M. Feldman

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MICROSATELLITE FINE MAPPING OF *TRITICUM DICOCCOIDES*-DERIVED STRIPE-RUST RESISTANCE GENE *YRH52* AND THE POTENTIAL APPLICATION IN MARKER-ASSISTED SELECTION

J. H. Peng[1], T. Fahima[1], M. S. Röder[2], Y. C. Li[1], A. Grama[3], and E. Nevo[1]

[1]*Institute of Evolution, University of Haifa, Mount Carmel, Haifa 31905, Israel;* [2]*Institute for Plant Genetics and Crop Plant Research, Correnssstrasse 3, D-06466 Gatersleben, Germany;* [3]*Agricultural Research Organization, The Volcani Center, P. O. Box 6, Bet Dagan 50250, Israel*

Objective: A stripe-rust resistance gene *YrH52* derived from the unique Mt. Hermon population of wild emmer in Israel has been located onto chromosome 1B (Peng et al. 1999, TAG in press). The marker-based cloning and marker-assisted selection greatly depends on the fineness of the map. The present study is to conduct fine mapping of *YrH52* using more microsatellite markers and evaluate the accuracy and efficiency of marker-assisted selection. ***Method***: Using 70 new microsatellite primer pairs, 150 individuals of the F_2 mapping population were genotyped. The 150 F_3 families were tested using Israeli new stripe-rust race *134E132*. The accuracy and efficiency of marker-assisted selection were calculated as AMAS and EMAS, respectively, for homozygous genotypes of *YrH52* in F_2. ***Results***: Among 203 marker loci, 20 were found to be linked to *YrH52* with LOD scores from 3.84 to 59.41, and recombination frequencies from 0.01 to 0.34. A genetic map of chromosome 1B consisting of 23 markers and the gene, *YrH52*, was constructed with a total map length of 149.5 cM. Most of the markers located in the region close to *YrH52* that was bracketed by *Nor1* and *Xgwm273a* with map distance of 1.3 and 2.7 cm from either side, respectively. AMAS and EMAS of nine markers were higher than 85%. **Conclusion:** The molecular map of *YrH52* region on chromosome 1B is significantly improved compared to the previous one. Microsatellite marker is effective to conduct marker-assisted selection of *YrH52* in F_2 generation when the linkage distance is less than 5 cM. AMAS can be dramatically improved when two markers bracketing the target gene are used, whereas EMAS mainly depends on the linkage distance.