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SNP MARKERS ENABLED TO ASSESS GENETIC DIVERSITY IN A DURUM WHEAT COLLECTION

TARANTO F.*, D'AGOSTINO N.**, PETRUZZINO G.*, MINERVINI A.P.*, FICCO S.*, PECORELLA I.*, FICCO D.B.M.*, MANGINI G.***, BLANCO A.***, MARGIOTTA B.****, LAGHETTI G.****, SAIA S. *****, PECCHIONI N.*, PAPA R.******, DE VITA P.*

*) CREA Centro di Ricerca Cerealicoltura e colture Industriali, S.S. 673, km 25.200, 71122 Foggia (Italy)
**) CREA Centro di Ricerca Orticoltura e Florovivaismo, Via Cavalleggeri 25, Pontecagnano Faiano, 84098 Salerno (Italy)
***) DISSPA, Università degli Studi di Bari, Via G. Amendola 165/A, 70126 Bari (Italy)
****) CNR Istituto di Bioscienze e Biorisorse, Via G. Amendola 165/A, 70126 Bari (Italy)
*****) CREA Centro di Ricerca Cerealicoltura e Colture Industriali, SS 11 km 2,500, 13100 Vercelli (Italy)
******) Dipartimento D3A, Università Politecnica delle Marche, Piazza Roma 22, 60121 Ancona (Italy)

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Durum wheat (*Triticum turgidum* ssp. *durum*) is one of the most important staple crop cultivated in Italy and for that reason, it has been subjected to demanding breeding programs in the last century. How these breeding programs have influenced the genetic diversity within Italian durum wheat germplasm is still under debate.

The present study aims to explore genetic diversity and the extent of gene flow in a wide durum wheat collection that includes 603 accessions spread in Italy from 1800 to 2015. The collection consists of landraces, old and modern cultivars and 12 populations of two main Sicilian landraces, namely Timilia and Russello, collected directly in the farmers' fields.

For this purpose, a 15K SNP Illumina Infinium assay was used to identify and score of over 2,500 high quality polymorphic SNP markers covering the whole genome of tetraploid wheat.

In general, the population structure was associated to the different evolutionary steps determined by modern plant breeding with the development of old cultivars and modern varieties. Indeed, a clear genetic differentiation among landraces, old and modern cultivars appeared evident. Loss of genetic diversity was observed moving from landraces to old cultivars; while, an increase was seen in modern cultivars compared to old cultivars.

The results of this study will have important implications for future breeding programs and for the conservation of wheat genetic resources. Indeed, we found higher genetic diversity in landraces that could be exploited to identify "novel" beneficial alleles not present in the pool of modern varieties. Considering the wide adaptability that these genetic materials have with respect to the Italian cultivation environment, old population and landraces represent a an extremely rich source of alleles and traits of interest to be introgressed into durum wheat varieties. The germplasm collection under investigation will be used to assess the genetic value of the agronomic traits under selection through genome-wide association studies.