Are We Growing Yet?

Welcome to our second issue of The Plant Genome. There are many signs that there is a growing interest in this journal. First and most important to the genomics community, The Plant Genome site experiences an impressive 700 visits per week. The open source electronic format offers our authors the broadest possible exposure to the scientific community. Second, in this issue, we feature seven contributed research articles, up from four in the previous issue. While this was not the doubling of submission growth that extreme optimists like me had hoped for, journal growth appears to be headed in the right direction based on the current article submission rate. Third, we are receiving articles on a diversity of agronomic and horticultural crops as well as the newest crop category—plants grown for the production of biomass to be converted into renewable fuels. And finally, we have received a few articles from authors outside the U.S., which suggests that the journal is being recognized internationally. These are all promising indicators of journal growth, but certainly it is too early to declare success and we remain committed to growing article submission. And so we ask you, to also assist us in promoting The Plant Genome to your colleagues by communicating through your scientific networks. Please share our promotional letter with your genomics colleagues. Extending awareness of The Plant Genome will increase journal growth rate and thereby provide greater readership of your articles.

The Model Crop
In this issue of The Plant Genome we are pleased to feature our first invited review article “The Rice Genome Research: Current Status and Future Perspectives” generously contributed by Bin Han and Qifa Zhang. As they describe, the rice genome was sequenced in 2005. This crop, which feeds nearly half of the world’s population, is a nearly ideal genomics model because of its compact genome and extensive germplasm resources including large mutant and insertional libraries, and its relative ease of transformation. However, as they state “there is still a huge gap of knowledge between the genotype and phenotype; a gap which must be bridged in order to breed elite varieties suitable for sustainable agriculture.” Towards closing the gap they propose the International Rice Functional Genomics Project (IRFGP) with the ultimate goals of determining the function of every gene in the rice genome by 2020, to identify functional diversity of alleles for agriculturally useful genes from the primary gene pool and to apply the findings of functional genomics research to rice crop genetic improvement and beyond.” Rice provides a model for approaching similar goals in crops with larger genomes and that are not quite as amenable to functional genomics research as rice or other models such as Arabidopsis. The ultimate question is how much the understanding of rice functional genomics from the IRFGP can serve as a framework to gain the same insights to closing the genotype to phenotype gap in the less tractable but equally important cereal genomes.

Paradigm Shifting
We all know that genomics is in an era of accelerating sequence data acquisition and analysis. Many of us remember when sequencing a single 2 or 3 kb of DNA was a major, costly undertaking including both lab work and data analysis. The establishment of sequencing centers accompanying the paradigm shift brought about by the automated sequencers made single gene and small genome sequencing easily feasible, resulting in the complete sequencing of the Arabidopsis and rice genomes in 2000 and 2005, respectively, and many other crops are following suit. More recently, we have experienced another jump in sequencing productivity from a new generation of sequencing technologies that dovetail nicely with standard sequencing, closing in on the NIH sponsored target of the $1000 genome. This revolution in
sequencing represents a reduction from $10.00 to a few cents per finished bp in less than 20 years (Service, 2006, Science 311:1544–1546). While this is incredible progress, there are indications that a next generation of technologies promise to cheaply sequencing multiple gigabase runs in just hours. Accompanied with the requisite data analysis advances, these technologies promise to again shift our genome sequencing paradigm making it feasible to sequence the large genomes of most crop plants rapidly and at low cost. Without promoting any particular technical approach or company involved in these next generation sequencing technologies, these advances are promised by 2010. It is a wonderful age to be a plant genomics researcher, …but are we ready for this next paradigm shift in sequencing?

The What If Challenge

Because it now seems likely that sequencing a crop genome for under $1000 will become a reality sooner than later, it is important that the plant genomics community is prepared to benefit. For our next issues of The Plant Genome, an open forum series of short “Vision” articles will be invited that address how ultra high throughput genome sequencing will impact plant breeding, functional genomics, systems biology, and related fields. To ensure that “The What if Challenge” reviews are not obsolesced due to further advances in sequencing technology before they are published, I am setting the costs of sequencing a typical crop genome at $1, three orders of magnitude lower than the $1000 target. This makes sequence capacity and acquisition unlimited. Authors will be “challenged” to forecast the impacts on crop improvement, biology, and how we will do research—all towards closing the gap in knowledge between the genotype and phenotype. For articles to be featured in the next issue, authors will be invited, but in the spirit of the open source world we are interested in a diversity of visions and opinions. If you are interested in submitting an article, please send your proposed topic to dsomers@crops.org.

Sincerely yours,
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