Fine Mapping of Genes of Economic Importance in Diploid Wheat, Triticum monococcum, and Their Transfer to Rainfed Cultivar Background

The project aimed at achieving four major objectives; generating a linkage map in diploid A genome wheat, mapping of leaf rust and stripe rust resistance in the diploid wheat, transferring these in hexaploid wheat background and improving drought tolerant hexaploid wheat lines for rust resistance.

Progress made in achieving these objectives is presented briefly. A linkage map of diploid A genome of wheat has been generated with 179 loci. The data were published submitted to GrainGenes (http://wheat.pw.usda.gov/report?class=mapdata&name=T.%20boeoticum%20x%20monococcum, database and information site). For stripe rust resistance data was recorded in the recombination inbred line (RIL) population again during 2006-07 by testing an additional Puccinia striformis tritici (Pst) race 78S84, which was released for field evaluation only during 2006-07. Two quantitative trait loci (QTL) for stripe rust resistance, designated as QYrtm.pau-2A and QYrtb.pau-5A, contributed by T. monococcum and T. boeoticum respectively, were mapped on chromosomes 2A and 5A and the results published. T. monococcum and three RILs were crossed to hexaploid wheat cvs WL 711 and PBW 343, using T. durum as a bridging species. Despite suppression of stripe rust resistance by the B genome of T. durum, one stripe rust resistance gene has been transferred from one of the RILs, which apparently is a gene from T. boeoticum as revealed by introgression of markers linked to stripe rust QTL, QYrtb. pau-5A. Homozygous resistant progenies have been identified in both the cultivars and their chromosome number ranged from 40-42. A BC,F2 progeny (derived from a single BC,F2 plant) derived from the cross N59/T. monococcum//2*WL711 showed segregation for stripe rust resistance when evaluated against mixture of four Pst pathotypes. This population is being used for fine mapping of the stripe rust resistance gene transferred from A genome species.

For leaf rust resistance, mapping could not be achieved using the RIL population, probably because the population did not segregate at adult plant stage and at seedling stage it showed segregation against one pathotype only. Both seedling and adult plant resistance genes for leaf rust resistance have been transferred from the diploid to hexaploid wheat. Transfer of leaf rust resistance was monitored at seedling stage. Several thousand plants were screened at seedling stage against the most virulent pathotype 77-5 but genetics of leaf rust resistance was studied in some selected progenies only. A total of 1425 BC,F2 plants in the genetic background of PBW 343 was screened. 1114 plants were resistant and 311 susceptible which fits well to 3:1 segregation as expected for a single gene. Similarly in the background of WL711, of the 408 BC,F2 plants, 287 were resistant and 121 susceptible, which again fits to a one-gene segregation. These have been confirmed during 2007-08 crop season after screening F3 progenies of various backcross generations. Thus one gene for resistance to leaf rust at the seedling stage has been transferred from the diploid A genome of wheat into hexaploid wheat varieties PBW 343 and WL711. These populations are now being used for mapping leaf rust resistance gene transferred from T. monococcum into hexaploid wheat background. An off-shoot of the project was the recovery of introgression lines having high grain number per spike from T. monococcum which could prove useful for further improving the productivity.