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Global Climate Change Amplifies Aquatic Invasive Species Impacts

PROGRAM AND ABSTRACTS

Netherlands Food and Consumer Product Safety Authority
Ministry of Agriculture, Nature and Food Quality

RESEARCH INSTITUTE **NATURE AND FOREST**

Invasive Species Centre

Phylogenetic analyses reveal a new old introduced red algal species in Europe

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The detection of invasive species is commonly challenging in marine environments, often related with the insufficient taxonomic knowledge of the local diversity. Using DNA sequences in diversity surveys and their phylogenetic analysis can assist us to clarify the native or introduced origin of some species. We applied this approach to study the red algae *Aphanocladia stichidiosa*. It was originally described in the Mediterranean (1955), later recorded in Portugal (1960), the Canary Islands (1986), the northwestern Spain (1990) and the Azores (2012). Unexpectedly, our diversity surveys in Australia revealed its presence in Victoria in 2015, finding that European and Australian specimens had identical DNA sequences (*rbc*L gene) and suggesting that it is introduced in one of the regions. Phylogenetic analysis resolved A. stichidiosa in a highly supported clade with species restricted to the southern hemisphere, mainly from Australia. Accordingly, we conclude that *A. stichidiosa* is native from Australia, although it has never been recorded there before, and that it represents a relatively old introduction in Europe. In both native and introduced regions, it is frequent in algal turfs, a type of assemblage composed by a carpet of small, morphologically similar species whose identification is often difficult. The type of growth of this species explains the absence of previous records in Australia, where the number of taxonomists studying this assemblage is lower than in Europe. Sequential reports of *A. stichidiosa* in different European regions suggest that it is expanding its distribution, as well as its abundance is increasing. The invasive character of this species needs to be determined yet, and its small size should not lead to underestimate its potential harmfulness. In the current context, in which kelp forests are globally declining and algal turfs are expanding, this species might play a relevant role in the transformation of the European marine ecosystems.

Identifying EU-listed Aquatic Invasive Species by DNA-barcoding using currently available sequence data

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The introduction of Invasive Alien Species (IAS), whether by accident or deliberately, can have negative consequences when they manage to establish viable populations in new environments. Because IAS can be disruptive and hard to eradicate, measures to prevent initial introduction and spread are the most cost-effective management approach. This requires an early detection and accurate identification of intercepted specimens of potential IAS. Because morphology-based species identifications are not always possible (e.g. cryptic species, trace material, early life-stages), the Barcoding Facility for Organisms and Tissues of Policy Concern (BopCo; https://bopco.myspecies.info/) investigated and evaluated the usefulness of DNA sequences to identify each of the 24 aquatic species currently listed on the European Regulation regarding IAS (2016/1141 and later additions). The reliability of DNA-based species identifications, however, depends on the completeness and correctness of the available sequence data, as well as on the evolutionary rate of the selected DNA marker, which determines its ability to distinguish taxa at the species level.

BopCo produced concise factsheets for each of the 24 species containing information on species taxonomy and current distribution in Europe, as well as a discussion on the usefulness of publicly available DNA sequence data to identify samples to the taxonomic level applied in the EU list (https://bopco.myspecies.info/content/invasive-alien-species-ias-factsheets). Recommendations are made on which DNA marker(s) to use when identifying a potential IAS sample. An overview will be presented how well the data cover the identification needs, highlighting the encountered issues (e.g. lack of sequence data, erroneous taxonomic assignments), their frequency of occurrence and the implications for assuring reliable identifications of invasive alien species.