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INVESTIGATIONS AND AUTHOR SUMMARIES

- 145–152 **Molecular Characterization of Sexual Diversity in a Population of *Serpula lacrymans*, a Tetrapolar Basidiomycete**
Inger Skrede, Sundy Maurice, and Håvard Kausserud
The authors report on the diversity of mating types in the European population of the wood-decay fungus *Serpula lacrymans*, which possesses a tetrapolar multi-allelic mating system. Using annotation of the mating type loci, they identified synteny of *S. lacrymans* and other basidiomycetes and the presence of a retrotransposon in one mating type locus (MAT A). Genetic markers linked to the MAT loci combined with *in vitro* crossing experiments demonstrated low diversity of mating types in the European *S. lacrymans* population. The authors hypothesize that the low diversity of mating types restrains the dispersal and further establishment of the fungus in Europe.
- 153–165 **Fosmid-Based Structure-Function Analysis Reveals Functionally Distinct Domains in the Cytoplasmic Domain of *Drosophila* Crumbs**
Sven Klose, David Flores-Benitez, Falko Riedel, and Elisabeth Knust
Drosophila Crumbs (Crb) is a large transmembrane protein that regulates epithelial cell polarity in the embryo. Its small cytoplasmic domain contains a FERM-binding and a PDZ-binding motif. To analyze the function of each of these domains, the authors designed various fosmid-based transgenes containing the entire *crb* locus, with mutations in individual domains. They found that embryos expressing a Crb protein that lacks the PDZ-binding motif lose epithelial cell polarity and fail to invaginate salivary gland, but not tracheal primordia. Strikingly, the FERM-binding domain is only required at later stages for dorsal closure and germ band retraction, a function not revealed in rescue experiments performed previously using the GAL4/UAS system.
- 167–180 **RNA Polymerase II Mutations Conferring Defects in Poly(A) Site Cleavage and Termination in *Saccharomyces cerevisiae***
Charles E. Kubicek, Robert D. Chisholm, Sachiko Takayama, and Diane K. Hawley
In eukaryotic nuclei, pre-mRNA polyadenylation and transcription termination are coupled and share required proteins and nucleic acid elements. RNA polymerase II is known to play a central role in the coupling, but the mechanism is still unclear. This article describes the first genetic screen for polyadenylation and termination mutants targeted to an RNA polymerase II subunit in the yeast *Saccharomyces cerevisiae*. The screen successfully identified mutations that reduced the efficiency of RNA cleavage at the poly(A) site and at least one mutation that uncoupled cleavage from termination, providing a novel tool to understand the relationship between these two essential processes.

- 181–195 **Redundant Canonical and Noncanonical *Caenorhabditis elegans* p21-Activated Kinase Signaling Governs Distal Tip Cell Migrations**
Eldon C. Peters, Andrea J. Gossett, Bob Goldstein, Channing J. Der, and David J. Reiner
 Pak S/T kinases are well-characterized effectors of Rac and Cdc42. However, humans have six Paks and multiple Rac and Cdc42 isoforms, and thus their functional requirements and pathway relationships are unclear. The authors analyzed the three *Caenorhabditis elegans* Group A Paks, along with Rac, RhoG and Cdc42. PAK-1 and MAX-2 are redundant for distal tip cell migration, locomotion, embryonic epiboly, and fertility. In cell migration the atypical Dock/ELMO RacGEF, working without MIG-2/RhoG, activates CED-10/Rac. CED-10 activates MAX-2, but CDC-42 does not. Conversely, PAK-1 functions in the non-canonical Pak-Pix-Git complex, but surprisingly requires kinase activity and perhaps Rac input.
