

## Development and Application of Environmental DNA techniques for Evaluating Distribution and Population Status of Rare/Invasive Species

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[Abstract]

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Maintenance of biodiversity and local ecosystems is crucial for ecosystem services. However, the extent of monitoring biodiversity and ecosystems, particularly for rare and invasive species, has been constrained due to the costs and time limitations associated with traditional catch surveys. On the other hand, recently developed environmental DNA (eDNA) methods, which utilize DNA in environmental media for estimating distributions, can significantly reduce the costs and time required for wildlife monitoring. In this project, we aimed to further develop the eDNA methods for estimating distributions, biomass, intra-genetic variations, and long-term population dynamics of rare and invasive aquatic organisms at the same time. For now, its applicability is rather limited to the presence/absence of wild organisms, but with the technical advances we aimed for, we believe that one can apply an eDNA method to estimate not only distributions of rare/invasive animals but also their status and past population dynamics based both on water and aquatic sediment core samples. Our results indeed suggest that our new methods can be used for estimating haplotype distributions of both rare and invasive species, from which we understand their distribution histories without catching them. Analyses of sediment core samples also suggest historical changes in biodiversity as well as population/genotype dynamics of target species. We illustrated such a capability by applying the eDNA methods to real-world problems with a variety of endangered species such as Sakhalin taimen (*Parahucho perryi*) and Honmoroko (*Gnathopogon caerulescens*), and invasive species such as Largemouth bass (*Micropterus salmoides*) and Bluegill (*Lepomis macrochirus*). Overall, we show the great capability of eDNA as a tool to provide a scientific basis for management priorities on rare or invasive species, simply by collecting environmental media.

[References]

- 1) T. MINAMOTO, M. MIYA, T. SADO, S. SEINO, H. DOI, M. KONDOH, K. NAKAMURA, T. TAKAHARA, S. YAMAMOTO, H. YAMANAKA, H. ARAKI, W. IWASAKI, A. KASAI, R. MASUDA and K. UCHII: Environmental DNA, 3, 8-13 (2021) (IF : 6.9) An illustrated manual for environmental DNA research: Water sampling guidelines and experimental protocols.
- 2) H. MIZUMOTO, T. MITSUZUKA and H. ARAKI: Frontiers in Ecology and Evolution 8: 569425 (2020) (IF : 4.493) An environmental DNA survey on distribution of an endangered salmonid species, *Parahucho perryi*, in Hokkaido, Japan.
- 3) T. JO, and H. YAMANAKA: Ecology and Evolution, 12: e9234 (2022) (IF : 3.167) Fine-tuning the performance of abundance estimation based on environmental DNA (eDNA) focusing on eDNA particle size and marker length.
- 4) K. WAKIMURA, K. UCHII and T. KIKKO: Environmental DNA, 00, 1-14 (2023) (IF : 6.9) Evaluation of genetic diversity in an endangered fish *Gnathopogon caerulescens* using environmental DNA and its potential use in fish conservation.
- 5) H. DOI, M. YASUHARA and M. USHIO: Biology Letters 17: 20200666 (2021) (IF : 3.904) Causal analysis of the temperature impact on deep-sea biodiversity.