

## Contents

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### GENOME REPORT

- 2015–2022 **Insight into the Recent Genome Duplication of the Halophilic Yeast *Hortaea werneckii*: Combining an Improved Genome with Gene Expression and Chromatin Structure**  
*Sunita Sinha, Stephane Flibotte, Mauricio Neira, Sean Formby, Ana Plemenitaš, Nina Gunde Cimerman, Metka Lenassi, Cene Gostinčar, Jason E. Stajich, and Corey Nislow*
- Using long-read single molecule sequencing Sinha *et al.* present a high-quality genome sequence for the extremely halotolerant yeast *Hortaea wernickii*. This new genome assembly permits a comprehensive comparison of the paralogous gene pairs with respect to their patterns of gene expression and chromatin architecture. In contrast to the model yeast *Saccharomyces cerevisiae*, the authors find that the majority of gene pairs in *Hortae* are quite similar, supporting the idea that this yeast underwent a recent whole genome duplication. Sinha *et al.* discuss the implications of this genome duplication and the potential applications of this extreme halophile in basic and applied research.

### MUTANT SCREEN REPORT

- 2023–2038 **RNAi-Mediated Reverse Genetic Screen Identified *Drosophila* Chaperones Regulating Eye and Neuromuscular Junction Morphology**  
*Sandeep Raut, Bhagaban Mallik, Arpan Parichha, Valsakumar Amrutha, Chandan Sahi, and Vimlesh Kumar*
- The role of chaperones in neuronal development and functions is not well understood. In this manuscript, Raut *et al.* report a targeted RNAi-mediated reverse genetic screen which led to the identification of *Drosophila* chaperones that play a crucial role in eye/rhabdomere morphogenesis and NMJ development. The outcome of this screen should provide a useful resource for further elucidating the role of individual chaperones in *Drosophila* eye morphogenesis and synaptic development.

### INVESTIGATIONS

- 2039–2045 **Assessment of Single Cell RNA-Seq Normalization Methods**  
*Bo Ding, Lina Zheng, and Wei Wang*
- Ding, Zheng, and Wang have assessed the performance of seven normalization methods for single cell RNA-seq using data generated from dilution of RNA samples. The analyses in this study showed that methods considering spike-in ERCC RNA molecules significantly outperformed those not considering ERCCs. This work provides a guidance of selecting normalization methods to remove technical noise in single cell RNA-seq data.
- 2047–2054 **Construction of a Recyclable Genetic Marker and Serial Gene Deletions in the Human Pathogenic Mucorales *Mucor circinelloides***  
*Alexis Garcia, Gloria Adedoyin, Joseph Heitman, and Soo Chan Lee*
- Garcia *et al.* developed a recyclable genetic marker to provide a robust genetic system in *Mucor circinelloides*. *M. circinelloides* is one of the causal agents of mucormycosis, which is recognized as an emerging fungal infectious disease. *Mucor* serves as a model system to study pathogenesis in mucormycosis, RNAi silencing, and light sensing. *Mucor* is also known as a biodiesel producer. However, genetics and molecular biology in this fungal system is less well developed compared with model and even other pathogenic fungi. This study provides a novel forum in the molecular biology and genetics of this understudied model fungal system.