- 197–203 **Genomic Prediction of Northern Corn Leaf Blight Resistance in Maize with Combined or Separated Training Sets for Heterotic Groups**
Frank Technow, Anna Bürger, and Albrecht E. Melchinger
 The fungal disease northern corn leaf blight (NCLB) is a threat to maize cultivation worldwide. It can be most effectively controlled by cultivation of resistant varieties. In this article, the authors report the first empirical results for genomic prediction of NCLB resistance. They show that prediction accuracy for this trait can be increased by using training sets that combine different heterotic groups.
- 205–215 **Fine-Scale Mapping of the *Nasonia* Genome to Chromosomes Using a High-Density Genotyping Microarray**
Christopher A. Desjardins, Jürgen Gadau, Jacqueline A. Lopez, Oliver Niehuis, Amanda R. Avery, David W. Loehlin, Stephen Richards, John K. Colbourne, and John H. Werren
Nasonia, a genus of small insects, is a model system for studying the genetics of complex traits and speciation. To assist quantitative trait locus (QTL) mapping studies using *Nasonia*, the authors developed and utilized a genotyping microarray to infer a high-resolution genetic map of the *Nasonia* genome. They used the microarray to characterize 26 segmental introgression lines (SILs) that can be screened for rapid mapping of QTLs. The microarray can also be used for bulk-segregant analysis to map species differences in a hybrid population. These resources should further expand the usefulness of *Nasonia* as a genetic model.
- 217–223 **Genome-Wide Copy Number Variant Analysis in Inbred Chickens Lines With Different Susceptibility to Marek's Disease**
Juan Luo, Ying Yu, Apratim Mitra, Shuang Chang, Huanmin Zhang, George Liu, Ning Yang, and Jiuzhou Song
 Breeding of chickens genetically resistant to Marek's disease (MD) is a vital strategy to poultry health. To find the markers underlying the genetic resistance to MD, the authors examined copy number variation (CNV) in inbred MD-resistant and -susceptible chicken lines. They found a total of 45 CNVs in four lines of chickens. Twenty-eight of them were potentially involved in immune response and cell proliferation, *etc.* Importantly, two CNVs related with MD-resistance were transmitted to descendent recombinant congenic lines that differ in susceptibility to MD. These findings may lead to better strategies for genetic improvement of disease resistance in poultry.
- 225–230 **Tissue-Specific Transcriptomics in the Field Cricket *Teleogryllus oceanicus***
Nathan W. Bailey, Paris Veltsos, Yew-Foon Tan, A. Harvey Millar, Michael G. Ritchie, and Leigh W. Simmons
 Genomic studies of non-model organisms depend on availability of transcriptomic data across and within species, plus the development of bioinformatics techniques to handle that data. The authors addressed these two objectives by examining transcriptome differences among three tissue types of the field cricket *Teleogryllus oceanicus*. Uniquely expressed sequences in both testis and accessory gland showed a significantly lower rate of matching to annotated *Drosophila melanogaster* genes compared with those from general body tissue. These results correspond with empirical evidence that genes expressed in testis and accessory gland tissue are rapidly-evolving targets of selection.

- 231–249 **Cytological Characterization and Allelism Testing of Anther Developmental Mutants Identified in a Screen of Maize Male Sterile Lines**
Ljudmilla Timofejeva, David S. Skibbe, Sidae Lee, Inna Golubovskaya, Rachel Wang, Lisa Harper, Virginia Walbot, and William Zacheus Cande
- For a plant to reproduce, flowers need to properly develop. Anthers, the male floral organ, produce pollen. A defect or absence of any anther cell type results in male sterility. These authors conducted a cytological screen of maize male-sterile mutants. The screen yielded 42 new mutants, including 22 mutants with pre-meiotic cytological defects (five times more than were previously known), 7 mutants with post-meiotic defects, and 13 mutants with irregular meiosis. Cytological and genetic analysis of these mutants has led to a deeper understanding of how an anther develops.
