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To the editors of *Molecular Ecology Resources*:

Enclosed, please find a manuscript my co-authors and I believe would be ideally suited for *Molecular Ecology Resources*. In this article, entitled, “Effects of environmental contamination on diet DNA metabarcoding data of invertebrate consumers in mesocosms and natural environments”, we present results from a surface sterilization treatment of invertebrate consumers prior to DNA metabarcoding aimed at exploring the effects of surface contaminants on diet DNA data. We believe this study directly relates to the scope of *Molecular Ecology Resources* by providing validation and improvement of DNA metabarcoding as a molecular tool for diet studies across taxa in a wide range of environmental contexts.

Our findings provide evidence from an open terrestrial environmental context that surface contamination does not systematically alter DNA metabarcoding-derived diet data, but that in a contained, mesocosm environment, surface contaminants from shared space with a diet item could inflate estimates of consumption. We believe this study to be timely and of general interest as DNA metabarcoding continues to provide valuable insight into a range of consumptive interactions in invertebrate consumers (e.g. host-parasitoid, predator-prey, consumer-fungus) across environmental contexts, including aquatic, marine, terrestrial, and experimental mesocosms. However, the field has not addressed the potential problem of environmental contamination and systematic fixes (e.g. surface sterilization). Our results suggest that environmental, ecological, and methodological aspects of diet DNA metabarcoding studies can play a role in the risk of surface contamination and we suggest next directions in validating DNA metabarcoding across environments and invertebrate consumer taxa. Diet DNA metabarcoding is a promising approach for revealing consumptive interactions in a range of taxa, including invertebrates, that have been foundational to the study of biodiversity. Refining methods and protocols in this field will continue to expand our understanding of ecological communities and functions.

We look forward to hearing your thoughts on this work. Please feel free to contact me with any questions about this material. On behalf of my co-authors, I thank you for your consideration of our submission.

Sincerely,

Ana Miller-ter Kuile