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## P0778: Genomic Selection for Water Use Efficiency in japonica Rice and Evaluation of Different Parameters Implicated on the Accuracy Level

### POSTER

Conjunction of high-throughput marker technologies and new statistical methods has recently given birth to a new breeding strategy called genomic selection (GS). The method use genome-wide dense marker genotyping for the prediction of genetic values (GEBV) with enough accuracy to allow selection based on GEBV alone. We present here GS for water use efficiency in rice, in the framework of a pedigree breeding scheme. The training population (TP) was composed of 284 accessions belonging to temperate and tropical japonica rice groups. The candidate population (CP) was composed of 99 F5-F7 lines derived from 36 crosses involving 32 accessions of TP. The two populations were genotyped with an average marker density of 4.8 per kb, with MAF 2.5%. Phenotypic traits considered included flowering time (FL), grain yield (GY) and nitrogen balance index (NI) under conventional irrigation (CI) and aerobic system (AS). Phenotypes were modeled using two statistical regression methods: genomic best linear unbiased prediction (GBLUP) and reproducing kernel Hilbert Space (RKHS). The models were tested with three incidence matrixes corresponding to densities of 4.8, 9.5 and 13.8 marker per kb, and to linkage disequilibrium (LD) thresholds of  $r^2 \leq 1$ ,  $r^2 < 0.98$  and  $r^2 < 0.81$  to investigate effect of the method and level of LD. Results of interpopulation prediction in rice breeding provided accuracies of GEBV prediction reasonably high for GY (0.41; Sd=0.03) and for NI (0.36; Sd=0.04), low for FL (0.26; Sd = 0.07), that need to be optimized by exploring potential effect of population structure within both TP and CP.

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