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Full Length Research Paper

Application of randomly amplified polymorphic DNA (RAPD) markers and polyphenol oxidases (PPO) genes for distinguishing between the diploid (*glaucum*) and the tetraploid (*leporinum*) accessions in *Hordeum murinum* complex

Haddad El Rabey* and Abdulrahman L. Al-Malki

Biochemistry Department, Faculty of Sciences, King Abdul Aziz University, Jeddah, Kingdom of Saudi Arabia.

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The genome of 12 wild barley accessions belonging to *Hordeum murinum* complex (eight out of them belong to *H. m. glaucum* and four belong to *H. m. leporinum*) was characterized using RAPD-PCR markers and polyphenol oxidases genes (PPO). A total of 123 RAPD markers with 22 arbitrary decamer primers were used. 56 out of the RAPD markers were common to all accessions, and the other 67 markers were polymorphic. 35 out of the polymorphic markers are distinguishable between the two taxa but not among all accessions, 15 RAPD markers are specific to *H. m. glaucum* and 17 are specific to *H. m. leporinum*. The PCR amplification of PPO genes revealed that amplified fragments from these genes are randomly distributed among the studied accessions regardless of their taxonomy. All data were analyzed using NT-SYS-pc (numerical taxonomy and multivariate analysis system) program to address the phylogenetic relationships between the studied taxa. The examined accessions were clustered into two main groups; the first one consists of 4 accessions representing the *H. m. leporinum* (diploid) and the other one consists of eight accessions representing the *H. m. leporinum* (tetraploid).

Key words: *Hordeum, glaucum*, *murinum, leporinum*, random amplified polymorphic DNA polymerase chain reaction (RAPD-PCR), polyphenol oxidases (PPO), numerical taxonomy and multivariate analysis system (NTSYS-pc).

INTRODUCTION

Wall barley (*Hordeum murinum*) consists of three subspecies, naturally distributed from southern Central Asia through the Mediterranean region to northwestern Europe, but now an invasive weed in many parts of the world (Jakoba and Blattner, 2010). Polymerase chain reaction (PCR) based molecular markers have become increasingly popular for fingerprinting and cultivars identification since the development of PCR technology (Saiki et al., 1988). RAPD-PCR (randomly amplified polymorphic DNA) was first conducted by Williams et al. (1990). It is based on amplification using arbitrarily 10-mer primers, and has been successfully used for *Hordeum* genome characterization, for major quantitative trait loci mapping, facilitating positional cloning of genes, studying genetic diversity and genetic fingerprinting for phylogeny studies (Marillia and Scoles, 1996; Lainé et al., 2000; Waldron et al., 2002; Blattner, 2004).

The *Hordeum murinum* complex is a group of in-breeding annual plants, belonging to section *Campestria* (Åberg, 1940) or section *Hordeum* (Bothmer et al., 1987) of the genus *Hordeum*, family *Poaceae*. Taxa of the complex are distributed in central Europe, Mediterranean region, North Africa, southwestern Asia, Caucasus, Southern Uzbekistan, Tadzjikistan, Iran, and Afghanistan, and as weeds, have colonized most parts of the world (Bothmer et al., 1995). Morphologically, size of seed triplets and the relatively large inflated lateral spikelets,

*Corresponding author. E-mail: elrabey@hotmail.com. Tel: 009662640000-68972. Fax: 00966026951945.