- 2055–2063 **Novel Mutations in Synaptic Transmission Genes Suppress Neuronal Hyperexcitation in *Caenorhabditis elegans***  
*Katherine A. McCulloch, Yingchuan B. Qi, Seika Takayanagi-Kiya, Yishi Jin, and Salvatore J. Cherra III*  
 Acetylcholine receptors regulate neural circuit activity in multiple contexts. In humans, mutations in acetylcholine receptors can cause neurological disorders, such as epilepsy. Here, McCulloch *et al.* used a *Caenorhabditis elegans* model to dissect genetic pathways in response to altered acetylcholine signaling. Through genetic suppressor studies of a gain-of-function mutation in the *acr-2* receptor subunit, which causes defective locomotion as well as spontaneous convulsions, the authors identified roles for genes that mediate synaptic vesicle release. McCulloch *et al.* defined a role for a conserved major facilitator superfamily domain family protein, *mfsd-6*, and the sphingosine kinase, *sphk-1* in regulating neural circuit activity.
- 2065–2080 **Manipulating the Mitochondrial Genome To Enhance Cattle Embryo Development**  
*Kanokwan Srirattana and Justin C. St. John*  
 Srirattana and St. John successfully produced embryos using somatic cell nuclear transfer (SCNT) that possessed recipient oocyte only mitochondrial DNA (mtDNA) by using mtDNA-depleted cells as donors. The developmental potential of embryos was further enhanced by using a reprogramming agent. Depleting donor cells of their mtDNA prior to SCNT effectively regulated mtDNA copy number at the blastocyst stage, which is important to developmental outcome. Gene expression profiles for the embryos derived from depleted cells were different to those of non-depleted cells. This approach validates the use of mtDNA depleted cells and a reprogramming agent to enhance livestock production traits.
- 2081–2094 **Validated Bayesian Differentiation of Causative and Passenger Mutations**  
*Frederick R. Cross, Michal Breker, and Kristi Lieberman*  
 The problem of determining a causative mutation from a larger collection of mainly passenger mutations occurs in many contexts. Cross, Breker, and Lieberman present a Bayesian approach for a quantitative determination of probability that a given mutation is causative.
- 2095–2106 **Effects of the Ordering of Natural Selection and Population Regulation Mechanisms on Wright-Fisher Models**  
*Zhangyi He, Mark Beaumont, and Feng Yu*  
 The results show that under the Wright-Fisher model, different mechanisms of natural selection can cause different behaviors in the resulting population. Specifically, viability and fecundity selection can affect the distribution of haplotype frequencies trajectories evolving under genetic recombination, but the difference in the distribution of trajectories is only appreciable when the population is in significant linkage disequilibrium. As linkage disequilibrium decays, the trajectories for the two different models rapidly become indistinguishable. The effect may be significant when factors such as gene migration maintain a degree of linkage disequilibrium.
- 2107–2114 **Exploring the Impact of Cleavage and Polyadenylation Factors on Pre-mRNA Splicing Across Eukaryotes**  
*Gildas Lepennetier and Francesco Catania*  
 In human, mouse, and *Drosophila*, the spliceosomal component U1 snRNP (U1) protects nascent transcripts from premature cleavage and polyadenylation at cryptic intronic polyadenylation signals (PAS). U1 may suppress PAS by directly interacting with and/or disturbing the recruitment of cleavage and polyadenylation factors (CPFs). Here Lepennetier and Catania asked: are CPFs simply patrolled or do they, in turn, antagonize U1 recruitment? The observations imply a pattern of dynamic competition between U1 and CPFs that is widespread across eukaryotes. They suggest that U1 and CPFs regulate one another to control transcriptional outputs.
- 2115–2124 **Linkage Map of *Lissotriton* Newts Provides Insight into the Genetic Basis of Reproductive Isolation**  
*Marta Niedzicka, Katarzyna Dudek, Anna Fijarczyk, Piotr Zieliński, and Wiesław Babik*  
 Linkage maps empower studies on the genomic architecture of reproductive isolation. A linkage map for newts of the *Lissotriton vulgaris* species complex was constructed using F2 interspecific hybrids. It consists of 1146 protein coding genes on 12 linkage groups, equal to the chromosome number. With a length of 1484 cM it is notably shorter than two other maps available for salamanders. Thus large salamander genomes do not necessarily, as previously suggested, translate into long linkage maps. A complex pattern of transmission ratio distortion consistent with environment-dependent mortality of some genotypes provides insights into the genetic basis of reproductive isolation.

