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## Patterns of intraspecific genetic variation of *Andoa berthelotiana* (Myuriaceae, Bryophyta) in the Azores (Macaronesia)

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### Abstract

Macaronesia is home to several endemic bryophytes, such as *Andoa berthelotiana*. Recent genetic studies revealed the existence of two intraspecific lineages within this species, one in Madeira and the Canary Islands and another in the Azores. However, patterns of intraspecific variation within archipelagos, remain a relatively unexplored area of research. In this study we investigate patterns of intraspecific variation of *Andoa berthelotiana* within the Azorean archipelago and potential associations with elevation. Our investigation is based on the analysis of chloroplast DNA sequences and AFLP data.

The dataset includes *trnL-trnF* sequences from 23 samples and AFLP data from 34 samples collected in seven of the nine Azorean islands, encompassing elevations of up to 1200 m. For the DNA sequence data haplotype diversity, nucleotide diversity and a statistical parsimony haplotype network were calculated. The AFLP data were analyzed by AMOVA (Analysis of Molecular Variance) and PCoA (Principal Coordinates Analysis). A Chi-Square test was carried out to assess the significance of the relationship between elevation and AFLP groups or *trnL-trnF* haplotypes, respectively.

The observed intraspecific genetic variation clustered into three *trnL-trnF* haplotypes and two AFLP groups, without a clear geographical structure across the Azorean archipelago. Group AFLP1 and haplotypes trnL\_F1 and trnL\_F3 only appeared below 600 m elevation, where low-elevation vegetation (coastal woodlands, lowland forests and montane *Laurus azorica* forests) prevails, while group AFLP2 and haplotype trnL\_F2 occurring along the whole elevational range, but with most samples above 600 m. Associations between elevation and molecular groups were significant according to the Chi-Square test.

Our study reveals the presence of genetic variation within *Andoa berthelotiana* in the Azorean archipelago. The two main genetic groups do not seem to be related to geographical location of islands nor groups of islands, but rather to elevation. One group exhibits a broader ecological amplitude, whereas the other may be genetically adapted to environmental conditions at lower elevations (below 600 m), which includes the area where the native laurel forests dominate and where anthropogenic activities have altered the majority of natural vegetation. Conservation efforts should therefore not only consider the species *Andoa berthelotiana* itself, which is associated with natural forest, but also intraspecific genetic diversity of *Andoa* populations, in particular genotypes restricted to lower elevations.

**Key words:** AFLP, conservation, ecology, elevation, haplotypes, *trnL-trnF*

### Introduction

Macaronesia (comprising the Azores, Madeira, Selvagens, Canary Islands, and Cape Verde archipelagos) is home to several endemic bryophytes, some of which are present in all but the driest Macaronesian archipelagos Selvagens and

Cape Verde (Vanderpoorten *et al.* 2011). One example is *Andoa*, a monospecific genus of pleurocarpous mosses, which occurs in the Canary Islands (Tenerife, Fuerteventura, La Palma), Madeira Island, and the Azores (all nine islands) (Martins *et al.* 2021 and references therein).

A recent study based on DNA sequences and AFLP data revealed the existence of two intraspecific lineages within *Andoa berthelotiana* Montagne (1840:4) Ochyra (1982:31), one occurring in Madeira and the Canary Islands, and the other in the Azores (Martins *et al.* 2021). The presence of morphological differences corresponding with the molecular lineages, but also considerable morphological overlap, led to the interpretation of both lineages as semi-cryptic species (Martins *et al.* 2021).

Recent studies indicated the ecological and evolutionary importance of intraspecific variation (e.g. Godhe & Rynearson, 2017, Mimura *et al.* 2017, Garcia-Cisneros *et al.* 2018, Des Roches *et al.* 2021). Not incorporating local adaptation in species distribution models hampers our capacity to predict distribution ranges, leading to the concern of whether modelling should be done at the species or intraspecific level (Collart *et al.* 2021). As far as pleurocarpous mosses are concerned, already Cronberg (2004) indicated that alpine and subalpine populations of *Hylocomium splendens* (Hedwig:1801:262) Schimper (1852:173) were genetically differentiated at the molecular level. Désamoré *et al.* (2012) analyzed patterns of intraspecific molecular variation in *Homalothecium sericeum* Hedwig (1801:228) Schimper (1851:93) in Europe in relation to climate change using species distribution modelling. Hedenäs (2016, 2019), based on comparative analysis of several acrocarpous and pleurocarpous species, stated that examining intraspecific variation is vital for biodiversity studies and conservation management, and that each individual species should be investigated instead of relying solely on data from other taxa, due to large differences between species and geographical areas.

Within Macaronesia, Patiño *et al.* (2010) and Sim-Sim *et al.* (2015) investigated patterns of intraspecific genetic diversity in the Canary Islands and Madeira Island, respectively. The latter study explored for the first time relationships between intraspecific genetic variation and elevation in four different bryophyte species, and is still the only such bryological study in Macaronesia.

Since the molecular variation in *Andoa berthelotiana* seemed largest within the Azores (Martins *et al.* 2021), with the current study we aim to provide the first insights into patterns of intraspecific variation within the Azorean archipelago. Specifically, we aim to determine possible relations between genetic variation and geographical (island or group of islands) factors and abiotic (elevation) factors. Although *Andoa berthelotiana* is not currently under threat in the Azores as a whole (cf. Martins *et al.* 2021), this species is considered Vulnerable (Hodgetts *et al.* 2019) in the European IUCN Red List. The results may thus inform future conservation actions to preserve this species and its genetic diversity within the Azorean archipelago.