- 251–262 **Origin and Evolution of Dishevelled**
Adler R. Dillman, Paul J. Minor, and Paul W. Sternberg
- The authors discovered that *Caenorhabditis* is unique among nematodes in having three Dishevelled (Dsh) orthologs (*dsh-1*, *dsh-2*, and *mig-5*). Here they describe a likely origin of this expansion. They found that basal-branching nematode lineages have one Dsh, while other sequenced taxa have two. They identify a new protein domain conserved in some nematode orthologs, the conservation of an SH3 binding motif in two of the three *Caenorhabditis* orthologs, and a conserved nuclear localization signal in Dsh orthologs across animals. They present many testable hypotheses concerning the functional specialization of Dsh orthologs in animals.
- 263–272 **Accuracy of Across-Environment Genome-Wide Prediction in Maize Nested Association Mapping Populations**
Zhigang Guo, Dominic M. Tucker, Daolong Wang, Christopher J. Basten, Elhan Ersoz, William H. Briggs, Jianwei Lu, Min Li, and Gilles Gay
- The authors focus on evaluating accuracy improvements of across-environment genome-wide prediction (GWP) by utilizing genetic and residual covariance across correlated environments. They evaluated predictions with a multi-environment (ME) model for two corn polygenic leaf structure traits, leaf length (LL) and leaf width (LW), based on within-population (WP) and across-population (AP) experiments using a large maize nested association mapping (NAM) data set consisting of 25 populations of recombinant inbred-lines (RILs). To make their study more applicable to plant breeding, they employed two cross-validation schemes by evaluating accuracies of (CV1) predicting unobserved phenotypes of untested lines and (CV2) predicting unobserved phenotypes of lines that have been evaluated in some environments but not others. The authors conclude that (i) GWP gave higher prediction accuracies than traditional QTL-based prediction (QP) in both WP and AP, and provided more advantages over QP for WP than for AP; (ii) prediction accuracy with ME was significantly higher than that attained by single-environment (SE) model in CV1 and CV2, and gains with ME over SE were greater in CV2 than in CV1; these gains were also greater in WP than in AP in both CV1 and CV2; and (iii) gains with ME over SE attributed to genetic correlation between environments, with little effect from residual correlation.
- 273–282 ***Saccharomyces cerevisiae* Genetics Predicts Candidate Therapeutic Genetic Interactions at the Mammalian Replication Fork**
Derek M. van Pel, Peter C. Stirling, Sean W. Minaker, Payal Sipahimalani, and Philip Hieter
- Synthetic lethality can rationally predict unlinked therapeutic targets whose disruption is lethal in combination with recurrent somatic mutations in cancer. In this study, the authors created and analyzed synthetic sick/lethal networks of chromosome instability (CIN) genes in *Saccharomyces cerevisiae* to demonstrate that essential and nonessential DNA replication fork proteins are hubs of genetic interactions with CIN cancer genes. Biological functional information predicted synthetic lethal interactions between additional replication fork and cancer genes, which the authors show are conserved from yeast to human cells. This work validates the idea that yeast high-throughput genetics can be used to identify pathways and complexes of therapeutic relevance to cancer.

- 283–295 **Genetic Control and Comparative Genomic Analysis of Flowering Time in *Setaria* (Poaceae)**
Margarita Mauro-Herrera, Xuewen Wang, Hugues Barbier, Thomas P. Brutnell, Katrien M. Devos, and Andrew N. Doust
- The panicoid grass genus *Setaria* is an emerging model for architecture, biofuels, and C4 photosynthesis. QTL analyses of mapping populations in varying environments reveal a conserved pattern of genetic regulation of flowering time, although marked genotype X environment interactions are evident. In this study, the authors found multiple syntenic QTL regions among *Setaria*, sorghum, and maize, with candidate genes in these regions known to control flowering in other plants. However, many flowering time genes cloned in maize do not colocalize with *Setaria* QTL, suggesting that variation in flowering time in separate grass lineages is controlled by a combination of conserved and lineage-specific genes.
