
Adaptive variation in five conifer species across the Italian alpine ecosystems

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Forest ecosystems form a dominant landscape in many alpine environments where natural populations of coniferous species are found across steep environmental gradients. Such populations are supposed to be tightly genetically adapted to these diverse environments; however the genetic basis of these adaptations is poorly understood. A preliminary investigation was conducted on five ecologically and economically important conifer species for the Italian Alps and Apennines: *Abies alba*, *Larix decidua*, *Picea abies*, *Pinus cembra* and *Pinus mugo*. To understand genetic patterns of adaptive variation, natural populations of these species were sampled along an altitudinal gradient and genotyped for single nucleotide polymorphisms (SNPs) markers. Population structure was estimated using Bayesian clustering analyses and a multivariate method, revealing the presence of 3 genetic clusters for *A. alba* and *L. decidua*, and 4 for *P. abies*, *P. cembra* and *P. mugo*. Inferred genetic structure was tested for correlation with latitude, longitude and the altitudinal gradient using multivariate analysis. Genetic variation resulted significantly correlated with geographic location in all five species: latitude was highly significant for *A. alba* and longitude for the other species. Further analysis on a local scale are needed to deeply investigate the altitudinal gradient effect and possibly detect outlier loci associated to climatic and environmental parameters.

Lack of genetic structure in natural sylvatic *Rhodnius robustus* in a recently fragmented landscape of the Brazilian Amazon Forest

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Actually, there is a growing concern that the Amazon becomes an area with an increasing risk of exposure to Chagas Disease. Anthropogenic disturbances with deforestation of Amazon tropical wet forest leads to a mosaic of landscapes composed of natural forest, secondary vegetation (secondary forest, palm groves, fallows) and pasture. These changes result in the proliferation of invasive heliophilous palm trees of the *Attalea* genus, the principal natural ecotope of *Rhodnius* species, bloodsucking insect vectors of *Trypanosoma cruzi*, the etiologic agent of Chagas disease in Latin America. To understand the genetic structure of wild populations of *Rhodnius robustus* in *Attalea* palm trees through different land cover classes, a population genetic study was conducted with both mitochondrial (cytochrome b) and microsatellites (10 loci) markers. *Rhodnius robustus* specimens were sampled in palm trees located in three rural communities representative of a temporal gradient of settlement time (20-80 years). The landscape of the communities was composed of 6 different land cover classes representative of an anthropic gradient from forest to pasture. This study reveals significant gene flow insensitive to the fragmentation of the environment, suggesting that invasive dynamics of palm trees provide insect vectors a functional connectivity between different landscape units and communities.