## Material and methods

### Study area

The Azores are divided into three island groups. The Eastern group (São Miguel and Santa Maria Islands, and Formigas Islets; Pacheco *et al.* 2013) and the Central group (Faial, Pico, São Jorge, Terceira and Graciosa Islands) are distributed on the Nubia-Eurasia tectonic plate boundary (Mitchell *et al.* 2018, Silva *et al.* 2021). The Western group comprises Flores and Corvo Islands, both located on the North American tectonic plate (Fernandes *et al.* 2006, Mitchell *et al.* 2018, Silva *et al.* 2021). Except for Pico (2350 m a.s.l.), peak elevations of the Azorean islands ranges approximately between 400 and 1100 m a.s.l. (Graciosa 405, Santa Maria 587, Corvo 718, Flores 911, Terceira 1021, Faial 1043, São Jorge 1053, São Miguel 1105 m a.s.l.) (Forjaz *et al.* 2004).

Since the beginning of continuous human settlement in the early 15<sup>th</sup> century, the natural vegetation in the Azores has been under constant anthropogenic pressure, causing permanent changes in vegetation, according to studies from Flores, Pico and S. Miguel islands (Connor *et al.* 2012, 2013, Rull *et al.* 2017). About 56% of the archipelago territory is occupied by agriculture and pasture, while forests and natural vegetation occupy 35% (Monteiro *et al.* 2008), of which an estimated less than five percent still is original native forest (Triantis *et al.* 2010). Almost one fifth (19%) of the bryophyte species are considered threatened or near threatened (Gabriel & Sérgio 1995, Hodgetts *et al.* 2019). The vast majority of human activities that caused the transformation or degradation of most of the natural vegetation of the Azores, with a larger influence in the laurel forests, occurred in elevations below 600 m, while above 600 m we find the best-preserved vegetation belts (Elias *et al.* 2016).

The laurel forest (Laurissilva) dominated by *Laurus azorica* Seubert (1844:29) Franco (1960:101) and *Myrica*

*faya* Aiton (1789:397) seems to be the climax vegetation type up to approximately 600 m a.s.l., above which it is gradually replaced by *Erica azorica* Hochstetter ex Seubert (1844:40) and eventually by *Juniperus brevifolia* (Seubert 1844:26) Antoine (1857:16) (Tutin, 1953). More recently, Elias *et al.* (2016) distinguished eight vegetation types in the Azores based on studies in four islands from the three islands groups (São Miguel, Pico, Terceira and Flores). Below 600 m there are *Erica-Morella* coastal woodlands, *Picconia-Morella* lowland forests and *Laurus* submontane forests, while above 600 m five vegetation types occur, namely *Juniperus-Ilex* montane forests, *Juniperus* montane woodlands, *Calluna-Juniperus* altimontane scrublands, and two high elevation vegetation types not considered here because our study altitudinal limit is 1200 m.

### Plant material

A total of 34 Azorean *Andoa* specimens, collected between 2008 and 2011, were analyzed, covering seven Azorean islands, all except Corvo and Graciosa, the two smallest islands, virtually without native forests. Collection sites are shown in Fig. 1. The Azores shape files were supplied by the University of Azores, Azores Biodiversity Group, loaded on QGIS Desktop 3.22.1 and exported to Paint. Voucher information per specimen is given in Table 1.

### Molecular analysis

For further details on DNA extraction, PCR, Sanger sequencing, and AFLP analysis see Martins *et al.* (2021). Of the three molecular markers used in that study (*trnL-trnF*, ITS, *nad5*) most sequences from Azorean specimens were obtained for the chloroplast marker *trnL-trnF*; therefore, we compared that marker with the AFLP data in the present study. We included *trnL-trnF* sequences from 23 *Andoa* samples for which also AFLP data were available (Table 2). For the other 11 samples for which AFLP data were present, no properly readable sequences could be obtained. For GenBank accession numbers see Appendix 1 in Martins *et al.* (2021). DNA sequences were manually aligned in PhyDE v0.995 (Müller *et al.* 2006). Absence/presence information of AFLP fragments obtained for two selective primer combinations from 34 specimens (Table 2) was transformed into a binary matrix (0 – fragment absent / 1 – fragment present).

