

THE *EREbia tyndarus* SPECIES COMPLEX IN THE ALPS AND APENNINES: NEW GENETIC DATA ON A BIOGEOGRAPHIC RIDDLE

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The *Erebia tyndarus* species complex is a cluster of closely related alpine taxa, which have represented an intriguing issue for taxonomists, evolutionary biologists and biogeographers (eg. Lorković, 1958; Descimon & Mallet, 2009).

The species within the ‘*tyndarus*’ group were defined using morphological and ecological characters, cross-breeding experiments, karyology, and molecular data from allozymes and mitochondrial DNA (mtDNA). However, the delimitation of species, their interrelationships, as well as the origin of their non-obvious geographic distribution, are still largely unclear, especially as far as the species inhabiting Alps and Apennines are concerned.

Since Warren’s monography (1936), allowing for only one species, *Erebia tyndarus*, up to five different species have been described in the Alps, though most taxonomists currently consider four species: *E. tyndarus*, *E. cassioides*, *E. calcaria* and *E. nivalis*, all of them belonging to a unique “Alpine” clade (Albre et al., 2008). Figure 1a illustrates the distribution range of these taxa. Three species (*E. tyndarus*, *E. nivalis*, *E. calcaria*) are endemic to the Alps, while *E. cassioides* stretches its patchy distribution from the Alps into Apennines, Pyrenees and Balkans. This distribution pattern includes

instances of allopatry, parapatry and quasi-sympatry; the latter case represented by *E. nivalis* narrowly overlapping along an altitudinal gradient with *E. cassioides* or (in a single site) *E. tyndarus*.

As stenoecious butterflies with low dispersal ability, members of the ‘*tyndarus*’ group represents a valuable model for historical dynamics of alpine habitats in Italian mountain ranges.

Here we present the progress of a PRIN2009 project, entitled “Comparative phylogeography of butterflies from Apennines addressed to the development of descriptive and predictive bioclimatic models”, aiming at elucidating the genetic relationships within the “Alpine” clade and the population range dynamics along Alps and Apennines.

A fragment (1190 bp) of the mtDNA *cox1* gene was sequenced in a sample of 112 individuals representative of the distribution of all the species of the “Alpine” clade in the Alps and Apennines, plus 3 individuals from the Pyrenean range of *E. cassioides* and 1 *E. rondoui* as an outgroup (Figure 1a). Restriction sites associated DNA (RAD) from the whole genomes of a subset of 45 individuals was sequenced on a single lane of a HiSeq Illumina machine.

Our preliminary analysis of RAD data provide the first molecular support for the traditional 4-species taxonomy (Figure 1c) of the “Alpine” clade, which is not resolved by mtDNA data (Figure 1b). Both mtDNA and RAD data detect some geographic structure within *E. cassioides*, indicating relatedness between Apennine and western Alps (especially Maritime Alps) populations. Interestingly, RAD data show a rather continuous genetic gradient from Pyrenees to Alps and Apennines, while mtDNA highlights the genetic distinctiveness of Western Alpine and Apenninic populations from the rest of *E. cassioides*, consistent with the hypothesis of colonization of the Apennine range from Western Alps.

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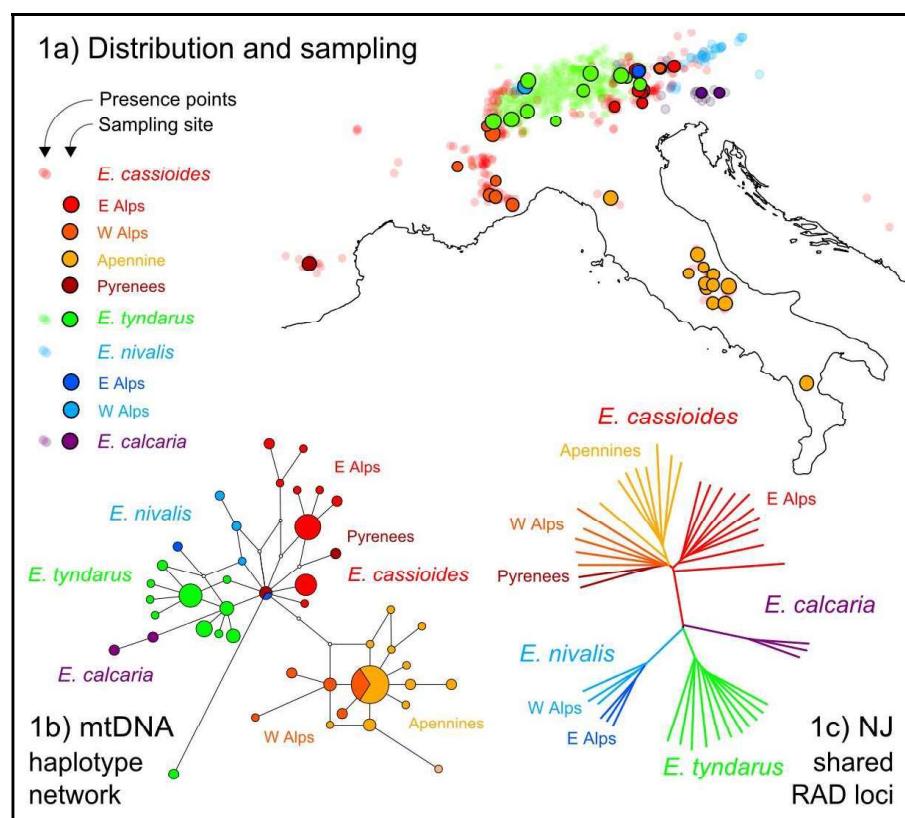


Figure 1. The *Erebia tyndarus* species complex: sampling localities and results of the genetic analysis.