GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Assessment of genetic diversity of wheat genotypes by resistance gene analog-EST markers

O. Karakas[1], F. Gurel[2] and A.A. Uncuoglu[3]

[1]The Scientific and Technological Research Council of Turkey, Marmara Research Center, Genetic Engineering and Biotechnology Institute, Gebze-Kocaeli, Turkey
[2]Department of Molecular Biology and Genetics, Istanbul University, Istanbul, Turkey
[3]Department of Bioengineering, Faculty of Engineering, Marmara University, Goztepe, Istanbul, Turkey

Corresponding author: A.A. Uncuoglu
E-mail: ahu.uncuoglu@marmara.edu.tr

Genet. Mol. Res. 10 (2): 1098-1110 (2011)
Received September 15, 2010
Accepted November 26, 2010
Published June 14, 2011
DOI 10.4238/vol10-2gmr1065

ABSTRACT. Resistance gene analog-expressed sequence tag (RGA-EST)-based markers have been used for variety discrimination and studies of genetic diversity in wheat. Our aim is to increase the competitiveness of public wheat breeding programs through intensive use of modern selection technologies, mainly marker-assisted selection. The genetic diversity of 77 wheat nucleotide binding site (NBS)-containing RGA-ESTs was assessed. Resistant and susceptible bread wheat (*Triticum aestivum*) genotypes were used as sources of DNA for PCR amplifications. In our previous studies, the F_2 individuals derived from the combinations PI178383 x Harmankaya99, Izgi2001 x ES14, and Sonmez2001 x Aytin98 were evaluated for yellow rust resistance at both seedling and adult stages to identify DNA markers. We have now examined the genetic variability among the resistant and susceptible Turkish wheat cultivars for yellow rust disease and the mean genetic distance between the cultivars. The highest similarity was 0.500 between Harmankaya99 and Sonmez2001. The lowest similarity was 0.286 between Aytin98,

PI178383 and Aytin98, ES14. A relatively high level (49.5%) of polymorphism was observed with 77 RGA-EST primers across the six wheat genotypes, despite the fact that all of them were local cultivars from geographically close locations. RGA-EST sequences were compared by BlastX algorithms for amino acid sequences to determine the polymorphic categories among the combinations. BlastX analyses of six RGA-ESTs that gave polymorphic patterns for all combinations were NBS-LRR class RGA, NB-ARC domain containing protein, NBS-type resistance protein RGC5, NBS-LRR-S/TPK stem rust resistance protein, and putative MLA1 proteins, while 38 RGA-EST gave a monomorphic pattern.

Key words: *Triticum*; Biodiversity; RGA-EST; Genetic diversity; Yellow rust

