Molecular approaches to macrophytic biodiversity monitoring in the Venice Lagoon

Filippo Drigo[1,2*], Chiara Frasson[3], Chiara Stefanelli[1], Riccardo Trentin[1,4], Emanuela Moschin[1], Davide De Battisti[1], Isabella Moro[1,2,5], Cristiano De Pittà[1,2]

*lead presenter: filippo.drigo@studenti.unipd.it
1 Department of Biology, University of Padova, Padova, Italy
2 National Biodiversity Future Centre (NBFC), Italy
3 Pediatric Research Institute "Città della Speranza", Padova, Italy
4 Centro de Ciências do Mar do Algarve (CCMAR/CIMAR LA), Campus de Gambelas, Universidade do Algarve, Faro, Portugal
5 Department of Integrative Marine Ecology, Stazione Zoologica Anton Dohrn, Villa Comunale, Napoli, Italy

The Venice Lagoon is the largest transitional environment within the Mediterranean Sea (almost 550 km^2). Due to this characteristic, it contains many different ecological niches, hence the biodiversity in this environment is very high. At the same time, this lagoon system is under constant pressure from global climate change and human activities, and it has been greatly modified by humans during the centuries.

Three field monitoring campaigns were conducted across salt marshes and wood poles in the Venice Lagoon between 2023 and 2025. All collected samples were classified using an integrated morphological and molecular approach, in which morphological observations guided the selection of appropriate gene marker for species identification through DNA barcoding. To further increase identification reliability, a phylogenetic tree was reconstructed for each major taxon to evaluate clustering patterns and sequence relationships, and two independent species delimitation approaches, ASAP and GMYC, were applied.

Reliable sequences were obtained for 50% of the samples and aligned with reference databases. Overall, morphological and molecular approaches yielded consistent identifications in approximately 50% of cases for seaweeds and approximately 75% for higher plants. In total, 73 species were identified, comprising 13 Chlorophyta, 11 Heterokontophyta, 25 Rhodophyta, and 24 Tracheophyta, with 8 out of 35 NIS listed for the Venice Lagoon being recorded. Additionally, the presence of *S. x townsendii* was confirmed in the Southern and Central lagoon, and a higher abundance of the NIS *S. anglicus* was observed relative to the native *S. maritimus*.

Overall, this study highlights the importance of integrating morphology-based identification with molecular tools to achieve reliable species assessment, which is fundamental for long-term monitoring activities, especially in threatened environments such as the Venice Lagoon.