Canadian Journal of Biotechnology

Poster Presentation   OPEN ACCESS

Category: Plant Genomics

Allele Mining and Allelic Diversity of Genes Governing Grain Size Related Traits in Rice (*Oryza sativa* L.)

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Abstract

Mining elite alleles for grain size is one of the key aspects for the improvement of cultivated rice to suit diverse global consumer preferences. Thus with the goal of identification of novel and superior alleles from the genes governing the grain size related traits by exploring the natural variability present in the rice germplasm, the present study was conducted. 124 rice genotypes were evaluated for different grain traits such as grain length (GL), grain width (GW), grain length to width ratio (GL/GW), and 1000-grain weight (TGW). The germplasm of 124 rice genotypes presented substantial variation for grain size traits. Significant correlations were detected among the grain size traits. All the four traits exhibited normal distribution in the germplasm indicating quantitative inheritance of these traits. In total, 32 molecular markers comprising of 8 grain size gene-specific markers and 24 SSR markers covering all 12 chromosomes were used in this study and all markers showed polymorphism and produced a total of 86 alleles among the 124 rice varieties. Number of alleles ranged from 2 to 4 with an average of 2.68 alleles per locus. The mean polymorphism information content (PIC) value was 0.34. Analysis revealed 124 genotypes could be made into two groups, A and B. The group A exclusively includes the extra-long grain length basmati genotypes. However, the group B again divided into two groups *i.e.,* B1 and B2. The group B1 includes mostly long grain genotypes. The group B2 comprised of all classes of grain length and size genotypes. Based on the population structure Q matrix data the 124 accessions are divided into four clusters/subpopulations, viz., from POP1 to POP4. POP1 subpopulation was grouped under extra-long grain type, POP2 was grouped under long grain type, POP3 and POP4 includes all the four grain size classes. Eight marker-trait associations were identified by screening 124 genotypes with grain size specific primers for GL, GW, L/B and TGW traits. One *GS*3 gene-specific marker, GS3RGS1 was found to be associated with GL, GW, L/B and TGW traits with their PVE as 15.2%, 16.9%, 10.3% and 7.8%, respectively. Earlier results also reported that the *GS*3 is the major gene governing the grain length and minor gene for grain width. Similarly, one SSR marker, RM505 was showed association with GL, GW, L/B and TGW traits with their PVE as 4.4%, 2.6%, 1.9% and 3.8%, respectively. The present investigation reinforces the fact that grain size is a complex trait regulated by many genes located on different chromosomes. However, the gene specific markers, for GL, GW, TGW and L/B traits, such as GS3RGS1 and RM505 have potential to be used as foreground markers in marker-assisted breeding. Mining of complete gene sequences and other genes governing grain size traits is warranted further investigation adding some more germplasm.