

Brief summary of dissertation

As a non-invasive genetic method, eDNA based approaches have become an important component of ecologists' and environmental managers' toolkits for biomonitoring in conservation and an increasingly important source of ecological knowledge. This thesis focuses on aquatic eDNA based approaches beyond detections of species presence by 1) enhancing the knowledge of the characteristics of aquatic eDNA particle size distribution (PSD), 2) exploring the possibility of eDNA analysis in physiological investigation and 3) performing functional gene analysis across species. Aquatic eDNA PSD changes with degradation interacting with environmental factors and species. This knowledge supports the capability of eDNA PSD analysis in assessing false- and real-positive of species presence, as well as contributing to abundance assessment and guiding sampling strategy development when using eDNA based approaches. eDNA methylation varies between life stages, and supports life stage evaluations, and brings up the possibility of using eDNA methylation analysis in assessing physiological information. eDNA based approaches support functional gene analysis across species. Functional gene analysis promotes investigating ARGs pollution and the interaction of pollution between different types of agricultural regions. Thanks to the continuously increasing insights on environment-related gene function and expression level, it becomes potentially possible to use eDNA functional gene (and methylation) analysis to evaluate environmental changes. Overall, this thesis contributes to expanding the application of aquatic eDNA based approaches beyond detections of species presence, and provides efficient and non-invasive approaches for biomonitoring and ecological assessments.