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APRIL 2013 • VOLUME 3 • ISSUE 4 • [www.g3journal.org](http://www.g3journal.org)

### INVESTIGATIONS AND AUTHOR SUMMARIES

- 585–595 **Assembly of the Synaptonemal Complex Is a Highly Temperature-Sensitive Process That Is Supported by PGL-1 During *Caenorhabditis elegans* Meiosis**  
*Ceyda Bilgir, Carolyn R. Dombecki, Peter F. Chen, Anne M. Villeneuve, and Kentaro Nabeshima*  
In this article, the authors report that assembly of the synaptonemal complex (SC) exhibits extremely high temperature sensitivity during *Caenorhabditis elegans* meiosis and that a germline-specific P-granule component plays a role in SC assembly at high temperatures. Their work also has broader relevance to the *C. elegans* community in that it provides a potential mechanistic explanation for a commonly used procedure for obtaining males and highlights the risks of using high temperatures in *C. elegans* research. It also describes a useful experimental resource for studying chromosome dynamics in germlines and embryos using GFP-LacI/lacO.
- 597–605 **Genome-Wide Detection of Gene Coexpression Domains Showing Linkage to Regions Enriched with Polymorphic Retrotransposons in Recombinant Inbred Mouse Strains**  
*Marie-Pier Scott-Boyer and Christian F. Deschepper*  
Although gene coexpression domains have been reported in most eukaryotic organisms, data available to date suggested that coexpression rarely concerned more than doublets or triplets of adjacent genes in mammals. In this study, the authors performed genetic analyses of gene expression data from tissues of recombinant inbred mouse strains. They found that mammalian genomes do harbor small domains containing more than four coexpressed genes. The expression levels of all such coexpressed genes could all be linked to common polymorphic loci. These domains showed enrichment for polymorphic transposable elements, the latter showing enrichment for the motifs of binding sites for several regulatory factors.
- 607–616 **Plastome Sequence Determination and Comparative Analysis for Members of the *Lolium-Festuca* Grass Species Complex**  
*Melanie L. Hand, German C. Spangenberg, John W. Forster, and Noel O. I. Cogan*  
This article describes the comprehensive characterization of the full chloroplast genome (plastome) sequences for representative diploid members of the *Lolium-Festuca* species complex, which includes some of the world's most important cool-season pasture grasses. The authors analyze the sequence data in terms of gene content and annotation and conduct a comparative analysis across the Poaceae family of grasses and cereals and other flowering plant species. They interpret their results in terms of evolutionary processes and discuss the implications of the study for plastid genome-mediated plant transgenesis.

- 617–631**     **An Ultra-High-Density, Transcript-Based, Genetic Map of Lettuce**  
*Maria José Truco, Hamid Ashrafi, Alexander Kozik, Hans van Leeuwen, John Bowers, Sebastian Reyes Chin Wo, Kevin Stoffel, Huaqin Xu, Theresa Hill, Allen Van Deynze, and Richard W. Michelmore*
- Comprehensive genetic maps that contain much of the gene coding component of genomes have a multitude of uses. These authors generated an ultra-high-density genetic map for lettuce, an economically important member of the Compositae. The map orders approximately a third of all known genes on the nine chromosomal linkage groups. This was achieved by hybridizing genomic DNA to a custom Affymetrix oligonucleotide array. The authors analyzed segregation of DNA polymorphisms using F<sub>7,8</sub> recombinant inbred lines from a cross between cultivated *Lactuca sativa* and *L. serriola*, the wild progenitor. Integration of this map with previously published data provides candidate genes for multiple phenotypes.
- 633–644**     **Trans-Lesion DNA Polymerases May Be Involved in Yeast Meiosis**  
*Ayelet Arbel-Eden, Daphna Joseph-Strauss, Hagit Masika, Oxana Printzentel, Eléonor Rachi, and Giora Simchen*
- Trans-lesion DNA polymerases (TLSPs) bypass DNA lesions during replication and thus generate new mutations. This study shows that these proteins are strongly induced during yeast meiosis, when DNA double-strand breaks (DSBs) are formed and chromosomes recombine. TLSPs-deleted strains undergo an apparent normal meiosis; however, strains devoid of all three TLSPs show a reduction in recombination events. The authors also found meiosis-specific associations of TLSPs with DSB proteins, which suggests that TLSPs may participate in processing of meiotic DSBs and recombination. This explains the previously reported 6–20-fold increase in mutations during meiosis, which would lead to greater genome diversity and faster evolutionary divergence.
- 645–655**     **Activation-Induced Cytidine Deaminase Does Not Impact Murine Meiotic Recombination**  
*Catarina S. Cortesao, Raquel F. Freitas, and Vasco M. Barreto*
- A number of parallels have been drawn between the physiological reactions of DNA recombination in somatic and germline cells. AID is the enzyme that edits the immunoglobulin genes in B lymphocytes. Its apparent additional functions and its reported expression in the germline raise the hypothesis that AID is also involved in meiosis. Here the authors directly address that question and exclude the contribution of AID to the frequency of meiotic recombination in mice. The data show that the few mammalian enzymes able to trigger physiological double-strand breaks in the genome have nonoverlapping roles.
- 657–664**     **Donor DNA Utilization During Gene Targeting with Zinc-Finger Nucleases**  
*Kelly J. Beumer, Jonathan K. Trautman, Kusumika Mukherjee, and Dana Carroll*
- When performing a gene targeting experiment, it is important to know how the donor DNA should be designed and what outcomes can be expected. This study examines targeted gene replacements in *Drosophila*, stimulated by cleavage of the target locus with zinc-finger nucleases (ZFNs). Issues addressed include the minimum length of homology needed to support recombination between donor and target, the length of conversion tracts, the incorporation of large insertions and deletions, and the use of oligonucleotides as donors. The results are important not only for *Drosophila* but for nuclease-mediated gene targeting in other organisms as well.
- 665–673**     **ZRT1 Harbors an Excess of Nonsynonymous Polymorphism and Shows Evidence of Balancing Selection in *Saccharomyces cerevisiae***  
*Elizabeth K. Engle and Justin C. Fay*
- Many species show genome-wide evidence of positive selection based on patterns of DNA variation within species compared to divergence between species. Yet evidence for positive selection in the budding yeast *Saccharomyces cerevisiae* is absent. In this study, the authors examined the hypothesis that balancing selection on some genes obscures genome-wide evidence of positive selection. They found that one out of the five genes tested, *ZRT1*, exhibits evidence of balancing selection. While it is difficult to determine the frequency of balancing selection in the yeast genome, these results suggest that balancing selection is important to consider when estimating the frequency of positive selection across the yeast genome.

