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INVESTIGATIONS

- 2105–2114 **Increased Genomic Prediction Accuracy in Wheat Breeding Through Spatial Adjustment of Field Trial Data**
Bettina Lado, Ivan Matus, Alejandra Rodríguez, Luis Inostroza, Jesse Poland, François Belzile, Alejandro del Pozo, Martin Quincke, Marina Castro, and Jarislav von Zitzewitz
- The possibility to predict important and complex traits in plant breeding programs could greatly increase efficiency of selection. In this study, the authors applied currently proposed SNP discovery methods in a wheat breeding germplasm that was field-tested for adaptation in three different Mediterranean climatic conditions. They found that a mixed-model using moving-means as a covariate for spatial adjustment was the best fit for the complex agronomic data. A Gaussian kernel model presented the highest accuracy. The genotyping strategy was effective for predicting traits, and correction of spatial variation increased prediction accuracies. This may be the first article showing positive results towards wheat genomic selection in South America.
- 2115–2120 **Coupling Between Noise and Plasticity in *E. coli***
Gajinder Pal Singh
- Expression levels of genes change under different conditions and also vary among identical cells in the same environment. These two parameters – known as plasticity and noise – positively correlate with each other in yeast, suggesting linkage by a common expression mechanism. Further, different classes of genes show different levels of coupling. Are these results specific to yeast? Here the author shows that such a correlation exists in *E. coli*, and factors influencing this correlation are also very similar. The results of the study indicate that noise-plasticity correlation is a common phenomenon and that its mechanism might be similar across evolutionarily distant organisms.
- 2121–2130 **Rapid Degeneration of Noncoding DNA Regions Surrounding *SLAP3X/Y* After Recombination Suppression in the Dioecious Plant *Silene latifolia***
Kotaro Ishii, Rie Nishiyama, Fukashi Shibata, Yusuke Kazama, Tomoko Abe, and Shigeyuki Kawano
- The heteromorphic XY chromosomes of the *Silene latifolia* are thought to have evolved with a gradual divergence. The authors' analysis of 115 kb and 73 kb sequence containing the XY-linked paralogs *SLAP3X* and *SLAP3Y*, respectively, demonstrate that most parts of noncoding sequences are repetitive and not homologous between X and Y. Nucleotide divergence analyses reveal that the recombination of these genes stopped about 3.4 million years ago, and that all insertion events of transposons occurred after the recombination stopped. The insertions and deletions in these regions after the recombination stop may have caused gradual divergence of the XY chromosomes.

- 2131–2146 **Linkage Relationships Among Multiple QTL for Horticultural Traits and Late Blight (*P. infestans*) Resistance on Chromosome 5 Introgressed from Wild Tomato *Solanum habrochaites***
J. Erron Haggard, Emily B. Johnson, and Dina A. St. Clair
- A QTL for *Phytophthora infestans* resistance on chromosome 5 was introgressed from wild *Solanum habrochaites* into cultivated tomato (*S. lycopersicum*); fine-mapping revealed multiple resistance QTL and coincident/linked QTL with undesirable effects on horticultural traits. In this study, the authors evaluated chromosome 5 sub-near-isogenic lines for 17 horticultural traits in field experiments over two years. Each previously detected horticultural trait QTL fractionated into two or more QTL. Forty-one QTL were detected across all traits and 30% exhibited QTL × environment interactions. Co-location of QTL for multiple traits suggests pleiotropy or tightly-linked genes and a complex genetic architecture, presenting challenges for breeding efforts.
- 2147–2149 **MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses**
Ronald M. Nelson, Carl Nettelblad, Mats E. Pettersson, Xia Shen, Lucy Crooks, Francois Besnier, José M. Álvarez-Castro, Lars Rönnegård, Weronica Ek, Zheyu Sheng, Marcin Kierczak, Sverker Holmgren, and Örjan Carlborg
- MAPfastR is a software package developed to analyze QTL data from inbred and outbred line-crosses. The package is written in the R language and is able to handle large datasets for fast and accurate QTL analyses.
- 2151–2161 **Detecting Selection Using Time-Series Data of Allele Frequencies with Multiple Independent Reference Loci**
Jo Nishino
- Here the authors present a neutrality test at a single diallelic locus using time-series data of allele frequencies. This test is an extension of Feder *et al.*'s (2013) frequency increment test (FIT) and explicitly allows for changes in population size by using information from independent reference loci. Various demographic models suggest that the authors' proposed test is unbiased when sampling noise can be ignored and that it has greater power to detect selection than the FIT. These findings may facilitate the development of more sophisticated methods using independent reference loci, including a method that can estimate the strength of selection.
- 2163–2171 **Genomic Sequence Diversity and Population Structure of *Saccharomyces cerevisiae* Assessed by RAD-seq**
Gareth A. Cromie, Katie E. Hyma, Catherine L. Ludlow, Cecilia Garmendia-Torres, Teresa L. Gilbert, Patrick May, Angela A. Huang, Aimée M. Dudley, and Justin C. Fay
- The yeast *S. cerevisiae* is important for the production of fermented foodstuffs and as a laboratory model for basic cellular processes. To explore the genetic diversity of the global population of *S. cerevisiae*, the authors used a cost-effective genotyping method that permits the sequencing of a common ~1% of every strain's genome. Their results suggest that major subpopulations correspond to geography and that human activity has dispersed strains around the globe. In contrast, the small subset of strains used in the laboratory is mostly related to European strains and contains only one quarter of the sequence diversity of the larger population.
- 2173–2185 **STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma**
Jennifer Hardee, Zhengqing Ouyang, Yuping Zhang, Anshul Kundaje, Philippe Lacroute, and Michael Snyder
- Dysregulation of the transcription factor STAT3 is implicated in many types of cancer, including diffuse large B cell lymphoma. Comparative genomic analysis of STAT3 binding and transcriptome expression in the two subtypes of DLBCL provide novel insights into its genetics and genes downstream of STAT3 that may contribute to oncogenesis. In this article, the authors suggest new avenues of investigation for DLBCL drug targets and for understanding the dysregulation of STAT3 in many other cancers. Overall, the study makes a significant contribution to our knowledge of the genetic basis of aggression in hematological cancers and provides ChIP-Seq and RNA-Seq datasets for further research.

