

Genetic structuring in island endemics – analysing the effects of topography and climate on population differentiation

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Background

Island endemics evolved by species radiations on oceanic archipelagos are ideally suited to analyse population differentiations and adaptive speciation processes due to 1. restricted species ranges and the possibility to respectively take the total populations into account and 2. direct comparability and reference between closely related species and environments. The genus *Aeonium* WEBB & BERTHEL. (Crassulaceae) is one of the most popular examples of plant species radiations on islands. In a relatively short evolutionary time period various ecological niches have been realized and a great variety of morphological forms and ecophysiological characteristics have developed. The Canarian archipelago can be regarded as the clear species diversity centre and recent research results imply a phylogenetic origin on that archipelago, stating *Aeonium* as neoendemic (Mort et al. 2002). Most of the species occur only on single islands and clear intrageneric lineages with vicariant island distributions can be seen, which, with respect to the young geological age of some of the Canary Islands, indicates recent speciation and ongoing intense evolutionary processes (Fig. 1).

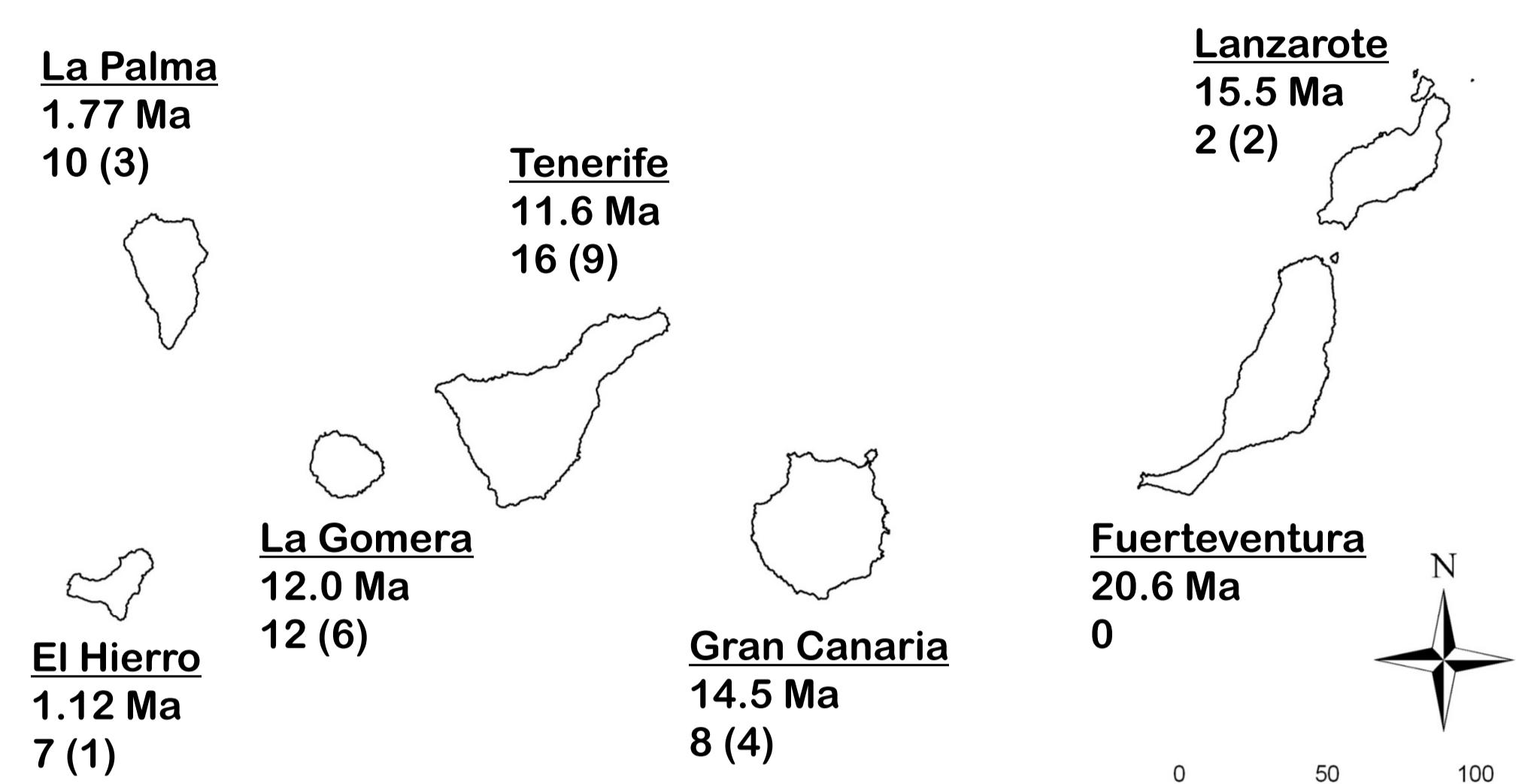


Fig. 1: The Canarian archipelago with geological ages and numbers of *Aeonium* species of the single islands (including *Greenovia*; island endemics in brackets) (Carracedo et al. 2002, Liu 1989).

