ISSUE HIGHLIGHTS

Targeted genome modification in mice using zinc-finger nucleases, pp. 451–459

Iara D. Carbery, Diana Ji, Anne Harrington, Victoria Brown, Edward J. Weinstein, Lucy Liaw and Xiaoxia Cui

These investigators reduced the time to make knockout mice from years to months by introducing zinc-finger nucleases (ZFNs) into one-cell embryos, thus avoiding selection, culturing of embryonic stem cells, or breeding of chimeric animals. They show that generation of stable mutations using ZFNs is quick and efficient. The ZFN technology promises to facilitate rapid creation of mouse models for biomedical research.

Bacterial DNA uptake sequences can accumulate by molecular drive alone, pp. 613–627

H. Maughan, L. A. Wilson and R. J. Redfield

Many bacteria take up DNA fragments from their surroundings, but is this a bacterial version of sex or just an efficient way to get nucleotides for food? The answer must explain why some bacterial genomes contain many hundreds of copies of a sequence motif preferred by their DNA uptake machinery. Accumulation of these genomic uptake sequences by natural selection is especially puzzling because they cannot act until their cell is dead. The authors solve this problem by showing that selection isn't needed; if DNA uptake is biased, simulated uptake sequences passively accumulate by recombination, reaching densities and distributions like those in real genomes. This result frees researchers to focus on why DNA uptake is sometimes biased, and on the relative importance of genetic variation and food.

Detection of a gravitropism phenotype in *glutamate receptor-like 3.3* mutants of *Arabidopsis thaliana* using machine vision and computation, pp. 585–593

Nathan D. Miller, Tessa L. Durham Brooks, Amir H. Assadi and Edgar P. Spalding

Many single gene knockouts produce no obvious phenotypes in plants. Improved methods for detecting and quantifying the effects of gene mutations would likely make reverse genetics more effective for defining gene functions. These investigators record and analyze Arabidopsis seedlings' response to gravity (gravitropism) with high spatial and temporal resolution by digital image capture and processing (machine vision). Computational analysis of the results for a glutamate receptor mutant reveals an otherwise unobservable phenotype.

Trivalent arsenic inhibits the functions of chaperonin complex, pp. 725–734

Xuewen Pan, Stefanie Reissman, Nick R. Douglas, Zhiwei Huang, Daniel S. Yuan, Xiaoling Wang, J. Michael McCaffery, Judith Frydman and Jef D. Boeke

Arsenic is a ubiquitous environmental pollutant that causes severe health problems in humans. It is also used as an effective therapeutic agent against various diseases and infections. Using advanced genomic tools in the model organism yeast and biochemical experiments, these investigators demonstrate that arsenic disturbs functions of the chaperonin complex required for proper folding and maturation of a large number of proteins. This mechanism of action by arsenic is conserved in various biological systems. Such an understanding should help in exploring possible ways to overcome toxic effects caused by exposure to arsenic.

Parallel adaptation: One or many waves of advance of an advantageous allele?, pp. 647–668

Peter Ralph and Graham Coop

There are many examples of repeated evolution of an adaptive phenotype within a species through independent mutations. These authors model the probability of such parallel adaptive mutations in a geographically spread population. They find that the characteristic geographic scale on which parallel adaptations occur can be expressed as a simple function of population genetic parameters. They demonstrate for realistic parameters that parallel adaptation is probably a more common outcome than appreciated.

The rapidly evolving centromere-specific histone has stringent functional requirements in *Arabidopsis thaliana*, pp. 461–471

Maruthachalam Ravi, Pak N. Kwong, Ron M. G. Menorca, Joel T. Valencia, Joseph S. Ramahi, Jodi L. Stewart, Robert K. Tran, Venkatesan Sundaresan, Luca Comai and Simon W.-L. Chan

The rapid evolution of the centromere-specific histone CENH3 has been proposed to contribute to speciation. This article shows that while *Arabidopsis thaliana cenh3* can be complemented by CENH3 from a sister species, *Brassica* and maize CENH3s are not functional in Arabidopsis, despite localizing to kinetochores. These results are consistent with the idea that rapid centromere evolution can cause chromosome segregation defects and reduce fertility in interspecies crosses.

Promoter strength influences the S phase requirement for establishment of silencing at the *Saccharomyces cerevisiae* silent mating type loci, pp. 551–560

Jie Ren, Chia-Lin Wang and Rolf Sternglanz

Establishment of silencing of the yeast silent mating type locus *HMR* requires passage through the cell cycle. This article shows that silencing of the *HML* locus, the counterpart of *HMR*, can occur in the absence of cell-cycle progression. The difference is attributed to differing promoter strengths at the two loci. The stronger the promoter, the greater the cell-cycle requirement. Thus, transcriptional activity counteracts the establishment of silencing but can be overcome by passage through S phase.

A Drosophila chromatin factor interacts with the Piwi-interacting RNA mechanism in niche cells to regulate germline stem cell self-renewal, pp. 573–583

Tora K. Smulders-Srinivasan, Akos Szakmary and Haifan Lin

This article reveals the role of epigenetic programming of niche cells in regulating stem cell self-renewal. While niche signaling and epigenetic programming of stem cells have been well studied, epigenetic programming of niche cells has not been explored. This study investigates the important role of the epigenetic factor Corto in antagonistically interacting with the Yb–Piwi–Hedgehog niche signaling pathway in maintaining germline stem cells in the Drosophila ovary.

A two-pathway analysis of meiotic crossing over and gene conversion in *Saccharomyces cerevisiae*, pp. 515–536

Franklin W. Stahl and Henriette M. Foss

The relationships between gene conversion (nonreciprocal recombination) and crossing over (reciprocal recombination) in meiosis have long intrigued—and baffled—yeast geneticists. Stahl and Foss explain how these relationships can be understood within a model for DNA double-strand break repair that assumes two pathways differing in several respects, most notably in the action of enzymes that rectify the mispaired bases that arise during double-strand break repair. The model accounts for multiple aspects of previously published studies and makes a number of distinctive, testable predictions.

This Month in Genetics Research

Inference of unexpected genetic relatedness among individuals in HapMap Phase III, Am. J. Hum. Genet. **87**(4)

Trevor J. Pemberton, Chaolong Wan, Jun Z. Li and Noah A. Rosenberg

The International HapMap Project propelled studies of human population genetics and genome-wide association studies. This article reports an analysis of the most recent results of the HapMap Project, which increases the number of individuals sampled fivefold. Remarkably, the authors identify numerous pairs of close relatives, among the 1,397 individuals sampled, whose relationship was not known. They cull the panel of individuals to a standardized subset of unrelated people for use in studies in which it is important that relatedness be clearly defined.