- 2125–2138 **Comparative Transcriptomic Analysis of Race 1 and Race 4 of *Fusarium oxysporum* f. sp. *cubense* Induced with Different Carbon Sources**  
*Shiwen Qin, Chunyan Ji, Yunfeng Li, and Zhenzhong Wang*  
 A comprehensive transcriptome resource for *Fusarium oxysporum* f. sp. *cubense* (Foc) was generated and the gene expression profiles of Foc grown in the presence of host cell wall polysaccharides were characterized using RNA-seq. Comparative transcriptome analysis allowed the identification of differentially expressed genes that are specifically expressed during decomposition of different plant cell wall polysaccharides, revealing the molecular mechanisms of pathogenesis in banana and the genetic basis of host specificity in Foc. Genes involved in penetration of the host cell wall, signalling and transportation may have a significant impact on Foc race 4 virulence.
- 2139–2149 **The Immune Phenotype of Three *Drosophila* Leukemia Models**  
*Badrul Arefin, Martin Kunc, Robert Krautz, and Ulrich Theopold*  
 Many leukemia patients suffer from dysregulation of their immune system, which renders them more susceptible to infections and leads to general weakening (cachexia). Using *Drosophila* models for myeloid leukemia, Arefin *et al.* observe that affected larvae display normal immune competence and lack gross behavioral abnormalities. Using more subtle assays, the authors find that in the presence of leukemic cells a proinflammatory status is induced and larvae are more susceptible towards insect-pathogenic nematodes. Similarly, Arefin *et al.* detect subtle differences in avoidance behavior of leukemic larvae towards nematodes. The leukemia models will allow screens for genetic and chemical modifiers of altered immunity and behavior.
- 2151–2159 **Two Loci Contribute Epistatically to Heterospecific Pollen Rejection, a Postmating Isolating Barrier Between Species**  
*Jennafer A. P. Hamlin, Natasha A. Sherman, and Leonie C. Moyle*  
 Plants are among the many sexually reproducing organisms able to recognize and reject the gametes of other species. Hamlin, Sherman, and Moyle investigated genetic interactions involved in the postmating rejection of heterospecific pollen during growth down the female reproductive tract ('pistil') to the ovary. The authors found that a small number of loci are jointly necessary and sufficient to express this reproductive barrier when acting together, even though they do not have effects individually. At least one of these loci likely also contributes to conspecific self-incompatibility, consistent with a partially shared basis for inter- and intraspecific mechanisms of postmating prezygotic female choice.
- 2161–2170 **Phased Genotyping-by-Sequencing Enhances Analysis of Genetic Diversity and Reveals Divergent Copy Number Variants in Maize**  
*Heather Manching, Subhajit Sengupta, Keith R. Hopper, Shawn W. Polson, Yuan Ji, and Randall J. Wisser*  
 In the article by Manching *et al.*, an imputation-less genotyping-by-sequencing (GBS) procedure was developed for genotyping heterozygous individuals from non-pedigree populations. The procedure was demonstrated in maize where it was determined that there was enrichment for scoring SNPs around genes and genotyping accuracy was >99.4%. The authors also introduced new software for phased genotyping of multi-nucleotide variants. Phased GBS enhanced the characterization of genetic diversity and led to the discovery of diverged copy number variants that are unobservable in the underlying SNP data. This study extends the usefulness of GBS, which has emerged as the dominant platform for genome-wide genotyping.
- 2171–2184 **A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia**  
*Jordi Leno-Colorado, Nick J. Hudson, Antonio Reverter, and Miguel Pérez-Enciso*  
 The pig is an excellent model to study domestication, given the wide distribution of its wild ancestor. Leno-Colorado *et al.* studied pig domestication using 163 wild and domestic pig genomes with metabolic pathway as the unit of analysis. This approach is attractive since it considers the interrelated functions of genes. The authors found significant pathways related to behavior and reproductive performance, both important targets during domestication. Pathways were interrelated, and clustered according to whether they were under hormone or sympathetic nervous system control. These results can be partly explained by a relaxation of purifying selection in genes associated with the domestication process.

