of acquired resistance.

Evolution of mating systems in basidiomycetes and the genetic architecture underlying mating-type determination in the yeast Leucosporidium scottii, pp. 75–89
Teresa M. Maia, Susana T. Lopes, João M. G. C. F. Almeida, Luís H. Rosa, José Paulo Sampaio, Paula Gonçalves, and Marco A. Coelho

The tetrapolar system, in which mating is dictated by two alternate MAT genes at genetically unlinked regions, has been proposed to be the ancestral state in basidiomycete fungi. Support for this model has however been gathered only from two recently derived lineages. Maia et al. show that Leucosporidium scottii, a basidiomycete belonging to the earliest-branchoing lineage, has a tetrapolar system, a finding that strongly reinforces tetrapolarity as the ancestral state.

Bayesian nonparametric inference of population size changes from sequential genealogies, pp. 281–304
Julia A. Palacios, John Wakeley, and Sohini Ramachandran

Inferring population size changes from whole genomes is hampered by the intractable size of the ancestral recombination graph. Palacios et al. present a method using realizations of the sequentially Markov coalescent (SMC) instead of sequence data. They implement a novel Bayesian nonparametric approach for estimating population sizes with measures of uncertainty and show the method outperforms recent likelihood-based methods that rely on discretization of the parameter space. They find the state space for estimating population size changes is substantially reduced by considering ranked tree shapes instead of labeled topologies.

The genetic basis of composite spike form in barley and ‘Miracle-Wheat’, pp. 155–165
Naser Poursarebani, Tina Seidensticker, Ravi Koppolu, Corinna Trautewig, Piotr Gawroński, Federico Bini, Geetha Govind, Tuan Rutton, Shun Sakuma, et al. identify the NF-kappaB subunit p50 effector molecule, leading the authors to suggest that haploinsufficiency of the NF-kappaB1 subunit p50 in common variable immunodeficiency. Now, Fliegauf et al. describe a framework for modeling patterns of covariance in ancestry among loci that are generated from admixture—genotype mixing in two formerly isolated populations. Their model explicitly incorporates geographic structure in admixture, with two populations coming into contact and mixing by diffusive local migration. The results also highlight the importance of model choice in inferring population history from genomic data.

A male-specific genetic map of the microcrustacean Daphnia pulex based on single-sperm whole-genome sequencing, pp. 31–38
Sen Xu, Matthew S. Ackerman, Hongan Long, Lydia Bright, Ken Spitze, Jordan S. Ramsdell, W. Kelley Thomas, and Michael Lynch

Xu et al. developed a high throughput approach for constructing genetic maps using single sperms. The method combines fluorescence-activated cell sorting, whole-genome amplification, short-read sequencing, and a computational algorithm for analyzing single sperm whole-genome sequencing data. These methods allowed the authors to rapidly build a male-specific genetic map for the freshwater microcrustacean Daphnia pulex, which shows significant improvements compared to a previous map. The approach holds great promise for the study of recombination rate variation in many organisms.

This Month in the American Journal of Human Genetics

Haploinsufficiency of the NF-kB1 subunit p50 in common variable immunodeficiency, Am. J. Hum. Genet. 97(3)
Manfred Fliegauf, Vanessa Bryant, Natalie Frede, Charlotte Slade, See-Turn Woon, Klaus Lehnter, Sandra Winzer, Alia Balashkasva, Thomas Scrirrs, Ephymia Leung, Anthony Jordan, Baerbel Keller, Esther de Vries, Hongzhi Cao, Fang Yang, Alejandro A. Schaeffer, Klaus Warnats, Peter Browett, Jo Douglass, Rohan V. Ameratunga, Jos W.M. van der Meer, and Bodo Grimbacher

The NF-kB pathway plays a key role in mediating the host response to a variety of pathogens. Decades of research has uncovered many complexities in this pathway, and mutations in various pathway members have been identified in a range of disorders. Strikingly, however, no mutations have been identified in NFKB1, which encodes p105, the key mediator of canonical NF-kB signaling. Now, Fliegauf et al. identify heterozygous NFKB1 mutations in individuals with common variable immunodeficiency, a disorder characterized by recurrent infection and autoimmune disease. Functional work shows that these mutations abolish processing of p105 into the p50 effector molecule, leading the authors to suggest that haploinsufficiency for NFKB1 is pathogenic in these families.