

Macaronesia: a source of hidden genetic diversity for post-glacial recolonization of western Europe in the leafy liverwort *Radula lindenbergiana*.

Benjamin Laenen¹, Aurélie Désamoré¹, Nicolas Devos¹, A. Jonathan Shaw², Juana Maria González-Mancebo³, Mark A. Carine⁴ and Alain Vanderpoorten¹

✓ Introduction

Bryophytes exhibit apparently low rates of endemism in Macaronesia and differ in diversity patterns from angiosperms by the widespread occurrence of endemics within and among archipelagos. With a phylogeography of the leafy liverwort *Radula lindenbergiana* (top right) using molecular markers, we aim to address two main questions :

- Is there an evidence of morphologically cryptic diversification in Macaronesia?
- What are the past and present relationships between Macaronesia and the continent in this taxa?



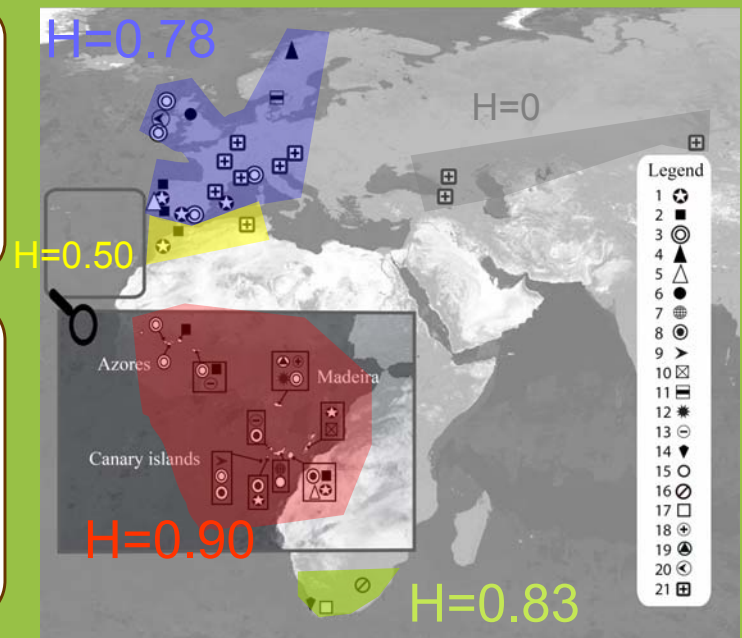
Radula lindenbergiana

✓ Materials and methods

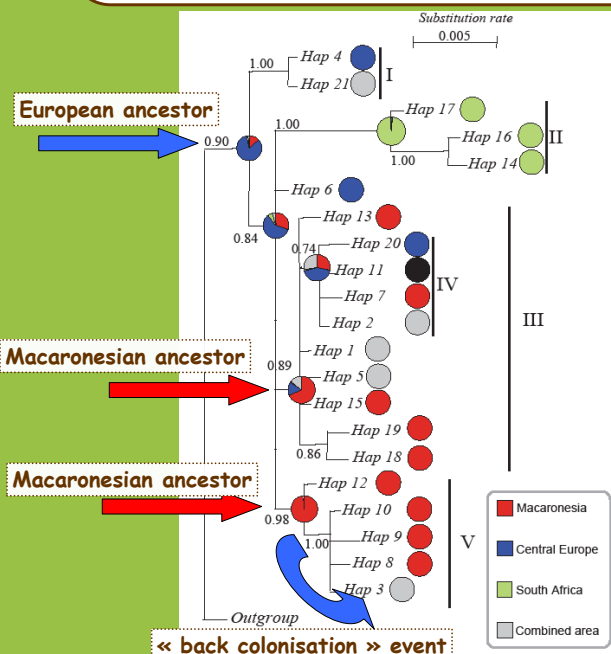
- 84 sampled populations
- 4 cpDNA loci : *atpB-rbcL*, *trnL*, *trnG* and *rps4*
- Genetic diversity index (H, pi)
- Bayesian ancestral area reconstruction
- Fst/Nst to test for phylogeographical signal

✓ Results

- High genetic diversity (H) in Macaronesia (right map) with endemic haplotypes
- Low genetic diversity (H) in Caucasus/Asia and North Africa
- Non monophyly of macaronesian haplotypes
- Macaronesian origin of current european atlantic coast haplotypes (tree below)
- Nst>Fst → geographical structure of haplotypes



Haplotype map with regions in color and haplotypic diversity (H) associated.



✓ Main Conclusion

In *Radula lindenbergiana*, molecular markers have revealed a cryptic diversification in Macaronesia.

→The apparent lack of radiation among macaronesian bryophytes may thus reflect the reduced morphology of bryophytes in comparison with angiosperms.

The high genetic diversity, the phylogeographic signal coupled with the macaronesian origin of current european haplotypes point macaronesian islands as potential glacial refugium.

→Buffered climatic conditions may have favoured refugium during glacial period with subsequent « back colonisation » from island to the continent.

	Sample size	Nb of haplotypes	Haplotypic diversity (S.D.)	Nucleotidic diversity (S.D.)
Macaronesia	39	13	0.90 (0.03)	0.0038 (0.0019)
South Africa	4	3	0.83 (0.22)	0.0013 (0.0010)
Europe	28	9	0.78 (0.06)	0.0025 (0.0014)
North Africa	4	2	0.50 (0.27)	0.0002 (0.0003)
western Asia	9	1	0.00 (0.00)	0.0000 (0.0000)

50% consensus majority rule from the Bayesian analyses based on the four cpDNA loci. Pie diagrams on node represent the results of ancestral area reconstruction.