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JUNE 2013 • VOLUME 3 • ISSUE 6 • www.g3journal.org

EDITORIAL

927 HeLa Cell Sequela

INVESTIGATIONS AND AUTHOR SUMMARIES

929–940 A Nucleosomal Region Important for Ensuring Proper Interactions Between the Transcription Elongation Factor Spt16 and Transcribed Genes in *Saccharomyces cerevisiae*

Hoai-Trang T. Nguyen, William Wharton II, Jennifer A. Harper, James R. Dornhoffer, and Andrea A. Duina

The histone chaperone FACT complex assists in the elongation phase of transcription first by facilitating the removal of histones from DNA in front of a transcribing RNA polymerase II complex and then by reassembling the histones into nucleosomes in its wake. These authors provide evidence for the existence of a nucleosomal region with an important role in ensuring proper interactions between the Spt16 component of yeast FACT and chromatin during elongation. This region may directly interact with FACT to promote its dissociation from chromatin at the 3' ends of genes and possibly also to recruit it to transcribed genes.

941–947 Resistance to Germline RNA Interference in a *Caenorhabditis elegans* Wild Isolate Exhibits Complexity and Nonadditivity

Daniel A. Pollard and Matthew V. Rockman

Two fundamental questions in genetics are 1) How many genes contribute to common trait differences within populations and 2) How do those genes interact? The authors approached these questions by studying the genetic basis for differences in sensitivity to gene expression knockdown via RNAi in the germline of roundworm *Caenorhabditis elegans* strains. Using classical and quantitative techniques, they found that RNAi variation is most simply explained by one large effect gene plus the nonadditive enhancing and suppressing activities of several additional genes. Their study adds to the growing list of traits with complex genetic architectures.

949–957 The Use of RelocaTE and Unassembled Short Reads to Produce High-Resolution Snapshots of Transposable Element Generated Diversity in Rice

Sofia M. C. Robb, Lu Lu, Elizabeth Valencia, James M. Burnette III, Yutaka Okumoto, Susan R. Wessler, and Jason E. Stajich

These authors have developed a new tool called RelocaTE to identify polymorphic transposable element insertion sites using next generation sequence and an organism's genome sequence. In this study, they used RelocaTE to compare genomes of sibling rice plants and identified variation in the extremely active *mPing* element. Their approach shows that resequencing is sensitive enough to detect transpositions occurring even in somatic tissue. RelocaTE assigns a genotype to each insertion site to distinguish heterozygous from homozygous insertions. It is designed to be used with any transposable element and is available as open source software.

- 959–969 **Resequencing and Comparative Genomics of *Stagonospora nodorum*: Sectional Gene Absence and Effector Discovery**
Robert Andrew Syme, James K. Hane, Timothy L. Friesen, and Richard P. Oliver
 As the first Dothideomycete with a published genome sequence, *Stagonospora nodorum* has emerged as a model organism for this agriculturally important fungal class. An important component of Dothideomycete infection is the secretion of a suite of effector molecules. Different strains of *Stagonospora nodorum* often secrete a different suite of effectors. Here the authors present the comparison of two new genome sequences, each of which are known to produce a distinct set of effectors. Their article describes an unusual pattern of genomic conservation and outlines a new method for effector candidate discovery.
- 971–977 **Genetic Polymorphisms in Host Innate Immune Sensor Genes and the Risk of Nasopharyngeal Carcinoma in North Africa**
Khalid Moumad, Jesus Lascorz, Melanie Bevier, Meriem Khyatti, Moulay Mustapha Ennaji, Abdellatif Benider, Stefanie Huhn, Shun Lu, Lotfi Chouchane, Marilys Corbex, Kari Hemminki, and Asta Försti
 In this study, the authors found that polymorphisms in the host innate immunity genes CD209, DDX58 and TLR3 were associated with the risk of Epstein-Barr virus-related nasopharyngeal carcinoma (NPC) in a high incidence population from North Africa. Their results suggest that these polymorphisms are important regulators of host response to infection and to NPC.
- 979–991 **Identification of Cilia Genes That Affect Cell-Cycle Progression Using Whole-Genome Transcriptome Analysis in *Chlamydomonas reinhardtii***
Alison J. Albee, Alan L. Kwan, Huawen Lin, David Granas, Gary D. Stormo, and Susan K. Dutcher
 Cilia are microtubule-based organelles that project from most cells in the human body. Defects in cilia are associated with respiratory infections, male infertility, congenital heart disease, kidney disease, and retinal degeneration. Transcriptome analysis in *Chlamydomonas* identifies 1,850 genes upregulated during ciliogenesis. The authors asked if four of these upregulated genes are involved in cilia-related processes using shRNA knockdown in human retinal pigment epithelial cells. These four genes have cilia-related phenotypes. Surprisingly, knockdown of GLOD4 and SPATA4 also affects cell cycle progression. This technique provides a powerful tool to gain insight into the molecular mechanism by which cilia and centrosomes are assembled.
- 993–1001 **Widespread Selection Across Coding and Noncoding DNA in the Pea Aphid Genome**
Ryan D. Bickel, Joseph P. Dunham, and Jennifer A. Brisson
 This article presents a genome-wide population genetic analysis of the pea aphid using resequencing data from 21 pea aphid lines collected from alfalfa in North America. Population genetic statistics suggest that founding events and subsequent population expansion in North America have had a large influence on the genome. Furthermore, genome-wide coding and noncoding DNA seems to be evolving nonneutrally, suggesting that the majority of the genome exhibits significant evolutionary constraint. The authors found this pattern on both autosomes and the X chromosome, but the magnitude of the effect differed on the sex chromosome. These results provide an important look at the factors influencing genome evolution, particularly in aphids.
- 1003–1013 **Retrospective View of North American Potato (*Solanum tuberosum* L.) Breeding in the 20th and 21st Centuries**
Candice N. Hirsch, Cory D. Hirsch, Kimberly Felcher, Joseph Coombs, Dan Zarka, Allen Van Deynze, Walter De Jong, Richard E. Veilleux, Shelley Jansky, Paul Bethke, David S. Douches, and C. Robin Buell
 Potato is a unique breeding system compared to grain and legume crop species because it is an autotetraploid and vegetatively propagated. Potato breeding over the last 150 years has focused on phenotypic rather than genotypic selection to improve agronomic quality, yield, and market class specific traits. These authors genotyped a 250 clone diversity panel that included potato cultivars released from 1857 to 2011, advanced breeding lines, and wild species. They detected enrichment of alleles in biosynthetic pathways important for market class specific traits, limited population structure within cultivated potato, and significantly more heterozygosity in cultivated potato compared to wild species.

