

Introduction

The globally threatened butterflies in the genus *Maculinea* are social parasites of *Myrmica* ant colonies, gaining access to the colonies by mimicking the specific cuticular hydrocarbons (CHCs) of their host ants. *Maculinea* butterflies have been heavily impacted by changes in land use over the last century, and now exist primarily in fragmented, isolated populations with little gene flow, and hence are thought to be in danger of extinction not only due to small population sizes, but also due to reduced genetic variation, which could reduce their ability to adapt to new environments and to climate change. *Maculinea alcon* exploits different host *Myrmica* species in different parts of Europe, and has been shown to be in a coevolutionary arms race with at least one of its hosts, involving evolution of the CHC profiles of both parties. Locally, *Maculinea alcon* is rather host-specific, showing local adaptation to one or two host *Myrmica*, often the most common species. However, there is large variation across Europe in the hosts with which *Maculinea alcon* associates. This study therefore set out to investigate the geographical variation in host specificity, CHCs and genetic variation in *Maculinea alcon*, comparing populations from the core of the species distribution with more peripheral populations

Methods

Populations of *Maculinea alcon* that either specialised on a single *Myrmica* host species, or exploited two hosts simultaneously were identified in a core area of the species range (Hungary & Rumania) and a peripheral area (Denmark & Sweden: Fig 1a), and samples were collected to test two main hypotheses: 1) That populations using multiple host species are more variable than populations using a single host species, and 2) That populations at the core of the species range are more variable than those at the periphery. Variation in CHCs was tested using Gas Chromatography of cuticular extracts, and genetic variation was tested using a number of variable microsatellite markers. In addition, host-use data was collected from a large number of studies of *Maculinea* populations across Europe to test the hypothesis that peripheral populations were more likely to specialize on a single host *Myrmica* species.

Results

Although all data has been collected, the analysis of genetic variation is still underway, so I report here only the preliminary analysis of CHCs. The hydrocarbon profiles of *Maculinea alcon* were significantly different between the core and the peripheral populations (Fig 1b; $F_{1,254} = 69.4$, $p < 0.0001$). They were also significantly more variable in populations from the core area (Fig 1c; $F_{1,259} = 40.53$, $p < 0.0001$), but not more variable in those populations which exploited two hosts rather than one – in fact those that exploited a single host were significantly more variable ($F_{1,259} = 4.04$, $p = 0.045$), primarily due to the low variation in the population from the island of Læsø (excluding Læsø; $F_{1,233} = 1.67$, $p = 0.197$).

Overall, there was no pattern as to whether core or peripheral populations exploited one or more host species (Fig 4), but two groups of populations were found, one in the North West, which exploited hosts in the *Myrmica rubra* species group, and a southern set that exploited hosts in the *Myrmica scabrinodis* species group. Within the latter, all populations that exploited more than one host species were found in the core, eastern area of the range of *Maculinea alcon* (Fig 1d).

Discussion

The predicted pattern of increased variation in the populations from the core area of *Maculinea alcon*'s distribution was found for the cuticular hydrocarbons of this species. However, the predicted increase in variation in CHCs in populations using two hosts was not found, suggesting that the caterpillars produce a compromise profile rather than individuals producing profiles that may match one host of the other.

Host use data confirmed the existence of two sets of populations, a north-western group that exploit hosts in the *Myrmica rubra* species group, and a larger, southern group that exploit hosts in the *Myrmica scabrinodis* species group. Within the latter, multiple host ant use is only found in the core of the range of *Maculinea alcon*, supporting predictions that the lower genetic variation in peripheral populations may reduce their ability to mimic multiple hosts.

