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Unlocking Genetic Variation Stored in Gene Banks for the Benefit of Resource-Poor Farmers

MATTHIAS WISSUWA

Japan International Research Center for Agricultural Sciences (JIRCAS), Crop, Livestock and Environment Division, Japan

Abstract

Over the past two decades, molecular approaches in crop science have moved from basic research to applications in plant breeding, plant pathology or food chemistry. In breeding these applications have typically developed out of QTL mapping approaches that fine-mapped loci or cloned candidate genes controlling the trait of interest, which allowed for the development of molecular markers for use in marker assisted selection (MAS). To date the improvement of flooding tolerance of popular rice varieties through MAS for the *sub1* gene is one of the most successful examples of molecular approaches being used for development.

Rapid advances in genome sequencing technologies that have driven down costs to a level where representative sub-sets of crops stored in gene bank collections can now be sequenced promises to provide a new boost for molecular breeding efforts. In rice 3000 gene bank accessions have been sequenced and the data made publicly available through the SNP-Seek website hosted by the International Rice Research Institute (IRRI). Seeds of these sequenced rice accessions are also publicly available and are being phenotyped under a number of environments and stresses. Own work is currently evaluating genotypic variation for nutrient efficiency and grain yield under low-input conditions in Madagascar, as practised by the predominantly resource-poor farmers there. Through genome-wide association studies (GWAS) and allele mining within SNP-Seek, rare alleles ‘hidden’ in gene banks are now being identified as enhancing nutrient efficiency. Carriers of such rare but useful alleles are often traditional varieties developed by farmer-breeders under low-input conditions. After further confirmation of allele effects in subsequent candidate gene studies, the objective will be to introgress such alleles into modern rice varieties through MAS, using traditional varieties as donors. Thus, advances in molecular approaches have provided new impetus for the utilisation of genetic resources present in gene banks.

Keywords: Gene banks, genome sequencing