- 2185–2193 **Assessment of Gene Flow Between *Gossypium hirsutum* and *G. herbaceum*: Evidence of Unreduced Gametes in the Diploid Progenitor**  
*E. Montes, O. Coriton, F. Eber, V. Huteau, J. M. Lacape, C. Reinhardt, D. Marais, J. L. Hofs, A. M. Chèvre, and C. Pannetier*
- In the framework of gene flow assessment, reciprocal crosses were performed without emasculation between *Gossypium hirsutum* (AADD) and *Gossypium herbaceum* (AA). Of the 148 plants produced from the cross *G. herbaceum* × *G. hirsutum*, three showed a hybrid phenotype. Combined analyses based on cytometry, fluorescent in-situ hybridization, chromosome counting indicated that two hybrids were triploids (AAD) and, remarkably, the 3rd one was a tetraploid carrying three A genomes and a single D genome. This plant material could provide a useful tool for the study of the expression of genes duplicated in the A and D cotton genome.
- 2195–2207 **Cold Fusion: Massive Karyotype Evolution in the Antarctic Bullhead Notothen *Notothenia coriiceps***  
*Angel Amores, Catherine A. Wilson, Corey A. H. Allard, H. William Detrich III, and John H. Postlethwait*
- The common ancestor to half of all vertebrate species halved its chromosome number ~ 300 million years ago. To model mechanisms, Amores *et al.* investigated a similar event in Antarctic Bullhead fish. Bullhead has 11 chromosome pairs but its ancestors had 24. A meiotic map for Bullhead allowed comparative genomic analyses. Results showed that 22 of 24 ancestral haploid chromosomes first fused strictly pairwise; the two remaining, smallest ancestral chromosomes independently joined a different previously fused chromosome. Regimented pairwise fusion leaving the smallest chromosomes to last suggests not yet understood rules that may have governed chromosome reductions preceding origins of teleost fish.
- 2209–2218 **Development of a Medium Density Combined-Species SNP Array for Pacific and European Oysters (*Crassostrea gigas* and *Ostrea edulis*)**  
*Alejandro P. Gutierrez, Frances Turner, Karim Gharbi, Richard Talbot, Natalie R. Lowe, Carolina Peñaloza, Mark McCullough, Paulo A. Prodöhl, Tim P. Bean, and Ross D. Houston*
- A combined-species medium density SNP array was created for two ecologically and economically important oyster species; Pacific oyster (*Crassostrea gigas*) and European flat oyster (*Ostrea edulis*). The array was tested in diverse wild and hatchery populations and contains ~ 27 K high quality SNPs for *C. gigas* and ~ 11 K high quality SNPs for *O. edulis*. The array is effective at detecting both population and family structure, and will be applied for genome-wide association and evolutionary genetic studies, and for genomic selection in oyster breeding programs.
- 2219–2226 **Whole-Genome Sequence and Variant Analysis of W303, a Widely-Used Strain of *Saccharomyces cerevisiae***  
*Kinnari Matheson, Lance Parsons, and Alison Gammie*
- Here Matheson, Parsons, and Gammie present the genome sequence of a widely-used laboratory strain of *Saccharomyces cerevisiae*. The authors provide a list of sequence variants between the strains and comparative analysis that identifies remnants of wine strain ancestry across the genome. The authors show the utility of this genome with more accurate variant calling of passaged mismatch repair deficient strains, which mutate rapidly.
- 2227–2234 **A Generalized Linear Model for Decomposing *Cis*-regulatory, Parent-of-Origin, and Maternal Effects on Allele-Specific Gene Expression**  
*Yasuaki Takada, Ryutaro Miyagi, Aya Takahashi, Toshinori Endo, and Naoki Osada*
- Joint quantification of genetic and epigenetic effects on gene expression is important for understanding the establishment of complex gene regulation systems in living organisms. In this study, Takada *et al.* propose a simple method to decompose *cis*-regulatory (i.e., allelic genotype, AG), genomic imprinting (i.e., parent-of-origin, PO), and maternal (i.e., maternal genotype, MG) effects on allele-specific gene expression using RNA-seq data obtained from reciprocal crosses. The authors applied the method to whole-body *Drosophila* and mouse trophoblast stem cell (TSC) and liver RNA-seq data.
- 2235–2247 **Metabolic Adaptation to Nutrients Involves Coregulation of Gene Expression by the RNA Helicase *Dbp2* and the *Cyc8* Corepressor in *Saccharomyces cerevisiae***  
*Siwen Wang, Zheng Xing, Pete E. Pascuzzi, and Elizabeth J. Tran*
- The study from Wang *et al.* reveals that the RNA helicase *Dbp2* co-regulates metabolic gene expression with the *Cyc8* co-repressor. The authors found that *Dbp2* maintains glucose repression of respiration, gluconeogenesis, and utilization of nonfermentable carbon sources. This is achieved by regulating the association of the *Cyc8* co-repressor at lncRNA-targeted, co-regulated genes. The study elucidates the RNA helicase *Dbp2* as a regulator of cell metabolism that links gene regulation to adaptation to nutrient availability.