Aims and hypotheses

Recent reconstructions of the *Aeonium* phylogeny and molecular dating results show high evolutionary rates (Kim et al. 2008, Thiv et al. 2010) and a wide range of habitat types and evolutionary opportunities on most of the Canary Islands give rise to the assumption of explicit genetic population structures within some of the species depending on ecological and spatial factors. To evaluate the significance of these factors to population structuring and associated evolutionary processes within species of *Aeonium* we test the following hypotheses:

- intraspecific genetic variabilities reveal clear population differentiations and restricted gene flow between populations
- population structures match with geographical patterns – topography, potential gene flow barriers, distance, climatic parameters (precipitation and temperature differences), geological age of islands, geological underground, position in altitudinal zonation
- interspecific differences in population structuring can be explained by specific biological characteristics - population sizes (total and subpopulations), specific reproductive characteristics, phylogenetic species ages
- population genetic differentiations correlate with intraspecific morphological variabilities

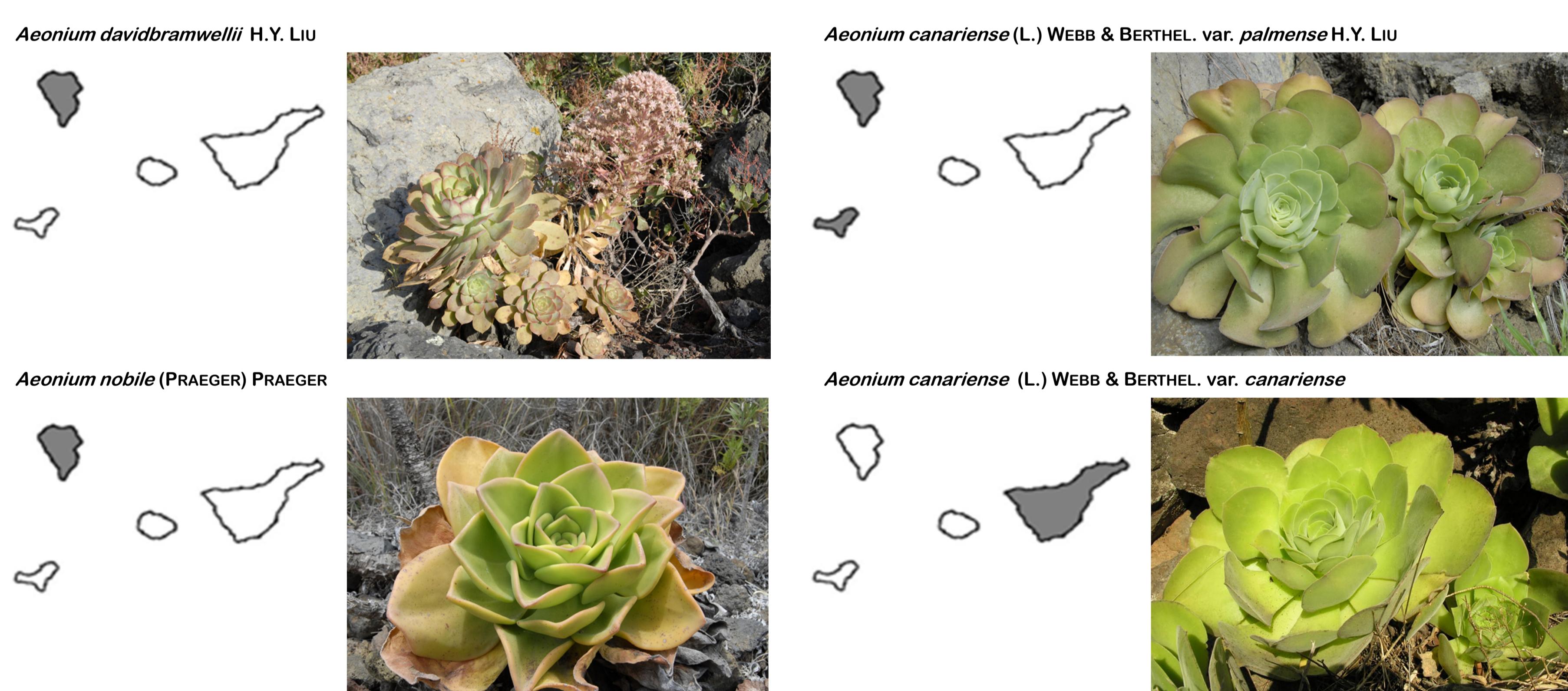


Fig. 2: Target species and their occurrence on the single Canary islands.