- 297–304 **A Compendium of *Caenorhabditis elegans* RNA Binding Proteins Predicts Extensive Regulation at Multiple Levels**
Alex M. Tamburino, Sean P. Ryder, and Albertha J. M. Walhout
- Gene regulatory networks are a popular topic in systems biology. Existing studies have focused on transcription factors and microRNAs. Another important type of network involves RNA binding proteins (RBPs) that bind mRNAs to affect splicing, transcript stability, localization, and translation. Transcriptional network studies have been facilitated by predictions of which genes encode transcription factors. The authors provide a high-quality compendium of predicted RBPs encoded by the *Caenorhabditis elegans* genome. Using this compendium along with publicly available data, they conducted genome-scale analyses of RBPs, and demonstrate that RBPs are extensively regulated at multiple levels.
- 305–313 ***Caenorhabditis elegans* POT-1 and POT-2 Repress Telomere Maintenance Pathways**
Ludmila Shtessel, Mia Rochelle Lowden, Chen Cheng, Matt Simon, Kyle Wang, and Shawn Ahmed
- These authors employed genetic tests to illustrate that *Caenorhabditis elegans* POT-1 and POT-2 are both negative regulators of telomerase. This is an unexpected common function for these proteins. The results of this study also suggest that *pot-1* and *pot-2* independently repress the telomerase-independent telomere maintenance pathway ALT, allowing ALT to occur when small populations of *C. elegans* animals are transferred. The authors used a transgene that expresses mCherry-tagged POT-1 to complement the telomere elongation phenotype of a *pot-1* deletion mutation and to demonstrate that POT-1 physically associates with telomeres *in vivo*. Their POT-1::mCherry construct confers, for the first time, the ability to monitor live telomere dynamics *in vivo* in *C. elegans*.
- 315–322 **Regulation of the S-Locus Receptor Kinase and Self-Incompatibility in *Arabidopsis thaliana***
Susan R. Strickler, Titima Tantikanjana, and June B. Nasrallah
- The S-locus receptor kinase (SRK) is responsible for the ability of the stigma to inhibit self-pollination in the self-incompatibility (SI) response of the Brassicaceae. Different accessions of self-fertile *Arabidopsis thaliana* differ in the ability of their stigmas to inhibit self-pollination upon transformation with a functional SRK gene from self-incompatible *Arabidopsis lyrata*. These authors analyzed a loss-of-function mutation in NRPD1a that abolishes the ability of stigmas to inhibit self-pollination in some accessions. Their study reveals that this variability is associated with variable regulation of the SRK transgene in different accessions, with involvement of epigenetic and genic factors that converge on the SRK promoter.
- 323–331 **Genetic and Physiological Characterization of Two Clusters of Quantitative Trait Loci Associated With Seed Dormancy and Plant Height in Rice**
Heng Ye, Donn H. Beighley, Jiujuan Feng, and Xing-You Gu
- Despite years of detached genetic research on seed dormancy and plant height, the relatedness of these traits and their shared regulatory mechanisms in natural variants remains unclear. The introgression of chromosomal segments from weedy into cultivated rice prompted the detection of two clusters of quantitative trait loci both associated with seed dormancy and plant height, with the alleles inhibiting germination also reducing stem elongation. Natural mutants of these two clusters were sensitive and insensitive to gibberellin (GA), respectively. The authors found that the sensitive mutant coincided with a functional mutation at a GA biosynthesis gene. They hypothesize that the insensitive mutant works on the GA signaling pathway.

- 333–341 **A High Load of Non-neutral Amino-Acid Polymorphisms Explains High Protein Diversity Despite Moderate Effective Population Size in a Marine Bivalve With Sweepstakes Reproduction**
Estelle Harrang, Sylvie Lapègue, Benjamin Morga, and Nicolas Bierne
- Marine bivalves exhibit unusually high protein variation, but is this simply a consequence of their large population sizes, or of selection? Here the authors show that diversity in non-coding DNA is actually only moderate in the flat oyster, whereas amino acid-changing polymorphisms are comparatively abundant. Furthermore, amino acid-changing mutations tend to segregate at low frequencies, in accordance with their being mildly deleterious. The authors conclude that elevated protein diversity in oysters is predominantly a result of high genetic load rather than large population sizes. Skewed offspring distributions may explain the decoupling between neutral and non-neutral diversities.
