GENETIC DIVERSITY IN COMMERCIAL AND LOCAL VARIETIES OF SQUASH (CUCURBITA PEPO L.) AS ESTIMATED BY MULTIPLEX SSR MARKER APPROACHES

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_Cucurbita pepo_ L. belongs to the genus Cucurbitaceae (2x=2n=40) and is among the economically most important vegetable crops. Generally, the edible round-fruited members of this specie are called “pumpkins” while the non-edible sorts are called “gourds” and the edible non-round-fruited sorts, like zucchini, are called “squash”.

_Zucchini (Cucurbita pepo subsp. pepo), morphotype zucchini_ is one of the most popular vegetable crops of the genus. According to FAOSTAT (2011) estimates, more than 24.3 million tons of pumpkin, squash and gourds were produced annually on an area of approximately 1.8 million hectares. In the same year, ISTAT estimated that the Italian production of Zucchini was about 577.718 tons, on a cultivated area of approximately 18.000 hectares.

Various DNA- sequence polymorphisms have been employed to study the genetic relationships of different _Cucurbita pepo_ sub-species with ever-increasing precision. Recently, large repositories of microsatellites, which are simple sequence repeats highly polymorphic in their length and widely distributed through the genome, were developed and exploited to study the genetic relationships among diverse _C. pepo_ accessions.

Despite the economic relevance of Zucchini and the current availability of large sets of markers and genetic maps, only a few researches focused on marker assisted selection and marker assisted breeding programs were published during the last years. Hence, the aim of our study was to assess the genetic diversity of 18 commercial F1 varieties and four inbred lines of Zucchini with different fruit morphology, by using a set of mapped SSR molecular markers. To this end, we developed a multiplex SSR marker assay based on the use of four different oligonucleotide anchors, which allowed the amplification of up to 16 SSR loci in single multiplex reactions. Finally, the molecular analyses focused on a panel of 21 marker loci selected according to their linkage map position and polymorphism information content (PIC). The degree of heterozygosity (H) and the coefficients of inbreeding (F) were used to study the genetic structure of each variety. The estimation of the extent of genetic variation within varieties and genetic differentiation between varieties was carried out using specific software.

A main finding arising from the molecular analysis was a low degree of heterozygosity (H_0) observed in the analyzed F1 commercial hybrids (0.31). Values of mean genetic similarities calculated within and between _C. pepo_ varieties were an average high, indicating little genetic variation among the considered varieties. Noteworthy, a principal coordinate analysis based on the mean values of genetic similarity estimated within and between squash accessions clustered all varieties characterized by the Zucchini fruit morphotype in a single group, suggesting the possibility that one or more SSR loci could be associated with genes controlling this character.
In conclusion, this research describes the development of a multiplex SSR marker assay that proved to be suitable for fast and cost-effective genotyping Zucchini and its possible exploitation for marker-assisted breeding programs in this species.