
DNA metabarcoding to quantify the response of insect diversity to mountain forest die-offs in the French Pyrenees

Lucas Sire^{*†1}, Rodolphe Rougerie², Annie Bézier³, Béatrice Courtial, Christophe Bouget⁴, Elisabeth Herniou⁵, and Carlos Lopez-Vaamonde^{‡6,7}

¹IRBI – CNRS : UMR7261 – France

²Muséum national d'histoire naturelle (MNHN) – Ministère de l'Ecologie, du Développement Durable et de l'Energie, Ministère de l'Enseignement Supérieur et de la Recherche, Muséum National d'Histoire Naturelle (MNHN) – 57, rue Cuvier - 75231 Paris Cedex 05, France

³Institut de recherche sur la biologie de l'insecte (IRBI) – CNRS : UMR7261, Université François Rabelais - Tours – Av Monge 37200 TOURS, France

⁴Ecosystèmes forestiers (UR EFNO) – Irstea – Domaine des Barres, F-45290 Nogent-sur-Vernisson, France

⁵Institut de Recherche sur la Biologie de l'Insecte (IRBI) – CNRS : UMR7261, Université François Rabelais - Tours – Av Monge 37200 Tours, France

⁶Zoologie Forestière (URZF) – Institut national de la recherche agronomique (INRA) : UR633 – Orléans, France, France

⁷Institut de recherche sur la biologie de l'insecte (IRBI) – Université de Tours, Centre National de la Recherche Scientifique : UMR7261 – Av Monge 37200 TOURS, France

Abstract

Mountain forests suffer from an increase in frequency and severity of summer droughts and infestations of pathogens and insects. Those factors are causing high mortality of some keystone tree species (forest die-offs). Yet, how tree diebacks and associated changes in forest composition will affect local diversity and ecosystem functions remains unknown. Here, we aim at quantifying the impact of climate-induced forest decline on biodiversity by measuring changes in taxonomic structure of invertebrate communities along gradients of silver fir (*Abies alba*) dieback in the French Pyrenees.

We use DNA metabarcoding to analyse 224 samples of Malaise traps placed on 56 silver fir dominated plots in the French Pyrenees from May to September 2017. Samples were sequenced using Illumina MiSeq and analysed using the DAME twin-tagging pipeline approach. We conducted taxonomic assignment against reference DNA barcode libraries to streamline identification and recover biological information for ecological analysis.

We discuss the results of our metabarcoding analysis and the utility of our approach to conduct biomonitoring across a large geographical scale.

*Speaker

†Corresponding author: lucas.sire.17@gmail.com

‡Corresponding author: Carlos.lopez-vaamonde@orleans.inra.fr