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INVESTIGATIONS

- 157–166 **Maternal Germline-Specific Genes in the Asian Malaria Mosquito *Anopheles stephensi*: Characterization and Application for Disease Control**
James K. Biedler, Yumin Qi, David Pledger, Anthony A. James, and Zhijian Tu
Mosquitoes transmit several infectious diseases including malaria that impose a serious cost to human health and economy. Understanding mosquito biology and reproduction is essential for devising strategies for mosquito control. Biedler *et al.* focus on the identification and characterization of genes that are expressed primarily in the female germline before bloodfeeding. The authors demonstrate the use of promoters derived from these genes in transgenic cassettes to express and deliver mRNA/protein/microRNAs to the ovaries and progeny embryos. This can serve as a tool for functional studies and for developing applications that replace wild mosquito populations with disease refractory populations.
- 167–174 **Exome Sequencing Identifies a Rare *HSPG2* Variant Associated with Familial Idiopathic Scoliosis**
Erin E. Baschal, Cambria I. Wethey, Kandice Swindle, Robin M. Baschal, Katherine Gowan, Nelson L.S. Tang, David M. Alvarado, Gabe E. Haller, Matthew B. Dobbs, Matthew R.G. Taylor, Christina A. Gurnett, Kenneth L. Jones, and Nancy H. Miller
Idiopathic scoliosis is a complex disease which affects 3% of the pediatric population and can have life-long implications. Genetic findings are hampered by incomplete penetrance, subclinical disease in control populations, unknown modes of inheritance, and genetic heterogeneity. Through exome sequencing in a multigenerational family with idiopathic scoliosis, this study identified a variant in the *HSPG2* gene that potentially contributes to the disease phenotype in this family. Additional sequencing in two independent cohorts of idiopathic scoliosis patients demonstrated enrichment of this variant, giving further evidence that rare variants in the *HSPG2* gene potentially contribute to idiopathic scoliosis susceptibility.
- 175–182 **Behavior of Aberrant Chromosome Configurations in *Drosophila melanogaster* Female Meiosis I**
William D. Gilliland, Eileen M. Colwell, Fiona M. Lane, and Ashley A. Snouffer
Gilliland *et al.* performed genetic and cytological analysis of female meiosis I in *Drosophila melanogaster* with aberrant chromosome arrangements, including females that are XXY or carrying one or more compound chromosomes. The authors show that even unpaired chromosomes still move onto the spindle during prometaphase and complete congression, but when free 4s are not present this movement is reduced. They also show that chromosomes with multiple partners are cooriented at metaphase arrest at the same rates inferred genetically, and that chromatin threads can be found coming from heterologous chromosomes. Together these results suggest a mechanism for how heterochromatin can establish heterologous chromosomal coorientations.

