

## In full bloom

“A weed is a plant whose virtues have not yet been discovered.”

—Emerson

In March 2003, *Nature Genetics* published *A Ten-Year Retrospective*, a collection of review articles chronicling a decade of achievements from diverse genetic fields. Included among these was a solitary contribution devoted to plant genetics.

In an accompanying editorial, we remarked that *Nature Genetics* publishes fewer plant genetics papers than we would like. Indeed, in 2003, only four plant studies found their way into the pages of the journal, representing just 2% of all studies published during the year.

Given this history, you might be surprised to see that this issue boasts four contributions from the plant community. Frankly, the editors are a bit surprised too (though we suspect Mendel would have approved). So, what can human geneticists and otherwise zoologically minded researchers learn from their botanically inspired colleagues? The answer, it seems, is much.

On page 138 of this issue, Kiyotaka Nagaki and colleagues, through their work on rice chromosome 8, present the first complete sequence of a native centromere from a multicellular eukaryotic organism—a pioneering study that offers a welcome glimpse into these highly repetitive and heretofore intractable sequences aptly described by the authors as “the last frontiers of higher eukaryotic genomes”.

We are also pleased to present a trio of flowering papers from the *Arabidopsis* community, a hopeful reminder, of sorts, for readers in the Northern Hemisphere currently languishing in the dreags of winter. In the first of these, Hao Yu and colleagues (page 157) offer fresh insights into the genetic circuitry underlying the establishment of floral meristem identity. This new work illustrates how the transcription factors LEAFY and APETALA1 serve both activator and repressor roles during the

transition from vegetative to reproductive growth, promoting floral organ identity while simultaneously suppressing floral reversion to a ground state known as inflorescence. The logic of this system provides a general framework for understanding how cell fates are specified and stably maintained by transcriptional networks in the context of highly differentiated, multicellular organisms.

Studies from Israel Ausín *et al.* (page 162) and Hyoun-Joung Kim *et al.* (page 167) examine a new link between histone modifications and the regulation of both flowering time and cold response, discussed in an accompanying News and Views article by Richard Amasino (page 111). In the former study, Ausín and colleagues identified the product of the classical flowering time locus *FVE* as a retinoblastoma-associated protein that interacts with the histone deacetylation machinery to regulate the chromatin structure of the flowering repressor locus *FLC*. As this study reminds us, the use of epigenetic programming to regulate key developmental transitions is a universal theme in eukaryotic gene regulation, providing the incentive for productive cross-pollination between what might appear, at first glance, to be among the most disparate of model organisms.

The work by Kim and colleagues offers an additional perspective on *FVE* by showing that this same gene also regulates the physiological response of plants to cold temperatures. This study integrates concepts from the fields of physiology, development and gene regulation to address a topic of broad evolutionary significance. The underlying principles, as is often the case, transcend the organism.

Does this sudden eruption of plant papers mark a shift in the journal’s coverage of this historically rich field? It is too early to tell. We anticipate, however, that embracing a comparative view of nature’s two grand experiments in the evolution of multicellularity will continue to unveil shared logic and common themes. In the meantime, we hope you enjoy these latest seedlings from the plant community.