- 2187–2194 **Divergence of Iron Metabolism in Wild Malaysian Yeast**
Hana N. Lee, Yulia Mostovoy, Tiffany Y. Hsu, Amanda H. Chang, and Rachel B. Brem
 Interpreting the phenotypic relevance of gene expression variation is one of the primary challenges of modern genomics. Observing striking changes in iron metabolism gene expression between wild yeast populations, the authors hypothesized that these microbes would differ with respect to growth during iron challenge. Fitness measurements validated this prediction, revealing a growth defect in wild Malaysian yeast under conditions of high iron; molecular-genetic dissection identified three genes that contribute to molecular and cellular divergence in iron metabolism between yeast strains. These results clearly indicate that expression profiles can be used to generate hypotheses for the study of trait variation.
- 2195–2204 **Genotype to Phenotype Maps: Multiple Input Abiotic Signals Combine to Produce Growth Effects via Attenuating Signaling Interactions in Maize**
G. Buddhika Makumburage, H. Lee Richbourg, Kalindi D. LaTorre, Andrew Capps, Cuixen Chen, and Ann E. Stapleton
 Predicting gene by environment interaction is key in understanding the non-linear functions relating alleles to phenotypes. The authors identified chromosomal loci important for maize growth responses to drought, ultraviolet radiation stress, and to drought and high UV applied together. The loci important for the combination stress could not be explained as simple AND/OR circuitry creating combinations of single-stress loci. Instead, the combination-stress locus patterns were consistent with attenuating feedback in the circuitry for the plant stress-affected growth responses. These results suggest that screening of diverse populations for small-effect, limited interaction-circuit networks in combined-stress environments early in the selection process could lead to more efficient breeding.
- 2205–2217 **Immune-Related Functions of the *Hivep* Gene Family in East African Cichlid Fishes**
Eveline T. Diepeveen, Olivia Roth, and Walter Salzburger
 Relatively little is known about the contribution of immune-related genes to adaptive radiations. However, the exploitation of empty niches in a radiation is likely associated with new parasite communities, with which the emerging species must cope. Here the authors show that members of the *Hivep* gene family are characterized by signatures of positive selection in East African cichlid fishes. They further demonstrate that several *Hivep* paralogs are involved in the cichlids' immune response, as shown for non-teleost species, linking the observed adaptive protein evolution to host-pathogen interactions. The *Hivep* loci emerge as promising new candidate genes for teleost immune responses.
- 2219–2232 **Mated Progeny Production Is a Biomarker of Aging in *Caenorhabditis elegans***
Christopher L. Pickett, Nicholas Dietrich, Junfang Chen, Chengjie Xiong, and Kerry Kornfeld
 Reproduction has been proposed to influence aging. To analyze relationships between progeny production, reproductive aging, and somatic aging, the authors used two experimental approaches. First, longitudinal studies of *C. elegans* hermaphrodites demonstrated that high levels of progeny production were positively correlated with delayed somatic and reproductive aging. Second, increasing progeny production by mating hermaphrodites to males did not accelerate somatic aging. These results indicate that progeny production does not cause age-related degeneration of reproductive or somatic function and are consistent with the model that reproductive aging is an adaptive trait that promotes the generation of an optimal number of progeny.
- 2233–2238 **RNA-Guided Genome Editing for Target Gene Mutations in Wheat**
Santosh Kumar Upadhyay, Jitesh Kumar, Anshu Alok, and Rakesh Tuli
 These authors report RNA-guided genome editing in wheat, one of the most important food crops. They used the CRISPR-Cas system to achieve editing of multiple target sites, thereby demonstrating the applicability of the technique to one of the largest and most complex genomes in food crops.

