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INVESTIGATIONS AND AUTHOR SUMMARIES

- 523–530 **High-Resolution SNP/CGH Microarrays Reveal the Accumulation of Loss of Heterozygosity in Commonly Used *Candida albicans* Strains**
Darren Abbey, Meleah Hickman, David Gresham, and Judith Berman
 To quickly detect large-scale genome changes, we designed a high-resolution microarray that simultaneously detects single nucleotide polymorphism (SNP) alleles and independently measures copy number variation (CNV) loci by comparative genome hybridization (CGH) at 40,000 loci in the genome of *Candida albicans*, a fungal resident and pathogen of humans. By analyzing the SNPs as a function of chromosome copy number, we assembled a haplotype map, which assigns specific SNPs to specific chromosome homologs. Using the array and map, we detected genetic alterations that appeared in common lab strains and found that strain fitness generally decreases with increasing numbers of genome alterations.
- 531–538 **Transposon-Mediated Transgenesis in the Short-Lived African Killifish *Nothobranchius furzeri*, a Vertebrate Model for Aging**
Dario Riccardo Valenzano, Sabrina Sharp, and Anne Brunet
 This study is the first report of transgenesis in the African killifish *Nothobranchius furzeri*, an extremely short-lived vertebrate species that is a promising model for aging research. Using the Tol2 transposase system, we generated stable lines of transgenic fish that express green fluorescent protein under the control of two different promoters. We also report successful integration of the transgene in the genome, and transmission through the germline. Our results pave the way for the use of *N. furzeri* as a genetically-tractable model system to study the mechanisms of vertebrate aging and longevity.
- 539–548 **Genome Evolution in the *Eremothecium* Clade of the *Saccharomyces* Complex Revealed by Comparative Genomics**
Jürgen Wendland and Andrea Walther
 This article demonstrates the power of comparative genomics/phylogenomics within *Saccharomyces*-complex species. We established the essentially complete genome sequence of *Eremothecium cymbalariae*. Comparisons to its relative *Ashbya (Eremothecium) gossypii* and to the ancestral yeast genome provide insight into the evolutionary history of *Eremothecium* genomes. *E. cymbalariae* exhibits several ancestral properties, e.g. eight chromosomes, mating-type cassettes on one chromosome, a TY-transposon, and low GC compared to the *A. gossypii* genome with only seven chromosomes, dispersed mating-type loci, no TY-elements, and a high GC-content. Thus comparative genomics of *E. cymbalariae* allowed us to identify a missing link between ancestral yeasts and *A. gossypii*.
- 549–558 **Genome-Wide Analysis of Nascent Transcription in *Saccharomyces cerevisiae***
Anastasia McKinlay, Carlos L. Araya, and Stanley Fields
 Transcription by RNA polymerase II determines the protein complement of a cell; thus it is critical to assess the activity of this polymerase throughout the genome. We carried out this assessment for the polymerase of the yeast *Saccharomyces cerevisiae* by isolating nascent RNA and using it to prepare libraries for high-throughput DNA sequencing. The resulting sequence data allowed us to examine nascent transcript levels for approximately 4200 yeast genes, yielding measures both of the contribution

of transcriptional activity to transcript abundance and of transcript stabilities. This study provides evidence for the regulation of yeast transcriptional activity at multiple steps in the transcription process.

559–570 **Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the *Arabidopsis* Transcriptome**

Amber M. Hotto, Robert J. Schmitz, Zhangjun Fei, Joseph R. Ecker, and David B. Stern

Noncoding RNAs (ncRNAs) are comprised of structural and regulatory RNAs, the latter class including micro-RNAs and antisense RNAs. Some ncRNAs have well-defined functions, and while fragmentary evidence showed that plant chloroplasts contain ncRNAs, no comprehensive study had been undertaken. Here, high-throughput RNA sequencing identified 107 chloroplast ncRNAs, many of which were verified by additional methods, and their biogenesis studied by analysis of chloroplast ribonuclease-deficient mutants. We speculate that ncRNAs could have a previously underappreciated role in chloroplast gene regulation.

571–579 **An Evaluation of *Arabidopsis thaliana* Hybrid Traits and Their Genetic Control**

Siobhan Moore and Lewis Lukens

Heterosis is a phenomenon in which the hybrid offspring of two parental lines has trait values that surpass the trait values of the parents. To investigate the genetic basis of heterosis in a model system, we evaluated five *Arabidopsis thaliana* parental lines for their effects on hybrid flowering time, biomass, and reproductive traits. Hybrids derived from different parental lines greatly differed. We show that epistatic interactions of two flowering time genes, *FRIGIDA (FRI)* and *FLOWERING LOCUS C (FLC)*, can explain heterosis for flowering time traits, contribute to heterosis for biomass traits, and can reduce heterosis for reproductive traits.

581–591 **Major Families of Multiresistant Plasmids from Geographically and Epidemiologically Diverse Staphylococci**

Julia E. S. Shearer, Joy Wireman, Jessica Hostetler, Heather Forberger, Jon Borman, John Gill, Susan Sanchez, Alexander Mankin, Jacqueline LaMarre, Jodi A. Lindsay, Kenneth Bayles, Ainsley Nicholson, Frances O'Brien, Slade O. Jensen, Neville Firth, Ronald A. Skurray, and Anne O. Summers

Staphylococci are a leading cause of hospital infections and of fatal infections in otherwise healthy people. They often carry antibiotic resistances and virulence genes on mobile elements called plasmids. Among 280 human and animal staphylococci isolated on three continents, we found 80% had plasmids large enough to carry multiple resistance genes. Of the 93 plasmids we sequenced, 59 were >20 kb, tripling the number of published large staphylococcal plasmid sequences. This large dataset revealed the intercontinental spread over seven decades of three highly conserved plasmid families residing in both human and animal strains, underscoring their remarkable stability and promiscuity.

