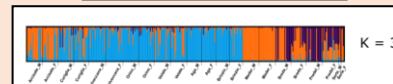
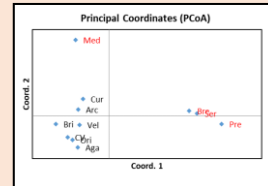
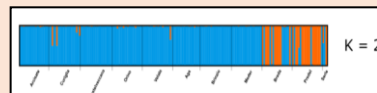


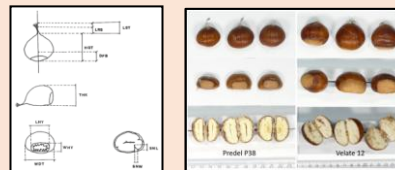
CASTADIVA: Biodiversity and multi-functionality of the chestnut tree. Leveraging genetic resources for the development of Lombardy sub-mountain areas.



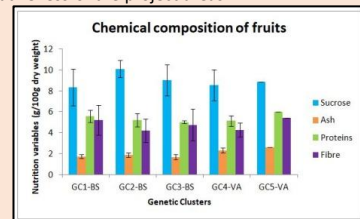
Thereafter mother plants and embryos genetic data were together analysed. Even in this case we found the same results, STRUCTURE and PCoA (not shown) analyses showed high genetic similarity between individuals of the same area. Notably, we found high genetic divergence between mother and embryos only for Serle area (Breda and Predel sites).

Morphological, pomological analyses and chemical composition of fruits

Morphological and anatomical parameters were measured on the whole fruit and on the sectioned fruit (20 fruits per plant) on the entire set of plants analysed for genetic diversity.



A subset of about 50 plants were selected for in-depth analysis of leaf and inflorescence morphology, and chemical composition of the fruit. The plants of this subgroup were chosen according to the criteria of genetic differentiation and territorial distribution, to ensure the representativeness of the project areas.



Flours of fruit sampled from 23 plants (19 from Serle-BS and 4 from the Varese-VA province) from the subset of 50 previously mentioned and representing 3 and 2 genetic clusters (GC) for geographic locations (BS and VA), were analysed. The data obtained show a discrete variability in the content of the various compounds between the GCs and in accordance with published data for chestnut. Lipids and starch content analyses are still in progress.

SUMMARY AND CONCLUSIONS

The results obtained show a genetic diversity of the chestnut groves in the two areas of Lombardy, probably resulting from different chestnut management: in the Serle area, a higher number of clonal individuals identified as "Marrone" were found, while in the Varese area, analyses are underway. Instead, the data obtained show a fair variability in the content of the different compounds among the samples, in particular: sucrose content varies between 8 and 11%, dry matter 40-55%, ash 1.5-2.5%, protein 5-6%, fibre 4-6%.

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BACKGROUND

Over the centuries, the chestnut tree, cultivated for its fruits and timber, has become an essential element of subsistence for many societies in mountain and sub-mountain areas, revealing its potential as a multifunctional species. Today most chestnut forests are in a state of decline and abandonment, mainly due to the depopulation of rural areas, global climate changes and recent outbreaks of exotic pests.

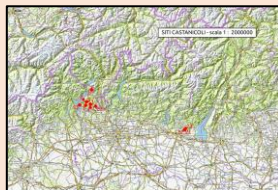
With a view to the recovery and enhancement of chestnut genetic resources, the CASTADIVA project mainly aims to map the chestnut groves in pilot areas of the Lombardy Region (Municipality of Serle, BS and in the Varese Prealps, VA), to evaluate the genetic diversity of chestnut stands, and to genetically characterize local varieties. In parallel, the project includes a characterization of the fruits through morphological, pomological, qualitative and nutritional analyses. CASTADIVA will require integration of data obtained from genetic and morphometric analyses with ecological, silvicultural and possibly socio-economic data, in order to identify the best practices and management criteria for the conservation and enhancement of chestnut genetic resources. Transferring information to local administrations and the agricultural stakeholders will be a final step of crucial importance.

RESULTS: Spatial prospecting

Territorial prospecting, mapping, ecological and silvicultural characterization of two Lombardy's chestnut areas (Serle, BS and different locations in Varese province) has been performed in order to select the representative sites for sampling plant material.

Genetic diversity analysis of chestnut

Leaf and fruit samples of 20 plants for 4 different sites in Serle and 7 in Varese were collected and analysed using 12 genomic microsatellites (SSRs) as molecular markers. The data analysis performed through GeneAlix software showed an higher number of clones in Serle area (Breda and Predel) than in Varese area and in both, genetic diversity indices highlighted a similar genetic variability.



Pop	N	Ns	Nv	I	Hs	Hv	alle	F
Pop Varese	Mean 139,500	10,000	4,202	1,591	0,661	0,715	0,718	0,085
SE	0,230	1,311	0,571	0,136	0,061	0,014	0,014	0,072
Pop Serle	Mean 63,000	7,917	4,389	1,591	0,815	0,738	0,744	0,114
SE	0,000	0,941	0,456	0,118	0,025	0,031	0,032	0,028

STRUCTURE analyses, used to identify population gene pools, showed two different gene pools (K=2) representing the two geographical areas and together with Principal Coordinates analysis (PCoA) highlighted a correlation between geographical proximity and genetic similarity.