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MOLECULAR CHARACTERIZATION AND DISCRIMINATION OF ITALIAN TOMATO CULTIVARS

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The tomato, *Solanum lycopersicum* (L.), is an autogamous species with a narrow genetic base. The introduction of the species in Europe, from Mexico, was crucial in the reduction of genetic variability, since in the European habitat tomatoes were generally cultivated in protected environments.

The high degree of genetic uniformity in tomato cultivars is not only strongly influenced by domestication far from the center of origin, but above all by genetic improvement which, *per se*, culminated in the achievement of uniform forms, apart from the fact that only a limited number of genotypes were used for breeding.

Tomato is nowadays one of the most economically important and widely grown plants in *Solanaceae* family. The popularity of tomato as fresh and processed crop has made it an important source of vitamin A and C in diets. In addition to its worldwide agricultural and economic importance as a crop, tomato is a preeminent model system for genetic studies in plants.

Simple sequence repeat (SSR) markers can be useful in variety identification and to analyze the relationships among cultivars. SSR analyses were conducted on four tomatoes sauces and 51 modern and vintage cultivated tomato cultivars, using eleven selected SSR primers. Cluster analysis allowed us to distinguish tomato in two major groups, the first included most of the fresh market varieties and the second included most of the modern processing varieties. The analysis showed a significant variation among varieties. The SSR approach showed considerable potential for tomato variety identification and discrimination. DNA profiles of these crops are even useful for quality control in agri-food chain, considering the possibility to identify the varieties present in the processed tomato.