Spatial genetic structure of the parasitoid wasp
Hyposoter horticola

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INTRODUCTION

Host-parasitoid system

Host population is **fragmented**
with **high turnover rate** of the local populations [1]

Parasitoid wasp is **more mobile** than its butterfly host [2]
could lead to little genetic structure

→ **Spatial genetic structure of a parasitoid
that uses a locally unstable host?**

References: (1) Hanski I., Pakkala T., Kuussaari M. and Lei G. 1995. Metapopulation persistence of an endangered butterfly in a fragmented landscape. Oikos 72: 21–28. (2) Van Nouhuys S. and Hanski I. 2002. Colonization rates and distances of a host butterfly and two specific parasitoids in a fragmented landscape. Journal of Animal Ecology 71: 639-650.

MATERIAL & METHODS

Female *H. horticola* parasitizing a *M. cinxia* egg cluster
(Photo by C. Couchoux)

Hyposoter horticola
Egg-larval endoparasitoid
Specialist of butterfly *Melitaea cinxia*

Population in the Åland islands, Finland
M. cinxia lives in a **metapopulation**
Patches of suitable habitat organised in **networks**

407 female wasps from 168 habitat patches / 40 networks
Genotyped at **14 microsatellite loci**


M. cinxia
(Photo by S. van Nouhuys)

RESULTS

Spatial clustering (map)

Bayesian clustering of **networks** showed that the
population was **genetically structured**
(Spatial clustering in BAPS, p = 0.97 for **K = 8**).
But some genetic clusters were widespread (●)
and not always continuous (●●).

Isolation By Distance (graph)

IBD analysis showed a significant correlation
between pairwise **genetic distance** and
geographic distance at the **patch level**.
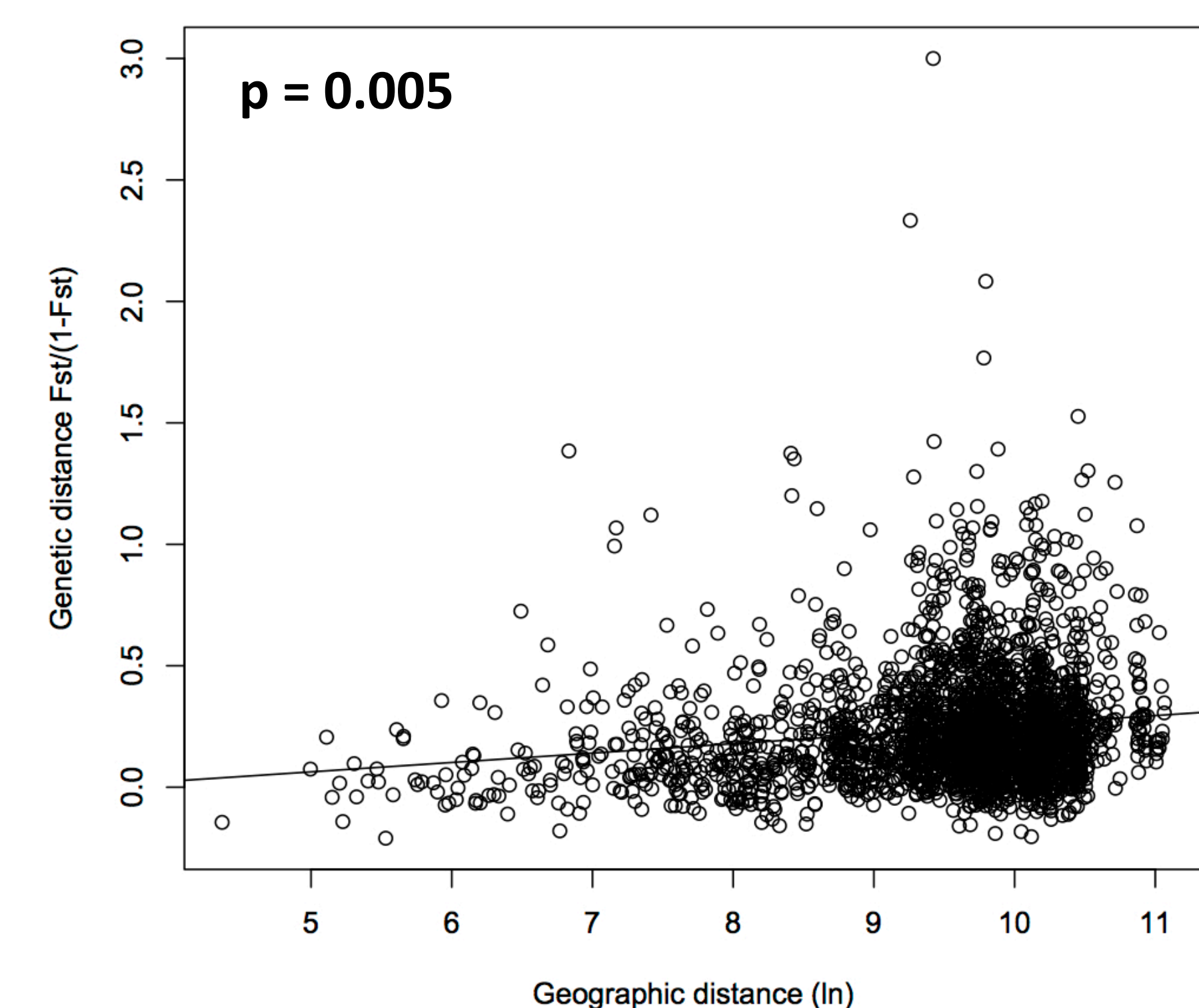
Hierarchical analysis of genetic variation (table)

Analysis of molecular variance (AMOVA) showed that all
three levels - **patch**, **network** and **genetic cluster** - explain
a significant proportion of the variation in the data.

Source of variation	Variation (%)	F
Model = Patches nested within networks		
Among networks	5.62	$F_{NT} = 0.06$ ***
Among patches within networks	10.10	$F_{PN} = 0.11$ ***
Among individuals within patches	-4.96	$F_{IP} = -0.06$
Within individuals	89.24	$F_{IT} = 0.11$ ***
Model = Networks nested within genetic clusters		
Among genetic clusters	4.09	$F_{CT} = 0.04$ ***
Among networks within genetic clusters	5.93	$F_{NC} = 0.06$ ***
Among individuals within networks	2.48	$F_{IN} = 0.03$
Within individuals	87.51	$F_{IT} = 0.12$ ***

Abbreviations for F indices: P = patch, N = network, C = genetic cluster, I = individual and T = total.

DISCUSSION & CONCLUSION

H. horticola
(Photo by C. Couchoux)

- The parasitoid population is **spatially structured**, even though some genetic clusters are discontinuous.
- The genetic structure is **hierarchical**, with 3 levels – **habitat patches**, **networks of patches** and **genetic clusters**.
  However, **founder effect** and **small effective population size** of the local habitat patches seem to overestimate the importance
  of patch level in spatial structuring. **Inbreeding values** (F_{IP}, F_{IN}) indicate that **networks** probably define the **breeding population.**
- Apart from the hierarchical structure, **geographic distance** also affects genetic differentiation.

→ **The genetic structure of the parasitoid matches the spatial structure of its host.**