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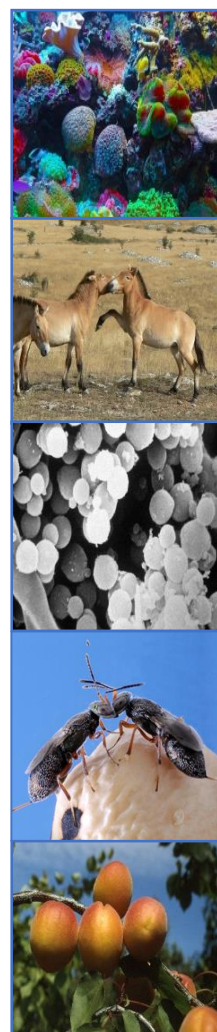
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DNA metabarcoding of passive trap collection media for forest insect biomonitoring

Lucas Sire^{*1}, Paul Schmidt Yáñez², Annie Bézier¹, Béatrice Courtial³, Susan Mbedi⁴, Sarah Sparmann⁴, Rodolphe Rougerie⁵, Christophe Bouget⁶, Michael T. Monaghan^{2,7}, Elisabeth Herniou¹, and Carlos Lopez-Vaamonde^{1,3}

¹Institut de recherche sur la biologie de l'insecte UMR7261 – Université de Tours, Centre National de la Recherche Scientifique : UMR7261 – Av Monge 37200 TOURS, France

²Leibniz Institute of Freshwater Ecology and Inland Fisheries – Berlin-FriedrichshagenNeuglobsowBerlin-AdlershofBerlin Center for Genomics in Biodiversity Research (BeGenDiv), Germany

³INRAE UR0633 Zoologie Forestière – INRAE, UR063 Zoologie Forestière - Orléans, France – Orléans, France, France

⁴Berlin Center for Genomics in Biodiversity Research (BeGenDiv) – Berlin, Germany, Germany

⁵Institut de Systématique, Evolution, Biodiversité – Université des Antilles, Museum National d'Histoire Naturelle, Ecole Pratique des Hautes Etudes, Université Paris sciences et lettres, Centre National de la Recherche Scientifique : UMR7205, Sorbonne Université – 57 rue Cuvier - CP 50 - 75005 Paris, France

⁶Ecosystèmes forestiers – Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement : UR1455 – Domaine des Barres, F-45290 Nogent-sur-Vernisson, France

⁷Freie Universität Berlin – Kaiserswerther Str. 16-18, 14195 Berlin, Germany

Abstract

Insect decline has been increasingly reported in the past years due to global change. Large-scale biomonitoring has thus become necessary to better understand the dynamics of insect communities and to preserve their essential role in ecosystem functioning. In that sense, coupling high-throughput sequencing and DNA metabarcoding has exponentially increased our potentiality to monitor insect communities over wider geographic regions and time scales. However, biomonitoring of entomofauna using molecular tools often results in destructive DNA extraction through voucher grinding, impeding primordial morphological back-up. Here, we filter unprocessed collection medium to assess insect communities through environmental DNA metabarcoding. We demonstrate that recovered communities are different yet complementary and that insect response to environmental changes remains similar to homogenate bulk metabarcoding. We also show that insect orders-by their contrasting sclerotization ratio-, and collection medium type, are unequal in yielding metabarcoding results. Overall, we believe it as an efficient alternative for biomonitoring insect response to ecological changes while preserving insect vouchers for identification and description, especially in tropical regions where singletons or undescribed species can be very common in trap samples.

^{*}Speaker