

## Contents

June 2019 • VOLUME 9 • ISSUE 6 • [www.g3journal.org](http://www.g3journal.org)

### GENOME REPORTS

- 1785–1793 **Whole Genome Sequencing and Re-sequencing of the Sable Antelope (*Hippotragus niger*): A Resource for Monitoring Diversity in *ex Situ* and *in Situ* Populations**  
*Klaus-Peter Koepfli, Gaik Tamazian, David Wildt, Pavel Dobrynin, Changhoon Kim, Paul B. Frandsen, Raquel Godinho, Andrey A. Yurchenko, Aleksey Komissarov, Ksenia Krasheninnikova, Sergei Kliver, Sofia Kolchanova, Margarida Gonçalves, Miguel Carneiro, Pedro Vaz Pinto, Nuno Ferrand, Jesús E. Maldonado, Gina M. Ferrie, Leona Chemnick, Oliver A. Ryder, Warren E. Johnson, Pierre Comizzoli, Stephen J. O'Brien, and Budhan S. Pukazhenthi*
- 1795–1805 **The Genome of C57BL/6J “Eve”, the Mother of the Laboratory Mouse Genome Reference Strain**  
*Vishal Kumar Sarsani, Narayanan Raghupathy, Ian T. Fiddes, Joel Armstrong, Francoise Thibaud-Nissen, Oraya Zinder, Mohan Bolisetty, Kerstin Howe, Doug Hinerfeld, Xiaoran Ruan, Lucy Rowe, Mary Barter, Guruprasad Ananda, Benedict Paten, George M. Weinstock, Gary A. Churchill, Michael V. Wiles, Valerie A. Schneider, Anuj Srivastava, and Laura G. Reinholdt*

### FEATURED ARTICLE

- 1807–1813 **Evolution of Antibiotic Synthesis Gene Clusters in the *Streptomyces globisporus* TFH56, Isolated from Tomato Flower**  
*Gyeongjun Cho and Youn-Sig Kwak*

### MUTANT SCREEN REPORT

- 1815–1823 **Negative Regulation of the Mis17-Mis6 Centromere Complex by mRNA Decay Pathway and EKC/KEOPS Complex in *Schizosaccharomyces pombe***  
*Xingya Xu, Norihiko Nakazawa, Li Wang, Orié Arakawa, and Mitsuhiro Yanagida*

### SOFTWARE AND DATA RESOURCES

- 1825–1830 **DPAC: A Tool for Differential Poly(A)–Cluster Usage from Poly(A)–Targeted RNAseq Data**  
*Andrew Routh*

### INVESTIGATIONS

- 1831–1838 **Full-Length Transcriptome Sequencing and the Discovery of New Transcripts in the Unfertilized Eggs of Zebrafish (*Danio rerio*)**  
*Rumana Mehjabin, Lv Xiong, Rong Huang, Cheng Yang, Geng Chen, Libo He, Lanjie Liao, Zuoyan Zhu, and Yaping Wang*
- 1839–1850 **Mutation of the ATPase Domain of MutS Homolog-5 (MSH5) Reveals a Requirement for a Functional MutS $\gamma$  Complex for All Crossovers in Mammalian Meiosis**  
*Carolyn R. Milano, J. Kim Holloway, Yongwei Zhang, Bo Jin, Cameron Smith, Aviv Bergman, Winfried Edelmann, and Paula E. Cohen*
- 1851–1867 **The Effect of Neutral Recombination Variation on Genome Scans for Selection**  
*Katie E. Lotterhos*

