ISSUE HIGHLIGHTS

Mek1 suppression of meiotic double-strand break repair is specific to sister chromatids, chromosome autonomous and independent of Rec8 cohesin complexes, pp. 771–782
Tracy L. Callender and Nancy M. Hollingsworth

Mistakes in chromosome segregation during meiosis, which can lead to infertility and birth defects, may result if homologs are not physically connected by crossovers. The Mek1 protein kinase acts to promote recombination between homologs in yeast by suppressing recombination between sister chromatids. This article describes how Mek1 acts to regulate recombination during meiosis. It is important to understand the constraints on Mek1 function because that may facilitate identification of Mek1 substrates involved in suppressing intersister chromatid recombination.

Genetic variation gleaned from 94 mouse strains containing region of the genome. This article reports a dense map of understanding the genetic relationships between strains in each

understudied trait is increasing, and this might be due to a global shift in the population mean of underlying genetic variants or to increased variance underlying endophenotypes (such as body weight) in response to changing lifestyles. Using inbred lines of Drosophila melanogaster raised with different diets, the authors of this article show that population level genotype-by-diet interactions are pervasive and result in changes in both the population mean and the variance of metabolic phenotypes.

The rate and spectrum of spontaneous mutations in a plant RNA virus, pp. 983–989
Nicolas Tromas and Santiago F. Elena

RNA viruses are well known for their tremendous evolutionary potential. The lack of a proofreading ability of their RNA replicases contributes to this evolvability. These authors sought to estimate the mutation rate of a plant RNA virus and characterize the spectrum of spontaneous mutations. They find that the mutation rate is lower than that of animal RNA viruses.

Expression quantitative trait loci: Replication, tissue- and sex-specificity in mice, pp. 1059–1068
Atila van Nas, Leslie Ingram-Drake, Janet S. Sinsheimer, Susanna S. Wang, Eric E. Schadt, Thomas Drake and Aldons J. Lusis

Mapping genes that control transcript abundance has proven useful for modeling networks underlying complex traits such as obesity and diabetes. However, neither the reproducibility of these expression quantitative trait loci (eQTL) nor their tissue- and sex-specificity have been thoroughly evaluated. This article reports the analysis of these characteristics in four tissues from two large genetic crosses in mice. The conclusion is that local eQTL—the ones near the gene encoding the transcript and likely acting in cis—are highly reproducible, but distal, trans-acting eQTL are only modestly reproducible.

This Month in Genetics Research

Spoiling the whole bunch: Quality control to preserve the integrity of high throughput genotyping, Am. J. Hum. Genet. 87(1): DOI: 10.1016/j.ajhg.2010.06.005.
Anna Pluzhnikov, Jennifer E. Below, Anuar Konkashbaev, Anna Tikhomirov, Emily Kistner-Griffin, Cheryl A. Roe, Dan L. Nicolae and Nancy J. Cox

Successful genome-wide association studies (GWASs) require navigating the shoals of undetected genotyping errors, which will likely loom larger as investigators tap existing public databases for GWAS control samples. This article describes how to deal with this problem by utilizing additional sources of information, including raw signal intensity data.