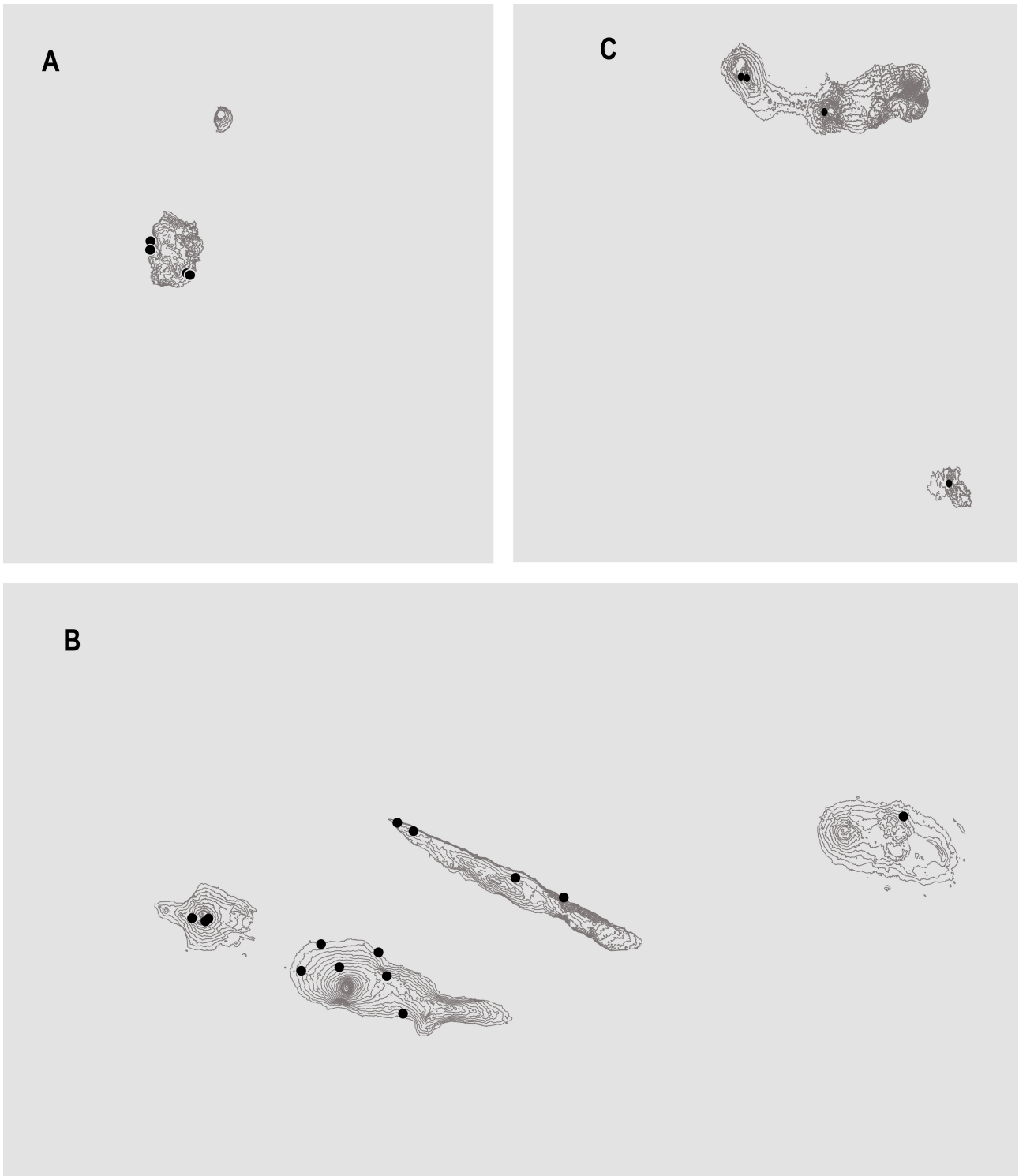
### Data analysis

A statistical parsimony (TCS) haplotype network (Clement *et al.* 2002) of *trnL-trnF* sequences of 23 *Andoa* samples was carried out with PopArt (Leigh & Bryant, 2015). Haplotype diversity (Hd) and nucleotide diversity ( $\pi$ ) were calculated in DNAsp5 (Librado and Rozas 2009).

The AFLP data were analyzed by AMOVA (Analysis of Molecular Variance) and PCoA (Principal Coordinates Analysis), using GenAlex 6.5 (Peakall & Smouse 2012). In PCoA, the data analyzed is a similarity or distance matrix for a set of objects. The similarity or distance matrix is assembled from the data variables (Gower 1966), here the scored AFLP fragments. The AMOVA was carried out to calculate pairwise PhiPT values (Fst analogue for binary data in GenAlex; Bolibok-Brągoszewska *et al.* 2014) to estimate genetic differentiation between two elevational groups (0–600 m, *Picconia-Morella* lowland forests and *Laurus* submontane forests; 600–1200 m, *Juniperus-Ilex* forests and *Juniperus* woodlands). The number of permutations used to estimate the probability values was 999 (Yamasaki and Ideta 2013). Following Yaacov *et al.* (2012), we considered PhiPT values 0.15–0.25 representing large, 0.05–0.15 moderate, and <0.05 little genetic differentiation with p-value = 0.001.

A Chi-Square test was carried out in Past 4.03 (Hammer 2021) to assess the significance of the relationship between elevation and AFLP groups or *trnL-trnF* haplotypes, respectively. In this analysis, we divided the 34 AFLP samples into four elevational groups (0–300 m, 300–600 m, 600–900 m, 900–1200 m). For *trnL-trnF*, the 23 samples were divided into two elevational groups (0–600 m, 600–1200 m) due to the lower number of samples available, in order to obey the Chi-Square test principles (Zar 2010). Significance levels were considered significant if p-values were below 0.05.

When 20% of the samples are below five, it is required to apply the Chi-Square test by Monte Carlo simulation, which comprises a comparison of the observed data with random samples that are generated in accordance with the tested hypothesis. In the present case, the analyzed p-values are those from Monte Carlo simulation. We used the Bonferroni correction for corrections of p for multiple comparisons, concerning AFLP and *trnL-trnF* samples. The significance level (p=0.05) was divided by the number of samples, respectively eight and six.



**FIGURE 1.** Azorean islands with altimetry maps of 100 m altitudinal curves and sampling locations (black dots). A. Western island group (Flores), B. Central island group (Faial, Pico, S. Jorge, Terceira). C. Eastern island group (S. Miguel and Sta Maria).

**TABLE 1.** Voucher information for the analyzed *Andoa berthelotiana* specimens. CG Central Group, EG Eastern group, WG Western group.

