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Exploiting the extraordinary genetic polymorphism of *Ciona* for developmental genetics with whole genome sequencing, pp. 49–59

Sarah Abdul-Wajid, Michael T. Veeman, Shota Chiba, Thomas L. Turner, and William C. Smith

Tunicates such as *Ciona* are key for understanding the evolutionary origins of chordate development. This study used a whole-genome sequencing approach to map spontaneous developmental mutations in outbred *Ciona* populations. The smaller genomes and higher polymorphism rate of *Ciona* allowed the authors to define much narrower candidate regions than has been reported for other vertebrate models. *Ciona* methods and resources were also the focus of a recent Toolbox Review on *Ciona intestinalis*.

TargetOrtho: a phylogenetic footprinting tool to identify transcription factor targets, pp. 61–76

Lori Glenwinkel, Di Wu, Gregory Minevich, and Oliver Hobert

It has proven difficult to use experimental knowledge of transcription factor binding sequences to reliably predict target genes in genomic sequence space. This article describes TargetOrtho, a bioinformatic pipeline aimed at predicting functionally relevant transcription factor target genes. Among the key features of this pipeline is the use of sequence conservation of binding sites in related species. The authors validate TargetOrtho by identifying novel targets of a transcription factor in motor neurons of *Caenorhabditis elegans*.

The fate of chromosomes and alleles in an allohexaploid *Brassica* population, pp. 273–283

Annaliese S. Mason, Matthew N. Nelson, Junko Takahira, Wallace A. Cowling, Gustavo Moreira Alves, Arkaprava Chaudhuri, Ning Chen, Mohana E. Ragu, Jessica Dalton-Morgan, Olivier Coriton, Virginie Huteau, Frédérique Eber, Anne-Marie Chèvre, and Jacqueline Batley

Production of stable allohexaploid (three-genome) hybrids in the agriculturally significant *Brassica* genus has been a goal of geneticists and breeders for 100 years. However, synthetic allohexaploids in *Brassica* are usually unstable and lose chromosomes from generation to generation. Why this happens is unknown, as naturally-occurring stable allopolyploid species are common in this genus. Mason *et al.* used a combination of SNP marker and cytogenetics techniques to comprehensively assess karyotype stability and chromosome behaviour in allohexaploid *Brassica*. Their results show promise for the development of stable synthetic hybrids.

Modular skeletal evolution in sticklebacks is controlled by additive and clustered quantitative trait loci, pp. 405–420

Craig T. Miller, Andrew M. Glazer, Brian R. Summers, Benjamin K. Blackman, Andrew R. Norman, Michael D. Shapiro, Bonnie L. Cole, Catherine L. Peichel, Dolph Schluter, and David M. Kingsley

Stickleback fish have repeatedly evolved changes to their skeleton as they adapt from oceanic to freshwater environments. Miller *et al.* analyze a large genetic cross between marine and freshwater sticklebacks and identify over 100 quantitative trait loci controlling skeletal traits. Loci underlying evolved changes in skeletal pattern tend to have additive genetic effects, typically act in anatomically regional domains, and cluster in the genome. This suggests concerted changes in traits may occur when sticklebacks inherit alleles at linked or possible "supergene" regions of the genome.

A penalized likelihood method for estimating the distribution of selection coefficients from phylogenetic data, pp. 257–271

Asif U. Tamuri, Nick Goldman, and Mario dos Reis

Estimation of the distribution of selection coefficients (S) is a long-standing issue in molecular evolution. This article describes a penalized likelihood method to estimate the distribution in protein-coding genes from phylogenetic data. Results for three real data sets indicate a high proportion of deleterious mutations as predicted by population genetics theory and as seen in mutation experiments.

Birth, death, and diversification of mobile promoters in prokaryotes, pp. 291–299

Mark W.J. van Passel, Harm Nijveen, and Lindi M. Wahl

Mobile promoters are homologous promoter sequences associated with non-homologous coding sequences, which may be a new class of mobile genetic element. This study identifies the full complement of mobile promoters in sequenced prokaryotic genomes. The authors develop a model of the gain and loss of mobile promoters in these genomes; by fitting this model to the data, they predict the relative importance of horizontal gene transfer, duplication and diversification in maintaining mobile promoter families.

High-resolution sex-specific linkage maps of the mouse reveal polarized distribution of crossovers in male germline, pp. 91–106

Eric Yi Liu, Andrew P. Morgan, Elissa J. Chesler, Wei Wang, Gary A. Churchill, and Fernando Pardo-Manuel de Villena

Liu *et al.* used high-density genotyping of the mouse Collaborative Cross to investigate the roles of sex and genetic background in mammalian recombination. This revealed a striking concentration of recombination events in the distal ends of autosomes in male meiosis that is absent in female meiosis. The authors also identify large recombination-poor regions that cover 5% of the genome. These regions are enriched for segmental duplications, suggesting an inverse local correlation between recombination rate and mutation rate for large copy number variants.

Genetic and genomic tools for the marine annelid *Platynereis dumerilii*, pp. 19–31

Juliane Zantke, Stephanie Bannister, Vinoth Babu Veedin Rajan, Florian Raible, and Kristin Tessmar-Raible

and

TALENs mediate efficient and heritable mutation of endogenous genes in the marine annelid *Platynereis dumerilii*, pp. 77–89

Stephanie Bannister, Olga Antonova, Alessandra Polo, Claudia Lohs, Natalia Hallay, Agne Valinciute, Florian Raible, and Kristin Tessmar-Raible

The bristle-worm *Platynereis dumerilii* is a model system for studies of evolution, development and neuroscience, as well as for the molecular basis of circalunar reproductive timing. This manuscript marks a breakthrough for the *Platynereis* model, as it describes the first method for generation of specific and inheritable mutations in the species. The authors also provide a streamlined workflow and technical tricks that are of wider relevance for the establishment of targeted genome editing technology in other non-conventional model species. *Platynereis dumerilii* genetic methods are also the focus of a Toolbox Review in this issue.

This Month in the American Journal of Human Genetics

Maternal history of Oceania from complete mtDNA genome sequences: contrasting ancient diversity with recent homogenization due to the Austronesian expansion, Am. J. Hum. Genet. 94(5)

Ana T. Duggan, Bethwyn Evans, Françoise R. Friedlaender, Jonathan S. Friedlaender, George Koki, D. Andrew Merriwether, Manfred Kayser, and Mark Stoneking

There are still many questions regarding human migrations in Oceania. In this study, Duggan *et al.* evaluate approximately 1,330 whole mitochondrial genome sequences from 34 Oceanic populations to better understand the maternal contribution to the migrations that have occurred in this region. Because of the distribution of the Austronesian-associated haplogroups, the authors suggest that the Austronesians became very well integrated into the existing populations. Of the non-Austronesian haplogroups that might have originated in Oceania, the coalescence times are more than 60 thousand years ago suggesting an ancient origin, are region-specific suggesting long periods of isolation, and also suggest that there were lesser migrations throughout the history of this region.