

Characterization of Wheat (*Triticum aestivum* L.) Genotypes with Respect to Heat Stress Tolerance and Spot Blotch Resistance

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Abstract—Twelve wheat (*Triticum aestivum* L.) genotypes were characterized with respect to heat stress and spot blotch disease under four environmental conditions viz no stress (E_1), stress due to spot blotch (E_2), heat stress (E_3) and combined stress (E_4) along with molecular characterization using 28 SSR markers (associated with heat tolerance as well as spot blotch). Morphological parameters such as 1000 grain weight, grain filling duration (GFD), plant height, peduncle length, spike length, disease severity and area under disease progress curve (AUDPC) were recorded. The individual impact of heat stress with respect to performance of the genotype was found significantly higher than that caused by spot blotch. On the basis of stress susceptibility index (SSI) the genotypes WH 760, DBW 14, and Raj 3765 were found better for the characters 1000 grain weight and GFD. The overall disease severity was found maximum under heat stress condition. As considered 28 SSR markers detected total 244 alleles in 12 genotypes, the number of alleles per locus varied from four in Xgwm133a and Xgwm456 to twenty three in Xgwm293 with an average of 6.5 alleles per locus. A total 158 unique alleles were observed at 37 SSR loci, with an average of 5.6 unique alleles per locus. The number of unique alleles per locus ranged from one in Xgwm273 to twenty three in Xgwm293. In spite of that six SSR loci also showed null alleles with respect to primer Xbarc1047, Xgwm133a, Wmc168, cfd144, Xbarc147 and Xgwm126. The polymorphism information content (PIC) values were varied from 0.292 in case of Wmc273 to 0.902 in the case of Xgwm356. Pair wise genetic similarity coefficient for Sonalika and HD 2967 were most distantly related. Cluster analysis grouped 12 wheat genotypes into four different clusters at 35 phenon level, the use of 28 SSR markers allowed unique genotyping and analysis.