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Genome studies and molecular genetics

Genomics – deeper and wider in order to understanding plant diversity

Editorial overview

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In about a decade, plant genomics have evolved from the effort to sequence the *Arabidopsis* genome into an approach that could be used to study most questions with importance for plant biology. The reviews in this issue to *Current Opinion in Plant Biology* illustrate, in a broad sense, how genomics has helped molecular biologists not only to dig deeper into the biology of a species but also to go wider and apply the toolbox of genomics to new species and to address new problems. Several reviews address issues related to chromosomes and chromosome evolution. [Schubert](#) describes some of the evolutionary constraints on chromosomes and chromosome fusion, why species may have limited range in the number of chromosomes, and the important implications chromosomes could have for speciation. [Lamb et al.](#) describe our latest understanding of the structures of plant chromosomes from the centromeres, neocentromeres, to the telomeres. This understanding of chromosome structure is making it possible to start engineering artificial plant chromosomes. Sex chromosomes are a special case. Unlike animals, rather few plant species are dioecious, and out of those, only a few have specialized sex chromosomes. [Ming and Moore](#) review our understanding of the evolution of sex chromosomes, which is still only in its infancy. The sex chromosomes of plants have peculiarities, some apparently shared with animal systems, but the heterogeneity in patterns of recombination, gene loss and gene acquisition on plant sex chromosomes is remarkable.

Recombination is a central element in the ability of plants to evolve, and the review by [Li et al.](#) describes how the rules controlling recombination are being unraveled. For example, these rules determine how recombination deals with the repetitive nature of plants and the role played by homology. Finally, there are exciting prospects for gene targeting and homologous recombination in plants.

One of the areas where technical developments have fundamentally changed the way scientists generate data is expression profiling. Quantitative RT-PCR, microarrays including tiling arrays, and deep sequencing are increasingly important for expression profiling, as described in the review by [Busch and Lohman](#). Not only can the 'known' genes be profiled, but deep sequencing and tiling arrays have made it possible to identify novel transcripts in *Arabidopsis*. The need for each researcher to carry out expression profiling is also gradually decreasing as public expression profiling databases are developed and extended. [Zhang et al.](#) review some of technical issues involved in dealing with both genetic diversity and expression variation.

The father of systematics, Carl Linneus — whose 300th birthday we celebrate this year — used morphological characters to classify the plant species, without knowledge of genes and genomes. The majority of reviews in this issue address, in different ways, diversity within and between species using genomic techniques. Although diversity at the phenotype level has been exploited for over a century using genetics, the extent to which the genetic material varies within one species, but at the same time can be conserved between distant species, still astonishes scientists. The enormous complexity in the maize genome, described in the review by [Morgante *et al.*](#), must give nightmares to those that try to explain species as products of ‘intelligent design’; an colossal amount of genetic variation is continuously generated and then passed through the filter of selection, giving rise to allelic variants that can not be understood unless looked at in the light of evolution. Two other reviews also address how variation within species is analyzed. [Holland](#) reviews our current understanding of genetic architectures of plants, including the magnitude of quantitative trait loci (QTL) effects, their interactions with one another, and how these play a role in heterosis. The [Zhang](#) review provides additional insights in how new expression technologies can be used to partition the *cis* and *trans* components of gene regulatory mechanisms that are revealed by expression profiling and the mapping of expression QTL. Exciting new experiments are looking at the global interaction with methylation.

Trees present very some unique challenges to plant scientists. They usually have a genetic variation that exceeds the typical plant, and their very long generation times makes analyses of crossing populations, for example QTL studies, less useful as a standard tool. Instead, they are well suited for association studies, as they typically have much less of population structure owing to their large population sizes and outbreeding habit. This is described in the review by [Savolainen and Pyhäjärvi](#). Other types of variation can be detected if the genomes between closely related species are compared. [Schranz *et al.*](#) lay out the benefits and advantages in being able to contrast *Arabidopsis* genomics with the genomics of related species. This includes being able to identify critical non-coding sequences and find adaptations beyond those present in *Arabidopsis*. The review by [Bennetzen](#) describes the increasingly comprehensive, species-rich, and large-scale comparisons of genome structure that are possible within the grasses. Researchers are beginning to identify the functional outcomes of the many and various changes in genomic structure that have occurred in different grass lineages.

The genomes of the moss *Physcomitrella patens* and the green algae *Chlamydomonas reinhardtii* are currently being deciphered, and the reviews by [Quatrano *et al.*](#) and

[Grossmann *et al.*](#) give us a preview of what their full genome sequence might tell us. One rationale for choosing these organisms for genome sequencing is their unique properties as model systems, but their positions in the deeper branches of plant phylogeny also make it possible to retrieve information about the genomes of the last common ancestors shared by these species and higher plants, ancestors that lived many hundreds of millions year ago. *Chlamydomonas* metabolism can, according to [Grossman *et al.*](#), be better understood when the genome sequence is analyzed, and several surprising findings have been made regarding fermentation, selenoprotein function and vitamin biosynthesis. [Quatrano *et al.*](#) focus on how we can investigate whether gene regulation networks are conserved between mosses and higher plants. The ABA signaling system seems have a high degree of conservation, whereas the LFY regulatory network has apparently evolved in the higher plants lineage since the last common ancestor.

Now that the full genome sequence of several plants is available, efforts are being made to identify the ‘core’ genes that are shared by many plants, and then to see how different species have expanded this set of genes. [Sterck *et al.*](#) argue that the ancestral plant genome contained 12–14 000 genes, and that retention of genes after whole-genome duplications or smaller-scale duplications can be analyzed to provide information about the selection pressures that have created extant genomes.

Finally, not only the genomes of plants themselves needs to be studied to understand plant diversity. Micro-organisms that interact with plants can, in many cases, negatively influence plant growth and vigor. However, interactions that are of mutual benefit, like ectomycorrhizal, are of paramount importance for most plants. [Martin *et al.*](#) describe how the toolbox of genomics is being used both to seek ‘master symbiotic genes’ and to understand fine details about the signaling and metabolic interactions between the plants and fungi that form ectomycorrhizal symbioses.

Taken together, the reviews in this issue demonstrate how genomics is going both ‘deeper’, to help us understand the fine details in plant function, and ‘wider’, making it possible to study not only the most-studied model plants but also the whole complexity of plant species. Two hundred and fifty years ago, Carl Linneus could not have anticipated the extent to which we would be able to understand plant diversity: plant researchers of today might have problems anticipating where the scientific frontiers will be only a decade from now. Nevertheless, it is safe to say that between- and within-species differences will provide one major source of knowledge that will be exploited by genomics and molecular biology.