- 2249–2258 **Definition of a RACK1 Interaction Network in *Drosophila melanogaster* Using SWATH-MS**  
*Lauriane Kuhn, Karim Majzoub, Evelyne Einhorn, Johana Chicher, Julien Pompon, Jean-Luc Imler, Philippe Hammann, and Carine Meignin*
- In this study, Kuhn *et al.* report a proteomic characterization of the interactome of RACK1 in *Drosophila* S2 cells using Label-Free quantitation mass spectrometry. These data represent the first SWATH-MS spectral library available for *Drosophila* and will be a useful resource for the community. The 52 interacting proteins identified are significantly enriched for the functions translation and nucleic acid binding, reflecting the engagement of RACK1 at the ribosome. A functional screen did not reveal any protein required for IRES-dependent translation and not essential for cell viability, like RACK1. However, 10 of the RACK1 partners identified were found to restrict viral replication.
- 2259–2270 **Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common *Brassica rapa* Mapping Population**  
*R. J. Cody Markelz, Michael F. Covington, Marcus T. Brock, Upendra K. Devisetty, Daniel J. Kliebenstein, Cynthia Weinig, and Julin N. Maloof*
- This article utilizes a large RNA-seq data set to densely genotype a Recombinant Inbred Line population of *Brassica rapa* that has been used extensively for answering development, evolution and agronomic questions across many labs and environments. With this data set we also placed genomic scaffolds to relative locations within the reference genome and created a new genetic map with known genomic coordinates for the markers. This dense, physically anchored genetic map improves mapping resolution and can aid in candidate gene identification.
- 2271–2279 **A Systemic Analysis of Transcriptomic and Epigenomic Data To Reveal Regulation Patterns for Complex Disease**  
*Chao Xu, Ji-Gang Zhang, Dongdong Lin, Lan Zhang, Hui Shen, and Hong-Wen Deng*
- Human complex diseases are induced by various genomic and epigenomic alterations. Xu *et al.* presented a novel integrative analysis framework, which can not only identify disease-associated (epi-)genomic factors from diverse omics data, but also can infer the regulatory interactions of these factors. Applying this strategy to GBM (Glioblastoma multiforme) samples with genome-wide gene expression, DNA methylation, and miRNA expression data, the authors identified three regulatory modules of dysregulated (epi-)genomic factors and revealed a global regulatory pattern critical for GBM survival time. The author s integrative analysis framework represents an innovative strategy to enhance the understanding of molecular genomic mechanisms underlying human complex diseases.
- 2281–2293 **Genetic Subtraction Profiling Identifies Candidate miRNAs Involved in Rice Female Gametophyte Abortion**  
*Liyu Yang, Ya Wu, Wenliang Wang, Bigang Mao, Bingran Zhao, and Jianbo Wang*
- To investigate the potential regulatory effects of miRNA on the abortive mechanism in rice female gametophyte, Yang *et al.* report a comprehensive miRNA transcriptome analysis of ovules in high frequency female-sterile rice line (*fsv1*) and rice wild type line (Gui 99). As a result, 100 known miRNAs exhibited significant differential expression between the ovules of these two rice lines. The coherent targets of these miRNAs were associated with many biological pathways such as protein degradation, auxin signal transduction and transcription factor regulation. These results will serve as blueprint for further investigation of the regulatory roles of miRNAs in rice female gametophyte abortion.
- 2295–2304 **The Mapping of Predicted Triplex DNA:RNA in the *Drosophila* Genome Reveals a Prominent Location in Development- and Morphogenesis-Related Genes**  
*Claude Pasquier, Sandra Agnel, and Alain Robichon*
- Non canonical DNA structures Triplex DNA:RNA make stable structures according to Hoogsteen rules. Pasquier, Agnel, and Robichon propose a *Drosophila* genome wide scale computational analysis of triplex motifs by the association DNA:RNA. The conclusions reside in the facts: more than 10 000 loci shelter triplex compatible sequences ii) particular TFOs (triplex forming oligonucleotides) in mRNA or in LncRNA match in multiple locations in the genome; iii) the theoretical prediction of triplex amazingly reveal that they restrictively target developmental and morphogenesis gene networks. The authors think that these data might provide new insights in epigenetic regulation across species from plants, invertebrates to mammals.

