

IN BRIEF

PLANT GENOMICS**The wild side of soybeans**

Domesticated crops often lose a great deal of genetic diversity over time, which makes them less able to adapt to novel conditions than their wild relatives. Now, Li *et al.* have sequenced the wild relatives of the soybean plant — one of the world's largest sources of vegetable oil and plant protein — and identified several genes associated with resistance to various abiotic and biotic stresses. Knowledge of these candidate genes can inform crop breeding programmes to create new varieties of soybeans that can survive in diverse environments. This study also provides further insights into the evolutionary divergence of domesticated and wild soybeans.

ORIGINAL RESEARCH PAPER Li, Y. H. *et al.* *De novo* assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. *Nature Biotech.* <http://dx.doi.org/10.1038/nbt.2979> (2014)

HUMAN EVOLUTION**Who do you think you are?**

A new study shows that modern Europeans have derived from three main populations rather than two as previously thought. Lazaridis *et al.* sequenced the genomes of several ancient humans from Germany, Luxembourg and Sweden, and compared them with the genomes of modern humans. The authors found that most but not all modern Europeans are descended from western European hunter-gatherers, ancient north Eurasians and early European farmers. This study provides insights into the evolutionary history of modern Europeans. Further work will determine when these three main groups converged to produce modern combinations of European alleles.

ORIGINAL RESEARCH PAPER Lazaridis, I. *et al.* Ancient human genomes suggest three ancestral populations for present-day Europeans. *Nature* <http://dx.doi.org/10.1038/nature13673> (2014)

TRANSLATION**To each their own — use of distinct tRNA pools**

Two distinct translation programmes exist for proliferation and differentiation, indicates a new study by Gringold *et al.* Using microarrays to measure the expression levels of tRNAs from differentiating or proliferating cells, the researchers show that the expression of pools of tRNAs expressed in either cellular state is mutually exclusive: tRNAs that are induced in proliferating cells are repressed in differentiating cells and vice versa. In addition, the tRNAs associated with each particular cell type carried anticodons that are part of a codon usage signature particular to proliferation or differentiation. These distinct translational programmes may have arisen to ensure stable cell fate decisions.

ORIGINAL RESEARCH PAPER Gringold, H. *et al.* A dual program for translation regulation in cellular proliferation and differentiation. *Cell* **158**, 1281–1292 (2014)

DEVELOPMENT**Daddy issues — paternal contribution in plants**

In contrast to mammals, in which maternal RNA and proteins drive early embryogenesis, the contribution of maternal and paternal genomes to early plant embryogenesis varies by gene, a new study has shown. Del Toro-De León *et al.* find that paternal genes are not activated in plant zygotes in a discrete step but rather show gradual activation. This latter finding reconciles conflicting reports regarding paternal gene contributions in plants.

ORIGINAL RESEARCH PAPER Del Toro-De León, G., García-Aguilar, M. & Gillmor, C. S. Non-equivalent contributions of maternal and paternal genomes to early plant embryogenesis. *Nature* <http://dx.doi.org/10.1038/nature13620> (2014)