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InDel Marker Based Estimation of Multi-Gene Allele Contribution and Genetic Variations for Grain Size and Weight in Rice (*Oryza sativa* L.)

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Abstract

The market success of any rice cultivar is exceedingly dependent on its grain appearance, as well as its grain yield, which define its demand by consumers as well as growers. The present study was undertaken to explore the contribution of nine major genes, qPE9~1, GW2, SLG7, GW5, GS3, GS7, GW8, GS5, and GS2, in regulating four size and weight related traits, i.e., grain length (GL), grain width (GW), grain thickness (GT), and thousand grain weight (TGW) in 204 diverse rice germplasms using Insertion/Deletion (InDel) markers. The studied germplasm displayed wide-ranging variability in the four studied traits. Except for three genes, all six genes showed considerable association with these traits with varying strengths. Whole germplasm of 204 genotypes could be categorized into three major clusters with different grain sizes and weights that could be utilized in rice breeding programs where grain appearance and weight are under consideration. The study revealed that TGW was 24.9% influenced by GL, 37.4% influenced by GW, and 49.1% influenced by GT. Hence, assuming the trend of trait selection, i.e., GT > GW > GL, for improving TGW in the rice yield enhancement programs. The InDel markers successfully identified a total of 38 alleles, out of which 27 alleles were major and were found in more than 20 genotypes. GL was associated with four genes (GS3, GS7, GW8, and GS2). GT was also found to be regulated by four different genes (GS3, GS7, GW8, and GS2) out of the nine studied genes. GW was found to be under the control of three studied genes (GW5, GW8, and GS2), whereas TGW was found to be under the influence of four genes (SLG7, GW5, GW8, and GS5) in the germplasm under study. The Unweighted Pair Group Method with Arithmetic means (UPGMA) tree based on the studied InDel marker loci segregated the whole germplasm into three distinct clusters with dissimilar grain sizes and weights. A two-dimensional scatter plot constructed using Principal Coordinate Analysis (PCoA) based on InDel markers further separated the 204 rice germplasms into four sub-populations with prominent demarcations of extra-long, long, medium, and short grain type germplasms that can be utilized in breeding programs accordingly. The present study could help rice breeders to select a suitable InDel marker and in formulation of breeding strategies for improving grain appearance, as well as weight, to develop rice varieties to compete international market demands with higher yield returns. This study also confirms the efficient application of InDel markers in studying diverse types of rice germplasm, allelic frequencies, multiple-gene allele contributions, marker-trait associations, and genetic variations that can be explored further.

Key words: Insertion/Deletion (InDel) markers; genetic variation; multi-gene allele contributions; rice (*Oryza sativa* L.), grain size and weight; rice germplasm

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