



Conference Abstract

Environmental DNA methods for the analysis of macroorganismal populations

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Abstract

Environmental DNA (eDNA) methods have been widely used to investigate the distribution and abundance/biomass of macroorganisms. eDNA methods analyze DNA collected directly from the environment, such as from water, soil, and air. The techniques have been applied to many taxa inhabiting various aquatic and terrestrial ecosystems. The recent development of eDNA methods has revolutionized the way we assess macroorganisms in natural environments.

In this talk, I will present current developments of eDNA methodology, especially with regard to population analysis using various DNA measurement methods. For example, 1) eDNA was used to assess fish species distributions and abundance/biomass (Takahara et al. 2012, Doi et al. 2017a), 2) quantitative PCR of sedimentary DNA was applied to sediment core samples to detect the DNA of three dominant fish species spanning the last 300 years (Kuwaie et al. 2020), and 3) new methods for sampling eDNA from water (Doi et al. 2017b) and on-site measurement (Doi et al. 2020) will be presented. I end by addressing the need for standardized protocols for eDNA monitoring to enable broader uptake of eDNA technology (Minamoto et al. 2021).

Presenting author

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