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AUGUST 2011 • VOLUME 1 • ISSUE 3 • www.g3journal.org

INVESTIGATIONS AND AUTHOR SUMMARIES

- 171–182 **Stacks: Building and Genotyping Loci De Novo From Short-Read Sequences**
Julian M. Catchen, Angel Amores, Paul Hohenlohe, William Cresko, and John H. Postlethwait
- Advances in sequencing technology provide special opportunities for genetic analysis but lack of software has hindered progress. *Stacks* software uses short-read DNA sequence data for genetic analysis either *de novo* or by comparison to reference genomes. From short DNA sequence reads obtained with thrift and speed, *Stacks* can recover thousands of single nucleotide genetic variants (SNPs) for genetic analysis of crosses or populations. *Stacks* can generate markers for ultra-dense genetic maps, for analysis of population histories in geographical space, and for help in reference genome assembly. *Stacks* thus makes genomic analysis accessible for organisms with no previous genomic information.
- 183–186 **Mutation Rate Inferred From Synonymous Substitutions in a Long-Term Evolution Experiment With *Escherichia coli***
Sébastien Wielgoss, Jeffrey E. Barrick, Olivier Tenaillon, Stéphane Cruveiller, Béatrice Chane-Woon-Ming, Claudine Médigue, Richard E. Lenski, and Dominique Schneider
- The quantification of spontaneous mutation rates is crucial for a mechanistic understanding of the evolutionary process. In bacteria, traditional estimates using experimental or comparative genetic methods are prone to statistical uncertainty, and consequently estimates vary by over one order of magnitude. With the advent of next-generation sequencing, more accurate estimates are now possible. Applying neutral theory, we directly inferred the mutation rate from the synonymous substitutions found in 19 *Escherichia coli* genomes that were derived from a 40,000-generation evolution experiment. Given the power of our approach, our estimate represents the most accurate measure of bacterial base-substitution rates available to date.
- 187–196 **High-Resolution Genotyping of Wild Barley Introgression Lines and Fine-Mapping of the Threshability Locus *thresh-1* Using the Illumina GoldenGate Assay**
Inga Schmalenbach, Timothy J. March, Thomas Bringezu, Robbie Waugh, and Klaus Pillen
- Wild species introgression lines (ILs) are an ideal resource to identify and clone exotic alleles, which control monogenic or polygenic traits. We report on a set of 73 wild barley ILs. The genomic extension of the individual introgressions was characterized with an Illumina SNP array. In addition, for most ILs segregating high-resolution mapping populations (HRs) were developed to facilitate fine-mapping and cloning of QTLs. As a case study we used HR lines to fine-map the novel locus *thresh-1* on barley chromosome 1H. We show that wild barley ILs and derived HR lines are ideal tools to support dissecting of QTL effects.

- 197–208 **Genome-Wide Analysis to Identify Pathways Affecting Telomere-Initiated Senescence in Budding Yeast**
Hsin-Yu Chang, Conor Lawless, Stephen G. Addinall, Sarah Oexle, Morgan Taschuk, Anil Wipat, Darren J. Wilkinson, and David Lydall
- In telomerase-deficient yeast cells, like equivalent mammalian cells, telomeres shorten over many generations until a period of senescence/crisis is reached. After this, a small fraction of cells can escape senescence. To investigate the pathways that affect entry into and recovery from telomere-driven senescence, we combined a gene deletion disrupting telomerase (*est1Δ*) with the systematic yeast deletion collection and measured senescence characteristics in high-throughput assays. Our genome-wide analysis identifies genes that affect entry into and/or exit from telomere-initiated senescence and will be of interest to those studying telomere biology, replicative senescence, cancer, and aging.
- 209–218 **Mixed Model Association Mapping for Fusarium Head Blight Resistance in Tunisian-Derived Durum Wheat Populations**
Farhad Ghavami, Elias M. Elias, Sujun Mamidi, Omid Ansari, Mehdi Sargolzaei, Tika Adhikari, Mohamed Mergoum, and Shahryar F. Kianian
- The results of association analysis of a complex trait (Fusarium head blight in wheat) using a mixture of lines from breeding populations complemented by traditional QTL analysis indicate a presence of an important region in proximity to a locus previously identified from hexaploid wheat sources of resistance. This implies that selection in two different species at two disparate locations for the same disease was for a region on the same chromosome. Additionally, our results indicate a presence of a suppressor of resistance locus in the cultivated durum wheat, thus implying that successful removal of this locus could lead to the development of resistant varieties.
- 219–231 **A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance**
Shawn Hoon, Marinella Gebbia, Michael Costanzo, Ronald W. Davis, Guri Giaever, and Corey Nislow
- We performed a global analysis of the cellular response to carbonyl stress and identified genes that confer both resistance and sensitivity when gene dose is modified. We also identified key pathways and gene products essential for the response to carbonyl stress, a key intracellular and environmental toxin.
- 233–243 **Integrating Rare-Variant Testing, Function Prediction, and Gene Network in Composite Resequencing-Based Genome-Wide Association Studies (CR-GWAS)**
Chengsong Zhu, Xianran Li, and Jianming Yu
- High-density array-based genome-wide association studies (GWAS) are complemented by exome sequencing and whole-genome resequencing-based association studies. Here we present a composite resequencing-based genome-wide association study (CR-GWAS) strategy to demonstrate specifically how biological function predictions can be incorporated in the testing of rare variants, and broadly how function prediction, genome database, and network information can be integrated into the process of identifying robust associations. Applying this composite analysis strategy to Arabidopsis resequencing data, we showcase that both common and rare variants are underlying the variation of flowering time in Arabidopsis.