

Environmental DNA metabarcoding reveals comparable responses to agricultural stressors on different trophic levels of a freshwater community

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Abstract

Freshwater habitats are under stress from agricultural land use, most notably the influx of neonicotinoid pesticides and increased nutrient pressure from fertilizer. Traditional studies investigating the effects of stressors on freshwater systems are often limited to a narrow range of taxa, depending heavily on morphological expertise. Additionally, disentanglement of multiple simultaneous stressors can be difficult in field studies, whereas controlled laboratory conditions do not accurately reflect natural conditions and food webs. To overcome these drawbacks, we investigated the impacts of two agricultural stressors (the neonicotinoid insecticide thiacloprid and fertilizer) in full-factorial design in a semi-natural research site, using environmental DNA sampling to study three different taxonomic groups representing three trophic levels: bacteria (decomposers), phytoplankton (primary producers), and chironomids (consumers). The results show considerably impact of both stressors across trophic levels, with an additive effect of fertilizer and thiacloprid on community composition at all levels. These findings suggest that agricultural stressors affect the entire food web, either directly or through cascade reactions. They are also consistent with morphological assessments that were performed in the same study site, even at a lower number of replicates. The study presented shows that the use of multi-marker environmental DNA provides a more comprehensive assessment of stressor impacts across multiple trophic levels, at a higher taxonomic resolution than traditional surveys. Additionally, over a thousand putative novel bio-indicators for both agricultural stressors were discovered. We encourage further investigations into stressors impacts at different trophic levels, which will lead to more effective monitoring and management of freshwater systems.

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