Multilevel selection 1: Quantitative genetics of inheritance and response to selection, pp. 277–288
Piter Bijma, William M. Muir and Johan A. M. Van Arendonk

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These two articles mark a major contribution for prediction of selection response when the trait under selection is influenced by interactions between pairs of individuals. By adding a level of individual-by-individual interaction to the classical variance components, the authors show that classical approaches to quantitative genetics can be nearly blind to these interactions. When appropriately modeled, the authors show, using real examples, that breeding populations can have quite strong interactions with substantial impacts on selection response. Just when we all thought that the only remaining frontier for quantitative genetics entailed molecular markers, these articles develop a whole new level to components of genetic variation and demonstrate their importance in selection response.

A specific subset of transient receptor potential vanilloid-type channel subunits in *Caenorhabditis elegans* endocrine cells function as mixed heteromers to promote neurotransmitter release, pp. 93–105
Antony M. Jose, I. Amy Bany, Daniel L. Chase and Michael R. Koelle

Most forms of sensation require transient receptor potential (TRP) family cation channels composed of four subunits. While single knockouts have revealed the functions of many homeric channels, which are composed of identical subunits, the functions of heteromeric channels composed of two or more different subunits remain largely unclear. This article shows that heteromeric TRP channels regulate egg laying in *Caenorhabditis elegans*. The authors present a model in which mechanical deformation of specific uterine cells by eggs relays a signal via the heteromeric TRP channels to promote egg laying.

Comparing likelihood and Bayesian coalescent estimation of population parameters, pp. 155–165
Mary K. Kuhner and Lucian P. Smith

The authors develop a Bayesian version of LAMARC, their likelihood-based Markov chain Monte Carlo genealogy sampler that fits population sample data to demographic population genetic models. Although this may seem like a technical detail, the comparison of merits of these two estimation approaches is of great importance to statistical geneticists who basically must take a leap one way or the other, and almost nobody goes to the effort to compare the two approaches. The authors use simulated DNA sequence data to assess accuracy of estimates of $\Theta (4N_e \mu)$ and rates of migration and recombination. In all cases the two methods have very similar results, although the Bayesian approach tends to exclude the true parameter estimates less often.

Disruption of genetic interaction between two autosomal regions and the X chromosome causes reproductive isolation between mouse strains derived from different subspecies, pp. 185–197
Ayako Oka, Toshinori Aoto, Yoshikazu Totsuka, Riichi Takahashi, Masatsugu Ueda, Akihiko Mita, Noriko Sakurai-Yamazaki, Hiromi Yamamoto, Satoshi Kuriki, Nobuo Takagi, Kazuo Moriwaki and Toshikiko Shiroishi

Laboratory mouse strains are not all completely interfertile, mostly because they were founded from various introgressions of *Mus musculus* domesticus, *M. m. musculus*, and *M. m. molossinus*. This article takes an elegant genetic approach to identify specific Dobzhansky–Muller type interactions using a consomic X chromosome line and then mapping quantitative trait loci that interact with the X chromosome to produce hybrid sterility. Mice whose autosomal complement is *C57BL/6J* but who have the X chromosome of *M. m. molossinus* produce spermatozoa with a defect in penetration through the zona pellucida of eggs and are male sterile.

Two unlinked double-strand breaks can induce reciprocal exchanges in plant genomes via homologous recombination and nonhomologous end joining, pp. 21–29
Michael Pacher, Waltraud Schmidt-Puchta and Holger Puchta

Double-strand breaks (DSBs) can occur simultaneously in a genome. To analyze the mutagenic potential of such a situation the authors establish an experimental system in tobacco harboring two unlinked transgenes, each carrying an I-sceI site. After expression of I-sceI, a kanamycin-resistance marker can be restored by joining two previously unlinked broken ends by homologous recombination or by nonhomologous end joining. Despite the fact that no selection was applied for joining the two other ends, the respective linkage can be detected in most cases tested, demonstrating that the respective exchanges are reciprocal. DSB-induced translocations events greatly exceed ectopic gene conversion events in somatic cells. Thus, DSB-induced reciprocal exchanges might play a significant role in plant genome evolution.

Components of the spindle assembly checkpoint regulate the anaphase-promoting complex during meiosis in *Caenorhabditis elegans*, pp. 107–123
Kathryn K. Stein, Edward S. Davis, Thomas Hays and Andy Golden

Temperature-sensitive mutations in subunits of the *Caenorhabditis elegans* anaphase-promoting complex (APC) arrest at metaphase of meiosis I at the restrictive temperature. To identify regulators and potential substrates of the APC, the authors perform a genetic suppressor screen using a weak allele of the APC subunit MAT-3, whose defects are specific to meiosis. Twenty-seven suppressors that resulted in embryonic viability and larval development at the restrictive temperature are isolated. The genes defined by these suppressor mutations include the APC co-activator Gyr-1 and in three spindle assembly checkpoint genes, mdf-1, mdf-2, and mdf-3/asan-1, orthologs of Mad1, Mad2, and Mad3, respectively. These studies provide evidence that components of the spindle assembly checkpoint may regulate the metaphase-to-anaphase transition in the absence of spindle damage during C. elegans meiosis.

Cytological visualization of DNA transposons and their transposition pattern in somatic cells of maize, pp. 31–39
Weichang Yu, Jonathan C. Lamb, Fangpu Han and James A. Birchler

Cytological methods have not been used in plants to study DNA transposition since McClintock’s initial work, principally because they lack the resolution necessary to follow movement of individual transposons (McClintock used transposon-induced chromosome breaks to assess movement). This article from the Birchler lab remedies the situation and describes improved cytological techniques for detecting single-copy genes. The method is used to monitor the chromosomal location and movement of several maize transposable elements including the genetically engineered RescueMu element. The method likely will be rapidly employed by a number of labs studying plant chromosome dynamics.