DNA no.	Island group	Island	Collecting site	Elevational group (m)	Main vegetation	Herbarium number
1328	2_CG	Pico	Perto da Furna Henrique Maciel	0–200	Forest with <i>Pittosporum undulatum</i> , <i>Picconia azorica</i> (Tutin 1933:101) Knoblauch (1934:1128)	267264 (LISU)
1329	2_CG	Pico	Transversal road to Pico	0–200	Forest with <i>Pittosporum undulatum</i> ?	267265 (LISU)
1330	2_CG	Pico	Furna da Agostinha	0–200	Vineard in ancient clearing invaded and surrounded by forest with <i>Pittosporum undulatum</i> , <i>Myrica faya</i> and <i>Picconia azorica</i>	267266 (LISU)
1117	1_WG	Flores	Aldeia da Cuada	0–200	Forest with <i>Laurus azorica</i> and <i>Pittosporum undulatum</i>	267244 (LISU)
1126	1_WG	Flores	Aldeia da Cuada	0–200	Forest with <i>Laurus azorica</i> and <i>Pittosporum undulatum</i>	267246 (LISU)
1168	1_WG	Flores	Faja Grande - Poço do Bacalhau	0–200	Forest	L.4518907 (L)
1169	1_WG	Flores	near Lombas	0–200	Forest	L.4518940 (L)
1212	1_WG	Flores	near Lombas	0–200	Forest with <i>Laurus azorica</i>	267254 (LISU)
1213	1_WG	Flores	Aldeia da Cuada	0–200	Forest with <i>Laurus azorica</i> and <i>Pittosporum undulatum</i>	267255 (LISU)
1214	1_WG	Flores	Aldeia da Cuada	0–200	Forest with <i>Laurus azorica</i> and <i>Pittosporum undulatum</i>	267256 (LISU)
1118	2_CG	S. Jorge	Lagoa	0–200		267245 (LISU)
1217	2_CG	S. Jorge	Lagoa	0–200		267259 (LISU)
1327	2_CG	Pico	Gruta das Torres	200–400	<i>Pittosporum undulatum</i> , <i>Juniperus brevifolia</i> , <i>Laurus azorica</i>	267263 (LISU)
1170	2_CG	S. Jorge	Near to the road, close to Pico dos Cutelos	200–400	Forest	L.4518981 (L)
1116	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i>	267243 (LISU)
1127	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i>	267247 (LISU)
1215	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i>	267257 (LISU)
1216	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i> , <i>Erica azorica</i> and <i>Pittosporum undulatum</i> .	267258 (LISU)
1219	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i>	267261 (LISU)
1220	2_CG	Terceira	Escaleira	200–400	Forest with <i>Laurus azorica</i> , <i>Erica azorica</i> and <i>Pittosporum undulatum</i> .	267262 (LISU)
1218	2_CG	S. Jorge	Sete Fontes Park	400–600		267260 (LISU)
1529	3_EG	S. Miguel	Forest track on Caldeira das Sete Cidades	400–600	Forest with <i>Cryptomeria japonica</i> (Thunberg ex. Linnaeus 1782:421) D. Don (1839:167)	GM Dirkse 27212
1149	3_EG	Sta Maria	Pico Alto	400–600		267250 (LISU)
1128	2_CG	S. Jorge	Ribeira d'Areias. Perímetro Florestal.	400–600	Forest	267248 (LISU)
1159	2_CG	Faial	Forest very close to Road Cabeço dos 30	600–800	Forest - <i>Laurus azorica</i> ?	267252 (LISU)

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**TABLE 1.** (Continued)

DNA no.	Island group	Island	Collecting site	Elevational group (m)	Main vegetation	Herbarium number
1542	2_CG	Faial	Forest very close to Road Cabeço dos 30	600–800	Forest - <i>Laurus azorica</i> ?	L267270 (LISU)
1343	2_CG	Pico	Mistério de Santa Luzia	600–800	Forest with <i>Erica azorica</i>	267267 (LISU)
1359	2_CG	Pico	Close to Lagoa do Capitao	600–800	Pasture	267268 (LISU)
1148	3_EG	S. Miguel	Lagoa do Canário	600–800		267249 (LISU)
1158	2_CG	Faial	Caldeira	800–1000		267251 (LISU)
1541	2_CG	Faial	Caldeira	800–1000		267269 (LISU)
1528	3_EG	S. Miguel	Mountain area along the road from Lagoa to Ribeira Grande	800–1000	Forest with <i>Laurus azorica</i> , <i>Ilex canariensis</i> Poir (1813:67), <i>Calluna vulgaris</i> (Linnaeus 1753:352) Hull (1808:114)	GM Dirkse 27259
1160	2_CG	Faial	Geodesic mark	1000–1200	Pasture area	267253 (LISU)
1543	2_CG	Faial	Geodesic mark	1000–1200	Pasture area	267271 (LISU)

**TABLE 2.** DNA numbers of samples analyzed for AFLP (all) and *trnL-trnF* haplotypes (gray shade), respectively, per 200 m a.s.l. interval. For further specimen information see Table 1.

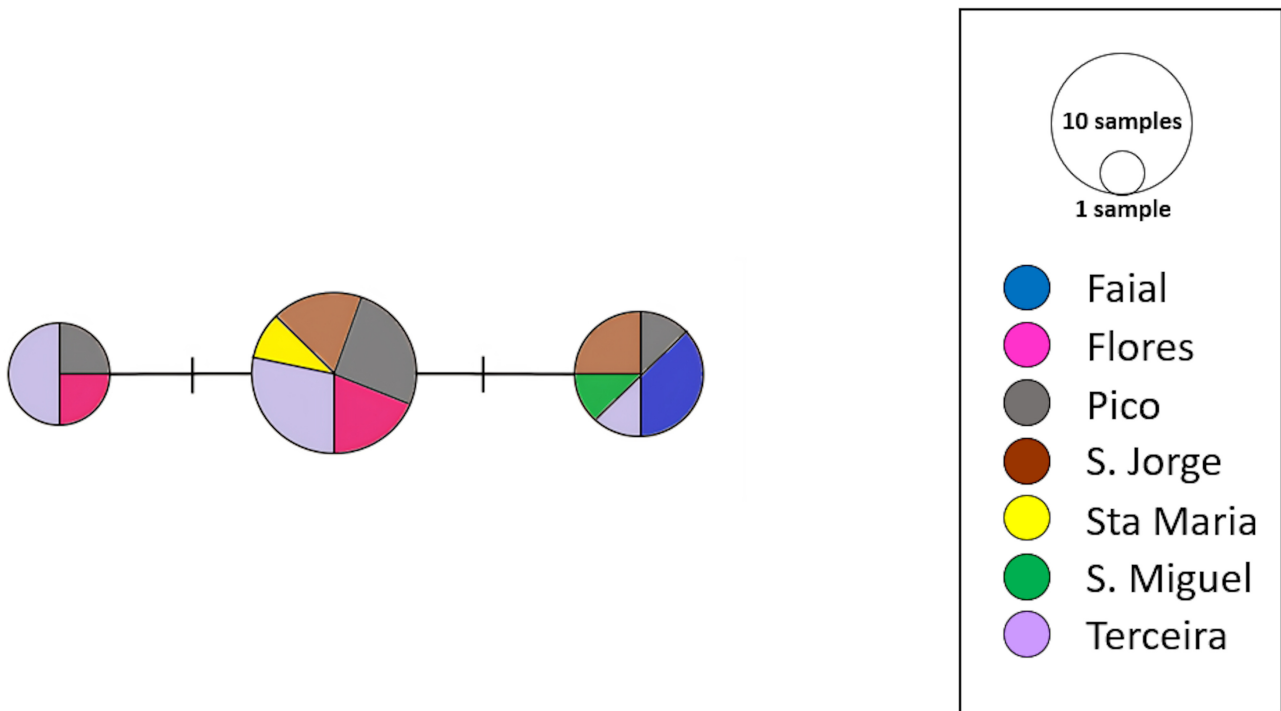
0–200 m	200–400 m	400–600 m	600–800 m	800–1000 m	1000–1200 m
1117	1116	1128	1148	1158	1160
1118	1127	1149	1159	1528	1543
1126	1170	1218	1343	1541	
1168	1215	1529	1359		
1169	1216		1542		
1212	1219				
1213	1220				
1214	1327				
1217					
1328					
1329					
1330					