- 183–193 **Genotyping of Endosperms to Determine Seed Dormancy Genes Regulating Germination Through Embryonic, Endospermic, or Maternal Tissues in Rice**
Xing-You Gu, Jinfeng Zhang, Heng Ye, Lihua Zhang, and Jiuhuan Feng
 Seed dormancy is imposed by one or more of the embryo, endosperm, and maternal tissues and has been associated with multiple quantitative trait loci in many crop or model plants. This research developed an endosperm genotype-based genetic approach to determine seed dormancy loci involved in the regulation of germination through seed component tissue(s) and applied this approach to the *SD₁₂*, *SD₁₋₂*, and *SD₇₋₁* loci in rice. This new genetic approach can be used for research on heritable traits expressed in endospermic seeds and for marker-assisted selection before or immediately after germination in crop breeding programs.
- 195–203 **The BLI-3/TSP-15/DOXA-1 Dual Oxidase Complex Is Required for Iodide Toxicity in *Caenorhabditis elegans***
Zhaofa Xu, Jintao Luo, Yu Li, and Long Ma
 Iodine is an essential trace element for life. However, for unclear reasons, excess iodide intake is also linked to severe human diseases. Xu *et al.* found that excess iodide had toxic pleiotropic effects on the nematode *Caenorhabditis elegans*. Through genetic screen and mutant characterization, the authors provided evidence that the BLI-3/TSP-15/DOXA-1 dual oxidase complex is required for this toxicity. They detected dramatically increased ROS production in animals treated with excess iodide, which can be partially reduced by mutations in the *bli-3* or *tsp-15* gene. They propose that the BLI-3/TSP-15/DOXA-1 dual oxidase complex is required for the toxic biological effects of excess iodide.
- 205–217 **A Rapid One-Generation Genetic Screen in a *Drosophila* Model to Capture Rhabdomyosarcoma Effectors and Therapeutic Targets**
Kathleen A. Galindo, Tiana R. Endicott, Usha Avirneni-Vadlamudi, and Rene L. Galindo
 Childhood cancer is the leading cause of disease-related mortality in the U.S. among children one-to-14 years of age, which underscores the need to elucidate the underpinnings of pediatric malignancy. Galindo *et al.* have genetically engineered *Drosophila melanogaster* to model the most common pediatric soft tissue sarcoma, rhabdomyosarcoma (RMS). With the “simpler” genetic composition of *Drosophila*, and its amenability to genetic probing, the authors are exploiting this model to uncover genes that drive RMS. They are hopeful that the cancer community will exploit this model with the goal of finding new means to target these aggressive and deadly childhood malignancies.
- 219–233 **Multiple QTL for Horticultural Traits and Quantitative Resistance to *Phytophthora infestans* Linked on *Solanum habrochaites* Chromosome 11**
J. Erron Haggard, Emily B. Johnson, and Dina A. St. Clair
 A QTL for *Phytophthora infestans* resistance on chromosome 11 of *Solanum habrochaites* was introgressed into cultivated tomato (*S. lycopersicum*) previously. Fine-mapping with near-isogenic lines (NILs) revealed multiple resistance QTL within this region and coincident/linked QTL with undesirable effects on horticultural traits. In this study, sub-NILs were evaluated for 17 horticultural traits in field experiments over two years. Each previously detected horticultural trait QTL fractionated into two or more QTL. Thirty-four QTL were detected across all traits with 14% exhibiting QTL x environment interactions. Co-location of QTL for multiple traits suggests pleiotropy or tight linkage and a complex genetic architecture.
- 235–239 **Segregation of a Spontaneous *Klr1* (CD94) Mutation in DBA/2 Mouse Substrains**
Dai-Lun Shin, Ashutosh K. Pandey, Jesse Dylan Ziebarth, Megan K. Mulligan, Robert W. Williams, Robert Geffers, Bastian Hatesuer, Klaus Schughart, and Esther Wilk
 DBA/2 is the oldest inbred strain of mice and has been widely used to study the genetic basis of many common diseases. This strain is also the paternal parent of the large family of BXD recombinant inbred strains. Shin *et al.* found differences regarding the *Klr1* gene in two DBA/2 strains from different breeders. This work revealed two isogenic mouse lines being a potential tool to study the functional role of the protein encoded by *Klr1*, *CD94* and highlights the relevance of the epoch effect in BXD mice.

