IN BRIEF

POPULATION GENOMICS

Population-scale sequencing in Iceland

The largest genome sequencing effort for a single population is reported in a focus issue of *Nature Genetics* (http://www.nature.com/ng/focus/icelanders/index.html). The research included whole-genome sequencing of 2,636 individuals from Iceland, as well as characterization of patterns of genetic variation, population structure, mutation rate and evolution. The authors also examined disease predisposition and identified loss-of-function variants in *ABCA7* that increase risk of Alzheimer's disease. Of note, Sulem *et al.* catalogued autosomal genes showing complete knockout from rare loss-of-function mutations. An accompanying Data Descriptor in *Scientific Data* details the data sets and resources available. Together, this work provides a valuable genomic resource and exemplifies the insights that can be obtained from population-scale sequencing.

ORIGINAL RESEARCH PAPERS Steinberg, S. *et al.* Loss-of-function variants in *ABCA7* confer risk of Alzheimer's disease. *Nature Genet.* http://www.dx.doi.org/10.1038/ng.3246 (2015) | Sulem, P. *et al.* Identification of a large set of rare complete human knockouts. *Nature Genet.* http://www.dx.doi.org/10.1038/ng.3243 (2015) | Helgason, A. *et al.* The Y-chromosome point mutation rate in humans. *Nature Genet.* http://www.dx.doi.org/10.1038/ng.3171 (2015) | Gudbjartsson, D. F. *et al.* Large-scale whole-genome sequencing of the Icelandic population. *Nature Genet.* http://www.dx.doi.org/10.1038/ng.3247 (2015) | Gudbjartsson, D. F. *et al.* Sequence variants from whole genome sequencing a large group of Icelanders. *Sci. Data* **2**, 150011 (2015)

COMPLEX TRAITS

Genetic discovery, heritability and prediction

Moser *et al.* report a new statistical method that is based on a hierarchical Bayesian mixture model (BayesR) for analysis of genome-wide association studies for human complex traits. Their method enables simultaneous discovery of variants associated with a complex trait, estimation of the total single-nucleotide polymorphism (SNP)-based genetic variance and polygenic risk prediction. BayesR is also used to characterize genetic architecture and partition the genetic variance across chromosomes. The authors tested their method in simulations and on case–control data sets for seven common diseases, finding that although a small proportion (<4%) of all SNPs contribute to a trait, a majority of these associated SNPs show a small effect, consistent with a polygenic model. The estimated genetic architecture varied considerably between traits, with type 1 diabetes and rheumatoid arthritis showing a greater proportion of the variance attributable to SNPs with larger effects, many of which are found in the major histocompatibility complex.

ORIGINAL RESEARCH PAPER Moser, G. *et al.* Simultaneous discovery, estimation and prediction analysis of complex traits using a Bayesian mixture model. *PLoS Genet.* **11**, e1004969 (2015)

MODEL ORGANISMS

100 *S. cerevisiae* genomes

Strope *et al.* present a new "100-genomes" strains resource for the model organism *Saccharomyces cerevisiae*. For a selected 93 strains, representing a diversity of geographical and environmental origins, the authors report whole-genome sequencing, *de novo* assembly and manual annotation to near-reference quality. Comparison of strains from human-associated environmental or clinical strains allowed the identification of genetic and phenotypic factors associated with clinical origins and the emergence of *S. cerevisiae* as an opportunistic pathogen.

ORIGINAL RESEARCH PAPER Strope, P. K. *et al.* The 100-genomes strains, an *S. cerevisiae* resource that illuminates its natural phenotypic and genotypic variation and emergence as an opportunistic pathogen. *Genome Res.* http://www.dx.doi.org/10.1101/gr.185538.114 (2015)