Genetics, Vol. 188, August 2011, Copyright © 2011

Genome evolution and meiotic maps by massively parallel DNA sequencing: Spotted gar, an outgroup for the teleost genome duplication, pp. 799–808

Angel Amores, Julian Catchen, Allyse Ferrara, Quenton Fontenot, and John H. Postlethwait

Genomic resources for many species of evolutionary interest are lacking, due to the expense and difficulty of producing them. These investigators surmounted those limitations by using massively parallel DNA sequencing to make a genetic map of the spotted gar fish, using only the offspring of two wild-caught fish. They show that genome organization in gar is more similar to that of human than teleost fish, thus validating gar as an outgroup for the teleost genome duplication. This economical and rapid approach brings genomic analysis of nonmodel organisms within reach.

Anterior–posterior axis specification in *Drosophila* oocytes: Identification of novel *bicoid* and *oskar* mRNA localization factors, pp. 883–896

Chin-Wen Chang, Dmitry Nashchekin, Lucy Wheatley, Uwe Irion, Katja Dahlgaard, Tessa G. Montague, Jacqueline Hall, and Daniel St. Johnston

The *Drosophila* anterior–posterior axis is defined by the targeting of *bicoid* and *oskar* mRNAs to opposite ends of the oocyte. This article describes a genetic screen for suppressors of the artificial mislocalization of *oskar* mRNA to the oocyte anterior, which results in embryos with two abdomens. Several factors required for *bicoid* or *oskar* mRNA localization were identified, including Cappuccino, which acts downstream of Oskar to nucleate actin filaments that play a role in *oskar* mRNA anchoring.

The balance between mutators and nonmutators in asexual populations, pp. 997–1014

Michael M. Desai and Daniel S. Fisher

How do mutator alleles contribute to the evolution of mutation rate? Because most mutators accumulate deleterious mutations and are selected against, most observed mutators are young. These investigators analyze the dynamics of mutator alleles that are being continually produced from nonmutators. Their study of the fate of each mutator lineage and how the youth of most mutators changes the characteristics of the mutator population has implications for the evolution of mutation rates and for adaptation.

Inference of site frequency spectra from high-throughput sequence data: Quantification of selection on nonsynonymous and synonymous sites in humans, pp. 931–940

Peter D. Keightley and Daniel L. Halligan

Interpreting high-throughput sequence data in a population genetics context requires unbiased inference of the distribution of allele frequencies. These authors present a method for achieving this that takes into account sequencing errors and random sampling of reads in individuals sequenced at low coverage. They validate their approach by simulations and by analyzing high-throughput human-genome sequence data.

Insight into the mechanism of nucleosome reorganization from histone mutants that suppress defects in the FACT histone chaperone, pp. 835–846

Laura McCullough, Robert Rawlins, Aileen Olsen, Hua Xin, David J. Stillman, and Tim Formosa

FACT (FAcilitates Chromatin Transcription/Transactions) is an essential histone chaperone with multiple roles in modulating chromatin structure by forming and destabilizing nucleosomes. To probe the mechanism of FACT function, these investigators identify histone mutations that suppress a FACT defect in yeast. The mutations reveal the importance of rapid interconversion between stable nucleosomes and reorganized forms. This study provides new insight into FACT activity and the dynamic properties of chromatin.

Genome-wide epigenetic perturbation jump-starts patterns of heritable variation found in nature, pp. 1015–1017

Fabrice Roux, Maria Colomé-Tatché, Cécile Edelist, René Wardenaar, Philippe Guerche, Frédéric Hospital, Vincent Colot, Ritsert C. Jansen, and Frank Johannes

This study reveals significant interaction between epigenetic and genetic inheritance in plants. By extensively phenotyping 6000 *Arabidopsis* plants with experimentally perturbed DNA methylomes, the authors find that epigenetically induced and naturally occurring variation in complex traits share part of their polygenic architecture and may offer complementary routes to adaptation in ecological settings.

Hox and a newly identified E2F co-repress cell death in *Caenorhabditis elegans*, pp. 897–905

Jennifer Winn, Monique Carter, Leon Avery, and Scott Cameron

How does a cell choose one particular fate among myriad possible fates? Here, the authors identify the mechanism by which two major developmental pathways, Hox and E2F, are able to specify cell fate in a manner that converges on a cell death gene to determine cell life *vs.* death. By observing the expression pattern of the *egl-1* BH3-only gene, the authors discover that Hox and E2F work in a highly context-specific, and sometimes cooperative, manner to regulate cell fate.

Inhibition of RNA interference and modulation of transposable element expression by cell death in *Drosophila*, pp. 823–834

Weiwu Xie, Chengzhi Liang, and James A. Birchler

This article reports the surprising observation that cell death suppresses RNA interference (RNAi) in adjacent cells. This is because the conversion of double-stranded RNA (dsRNA) to short interfering RNA (siRNA) is blocked. The authors show that expression of endogenous transposable elements, which are regularly silenced by RNAi, increases when cell death occurs due to a reduced level of siRNA. Thus, developmental perturbations, disease states, or environmental insults that cause ectopic cell death will alter transposon expression patterns.