An integrated molecular and ecological trait dataset for the Tuscan Archipelago butterflies: a resource to understand the evolution and extinction of island biodiversity


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What?
Characterize species diversity in an island system and infer the species traits that are associated with diversification emergence, maintenance and loss

Who?
The butterfly communities

Where?
The Tuscan Archipelago, Corsica, Sardinia, Tuscany

Methods

- We carried out surveys in the study area, during the last 15 years, and gathered occurrence data from the literature of the last 115 years
- We sequenced the COI gene for 1303 specimens, representing the 46 butterfly taxa reported in the Tuscan Archipelago, including comparative material from Sardinia, Corsica and Tuscany
- We calculated the Dst and Gst to measure the genetic differentiation among populations, and we also estimated island haplotype uniqueness
- We assessed 12 species traits related to: feeding (the number of host plants), morphology (wingspan), life history (volitism, length of flying period), physiology (mean annual temperature and precipitation)
- We evaluated the relationships between different species traits and population diversification, using stepwise phylogenetic regressions
- We assessed the traits that could have influenced species extinctions on Elba and Capraia

Results

- We identified the species that probably became extinct or strongly declined on these islands: five on Elba, three on Giglio and six on Capraia (Table 1)
- Gst values had an almost bimodal distribution: 10 species with Gst<0.25 and 9 species with Gst>0.75 (Table 1, Figure 2)
- All three indices (Dst, Gst and Uni) showed that, together with the endemics, several common and widespread species provided a large contribution to diversity (Table 1)
- The phylogenetic regressions showed that small-sized, more generalist species that are occurring in drier areas have a higher genetic structure and/or haplotype uniqueness (Table 2)
- The overall spatial pattern of genetic variation corresponded to the proximity of the areas, but we identified strong contrasts between geographically close areas (Figure 3)

Figure 2. Phylogenetic tree based on cytochrome c oxidase subunit 1 (COI) sequences of the butterfly fauna occurring in the Tuscan Archipelago, with their Gst, Dst and Uni plots. The values of Dst are superimposed on the tree, while the square-root values for Gst and Uni are represented by different colors from the RGB scale. Black sectors of Phoeonil and 2 represent the time frame of the flight period (the top sector corresponds to January). Host plants represent the number of plant genera on which the larvae of a species has been reported: one leaf means two or four genera, three leaves means three or four genera, four leaves means five or more genera. The size of the butterfly silhouettes is directly correlated with the species size (inmillimeters). The icons for Ecophy1 and 2 represent mean values of the annual temperature and precipitation that each species experiences where it occurs. Ecophy 1 is illustrated by a blue (low rate) to red (high rate) scale, while Ecophy 2 is represented by the dimension of the drap.

Figure 3. Overall genetic patterns obtained after comparisons among islands, based on Gst. (a) The colours obtained in the RGB projection of the Principal Coordinate Analysis (PCoA) have been included in (b) the map of the studied region to show similarity and contrast among areas. Locality codes are: Aro, Argentario; Cap, Capraia; Cia, Corsica; Elb, Elba; Gis, Giglio; Gl, Giglio; Gor, Gorgona; Mon, Montenero; Pi, Pianosa; So, Sardinia; Tu, Tuscan; Tc, central Tuscan coast; Ta, northern Tuscan coast; Ts, southern Tuscan coast. (b) Haplotype networks based on COI for nine particularly interesting species, obtained by comparing haplotypes from the study area with other regions of Europe.

Conclusions

There was considerable degree of population diversification in many species, which confirms that the Tuscan Archipelago hosts highly diverse butterfly communities. Phylogenetic regressions showed that smaller-sized and more specialized species, with a preference for drier regions, display greater genetic structure and/or uniqueness. Moreover, species adapted to colder and wetter areas and with shorter flight periods are more likely to become extinct.

The methodology used here can be applied to reveal fine-scale diversity patterns, their origins and the vulnerability of taxa to current and future environmental changes, thus providing a valuable tool for evidence-based conservation prioritization.

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