- 241–251 **A High-Density Linkage Map for *Astyanax mexicanus* Using Genotyping-by-Sequencing Technology**
Brian M. Carlson, Samuel W. Onusko, and Joshua B. Gross
- Owing to the presence of cave- and surface-dwelling counterparts, *Astyanax mexicanus* has illuminated the genetic basis of many extreme phenotypes. Densely-populated linkage maps are critical for candidate gene identification in genetic studies. Using a cave × surface hybrid F₂ pedigree, the authors present the most comprehensive and informative linkage map for this species to date using inexpensive genotyping-by-sequencing technology. Unaligned scaffolds from the *Astyanax* Genome Project were successfully assembled into putative chromosomes using linkage groups as templates. This resource will help resolve the genetic basis of extreme traits and catalyze assembly of the genome of this remarkable model system.
- 253–259 **Plant Genetic Archaeology: Whole-Genome Sequencing Reveals the Pedigree of a Classical Trisomic Line**
Patrice A. Salomé and Detlef Weigel
- George Redei conducted some of the first *Arabidopsis* mutant screens in the 1960s, but cloning of the corresponding genes only happened in the last 10 years, leaving ample time for further mutation accumulation and outcrossing. While investigating circadian phenotypes in trisomic lines he generated, Salomé and Weigel discovered that one line displayed a complex genetic origin with evidence of outcrossing between two accessions, as well as the presence of a classical late-flowering mutation in the *GIGANTEA* gene. The results show that such complexity can be deduced from whole-genome sequencing and illustrate how community resources can benefit research.
- 261–270 **Abiotic and Biotic Stressors Causing Equivalent Mortality Induce Highly Variable Transcriptional Responses in the Soybean Aphid**
Laramy S. Enders, Ryan D. Bickel, Jennifer A. Brisson, Tiffany M. Heng-Moss, Blair D. Siegfried, Anthony J. Zera, and Nicholas J. Miller
- Environmental stress profoundly affects basic cellular functions, but whether important differences exist between variable forms of stress remains a mystery in many animals. The authors used aphids to test whether stressors causing equivalent mortality (heat, starvation, host plant defenses) produce similar changes in gene expression. Patterns of gene expression were highly variable and unique to each stressor. Starvation altered thousands of genes, heat changed several hundred, but plant defenses affected less than fifteen. Although stressors may appear to have similar effects when focusing only on survival, what lies beneath can be extremely different.
- 271–279 **Overdominance Effect of the Bovine Ghrelin Receptor (*GHSR1a*)-*DelR242* Locus on Growth in Japanese Shorthorn Weaner Bulls: Heterozygote Advantage in Bull Selection and Molecular Mechanisms**
Masanori Komatsu, Yoichi Sato, Tatsuki Negami, Tohru Terada, Osamu Sasaki, Jumpei Yasuda, Aisaku Arakawa, Chikara Yoshida, Hideaki Takahashi, Aduli E. O. Malau-Aduli, Keiichi Suzuki, and Kentaro Shimizu
- Ghrelin and the ghrelin receptor (*GHSR1a*) are involved in growth hormone secretion, food intake, and other important functions. In investigating the reasons for the higher frequency of the *3R* allele of *GHSR1a* in Japanese Shorthorn bulls than in other cattle breeds, Komatsu *et al.* found a significant sex difference in the frequency of the *3R* allele and a significant overdominance effect of the *DelR242* locus on growth in weaner bulls. *4R/3R* heterozygotes showed a selective advantage in the form of higher average daily gain than homozygotes. The authors discuss possible molecular mechanisms for this overdominance effect.
- 281–289 **Genetic Dissection of Internode Length Above the Uppermost Ear in Four RIL Populations of Maize (*Zea mays* L.)**
Lixia Ku, Liru Cao, Xiaomin Wei, Huihui Su, Zhiqiang Tian, Shulei Guo, Liangkun Zhang, Zhenzhen Ren, Xiaobo Wang, Yuguang Zhu, Guohui Li, Zhiyong Wang, and Yanhui Chen
- Analyzing the genetic characteristics of internode length is critical for improving plant population structure and increasing photosynthetic efficiency. In this study, QTLs for ILAU were identified using four sets of RIL populations in three environments. Seventy QTLs were identified in the four populations. Individual effects ranged from 5.36% to 26.85% of phenotypic variation. Of the 70 initial QTLs, 46 were integrated in 14 mQTLs by meta-analysis. mQTL2-2, mQTL3-2, mQTL5-1, mQTL5-2, and mQTL9 with initial QTLs displayed $R^2 > 10\%$ might be hot spots. These results may provide useful information for marker-assisted selection to improve canopy architecture.

- 291–300 **Threshold Models for Genome-Enabled Prediction of Ordinal Categorical Traits in Plant Breeding**
Osva A. Montesinos-López, Abelardo Montesinos-López, Paulino Pérez-Rodríguez, Gustavo de los Campos, Kent Eskridge, and José Crossa

Categorical scores for disease susceptibility or resistance are often recorded in plant breeding. The aim of this study was to assess the genomic predictive ability for ordered categorical phenotypes using a threshold model. Montesinos-López *et al.* present an empirical application with a total of nine models, some including genomic \times environment (G \times E) interaction. They used real data consisting of maize lines genotyped with 46,347 SNPs and evaluated for disease resistance [ordinal scores from 1 (no disease) to 5 (complete infection)]. Relative to models based on main effects only, the threshold models that included G \times E interaction achieved 9-14% gains in genomic prediction accuracy.

MUTANT SCREEN REPORT

- 301–313 **Ectopic Expression Screen Identifies Genes Affecting *Drosophila* Mesoderm Development Including the HSPG Trol**
Nathanie Trisnadi and Angelike Stathopoulos

An ectopic expression screen was conducted to provide insight into mesoderm migration during *Drosophila* gastrulation. Over twenty genes were isolated and ten were further characterized, including integrins, cadherins, and EGFR and JAK/STAT signaling components, supporting the view that multiple inputs are integrated to facilitate this process. Heparan sulfate proteoglycan (HSPG) Trol was one gene identified. Trol supports FGF-dependent mesoderm spreading and muscle founder cell migration, while another HSPG Syndecan functions in FGF-dependent processes of mesoderm cell intercalation and differentiation. The authors propose that FGF signaling can be differentially regulated by specificity of HSPG cofactors Trol and Syndecan.

- 315 **CORRIGENDUM**