M. Feldm

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Molecular Mapping of Stripe Rust Resistance and Other Important Agronomic Traits in Wild Emmer Wheat, *Triticum dicoccoides*

J. Peng[1], T. Fahima[1], M. S. Roeder[2], L. E. Talbert[3], T. Blake[3], A. Grama[4], A. B. Korol[1], and E. Nevo[1]

[1]Institute of Evolution, University of Haifa, Haifa 31905, Israel; [2]Institute for Plant Genetics and Crop Plants, D-06466, Gatersleben, Germany; [3]Depart. of Plant, Soil, and Environmtal. Sci., Montana State University, Bozeman, MT 59717, U. S. A; [4]Volcani Center, Agricultural Research Organization, P. O. Box 6, Bet Dagan, 50250, Israel

Wild emmer wheat, *Triticum dicoccoides*, was found to be a valuable source for novel stripe resistance genes, as well as other agronomically important traits (Nevo, 1995). In this study, we have developed two mapping populations by crossing *T. durum* wheat cultivar Langdon 16 with two *T. dicoccoides* accessions Nahef 32-26 and Hermon G52. These mapping populations consist of 230 and 237 F_2 plants (F$_3$ families) in Nahef and Hermon populations, respectively. Highly significant differences between the parents were established for stripe rust resistance, heading date, plant height, grain yield/plant, grain number/plant, 100-grain weight, spike number/plant and grain number/spike. Obvious transgressive segregation was observed for the traits in F_2 generation. In Nahef population, the range of variation (R) for heading date, plant height, grain yield/plant, grain number/plant, 100-grain weight, spike number/plant and grain number/spike was 114 -185 days, 66-188.4 cm, 0.42-13.33 g, 13-303, 1.96-6.39 g, 1-13, and 5.5-32.4, respectively. In Hermon population, R of heading date, plant height, grain yield/plant, grain number/plant, 100-grain weight, spike number/plant and grain number/spike was 122-218 days, 41.9-174.3 cm, 0.20-11.28 g, 7-360, 2.18-5.72 g, 1-20, and 4.2-36.2, respectively. The genetic polymorphism between parents in each of the two populations has been tested using various molecular markers. Among 59 wheat microsatellite (WMS) markers, 49 detected polymorphism in Nahef population, and 52 in Hermon population. Among 72 STS markers, 67 revealed polymorphism in Nahef population, and 69 in Hermon population. Out of 720 RAPD primers, 230 detected polymorphism in Nahef population, and 215 in Hermon population. Therefore, significant genetic polymorphism and phenotypic variation exist in the two mapping populations. Construction of fine molecular map using WMS, STS and RAPD markers for each of the two mapping populations is underway. The multiple trait QTL mapping analysis will be conducted using these molecular markers to locate the QTLs of the examined traits and to reveal the relationships between stripe rust resistance and other agronomically important characters (due to linkage or pleiotropy of genes).

Nevo, E., 1995. Genetic resources of wild emmer, *Triticum dicoccoides*, for wheat improvement: news and views. Proc. Intern. 8th Wheat Genetics Sympos., pp.79-87, Beijing, China, 20-25.7. 1993, China Agricultural Scientech Press