GS-RUSE

Genomic selection for resource use efficiency in rice

ABSTRACT

Recently, the conjunction of access to very large number of molecular markers and the emergence of new statistical approaches has shifted the paradigm of animal & plant breeding for complex traits from "breeding by design", based on knowledge of specific functional polymorphism, to a "genome wide" approach, predicting genetic values, without prior hypotheses on causal relationships between markers and target traits, with enough accuracy to allow selection on that prediction alone. Complementary research are needed to harness the potential of this new paradigm to accelerate genetic gains.

Keywords : Drought, Conservation, Operation, Genomics, Plant, Modelling, Selection, Rice

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Project leader's institution : CIRAD
Project leader's RU : AGAP

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Funding : Labex

GOAL

The GS-Ruse project aims at contributing to tackle some of the conceptual issues of genomic selection (GS) in plants and at providing rice breeders with tailored methods and tools for the integration of GS approach in their breeding strategies. GS-Ruse research strategy is based on methodological development and proof of concept of GS within three breeding programs of complementary agro-socio-economic stakes and genetic futures. As the ultimate goal of the GS-Ruse project is to contribute to ecological intensification of rice production systems, we also take interest in agronomic and/or economical drivers of the target traits of these breeding programs, to promote system-level options of sustainable rice cropping.

RESULTS

GS can accelerate genetic gain in both pedigree and population rice 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. On the other hand, selection of SNP on the base of the degree of their linkage with the target trait, i.e. results of association analysis,

enhance significantly the predictive ability of genomic predictions. The key message is that, rice breeding programs based on pedigree schemes can use a genomic model trained with data from their working collection to predict performances of progenies produced through rapid generation advancement.

Results also include :

- R package "breedgenr", a simulation tool dedicated to meet breeder's needs to rationalize the different steps of a breeding scheme.
- R package "KRAM" for the implementation of a large set of genomic prediction methods;
- A multi-objective agro-economical model to explore economic and water saving results of different water management options.

PERSPECTIVES

In the light of our results, we have proposed a strategy to embed the international rice gene discovery and ecophysiological ideotype modeling research in a GS based rice breeding program.
- Further simulation studies are planned in relation with IRRI and CIAT to assess the impact of GS on long-term genetic gain and diversity, to adjust the GS strategy accordingly.