



Monitoring environmental health using eRNA

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Text While environmental DNA has been widely adopted for recovering biodiversity trends, the use of environmental RNA (eRNA) for biomonitoring is very much lagging behind. This can come across as surprising given that RNA provides a layer of functional information beyond species detection, as actively transcribed genes can reflect the health of organisms and communities, and consequently ecosystems. We harnessed functional information from eRNA, defined as RNA extracted from the environment, which includes extra-organismal RNA (eoRNA) from macroorganisms as well as whole microorganisms. We applied heat stress first to a simple and, then to a more complex freshwater community composed of bacterio- zoo- and phyto-plankton. We collected and sequenced eRNA (water samples) as well as organismal RNA (oRNA) directly from bulk zooplankton samples, enabling comparisons between eoRNA and oRNA based gene expression profiles. In the simple community, based on eoRNA alone, we detected 3941 *Daphnia* genes and identified 42 as differentially expressed (DE) following heat stress. Of these, 62% were also DE in oRNA and exhibited similar levels of relative expression in both RNA types. Within the whole community of eRNA, we detected heat stress responses across the major classes of zooplankton and phytoplankton, and community-wide shifts in functional KEGG orthologs. Our study demonstrates that transcriptomic profiling based on eRNA has the potential to reveal not only the community assemblage but also the health status of diverse communities of organisms, with broad potential implications for biological monitoring across the trophic chain.

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