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### INVESTIGATIONS AND AUTHOR SUMMARIES

- 843–851 **Expression Profiling of Attenuated Mitochondrial Function Identifies Retrograde Signals in *Drosophila***  
*William A. Freije, Sudip Mandal, and Utpal Banerjee*  
Cytochrome oxidase Va subunit is a key gene controlling cell growth in the *Drosophila* third instar larval process. These authors employed microarray-based transcriptional profiling to define the changes associated with loss of Cytochrome oxidase Va in *Drosophila* S2 cells. The authors used this discovery-driven approach to understand the mechanism of changes in growth kinetics. The transcriptome studies reveal a metabolic shift towards glycolysis and direction of metabolites away from the ailing mitochondrion. The authors, using a systems-based interpretation to summarize the data of the 21 most highly differentially-expressed genes, reveal a portrait of how energy substrates are managed through conserved mitochondrial retrograde signaling mechanisms.
- 853–864 **Genome-Wide Association Mapping in Tomato (*Solanum lycopersicum*) Is Possible Using Genome Admixture of *Solanum lycopersicum* var. *cerasiforme***  
*Nicolas Ranc, Stephane Muñoz, Jiaxin Xu, Marie-Christine Le Paslier, Aurélie Chauveau, Rémi Bounon, Sophie Rolland, Jean-Paul Bouchet, Dominique Brunel, and Mathilde Causse*  
As an inbred crop, the tomato exhibits low molecular polymorphism and high linkage disequilibrium, which reduces genome-wide association (GWA) resolution. The genome of cherry tomatoes is an admixture between the cultivated tomato and its wild ancestor. The authors used this admixture to improve the resolution of association mapping in the tomato. As a proof of concept, they sequenced 81 DNA fragments distributed on chromosome 2 in a core collection of 90 accessions, including mostly cherry tomato accessions. Three hundred and forty SNPs and indels were identified, and linkage disequilibrium decrease studied. The core collection was characterized for three fruit traits and several associations between polymorphism and phenotype were detected, validating several candidate genes and QTL previously identified.
- 865–871 **Proper Cyclin B3 Dosage Is Important for Precision of Metaphase-to-Anaphase Onset Timing in *Caenorhabditis elegans***  
*Maja Tarailo-Graovac and Nansheng Chen*  
Precision of anaphase onset is crucial for proper segregation of genetic material to daughter cells. This study demonstrates the importance of the Mos1-mediated single-copy insertion (MosSCI) method to manipulate gene dosage in controlled manner. In particular, using the MosSCI, the authors generated worms with additional copies of the *cyb-3* (Cyclin B3) gene and show that tripling the CYB-3 dosage results in significantly variable anaphase onset. This variability is skewed towards the delayed anaphase onset and is independent of the functional MDF-1/Mad1, a conserved component of the spindle assembly checkpoint that monitors anaphase onset and prevents chromosome instability.

- 873–882 **Microarray-Based Capture of Novel Expressed Cell Type-Specific Transfrags (CoNECT) to Annotate Tissue-Specific Transcription in *Drosophila melanogaster***  
*X. Hong, H. Doddapaneni, J. M. Comeron, M. J. Rodesch, H. A. Halvensleben, C. Y. Nien, F. Bolei, R. Metpally, T. A. Richmond, T. J. Albert, and J. R. Manak*
- Having developed a new methodology called CoNECT (capture of novel expressed cell type-specific transfrags) these authors enrich for transcript isoforms on a microarray, followed by next generation sequencing. This technique allows them to not only identify novel transcript isoforms in fly testes and ovaries, but also to identify transcriptional signatures of minority cell types in a tissue. For example, genes expressed in only two pairs of nerves in *Drosophila* ovaries were identified with CoNECT even though the neurons make up less than 0.01% of the total cell number in the ovary.
- 883–889 **Alignment-Free Population Genomics: An Efficient Estimator of Sequence Diversity**  
*Bernhard Haubold and Peter Pfaffelhuber*
- Sequence diversity is a central quantity in population genetics. It is usually estimated from alignments, but these are difficult to compute for genomes. These authors have therefore derived and implemented an efficient alignment-free estimator of sequence diversity based on the distribution of the lengths of exact matches between pairs of sequences. When applying their software to pairs of *Drosophila* genomes, they obtain diversity measurements that broadly agree with slower alignment-based analyses.
- 891–904 **Incidence of Genome Structure, DNA Asymmetry, and Cell Physiology on T-DNA Integration in Chromosomes of the Phytopathogenic Fungus *Leptosphaeria maculans***  
*Salim Bourras, Michel Meyer, Jonathan Grandaubert, Nicolas Lapalu, Isabelle Fudal, Juliette Linglin, Benedicte Ollivier, Françoise Blaise, Marie-Hélène Balesdent, and Thierry Rouxel*
- In current whole-genome sequence initiatives in eukaryotes, a large proportion of predicted proteins have no known function. For functional annotation, the production of collections of mutants using *Agrobacterium tumefaciens*-mediated transformation (ATMT), associated with genotyping and phenotyping has gained wide acceptance. In this study, the authors analyzed the genome features linked with T-DNA integration events in the compartmentalized genome of the phytopathogenic fungus *Leptosphaeria maculans*. Three hundred eighteen T-DNA tags were recovered. The T-DNA integration was mainly targeted to gene-rich, transcriptionally active regions and favored biological processes consistent with spore physiology. T-DNA integration was strongly biased towards regulatory regions, and mainly promoters.
- 905–911 **Resampling QTL Effects in the QTL Sign Test Leads to Incongruous Sensitivity to Variance in Effect Size**  
*Daniel P. Rice and Jeffrey P. Townsend*
- Quantitative trait loci (QTL) have long represented key outcomes of the analysis of the genetic basis of quantitative traits. They also seem to provide key data for revealing the evolutionary history of diverged populations, in that multiple loci with a common directional effect imply the action of natural selection rather than neutral drift. However, a popular test for selection based on quantitative trait locus effect directions and magnitudes is shown here to exhibit high sensitivity to QTL effect size variance. By applying the test to QTL data simulated under selection, the authors demonstrate that conditioning on the phenotypic difference results in a loss of power to reject the neutral hypothesis, and marked sensitivity to variation in locus effect magnitude that has no clear justification in evolutionary models.
- 913–920 **Genetic Interactions Between Arabidopsis *DET1* and *UVH6* During Development and Abiotic Stress Response**  
*Esther Kim, Valentina Ly, Avril Hatherell, and Dana F. Schroeder*
- The sun provides plants with visible light for photosynthesis but is also a source of damaging UV rays and heat. How do plants co-ordinate their development in order to maximize the beneficial effects of sunlight while protecting themselves from harm? Here the authors examine genetic interactions between the Arabidopsis genes *DE-ETIOLATED 1*, a regulator of visible light signaling, and *UV-HYPERSENSITIVE 6*, which is involved in repair of UV damaged DNA and heat response. They find that these genes utilize both independent and common pathways to regulate plant development and response to heat, visible light and UV damage.