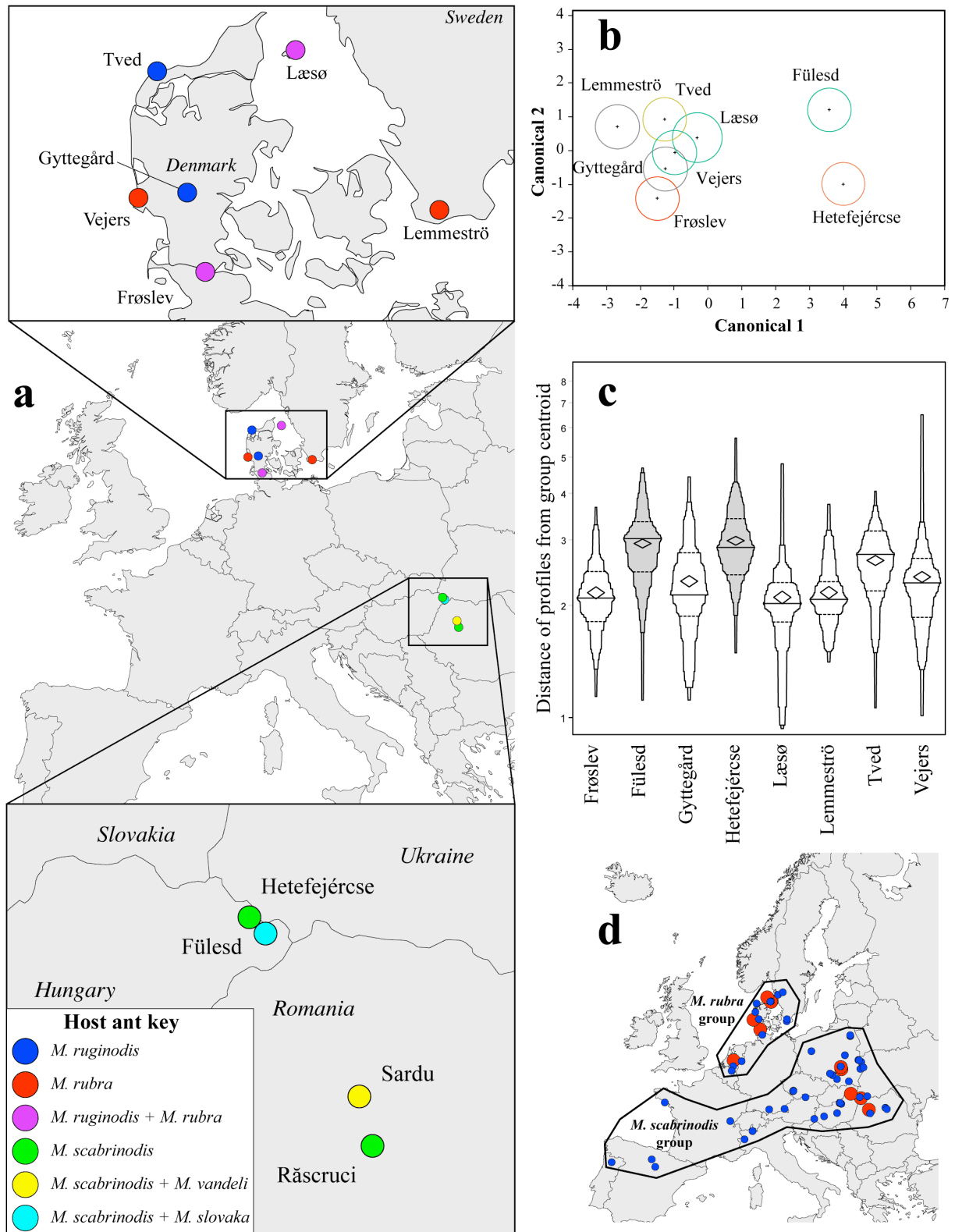


Figure 1: Provisional results of CHC analysis of *Maculinea alcon* across its range in Europe.

a) Map showing the location of the ten *Maculinea alcon* populations studied in detail, and their host ant associations. The two Romanian populations have been used for genetic analysis only.

b) Ordination plot showing differences in the CHC profiles of *Maculinea alcon* from eight populations. For each population the centroid and 95% confidence circle for the centroid are shown.

c) Within-population variation in CHC profiles, shown as the distribution of distances of each caterpillar's profile from the population centroid. Means for each population are marked with diamonds. The two populations from core of the distribution are shaded grey.

d) Distribution of populations of *Maculinea alcon* exploiting one (shaded blue) or two (shaded red) host ants, and the species groups within the genus *Myrmica* that they exploit.