

GENETIC CHARACTERIZATION OF AN ENDANGERED SPECIES OF SICILIAN INLAND WATERS: THE MEDITERRANEAN TROUT (*Salmo cetti*)

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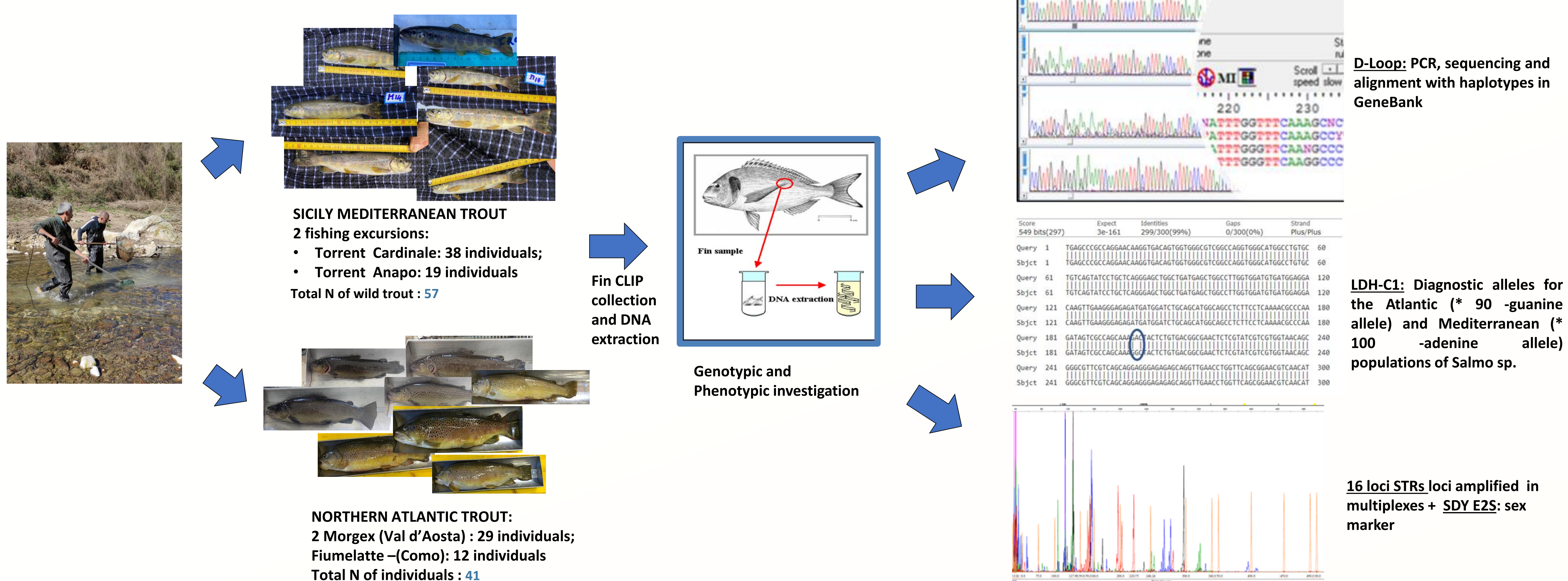
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1. INTRODUCTION