- 675–686 **Comparative Genomics of Serial Isolates of *Cryptococcus neoformans* Reveals Gene Associated With Carbon Utilization and Virulence**  
*Kate L. Ormerod, Carl A. Morrow, Eve W. L. Chow, I. Russel Lee, Samantha D. M. Arras, Horst Joachim Schirra, Gary M. Cox, Bettina C. Fries, and James A. Fraser*  
*Cryptococcus neoformans* is an important fungal pathogen responsible for an estimated 625,000 deaths each year. It is capable of surviving within the human host for long periods, necessitating long-term antifungal therapy. Changes occurring in the genome during this time may contribute to the development of antifungal resistance as well as strains better able to cope with the hostile host environment. In this article, the authors report the first whole genome comparison of two strains isolated sequentially from a single patient. The strains displayed differences in virulence profiles and nutrient acquisition and characterize a predicted transcriptional regulator responsible for many of the observed phenotypic changes.
- 687–693 **A Functional Comparison of the 3xP3 Promoter by Recombinase-Mediated Cassette Exchange in *Drosophila* and a Tephritid Fly, *Anastrepha suspensa***  
*Marc F. Schetelig and Alfred M. Handler*  
The artificial 3xP3 promoter has three binding sites for Pax-6/eyeless homodimers and has been used to promote eye-specific marker expression in many orders of insects. However, *Anastrepha suspensa*, transgenic flies identified by polyubiquitin (*PUB*)-regulated EGFP, did not express a 3xP3-regulated AmCyan fluorescent protein. To determine if 3xP3 is functional in a tephritid species, the authors developed a Cre/loxP-based recombinase-mediated cassette exchange system and used it to compare marker expression in the same genomic context. They found that the *PUB-DsRed* and 3xP3-*AmCyan* markers both expressed normally in *Drosophila*, while only the *PUB-DsRed* marker was expressed and detectable in the tephritid species.
- 695–708 **Transcriptome Profiling Following Neuronal and Glial Expression of ALS-Linked SOD1 in *Drosophila***  
*Emily L. Kumimoto, Taylor R. Fore, and Bing Zhang*  
Amyotrophic lateral sclerosis (ALS) is a devastating neural disease affecting people around the world. Several gene mutations have been linked to the disease, but currently it is incurable. This study models ALS in fruit flies and shows age-dependent changes of mutant SOD1 flies to oxidative stress by expressing an ALS-causing gene in two critical cells (motoneurons or glia) affected in the disease. The authors also identify gene expression altered by cell-specific expression of mutant SOD1. These observations may provide insight into the development or progression of ALS.
- 709–717 **Linkage Disequilibrium Estimation of Effective Population Size with Immigrants from Divergent Populations: A Case Study on Spanish Mackerel (*Scomberomorus commerson*)**  
*Gilbert Michael Macbeth, Damien Broderick, Rik C. Buckworth, and Jennifer R. Ovenden*  
Effective population size is an important ecological parameter which can be used to monitor changes in populations. These authors found that estimates of effective population size using the linkage disequilibrium method were sensitive to a small number of nontarget species or samples from divergent populations. The bias can be corrected by removing outlier genotypes using a correspondence analysis. In this article, the authors demonstrate the methods in a narrow barred Spanish mackerel population (*Scomberomorus commerson*).
- 719–726 **Involvement of MLPK Pathway in Intraspecies Unilateral Incompatibility Regulated by a Single Locus With Stigma and Pollen Factors**  
*Yoshinobu Takada, Takahiro Sato, Go Suzuki, Hiroshi Shiba, Seiji Takayama, and Masao Watanabe*  
In this study, the authors genetically characterized novel pollen-stigma unilateral incompatibility (UI) in *Brassica rapa*. This UI is only observed in crosses between stigma of a Japanese commercial line and pollen of a Turkish line in *B. rapa*. The authors did not find any difference between the UI and self-incompatibility (SI) phenotypes. Although the UI was not regulated by the S-locus (SI locus), the stigma and pollen factors of UI were closely linked to each other and inherited as a single locus, as well as the S-locus. Further genetic segregation analysis revealed that MLPK-dependent signal cascade is related to this UI recognition.