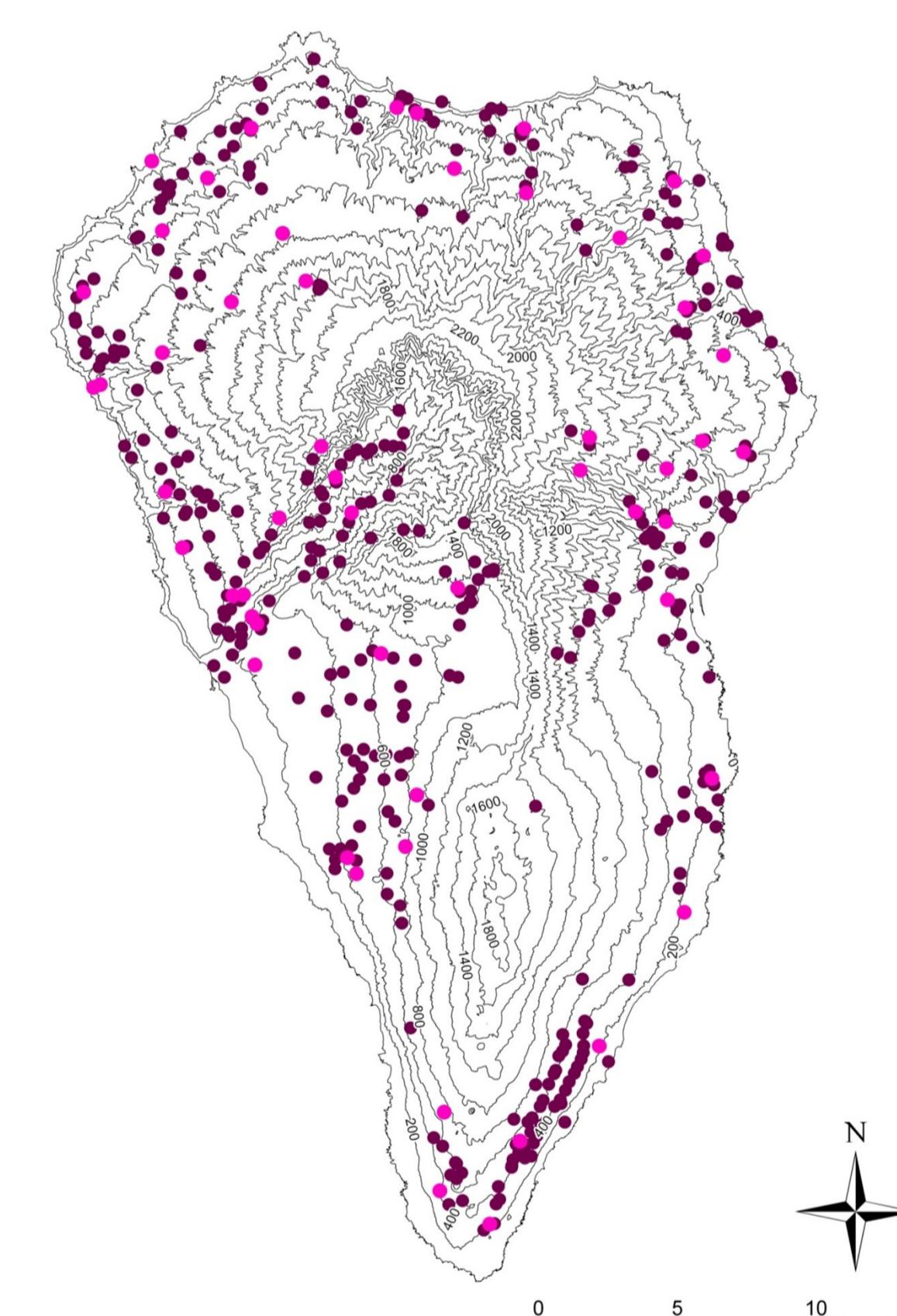


Fig. 3: Sampling results for *Ae. davidbramwellii* on La Palma. Deep purple marks: species occurrence locations, pink marks: populations where DNA-samplings were performed.

Materials and methods

Considering phylogenetic and biogeographical relationships, as well as differing ecological demands, we selected three single island endemic *Aeonium* species of Tenerife, El Hierro and in particular La Palma and one variety distributed across two islands (Fig. 2). From each taxon DNA-samples were taken comprehensively throughout the entire distribution range (e.g. for *Ae. davidbramwellii* see Fig. 3) with 5 DNA-samples per sampling site / (sub-)population, respectively.

Laboratory work is currently in progress to detect intraspecific genetic variabilities (ISSR-fingerprintings - Inter Simple Sequence Repeats, fragment analysis carried out on an automated sequencer). By population genetic data analyses (G_{ST} , AMOVAs, etc.) and referencing of these data to geography and climate by Mantel tests and GIS studies we aim to detect geographically or ecologically conditioned population differentiations. Further on, we took morphological data on the populations that are chosen for the DNA fingerprinting to compare and relate genetic and morphological population differentiations.

Beside these biogeographical and evolutionary investigations we will combine the genetic population structure data with regional climate models and future habitat suitability models to recognize potential impacts of climate change on the investigated *Aeonium* taxa and thus assess recent and future endangerment status of these spatially strongly restricted species.