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Association mapping for morphological traits under saline stress in wheat

Harpreet Singh

Maharishi Markandeshwar University, India

Introduction: Salinity is a major concern constraint to wheat production affects yield and its related parameters. In the present study association mapping was conducted for different morphological characters using diverse 90 wheat accessions. A total of 135 SSR markers distributed on all chromosomes of wheat were used to map rice genome association analysis was carried out by means of mixed linear model. To manage the spurious associations, population structure with kinship in the given panel was considered during association. Population structure analysis revealed three subgroups in the 90 wheat accessions. The admixture level was in range from 0.9%-23.2%. A total of 13 marker trait associations were identified and out of these five marker trait associations explained phenotypic variation of more than 10%. These identified marker trait associations could enhance breeding effectiveness by significantly reducing the time and labor consuming efforts which otherwise be needed in conventional breeding.

Findings: The entire panel was selected carefully by screening material from different geographical locations. The screening was done meticulously. A total of 13 marker trait associations were found and out of these traits panicle length explained phenotypic variance of 16.2%. Some of these QTLs share overlapping regions with other genes when BLAST was performed and shows 100% identity.

Conclusion & Significance: Salt tolerance is a posing threat for field crops like wheat with millions of hectares of land are affected by it. There is an urgent need to develop varieties that can withstand such harsh environment. The present study is one of the steps towards developing these varieties. Once the regions are identified, the genes could be introgressed to conventional varieties which can support food requirements of world population.

Biography

Harpreet Singh is a Ph.D. scholar in Maharishi Markandeshwar University from India.

harpreet13.bio@yahoo.com

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