- 343–352 **Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast**
Karl Waern and Michael Snyder
- Recent advances have allowed characterization of an organism's transcriptome at ever higher resolutions, most recently with RNA sequencing (RNA-Seq) technology. This study uses RNA-Seq to characterize the transcriptome of baker's yeast across 18 different environmental conditions, which triggers a large variety of gene regulation phenomena. By directly comparing transcriptomes between conditions, the authors found extensive differences in lengths of gene-encoding transcripts, which have important implications for the regulation of these genes. In addition, a large data set is made available to serve as a resource to the scientific community.
- 353–358 **How to Design a Genetic Mating Scheme: A Basic Training Package for *Drosophila* Genetics**
John Roote and Andreas Prokop
- For more than a century, the fruitfly *Drosophila melanogaster* has been used as a powerful model organism for biological research. Genetics is the essential and common instrument used by *Drosophila* groups. Training newcomers to fly genetics is a complex and time-consuming task, but too important to be left to chance. Surprisingly, suitable training resources are currently not available. Here the authors present a training package to be used as a resource in *Drosophila* laboratories.
- 359–368 **Allele Identification for Transcriptome-Based Population Genomics in the Invasive Plant *Centaurea solstitialis***
Katrina M. Dlugosch, Zhao Lai, Aurélie Bonin, José Hierro, and Loren H. Rieseberg
- These authors present a large dataset of 40 transcriptomes for wild genotypes of the invasive plant *Centaurea solstitialis* from across its worldwide distribution. They found that modest applications of sequencing effort recover most of the novel sequences present in the transcriptome of this species, including single-copy loci and a representative distribution of functional groups. The coverage of variable sites, observation of heterozygosity, and overlap among different libraries are all highly dependent on sequencing effort. Still, overlapping polymorphic sites revealed population structure and variation across the authors' samples, providing the first genetic evidence in support of hypothesized invasion scenarios.
- 369–378 **Functional Analyses of *Trichoderma reesei* LAE1 Reveal Conserved and Contrasting Roles of This Regulator**
Razieh Karimi-Aghcheh, Jin Woo Bok, Pallavi A. Phatale, Kristina M. Smith, Scott E. Baker, Alexander Lichius, Markus Omann, Susanne Zeilinger, Bernhard Seiboth, Catherine Rhee, Nancy P. Keller, Michael Freitag, and Christian P. Kubicek
- The putative methyltransferase LaeA is a global regulator that affects the expression of multiple secondary metabolite gene clusters in several fungi, and it can modify heterochromatin structure in *Aspergillus nidulans*. These authors recently showed that the LaeA orthologue of *Trichoderma reesei* (LAE1) regulates the expression of cellulases and polysaccharide hydrolases, which is unique in fungi. To learn more about the function of *T. reesei* LAE1, they assessed the effect of *lae1* manipulation on genome-wide gene expression. They found that LAE1 regulates genes of secondary metabolism, genes encoding ankyrin-proteins, iron uptake, heterokaryon incompatibility proteins, PTH11-receptors, and oxidases/monooxygenases. ChIP-seq with antibodies against histone modifications detected 4089 genes, but only 75 exhibited regulation by LAE1. *T. reesei lae1* did not rescue sterigmatocystin formation in a *laeA* null mutant of *A. nidulans* and did not interact with *A. nidulans* VeA in yeast two-hybrid assays, while it interacted with the *T. reesei* VeA orthologue. The results of this study show that the biological roles of fungal LaeA proteins are much less conserved than previously thought, and LAE1 appears to predominantly regulate genes increasing relative fitness in its environment.