

TWO DIFFERENT GENOTYPING METHODS SUGGEST UNCOMMON REPRODUCTIVE BEHAVIOUR IN *APIUM GRAVEOLENS* L. LOCAL POPULATIONS FROM THE LAZIO REGION

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Celery (*Apium graveolens* L.) belongs to the Apiaceae family and represents an important crop for the Italian agriculture from both an economic and cultural point of view. It is known for its different biotypes and botanical varieties. In the present study, we set up to investigate the distinctiveness of “Bianco di Sperlonga”, a landrace from Latium, from the white biotype. Ninety-six genotypes were genotypically characterized using SSR and SNP markers. Among the analyzed populations, 17 consisted in white celery including 12 local accessions and two commercial references of “Bianco di Sperlonga”, one of “Dorato d’Asti”, and two commercial lines. The remaining two populations included two black celeries, the “Nero di Trevi” landrace and a commercial line. SNPs were obtained through ddRADseq genotyping-by-sequencing approach. From the 8 EST-SSRs, 24 alleles were observed that allowed genetic similarity and statistics estimation, populations clustering and membership reconstruction of the analysed samples, although a few cases of missing data were present reducing the results informativeness and reliability for some celery accessions. In contrast, the GBS characterization produced 7281 SNPs, without missing data, shared among the accessions. The GBS information allowed higher reliability confirming the previous clustering, despite SSRs were less reliable. Both the adopted methods demonstrated their suitability for clustering samples depending on their biotype/origin, although SNPs were

more precise given their number. Despite this, populations distinctiveness was observed except for the "Bianco di Sperlonga" samples that closely grouped sharing high genetic similarity (GS) values. These 12 populations shared a mean GS from 95.7% (SSRs) to 98.5% (SNPs), while the other populations were clearly separated from them, "Bianco" commercial references included. Using both methods derived datasets, the clustering dendrograms, the ancestral reconstruction and the PCoA, concurred in confirming the strong relationship occurring between the local populations: an unexpected result, given the prevalently allogamous tendency of this crop species. Other genetic statistics suggesting reproductive strategy changes in these populations to autogamy were: the average homozygosity observed ($H_o > 92\%$), the gene flow values ($N_m < 0.1$) and the AMOVA results. Generally, both methods provided useful genotypic information for local population mapping, traceability or marker assisted breeding, although in this case ddRADseq approach proved to be much more informative than SSR approach given the 300X molecular loci identified. In conclusion, the results coming from this study allowed to establish the distinctiveness of the Bianco di Sperlonga landrace, to confirm its possible derivation from "Dorato d'Asti" and revealed an unexpectedly high degree of homozygosity. This suggested a loss of genetic load due to extremely strict inbreeding in traditional multiplication methods.