The hermes transposon of *Musca domestica* is an efficient tool for the mutagenesis of *Schizosaccharomyces pombe*, pp. 2519–2523
Adam G. Evertts, Christopher Plymire, Nancy L. Craig and Henry L. Levin

Transposons are terrific mutagens for genetic analysis, but none are currently available for mutagenesis of the fission yeast *Schizosaccharomyces pombe*. The authors have corrected this deficiency by employing the hermes transposon of the housefly to mutagenize *S. pombe*. It efficiently disrupts genes and makes it easy to identify them, thus enhancing the awesome power of fission yeast genetics.

The tetrad-pollen model fails to explain the bias in Mendel’s pea (*Pisum sativum*) experiments, pp. 2531–2534
Daniel J. Fairbanks and G. Bruce Schaalje

The tetrad-pollen model is often used to explain why the numbers of types of pea progeny Mendel observed were so remarkably (some say suspiciously) close to what his laws predict they should be. It proposes that during self-pollination of a heterozygous pea plant, each flower’s stigma samples pollen without replacement from a limited, nonrandomly distributed population of pollen grains. This should result in a bias toward expected numbers of progeny. These authors experimentally tested the tetrad-pollen model in peas and found no evidence to support the supposition that it explains this bias toward expectation.

Inferring human population sizes, divergence times and rates of gene flow from mitochondrial, X and Y chromosome resequencing data, pp. 2193–2207
Daniel Garrigan, Sarah B. Kingan, Maya M. Pilkinson, Jason A. Wilder, Murray P. Cox, Hmla Soodyall, Beverly Strassmann, Giovanni Destro-Bisol, Peter de Knijff, Andrea Novelletto, Jonathan Friedlaender and Michael F. Hammer

Accurate inference of past human demographic parameters is important for analysis of human genetic variation. The isolation-with-migration model was used here to simultaneously infer divergence times, rates of gene flow, and changes in population size for 10 globally distributed human populations based on sequences of mitochondrial, X, and Y chromosomes. Several interesting insights emerge, including severe population bottlenecks in the history of non-African populations, widely varying population sizes and rates of growth, and older divergence between African populations than between non-African populations.

Investigating the genetic circuitry of Mastermind in Drosophila, a Notch signal effector, pp. 2493–2505
Mark W. Kankel, Gregory D. Hurbut, Geeta Upadhyay, Vijay Yajnik, Barry Vedovnick and Spyros Artavanis-Tsakonas

Notch signaling is a well-studied signal transduction pathway that continues to yield significant insights. With this study the authors more than doubled the number of genes known to interact with Notch, indicating that this well-known signaling pathway is more complex than previously thought. This article also reports that Mastermind, a nuclear component of the Notch transcription complex, has a conserved and novel Notch-independent role in the regulation of Wnt signaling.

Zinc regulates the stability of repetitive minisatellite DNA tracts during stationary phase, pp. 2469–2479
Maire K. Kelly, Peter A. Jauert, Linnea E. Jensen, Christine L. Chan, Chinh S. Truong and David T. Kirkpatrick

Minisatellite sequences are a major source of variation in most genomes. Where does this variation come from? This article reports a surprising link between metal ion homeostasis and minisatellite stability. The authors used a novel colony morphology assay to screen for mutations that affect the stability of minisatellite DNA sequences. They found that mutations that affect zinc ion homeostasis increase the frequency of minisatellite tract alterations, which occur during the stationary phase of growth. Only minisatellite tracts are affected by abnormal zinc levels; other repetitive DNA sequences are immune to defects in zinc ion homeostasis.

Multiple functions and dynamic activation of MPK-1 extracellular signal-regulated kinase signaling in *Caenorhabditis elegans* germline development, pp. 2039–2062
Min-Ho Lee, Mitsue Ohmachi, Swathi Arur, Sudhir Nayak, Ross Francis, Diane Church, Eric Lambie and Tim Schedl

MAP kinase signaling cascades play major roles in many important cellular and organismal processes. This comprehensive study of the ERK MAP kinase MPK-1 in *Caenorhabditis elegans* provides significant insight into this familiar class of signal transduction pathway, revealing that through control of multiple cell biological processes and regulatory switches MPK-1 is a central regulator of germline development, which coordinates contemporaneous processes and integrates sequential processes.

Genomic spatial correspondence between nonsynonymous divergence and neutral polymorphism reveals extensive adaptation in *Drosophila*, pp. 2083–2099
J. Michael Macpherson, Guy Sella, Jerel C. Davis and Dmitri A. Petrov

Adaptive evolution leaves a spatial signature in both molecular polymorphism and divergence data. This article describes new evidence of extensive adaptation in Drosophila revealed by comparisons of these signatures across the genomes of *Drosophila simulans* and *D. melanogaster*, with special attention paid to the spatial scale of the associations. Regions of high divergence exhibit both reduced polymorphism and heterogeneity in polymorphism on the spatial scale expected of adaptive evolution.

Differential nuclear localization does not determine the silencing status of *Saccharomyces cerevisiae* telomeres, pp. 2019–2029
Michelle A. Mondoux, Jillian G. Scaife and Virginia A. Zakian

Genes near chromosome telomeres are transcriptionally repressed, or silenced. Could this be because telomeres are localized at the nuclear periphery? In yeast, different telomeres have different patterns and mechanisms of perinuclear localization as well as different levels of silencing. These authors ask whether localization of a telomere to the nuclear periphery contributes to gene silencing. They report that a truncated and a native telomere with distinctly different silencing properties seems to be localized identically in the nucleus, suggesting that something else about the chromosomal context of genes near telomeres determines their sensitivity to silencing.

Evidence for different origins of sex chromosomes in closely related Oryzias fishes: Substitution of the master sex-determining gene, pp. 2075–2081
Keita Tanaka, Yusuke Takehana, Kiyoshi Naruse, Satoshi Hamaguchi and Mitsuru Sakaizumi

The sex-determining gene *DMY/dmr1bY* of medaka fish (*Oryzias latipes*), absent in many other fishes, arose by a recent duplication of the *DMR1* gene. The sex chromosome of *O. luzonensis* is orthologous to a medaka autosome and fully pseudoautosomal. Phylogenetic analysis suggests that the *O. luzonensis* sex-determining gene acquired its sex-determination function <5 MYA. This study may lead to the first direct evidence for the substitution of the sex-determining gene in vertebrates and further motivates study of medaka and its relatives as a model for vertebrate sex chromosome evolution.