- 921–930 **Targeted Capture of Homoeologous Coding and Noncoding Sequence in Polyploid Cotton**  
*Armel Salmon, Joshua A. Udall, Jeffrey A. Jeddloh, and Jonathan Wendel*
- This article describes novel methods and results for high-throughput isolation and sequencing of homoeologous genes in allopolyploid plants. To capture and sequence both members of each gene pair (homoeologs) of wild and domesticated *Gossypium hirsutum*, the authors created custom hybridization probes to target 500 pairs of homoeologs using information from the cotton transcriptome. The methods and strategies developed here are of broad interest and appear well-suited for population genomics approaches, and may even be used for species in which genomic resources are quite limited.
- 931–941 **Satellite DNA-Like Elements Associated With Genes Within Euchromatin of the Beetle *Tribolium castaneum***  
*Josip Brajković, Isidoro Feliciello, Branka Bruvo-Madarić, and Đurđica Ugarković*
- In the beetle *Tribolium castaneum*, repeats of abundant pericentromeric satellite DNA are found dispersed in the vicinity of genes on all chromosomes and are statistically overrepresented near genes with immunoglobulin-like domains. The discovery of satellite DNA elements associated with genes in the euchromatic portion of the genome suggests a possible gene-regulatory role for these sequences.
- 943–959 **Loss of a 20S Proteasome Activator in *Saccharomyces cerevisiae* Downregulates Genes Important for Genomic Integrity, Increases DNA Damage, and Selectively Sensitizes Cells to Agents With Diverse Mechanisms of Action**  
*Kevin M. Doherty, Leah D. Pride, James Lukose, Brian E. Snyderman, Ronald Charles, Ajay Pramanik, Eric G. Muller, David Botstein, and Carol Wood Moore*
- In many human diseases, aggregated, unfolded, misfolded, and nonfunctional proteins accumulate. Functional proteasomes degrade such proteins. In studies of cells without a universally-conserved proteasome activator the authors found that numerous genes required for accurate chromosome structure, assembly, and repair were downregulated, a particular subset of genes encoding protein-folding chaperones was upregulated, massive chromosomal damage and cell death followed DNA-damaging treatments, and cells were hypersusceptible to agents with diverse mechanisms of action. The protective functions provided by the activator have implications for ubiquitin-independent targeting in anticancer therapy, and preservation of these functions without the carboxyl-terminus has implications for structural studies of the activator.
- 961–975 **Forward Genetic Analysis to Identify Determinants of Dopamine Signaling in *Caenorhabditis elegans* Using Swimming-Induced Paralysis**  
*J. Andrew Hardaway, Shannon L. Hardie, Sarah M. Whitaker, Sarah R. Baas, Bing Zhang, Daniel P. Bermingham, Ariana J. Lichtenstein, and Randy D. Blakely*
- This study uses the powerful model organism in a screen to identify novel genes that regulate endogenous dopamine signaling. The authors validate the utility of the screen via proof of concept studies demonstrating that the screen is capable of identifying mutations in the presynaptic dopamine transporter. They also describe the isolation and pharmacological, biochemical, and genetics analysis of two mutants, *vt25* and *vt29*, which bear mutations in unique, novel genes that regulate dopamine signaling through actions in distinct pathways.