- 2239–2255 **Identification and Characterization of FGF2-Dependent mRNA: microRNA Networks During Lens Fiber Cell Differentiation**
Louise Wolf, Chun S. Gao, Karen Gueta, Qing Xie, Tiphaine Chevaller, Nikhil R. Poddaturi, Jian Sun, Ivan Conte, Peggy S. Zelenka, Ruth Ashery-Padan, Jiri Zavadil, and Ales Cvekl
 Using conditional gene inactivation, the present data establish novel roles of Dicer1 in lens fiber cell differentiation and suggest that miRNAs are involved in the unique process of lens fiber cell denucleation. The authors identified differentiation-specific mRNAs and miRNAs in lens explants stimulated by FGF2. They found that multiple regulatory genes of lens fiber cell differentiation, including c-Maf, Nfat5/OREBP, N-Myc (transcription factors), Kdm5b/Jarid1b (histone lysine demethylase), and Med1/PBP (Gata co-activator), are connected by specific shared miRNAs. Collectively, the present studies identified FGF-dependent mRNA: miRNA gene regulatory networks (GRNs) that control lens differentiation.
- 2257–2271 **Genome of *Drosophila suzukii*, the Spotted Wing *Drosophila***
Joanna C. Chiu, Xuanting Jiang, Li Zhao, Christopher A. Hamm, Julie M. Cridland, Perot Saelao, Kelly A. Hamby, Ernest K. Lee, Rosanna S. Kwok, Guojie Zhang, Frank G. Zalom, Vaughn M. Walton, and David J. Begun
Drosophila suzukii Matsumura (Spotted Wing *Drosophila*) has recently caused substantial yearly losses of a wide variety of fruit crops in the United States as well as in Europe. To enable basic and applied research of this serious pest, the authors sequenced the *D. suzukii* genome to obtain a high quality reference sequence. Here they discuss the basic properties of the genome and transcriptome and describe patterns of genome evolution in *D. suzukii* and its close relatives. To facilitate public access, the authors have presented their analyses and genome annotations in a Web portal, SpottedWingFlyBase.
- 2273–2280 **Regulation of Gene Expression in *Neurospora crassa* with a Copper Responsive Promoter**
Teresa M. Lamb, Justin Vickery, and Deborah Bell-Pedersen
 The authors have developed a new system to control target gene expression in *Neurospora* using the promoter of the copper responsive gene, *tcu-1*. This promoter is specifically sensitive to copper levels, which are easily adjusted by the addition of CuSO₄ or BCS, a copper chelator, to the growth medium. Genetic alteration of the target gene promoter is via integration of a fusion-PCR-generated fragment that contains the *tcu-1* promoter and *bar* selection, allowing rapid strain construction. Conveniently, both over-expression and repression of the target gene can be accomplished in the same strain, and the range of expression levels achieved exceed thirty-fold.
- 2281–2288 **Comparative Genome Mapping Between Chinook Salmon (*Oncorhynchus tshawytscha*) and Rainbow Trout (*O. mykiss*) Based on Homologous Microsatellite Loci**
Kerry A. Naish, Ruth B. Phillips, Marine S. O. Brieuc, Lyndsay R. Newton, Anna E. Elz, and Linda K. Park
 This article provides novel insight into genome rearrangements following whole genome duplication in an ancestral autotetraploid, and thus is of broader appeal to studies of processes governing rediploidization. The results presented here also contribute significantly to the study of the salmonid genome, which is very relevant to the evolution of this species flock. Finally, the genome maps are applicable in aquaculture and conservation settings because they will facilitate the rapid transfer of genomic resources from two better described species – Atlantic salmon and rainbow trout – to this less described species, Chinook salmon.
- 2289–2295 **Assignment of Chinook Salmon (*Oncorhynchus tshawytscha*) Linkage Groups to Specific Chromosomes Reveals a Karyotype with Multiple Rearrangements of the Chromosome Arms of Rainbow Trout (*Oncorhynchus mykiss*)**
Ruth B. Phillips, Linda K. Park, and Kerry A. Naish
 In this study, the authors assigned Chinook salmon (2N=68) genetic linkage groups to specific chromosomes and compared them with the rainbow trout chromosome map (2N=60). The resulting data shows that there has been conservation of large syntenic blocks between the two species corresponding to entire chromosome arms. Only about one-third of the chromosomes are conserved between the two species.

