

more clonal, with very low number of polymorphisms. Notably, in *C. albicanan* intriguing genomic plasticity have been observed. Indeed, over the high polymorphism, strain-specific gene losses, acquisition, and several miss-sense genes were found. Moreover, in *C. albicans* isolates, the most polymorphic genes codify proteins related to the cell wall and hyphal formation, external encapsulation structure and cell periphery, suggesting a continuous adaptation to adverse environments or stress conditions. Our data are confirmed by phenotypical characterization that show changes in virulence related traits (invasive growth, hyphal formation and switch from smooth to myceliated colonies) for the majority of *C. albicans* strains. Also in two *C. parapsilosis* strains similar pathogenic traits were found. Interestingly, the cytokine milieu released by human PBMCs and DCs showed that specific inflammatory responses are produced by strains with the most virulent phenotype. Overall these results provide significant insights regarding the link between host adaptation, pathogenesis and evolution.

“Bad” species? Restriction sites associated DNA sheds light on the evolution of the *Erebia tyndarus* species complex

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The *Erebia tyndarus* species complex is a cluster of closely related alpine butterflies, representing an intriguing riddle for taxonomists, evolutionary biologists and biogeographers and a still underexploited model for understanding the role of neutral and adaptive processes in speciation. Members of the ‘tyndarus’ group have been characterized so far by morphological and ecological characters, cross-breeding experiments, karyology, and molecular data from allozymes and mitochondrial DNA (mtDNA). However, the delimitation of species, their relationships, as well as the origin of their peculiar geographic distribution, are still unclear. So much so that these taxa were cited as an example of ‘bad species’, for which the establishment of a phylogenetically ‘correct’ taxonomy could represent a desperate and almost meaningless endeavour (Descimon & Mallet, 2009). Up to five different species belonging to the ‘tyndarus’ group have been described in the Alps: *E. tyndarus*, *E. calcaria*, *E. nivalis*, *E. cassioides* and *E. carmentis* (with the latter often considered a subspecies of *E. cassioides*) all of them belonging to a unique “Alpine” clade (Albre et al., 2008). Figure 1 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 Eastern Alps into the Balkans and *E. carmentis* from Western Alps into Apennines and Pyrenees. 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*. In this ongoing study, we are employing restriction sites associated DNA (RAD) along with more traditional mtDNA sequencing in order to clarify the systematic and genetic relationships among taxa of the *E. tyndarus* “Alpine” clade, as a basis for further evolutionary studies. Our preliminary analyses show that our RAD data are able to provide, for the first time, a clear molecular support for the recognition of four well-defined genetic units, corresponding to the species *E. tyndarus*, *E. nivalis*, *E. calcaria* and *E. cassioides+carmentis* (Figure 1c). Interestingly, these lineages do not show any synapomorphies at 1200 bp of mtDNA (Figure 1b). In striking contrast, the distribution of mtDNA haplotypes highlights a strong geographical structure within *E. cassioides+carmentis*, where RAD shows a rather continuous genetic gradient from Pyrenees to Alps and Apennines, highlighting the historical role of nuclear gene-flow and recombination in maintaining the genetic cohesion of a single evolutionary unit. Finally, RAD data are providing provisional evidence for gene flow between *E. tyndarus* and *E. nivalis* (whose range overlap is very limited), while hybridization between *E. cassioides* and *E. nivalis* (occurring in quasi-syntopy at several sites) seems to lack altogether, which suggests an intriguing correlation between reproductive isolation and ability to coexist by niche-splitting.

A framework for the evolutionary study of uncharacterised microbial communities

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Complex microbial environments such as those analysed in metagenomic studies present a challenge in how these communities change and adapt to external stimuli. One such environment is present in the rumen of herbivores, which use a multi-chambered digestive system to host a complex microbial community that can break down the lignocellulosic