

CAMELLIA JAPONICA L. GENOTYPES IDENTIFIED BY SSRs FOR IMPROVING CULTIVARS

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The need to preserve genetic variability has been realized in crop field since a long time through the development of germplasm conservation programmes and the establishment of gene banks. On the contrary, the safeguard of varietal variability has been only recently undertaken on ornamental species. Genetic erosion assumes an alarming significance especially in those species in which genetic improvement has originated an extremely high number of cultivars, with a consequent loss or oversight of the ancient ancestors. Among these, *Camellia japonica* L. (Theaceae) represents a bright example, totaling currently about 30,000 cultivars. *Camellia* cultivation has a long history and the wide range of flower forms (e.g. single, anemone, formal), colours, and sizes is the result of many centuries of selection for desirable characteristics, first in China and Japan (Durrant, 1982, Chang and Bartholomew, 1984), then in Europe. The introduction of *Camellia japonica* L. in Italy is dated about 1760 (Remotti, 2002), but only during the XIXth century this species reached a high productive importance, with the selection of brand new cultivars (Corneo *et al.*, 2000).

Nowadays, the Italian production, even if it covers a considerable economic importance, is limited to the commercialization of about 200 cultivars, mostly derived from Eastern Asian ones.

A worrying phenomenon that involves Italian old *Camellia japonica* cultivars is the loss of identity, due to frequent cases of synonymy, homonymy and wrong naming (Remotti, 2002), so the need of restoring the correct names by the use of genetic traits.

The aim of this research is the genetic characterization of ancient *Camellia* cultivars from a historical Italian collection by using a set of four SSR primers developed in *Camellia japonica* (Ueno *et al.*, 1999; Caser *et al.*, 2010) and another set of 26 highly polymorphic microsatellites developed in *Camellia sinensis* (Freeman *et al.*, 2004; Hung *et al.*, 2008). A total of 197 *Camellia japonica* cultivars were selected in the Villa Anelli near Gonte di Oggebbio, (Vb) Italy. Results show that the SSR markers offer a suitable method for discriminate *Camellia japonica* genotypes. In fact, microsatellite allele frequency distribution was employed to describe genetic similarity among *C. japonica* cultivars and to assess the genetic relationships among the *Camellia* cultivars.

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