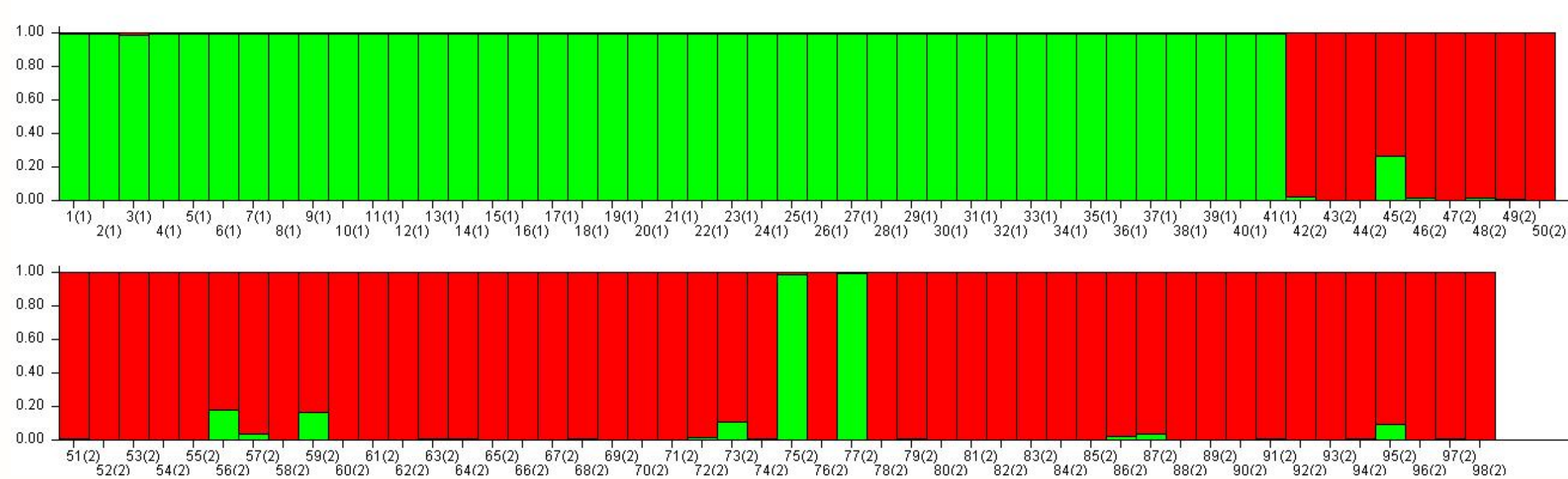
Mediterranean trout (*Salmo cetti*), is endemic species belonging to *Salmo trutta* group which is widespread exclusively in Sardinia, Sicily on a few areas of the Italian Tyrrhenian side. Following repopulation carried out with Atlantic trout, its presence on the Italian territory has undergone a strong contraction due to hybridization and introgression effects. At the moment, *Salmo cetti* is on the IUCN Red List, rated as Critically Endangered (CR). The selection of pure breeders with high genetic variability and the storage of their sperm in a cryobank become important tools to make the management of the conservation of endangered species more efficient. Recent pieces of evidence indicated the presence of a specific haplotype in the Iblei Mountains of Sicily suggesting the presence of some conserved areas with the endemic populations (Segherloo et al., 2021). The objective of the work was to genetically characterize a population of Mediterranean trout (*Salmo cetti*) caught in different waterways of the Iblei Mountains of Sicily in order to verify its level of introgression with the allochthonous Northern Atlantic haplotypes and evaluate the possibility to use this population as a precious resource for future restocking plans.

