



I think

B



Evoluzione

— 11th SIBE CONGRESS 2026



Book of Abstracts



A treasure in the forest: the high diversity and structuring of the alpine longhorn beetle *Rosalia alpina* in Italy

Lorenzo GARGINI^{1*}, Vincenzo BUONO¹, Alessandra Maria BISSATTINI¹, Alessandro CAMPANARO², Alice LENZI², Silvia GISONDI³, Alessio DE BIASE¹, Emiliano MANCINI¹

¹ Dept. of Biology and Biotechnologies “C. Darwin”, Sapienza University of Rome, Italy

² Council for Agricultural Research Economics, Research Centre for Plant Protection and Certification, CREA, Florence, Italy

³ Council for Agricultural Research Economics, Research Centre for Plant Protection and Certification, CREA, Rome, Italy

* Corresponding author: lorenzo.gargini1996@gmail.com

Rosalia alpina is a saproxylic longhorn beetle strictly protected under the European Habitats Directive and classified as Vulnerable by the International Union for Conservation of Nature. As a flagship and umbrella species, its conservation is crucial for the preservation of old-growth forest ecosystems, particularly in the current context of habitat fragmentation driven by land-use change, which represents a major threat to saproxylic beetle populations. We investigated the phylogeography and population structure of this species by sequencing a fragment of the mitochondrial cytochrome c oxidase subunit I (COI) gene and generating ddRAD data for 134 specimens from 37 sampling sites, covering a substantial portion of the species' Italian range. Our results highlighted the genetic uniqueness and variability of *R. alpina* populations in Italy, shaped by post-glacial recolonisation processes originating from southern Italian refugia in the Apennines and from Balkan source populations in the central-eastern Alps. Genomic analyses further revealed a clear separation between the above-mentioned evolutionary lineages, strongly supported by PCA (with PC1 explaining ~40% of the variance) and by high and significant pairwise F_{ST} values (0.60 and 0.69). Moreover, within the Apennines, two main genetic clusters were detected, separating central-northern and southern populations. This pattern likely reflects both historical and recent habitat fragmentation events that allowed limited gene flow across central Italy. Further sampling in the central Apennines and central Alps will be essential to better characterise gene flow dynamics and support conservation strategies aimed at preserving the genetic uniqueness of Italian populations in the face of ongoing old-growth forest loss and fragmentation.