

Genome-wide identification and characterization of novel non-coding RNA-derived SSRs in wheat

In the current study, scientists at DBT- National Agri-Food Biotechnology Institute (**NABI**), **Mohali has identified** a total of 661 SSRs dwelling in pre-miRNA (15), small nuclear (25) and long non-coding RNA (621). Of these, 46 were validated and 100% amplification success was observed in selected wheat genotypes. A set of 36 ncRNA-SSRs markers was utilized for genetic variability assessment in forty-eight Indian wheat genotypes (which includes bread wheat, durum wheat and relatives).



Number of alleles ranged from 1-4 with an average of 2 alleles per SSR locus. Mean PIC, observed heterozygosity and Shannon information index was found to be 0.258, 0.37 and 0.476 which suggests markers to show moderate to high polymorphism. Thirty-six ncRNA-SSRs showed transferability ranging from 42.1% to 100%. Average genetic dissimilarity among wheat genotypes was found to be 0.29 based on Jaccard's dissimilarity.

This is the first report of ncRNA-SSRs in wheat which will be useful for molecular breeding and genetic improvement of wheat. The work was published in the journal '*Molecular Biology Reports*'

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