

STUDY OF GENETIC DIVERSITY IN APRICOT (*PRUNUS ARMENICA*) USING SIMPLE SEQUENCE REPEATS

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Apricot (*Prunus armenica*) is an edible fruit cultivated all over the world, but the 60% of its production is concentrated into the Mediterranean basin, where it finds the best climate for its growth: hot-dry weather, fresh soil, and bright position. Italy with an extension of 17.000 hectares is one of the most productive European countries, whose national production supremacy is held by Campania (above all Vesuvian aerea) and Emilia Romagna Regions.

The aim of the present study is to characterize an apricot germplasm collection organized by the Regional Office for Agricultural Development and grown in the farm Improsta (SA) by highlighting the presence of simple sequence repeat polymorphism in genomic DNA.

Twelve primers (kindly supplied by Raffaele Testolin) related to 6 SSR loci were used to amplify 42 genomic DNA of apricot samples. Amplification products from these reactions were separated on 2% agarose gel and by capillary elettrophoresis on ABI PRISM 3100 automated sequencer (Applera).

Some SSR exhibited high level of genetic polymorphism. The size of fragments ranging from 76 to 218 base pair and the total number of alleles per locus varied from four to eleven, with a mean of 8.0. The most polymorphic locus was UDap-407 with eleven alleles. The CONVERT, MICROSAT and PHYLIP programs were used to analyze the data and to construct a neighbor-joining dendrogram based on allele frequency data calculated by Nei's genetic distance. The genetic relationship existing among the analysed samples are discussed as a mean to identify apricot varieties.