

Wildlife friendly agriculture: which factors do really matter?

A genetic study on the field vole

Chiara Marchi^{1,2}, Liselotte W. Andersen², Christian F. Damgaard³, Kent Olsen⁴, Thomas S. Jensen⁴ & Volker Loeschcke¹

¹Ecology and Genetics, Department of Biological Sciences, Aarhus University, Ny Munkegade 114, DK-8000 Aarhus C, Denmark

²Department of Wildlife Ecology and Biodiversity, National Environmental Research Institute, Aarhus University, Grenåvej 14, DK-8410 Rønde, Denmark

³Department of Terrestrial Ecology, National Environmental Research Institute, Vejløvej 25, 8600 Silkeborg, Denmark

⁴Natural History Museum, Universitetsparken 210, DK-8000 Aarhus C, Denmark



Introduction

The impact of landscape structure and land management on the dispersal of populations of wild species inhabiting the agricultural landscape was investigated by determining the genetic diversity and gene flow of field vole (*Microtus agrestis*) in three different areas. The main hypotheses were: I) organic farms act as genetic sources and diversity reservoirs for species living in agricultural areas, II) gene flow and genetic structuring in the agricultural landscape are influenced by the degree of landscape complexity and connectivity and III) the effective population sizes of the populations are determined by the available habitat.

It is well known that organic farming generally improves the biodiversity and abundance of species in the agricultural landscape (Hole et al., 2005). However, it has recently been shown that the benefits of organic farming are evident only at the landscape scale (Gabriel et al., 2010). Thus, to protect species living in the agricultural environment it is of extreme importance to investigate which landscape factors control their distribution and movements.

Landscape factors

The following landscape factors were determined for each sampling site: sampling site size; size of the undisturbed area within the sampling site; sampling site perimeter ("Perimeter"); core area perimeter ("Core Perimeter"); management (conventional or organic, "Management"); percentage of perimeter usable for dispersal (defined as the percentage of perimeter free from roads and water bodies, "% free perimeter"); connectivity index between sampling sites ("Connectivity"); permeability index ("Permeability") and side of the road ("Road"). Each factor was tested against the pattern of gene flow and genetic differentiation.

Results

The analysis of genetic structure performed with GENELAND (Figure 1) showed a higher degree of sub-structuring in the agricultural areas (five and four clusters in the two agricultural areas compared to only one cluster for the undisturbed area). The results by STRUCTURE analysis yield a lower number of clusters (Figure 2), but nonetheless showing a higher number of clusters in the agricultural areas. The analysis of landscape factors affecting genetic differentiation and gene flow showed no clear effect of management, instead the prevailing effect was due to landscape factors given in Table 1. The population size was influenced mainly by the size of un-disturbed habitat (Figure 3), but this tendency should be further investigated.

Conclusion

The distribution of genetic differentiation and the directions of gene flow were determined mainly by landscape factors: thus the expectation that organic fields act as genetic reservoir was not met. The fact that agricultural area presented more sub-populations than the undisturbed one, together with the importance of connectivity and habitat size in shaping gene flow and genetic differentiation, shows that switching to organic farming might not be enough to ensure the conservation of species in the agricultural environment. These results emphasize the need to include landscape structure in management policies.

