

Grasses. A Collective Model Genetic System

Since their domestication 10,000 years ago, the grasses have been of paramount importance to agriculture and human sustenance. This fact alone has been sufficient to make them the traditional focus of intensive scientific study. However, in this month's Special Issue, which is devoted entirely to the grasses, we offer a second reason for intensifying research efforts into the grasses—their emergence in recent years as a collective model genetic system that stands beside and complements *Arabidopsis*. This new role for the grasses has been fueled by several factors. These include the increased funding of research into the major cereals through the various plant genome initiatives, the accelerated sequencing of the complete rice (*Oryza sativa*) genome, the discovery of extensive synteny among the grasses, and the traditional and long-standing strength of the maize (*Zea mays*) genetics community. We hope that our readers, many of whose professional attentions have focussed primarily upon a single experimental organism, will be impressed by the many research articles in this issue in which the authors' navigation between related grass genomes has provided a powerful means of addressing fundamental questions in biology. Because rice, with its relatively simple genome, is the anchor species of this collective monocot genetic system, we have chosen Dorsett Trapnell's beautiful painting of rice cv Nipponbare to grace this month's cover.

Although rice is the major source of calories for more than one-half of the world's population, it is still not a major research organism in those areas of the world where most plant biologists reside. This situation is due, in part, to unwillingness by some government agencies to fund initiatives that focus on a crop plant that does not contribute to the local economy. Given the crucial nature of the rice genome sequence for research in all the grasses, two *Resources and Opportunities* articles are aimed at facilitating access to genomic resources and databases. Yuan et al. (pp. 1166–1174) describe the role of the International Rice Genome Sequencing Project in coordinating the multinational sequencing project. In addition to presenting the current status of this effort, they provide web links to the latest releases and to newly developed databases that integrate available sequence data from all grasses. In a second article, Barry (pp. 1164–1165) summarizes the rough draft sequence (representing approximately 85% of the rice genome) that was recently and laudably made public by Monsanto. It is estimated that the rice genome sequence will now be complete in 2004.

The idea that the grasses may be viewed as a single genetic system was first reviewed by Bennetzen and Freeling (1993). In this issue, Freeling (pp. 1191–1197) updates the reader about how the partial sequencing

of the rice genome as well as new mapping data have continued to build the case for extensive macro- and micro-synteny among the grasses. Freeling discusses how it should be possible to reduce any finely mapped character or quantitative trait locus to a nucleotide sequence, even in species with very large genomes. It is important that in many instances, these will be genes that could not be identified using the *Arabidopsis* sequence. Kellogg (pp. 1198–1205) similarly summarizes our current understanding of the evolutionary history of the grasses and how it too validates the idea of using grasses as a single genetic system.

Genomic mapping has fueled the comparative genetics approach that is proving so effective in understanding the basic biology of the grasses. However, fine mapping to less than 1 map unit will be required to convert traits and phenotypes into nucleotide sequences. For these reasons, many of the current grass genome projects involve the development of additional markers and tools for mapping and the generation of bacterial artificial chromosomes libraries and physical maps. For example, the utility of a comprehensive and integrated sorghum map to improve navigation between grass genomes is discussed by Draye et al. (pp. 1325–1341). Although the sorghum genome at 760 Mb is almost twice the size of the rice genome (430 Mb), this is still less than 30% of the 2,500-Mb maize genome. Because sorghum and maize are much closer relatives than rice and maize (approximately 24 million years ago versus 66 million years ago divergence, respectively), Draye et al. propose that the construction of a robust genetic map of sorghum will expedite gene identification and isolation in maize.

Another valuable and innovative mapping tool is the complete set of maize individual chromosome additions to the oat (*Avena sativa*) genome, which is reported by Kynast et al. (pp. 1216–1227) and employed by Okagaki et al. (pp. 1228–1235). These lines are especially useful in rapidly mapping maize sequences to a particular chromosome. Three other papers in this issue, namely Hirel et al. (pp. 1258–1270), Collins et al. (pp. 1236–1247), and Wang et al. (pp. 1271–1282), highlight how genetic maps are being used to identify genes involved in physiological and developmental processes.