- 1869–1880 **An Interaction Network of the Human SEPT9 Established by Quantitative Mass Spectrometry**  
*Matthias Hecht, Reinhild Rösler, Sebastian Wiese, Nils Johnsson, and Thomas Gronemeyer*
- 1881–1892 **Single and Multi-trait GWAS Identify Genetic Factors Associated with Production Traits in Common Bean Under Abiotic Stress Environments**  
*Atena Oladzad, Timothy Porch, Juan Carlos Rosas, Samira Mafi Moghaddam, James Beaver, Steve E. Beebe, Jimmy Burrridge, Celestina Nhagupana Jochua, Magalhaes Amade Miguel, Phillip N. Miklas, Bodo Ratz, Jeffery W. White, Jonathan Lynch, and Phillip E. McClean*
- 1893–1900 **Adenine Methylation in *Drosophila* Is Associated with the Tissue-Specific Expression of Developmental and Regulatory Genes**  
*Kinnary Shah, Weihuan Cao, and Christopher E. Ellison*
- 1901–1908 **Cyclin C Regulated Oxidative Stress Responsive Transcriptome in *Mus musculus* Embryonic Fibroblasts**  
*David C. Stieg, Kai-Ti Chang, Katrina F. Cooper, and Randy Strich*
- 1909–1919 **Toward Spider Glue: Long Read Scaffolding for Extreme Length and Repetitious Silk Family Genes AgSp1 and AgSp2 with Insights into Functional Adaptation**  
*Sarah D. Stellwagen and Rebecca L. Renberg*
- 1921–1931 **Genomic Prediction for Winter Survival of Lowland Switchgrass in the Northern USA**  
*Hari P. Poudel, Millicent D. Sanciangco, Shawn M. Kaeppler, C. Robin Buell, and Michael D. Casler*
- 1933–1943 **Tissue-Specific Split sfGFP System for Streamlined Expression of GFP Tagged Proteins in the *Caenorhabditis elegans* Germline**  
*Adam Hefel and Sarit Smolikove*
- 1945–1955 **Genome-Wide Association Study and Pathway-Level Analysis of Kernel Color in Maize**  
*Brenda F. Owens, Deepu Mathew, Christine H. Diepenbrock, Tyler Tiede, Di Wu, Maria Mateos-Hernandez, Michael A. Gore, and Torbert Rocheford*
- 1957–1973 **Genome-Wide Analyses Reveal Footprints of Divergent Selection and Drought Adaptive Traits in Synthetic-Derived Wheats**  
*Fakiha Afzal, Huihui Li, Alvina Gul, Abid Subhani, Ahmad Ali, Abdul Mujeeb-Kazi, Francis Ogbonnaya, Richard Trethowan, Xianchun Xia, Zhonghu He, and Awais Rasheed*
- 1975–1986 **Genomic Bayesian Confirmatory Factor Analysis and Bayesian Network To Characterize a Wide Spectrum of Rice Phenotypes**  
*Haipeng Yu, Malachy T. Campbell, Qi Zhang, Harkamal Walia, and Gota Morota*
- 1987–1998 **Little Evidence of Antagonistic Selection in the Evolutionary Strata of Fungal Mating-Type Chromosomes (*Microbotryum lychnidis-dioicae*)**  
*Anna Liza Bazzicalupo, Fantin Carpentier, Sarah Perin Otto, and Tatiana Giraud*
- 1999–2006 **A Novel QTL in Durum Wheat for Resistance to the Wheat Stem Sawfly Associated with Early Expression of Stem Solidness**  
*Andrea C. Varella, Hongtao Zhang, David K. Weaver, Jason P. Cook, Megan L. Hofland, Peggy Lamb, Shiaoan Chao, John M. Martin, Nancy K. Blake, and Luther E. Talbert*
- 2007–2016 **Generation of Inducible Gene-Switched GAL4 Expressed in the *Drosophila* Female Germline Stem Cell Niche**  
*Yi-Teng Ke and Hwei-Jan Hsu*
- 2017–2028 **Long-Term Conservation of Ohnologs Through Partial Tetrasomy Following Whole-Genome Duplication in Salmonidae**  
*Matthew A. Campbell, Matthew C. Hale, Garrett J. McKinney, Krista M. Nichols, and Devon E. Pearce*
- 2029–2036 **Transcriptome Analysis Reveals Unique Relationships Among *Eleusine* Species and Heritage of *Eleusine coracana***  
*Hui Zhang, Nathan Hall, Leslie R. Goertzen, Charles Y. Chen, Eric Peatman, Jinesh Patel, and J. Scott McElroy*

2037 **CORRIGENDUM**