

## IN BRIEF

**GENE REGULATION****Regulating transcription directionality**

Transcription often initiates divergently but it only proceeds in the sense direction. These authors, working in mouse embryonic stem cells, have elucidated a mechanism for regulating divergent transcription. They find that antisense transcripts are cleaved and polyadenylated shortly after initiation. This is due to asymmetric positioning of sequence elements: sense transcripts are depleted for polyadenylation sites and are enriched for binding sites for the U1 snRNP ribonucleoprotein. Depletion of the U1 snRNP led to promoter-proximal cleavage in the sense direction, indicating a regulatory role for this ribonucleoprotein.

**ORIGINAL RESEARCH PAPER** Almada, A. E. *et al.* Promoter directionality is controlled by U1 snRNP and polyadenylation signals. *Nature* <http://dx.doi.org/10.1038/nature12349> (2013)

**GWAS****Sexually dimorphic traits**

In this study the authors searched for sexually dimorphic genetic associations for human anthropomorphic traits — that is, associations that differ between men and women. They carried out a genome-wide association study (GWAS) meta-analysis of 270,000 individuals and found seven loci that show a sex difference in association. However, they found no loci for which there was an associated difference in directionality between men and women, as had been previously reported. Interestingly, the significant dimorphic loci that they did identify were only observed for waist size phenotypes, but not for height or body mass index phenotypes as might have been expected.

**ORIGINAL RESEARCH PAPER** Randall, J. C. *et al.* Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genet.* <http://dx.doi.org/10.1371/journal.pgen.1003500> (2013)

**GENOMICS****Sequencing historical plant pathogens**

The first complete pathogen genomes sequenced from historical herbarium (preserved plant) specimens are reported in this paper. The authors sequenced 11 herbarium samples of potato and tomato leaves infected with *Phytophthora infestans* (commonly known as potato blight) that were collected in the nineteenth century. The DNA obtained from the samples was of high quality and allowed genomic comparisons to be made between modern and historical strains to provide insights into the history of this important crop pathogen.

**ORIGINAL RESEARCH PAPER** Yoshida, K. *et al.* The rise and fall of the *Phytophthora infestans* lineage that triggered the Irish potato famine. *eLife* <http://dx.doi.org/10.7554/eLife.00731> (2013)

**EVOLUTION****A smooth path to C<sub>4</sub> photosynthesis**

C<sub>4</sub> photosynthesis is a CO<sub>2</sub>-concentrating mechanism that has evolved from conventional C<sub>3</sub> photosynthesis in various species, such as tropical plants. Heckmann *et al.* carried out theoretical modelling to characterize the fitness consequences of the various possible evolutionary paths to C<sub>4</sub> photosynthesis. They found that each step is typically accompanied by an incremental increase in fitness, thus showing how selective pressure can drive the stepwise assembly of complex biochemical systems.

**ORIGINAL RESEARCH PAPER** Heckmann, D. *et al.* Predicting C<sub>4</sub> photosynthesis evolution: modular, individually adaptive steps on a Mount Fuji fitness landscape. *Cell* **153**, 1579–1588 (2013)