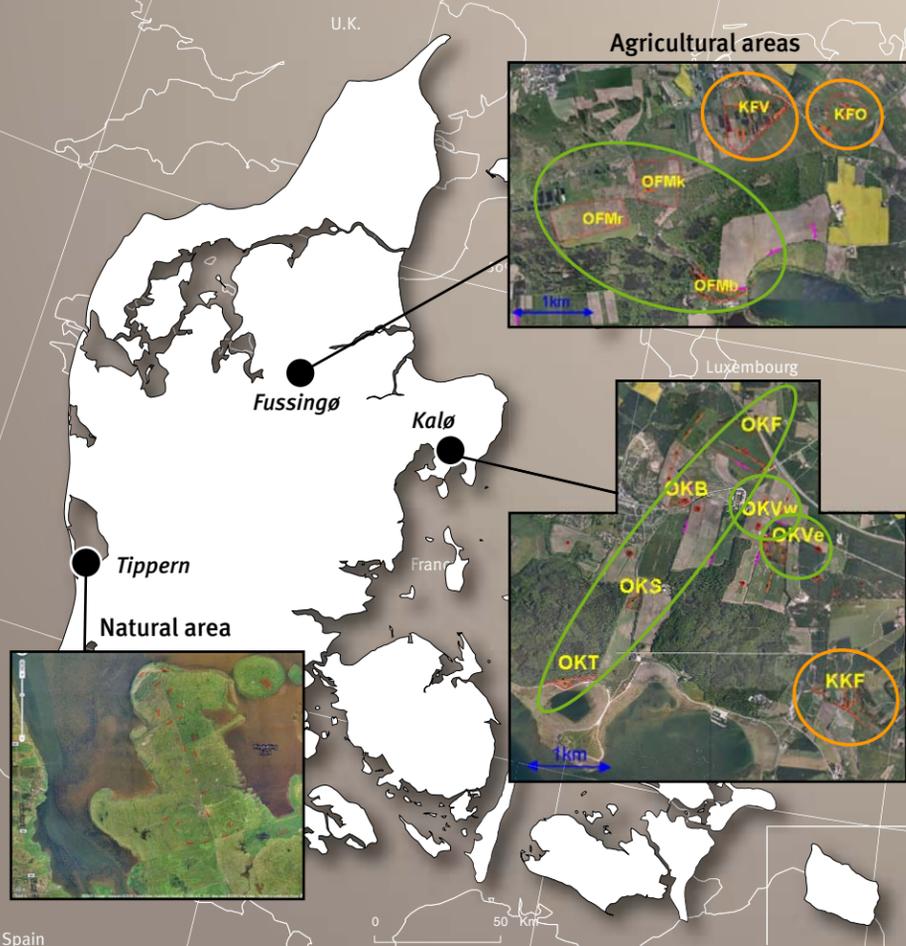


Figure 1: Sampling locations for the field vole (*Microtus agrestis*), samples were collected in year 2007 and 2008. Clusters based on GENELAND (50,000/200,000 iterations, max K = 8, coordinates as priors; Guillot et al., 2005) analyses are shown: each circle represents a genetic cluster, orange = the cluster showing conventional fields, green = the cluster showing organic fields

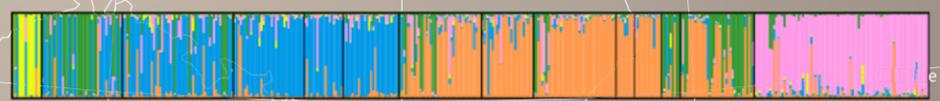


Figure 2: Bayesian clustering analysis performed in STRUCTURE (Pritchard et al., 2000) with K=5 and 100,000/1,000,000 iterations (admixture model, no prior information) for 15 microsatellite loci.

Factors affecting:	
Gene flow	Habitat size
Genetic differentiation	Distance
Effective population size	Distance
	Management
	Connectivity
	Size of undisturbed habitat

Table 1: Test of the relationship between gene flow/genetic diversity and landscape factors using BIMr (Faubet and Gaggiotti, 2008) and a simple Mantel test, respectively. The effective population size was calculated using LDNe (Waples and Do 2008) and the correlation with habitat and un-disturbed habitat size was investigated.

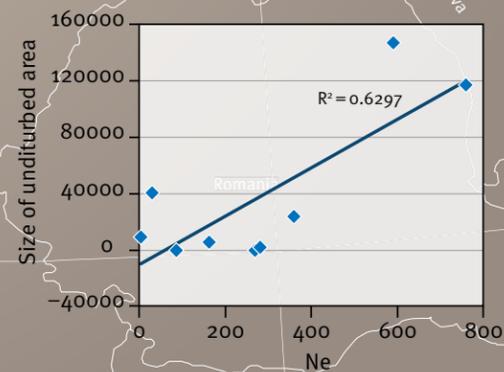


Figure 3: Correlation between estimated effective population size and undisturbed habitat size (for each sampling site in the agricultural areas).

Acknowledgements

This is a part of a PhD project that is funded by the Ministry of Food, Agriculture and Fisheries under the Finance and Appropriation Act, Sections 24.33.02.10 and by AGSoS (Aarhus Graduate School of Science).

References

Faubet, P., Waples, R.S. & Gaggiotti, O.E. (2007): Evaluating the performance of a multilocus Bayesian method for the estimation of migration rates. – *Molecular Ecology* 16, 1149–1166.
 Gabriel, D., Sait, S.M., Hodgson, J.A., Schmutz, U.A., Korin, W.E. & Benton, T.G. (2010): Scale matters: the impact of organic farming on biodiversity at different spatial scales. – *Ecology Letters*. Doi: 10.1111/j.1461-0248.2010.01481.x.
 Guillot, G., Mortier, F. & Estoup, A. (2005): GeneLand: a computer package for landscape genetics. – *Molecular Ecology Notes* 5, 712–715.
 Hole, D.G., Perkins, A.J., Wilson, J.D., Alexander, I.H., Grice, P.V. & Evans, A.D. (2005): Does organic farming benefit biodiversity? – *Biological Conservation* 122(3), 115–130.
 Pritchard, J.K., Stephens, M. & Donnelly, P. (2000): Inference of population structure using multilocus genotype data. – *Genetics* 157, 945–959.
 Waples, R.S. & Do, C. (2008): LDNe: A program for estimating effective population size from data on linkage disequilibrium. – *Molecular Ecology Notes* 8, 753–756.