IN BRIEF

PLANT GENETICS

Tunable plastic development

Plant development is highly plastic; that is, it can be extensively adjusted to different environments. These authors investigated whether the traits involved in this plasticity are controlled coordinately or independently. Specifically, they looked at plastic responses of *Arabidopsis thaliana* roots to two different nitrogen environments and used both genome-wide association mapping and gene expression analysis to identify the contributing genes. Their findings support the independent control of plastic traits, an insight that could be put to use in developing more robust crops.

ORIGINAL RESEARCH PAPER Gifford, M. L. *et al.* Plasticity regulators modulate specific root traits in discrete nitrogen environments. *PLoS Genet.* **9**, e1003760 (2013)

COMPLEX DISEASE

A SNP for disease prognosis

Genome-wide association studies (GWASs) have generally focused on susceptibility to disease, whereas the genetics of complex-disease progression and outcome has received little attention. Here, the authors use data from previous GWASs to identify a single-nucleotide polymorphism (SNP) in the forkhead box O3 gene (*FOXO3*) that is associated with the severity of, but not the susceptibility to, Crohn's disease, rheumatoid arthritis and malaria infection. This finding shows how new biological insights can be gained from re-analyses of GWAS data and has implications for predicting disease outcome and developing new therapies.

ORIGINAL RESEARCH PAPER Lee, J. C. *et al.* Human SNP links differential outcomes in inflammatory and infectious disease to a FOXO3-regulated pathway. *Cell* **155**, 57–69 (2013)

EVOLUTION

Interference follows duplication

One important source of genetic material for evolution is gene duplication followed by the partitioning of ancestral functions among the resulting paralogues. Using the duplication of a fungal transcriptional regulator as a case study, these authors showed — by reconstructing and testing the function of ancestral genes — that functional interference between paralogues occurs after gene duplication. Furthermore, this interference constrains subsequent evolution. Additional mutations were found to be required to minimize this interference and to lead to increased regulatory complexity.

ORIGINAL RESEARCH PAPER Baker, C.R., Hanson-Smith, V. & Johnson, A. D. Following gene duplication, paralog interference constrains transcriptional circuit evolution. *Science* **342**, 104–108 (2013)

CIRCADIAN BIOLOGY

MicroRNAs needed for time delay

The ~24-hour period of the circadian clock in mammals and other species requires a time delay that is built into a transcriptional negative feedback loop. The mechanisms of this time delay have been unclear, but these authors now provide evidence that microRNAs have an essential role. Using cells and mice that are deficient for the *Dicer* gene, they show that microRNAs generate a time delay by slowing down the translation of the period circadian clock 1 (PER1) and PER2 proteins, which are key components of the clock.

ORIGINAL RESEARCH PAPER Chen, R., D'Alessandro, M. & Lee, C. miRNAs are required for generating a time delay critical for the circadian oscillator. *Curr. Biol.* http://dx.doi.org/10.1016/j.cub.2013.08.005 (2013)