## Results

### Intraspecific variation of *Andoa berthelotiana* within the Azorean archipelago

Three *trnL-trnF* haplotypes were detected (Fig. 2), haplotype trnL-F1 with 11 samples from islands Flores, Terceira, São Jorge, Pico and Santa Maria, haplotype trnL-F2 with eight samples from São Jorge, Faial, Terceira, Pico and São Miguel islands, and haplotype trnL-F3 with four samples from Flores, Terceira and Pico islands. Overall Azorean haplotype diversity ( $H_d$ ) and nucleotide diversity ( $\pi$ ) were 0.642 and 0.00202, respectively.

According to the PCoA analysis of the AFLP results, two main groups can be distinguished (AFLP1 and AFLP2; Fig. 3), of which group AFLP1 was found on Flores, Pico, São Jorge, Santa Maria, São Miguel and Terceira islands and group AFLP2 on Faial, Flores, Pico, São Jorge, São Miguel and Terceira islands. AFLP group 2 includes all samples with *trnL-trnF* haplotypes trnL-F1 and trnL-F3, except for sample 1168 from Flores (haplotype trnL-F1) that belongs to group AFLP2. All samples with haplotype trnL-F2 correspond to group AFLP2.



**FIGURE 2.** Haplotype network resulting from an alignment of *trnL-trnF* sequences of 23 specimens. Center: haplotype trnL-F1, right: haplotype trnL-F2, left: haplotype trnL-F3.

### Relations between genetic variation and elevation

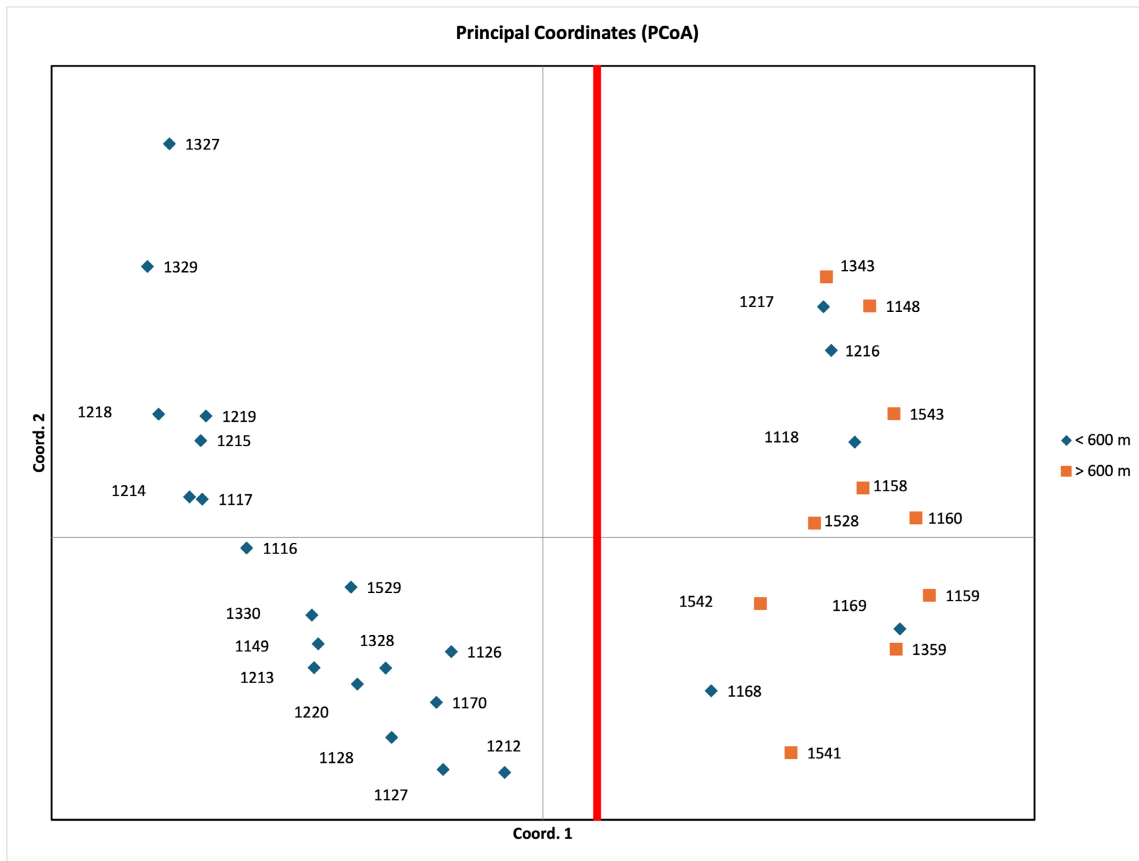
Of the three *trnL-trnF* haplotypes, trnL-F1 is only present below 600 m, while trnL-F3 is only present below 400 m. TrnL-F2 is the most widespread haplotype, occurring along the whole elevational range but with most samples above 600 m (Fig. 4). When grouping all samples from each haplotype into two intervals (0–600 m and 600–1200 m), the Chi-Square test indicated a significant difference between both elevation levels (Chi-Square: 11.979; Degrees of freedom: 2;  $p=0.0019$ ).

