Contacts
Franck Jabot
franck.jabot@inrae.fr
Fabien Laroche
fabien.laroche@inrae.fr

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ARTECO

Inferring arthropod spatial flows in ecotones between (semi-) natural and crop habitats

Backgrounds and challenges

Numerous empirical studies have documented the link between landscape structure and biodiversity, providing concrete guidelines for the ecological intensification of agricultural landscapes. However, they are based on ecological processes that are still poorly understood, and which shape the response of organisms to the multiplication of anthropogenic ecotones. Among these processes, the movement of organisms (foraging, dispersal, spill-over) and their habitat preferences play a central role. Quantifying these processes would enable us to better predict the effects of landscape and ecological infrastructures (hedges, grass strips).

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Objectives

We propose to work towards a better understanding of the ecological processes influencing the dynamics of organisms within heterogeneous landscapes, 1) by bringing together an interdisciplinary consortium (mathematics, ecology, molecular biology) of partners interested in ecotones and 2) by carrying out a pilot project to serve as a proof of concept. This project will aim to develop original methods for inferring arthropod flows at the interface between habitats, based on high-resolution species distribution data, both spatially (metric transects) and taxonomically (massive DNA barcoding), focusing on predatory taxa (beetles and spiders) for their biological control potential. We will concentrate our efforts on three types of interface: wheat crops on the one hand, forests, meadows or riparian zones on the other. These three interfaces allow us to study the role of semi-natural habitats (forests/grasslands/riparian forests) in the provision of ecosystem services for agriculture (pest regulation). Meetings of the consortium upstream and downstream of this project will enable us to prepare the setting up of an ANR-type project by the end of this project, capitalizing on the results of the exploratory project.

Approaches

We will sample terrestrial invertebrate communities along transects perpendicular to the interface, using suction-sampling methods (for a broad spectrum of arthropods - focusing on predatory invertebrates with a potential biological control role). The organisms sampled will be determined to species level by massive DNA barcoding, in order to determine abundance profiles along the transects for each population making up the communities. These abundance profiles (clines) will feed into the project's development of new inference methods, inspired by population genetics, to estimate invertebrate flows between plots. The project's originality is therefore twofold. From a biological point of view, the aim is to go beyond pattern analysis (distance and magnitude of edge effect) and delve deeper into the spatial processes involved, by explicitly estimating and integrating the flows of organisms between habitats. From a technical point of view, the aim is to implement recent and innovative methodologies known as "meGabarcoding", which involve the massive barcoding of tens of thousands of individuals, providing access not only to community diversity (like meTabarcoding), but also to the abundance of individuals of each species, and even to a certain level of intra-specific polymorphism. By coupling this megabarcoding approach with the acquisition of photographs of sampled individuals, we will contribute to the ongoing development of automatic image-based recognition systems (and AI) for terrestrial invertebrates, with a view to moving towards non-lethal monitoring methods. These methodological developments will help to modernize biodiversity monitoring methods and enable us to make a quantum leap in our understanding of ecotone ecology.