

Genetic influences on brain gene expression in rats selected for tameness and aggression, pp. 1277–1290

Henrike O. Heyne, Susann Lautenschläger, Ronald Nelson, François Besnier, Maxime Rotival, Alexander Cagan, Rimma Kozhemyakina, Irina Z. Plyusnina, Lyudmila Trut, Örjan Carlborg, Enrico Petretto, Leonid Kruglyak, Svante Pääbo, Torsten Schöneberg, and Frank W. Albert

For more than 64 generations, two lines of outbred rats have been selected for tameness or aggressiveness, and they now exhibit strikingly different behavior. Heyne *et al.* investigated the genetic basis of this difference by mapping eQTL affecting brain gene expression using a statistical approach that can identify QTL that have not reached fixation. By comparing the QTL affecting behavior with brain eQTL, the authors identified *Gltscr2*, *Lgi4*, *Zfp40* and *Slc17a7* as candidate genes.

Regulation of mitotic spindle disassembly by an environmental stress-sensing pathway in budding yeast, pp. 1043–1057

Adrienne Pigula, David G. Drubin, and Georjana Barnes

Microtubule-associated protein She1 promotes spindle disassembly, the timing of which is essential for coordinating mitotic exit with cytokinesis. Pigula *et al.* show that in budding yeast the stress-sensing HOG pathway is necessary for She1 localization to the anaphase spindle and for spindle disassembly, even in non-stress conditions.

Plasmid copy number underlies adaptive mutability in bacteria, pp. 919–933

Emiko Sano, Sophie Maisnier-Patin, John Paul Aboubechara, Semaury Quiñones-Soto, and John R. Roth

In the intensively-studied Cairns system, *E. coli* cells with a plasmid-borne leaky *lac* frameshift mutation are plated on lactose where they accumulate Lac⁺ revertant colonies above the non-growing lawn. Two opposing models explain the origin of these colonies: a) Mutagenesis induced by stress and b) Selection acting on pre-existing partial revertants. Sano *et al.* present evidence that all revertant colonies arise from pre-existing cells carrying multiple copies of the *lac* plasmid. They suggest that plasmid over-replication, rather than an increased mutation rate, leads to the observed revertants.

Msh4 and Msh5 function in SC-independent chiasma formation during the streamlined meiosis of *Tetrahymena*, pp. 983–993

Anura Shodhan, Agnieszka Lukaszewicz, Maria Novatchkova, and Josef Loidl

Crossing over occurs by two distinct pathways in animals, plants and fungi. One is linked to the presence of a synaptonemal complex (SC). Shodhan *et al.* show that components of this pathway function in the SC-less meiosis of the evolutionarily distant protist *Tetrahymena*. This simplified meiosis challenges the two-pathway paradigm and may reveal characteristics of the primordial meiotic process.

Hybrid incompatibility arises in a sequence-based bioenergetic model of transcription factor binding, pp. 1155–1166

Alexander Y. Tulchinsky, Norman A. Johnson, Ward B. Watt, and Adam H. Porter

Interspecies hybrids are often inviable or infertile because of incompatibility between interacting genes. To examine how incompatibility evolves at the molecular level, Tulchinsky *et al.* modeled gene expression as a function of binding energy between a transcription factor and DNA binding site. Under directional selection of gene expression, hybrid incompatibility evolved quickly, either due to non-recognition between transcription factor and binding site across species, or spurious binding. Under stabilizing selection, hybrid incompatibility evolved slowly, through compensatory mutations.

Novel distal eQTL analysis demonstrates effect of population genetic architecture on detecting and interpreting associations, pp. 879–893

Matthew Weiser, Sayan Mukherjee, and Terrence S. Furey

Standard eQTL mapping methods carry significant multiple testing burdens, limiting their ability to detect eQTL distal to the affected

gene. Weiser *et al.* describe a novel eQTL testing approach based on the pairwise conditional dependencies between genes' expression levels. They apply the method to data from yeast, mouse, and human, and identify thousands of novel eQTL. Genes implicated as distal eQTL were enriched for metabolism and biosynthesis annotations, suggesting they participate in feedback mechanisms.

Wild sex in zebrafish: loss of the natural sex determinant in domesticated strains, pp. 1291–1308

Catherine A. Wilson, Samantha K. High, Braedan M. McCluskey, Angel Amores, Yi-lin Yan, Tom A. Titus, Jennifer L. Anderson, Peter Batzel, Michael J. Carvan, Manfred Schartl, and John H. Postlethwait

Laboratory stocks of zebrafish have fluctuating sex ratios, but the sex determination mechanism in this important genetic model is unknown. Wilson *et al.* show that natural zebrafish populations have a single sex determining locus and a female-ZW/male-ZZ sex chromosome system. Unexpectedly, domesticated stocks lacked detectable sex-linked loci. These results suggest that key components of the sex determination system were lost during domestication, and variant mechanisms may have evolved or been unmasked over two decades of laboratory culture.

This Month's Perspective

Publication trends in model organism research, pp. 787–794

Michael R. Dietrich, Rachel A. Ankeny, and Patrick M. Chen

In 1990, the National Institutes of Health (NIH) gave some organisms special status as designated model organisms. This article documents publication trends for these NIH-designated model organisms over the past 40 years. The authors find that being designated a model organism by the NIH does not guarantee an increasing publication trend. An analysis of model and non-model organisms included in *GENETICS* since 1960 does reveal a sharp decline in the number of publications using non-model organisms yet no decline in the overall species diversity. They suggest that organisms with successful publication records tend to share critical characteristics, such as being well-developed as standardized, experimental systems and being used by well-organized communities with good networks of exchange and methods of communication.

This Month in the American Journal of Human Genetics

A selective sweep on a deleterious mutation in CPT1A in Arctic populations, *Am. J. Hum. Genet.* 95(5): 584–589

Florian J. Clemente, Alexia Cardona, Charlotte E. Inchley, Benjamin M. Peter, Guy Jacobs, Luca Pagani, Daniel J. Lawson, Tiago Antão, Mário Vicente, Mario Mitt, Michael DeGiorgio, Zuzana Faltyskova, Yali Xue, Qasim Ayub, Michal Szpak, Reedik Mägi, Anders Eriksson, Andrea Manica, Maanasa Raghavan, Morten Rasmussen, Simon Rasmussen, Eske Willerslev, Antonio Vidal-Puig, Chris Tyler-Smith, Richard Villems, Rasmus Nielsen, Mait Metspalu, Boris Malyarchuk, Miroslava Derenko, and Toomas Kivisild

As environmental factors change, adaptations that might have been previously advantageous can become harmful. In the study by Clemente *et al.*, a strong signal of selection is identified from whole genome sequencing of Northeastern Siberians residing in extremely cold regions where the traditional diet is high in fat. This variant in carnitine palmitoyltransferase 1A is also associated with hypoketotic hypoglycemia and sudden infant death syndrome, and the mutation decreases fatty acid oxidation and ketogenesis. This study suggests that this variant conferred a metabolic advantage when eating the traditional high-fat diet that has now become harmful as more carbohydrates are consumed.