

Title: Genetic connectivity of the carabid beetle *Abax parallelepipedus* in heterogeneous agricultural landscapes in Brittany and Picardy

Summary: In fragmented landscapes, functional connectivity plays a key role for long-term population viability by allowing the recolonization of habitats which have been emptied by local extinction, augmenting population sizes, reducing inbreeding depression and negative effects of genetic drift. Enhancing structural connectivity through the preservation or restoration of migration corridors is therefore a primary objective in species conservation to maintain functional connectivity of populations. However, the impact of landscape fragmentation on dispersal and gene flow is challenging since it depends on both species- and landscape-specific effects.

This M2 project is part of a multispecies project (\$) which targets European temperate forests. It aims at exploring the relationship between structural and functional connectivity and focuses especially on the carabid forest specialist *Abax parallelepipedus*, a species of interest for biocontrol in agricultural landscape. Genetic analyses will be *conducted* across heterogeneous landscapes in time and space. Three hypotheses will be tested - all consider dispersal as a trait coevolving with ecological specialization:

- i. generalists are more dispersive than specialists;
- ii. whatever the dispersal capacity, dispersal is counter-selected in specialists characterized by high movement cost;
- iii. whatever the dispersal capacity, dispersal is advantaged(?) in specialists characterized by low movement cost.

Populations of *A. parallelepipedus* will be sampled in Picardy (Thierache) and in Brittany (ZAA) linearly along hedgerows (potential corridor) and in forest patches (habitat). Next, the analysis of mitochondrial sequences and microsatellite multilocus genotypes will permit to assess the historical component of total genetic variation and quantify dispersal through measures of gene flow between populations. Finally, (i) multivariate and Bayesian clustering methods will be used to detect population genetic structure and potential immigrants between favorable habitats, and (ii) correlative analyses and graph theoretic approaches will be performed to understand genetic connectivity between populations and to investigate the relationship between of landscape quality and genetic structuring.

This M2 project is part of the EU (BiodivERsA) project WOODNET (<https://woodnetweb.wordpress.com/project/>) and the regional (Hauts-de-France) project PEGASE (<https://www.u-picardie.fr/edysan/pegase/>).

Duration: 6 months

Host Institute: EDYSAN (<https://www.u-picardie.fr/edysan/>) is a mixt research unity of CNRS and Université de Picardie Jules Verne. The research work developed in the laboratory aims at understanding natural and semi-natural ecosystem functioning and impacts environment changes over those systems. We are well placed in Amiens, a nice and active city in the Picardy region. The laboratory has an ongoing partnership with Regional Molecular Biology Centre (CRRBM) that dispose of state of the art equipment and infrastructure.

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Potential candidates should send a CV and cover letter (in English or French) to: annie.guiller@u-picardie.fr, vincent.Leroux@u-picardie.fr, ronan.marrec@u-picardie.fr

References :

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2. Garroway CJ, Bowman J, Carr D, Wilson PJ. 2008. Applications of graph theory to landscape genetics. *Evolutionary Applications*;1: 620-630. doi:10.1111/j.1752-4571.2008.00047.x.
3. Marrotte RR, Bowman J, Brown MGC, Cordes C, Morris KY, Prentice MB, Wilson PJ. 2017. Multi-species genetic connectivity in a terrestrial habitat network. *Movement Ecology*. 5:21. doi.org/10.1186/s40462-017-0112-2.