



## Spatial heterogeneity in landscape structure influence dispersal and the genetic structure of populations: empirical evidence from a grasshopper in an agricultural landscape

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## Bertrand Gauffre<sup>1,2</sup>, S. Mallez<sup>2,3</sup>, M.P. Chapuis<sup>4</sup>, R. Leblois<sup>4</sup>, I. Litrico<sup>5</sup>, S. Delaunay<sup>5</sup>, I. Badenhausser<sup>1,2</sup>

 $^1$  INRA, USC1339 (CEBC-CNRS), F-79360, Beauvoir sur Niort, France  $^2$  CEBC-CNRS (UPR 1934), F-79360, Beauvoir sur Niort, France  $^3$  INRA, UMR1355 Institut Sophia Agrobiotech, F-06903, Sophia Antipolis Cedex, France  $^4$  INRA, UMR CBGP, (INRA / IRD / Cirad / Montpellier SupAgro), Campus international de Baillarguet, F-34988 Montferrier-sur-Lez cedex, France  $^5$  INRA, URP3F, RD 150, site du chêne, F-86600, Lusignan, France.

- Dispersal may be strongly influenced by landscape and habitat characteristics that could either enhance or restrict movements of organisms. Therefore, spatial heterogeneity in landscape structure could influence gene flow and the spatial structure of populations.
- In the past decades, agricultural intensification has led to the reduction of grassland surfaces, their fragmentation and intensification. Since these changes are not homogeneously distributed in space, they have resulted in spatial heterogeneity with generally less intensified hedged farmland areas remaining alongside streams and rivers. Understanding the effect of landscape structure and habitat characteristics is thus critical for both studies in biodiversity conservation and insect management.
- In this study, we assessed spatial pattern of abundance and population genetic structure of a flightless grasshopper species, *Pezotettix giornae*, based on the surveys of 381 grasslands in a 450 km² agricultural landscape of western France. Data was analyzed using both geostatistical and landscape genetics approaches.
- Results suggested that small scale intense dispersal allows this species to survive in intensive agricultural landscapes. A complex spatial genetic structure related to landscape and habitat characteristics was also detected. Two *P. giornae* genetic clusters were inferred from Bayesian cluster analyses and were associated with a relictual hedged

farmland network. This network was characterized by high hedgerow and grassland density as well as higher grassland temporal stability which were suspected to slow down dispersal. Using computer simulations, we demonstrated that a linear zone where dispersal is more limited could be detected as a barrier to gene flow.

Interestingly, increasing the width of such heterogeneous zone could generate an additional genetic cluster. This study illustrates the relevance of using computer simulations to test hypotheses in landscape genetics studies.