

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Breeding Simulation
Keyword 2	: Breeding Strategy
Keyword 3	: Genomic selection
Title of Entry	: breedgenr: a non-parametric based breeding program simulator with applications in rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: For crop breeding programs to be able to effectively harness the genetic gains expected from the integration of genomic resources, high throughput phenotyping capabilities, and efficient statistical methods to model the complexity of empirical data requires adjustments of breeding strategies. Tools that simulate breeding features are thus needed to explore the effects of such adjustments and their potential interactions. Simulations are useful because they allow rapid replicated testing of a wide range of hypotheses at low cost, for example, the initial feasibility of genomic selection or the impact of the structure of the reference population. Simulating breeding strategies is well suited to investigate the long-term effects of selection, which is often not feasible using real experiments due to time and cost requirements. Different tools have been proposed to reflect the complexity of the studied population (genome structure, genetic architecture of the traits, and relatedness among individuals). However, few are specifically designed to simulate breeding strategies in crop species. We therefore developed breedgenr, a simulation tool dedicated to meet breeder's needs to rationalize the different steps of a breeding scheme and integrate new approaches such as genomic selection. breedgenr is an R package that has two distinctive features compared to existing tools. First, breedgenr uses real genotypic and phenotypic data from breeding programs to generate the reference population. Thus, it limits the number of possible hypotheses and scenarios regarding the evolutionary history and the structure of the breeding populations. Second breedgenr is based on non-parametric approaches to calibrate the genotype-phenotype relationship. Consequently, it does not rely on specific assumptions regarding the genetic model and the genetic architecture of the phenotypic traits considered. The robustness and functionality of breedgenr were evaluated using real datasets of

rice and different breeding schemes. The objective was to design breeding schemes that integrate different genomic selection scenarios. The results confirmed the robustness of the calibration of genotype-phenotype relationships based on non-parametric methods, and the capability of breedgenr to simulate breeding populations and different breeding schemes: pedigree breeding and recurrent selection. Further validation of the robustness of breedgenr and adjustment-expansion of its functionalities are presented.

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