IN BRIEF

GENETIC TESTING

Clinical whole-genome sequencing

Taylor *et al.* consider the utility of whole-genome sequencing for diagnosis of genetic disorders in routine clinical practice as part of the WGS500 project to sequence the whole genomes of 500 patients. The authors examine whole-genome sequencing data from 217 individuals (including 156 independent cases or families) with a range of genetic disorders for which previous genetic screening had not identified any pathogenic variants. They demonstrate that whole-genome sequencing now allows the identification of at least one variant with a high level of evidence of pathogenicity in 21% of cases (33/156), with higher rates seen for Mendelian disorders (34%; 23/68) or family trios (57%; 8/14). The authors consider analysis strategies that improve the accuracy of variant calling and detection rates, and they review challenges in sequence interpretation and in establishing the pathogenicity of variants.

ORIGINAL RESEARCH PAPER Taylor, J. C. *et al.* Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. *Nat. Genet.* http://dx.doi.org/10.1038/ng.3304 (2015)

HUMAN EVOLUTION

Out-of-Africa migration routes

The migration route of modern humans out of Africa into Europe and Asia 50,000–100,000 years ago has remained an unresolved question, with conflicting historical, archaeological and genetic evidence for either a Northern (via Egypt and Sinai) or Southern (via Ethiopia and the Arabian Peninsula) route. Pagani *et al.* now provide support for a Northern migration route, based on analysis of the whole-genome sequences of 100 Egyptians and 125 Ethiopians. They further estimate the timing of the divergence of modern Eurasians from Egyptians and Ethiopians at 55,000 and 65,000 years ago, respectively.

ORIGINAL RESEARCH PAPER Pagani, L. *et al.* Tracing the route of modern humans out of Africa by using 225 human genome sequences from Ethiopians and Egyptians. *Am. J. Hum. Genet.* **96**, 986–991 (2015)

PATHOGEN GENETICS

Rapid typing of *S.* Enteritidis clinical isolates

Quick *et al.* demonstrate the benefits of rapidly available and accurate prospective typing results during the course of an outbreak of *Salmonella enterica* subsp. *enterica* serovar Enteritidis (S. Enteritidis) in Birmingham, United Kingdom, in June 2014. The authors obtained 43 S. Enteritidis isolates from hospital patients, community samples and the environment. They sequenced isolates from 16 patients using a new rapid draft sequencing protocol on an Illumina MiSeq platform that provides results within 6 hours. They used these data to reconstruct the history of the outbreak and identify transmission occurring between hospital wards, allowing for early implementation of control measures to prevent further spread. In addition, they sequenced two samples on the MinION platform (Oxford Nanopore Technologies), demonstrating real-time analysis of long reads and species classification within 20 minutes, as well as the use of phylogenetic placement for rapid serotyping and genotyping. In summary, this study demonstrates the potential of these two technologies for use during rapidly progressing outbreaks.

ORIGINAL RESEARCH PAPER Quick, J. *et al.* Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of *Salmonella*. *Genome Biol.* **16**,114 (2015)