

Plant genomics in view of plant genetic resources – an introduction

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Abstract

Genetic resources form the basis of the new era of global food security. The food crises in many developing countries, reflected by food riots correlated with food prices, have been termed the Silent Tsunami. Plant genetic resources are clearly essential to food security for the future. Fortunately, genetic resources are generally considered a public good and shared internationally. Wild relatives of crop species and their derivatives represent the reservoir of genetic diversity that will help to meet the food demands of nine billion people by 2050. New technologies from genomics bolster conventional plant breeding for enhancing traits to meet these food demands. Genetic diversity is the lifeblood of traditional and modern plant breeding. The dramatic increase in the number of biotech crops reveals the value of new genetic resources. Genetic resources will provide a gateway to a new era of global food security. Although 7.4 million plant accessions are stored in 1750 germplasm banks around the world, only a small portion of the accessions has been used so far to produce commercial varieties. Our challenge is to find better ways to make more efficient use of gene bank materials for meeting food demands in the future.

Keywords: Genomics; variation; food security; gene banks; wide hybridization; sequencing; mutations

Borlaug legacy

Nobel Laureate Norman E. Borlaug certainly took advantage of plant genetic resources as he bred new varieties of wheat that are said to have saved the lives of perhaps one billion people via the Green Revolution (Vietmeyer, 2008, 2009, 2010, 2011). He used sources of stem rust resistance to stave off that devastating disease. His use of what became known as Shuttle Breeding using two breeding sites and selecting for superior yielding lines in each led to the development of photoperiod-insensitive lines that would give outstanding yields in a variety of environments such as Mexico, India and Pakistan. In addition, he utilized plant genetic resources that had genes to shorten and strengthen the wheat straw so that enhanced agronomic practices such as irrigation and fertilization would manifest in phenomenal increases in yield. This clearly illustrates that plant genetic resources are important for food security.

World population

World population has soared in recent human history. The current rate of growth is about one billion people added to this planet every 14 years. Ambassador Kenneth Quinn, President of the World Food Prize Foundation, said that ‘The last 50–60 years has been the single greatest period of food production and hunger reduction in all human history’ (pers. commun.). So, the question is whether we can sustain that history as we approach nine billion people by 2050.

Value of genetic resources

What is the value of genetic variation in crop breeding? Most studies reveal that 50% of the increase in crop productivity is due to genetic improvement. Genetic resources have played important roles – such as semi-dwarf wheat and rice. Agricultural productivity depends on genetic variation, and arguably, any additional knowledge of genetic variation is important in crop improvement. L. J. Stadler ushered in the era of induced mutations in plants 85 years

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ago (1928). The year 2013 is the 60-year anniversary since Watson and Crick (1953) have published on the structure of DNA and its mode of replication. Devos and Gale (2000) presented the comparative genomics of many grasses depicted by genome circles illustrating that information obtained for one species can be used to predict genes and gene locations in related species. These events and subsequent genomic techniques allow for the recognition and selection of useful genetic variation.

Applications

Early and continuing uses of genomics involve the employment of molecular markers to check purity, degree of inbreeding, and proof of patent infringement and many other applications. Additional exciting examples of the application of genomics now abound: (1) The International Rice Research Institute (IRRI) has bred at least ten megavarieties with the *submergence-1* gene using marker-assisted selection that allowed *sub-1* varieties to be developed in 2.5 years (Neeraja *et al.*, 2007). At least 100,000 farmers are now growing these varieties in flood-prone areas. (2) Pro-Vitamin A Golden Rice with the yellow carotenoid trait from maize is another exciting example in that it could save 500,000 children per year from going blind due to vitamin A deficiency (Potrykus, 2001). (3) Bt corn in the Philippines provides 40–60% higher yields than conventional varieties. Although the seed costs more, it still increases net income by about 34%. Food and feed are safer due to minimizing insect damage and lowering levels of harmful human carcinogens (Panopio and Mercado, 2011).

