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Poster Communication Abstract - 1.17

PHENOTYPIC EVOLUTION IN DURUM WHEAT (TRITICUM DURUM DESF.) BASED ON SNPS, MORPHOLOGICAL TRAITS, UPOV DESCRIPTORS AND KERNEL-RELATED TRAITS

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is a worldwide staple crop cultivated mainly Durum wheat in the Mediterranean basin. Progress in durum wheat breeding requires the genetic variation among the exploitation of gene pool enclosed in landraces, old cultivars and modern cultivars. The aim of this study was to provide a more comprehensive view of the genetic architecture evolution among 123 durum wheat accessions (41 landraces, 41 old cultivars and 41 modern cultivars), grown in replicated randomized complete block in two Metaponto (Basilicata) and Foggia (Apulia), using the Illumina areas, iSelect 15K wheat SNP array and 33 plant and kernel traits including the International Union for the Protection of new Varieties of Plants (UPOV) descriptors. Through DAPC and Bayesian population structure five groups were identified according to type of material data and reflecting the genetic basis and breeding strategies involved in their development. Phenotypic and genotypic coefficient of variation were low for kernel width protein content (1.03%). (6.43%)and for grain Highly significant differences between environments, genotypes and GEI (Genotype x Environment Interaction) were detected by mixed ANOVAs for agro-morphological-guality traits. Number of kernels per spike (h2=0.02) and grain protein content (h2=0.03) were not a heritability character and highly influenced by the environment. Nested ANOVAs revealed highly significant differences between DAPC clusters within environments for all traits except kernel roundness. Ten UPOV traits showed significant diversity for their frequencies in the two environments. By PCAmix multivariate analysis, plant height, heading time, spike length, weight of kernels per spike, thousand kernel weight, and the seed related traits had heavy weight on the differentiation of the groups, while UPOV traits discriminated moderately or to a little extent. The data collected in this study provide useful resources to facilitate management and use of wheat genetic diversity that has been lost due to selection in the last decades.