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A simple test identifies selection on complex traits, pp. 321–333

Tim Beissinger, Jochen Kruppa, David Cavero, Ngoc-Thuy Ha, Malena Erbe, and Henner Simianer

Important traits are often controlled by a large number of genes that each impact a small proportion of total variation; however, the majority of tools in population genomics are designed to identify single genes with large effects. Beissinger *et al*. describe an approach to identify selected traits controlled by many genes. Their technique uses additive effects estimates from all available markers coupled with estimates of allele frequency change over time. Based on simulations and analyses of maize and chicken breeding populations, they demonstrate the power of their approach for identifying traits controlled by many genes.

Accounting for errors in low coverage high-throughput sequencing data when constructing genetic maps using biparental outcrossed populations, pp. 65–76

Timothy P. Bilton, Matthew R. Schofield, Michael A. Black, David Chagné, Phillip L. Wilcox, and Ken G. Dodds

Next generation sequencing-based genotyping platforms allow for the construction of high density genetic linkage maps. However, data generated using these platforms often contain errors resulting from miscalled bases and missing parental alleles that are due to low sequencing depth. If not taken into account, these errors can lead to highly inflated linkage maps. Bilton *et al*. report a new statistical method for modeling low-coverage sequencing data in the construction of linkage maps, which is implemented in the package GUSMap.

Establishment of signaling interactions with cellular resolution for every cell cycle of embryogenesis, pp. 37–49

Long Chen, Vincy Wing Sze Ho, Ming-Kin Wong, Xiaotai Huang, Lu-yan Chan, Hon Kaoru Ng, Xiaoliang Ren, Hong Yan, and Zhongying Zhao

Intercellular signaling interaction plays a key role in breaking fate symmetry. Identifying such interaction at cellular resolution is technically challenging, especially in a developing embryo. To facilitate the identification of signaling interactions during *Caenorhabditis elegans* embryogenesis, Chen *et al*. generated a systems-level cell contact map consisting of 1,114 intercellular contacts. They also established a dedicated website to facilitate intuitive access to and visualization of contacting cell pairs.

Impulsive choice in mice lacking paternal expression of Grb10 suggests intra-genomic conflict in behavior, pp. 233–239

Claire L. Dent, Trevor Humby, Katie Lewis, Andrew Ward, Reiner Fischer-Colbrie, Lawrence Wilkinson, Jon Wilkins, and Anthony Isles

The imprinted gene *Grb10* is expressed in the brain from the paternal copy only. Here, Dent *et al*. show that paternal *Grb10* regulates impulsive choices, i.e. whether an animal chooses a smaller food reward now or is willing to wait for a larger food reward later. Loss of paternal *Grb10* makes animals more willing to wait. They previously demonstrated that mice lacking a different imprinted gene, maternal *Nesp55*, were less willing to wait and made more impulsive choices. This contrasting effect of oppositely imprinted genes fits with an evolutionary theory called intra-genomic conflict.

Genetics and genomics of social behavior in a chicken model, pp. 209–221

Martin Johnsson, Rie Henriksen, Jesper Fogelholm, Andrey Höglund, Per Jensen, and Dominic Wright

Johnsson *et al*. identify multiple genes affecting sociality-related behavior in chickens. They examine the genetic architecture of domestication in the chicken by studying pleiotropy and linkage in hypothalamus tissue. Statistical analyses of their eQTL data indicate that linkage, rather than pleiotropy, appears to be most relevant for domestication in the chicken.

Synaptogenesis is modulated by heparan sulfate in *Caenorhabditis elegans*, pp. 195–208

María I. Lázaro-Peña, Carlos A. Díaz-Balzac, Hannes E. Bülow, and Scott W. Emmons

The nervous system relies on synapses to transmit information between neurons and thereby direct behavior, but how the correct synaptic connections are genetically specified is poorly understood. By genetically ablating enzymes that modify heparan sulfate, Lázaro-Peña *et al.* show that the ability to modify heparan sulfate is required for normal male mating behaviors in *C. elegans,* as well as for the synaptic connections made by a set of sensory neurons. This leads them to conclude that components of the extracellular matrix play an important role in synapse formation in the male tail.

Inferring fitness effects from time-resolved sequence data with a delay-deterministic model, pp. 255–264

Nuno R. Nené, Alistair S. Dunham, and Christopher J. R. Illingworth

A broad range of approaches have considered the challenge of inferring selection from time-resolved genome sequence data. Models describing deterministic changes in allele or haplotype frequency have been highlighted as providing accurate and computationally rapid inferences in these analyses. Here, Nené, Dunham, and Illingworth show that a deterministic approach to inferring selection can produce severely flawed results in cases where mutation and selection cause a system to evolve into new haplotypes over time. They describe and demonstrate a new delay-deterministic inference approach, whereby the addition of a single model parameter substantially corrects for the deterministic error.

Assessing the genetic landscape of animal behavior, pp. 223–232

Ryan A. York

Recent years have seen an increase in studies that associate genomic loci with behavioral variation both within and across animal species. Ryan York compiles and analyzes over 1,000 of these loci, finding that the genetic bases of behaviors consistently vary across animal taxa and that this variation in recapitulated in the behavioral and genetic diversity of natural populations of *Drosophila*. These results suggest that behaviors may respond to evolutionary processes in predictable ways, enabling researchers to develop new hypotheses about the relationship between genes and behavior.