Genetic variation

We are learning that greater genetic diversity exists than ever before expected; for example, inbred lines of corn vary more from each other than humans differ from chimpanzees. Even more unexpected was the finding that many genes known in various lines are not present in the maize reference genome (B73). RNAseq on 500 inbreds revealed 8681 assembled transcripts that were not in the reference (Hansey *et al.*, 2012). The current concept is that there is a ‘pan genome’ comprising a ‘core genome’ and a ‘dispensable genome’. One can ask: ‘Are we selecting based on the dispensable genome? Does compensation by the dispensable genomes of two parents affect heterosis?’

Questions arising

Genomic information raises many other questions. We now know that copy number variation (CNV) is common in

crop genomes. Is the variation in some traits due to CNV? Soybean cyst nematode resistance appears to be due to ten copies of a sequence that increases the expression of a repeated multigene segment (Cook *et al.*, 2012). Having mutations in a variety of genes has always provided an important toolbox for genetic analysis. Today, there is an interest in having available a mutant for every gene; it is estimated that between 180,000 and 460,000 would be the number of mutant lines required in rice. There are currently about 200,000 mutant lines available for rice. Directed mutations are possible via zinc finger nucleases and Transcription Activator-Like Effector Nucleases and now by Clustered Regularly Interspaced Short Palindromic Repeats (Pennisi, 2013).

The first 50 plant genomes

DNA sequence data for more than 50 plant genomes have been published (Michael and Jackson, 2013). Even though 73% of these genomes are of crop species, still more data are necessary to assess the range of genetic resources that are available. Even partial genome assembly provides the basis for incorporating genomic information in breeding schemes.

Sequencing reference genomes and resequencing

The cost of sequencing a megabase of DNA is about \$0.10 today. In 2001, the cost was \$10,000. This allows extensive resequencing comparing against the reference genome. Phillips (2009) proposed to ‘sequence the entire rice germplasm collection of 100,000 accessions in the IRRI gene bank’. Since then, the IRRI and the Beijing Genome Institute (BGI) have sequenced 3000 rice lines. McCouch *et al.* (2012) discussed the role of genomics in assessing gene bank materials.

The relatively low cost of sequencing has led to the sequencing of multiple accessions of species. Varshney *et al.* (2013) sequenced the CDC Frontier variety of chickpea and resequenced 90 cultivated and wild genotypes. About 450 *Oryza rufipogon* accessions have been sequenced from different geographical regions (Huang *et al.*, 2012).

Molecular genetic markers

Single-nucleotide polymorphisms (SNPs) have been found to be extremely numerous. Based on 20 diverse varieties and landraces, McNally *et al.* (2009) reported 160,000 SNPs for rice. In chickpea, 76,000 SNPs were followed by Gaur *et al.* (2012). SNPs do not reveal all the variation. There are indels, inversions, translocations

and CNVs. Transposable elements allow forward and reverse genetics; some estimates indicate that there are perhaps a million tagged sites available in japonica rice.

Variation not present in the parents sometimes occurs in the progeny – termed *de novo* variation. Such variation can be from intragenic recombination, unequal crossing over, naturally occurring point mutations, transposable elements, DNA methylation, paramutation and gene amplification (Rasmusson and Phillips, 1997).

Wide hybridization followed by uniparental chromosome loss (Phillips and Rines, 2009) leads to the introgression of whole chromosomes or partial chromosomes (via irradiation of the addition lines). Every chromosome of maize has been introduced into oat by this approach. As oats is a C3 species and maize is a C4 species, the introduction of C4 characteristics into oat might be possible by this procedure (Kowles *et al.*, 2008; Tolley *et al.*, 2012).

Biotech crops

Individual genes or cassettes of genes can now be added to recipient varieties by genetic engineering (James, 2011). Biotech crops in which one or more important traits have been introduced via genetic engineering are now being grown on 700 million acres by seven million farmers. The acreage of biotech crops grown in developing countries has now surpassed that of crops grown in developed countries. This technology widens the range of available genetic resources.

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