

MORPHOLOGICAL, BIOCHEMICAL AND MOLECULAR EVALUATION OF *TRITICUM DURUM* DESF. GERMPLASM

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Durum wheat (*Triticum durum* Desf., $2n = 4x = 28$; AABB genomes) is an important grain-crop, particularly in the Mediterranean basin. Over time in Italy plant breeding programs have introduced a number of varieties with always higher and more stable yield and improved grain quality that have continuously replaced the varieties previously locally grown. In order to prevent the genetic erosion of the available durum wheat germplasm, a large number of germplasm collections are currently conserved ex situ in genebanks. Ex situ collections may have a considerable percentage of genetic diversity and useful traits for future breeding needs. So, different approaches can be adopted to explore these germplasm collections.

In this study 107 durum wheat accessions collected in Southern Italy and now preserved ex situ in genebanks were characterized. A set of morphological traits (heading date, plant height, spike length, number of spikelet per spike, number of seeds per spike and weight of 1000 seeds) were evaluated. Grain protein content (%) was determined and then gliadins and glutenins patterns were identified by biochemical methods (A-PAGE and SDS-PAGE, respectively). In addition, 30 SSRs markers were used to describe the genetic diversity of the whole collection.

According to the plant height, it was possible to divide the collection of accessions into three groups, whose morphological traits reflected the consequences of the introduction of dwarf gene varieties.

Grain protein content ranged from 13.6% to 21.7%, with an average of 17.8%. Biochemical characterization of gliadins and glutenins showed a high level of diversity. For gliadins, 100 different bands were identified; 14 patterns were observed in the α region, 23 in the β region, 51 in the γ region and 63 patterns in the ω region. The analysis of the high molecular weight glutenin subunits (HMW-GSs) evidenced that in the collection there were 13 bands and 16 different patterns. The molecular markers identified a total of 115 alleles, with a substantial level of genetic diversity in the whole collection of accessions.

The results suggested that genetic diversity was available in the whole germplasm collection, and that the collection can represent a valuable genetic resource for future breeding programs.