

Genetic diversity and structure of natural *Dactylis glomerata* L. populations revealed by morphological and microsatellite-based (SSR/ISSR) markers

P. Madesis^{1*}, E.M. Abraham^{2*}, A. Kalivas^{1,3}, I. Ganopoulos^{1,4} and A. Tsiftaris^{1,4}

¹Institute of Applied Biosciences, Centre for Research and Technology Hellas, Thessaloniki, Greece

²Laboratory of Range Science, Department of Forestry and Natural Environment, Aristotle University of Thessaloniki, Thessaloniki, Greece

³Cotton and Industrial Plant Institute, Cotton Institute and Industrial Crops ELGO-DEMETER, Thermi, Greece

⁴Department of Genetics and Plant Breeding, School of Agriculture, Aristotle University of Thessaloniki, Thessaloniki, Greece

*These authors contributed equally to this study.

Corresponding author: E.M. Abraham

E-mail: eabraham@for.auth.gr

Genet. Mol. Res. 13 (2): 4226-4240 (2014)

Received April 25, 2013

Accepted October 1, 2013

Published June 9, 2014

DOI <http://dx.doi.org/10.4238/2014.June.9.8>

ABSTRACT. *Dactylis glomerata* L. is an important forage species in the Mediterranean region, and in other regions with a similar climate. Genetic material from 3 locations in north, central, and south Greece was studied, using morphological traits, SSR, and ISSR molecular markers. Morphological analysis revealed differences among the geographic locations studied for all morphological traits, except the number of reproductive tillers. Moreover, the highest phenotypic variation was observed on the accessions from south, while the lowest was observed on the accessions from the north. Although the results of the molecular marker analysis are indicative, a high level of

genetic diversity at the species level was revealed by ISSRs ($G_{ST} = 0.291$) and SSRs ($F_{ST} = 0.186$). Analysis of molecular variance showed that a high level of genetic diversity existed for ISSRs and SSRs within populations (62 and 83%, respectively), rather than among populations (38 and 17%, respectively). Cluster analysis divided the 3 populations in 2 groups, with the population originating from the island of Crete forming 1 group, while the populations from north Greece (Taxiarchis) and central Greece (Pertouli) were clustered in a 2nd group. In general, the results indicate that SSRs are more informative compared to ISSRs about the genetic variation within a population, whereas the ISSRs were more informative about the genetic diversity among populations. However, a similar trend in diversity (genotypic and phenotypic) was observed in the morphological traits and microsatellite-based (SSR/ISSR) markers at the locations studied.

Key words: Cocksfoot; Fodder crop; Genotypic variation; Molecular markers; Phenotypic variation