

Application of Genomics to Enhance Utilisation of Plant Genetic Resources

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Genomics may greatly enhance utilisation of plant genetic resources (Brozynska *et al.*, 2016). This is especially critical with the prospects of major climate change (Aberton *et al.*, 2016). New cereal genotypes are needed to deliver desirable nutritional and functional characteristics in the environments of the future (Henry *et al.*, 2016). Analysis of wild and domesticated genetic resources may identify new sources of genetic variation for breeding. Genomic analysis of cereal (especially rice and wheat) genetic resources may contribute significantly to global food security. Whole genome sequencing and transcriptome sequencing can contribute to discovery of valuable new genes and alleles. Utilizing plant genetic resources requires analysis of large amounts of genomic data (Rossetto and Henry, 2014).

Rice

Sequencing of the genomes of wild rice (*Oryza*) populations has revealed new ancestral populations that widen the effective genepool of rice for breeding. These newly identified genetic resources will provide a new source of diversity for use in breeding for disease resistance and tolerance to climate change in rice. These resources and genomics tools facilitate the development of rice genotypes to satisfy the quality requirements of increasingly discerning rice consumers (Anacleto *et al.*, 2015).

The AA genome primary genepool of rice

The primary genepool of rice includes the wild *Oryza* species with AA genomes that are inter-fertile with domesticated rice. Analysis of the whole chloroplast genome of these species has been used to define their evolutionary relationships (Wambugu *et al.*, 2015). Diverse grain quality attributes may be found in this genepool (Wang *et al.*, 2015). This genepool also provides a source of biotic and abiotic stress tolerance genes for current and future environments.

New sources of genetic diversity for rice

Recent research has identified large poorly characterised populations of *Oryza* in northern Australia (Brozynska

et al., 2014). Phylogenetic analysis of the AA genome taxa indicates that they are sister groups to the clade including domesticated taxa suggesting that this region may be an important centre of diversity for rice. Reference genome sequences for these taxa have been produced recently as a tool to facilitate analysis of diversity in these wild populations.

Wheat

Sequencing of the transcriptome of developing seeds of diverse wheat germplasm has revealed genetic diversity that explains differences in carbon assimilation (Rangan *et al.*, 2016), flour yield in milling and bread quality on baking (Furtado *et al.*, 2015). Together these gene discoveries offer a significant opportunity to accelerate the rate of genetic gain in wheat breeding.

Carbon assimilation

Photosynthesis in the pericarp of wheat proceeds by a C₄ pathway. Genetic variation in grain photosynthesis by this recently defined pathway (Rangan *et al.*, 2016) may explain differences in yield due to re-fixation of carbon respired to support protein and starch biosynthesis during endosperm formation. Selection for enhanced photosynthesis in the grain may result in higher yields in environments limited by harsh conditions during late grain filling. The influence of heat stress on expression of this pathway and variation within the wheat genepool is being studied.

Flour yield

The yield of flour obtained when wheat is milled is controlled by genes that have been identified by analysis of levels of expression in wheat genotypes differing in flour yield. This discovery will avoid the need to have large amounts of grain to assess flour milling performance and provide tools for early generation selection.

Breadmaking quality

A highly differentially expressed gene encoding a small sulphur rich protein in wheat endosperm may explain differences in the breadmaking qualities of wheat

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(Furtado *et al.*, 2015). However, this gene may not be important for products such as chapatti. Knowledge of this gene may allow the development of wheat genotypes with acceptable end use quality at much lower grain protein contents improving the nitrogen use efficiency of the crop. The combination of selection for flour yield and bread quality will ensure wheat genotypes can be selected with acceptable grain quality. A modest number of genetic loci may require selection to ensure wheat breeding delivers acceptable end use quality allowing more selection pressure for grain yield.

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