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GENETIC STRUCTURE OF RADICCHIO (*CICHORIUM INTYBUS* L.) CULTIVATED VARIETIES: A COMPARISON BETWEEN F1 HYBRIDS AND SYNTHETICS

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Radicchio (*Cichorium intybus* subsp. *intybus* var. *foliosum* L.) is an important locally cultivated leafy vegetable, mainly used as component of fresh salads or typical dishes. This species is prevalently allogamous with an efficient self-incompatibility system that prevents autogamy.

Radicchio includes different biotypes, but the most important one is the Red of Chioggia. Traditionally, commercial varieties have been developed by recurrent mass selection. In recent years, synthetics have been constituted by breeders through intercrossing or polycrossing a number of mother individuals or clonal lines selected on the basis of their morpho-phenological and agronomic traits, eventually by performing also progeny tests in order to assess their general combining ability. Nowadays, newly released varieties are mainly F1 hybrids developed by Italian or European seed firms through large-scale single crosses between inbred lines selected according to their specific combining ability, exploiting also molecular marker-assisted breeding strategies.

This research has applied DNA genotyping using 29 mapped microsatellite markers scattered throughout the genome in order to assess the population structure of distinct commercial OP varieties as well as F1 hybrids along with their F2 progenies, for a total of 216 samples belonging to the biotype Red of Chioggia. Pair-wise comparisons among varieties were based on several genetic diversity statistics, including heterozygosity estimates, genotype frequencies, observed/expected number of alleles per locus, also by constructing or plotting genetic similarity trees and haplogroup histograms. The degree of heterozygosity of F1 hybrids ranged from 39% to 66%, with a mean estimate of 47% for synthetics. Differently from synthetics, a fixed genotype was found across several loci of the hybrid varieties. Moreover, the number of alleles for single loci was much greater in synthetics (more than 4 per locus up to 10 allele variants) than F1 hybrids and F2 progenies (usually 2 or 3 allele variants up to 4 per locus). The mean estimate of genetic similarity within populations was higher in hybrid varieties (95%, ranging from 92% to 96%) than synthetics (85%). As expected, both UPGMA dendrograms and STRUCTURE clusters revealed different sub-populations that corresponded to the single commercial varieties. Interestingly, F2 progenies were not discriminated from their related parental F1 hybrids.

On the whole, such molecular information will be crucial for breeders in order to understand the extent of genetic distinctiveness, uniformity, and stability of commercial and experimental varieties as well as genetic relationships and relatedness among commercial varieties.

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