



Flower Power

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A promotional banner for Cellecta. On the left, the text reads "CRISPR and RNAi Genetic Screening. Your new superpower." in white. In the center is a white-bordered box with the text "LEARN MORE". On the right is a photograph of a woman wearing a red mask and a red cape, with the Cellecta logo (a green molecular structure) and the word "CELLECTA" below it.

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Flower Power

*Once in a golden hour
I cast to earth a seed.
Up there came a flower,
The people said, a weed.*

—Alfred Lord Tennyson (from *The Flower*)

Spring is in the air and plant genome research is blossoming. In celebration, this issue of *Genome Research* highlights several papers describing budding research in plant comparative genomics. In our cover article, Laitinen and colleagues (p. 475), demonstrate the utility of complementing studies in model plants, such as *Arabidopsis*, with those in species from different families of flowering plants. In this work, the functional annotation of a *Gerbera* EST database with nearly 17,000 sequences constructed from various tissues is described and compared with the genome sequence data currently available from other plant species, revealing over 1600 unique *Gerbera* sequences not identified elsewhere in the plant kingdom. Analysis of the *Gerbera* transcriptome by cDNA microarray, the first constructed in the *Asteraceae* family, identified several transcription factors specifically up-regulated in flowers, which suggests a role for them in flower organ development and differentiation.

Two related papers by Ayele and colleagues (p. 487) and Katari and colleagues (p. 496) illustrate that even finished and well-annotated genomes benefit from comparative sequence analysis from closely related species. Although this approach has proven useful in the comprehensive annotation of animal genomes, these studies represent the first large-scale effort to identify conserved genomic regions across species for the purpose of improving gene annotation in plants. Both demonstrate the value of light shotgun coverage of the *Brassica oleracea* genome—a close relative of *Arabidopsis thaliana*—in finding genes not identified by EST matching or ab initio prediction, and now that the seeds have been sown, they advocate for more complete

sequencing of *Brassica* to considerably improve the annotation of the *A. thaliana* genome.

Along with improved annotation, substantial insight into the molecular mechanisms of plant genome evolution—including a greater understanding of polyploidy—is expected to stem from comparative analyses. For example, Yogeewaran and colleagues (p. 505) construct a genetic map of *Arabidopsis lyrata* ssp. *lyrata*, compare it with its close relative, *A. thaliana*, and *Capsella*, which has an $n = 8$ genome, and suggest a number of major chromosomal rearrangements that must have occurred in the evolutionary history of *A. thaliana* to result in the reduction of its genome from eight chromosome pairs to five. In a comprehensive analysis of haplotype structure and evolution in a polyploid system, sequences at the leaf rust resistance loci *Lr10* of the wheat A genomes from diploid, tetraploid, and hexaploid wheat species is presented by Isidore and colleagues (p. 526). These comparisons confirm the ancient origin of two haplotypes, H1 and H2, at the *Lr10* locus and, surprisingly, reveal that they were stable during genome evolution and polyploidization, a finding expected to spur future studies on balancing selection and haplotype stability. And in one of just a few studies that graph molecular cytogenetics onto phylogenetic data, Lysak and colleagues (p. 516) use comparative chromosome painting, corroborated by phylogenetic reconstructions based on chloroplast sequence, to confirm a triplication event for a large chromosomal segment across most of the tribe *Brassicaceae*, suggesting that most members are ancient hexaploids. While further clarification of the conflicting data on karyotype evolution in this family is required, this study, and those above, affirm that the time is ripe for plant biologists to begin reaping the benefits of genomic resources coupled with comparative and phylogenetic analyses.

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