

SNP-BASED MOLECULAR FINGERPRINTING OF THE ITALIAN “ACQUAVIVA RED ONION” LANDRACE

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Landraces of horticultural species represent unvaluable sources of agrobiodiversity, which can be employed in cultivation as such, or used in breeding to broaden the genetic base of modern cultivars. The landrace known as “Cipolla rossa di Acquaviva” (Acquaviva red onion, further referred to as ARO) is traditionally cultivated in a small area of the Apulia region (southern Italy) and is highly requested by the local market. Despite representing an important source of income for farmers, the ARO landrace lacks a solid genetic characterization necessary for its proper valorisation and protection from frauds. In this work, genotyping-by-sequencing (GBS) was used to characterize the genetic variation of seven onion populations commercialized as ARO, as well as one population of the landrace “Montoro”, which is phenotypically similar but is typical from a different cultivation area. A panel of 6,872 SNP markers was used to perform parametric and non-parametric structure analyses. Four ARO populations formed a homogeneous genetic group, clearly distinct from the other ARO and Montoro populations. A set of private alleles was identified and used to fingerprint the core set by means of SNP-based molecular barcode, suitable for traceability of marketable product. Overall, the results of provides insights on the genetic structure of onions marketed as ARO, and provide a framework for further breeding activities and product traceability.