

Gene /QTL Mining for Yield in Common Bean Germplasm (*Phaseolus vulgaris L.*) from Northern India

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Common bean is considered as one of the most valuable food consumed worldwide owing to innumerable nutritional and therapeutic benefits. Heretofore, multiple yield associated markers have been detected all over the world; even so, the present work is looked on as the first report on identification of novel/new potent markers associated with yield traits by exploiting the common bean germplasm of Northern India. Both the GLM and MLM were used to identify significant marker-trait associations using a panel of one hundred and thirty-five genotypes and ninety-eight microsatellite markers; a set of ninety six diverse common bean genotypes was selected for association analysis. The study here reports a total of 61 marker trait associations ($p \leq 0.005$) for the selected yield traits those were found distributed on all the chromosomes except chromosome 1. Only one marker PVBR213 associated with days to bud initiation was found common while using both the approaches. However, eighteen markers showed association with more than one trait. Phenotypic variation ranging from 3.31% to 32.7% strongly indicates the genetic complexity of the yield trait and supports the fact that such quantitative trait is controlled by several major ($R^2 \geq 25$) and minor ($R^2 \leq 25$) QTLs with small but cumulative effects. The authentication and stability of detected SSRs across environments comes from the previous reports where different genetic backgrounds were examined for analysis. Desirable traits such as early maturity and high yield detected in our study is highly recommended for the purpose of enhancement of agronomic trait performance, trait selection, development of bi-parental populations and in back cross breeding programs to achieve superior and sustainable genotypes for future generations.

Keywords: Common bean, Association mapping, Yield, Microsatellite markers