

## GENETIC IMPROVEMENT PROGRAMS AIMED AT THE ESTABLISHMENT OF NEW VARIETIES OF FLOWERING ORNAMENTAL SPECIES USING MOLECULAR SELECTION METHODS

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*plant breeding, marker-assisted breeding, plant genomics, horticulture, sustainability*

Flowering species constitute a choice of high interest among plants used for urban environments' landscape, due to their high ornamental potential. Furthermore, they can play an important role in providing several ecosystem services to cities, from pollution reduction to heat island phenomenon mitigation. The breeding of flowering ornamental species has been prosecuted so far almost exclusively with phenotypical approaches and it concentrated mostly on flowers' morphological and sensorial traits. Nevertheless, the development of new technologies, the reduction of sequencing costs and the increase in the available knowledges about the related genomes have made the molecular characterization now extendable also to these plants.

The development of a reliable set of molecular markers distinguishing a specific cultivar or a trait of interest is useful for breeding purposes, as well as for phylogeny studies. In order to determine which set of specific markers, like SSRs and SNPs, can be helpful to analyse plant accessions, it is important to know the taxonomy of the material of interest. A lot of flowering ornamental plants can produce vital offspring from interspecific crossing and have been obtained by breeders after decades of crosses without tracking. Hence, it is difficult to determine the original species from which they derive. *DNA barcoding* is a powerful technique to found genomic differences that uniquely identify single species and it has been widely used with successful results in plants. It consists in exploiting universal primers designed in nuclear and plastid coding and non-coding sequences, conserved at the species level.

The main objectives of this research project are the characterization, selection and enhancement of varietal genotypes of herbaceous and shrub species, particularly suitable for sustainable cultivation systems from an environmental, economic and social point of view. Here, we report the preliminary results of the general project, focusing the attention on a DNA barcoding analysis on different accessions of coleus (*Plectranthus* spp.), lantana (*Lantana* spp.), and purslane (*Portulaca* spp.), genera of increasing interest for the ornamental market. The plant material is derived from local germplasms, in order to valorise the typical populations of the territory and their genetic heritage. For the analysis three chloroplast sequences were considered: the *psbA-trnH* intergenic space region, the maturase K (*matK*) and ribonuclease large subunit (*rbcL*) genes, in addition to a nuclear sequence, the internal transcribed region (ITS). The sequencing output has been compared with the related sequences deposited in online databases, specific for DNA barcoding data. In addition to assess the belonging species, the genetic similarity degree between samples and references has been valued. It has been exploited to make a phylogeny tree reflecting the kinship and hence the breeding history of these flowering ornamental cultivars.