

Characterization of Wheat Genotypes for Resistance against Identified Isolates of Blotch Causing Fungal Species

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Abstract—Wheat is the most widely grown and consumed food crop of the world. Recent climate changes has aggravated the disease scenario which leads to increase in the incidence of Helminthosporium leaf blight of wheat i.e. spot blotch caused by the Bipolaris sorokiniana and it is one of the major disease that limits the cultivation of wheat. In this investigation, field screening of eighteen wheat (Triticum aestivum) genotypes were done for their tolerance against natural and artificial epiphytotic condition of spot blotch caused by Bipolaris sorokiniana during the year 2010-11 and 2011-12 at the spot blotch location of RAU, Pusa. The screening showed that the genotype PBW343 exhibited highest AUDPC value (1535.83 and 1706.75) and the minimum value was found to be in the genotype C-306(47.48 and 432.07) in both the years. Under molecular characterization, 18 wheat microsatellite markers were able to detect a total number of 304 alleles in all the 18 genotypes which has been taken for the study with an average of 9.21 alleles per locus. More alleles were identified in genome B (a total of 182 alleles) as compared to D(72) and A(34) genomes. It accounts for the higher polymorphism level in the B genome. PIC value ranged from 0.657 for the primer Xgwm44 to 0.925 for Xgwm389. A very high degree of similarity existed between variety Kauz/AA/Kauz and Raj3765 (0.930). The most distantly related cultivars were Sonalika and DL1012, HI1538, Agra local (0.625). Eighteen isolates of blotch causing fungal species were studied for their morphological characterization. On the basis of their growth pattern, the isolates were grouped into six different categories i.e. Olive black, Olive cream, Greyish, Black pink, Pink and Black cream. Among them Olive cream group has shown the maximum frequency of 38.88% whereas Black cream and Pink isolates displayed lowest frequency of 5.55%. Molecular characterization of the fungal isolates were done by

two fungus specific primer and nine Universal Rice Primer (URP) to observe the variability. Seven out of the ten isolates of fungus specific primer could amplified and identified as B.sorokiniana while rest of the three could not. URP resulted into 113 bands out of which 95 were polymorphic and 18 were monomorphic bands. The dendrogram constructed using genetic similarity ranges between isolates idicated the presence of genetic variability among the ten isolates under study. The two fungal isolates RAU-gtl-1 and RAU-gtl-5 showed the maximum genetic similarity, specific DNA bands were identified for selected isolates. The objective of this study was to gather information on the isolated B.sorokiniana causing blotch against wheat genotypes above.