

The Potential of Ultrahigh Throughput Genomic Technologies in Crop Improvement

THERE IS NO DOUBT this unlimited sequencing and genotyping capacity will significantly affect plant breeding, functional genomics, systems biology, and many other related fields. But its effect is probably analogous to that of the Internet, World Wide Web, Web browsing, and e-mail on globalization in the mid-1990s. In the book *The World is Flat*, author Thomas Friedman identified this “new” age of connectivity as one of 10 forces that flattened the world. Investment, or overinvestment, in sequencing and genotyping will likely drive the cost of these technologies down further, mirroring how fiber optics enabled virtually free data transmission. It is almost certain, however, that several other “flatteners” need to be in place for the final, grand-scale revolution in plant breeding.

A second flattener, methods of establishing genotype-phenotype relationship, requires further research. Continued efforts in fine-tuning available tools (e.g., mutational library, reverse genetics, QTL mapping, cloning and tagging, association mapping, comparative mapping, introgression library, etc.) and identifying new tools are warranted. Although more “-omics” will be added to our toolbox, we should never underestimate the complexity of biological processes for complex traits.

Essential genetic manipulation, physiological screening, and phenotyping processes that facilitate the breeding process, a third flattener, also need to be in place. Efficient protocols for double haploid and transformation do not exist for many crop species, and random mating cannot be conducted effectively in many self-pollinated crop species. Physiological screening methods for vari-

Using the knowledge between genotype and phenotype requires a fourth flattener, further breeding methodology research. Novel approaches of incorporating all these new tools into plant breeding practices need to encompass both science (e.g., genes, markers, marker assisted backcross, marker assisted recurrent selection, genome-wide selection, breeding value prediction, etc.) and art (e.g., generation, testing, germplasm, breeders’ knowledge, multiple traits, genotype × environment interaction, etc.).

A fifth flattener, training next-generation scientists in plant breeding, genetics, molecular biology, bioinformatics, quantitative genetics, population genetics, computer science, and even mathematicians for a world teeming with biological data requires that we focus more on the multidisciplinary nature of crop improvement. Hopefully, our efforts will not end with perfect tools but limited masters.

We may be very tempted to use the word “revolutionize” to describe the impact this ultrahigh-throughput technology on crop improvement; but remember, we have said it many times in the past—for isozyme, tissue culture, molecular markers, genetic engineering, genomics, and genome sequencing. Many flatteners must come together to transform the whole process of crop improvement. It would be safe to take a position as historians, to look back and declare the process after we are well into the post-revolution age, much like the way the official declaration of the current economic recession was made. Essentially, low-cost sequencing and genotyping is driven mostly by medical research, and we are along for the ride. To reach our goal with all flatteners in place, we will probably need to conduct further research of our own.

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