

## IN BRIEF

**PATHOGEN GENETICS****Evolution of host-adapted pathogens**

Langridge *et al.* characterized the evolution of a single lineage of *Salmonella enterica* subsp. *enterica*, a primary cause of foodborne gastroenteritis. This lineage comprises closely related members that exhibit differential host range, including host generalists (*S. enterica* serovar Enteritidis), as well as host specialists (*S. Gallinarum* and *S. Dublin*, which infect galiforme birds and cattle, respectively). The authors sequenced the whole genomes of 60 *Salmonella* isolates, which were selected to represent a range of serovar, sequence and geographical diversity, and reconstructed the phylogeny and evolutionary history of this *Salmonella* lineage. They tracked the order of adaptive events and pseudogene formation that resulted in differentially host-adapted pathogens. In particular, they found a degradation of common metabolic pathways in members showing host restriction rather than generalism, and confirmed the functional impact of gene loss with phenotyping assays. They identified a new clade within *S. Enteritidis*, which was demonstrated to show intermediate levels of pathogenicity between ancestral *S. Enteritidis* and *S. Gallinarum* in an avian model of infection. The authors suggest that this represents an intermediate stage in the evolution of host adaptation.

**ORIGINAL RESEARCH PAPER** Langridge, G. C. *et al.* Patterns of genome evolution that have accompanied host adaptation in *Salmonella*. *Proc. Natl Acad. Sci. USA* **112**, 863–868 (2015)

**PLANT GENOMICS****Maize evolution and spread**

Genomic analysis of ancient crop samples provides opportunities to more precisely characterize the evolutionary history of plants and to connect this with patterns of human-assisted migration. Da Fonseca *et al.* sequenced DNA extracts from 32 archaeological maize samples dated from 700–6,000 years ago, from the Southwest of the United States and Mexico, as well as modern maize isolates. Their analyses resolve conflicting hypotheses from previous studies about the origin of maize in the Southwestern United States, providing support for initial dissemination following a highland route about 4,000 years ago, prior to gene flow with maize from the Pacific coast about 2,000 years ago.

**ORIGINAL RESEARCH PAPER** da Fonseca, R. R. *et al.* The origin and evolution of maize in the Southwestern United States. *Nature Plants* **1**, 14003 (2015)

**HUMAN EVOLUTION****mtDNA and genetic ancestry**

The inference of human genetic ancestry based on mitochondrial DNA (mtDNA) haplogroups has been known to be less reliable than that based on genome-wide single-nucleotide polymorphism (SNP) platforms, but the extent of this has not been well characterized. Emery *et al.* now provide a quantification of this in analyses of individuals with the same mtDNA haplogroup from worldwide populations, making use of data sets from the Human Genome Diversity Project and the 1000 Genomes Project. They find that although mtDNA haplogroup membership alone provides some ancestry information, it has limited ability to predict continental ancestry and geographical origin. The authors recommend that these limitations should be made clear to consumers of commercial lineage-based ancestry testing products.

**ORIGINAL RESEARCH PAPER** Emery, L.S. *et al.* Estimates of continental ancestry vary widely among individuals with the same mtDNA haplogroup. *Am. J. Hum. Genet.* **96**, 183–193 (2015)