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Conference Abstract

Degradation factors of environmental DNA evaluated by experiments and meta-analysis

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Abstract

Environmental DNA (eDNA) methods have been developed to detect organisms' distributions and abundance/biomass in various environments. eDNA degradation is critical for eDNA evaluation, but, the dynamics and mechanisms of eDNA degradation are largely unknown, especially when considering different eDNA sources, e.g., cell-derived and fragmental DNA. In this study, we conducted the degradation experiments (Saito and Doi 2020a) and a meta-analysis (Saito and Doi 2020b). Firstly, we experimentally evaluated the degradation rates of eDNA derived from multiple sources, including fragmental DNA (the DNA of internal positive control, IPC), free cells from *Oncorhynchus kisutch*, and the resident species (Saito and Doi 2020a). We conducted the experiments with pond and seawater to evaluate the differences between freshwater and marine habitats. Our results showed that eDNA derived from the both cells and fragmental DNA decreased exponentially in the both sea and pond samples. The degradation of eDNA from the resident species showed similar behavior to the cell-derived eDNA.

As a meta-analysis, we complied the degradation rates of eDNA in laboratory experiment and field studies from 28 studies (Saito and Doi 2020b). We also collected the related factors, including water sources, water temperature, DNA regions, and PCR amplicon lengths of the measured DNA. Our results suggested that water temperature and amplicon length were significantly related to the degradation rate of eDNA. From the simulation based on the 95% quantile model, we predicted the maximum degradation rate of eDNA in various combinations of water temperature and PCR amplicon length.

Keywords

Environmental DNA, degradation, meta-analysis

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