

Title: Autonomous samplers and environmental DNA metabarcoding: sampling day and primer choice have greatest impact on fish detection probabilities

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Abstract:

Unprecedented rates of biodiversity loss and ecosystem function necessitate the use of rapid, efficacious, and cost-effective biomonitoring tools. The combination of autonomous samplers and high throughput sequencing (i.e., “metabarcoding”) of environmental DNA (eDNA) samples enables characterization of entire communities at high frequency and can be important tools for conservation and management, allowing researchers to track fluctuations in biodiversity. We deployed two autonomous samplers at two U.S. Geological Survey streamgage sites in the Upper Snake River (Wyoming and Idaho, USA) to collect eDNA samples from July-September 2021 and 2022 to characterize fish diversity. We used a probabilistic approach to evaluate the effects of water temperature, water discharge, filter pore size, water volume filtered, number of samples collected, timing, and primers on the probability of detecting eDNA from fish species known to be present. We detected eDNA from 11/15 species present in these areas of the Snake River. Overall, we did not find evidence that filter pore size, water volume filtered, water discharge, and water temperature affected the probability of detecting fish species’ eDNA. By contrast, primers and sampling day affected fish detection probabilities, indicating that primer choice and sampling day can either over- or under- estimate species diversity. These results indicate that researchers should consider spreading out sampling (i.e., not on consecutive days) and consider which primer set will maximize species detections.