



Category: Plant Genomics

Marker-assisted introgression of drought tolerance from wild ancestors into popular Indian rice varieties using a 7K Infinium SNP array

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Abstract

Recent advances in the area of genomics have led to the development of high throughput genotyping platforms that have immensely contributed to molecular breeding programs. Custom-designed single nucleotide polymorphism (SNP) arrays provide an efficient, cost effective, high throughput genotyping tool for QTL/gene mapping, variety identification, marker-assisted selection, etc. In the current study, two interspecific libraries of Chromosome Segment Substitution Lines (CSSLs) were evaluated under both drought and control conditions to identify lines with superior yield under drought. The CSSL libraries consisted of 48 BC₄F₃ lines derived from *O. sativa* cv. *Curinga (tropical japonica)* x *O. rufipogon*, and 32 BC₄F₃ lines derived from *O. sativa* cv. *Curinga (tropical japonica)* x *O. meridionalis*. The phenotypic screening of these 80 CSSLs led to the identification of MER-20 that yielded well under drought stress. This line was backcrossed with popular rice variety of India, Swarna-Sub1 to introgress wild chromosome segments responsible for reproductive stage drought tolerance. During backcrossing, tracking of wild introgressions and monitoring of recurrent parent genome recovery was facilitated by the use of the Cornell 6K and 7K Infinium rice SNP arrays. The 6K and 7K SNP arrays assayed 5275 SNPs and 7099 SNPs, respectively, distributed across the 12 chromosomes. In our populations of (MER-20X Swarna sub1) BC₂F₁ lines, 1775 SNPs were polymorphic using the 6K array. The percentage of recurrent parent genome in these backcrossed lines ranged from 33-92% and the percentage of wild donor genome ranged from 8-67%. Using genotypic selection, 5% of plants were identified for further marker assisted backcrossing, based on the presence of the target donor (wild) segment and maximum recovery of recurrent parent background. In the next generation, BC₃F₁ lines were genotyped using the 7K SNP array, which identified 2521 polymorphic SNPs. In the BC₃ generation, 60-95% of the recurrent parent genome was recovered and wild segments accounted for 5-40% of the genome. The best 5% progenies were again selected based on genotype, and selected BC₃F₂ individuals are now being evaluated for yield under drought stress. The use of the 6K and 7K SNP arrays improved the efficiency and accuracy of genotyping and greatly facilitated tracking of recurrent/donor genomes in backcross lines.

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