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ITS-DGGE ANALYSIS FOR CUCUMIS MELO L. CULTIVAR AUTHENTICATION

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Melon (*Cucumis melo* L.) is a climbing herbaceous annual fruit belonging to the Cucurbitaceae family. It is a cross-pollinated diploid (2n = 2x = 24) species. In Italy, the first region for melon cultivation is Sicily with 155 thousand tons, followed by Lombardy (118 thousand tons), Campania (68 thousand), Puglia (almost 50 thousand tons) and Emilia-Romagna (46 thousand tons). Regarding the cultivation method, the major part (86%) is cultivated in open fields, while the remaining 14% is in the greenhouse. Particularly, in Campania melon cultivation was born in Naples areas thanks to both extraordinary soil fertility conditions and favorable climatic conditions and later was extended to the province of Caserta and Salerno. The development of more extensive cultivation has led to an inevitable modification of the varietal structure with the introduction of new genetic material from other production areas. Local genotypes, therefore, are an excellent source of useful genes and could be cultivated in marginal areas where modern cultivars are less competitive. In order to protect niche products, it could be important the development of rapid and economical protocols apt to trace the product along the supply chain. In this work, we used a DGGE analysis to characterize melon commercial cultivars and local accessions. Primers for sequence isolation were designed on the ribosomal sequences belonging to the *Cucumis melo* L. genome deposited in the GenBank (a.n. EU312158). Amplified fragments were run into 6% polyacrylamide gel in a denaturation gradient (40-43%) and subjected to electrophoretic running at constant voltage (45V) for 16 hours. DGGE runs showed the presence of unique and non-unique bands. Fifty-five unique bands were eluted from the gel and sequenced after re-amplification. To validate the technique, we

used for each sequenced band a specific primers pair that present at the 3'end of the nucleotides variable. The nucleotide variation was considered an SNP only when the amplification product was obtained in a single variety and not in the others. Our results demonstrate that the DGGE is a flexible, cost-effective, and valid method for genotyping by SNPs.