- 2297–2304 **Mapping Polycomb Response Elements at the *Drosophila melanogaster giant* Locus**
Jumana AlHaj Abed, Connie L. Cheng, Chase R. Crowell, Laura L. Madigan, Erica Onwuegbuchu, Siddhi Desai, Judith Benes, and Richard S. Jones
- Polycomb-group proteins are highly conserved epigenetic transcriptional repressors. Recruitment of *Drosophila* Polycomb-group proteins to target loci requires the presence of at least one Polycomb Response Element (PRE). These authors map the locations of two PREs at the Polycomb-group target gene, *giant*, and provide further evidence for the difficulty in predicting PRE location by DNA sequence information alone. Components of all three major Polycomb-group protein complexes, PhoRC, PRC1, and PRC2, are shown to associate with these PRE regions in embryos.
- 2305–2312 **Dynamics of Adaptive Alleles in Divergently Selected Body Weight Lines of Chickens**
Mats E. Pettersson, Anna M. Johansson, Paul B. Siegel, and Örjan Carlborg
- These authors present a study of the genome-wide footprint of divergent selection on body weight in the Virginia chicken lines, experimental populations that have been under selection for either high or low body-weight for more than 50 years. Their findings include evidence for selection on standing variations in the early part of the experiment and for rapid fixation of a strong novel mutation in recent years. The article offers insight into the genetic architecture of complex traits and provides an interesting perspective on findings concerning growth-related traits in other species, such as horse, dog, and human.
- 2313–2319 **Rapid Recombination Mapping for High-Throughput Genetic Screens in *Drosophila***
Anne L. Sapiro, Robert J. Ihry, Derek L. Buhr, Kevin M. Konieczko, Sarah M. Ives, Anna K. Engstrom, Nicholas P. Wleklinski, Kristin J. Kopish, and Arash Bashirullah
- Chemical mutagenesis screens have fueled our knowledge of some of the most fundamental aspects of biology. But with the availability of collections of RNAi ectopic expression lines mutagenesis screens have fallen out of favor, primarily because of the time and effort involved in mapping mutations. Here the authors present a simple and rapid method for recombination mapping in *Drosophila* using pairs of dominant phenotypic markers. By facilitating the rapid identification of mutated genes, their mapping strategy removes a primary obstacle to the widespread use of chemical mutagenesis screens to understand fundamental biological phenomena.

MUTANT SCREEN REPORT

- 2321–2333 ***Saccharomyces cerevisiae* Genes Involved in Survival of Heat Shock**
Stefanie Jarolim, Anita Ayer, Bethany Pillay, Allison C. Gee, Alex Phrakayson, Gabriel G. Perrone, Michael Breitenbach, and Ian W. Dawes
- These authors screened the *Saccharomyces cerevisiae* deletion mutant collections for genes involved in the maintenance of heat-shock resistance. They found that there was little overlap between genes important for thermotolerance and those needed for maintenance of heat-shock resistance. There was also little overlap with genes that are activated or repressed during heat-shock. In addition to previously identified processes, the authors found cellular functions to be relevant. These included L-tryptophan metabolism, cytoplasmic ribosome biogenesis, DNA double-strand break repair, and mitochondrial respiration. The cell division transcription factor Swi6p and Hac1p mediating the unfolded protein response also play roles in maintenance of heat-shock resistance.

- 2335–2337 **REVIEWER INDEX**