- 727–731 **The Biotinidase Gene Variants Registry: A Paradigm Public Database**  
*Melinda Procter, Barry Wolf, David K. Crockett, and Rong Mao*
- These authors developed the *BTD* gene mutation database for Biotinidase deficiency. This database is designed to serve as a reference for the clinical diagnostic laboratory and as a scientific resource for the biotinidase research community. It has 168 entries for the most recently reported mutations and polymorphisms in the literature and includes several novel variants found in the authors' laboratory. The mutations have been defined according to the nomenclature required by the Human Genome Variation Society (HGVS).
- 733–740 **Genetic Basis of Ammonium Toxicity Resistance in a Sake Strain of Yeast: A Mendelian Case**  
*Cyrielle Reisser, Cynthia Dick, Leonid Kruglyak, David Botstein, Joseph Schacherer, and David C. Hess*
- Saccharomyces cerevisiae* has been domesticated by humans for over thousands of years for use in brewing and baking. For example, brewing strains have been specialized to ferment different substrates over a range of environments and conditions. In this study, the authors examined how natural isolates of *S. cerevisiae* responded to the stress of ammonium toxicity. They found one strain that was resistant to high levels of ammonium and identified a natural variant of a gene that conferred this resistance. Studying natural variation yields valuable insights into how the cell functions.
- 741–756 **A Whole Genome Screen for Minisatellite Stability Genes in Stationary-Phase Yeast Cells**  
*Bonnie Alver, Peter A. Jauert, Laura Brosnan, Melissa O'Hehir, Benjamin VanderSluis, Chad L. Myers, and David T. Kirkpatrick*
- Little is known about factors that influence the stability of repetitive DNA in quiescent, nondividing cells. These authors previously identified a novel yeast colony phenotype in which microcolonies arise on the surface of the main colony. The microcolonies derive from quiescent cells that have undergone repetitive DNA tract alterations. Using two different minisatellites as reporters, the authors conducted whole-genome screens to identify all yeast genes that influence DNA stability in stationary phase cells. While loss of some genes affected both reporters, the majority of the identified genes were unique, indicating that quiescent DNA stability is complex and dependent on the sequence examined.
- 757–762 **Parents Without Partners: *Drosophila* as a Model for Understanding the Mechanisms and Evolution of Parthenogenesis**  
*Therese Ann Markow*
- The evolution of parthenogenesis from sexual reproduction has occurred a number of times in animals, but the responsible genetic mechanisms are not well understood. *Drosophila* species exhibit a range of degrees of parthenogenetic development and thus offer a promising means to study the genetic basis of this reproductive transition.
- 763–770 **Functional Annotation and Comparative Analysis of a Zygopteran Transcriptome**  
*Alexander G. Shanku, Mark A. McPeck, and Andrew D. Kern*
- These authors generated a draft functional annotation of nearly 4000 genes in *Enallagma hageni's* transcriptome. It is the first examined and annotated transcriptome of any palaeopteran in the literature. They have also produced a strongly supported phylogenetic analysis that further strengthens support for Odonata's place in the Arthropoda tree.
- 771–780 **Physical and Genetic Interactions Between Uls1 and the Slx5–Slx8 SUMO-Targeted Ubiquitin Ligase**  
*Wei Tan, Zheng Wang, and Gregory Prelich*
- ULS1* is believed to encode a second SUMO-targeted ubiquitin ligase that functions redundantly or in parallel with Slx5-Slx8, a known heterodimeric SUMO-targeted ubiquitin ligase. The authors identified *ULS1* and two other genes in a screen designed to identify regulators of the SUMO pathway. A comparison of *ULS1* and *SLX5* deletion and overexpression phenotypes indicated that they are not redundant but might be antagonistic. The authors detected physical interactions between Uls1 and Slx5. They also found that deletion of a Uls1 region necessary for the interaction interferes with Uls1 function. Their results suggest a regulatory relationship between these two proteins.

## CORRIGENDUM

- 781 **Comparison of the Performance of Two Commercial Genome-Wide Association Study Genotyping Platforms in Han Chinese Samples**  
*Lei Jiang, Dana Willner, Patrick Danoy, Huji Xu, and Matthew A. Brown*