

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Genomic selection
Keyword 2	: Marker-assisted selection
Keyword 3	: Genomics-assisted breeding
Title of Entry	: 1K-RiCA (1K SNPs - Rice Custom Amplicon) a novel genotyping amplicon-based assay for genetics and breeding applications in rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Genomic selection (GS) using high-density SNPs data sets is promising to improve response to selection in rice breeding programs. However high-density SNP genotyping of all selection candidates each generation may not be cost effective. One way to reduce the routine cost in large number of lines in breeding programs is to genotype with a SNP panel of reduced density without drastically sacrificing accuracies. With this in mind we developed a low-density amplicon-based assay of 995 SNPs uniformly distributed across the rice genome (~1 marker every 1.53 cM), designed to be highly informative in populations derived from crosses with indica rice. An initial test using 700 rice samples showed an average SNP call rate of 95%. The SNP assay precision measured on 38 highly replicated accessions was of 99.7%. The SNP call accuracy between the 1K RiCA and other genotyping platforms with overlapping SNPs showed concordance values ranging from 97-100% with a mean of 99%. A test on 536 rice lines showed that the 1K-RiCA adequately capture the genetic diversity present in indica accessions and indica x indica elite crosses from IRRI's Favorable Environments Breeding Program, but was unable to do the same for aus, temperate or tropical japonica lines. The average number of polymorphic SNPs across pairwise comparisons for indica x indica, indica x japonica, and indica x aus crosses were 400, 465, and 452 respectively. Genotypic results on true F1 plants from 6 different crosses showed the robustness of the 1K-RiCA to called heterozygotes genotypes with an accuracy of 99%. A QTL analysis using 1K-RiCA data on 134 RILs derived from the cross IR64 x Azucena for three different AI-tolerance traits showed comparable results to those reported using high-density GBS data set. First attempts to use the 1K-RiCA for GS purposes show the utility of the assay to be deployed as a cost effective

tool for GS applications in indica rice breeding programs. The use of low-density genotyping with the 1K-RiCA followed by imputation can potentially provide a compromise between cost and accuracy that could promote the deployment of GS based strategies in several rice breeding programs around the world.

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