GENETICS, Vol. 215, July 2020, Copyright © 2020

Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, pp. 579–595

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Genetic analysis in autopolyploids is a very complicated subject due to the enormous number of genotypes at a locus that needs to be considered. For instance, the number of genotypes at a locus in a bi-parental cross is 36 for autotetraploids and 400 for autohexaploids. The statistical methods and companion software QTLpoly presented here specifically address this complicated nature and have been successfully tested in a hexaploid sweetpotato population. Orange-fleshed sweetpotato is an appealing crop for food and nutrition security in developing countries. The development of statistical methods for autopolyploids is expected to facilitate genomics-assisted autopolyploid breeding programs.

A decoy library uncovers U-box E3 ubiquitin ligases that regulate flowering time in *Arabidopsis*, pp. 699–712

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The ubiquitin proteasome system plays an essential role in the regulation of flowering time, a precisely timed developmental transition necessary for plant fitness. However, the full impact these proteins have on the timing of flowering is uncharacterized, and widespread functional redundancy in plants decreases the efficacy of traditional forward genetic screens. Feke *et al*. apply a reverse genetic screen utilizing dominant-negative E3 ligase "decoys" to identify, validate, and characterize three additional U-box E3 ubiquitin ligases involved in the regulation of flowering time. This work demonstrates the importance of dominant-negative strategies to identify regulators of complex biological processes in organisms with complex genetics.

Growth-dependent activation of protein kinases suggests a mechanism for measuring cell growth, pp. 729–746

Akshi Jasani, Tiffany Huynh, and Douglas R. Kellogg

Progression through the cell cycle occurs only when sufficient growth has occurred, which indicates that cells measure growth. Analysis of signals associated with growth in budding yeast suggests that signaling lipids delivered to the growing plasma membrane generate a growth-dependent signal that could be used to measure growth.

Amyotrophic lateral sclerosis modifiers in *Drosophila* reveal the phospholipase D pathway as a potential therapeutic target, pp. 747–766

Mark W. Kankel, Anindya Sen, Lei Lu, Marina Theodorou, Douglas N. Dimlich, Alexander McCampbell, Christopher E. Henderson, Neil A. Shneider, and Spyros Artavanis-Tsakonas

Amyotrophic lateral sclerosis (ALS) is a devastating neurodegenerative disorder lacking effective treatments. ALS pathology is linked to mutations in several different genes indicating a complex underlying genetic architecture that is effectively unknown. Here, in an attempt to identify genes and pathways for potential therapeutic intervention, Kankel *et al*. explore the genetic architecture that underlies *Drosophila* models of ALS through two independent genome-wide screens for modifiers of degenerative phenotypes associated with the expression of transgenic constructs carrying familial ALS -causing alleles of FUS ($hFUS^{R521C}$) and TDP-43 ($hTDP\text{-}43^{M337V}$). The authors uncover a complex array of genes affecting either - or both - of the two strains.

Lung function in African American children with asthma is associated with novel regulatory variants of the KIT ligand *KITLG/SCF* and gene-by-air-pollution interaction, pp. 869–886

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Baseline lung function is a standard diagnostic criterion used by clinicians to detect lung diseases. It is a complex trait significantly influenced by both genetics and environmental factors. Mak *et al*. identified a novel genetic association with lung function on chromosome 12 that also showed gene-by-air-pollution interaction in African American children with asthma. These variants showed physical interaction with Stem Cell Factor (KITLG/SCF) and their minor alleles were associated with increased *KITLG* gene expression in nasal epithelial cells. This is the first study that identified genetic association between lung function and *KITLG*, which has an established role in orchestrating allergic inflammation in asthma.

Genetic signatures of evolutionary rescue by a selective sweep, pp. 813–829

Matthew M. Osmond and Graham Coop

Inferring selective sweeps from genetic data has been a breakthrough in population genetics. The most prominent examples come from populations suddenly exposed to extreme stressors, such as insecticides. Such stressors may also induce population decline. When this decline is reverted by a sweep we say the population has been rescued by evolution. While evolutionary rescue has received wide theoretical and experimental attention it remains unclear if one can infer rescue from genetic data alone. Here, Osmond and Coop relax the common assumption that sweeps and demography are independent to determine the signatures rescue leaves in the genomes of the survivors.

Modular organization of *cis*-regulatory control information of neurotransmitter pathway genes in *Caenorhabditis elegans*, pp. 665–681

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Here, Serrano-Saiz *et al*. describe the *cis*-regulatory logic of how neurotransmitter identity is imposed onto individual, distinct neuron types. They provide support for a modular organization of *cis*-regulatory control elements.

The role of Y chromosome genes in male fertility in *Drosophila melanogaster*, pp. 623–633

Jiaying Zhang, Junjie Luo, Jieyan Chen, Junbiao Dai, and Craig Montell

The Y chromosome is comprised almost completely of heterochromatin and is rich in repetitive DNA, complicating DNA sequencing and genetic analyses. Over 100 years ago, Bridges found that the Y chromosome was required for male fertility, and since that time, six male fertility factors have been defined. Here, Zhang *et al*. interrogated known Y chromosome genes using CRISPR/Cas9 and RNAi, and provide molecular evidence supporting the identities of candidate coding sequences corresponding to male fertility factors. In addition, they provide evidence that some Y chromosome genes are not essential for male fertility.