593–601 **Physical Mapping in a Triplicated Genome: Mapping the Downy Mildew Resistance Locus *Pp523* in *Brassica oleracea* L.**

Jorge D. Carlier, Cláudia S. Alabaça, Nelson H. Sousa, Paula S. Coelho, António A. Monteiro, Andrew H. Paterson, and José M. Leitão

This article describes the construction of a physical map, encompassing a disease resistance locus, in the unusual conditions of a diploid species (*Brassica oleracea* L.) with a triplicated genome. The challenging issues posed to physical mapping by this atypical genome condition and by the presence of large amounts of transposable element-like sequences, in particular in what regards the exploitation of the genomic information on the related model species *Arabidopsis thaliana* L., are largely documented and discussed.

603–606 **Transcription Factor Binding Site Redundancy in Embryonic Enhancers of the *Drosophila* Bithorax Complex**

Robert A. Drewell

The bithorax complex in *Drosophila* contains three homeotic genes essential to normal development. The expression of these genes in the embryo is tightly controlled by *cis*-regulatory modules in the neighboring genomic DNA. The activity of the modules is mediated through the binding of protein transcription factors. In this article, I demonstrate that extensive redundancy exists for binding sites in the complex. This redundancy is selectively found at modules, which are known to recruit the transcription factors *in vivo*. The absence of compensatory binding sites is also demonstrated to be a potential source for two rare mutants in the complex.

- 607–613 **A Genetic Screen for Dominant Enhancers of the Cell-Cycle Regulator α -Endosulfine Identifies Matrimony as a Strong Functional Interactor in *Drosophila***
Jessica R. Von Stetina, Kimberly S. LaFever, Mayer Rubin, and Daniela Drummond-Barbosa
 The coordination of cell-cycle events with developmental processes is key for the success of organisms. *Drosophila* α -endosulfine (Endos) is an evolutionarily conserved protein required for meiotic maturation and early embryonic mitoses. Through a genetic screen, the authors identified the Polo kinase inhibitor *matrimony* (*mtrm*) as a strong dominant enhancer of *endos*⁰⁰⁰⁰³ heterozygotes. *endos*⁰⁰⁰⁰³ +/+ *mtrm*¹²⁶ females are sterile due to defects in early embryonic mitoses resulting from excessive Polo activity. *endos* promotes increased *Mtrm* expression in mature oocytes, suggesting the model that maternal *endos* antagonizes Polo activity in early embryos through effects on *Mtrm* during oogenesis.
- 615–626 **A Geographically Diverse Collection of *Schizosaccharomyces pombe* Isolates Shows Limited Phenotypic Variation but Extensive Karyotypic Diversity**
William R. A. Brown, Gianni Liti, Carlos Rosa, Steve James, Ian Roberts, Vincent Robert, Neil Jolly, Wen Tang, Peter Baumann, Carter Green, Kristina Schlegel, Jonathan Young, Fabienne Hirschaud, Spencer Leek, Geraint Thomas, Anders Blomberg, and Jonas Warringer
 The fission yeast *Schizosaccharomyces pombe* is widely used as a model for human cells, both healthy and diseased. While previous work has used a single strain of yeast, we have assembled and studied 80 different strains of *S. pombe* from around the world and have discovered that they vary significantly in size and that their chromosomes often have different structures. This variation will help us to understand the machinery that controls cell size and give us new information about chromosome stability—insights which should apply to human cells.
- 627–635 **Glypican Gene GPC5 Participates in the Behavioral Response to Ethanol: Evidence from Humans, Mice, and Fruit Flies**
Geoff Joslyn, Fred W. Wolf, Gerry Brush, Lianqun Wu, Marc Schuckit, and Raymond L. White
 Alcohol dependence is caused by the interaction of many individually weak genetic and environmental factors, making genes difficult to identify through human genome-wide association studies. Because many animals respond similarly to ethanol ingestion, we were able to perform a cross-species analysis. Comparative genetic analysis between mice and humans identified GPC5 as a gene that influences their ataxic response to ethanol. We then experimentally tested *Drosophila* strains carrying mutant alleles of the fly homologs of GPC5 and found alterations in their locomotor response to ethanol. As a genetic participant in ethanol response, GPC5 is a candidate alcohol dependence susceptibility gene.
- 637–645 **A Novel Retrotransposon Inserted in the Dominant *Vrn-B1* Allele Confers Spring Growth Habit in Tetraploid Wheat (*Triticum turgidum* L.)**
C.-G. Chu, C. T. Tan, G.-T. Yu, S. Zhong, S. S. Xu, and L. Yan
 Vernalization genes determine winter-spring growth habit of wheat. It was previously shown that allelic variation in the vernalization gene *VRN1* was due to deletions either in the promoter or the first intron. In this study, the authors report a novel dominant (*Vrn-B1*) allele of *VRN-B1* on chromosome 5B that has a 5.5 kb novel retrotransposon insertion in its promoter region. Sequence analysis shows that the retrotransposon has a low similarity to those found in wheat or other plant species. The retrotransposon in *Vrn-B1* functions similar to vernalization by inducing the transcription of *VRN-B1* and accelerating the flowering time of wheat plants.