Transposable elements have been important tools in the genetic and molecular dissection of plant genes underlying a variety of physiological and developmental processes. First discovered in maize by Barbara McClintock, transposable elements have in recent years been exploited for a number of functional genomics applications in plants. In this regard, one of the key features of certain maize elements that transpose through a DNA intermediate (class 2 elements)

is their propensity to insert into gene-rich regions rather than into intergenic DNA (primarily made up of retrotransposons in the large genome grasses). Complementing Pioneer Hibred's development of the first large Mu knockout collection in maize (Bensen et al., 1995), two large, publicly funded Mu-tagged collections in maize are currently under development. These collections are invaluable for both "reverse genetics"—(screen for insertions into known genes of interest), or "forward genetics"—(screen for desired mutant phenotypes) applications. In addition, publicly funded Ac-tagged collections are also being generated. Informational resources concerning the Mu and Ac collections and other Web sites of interest are available at www.agron.missouri.edu.

Because active class 2 elements have not been isolated from rice as yet, and because the importance of rice as a research tool has only recently been recognized, large rice knockout collections are not currently publicly available. In this issue, Greco et al. (pp. 1175–1177) summarize the progress of a consortium of rice researchers whose goal is the development of vectors and tagged populations based on the maize *Ac/Ds* system, which was shown previously to be active in rice. Although rice lacks endogenous active class 2 elements, Hirochika's research group has isolated several active retrotransposons (class 1). In this issue, Agrawal et al. (pp. 1248–1257) describe a forward genetics approach to clone a rice gene using an endogenous retrotransposon. Until such time that large knockout collections are available for rice, one of the primary strategies to determine the function of rice open reading frames will be the isolation of knockouts of maize orthologs using reverse genetics procedures.

In addition to their utility, transposable elements comprise the largest fraction of most grass genomes. The amplification of class 1 retrotransposons has been shown to be largely responsible for the huge difference in genome sizes of the grasses, thereby providing a molecular explanation for the "C-value paradox"—the huge differences in DNA content/haploid genome among the grasses. Dubcovsky et al. (pp. 1342–1353) extend these studies to the comparative analysis of colinear regions from barley (*Hordeum vulgare*) and rice where at least four genes reside.

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Because most of the sequence differences are restricted to transposons and introns, and because all of the identities are in coding exons, such intergeneric comparisons are an effective way to annotate grass genomes. The work of Vicient et al. (pp. 1283–1292) provides evidence that retrotransposons are active in many grass genomes. Lisch et al. (pp. 1293–1303) similarly report that elements related to *Mutator* in maize are potentially active in a wide variety of grasses. Finally, Feuillet et al. (pp. 1304–1313) use a combination of phylogenetic and genomic approaches to document the rapid genomic changes associated with polyploidization in wheat. Taken together, these studies add to a growing body of evidence that the grasses are in the midst of an extraordinary epic of genomic expansion, contraction, and rearrangement. As such, the grasses may be the best group of organisms in which to decipher the molecular mechanisms underlying the induction of genomic rearrangements and how this contributes to micro- and macro-evolutionary processes.

Although the primary emphasis of this Special Issue is to promote the grasses as a collective experimental system for basic research, we must not lose sight of the paramount importance of grasses to basic human welfare. Although most of the research presented here is largely basic and fundamental, it must be recognized that some of it may ultimately have tremendous potential consequences outside the ivory towers in which most of us exist. Ingo Potrykus' (pp. 1157–1161) personal account of the scientific and extra-scientific hurdles that he and his colleagues had to surmount before they could offer golden rice for free to the poor of the world underscores the need for scientists to be proactive and vocal in their support of the new molecular technologies.

LITERATURE CITED

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