

## DEVELOPMENT AND APPLICATION OF MOLECULAR MARKERS FOR GENETIC VARIATION ASSESSMENT IN A PIEDMONTESE LANDRACE OF CELERY

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In Piedmont, as well as in other Italian regions, a large number of vegetable landraces are still locally cultivated. These landraces have a certain genetic identity, are morphologically recognisable and their local demand is growing because of the added value consumers attributes to the taste, appearance, nutritive value of their production and their link with the culture and tradition of the area. Currently, organic farmers are also interested in introducing crop landraces in cultivation, because of their higher adaptation to local pedo-climatic conditions and/or supposed resistance to biotic stresses.

During the past years efforts have been made by the Piedmont Region, section Agricultural Development, to catalogue autochthonous local vegetable ecotypes ([www.regione.piemonte.it/agri/biodiversita/orticolo/schede.htm](http://www.regione.piemonte.it/agri/biodiversita/orticolo/schede.htm)). At present activities involving farmer organizations as well as research institutions are funded, with the main goal to obtain, for at least some of them, the registration as variety and fit the present seed trade regulations. However, as registered varieties are required to meet distinctiveness, uniformity and stability (D.U.S.) parameters, it is at first necessary to quantify the amount of genetic variation which is present in the germplasm in cultivation.

Here we report our preliminary results on the molecular assessment of genetic variation in a local ecotype of celery (*Apium graveolens* var. *dulce*): i.e. ‘Dorato d’Asti’, which is grown in south-east Piedmont and is well appreciated due to its flavour and the production of highly vigorous fleshy stalks with golden ribs.

We quantified genetic variation in tree populations by applying two complementary classes of molecular markers: amplified fragment length polymorphism (AFLP) and simple sequence repeats (SSR = microsatellites), the latter not available at the time of starting the work. Our first goal was thus the *in silico* mining of SSRs. We screened 2277 DNA accessions, downloaded from GenBank, and we found a total of 73 microsatellites containing sequences; the number of potential markers was reduced by means of a cluster analysis and using the sequence editor of MEGA software: redundant accessions and sequences presenting the repetitive motif at one end were discarded. After that, 39 sequences, all derived from ESTs, were selected for PCR amplification. On the whole we developed 11 dbEST-derived microsatellite markers, whose polymorphism was at first explored in sixteen celery commercial varieties, and marker transferability was tested on three accessions of celeriac (*A. graveolens* var. *rapaceum*).

The analysis of AFLP and SSR molecular variance in the three populations of celery ‘Dorato d’Asti’ provided useful information for future application of appropriate mass selection and

breeding strategies aimed at restricting the genetic basis of the material in cultivation and promote the registration of the landrace as a variety.