“Whole-genome resequencing-based characterization of a durum wheat landrace showing similarity to Senatore Cappelli”

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Abstract

Durum wheat (Triticum turgidum spp. durum) is a major cereal adopted since antiquity to feed humans. Due to its use, dating back several millennia, this species features a wide genetic diversity and landraces are considered important repositories of gene pools which constitute invaluable tools for breeders. The aim of this work is to provide a first characterization of a wheat landrace, referred to as ‘TB2018’, that was collected in the Apulia region (Southern Italy). ‘TB2018’ revealed, through visual inspection, characters reminiscent of the traditional variety ‘Senatore Cappelli’, while exhibiting a distinctive trait, i.e., reduced stature. Indeed, the comparison with a set of Italian durum wheat cultivars conducted in this study, in which 24 CPVO plant descriptors were adopted, placed the ‘TB2018’ landrace in proximity to the ‘Senatore Cappelli’ cultivar. In addition, the close similarity between the two genotypes was confirmed by the analysis of the seed protein pattern. A relative reduction was detected for ‘TB2018’ root elongation in the early stages of plant growth. The ‘TB2018’ genome sequence, obtained through low-coverage resequencing and comparison to the reference ‘Svevo’ cultivar is also reported in this study, followed by a genome-wide comparison against 259 durum wheat accessions that placed ‘TB2018’ close to the ‘Cappelli’ reference. Hundreds of genes putatively affected by variants that possess Gene Ontology descriptors were detected, among which some were shown to be putatively linked to the morphological traits that distinguish ’TB2018’ from ’Senatore Cappelli’, Overall, this study poses the basis for a possible exploitation of ’TB2018’ per se in cultivation or as a source of alternative alleles in the breeding of traditional cultivars. This work also presents a genomic methodology that exploits the information contained in a low-depth, whole-genome sequence to derive genotypic data useful for cross-platform (chip data) comparisons.