

Generation of Size Based (Ssrs and Isbps) And Gene Based Markers (Snps) from the 2A1 Chromosome of Wheat Using Ngs data and Their Validation For the Enrichment of Genetic Map of 2A

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Wheat is second most important cereal having genome size of 17 GB. Under IWGSC, flow sorted chromosomes of wheat have been used for the construction of BAC based physical maps which are being used for sequencing. Highly saturated genetic maps are essential for anchoring and for proper orientation of physical maps. Next generation data from 454 and illumina platforms of chromosome 2AL allows the identification of size based markers as well as gene based markers. A total of 425821 contigs (generated through hybrid assembly) have been examined for the prediction of SSRs and ISBPs. Using MISA tool 22,460 SSRs have been predicted in total out of which 5,542 SSRs can be used as markers. Using ISBPFINDER.pl a total of 2,16,414 ISBPs have been predicted out of which 12,706 can be used as markers. A set of 500 SSR markers and set of 50 markers have been used for the validation using ABI3730 XL genotyping platform and agarose gel respectively. Bin mapped ESTs of chromosome 2AL were used to identify full length cDNAs, which were then used to BLAST search against the assembled data. Contigs so identified were used for gene prediction using FGESH. A total of 215 primers have been designed from the 2AL assembly and are being mapped through generation of SNP markers. Parental polymorphism between *Triticum monococcum* and *Triticum boeoticum* using these markers have been done and ~60% polymorphism has been detected. Polymorphic markers are being used for the mapping using RIL population generated through cross between *Tm* and *Tb*.