

## “The What if Challenge”

**W**ELCOME TO OUR first 2009 issue of *The Plant Genome*. There continue to be indications that there is a growing interest in our journal. *The Plant Genome* site experiences an impressive 631 visits per day. This “visit” rate is of utmost importance because it demonstrates that the open source electronic format offers our authors the broadest possible exposure to the scientific community. Like the previous issue, this issue features seven contributed research articles and the current article submission rate promises journal growth. In addition, we are now publishing 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 United States suggesting that the journal is being recognized internationally. Once again, these are all promising indicators of journal growth. Nevertheless, we continue to ask your help to assist us in promoting *The Plant Genome* to your colleagues by communicating through your scientific networks. As I said in my last editorial, extending awareness of *The Plant Genome* will increase journal growth rate and thereby provide greater readership of your articles.

Recall that in our last issue, I initiated “*The What If Challenge*” for genome sequencing! This was based on the realization that we have experienced a huge jump in sequencing productivity from a new generation of sequencing technologies that dovetail nicely with standard sequencing. Furthermore, there are indications that a next generation of technologies promise to cheaply sequence 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.

I am extremely pleased to feature our first open forum series of short invited “Vision” articles 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 were not obsolesced due to further advances in sequencing technology before they are published, I set the costs of sequencing a typical crop genome at \$1, making sequence capacity and acquisition unlimited. The authors were “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 the articles featured in this and the next few issues, 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 a response, please send your proposed topic to [dsomers@crops.org](mailto:dsomers@crops.org).

Please join me in thanking Christian Tobias, Takashi Matsumoto and Baltazar A. Antonio, and Jianming Yu for volunteering their visions of and insights into our future in plant genomics in the unlimited sequencing capacity era. Their articles follow.

Sincerely,  
David A. Somers  
Editor, *The Plant Genome*

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