



Bulked segregant analysis for relative water content to detect quantitative trait loci in wheat under drought stress

M.R. Naroui Rad^{1,2}, M. Abdul Kadir¹, M.Y. Rafii³, H.Z.E. Jaafar⁴ and M.R. Naghavi⁵

¹Agrotechnology Department, Faculty of Agriculture, University Putra Malaysia, Serdang, Selangor, Malaysia

²Agriculture and Natural Resources Research Center, Sitan, Iran

³Institute of Tropical Agriculture, University Putra Malaysia, Serdang, Selangor, Malaysia

⁴Crop Science Department, Faculty of Agriculture, University Putra Malaysia, Serdang, Selangor, Malaysia

⁵Department of Agronomy and Plant Breeding, Faculty of Agriculture, University of Tehran, Karaj, Iran

Corresponding author: M.R. Naroui Rad

E-mail: narouirad@gmail.com

Genet. Mol. Res. 11 (4): 3882-3888 (2012)

Received February 7, 2012

Accepted July 3, 2012

Published November 12, 2012

DOI <http://dx.doi.org/10.4238/2012.November.12.5>

ABSTRACT. This study was carried out to evaluate the genetic effect of quantitative trait loci (QTLs) conferring drought tolerance in wheat. A population of 120 F₂ individuals from the cross between the drought-tolerant S-78-11 and drought-sensitive Tajan cultivars were analyzed for their segregation under drought stress conditions. The relative water content under drought stress conditions exhibited continuous variation, indicating the minor gene effects on the trait. Single-marker analysis (SMA) was carried out to detect the main QTL association with drought tolerance. The SMA results revealed that the simple sequence repeat markers GWM182 and GWM292 on chromosome 5D and GWM410 on

chromosome 5A exhibited significant association with drought tolerance, accounting for 30, 22, and 21% of the total variation, respectively. The 3 genetic loci, especially GWM182, can be used in marker-assisted selection methods in drought tolerance breeding in wheat.

Key words: Drought tolerance; Bulk segregant analysis; QTL; SSR markers; Wheat