- 2305–2314 **Essential Function of the Serine Hydroxymethyl Transferase (SHMT) Gene During Rapid Syncytial Cell Cycles in *Drosophila***  
*Franziska Winkler, Maria Kriebel, Michaela Clever, Stephanie Gröning, and Jörg Großhans*  
 Many metabolic enzymes are evolutionary highly conserved and serve a central function for catabolism and anabolism of cells. The serine hydroxymethyl transferase (SHMT) catalysing the conversion of serine and glycine and vice versa feeds into the tetrahydrofolate mediated C1 metabolism. Winkler *et al.* identified a *Drosophila* mutant in SHMT. Mutant embryos specifically arrest in interphase of nuclear cycle 13. The data suggest that SHMT mutant eggs contain maternally provided and SHMT-dependent metabolites in amounts which suffice for early development until interphase 13.
- 2315–2326 **Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population**  
*Xuecai Zhang, Paulino Pérez-Rodríguez, Juan Burgueño, Michael Olsen, Edward Buckler, Gary Atlin, Boddupalli M. Prasanna, Mateo Vargas, Félix San Vicente, and José Crossa*  
 Genomic selection increases genetic gain by reducing the length of the selection cycle, as has been exemplified in maize using rapid cycling recombination of bi-parental populations. No results of genomic selection applied to maize multiparental populations have been reported so far. This study shows realized genetic gains of rapid cycling genomic selection (RCGS) for four recombination cycles (C<sub>1</sub>, C<sub>2</sub>, C<sub>3</sub>, and C<sub>4</sub>) in a multiparental tropical maize population. Realized grain yield from C<sub>1</sub> to C<sub>4</sub> reached 0.225 ton ha<sup>-1</sup> per cycle, which is equivalent to 0.100 ton ha<sup>-1</sup> year<sup>-1</sup> over a 4.5-year breeding period from the initial cross to the last cycle. Genetic diversity narrowed only slightly during the last GS cycles (C<sub>3</sub> and C<sub>4</sub>).
- 2327–2335 **A Coding Variant in the Gene Bardet-Biedl Syndrome 4 (*BBS4*) Is Associated with a Novel Form of Canine Progressive Retinal Atrophy**  
*Tracy Chew, Bianca Haase, Roslyn Bathgate, Cali E. Willet, Maria K. Kaukonen, Lisa J. Mascord, Hannes T. Lohi, and Claire M. Wade*  
 Progressive retinal atrophy is a common cause of blindness in the dog and the basis for disease is unknown in many cases. Using genotyping array and whole genome sequencing data, Chew *et al.* identify a single nonsense SNP in *BBS4* that is highly associated with disease in the Hungarian Puli breed. In humans, *BBS4* is associated with a ciliopathy called Bardet-Biedl syndrome that includes a retinal degeneration phenotype. The authors find evidence that syndromic disease also occurs in the dog as they observe obesity and spermatozoa flagella defects. The dog is a promising model for Bardet-Biedl syndrome and for understanding *BBS4* cellular functions.
- 2337–2343 ***Drosophila simulans*: A Species with Improved Resolution in Evolve and Resequencing Studies**  
*Neda Barghi, Raymond Tobler, Viola Nolte, and Christian Schlötterer*  
 The combination of experimental evolution with high-throughput sequencing of pooled individuals – i.e. Evolve and Resequencing; E&R – is a powerful approach to investigate adaptation from standing genetic variation in controlled and replicated experimental settings. Nevertheless, E&R studies in *Drosophila melanogaster* have frequently resulted in inordinate numbers of candidate SNPs, particularly for complex traits. In the first E&R study in *Drosophila simulans*, narrower genomic regions carrying putatively selected loci and thus fewer false positives were identified. Barghi *et al.* propose that species such as *D. simulans* that lack large segregating inversions and have higher recombination rate are better suited for E&R studies.
- 2345–2352 **Whole-Genome Resequencing Identifies the Molecular Genetic Cause for the Absence of a Gy5 Glycinin Protein in Soybean PI 603408**  
*Jason D. Gillman, Won-Seok Kim, Bo Song, Nathan W. Oehrle, Nilesh R. Tawari, Shanshan Liu, and Hari B. Krishnan*  
 Through proteomic analysis, soybean PI603408, was identified whose seeds lacked a glycinin protein subunit. Through whole genomic resequencing, the molecular genetic cause was determined to be a two base deletion that introduces a frameshift mutation in Glycinin 5. A newly developed SIFT 4G database was used to predict the effect of the single nucleotide variants using ancestral conservation scoring across a range of diverse species. Gillman *et al.* anticipate the new SIFT 4G database, as well as the extremely high coverage depth (average 59.1-fold) resequencing information for PI 603408, will prove useful in future soybean gene diversity and gene function studies.

