

## IN BRIEF

**EVOLUTION****Orthologues undergo functional repurposing**

This paper presents a genetic interaction map of *Schizosaccharomyces pombe* and compares it with genetic interactions previously mapped in *Saccharomyces cerevisiae*. The authors found widespread conservation of interactions, but a subset of orthologous complexes seems to have different functions. They term this evolution of different partners or functional relationships ‘repurposing’ and link repurposing to important cellular processes, such as mitosis.

**ORIGINAL RESEARCH PAPER** Frost, A. *et al.* Functional repurposing revealed by comparing *S. pombe* and *S. cerevisiae* genetic interactions. *Cell* **149**, 1339–1352 (2012)

**MICROBIAL TRANSCRIPTOMICS****Features of virulence and non-coding RNAs**

To characterize the transcriptomic differences that may account for virulence further, Wurtzel *et al.* used high-throughput RNA sequencing to map the transcription start sites genome-wide of the pathogenic *Listeria monocytogenes* and non-pathogenic *Listeria innocua* bacteria. Focusing on non-coding RNAs, they characterized differences in expressed small RNAs and antisense RNAs between the species, including identifying >80 novel RNAs in *Listeria monocytogenes*. They also found unusual transcripts with long 5′ untranslated regions in both species that encroach into upstream genes in the opposite orientation and mediate downregulation of these neighbouring genes; these may be involved in a novel form of gene regulation.

**ORIGINAL RESEARCH PAPER** Wurtzel, O. *et al.* Comparative transcriptomics of pathogenic and non-pathogenic *Listeria* species. *Mol. Syst. Biol.* **8**, 583 (2012)

**GENOTYPING****Economical yet informative sequencing strategy**

Pasaniuc *et al.* simulated DNA sequencing on [1000 Genomes Project](#) data sets at different depths to determine whether low-depth sequencing could be an accurate and cost-effective alternative to array-based SNP genotyping in genome-wide association studies. They found that low-depth sequencing (at 0.1–0.5×) has comparable accuracy to high-resolution SNP arrays — a result confirmed by real low-depth exome sequencing data. At current costs, this sequencing approach was estimated to be six times cheaper than SNP arrays.

**ORIGINAL RESEARCH PAPER** Pasaniuc, B. *et al.* Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genet.* **44**, 631–635 (2012)

**GENOME EVOLUTION****Introgression and fixation of mimicry genes**

Sequencing the genome of *Heliconius melpomene* has enabled genome-scale analysis of introgression in *Heliconius*, which is a rapidly radiating genus of butterflies. This analysis has revealed a hybrid exchange of genes at genomic regions that control wing pattern mimicry, which is a protective mechanism whereby species mimic each others’ warning signals to warn off predators. The authors infer that closely related *Heliconius* species exchange protective colour pattern genes promiscuously and that hybridization can aid adaptation by transferring beneficial traits between species.

**ORIGINAL RESEARCH PAPER** The Heliconius Genome Consortium. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* 16 May 2012 (doi:10.1038/nature11041)