Group AFLP1 is formed exclusively by samples located below 600 m (Fig. 3 and Fig. 5), while group AFLP2 spans the whole elevational range but is observed mainly above 600 m. The PhiPT value between samples located between 0–600 m and 600–1200 m was 0.0151, indicating large genetic differentiation between these two altitudinal intervals. When grouping all samples from each AFLP group into four intervals (0–300 m, 300–600 m, 600–900 m, 900–1200 m; Table 3), the Chi-Square test indicated a significant difference between the frequencies of AFLP1 and AFLP2 among the four altitudinal levels (Chi-Square: 19.08; Degrees of freedom: 3;  $p=0.0001$ ).

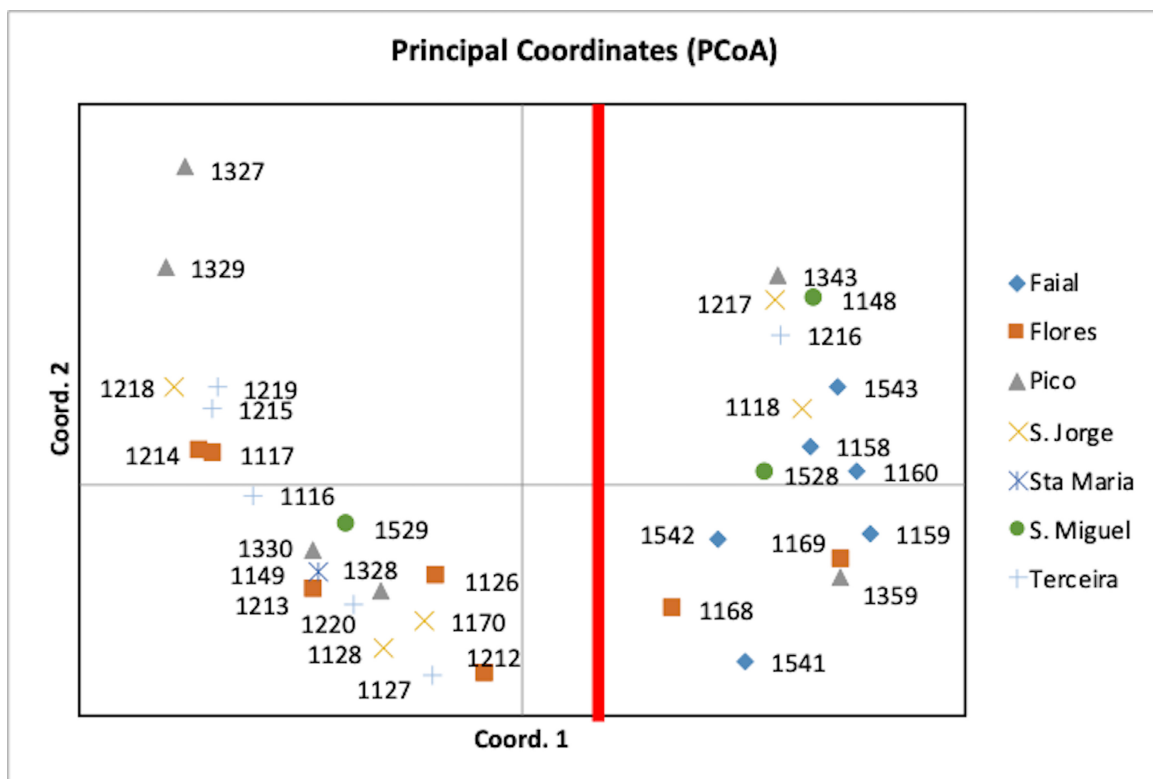
Using the Bonferroni correction, the corrected significance level is  $0.05/6=0.0083$  for *trnL-trnF* and  $0.05/8=0.00625$  for AFLP (both superior to the  $p$ -values obtained for *trnL-trnF* and AFLP, respectively 0.0019 and 0.0001), again confirming significant difference between both elevation levels for *trnL-trnF* haplotypes and indicating a significant difference between the presence of AFLP1 and AFLP2 considering the four altitudinal levels.

### Discussion

In addition to the intraspecific variation across Macaronesia (Martins *et al.* 2021), the current study explores the intraspecific variation within *Andoa berthelotiana* in the Azorean archipelago. Across Macaronesia the genetic variation is clearly geographically structured, leading to the presence of two semi-cryptic species, one in Canary Islands plus Madeira and another in the Azores (Martins *et al.* 2021). This differentiation, together with evidence at species level (e.g. *Echinodium spinosum* Mitten (1865:7) Juratzka (1866:178) in Madeira plus Canary Islands versus *Echinodium renauldii* (Cardot 1897:69) Brotherus (1909:1217) in the Azores; Stech *et al.* 2008) and comparison of whole bryophyte flora's (González-Mancebo *et al.* 2008), support the classification of the Macaronesian archipelagos into different biogeographic regions. For example, Rivaz-Martín *et al.* (2014) considered the Azores to belong to the Atlantic Central European sub-region, while Madeira belongs to Canarian-Madeirense biogeographic sub-region.