2. MATERIAL AND METHODS

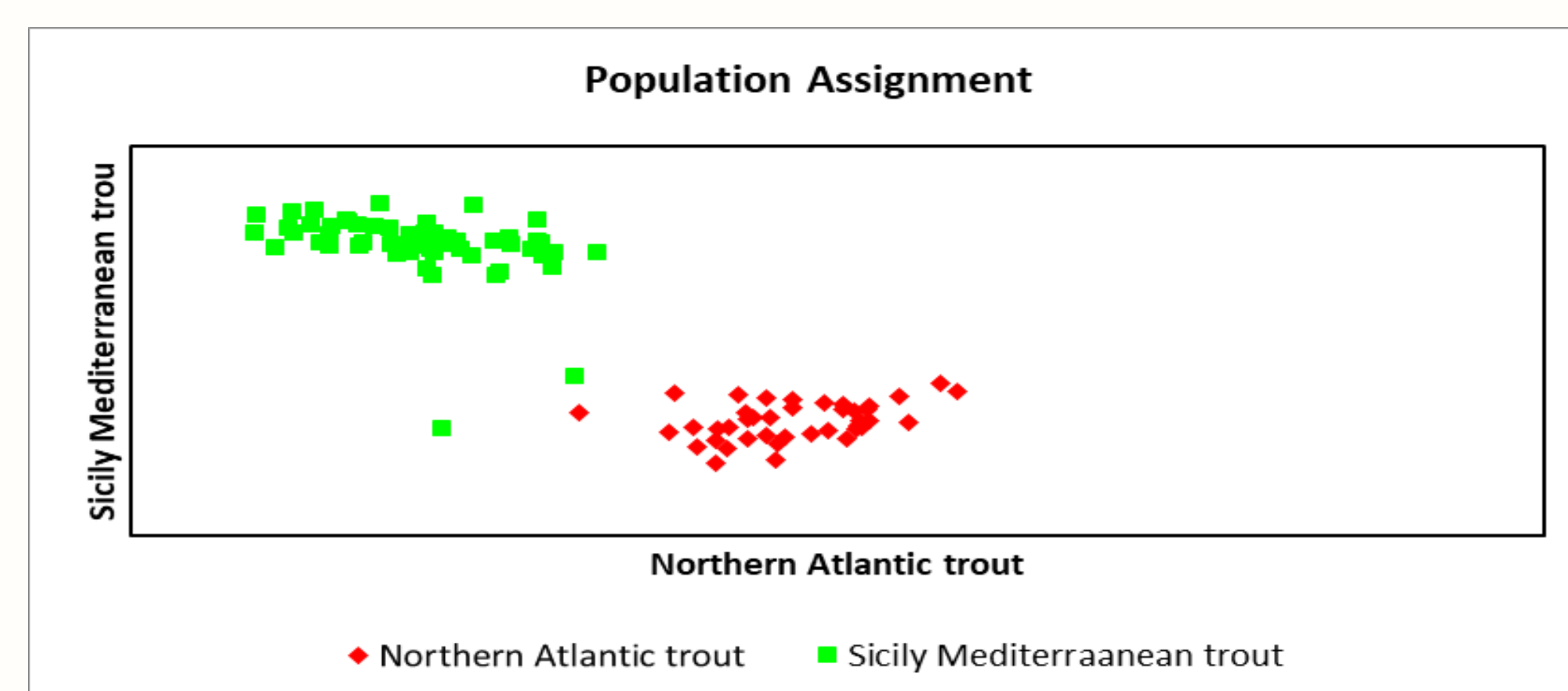


3. RESULTS

The analysis of the SDY-ES2 locus revealed that, out of the total Sicily Mediterranean trout, 42 were males and 15 females. The expected and observed heterozygosity (H_e : 0,630 and H_o : 0,627, respectively) was quite low, as was the actual number of alleles (N_e : 2,70). A deviation from a Hardy-Weinberg equilibrium was found for 9 out of 16 loci ($p < 0.05$). STRUCTURE and GenAIE 6.5 analysis clearly revealed the presence of 2 distinct populations, with few misassignments in the Northern Atlantic populations. The Locus D-loop mtDNA analysis showed that the Sicily Mediterranean population 100% matched with the haplotype sequence present in the database for *Salmo cetti* (GenBank MW251439.1, Segherloo et al., 2021), except for 3 individuals. The screening of the LDH-C1 Locus revealed the presence of 3 individuals with allele LDH-C1 * 90. The hybridization index indicated the 87% of individuals belonging to Class VI (zero potential of hybridization), 6% to Class V and only 8% to Class II (high potential of hybridization) (Pensierini et al., 2006).



Barplots of individual, STR-based admixture as obtained through the Bayesian clustering analysis in STRUCTURE



GenAIE assignment plot showing distinct clustering of all 2 sampled groups

4. DISCUSSION AND CONCLUSIONS

The results obtained in this study indicated that the Mediterranean trout population sampled in some waterways of Sicily Iblei Mountains showed a very low level of introgression with the Northern Atlantic lineage, despite the numerous releases of the allochthonous individuals occurred in the past. Probably, the extreme conditions of the waterways and the permanence to which they are forced make difficult the survival of the North Atlantic haplotype and the relative hybrids. At the same time, the geographic isolation of individuals, due to the characteristics of the waterways, represent a limit to the genetic variability of the population, which was found quite low. The genetic results obtained in this preliminary study suggests a potential use of the Sicily Iblei Mountains trout population as a precious resource for planning native fish restocking activities.

5. REFERENCE

Peakall R., Smouse P.E. GenAIE 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics*. 2012; 28:2537–2539.

Pensierini, M., F. Nomis Marzano, G. Gandolfi, M. Maldini, E. Marconato, and P. Gibertoni. 2006. Fenotipi della trota mediterranea: metodologia di indagine molecolare combinata e selezione morfologica per l'identificazione di esemplari autoctoni. Quaderni ETP - *Journal of Freshwater Biology* 34:69-75.

Segherloo, I.H.; Freyhof, J.; Berrebi, P.; Ferchaud, A.L.; Geiger, M.; Laroche, J.; Levin, B.A.; Normandeau, E.; Bernatchez, L. A genomic perspective on an old question: *Salmo* trouts or *Salmo trutta* (Teleostei: Salmonidae)? *Mol. Phylogenetics Evol.* 2021, 162, 107204.

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