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SPECIAL FEATURE: FOREWORD

Environmental DNA as a Practical Tool for Aquatic Conservation and Restoration

Special issue: Environmental DNA as a practical tool for aquatic conservation and restoration

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Environmental DNA (eDNA) analysis has been widely used to investigate the distribution and abundance/biomass of macro-organisms, and during the past decade, the application of eDNA-based biomonitoring has gained increasing interest (Goldberg et al. 2015; Thomsen and Willerslev 2015; Tsuji et al. 2019; Doi et al. 2021). eDNA, which comprises DNA fragments released by organisms into the environment is believed to be derived from mixtures of feces, skin cells, mucus, and secretions. eDNA techniques can be used to analyze DNA collected directly from environmental sources, such as water, soil, and air (Goldberg et al. 2015). With respect to water bodies, these methods have been applied in monitoring multiple species inhabiting a range of limnologic habitats, including rivers, lakes, and ponds, and eDNA detection and quantification have been performed for a diverse range of taxa, including fish, aquatic plants, mollusks, insects, crustaceans, reptiles, amphibians, birds, and mammals (Tsuji et al. 2019).

eDNA analysis involves the use of one or both of two detection techniques, namely, real-time PCR and metabarcoding via DNA sequencing (Tsuji et al. 2019; Doi et al. 2021). In addition, high-throughput DNA sequencing has recently been applied for the simultaneous detection of multiple taxa [e.g., the fish community (MiFish); Miya et al. 2015], a procedure referred to as “eDNA metabarcoding.” eDNA methods can be applied to perform two types of estimation, namely, the presence/absence and abundance/biomass of organisms. Of these two approaches, most eDNA studies conducted to date have sought to estimate the presence or absence of species based on the detection of DNA copies using real-time PCR or DNA sequencing with universal primers. However, comparatively few studies have attempted to estimate species biomass and abundance based on eDNA concentrations in water (Takahara et al. 2012; Doi et al. 2017).

By performing eDNA surveys of water bodies, we can obtain information on the distribution of species and changes in their populations with high taxonomic resolution. Consequently, it is anticipated that eDNA methods will revolutionize the scope and efficacy of biodiversity management and conservation surveys in aquatic habitats. Accordingly, eDNA methods can provide a practical tool for aquatic conservation and restoration. In this regard, recent advances in portable, field-friendly technology, and molecular genetics techniques (e.g., DNA metabarcoding for communities and species-specific eDNA detection of invasive or rare species) have provided additional approaches for the expansion of research in the conservation of aquatic habitats (Huerlimann et al. 2020).

However, despite these promising advances, further developments are still required to enhance the quality, reliability, and interpretability of aquatic eDNA analyses. In this special issue, we have collected articles with particular relevance to two main topics regarding the application of eDNA analysis for aquatic ecosystems: (1) eDNA methods for aquatic species/community detection and quantification and (2) eDNA surveys for the conservation and restoration of the aquatic ecosystems. Given the importance and paucity of information regarding eDNA, the case studies and review presented in this special issue highlight the potentially instrumental contribution of eDNA as a practical tool for aquatic conservation and restoration.

Data Availability In this preface article, we did not use any data.

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References

Doi H, Inui R, Akamatsu Y, Kanno K, Yamanaka H, Takahara T, Minamoto T (2017) Environmental DNA analysis for estimating the abundance and biomass of stream fish. Freshw Biol 62:30–39. https://doi.org/10.1111/fwb.12846

Doi H, Minamoto T, Takahara T, Tsuji S, Uchii K, Yamamoto S, Katano I, Yamanaka H (2021) Compilation of real-time PCR conditions toward the standardization of environmental DNA methods. Ecol Res 36:379–388. https://doi.org/10.1111/1440-1703.12217

Goldberg CS, Strickler KM, Pilliod DS (2015) Moving eDNA methods from concept to practice for monitoring aquatic macroorganisms. Biol Conserv 183:1–3. https://doi.org/10.1016/j.biocon.2014.11.040

Huerlimann R, Cooper MK, Edmunds RC, Villacorta-Rath C, Le Port A, Robson HLA, Strugnell JM, Burrows D, Jerry DR (2020) Enhancing tropical conservation and ecology research with aquatic environmental DNA methods: an introduction for non-environmental DNA specialists. Anim Conserv 23:632–645. https://doi.org/10.1111/acv.12583

Miya M, Sato Y, Fukunaga T, Sado T, Poulsen JY, Sato K, Minamoto T, Yamamoto S, Yamanaka H, Araki H, Kondoh M, Iwasaki W (2015) MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. R Soc Open Sci 2:150088. https://doi.org/10.1098/rsos.150088

Takahara T, Minamoto T, Yamanaka H, Doi H, Kawabata ZI (2012) Estimation of fish biomass using environmental DNA. PLoS ONE 7:e35868. https://doi.org/10.1371/journal.pone.0035868

Thomsen PF, Willerslev E (2015) Environmental DNA—an emerging tool in conservation for monitoring past and present biodiversity. Biol Conserv 183:4–18. https://doi.org/10.1016/j.biocon.2014.11.019

Tsuji S, Takahara T, Doi H, Shibata N, Yamanaka H (2019) The detection of aquatic macroorganisms using environmental DNA analysis—a review of methods for collection, extraction, and detection. Environ DNA 1:99–108. https://doi.org/10.1002/edn3.21