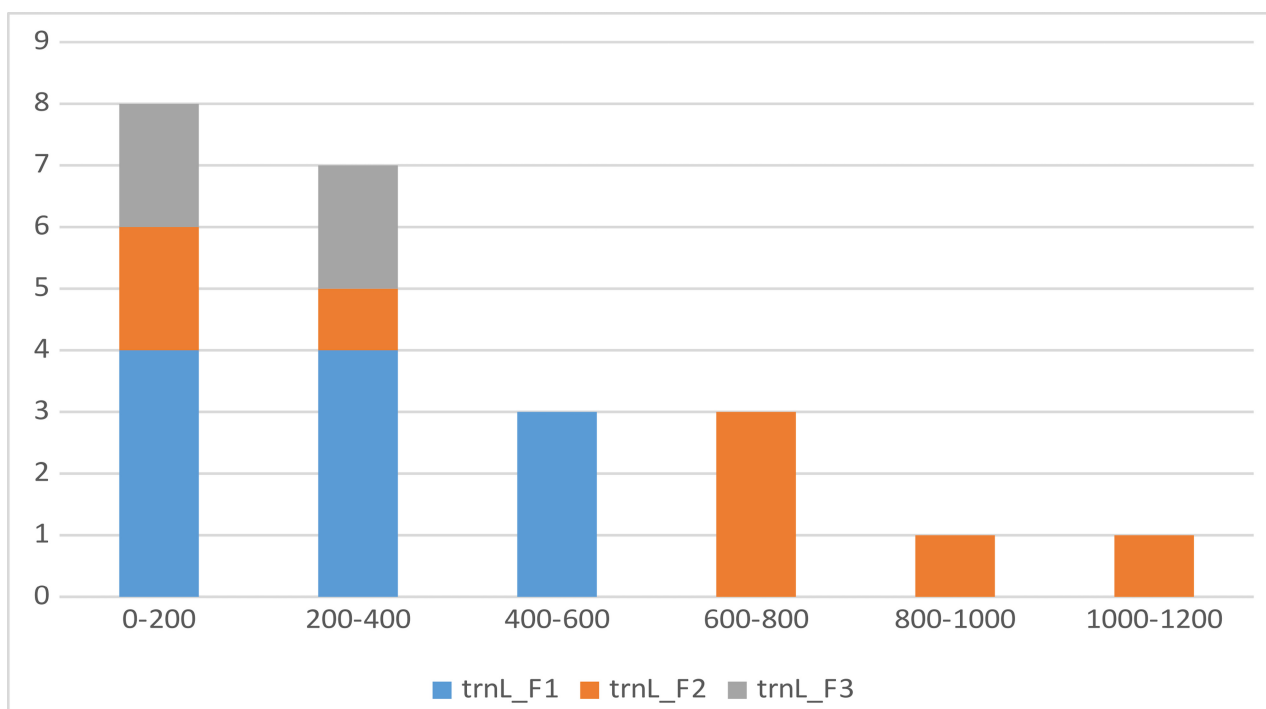


a)

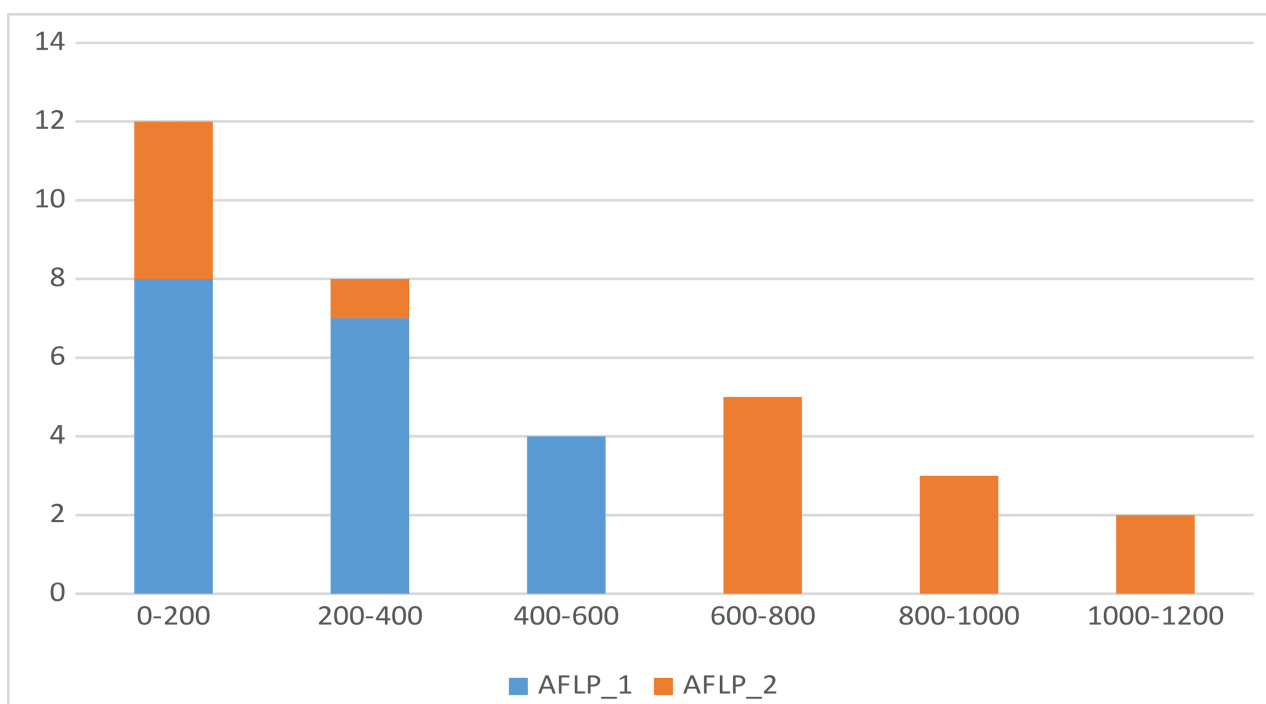


b)

**FIGURE 3.** PCoA analysis of *Andoa berthelotiana* samples from Azores archipelago: Faial, Flores, Pico, São Jorge, Santa Maria, São Miguel, Terceira islands, for the first two axes based on AFLP distance matrices. On the left and right sides samples cluster together, seemingly forming two groups, respectively AFLP1 and AFLP2. In a) symbols indicate elevation lower and higher than 600 m, in b) symbols indicate the different islands.



