Parameterizing the particle size distribution of macrobial eDNA using the Weibull distribution model

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May 25, 2022

Abstract

Knowledge of the persistent state of environmental DNA (eDNA) particles in water and modeling its particle size distribution (PSD) is crucial to refine the eDNA sampling strategy. Previous studies measured eDNA concentrations at different size fractions to infer eDNA PSDs, whereas such discrete PSDs greatly depend on filter pore sizes used and may potentially bias our understanding of eDNA states. Here, I evaluated the Weibull distribution model as a tool for parameterizing eDNA PSDs. First, of the selected models developed for PSDs, the Weibull model was fitted most accurately to the eDNA PSD. Second, the Weibull parameters significantly varied depending on target genetic regions (mitochondrial/nuclear), time passages, and species, which also substantially changed the eDNA capture efficiency at a given filter pore size. According to the results, the higher detectability of multi-copy nuclear eDNA than mitochondrial one could partly be accounted for differences in their PSDs, a larger pore size filter could be suitable to detect the eDNA releases associating incidental events, and the optimum filter pore size for sufficient eDNA detection could be different among the taxa. Although further consideration is needed, this study provided the groundwork for optimizing the strategy of aqueous eDNA sampling, which contributes to efficient biodiversity conservation and ecosystem management.

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