

DBT-NABI scientists develop and Characterise new markers in Wheat

New Delhi, July 08: Assessment of existing diversity is the key for germplasm conservation and crop improvement. Wheat (*Triticum aestivum* L.) is among the most important cereal crops and consumed by two billion world's populations. DNA-based markers are predominantly used for diversity characterization because they are easy to develop and not influenced by the environment. Among them microsatellites (simple sequence repeats, SSRs) are most suitable due to their genome-wide distribution, hyper variability and reproducibility for their applications in diversity, genetic improvement, and molecular breeding. bZIP transcription factors play major roles in plants in light and stress signaling, seed development, and defence.

A total of 846 SSRs were identified from 370 wheat cDNA sequences and a sub-set of 35 polymorphic TabZIPMS (*Triticum aestivum* bZIP Micro-Satellites) was used for diversity and genetic structure analysis of 92 Indian wheat varieties and related species.

114 SSR variants ranging from 2-5 per SSR locus were detected for the 35 SSRs in the varieties. Average polymorphic information content (PIC) and observed heterozygosity was found to be 0.135 and 0.838, respectively. Thirty-four SSRs showed cross-transferability into different related species.

Combined Bayesian model and Jaccard's similarity based genetic clustering analysis revealed two clusters of 80 bread wheat varieties and one separate cluster of related species. The findings provide resources for future utilization in genetic resource conservation, trait introgression, breeding and varietal development.

The above work was recently published in GENE (doi: 10.1016/j.gene.2020.144912)

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