

## ISSUE HIGHLIGHTS

**A mixed-model quantitative trait loci (QTL) analysis for multiple-environment trial data using environmental covariables for QTL-by-environment interactions, with an example in maize**, pp. 1801–1813

*Martin P. Boer, Deanne Wright, Lizhi Feng, Dean W. Podlich, Lang Luo, Mark Cooper and Fred A. van Eeuwijk*

Complex quantitative traits are the outcome of processes that depend on genotype and environment simultaneously. This article analyzes grain yield and grain moisture for 976 F<sub>2</sub> maize testcross progenies evaluated across 12 environments in the corn belt of the United States. The analysis was based on mixed models, incorporating both genotypic and environmental covariates. A majority of the detected QTLs showed significant QTL-by-environment interactions (QEI). Most QEI could be understood as a differential QTL expression conditional on longitude or year.

**Sex-specific splicing of the honeybee *doublesex* gene reveals 300 million years of evolution at the bottom of the insect sex-determination pathway**, pp. 1733–1741

*Soochin Cho, Zachary Y. Huang and Jianzhi Zhang*

In honeybees, sex is determined by the allelic composition of the complementary sex determination (*csd*) gene. However, the downstream genes of *csd* are unknown. The authors propose that the *doublesex* (*dsx*) gene, the most downstream gene in the *Drosophila* sex-determination cascade, is also a downstream gene of the honeybee sex-determination pathway. Here they demonstrate sex-specific alternative splicing of honeybee *dsx* and in doing so provide evidence for their hypothesis. These results reveal the conservation and modification of the bottom of the sex-determination pathway during 300 million years of holometabolous insect evolution.

**A ONECUT homeodomain protein communicates X chromosome dose to specify *Caenorhabditis elegans* sexual fate by repressing a sex switch gene**, pp. 1621–1637

*John M. Gladden and Barbara J. Meyer*

Sex is determined in *Caenorhabditis elegans* through a signal that communicates the number of X chromosomes relative to the number of autosomes. X chromosome number is relayed by the X signal elements (XSEs) that act cumulatively to repress the *xol-1* gene in XX animals, thereby inducing hermaphrodite fate. This article identifies a new XSE, the ONECUT homeodomain protein CEH-39, which acts as a dose-dependent repressor of *xol-1* transcript levels. Unexpectedly, other XSEs also repress *xol-1* predominantly, but not exclusively, at the transcript level. The twofold difference in X dose between XO and XX animals is translated into the male vs. hermaphrodite fate by the synergistic action of multiple, independent XSEs that render *xol-1* active or inactive, primarily through transcriptional regulation.

**Accelerated rate of gene gain and loss in primates**, pp. 1941–1949

*Matthew W. Hahn, Jeffery P. Demuth and Sang-Gook Han*

This article investigates the gain and loss of genes from the genomes of six fully sequenced mammals, including human, chimpanzee, and rhesus macaque. Evolution of many uniquely human characteristics appears to be accomplished via the addition of new genes rather than the modification of existing genes. Many of these differences are likely the product of natural selection, but go unnoticed in common analyses of nucleotide divergence between orthologous genes.

**The role of epistasis in the manifestation of heterosis: A systems-oriented approach**, pp. 1815–1825

*A. E. Melchinger, H. F. Utz, H.-P. Piepho, Z.-B. Zeng and C. C. Schön*

Heterosis is widely used in breeding, but the genetic basis of this biological phenomenon has not been elucidated. The authors

develop a generalized derivation to express heterosis as the sum of individual genetic effects for multiple QTL and all types of higher-order epistasis. They define a new type of heterotic effect denoted as augmented dominance effect, defined as the dominance effect at each QTL minus half the sum of additive × additive interactions with all other QTL. Genotypic expectations of genetic variances and QTL estimates obtained from testcrosses of recombinant inbred lines and composite-interval mapping are given.

**Genetic basis of heterosis for growth-related traits in *Arabidopsis* investigated by testcross progenies of near-isogenic lines reveals a significant role of epistasis**, pp. 1827–1837

*Albrecht E. Melchinger, Hans-Peter Piepho, H. Friedrich Utz, Jasmina Muminović, Thilo Wegenast, Otto Törjék, Thomas Altmann and Barbara Kusterer*

Investigations on the underlying causes of heterosis are hampered by its complex nature and the low power of detecting epistatic interactions among quantitative trait loci (QTL) in segregating populations. The authors studied heterosis in *Arabidopsis* hybrid C24 × Col-0 by testing near-isogenic lines and their triple testcross progenies. While the first approach revealed mostly overdominant QTL, the second approach allowed separation of dominance and epistasis and yielded substantial positive additive × additive effects and directional dominance. Positive epistatic effects reduced heterosis for growth-related traits in our materials.

**A mosaic genetic screen for *Drosophila* neoplastic tumor suppressor genes based on defective pupation**, pp. 1667–1677

*Laurent Menut, Thomas Vaccari, Heather Dionne, Joseph Hill, Geena Wu and David Bilder*

Mutations in *Drosophila* neoplastic tumor suppressor genes (TSGs) can model aspects of cancer in humans, but only a handful have been identified to date. This work describes an efficient screen to isolate new TSG mutations, using genetic mosaics in which eye imaginal discs are mutant in an otherwise wild-type larva. Surprisingly, while flies can live without eyes, the presence of overproliferating “tumorous” cells in the eye disc alone induces a robust block in metamorphosis. A genetic screen based on this phenotype identifies seven new neoplastic TSGs in the fly genome, opening the door to their molecular and genetic characterization.

**The role of Stn1p in *Saccharomyces cerevisiae* telomere capping can be separated from its interaction with Cdc13p**, pp. 1459–1474

*Ruben C. Petreaca, Huan-Chih Chiu and Constance I. Nugent*

The ends of linear chromosomes in budding yeast are thought to be protected by a three subunit protein complex consisting of Cdc13p, Stn1p, and Ten1p. It has been proposed that Cdc13p, a single-strand telomere binding protein, physically recruits Stn1p and Ten1p to chromosome ends. This article shows that the N-terminus of Stn1p, which interacts with Ten1p, but not the C-terminus, which interacts with Cdc13p, is sufficient to promote telomere capping and cell viability. The Stn1p–Cdc13p interaction contributes to telomere-length regulation.

**Extensive additivity of gene expression differentiates subspecies of the house mouse**, pp. 1553–1567

*Ruth Rottschmidt and Bettina Harr*

By crossing different subspecies of the house mouse and analyzing the expression levels of transcripts in F<sub>1</sub> hybrids relative to their parents, this article found evidence for pervasive within-locus additivity in gene expression in several tissues for most of the crosses analyzed. One cross, however, showed substantial nonadditivity in testis tissue, suggesting that this might be linked to hybrid sterility.