

Genomics of plant genetic resources: a gateway to a new era of global food security

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This special issue focuses on how genomics of plant genetic resources (PGRs) provides key information and materials to meet the challenges that agriculture will face in the next few decades to meet the fast-growing demand for plant-derived products. Sessions at the 3rd International Symposium on Genomics of Plant Genetic Resources (GPGR3; www.GPGR3.com) held in Jeju, Korea, from 16 to 19 April 2013 covered topics including basic plant genome diversity and its applications. This meeting followed on the successful previous two editions in Beijing, China (2005), and in Bologna, Italy (2010). In this special issue, a total of 35 short review and research articles have been selected from the 312 oral and poster presentations during GPGR3.

The overall objective of GPGR3 was to present and discuss state-of-the-art genomics research and how to best use it to harness PGR diversity for global food security. In view of the recent food crises, PGRs are critical for fulfilling the future food, feed, fibre and fuel needs of an expanding population, as well as for addressing the challenges posed by climate change and depletion of natural resources, water, in particular. This collection of articles and the references cited therein highlight the increasing strategic role of plant genomics in the interrogation of germplasm collections to discover agronomically beneficial superior alleles for use in conventional breeding and, subsequently, to determine gene function. Below, we present a brief introduction on the impact of emerging next-generation sequencing (NGS) technologies applied

to diversity studies of PGRs and the importance of public–private partnerships (PPPs) for more effective management of PGRs and the release of improved cultivars.

Although various biotechnologies have been developed and/or applied to crop improvement, the supply of plant-derived products is still insufficient to meet the needs of a rapidly increasing population. Therefore, global food demand is projected to increase steadily until 2050, while crop productivity will be negatively affected because of the growing competition for land, water, fertilizers and energy and the negative effects of climate change, which will inevitably result in higher food prices (Godfray *et al.*, 2010; Chang and Hsu, 2011). The increasing demand for not only food but also for biofuels as renewable sources of energy has resulted in competition for crop resources of energy (Fargione *et al.*, 2008). Food security must be solved and is one of the urgent challenges, e.g. feeding the projected nine billion people (Gregory and George, 2011).

In view of the growing concern for food security and preservation of biodiversity, the concept of PGRs was first developed in 1993, and since then, PGRs have been considered to be important for gene discovery and cultivar release and for developing more sustainable agricultural practices (Hammer, 2003). Both domestication and modern plant breeding have greatly reduced the genetic diversity in major crops (Tanksley and McCouch, 1997; Hyten *et al.*, 2009). Thus, many efforts have been taken to preserve *ex situ* and *in situ* PGRs (Gepts, 2006; van Zonneveld *et al.*, 2014). In early studies, genetic diversity was investigated based on the characterization of plant morphology, yield, quality and other simple phenotypic features (Gilbert *et al.*, 1999; Hoisington *et al.*, 1999).

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More recently, the development of NGS technologies has allowed for the massive production of whole-genome/transcriptome sequence data, which in turn enables a more in-depth exploration of PGR diversity while allowing to develop novel molecular markers and identify agronomically important loci (Edwards and Batley, 2010; Tuberosa *et al.*, 2014).

Recently, several NGS platforms including GS-FLX and Illumina HiSeq have been developed using which large amounts of sequence data can be produced in a relatively short period of time for either *de novo* assembly or resequencing (Van *et al.*, 2014). Whole-genome sequencing has been widely used in plant and animal species for the characterization of DNA sequence variations including the detection of single-nucleotide polymorphisms (SNPs). Genome-wide SNP genotyping can be implemented for association mapping and evolutionary analyses (Akhunov *et al.*, 2009; Varshney *et al.*, 2009; Waugh *et al.*, 2009). Evolutionary studies in wild species when compared with those in modern cultivars will be helpful in terms of crop improvement. e.g. to determine structural variations in chromosomes as such variation can be a driving force in plant evolution, thus allowing for the discovery of new genes and valuable traits (Barabaschi *et al.*, 2012). As we approach third-generation sequencing (Rusk, 2009), NGS technologies are powerful tools that can be used to conduct multiplexed genotyping and to develop genome-wide markers. These applications of NGS provide an important vehicle to the gateway to the new era of global food security (Gupta *et al.*, 2008).

Another major issue with regard to the more effective utilization of PGRs to meet the challenges posed by food security is related to our capacity to forge strong PPPs to create additional research opportunities, particularly in the area of translational genomics aiming to release improved cultivars (Varshney and Tuberosa, 2013; Baenziger *et al.*, 2014), including interactive forums and international research projects. Along this line, the purpose of the wrap-up session of GPGR3 was to inform on the opportunities offered by PPPs and discuss strategies on how to strengthen them and make them more effective.

The presentations addressing the first topic provided evidence that each PPP research project has its own peculiarities and can offer new and exciting opportunities to achieve win-win outcomes. To deal with global challenges, innovation is essential, especially through outward collaboration to develop new ways of thinking and seek better solutions. Valuable information, new platforms and strategies, and creative out-of-the-box ideas can be generated by properly putting together the puzzle pieces contributed by the different stakeholders from academia, governmental research centres, germplasm banks and seed companies. Notably, it has been reported that spontaneous collaborations outside

of established grant schemes are often successful. More in general, it has been observed that successful PPPs require that all partners be on the same level and provide complementary skills and expertise.

As to the second topic, i.e. international collaboration and sharing of PGRs and databases, international collaborations between the International Atomic Energy Agency (IAEA), Leibniz Institute of Plant Genetics and Crop Plant Research, and Federal University of Pelotas in Brazil were discussed. The IAEA is currently expanding collaboration in science, research and innovation for food security, food safety and sustainable agriculture. The intention is to conduct joint research projects, share knowledge and encourage staff to increase food system resilience, to promote the improved and sustainable utilization of agricultural and natural resources, and to enhance member states' capabilities in the application of nuclear techniques. Furthermore, international collaboration in terms of information sharing in support of scientific research is very important. Currently, genomic information on biological species is publicly available through genebanks (1750 genebanks worldwide including an estimated 7.4 million accessions). Therefore, within the PGR framework, extensive international collaboration is needed for sharing and characterizing mapping populations, core collections, TILLING populations and introgression libraries (Bovina *et al.*, 2011; Frison and Demers, 2014; Grandillo, 2014).

With the availability of whole-genome sequences in many crop species including, among others, rice (Goff *et al.*, 2002; Yu *et al.*, 2002), soybean (Schmutz *et al.*, 2010), pigeonpea (Varshney *et al.*, 2011), corn (Schnable *et al.*, 2009) and, hopefully soon, also wheat (Choulet *et al.*, 2014), crop improvement will be accelerated by means of genomics-assisted strategies aimed at more effectively harnessing allelic diversity based on sequence information (Moose and Mumm, 2008) and a better understanding of gene function (Harrison, 2012). This special issue offers a glimpse on how genomics can assist in the characterization of PGRs to (1) identify beneficial alleles the manipulation of which through marker-assisted selection and/or genetic engineering will be crucial for helping secure the future well-being of mankind while reducing the impact of agricultural practices on the environment and (2) optimize the collection, management and conservation of natural and artificially induced plant biodiversity.

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