IN BRIEF

FUNCTIONAL GENOMICS

Large-scale mouse phenotyping

To aid the characterization of gene–phenotype relationships, de Angelis *et al.* developed and implemented statistical methods to optimize the design and analysis of multicentre, large-scale, broad-based phenotyping of mouse knockouts. The authors analysed data from over 27,000 mice with a total of 449 mutant alleles representing 320 unique genes, and found at least one deviant phenotype in 83% of mutant lines and more than one in 65% of lines. Notably, there were significantly more phenovariant lines among homozygotes than heterozygotes, and phenotypic effects were stronger in homozygotes. Finally, the authors identified new phenotypes for 87.9% of genes with previously unknown function and identified a large number of candidate disease-associated genes, demonstrating the value of broad-based phenotying on a large scale.

ORIGINAL RESEARCH PAPER de Angelis, M. H. *et al.* Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. *Nat. Genet.* http://dx.doi.org/10.1038/ng.3360 (2015)

PATHOGEN GENETICS

Sequencing of clinical bacterial isolates

Roach *et al.* performed prospective whole-genome sequencing of almost all bacterial isolates collected from a hospital's intensive care units over the course of a year: 12% of isolates that had been assigned a species-level classification via traditional microbiological methods were identified as novel genomospecies, on the basis of *de novo* genome assemblies. Interestingly, pangenome analysis revealed significant variation in pangenome size between species, reflecting differences in genome flexibility. Exploring the infection dynamics of individual patients, the authors detected a high incidence of co-infection with multiple strains of the same species (polyclonal infection). Analysis of clonal lineages across multiple patients suggested the inter-patient transmission of several opportunistic pathogens, including *Staphylococcus epidermidis* and *Pseudomonas aeruginosa*. This study demonstrates the value of routine genomic surveillance of bacterial isolates in providing useful information that has the potential to improve patient treatment and infection control practices.

ORIGINAL RESEARCH PAPER Roach, D. J. *et al.* A year of infection in the intensive care unit: prospective whole genome sequencing of bacterial clinical isolates reveals cryptic transmissions and novel microbiota. *PLoS Genet.* http://dx.doi.org/10.1371/journal.pgen.1005413 (2015)

POPULATION GENETICS

One founding population, or two?

Two new studies investigate the population history of native Americans, and come to differing conclusions. One study, published in *Science*, reports a single migration via Siberia <23,000 years ago for the founding population, with subsequent gene flow with East Asians and Australo-Melanesians. The second study, published in *Nature*, reports evidence for two founding populations, one of which had ancestry closely related to Australasians. The results from these studies add to the ongoing debate, and analysis of larger numbers of Amazonian genomes will probably be needed to piece together the complex demographic history.

ORIGINAL RESEARCH PAPERS Raghavan, M. *et al.* Genomic evidence for the Pleistocene and recent population history of Native Americans. *Science* http://www.dx.doi.org/10.1126/science.aab3884 (2015) | Skoglund, P. *et al.* Genetic evidence for two founding populations of the Americas. *Nature* http://www.dx.doi.org/10.1038/nature14895 (2015)