- 2353–2361 **A Targeted Capture Linkage Map Anchors the Genome of the Schistosomiasis Vector Snail, *Biomphalaria glabrata***  
*Jacob A. Tennessen, Stephanie R. Bollmann, and Michael S. Blouin*
- Schistosomiasis, a prevalent and debilitating parasitic disease, is transmitted by aquatic snails. In order to combat this disease in the snail hosts, and to understand mollusk biology more generally, the snail genome was recently sequenced. However, the current genome draft is poorly assembled and consists of hundreds of thousands of scaffolds. The organization of genes within chromosomes is still largely unknown. Here, Tennessen, Bollmann, and Blouin have generated a dense linkage map targeting unique and gene-containing portions of the genome. The authors can now determine which genes are adjacent to a given genetic marker, and thus find and study the genes underlying snail-parasite interactions.
- 2363–2373 **The Evolutionary Basis of Translational Accuracy in Plants**  
*Salvatore Camiolo, Gaurav Sablok, and Andrea Porceddu*
- The present work deals with the evolution of the compositional determinants of translational accuracy in the main flowering-plant clades. The study from Camiolo, Sablok, and Porceddu shows that although signatures of selection for translational accuracy are evident in all plant species, the underlying factors vary in intensity between clades. The authors analyzed codon preferences at evolutionarily conserved sites in domain and non-domain regions of transcripts and in regions that form RNA stems and loops. The results suggest that both the domain and the structure factors play a role in the selection for translational accuracy in higher plants.
- 2375–2389 **Systematic Analysis of the DNA Damage Response Network in Telomere Defective Budding Yeast**  
*Eva-Maria Holstein, Greg Ngo, Conor Lawless, Peter Banks, Matthew Greetham, Darren Wilkinson, and David Lydall*
- Holstein *et al.* have systematically examined genome-wide genetic interactions that affect fitness of cells with different types of telomere defects, both chronic and acute. The authors also examined genetic interactions when aspects of the DNA damage response network were disabled. The results show there is no universal cellular response to telomere defects. The large volumes of data generated are made available via two interactive web-based tools. The authors observed that Chk1, a checkpoint kinase, shows particularly strong effects on telomere defective cells in the absence of the nuclease Exo1. This may be because Chk1 affects single stranded DNA production.
- 2391–2403 **The Genetic Architecture of Ovariole Number in *Drosophila melanogaster*: Genes with Major, Quantitative, and Pleiotropic Effects**  
*Amanda S. Lobell, Rachel R. Kaspari, Yazmin L. Serrano Negrón, and Susan T. Harbison*
- Ovariole number is a morphological trait in insects thought to impact reproductive fitness by controlling egg production. Lobell *et al.* investigated the genetic architecture of ovariole number with a genome-wide association study in *Drosophila melanogaster*. Twenty-four candidate genes for ovariole number were identified and verified using mutations and RNAi-mediated knockdown. Most genes had quantitative effects on ovariole number; however, two genes had major effects on ovariole morphology and offspring production. The authors also observed pleiotropic effects of seven of these genes on sleep. Traits were associated with different polymorphisms within genes and were not linked, suggesting that these polymorphisms might evolve independently.
- 2405 **CORRIGENDUM**