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MORPHOLOGICAL AND GENETIC CHARACTERIZATION OF A LARGE COLLECTION OF ITALIAN TOMATO LANDRACES

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Increased interest towards traditional tomato varieties is fuelled by the need to rescue desirable organoleptic traits and to improve the quality of fresh and processed tomatoes in the market. In addition, the phenotypic and genetic variation preserved in tomato landraces represents a means to understand the genetic basis of traits related to health and organoleptic aspects and to breed them in modern varieties. In the frame of Horizon 2020, the TRADITOM project "Traditional tomato varieties and cultural practices: a case for agricultural diversification with impact on food security and health of European population" (http://traditom.eu/) aims to the collection, characterization and valorisation of European traditional tomato germplasm. The project has the long-term objective to understand biochemical and molecular factors underlying the typicality of traditional tomatoes, in the perspective to genetically improve them without losing quality traits and to eventually breed quality alleles into modern genetic backgrounds. As a part of the whole project collection of over 1500 accessions, this presentation describes the characterization of the main collections preserved in Italy, listing a total of over 430 samples. In two different phenotypic trials, the material has been scored for 18 qualitative variables and measured for further eight plant and fruit traits. Image analysis was conducted with the Tomato Analyzer software allowing for 15 morphometric and nine colorimetric parameters to be detected. A subset of the collection was subjected to metabolic profiling. The accessions showed a wide variability for most scored traits, including, for example, a 90-fold variation for fruit weight, 8-fold for locule number and >4-fold for the soluble solid and carotenoid content. Correlation and ANOVA statistics indicated distinctive differences among groups of accessions belonging to recognized typologies. The classification based on morphology was compared with genotypic data collected through ‘genotyping by sequencing’.