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Conference Abstract

Applications of environmental DNA methods for charophyte biodiversity

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Abstract

The use of environmental DNA (eDNA) for qualitative species inventories offers great potential as a cost-effective tool for species identification. This requires that the target species release DNA, reference information is available and detection methods exist. Environmental DNA analyses are currently used routinely to inventory fish fauna (Wang et al. 2021), molluscs (Klymus et al. 2017) or insects (Uchida et al. 2020). For other groups, such as macrophytes, there is not much information available (Scriver et al. 2015). In plants, identifying suitable eDNA markers been much more challenging, as no single DNA region has been accepted for the purposes of barcoding.

Within this project, we assessed if stoneworts (Charophytes, Characeae) can be detected by using eDNA analysis and if it can be used to support macrophyte monitoring. Charophytes are macroscopic green algae which, because of their role as habitat engineers, are of special importance for aquatic ecosystems. Many charophyte species are bound to clean, nutrient-poor fresh and brackish waters (e.g. Melzer 1999) and are regarded bioindicators for water quality by national and international directives (e.g. Habitats Directive, EU Water Framework Directive). Being sensitive to anthropogenic pressures, a drastic decline in populations with increasing eutrophication has been reported (Sand-Jensen et al. 2017) . However, the diversity of Characeae is often underestimated due to difficulties in morphological determination, and the genetic identification of charophytes has been established only in the recent few years (e.g. Nowak et al. 2016).

We assessed the potential utility of eDNA to document the diversity of charophyte species. eDNA from a fresh water lake (Dreetzsee, Germany, 2018) and from a brackish water site (Darß-Zingst Lagoon System, Germany, 2018) was extracted from filtered or ethanol-precipitated water samples, and we designed and tested eDNA markers based on four regions of the chloroplast genome - *atp*B, *rbc*L, *psb*C, and *matK*. Of the four regions, *matK* and *rbc*L were most likely to amplify DNA from charophyte species. Both sites exhibit a diverse charophyte flora, which we successfully could identify to species/group level by eDNA analysis.

In a current study, the developed eDNA markers are used to scrutinize the charophyte population of the Schlei estuary (Germany, Schleswig-Holstein). Since conventional monitoring can only be carried out once a year at a few sites, Characeae have not been observed in recent years, or only very sporadically. As it is not possible to survey the entire Schlei, especially due to high water turbidity, the eDNA methodology is tested to assess the presence of Characeae species.

Keywords

environmental DNA; Characeae; plants; biodiversity

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