- 1015–1030** **The Transcriptional Response to Nonself in the Fungus *Podospora anserina***
Frédérique Bidard, Corinne Clavé, and Sven J. Saupe
- In fungi, heterokaryon incompatibility is a nonself-recognition process when different individuals belonging to the same species undergo cell fusion. The authors analyzed the gene expression changes occurring during the incompatibility reaction in the fungus *Podospora anserina*. They report an up-regulation of proteolytic and lipolytic activities, of secondary metabolism clusters, toxins, and effector-like proteins. The up-regulated genes are enriched on specific chromosomes and appear more rapidly diverging than the rest of the genome. Most importantly, the authors found that the transcriptional response during incompatibility bears a number of similarities to the transcriptional responses described in other types of biotic interaction involving fungi.
- 1031–1042** **Isolation and Diversity Analysis of Resistance Gene Homologues from Switchgrass**
Qihui Zhu, Jeffrey L. Bennetzen, and Shavannor M. Smith
- This work provides genome-level analysis of four resistance gene homologues (RGHs) in the switchgrass germplasm. The authors show that lowland and upland switchgrass ecotypes are less similar, even from nearby populations, than were more distant populations with similar growth environments. The results also revealed that the four RGHs were under positive selection in the studied switchgrass accessions. In addition, intragenic recombination was detected in switchgrass RGHs, thereby demonstrating an active genetic process that has the potential to generate new resistance genes with new specificities that might act against newly-arising pathogen races.
- 1043–1048** **A Hypomorphic Mutation Reveals a Stringent Requirement for the ATM Checkpoint Protein in Telomere Protection During Early Cell Division in *Drosophila***
Patrizia Morciano, Yi Zhang, Giovanni Cenci, and Yikang S. Rong
- How ATM functions in telomere protection remains poorly understood. Here the authors have characterized a hypomorphic mutation in the conserved ATM checkpoint protein in *Drosophila* that specifically disrupts telomere capping during early embryonic cell divisions. The amenability of *Drosophila* embryos to molecular and biochemical investigations ensures that this newly identified mutation will facilitate future studies of ATM in telomere maintenance.
- 1049–1059** **Quantitative Trait Locus and Haplotype Analyses of Wild and Crop-Mimic Traits in U.S. Weedy Rice**
Muhamad S. Mispan, Lihua Zhang, Jiujuan Feng, and Xing-You Gu
- Conspecific weeds retain characters from wild ancestors and develop crop mimics to enhance adaptation and competitiveness in agro-ecosystems. Using quantitative trait locus analysis, the authors identified a total of 49 loci associated with six wild and eight crop-mimic traits in an F₂ population from the cross between a cultivated and a U.S. weedy rice line, with 45 of the loci collocated as clusters on 14 genomic regions. Haplotype analysis for these cluster regions revealed that U.S. weedy red rice populations shared approximately 50% haplotypes with the AA-genome wild rice, incorporated haplotypes from cultivated rice, and can basically be classified into two groups.