

Genomic selection in rice: lessons learned from a large set of proof-of-concept studies embedded in current breeding programs

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The increase in rice production needed to meet future demand requires renewed cropping systems and rice varieties with enhanced resources use efficiency and adaptation to environmental stresses in the context of climate change. Genomic selection (GS) has the potential to accelerate the development of such varieties. We present an overview of the proof-of-concept studies conducted during the last decade with the aim of providing rice breeders with tailored GS methods and tools. These studies involved complementary breeding programs (pedigree breeding, population improvement, etc.), mobilising different compartments of rice genetic diversity (*indica*, tropical and temperate *japonica*), and targeting a wide range of traits (yield potential, nitrogen use efficiency, adaptation to alternate watering and drying, salinity tolerance, drought tolerance, exclusion of heavy metals, outcrossing and hybrid seed production abilities, etc.). The objective was to evaluate the importance of different factors known to influence the accuracy of genomic prediction: marker density, linkage disequilibrium, trait heritability and genetic architecture, characteristics of the training population, relatedness between training and candidate populations, statistical models, etc.). Our results showed notably that GS can accelerate genetic gain in both pedigree and population breeding schemes by increasing selection intensity and by shortening the selection cycle. Rice diversity panels provide accurate genomic predictions for complex traits in the progenies of biparental crosses involving members of the panel. Genomic prediction accounting for genotype-by-environment interactions offers an effective framework for breeding simultaneously for adaptation to an abiotic stress and for performance under normal cropping conditions. The degree of relatedness between the training and the candidate population matter more than the size of the training set per se. Whatever the genetic background of the training and the candidate populations (and the associated linkage disequilibrium), average marker density of more than one SNP every 20 kb does not improve prediction accuracy. Further simulation studies are needed to assess the impact of GS on long-term genetic gain and diversity, to adjust the GS strategy accordingly. In the light of these results, we propose a strategy for embedding international rice gene discovery and ecophysiological ideotype modeling research in a GS based rice breeding program.