TaSSRDb: The Putative Microsatellite DNA Marker-based Wheat Genomic Resource for Germplasm Management

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Abstract—For increasing global demand of wheat warrants genomic resources that can serve as tool for developing wheat cultivars with increased yield, tolerance to abiotic and biotic stresses and improved input use efficiency in changing climate scenario. There is no structured marker database with options to generate primer pairs for genotyping on desired chromosome/ physical location along with reported markers associated with different wheat traits. Constraints of in-vitro SSR marker discovery can be overcome by genome wide in-silico mining of SSRs. Triticum aestivum SSR database (i.e., TaSSRDb) is an integrated online relational database (http://webtom.cabgrid.res.in/wheatssr/) for chromosome-wise SSR calling from subgenomes along with motif types and primer generation for desired marker. From complex, hexaploid wheat genome of ~17 GB, our tool, TaSSRDb catalogues highest number of SSRs (476169) along with previously reported 268 SSR markers associated with 11 traits. We found highest (116.93 markers/Mb) and lowest (74.57 markers/Mb) SSR densities on 2D and 3A chromosome, respectively. E-PCR was done for 30 loci randomly selected for PCR validation. These putative markers can be used for linkage mapping, gene/OTL discovery, diversity analysis, traceability, variety identification, differentiation of EDV/IV, seed purity and hybrid wheat testing programs. If physical location of the gene is known, it can be introgressed using closely linked SSR loci having allelic size difference in parental lines. Phenotypic DUS testing limitations can be overcome by supplementation of SSR allelic profile based distinctness, uniformity among existing and stability among segregating population. This genomic resource can not only accelerate knowledge discovery, but also be used in germplasm management in endeavour of wheat productivity. Keyword: DUS, EDV, e-PCR, molecular marker, seed purity, SSR, Triticum aestivum.