**FIGURE 4.** Elevational gradient with 200 m intervals, between haplotypes trnL-F1, trnL-F2 and trnL-F3. 200 m intervals were considered to see if there were if there was any haplotype differentiation below or above 600 m.



**FIGURE 5.** Elevational gradient with 200 m intervals, between groups AFLP1 and AFLP2. 200 m intervals were considered to see if there were any AFLP group differentiation below or above 600 m.

Within the Azores, the present data do not show a clear geographical structure of genetic variation with *Andoa berthelotiana*. There seems to be a slight shift in *trnL-trnF* haplotype distribution from the Western to the Eastern island groups as well as some differentiation in frequency of occurrence of AFLP groups 1 and 2 (e.g. AFLP1 more frequent on Flores and Pico, and AFLP2 on Faial), but a higher number of samples needs to be analyzed to substantiate this observation. Due to the shorter distances between the islands of the Azores archipelago than between the Azores versus Madeira and Canary Islands, assuming more frequent dispersal events and genetic exchange in *Andoa* populations within the Azorean islands might be plausible. Though haplotype diversity is relatively high within the Azores, the low nucleotide diversity reveals small variation amid haplotypes.

**TABLE 3.** Distribution of samples from both AFLP groups between 300 m a.s.l. intervals, with pairwise significant differences. The column (Significance) indicates the significance letters assigned (a – b) to the altitude intervals based on the post-hoc test. Intervals that share the same letters do not significantly differ from each other, whereas intervals with different letters indicate significant differences in the AFLP distribution of *Andoa berthelotiana* across the four elevation intervals ( $p < 0.05$ ).

Intervals	AFLP1	AFLP2	Significance
0–300	9	4	a
300–600	10	1	a
600–900	0	6	b
900–1200	0	4	b

In contrast to a relationship with geographical location of islands or groups of islands, intraspecific variation within the Azores is related to the elevation at which the samples were collected. Elevation is well known as a propeller of species diversity and genetic diversity, also in bryophytes (Cronberg 2004, Sim-Sim *et al.* 2015), given that it influences temperature and precipitation, which in turn impact on plant species distribution and possibly intraspecific genetic variation (Sim-Sim *et al.* 2015). *Andoa* specimens with genotypes restricted to elevations below 600 m (AFLP group 1, haplotypes trnL-F1 and trnL-F3) may be genetically adapted to environmental conditions that prevail in those areas. There, most samples were collected in forests with *Laurus azorica* (endemic) and/or *Pittosporum undulatum* Ventenat (1802:76) (introduced invasive species) and sometimes also with *Erica azorica* (endemic). The other genotypes (AFLP group 2, haplotype trnL-F2), in contrast, seem to have a wider ecological amplitude, ranging from low- to high-elevation vegetation.

Within the Azores archipelago, anthropogenic activities have altered the majority of natural vegetation, in particular the laurel forests between 300 and 600 m a.s.l. (Elias *et al.* 2016). Beyond 600 m until about 900 m a.s.l., the best conserved vegetation belts are found, which include *Juniperus-Ilex* forests and *Juniperus* woodlands (Elias *et al.* 2016). Generally, bryophyte species richness in the Azores is highest at around 600 m a.s.l. (Gabriel & Bates, 2005, Gabriel *et al.* 2011, Henriques *et al.* 2017), with exception of the highest island Pico, where bryophyte richness peaks from 600 m to 1000 m a.s.l. (Coelho *et al.* 2021). Conservation of the remains of vegetation types below 600 m a.s.l. (*Erica-Morella* coastal woodlands, *Picconia-Morella* lowland forests and *Laurus* submontane forests) is thus crucial for the conservation of bryophyte diversity. As our data show, this does not only hold for the species *Andoa berthelotiana* itself, which is associated with natural forest (Gabriel *et al.* 2011), but also for the intraspecific genetic diversity of *Andoa* populations, i.e. the genotypes restricted to lower elevations. AFLP group 1 and haplotypes trnL-F1 and trnL-F3 might be related to habitats contained in *Picconia-Morella* lowland forests (generally between 100–300 m a.s.l., also down to coastal areas) and particularly *Laurus* submontane forests (frequently between 300 and 600 m a.s.l.). This observation was taken from the data concerning the main vegetation present at the collection site and the elevation. Other authors have found that environmental determinants, namely orographic mist layer, were important to predict bryophyte richness in the Macaronesian Islands (cf. Aranda *et al.* 2014), and these environmental factors may also be related to intraspecific variation. More research is required to infer whether the different genotypes correlate with environmental conditions and specific habitat types.

Hedenäs (2016) already concluded that intraspecific diversity may significantly vary in different regions and that reducing regional frequencies of bryophyte species could cause an important reduction of genetic variation. Population genetic diversity is usually not given proper consideration in conservation priorities (Kahilainen *et al.* 2014), despite the fact that genetic diversity can increase the probability of species survival and lessen fast anthropogenic environmental changes (Hughes and Tillman, 2004; Jump *et al.* 2009; Spagnuolo *et al.* 2009). For *Andoa*, the present data indicates that, in parallel to conserving populations across its distribution range, in particular the few remaining populations on Tenerife, Fuerteventura and La Palma, Canary Islands (González-Mancebo *et al.* 2008, 2009, 2019), efforts are required to create priority conservation areas or to improve extant ones that sustain the current genetic variation within *Andoa* on the Azores, mainly below 600 m.

## Conclusions

Together with the earlier study by Sim-Sim *et al.* (2015), the present study shows an avenue for the study of intraspecific variation within Macaronesian endemic bryophyte species in relation to elevation, where the preservation of one or

few populations with unique genotypes might be of importance to protect the future existence of species in a context of possible continuous anthropogenic environmental changes. Our analyses on the elevational distribution of intraspecific molecular variation in the endemic *Andoa berthelotiana* furthermore support the view that the conservation of vegetation types below 600 m is essential for the conservation of bryophyte diversity in the Azores.

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