

## Titre du projet : **Testing high-elevation quaternary climatic refugia for alpine plants (NUNATAKS)**

Volet : **Recherche**

Porteur du projet : **Sébastien Lavergne**

Laboratoires impliqués : **LECA - ISTerre**

## Bilan du projet pour l'année/la période

### Bilan d'activité (1 page max)

**Objective :** This project aims at revisiting fundamental, yet unresolved, problem of Pleistocene climatic refugia in the Alps. We study study the high-alpine cushion plant, siliceous specialist, *Androsace vandellii* (Fig 1), and test whether it survived

### Distribution data and distribution modelling :

In order to explore current and past distribution of *Androsace vandellii*, we collected current species distribution data of the species, modelled its ecological niche by the means of species distribution modeling (SDM). We now plan to hindcast niche preferences into the past conditions of the last glacial maximum (LGM).

First we compiled geo-referenced data about the species presence and absence, including CBNA phytosociological database, Silene database, database provided by University in Lausanne, internal LECA phytosociological database, presence data provided by University in Innsbruck and Civil Museum in Rovereto, and also the presence and absence data we gathered during our own fieldwork. All those sources combined together yield 695 presence and 16064 absence points across the Alps.

All these data were used to calibrate two different species distribution models: (i) A coarse-scale model of species distribution across whole Alpine arc, using topographic variables derived from 30x30m DEM, relevant BIOCLIM variables and bedrock information from PARMADO raster in resolution 1 x 1 km. This model was fitted using R package BIOMOD and used during field campaign for discovering populations with unknown location. (ii) A the moment we are developing a fine-scale model only for french Alps, where we have the most dense presence and absence sampling. In this model we substituted PARMADO by fine vector layer based on IGN data. We also added a layer forecasting current and LGM glacier cover based on, topographic and climatic variables and geomorphological evidence in hierarchical manner. Once finished the development, we'll be able to use its current predictions and hindcast them to the estimated climatic context of the LGM.

### Development of ddRAD sequencing :

We processed the material obtained by our 2017 field campaign or from our collaborators from University in Innsbruck (Fig 2) to extract nuclear DNA and performed genetic screening based on a ddRAD sequencing protocol. We extracted samples of all 233 individuals from 55 populations across the whole distribution range and performed library preparation. Resulting multiplexed libraries were sequenced by a subcontractor (FASTERIS). Using a reference plastome and mitochondrial genome, we selected only sequenced fragments coming from nucleus. We grouped homologous nuclear fragments using Stacks programme and selected randomly one variable site in each fragment, so called single nucleotide polymorphisms (SNPs), for subsequent population-genetic analyses. This procedure yielded 816 SNPs for 233 individuals entering the analysis.

### Analytical perspectives :

The SNP data retrieved from RAD sampling show that several populations have much higher genetic variability (Fig 3), suggesting that these might be the refugial populations that survived LGM. In order to further explore this pattern, we plan to fit current population genetic structures, e.g. site frequency spectra of populations, by several different coalescent population models (using R package Coala), standing for different scenarios of past population processes. Then we plan to use approximate bayesian computations (ABC) to evaluate which of the scenarios are most likely to explain observed data structure. The main working scenarios are (i) Equally isolated populations reestablished after overall bottleneck at time of LGM (ii) Equally isolated populations with strength of bottleneck related to habitat suitability in LGM (iii) Populations with strength of geneflow related to friction distance on current SDM and strength of bottleneck related to habitat suitability in LGM.

### Illustrations - avec légende et crédit (à envoyer également séparément)



Fig 1. The study species *Androsace vandellii*, Belledonne, 2017.

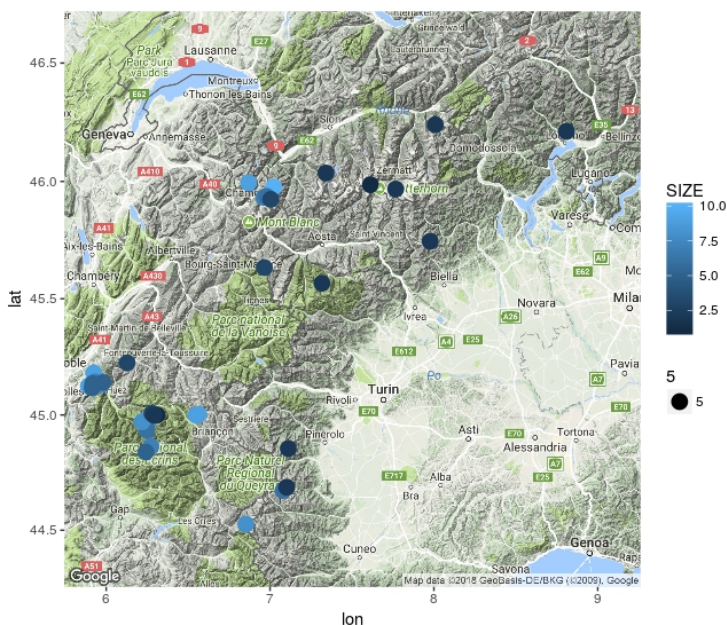


Fig 2. Map showing all sampled populations of Western Alps used in the genetic analyses. Populations of size larger than 5 samples will be used for coalescent modeling.

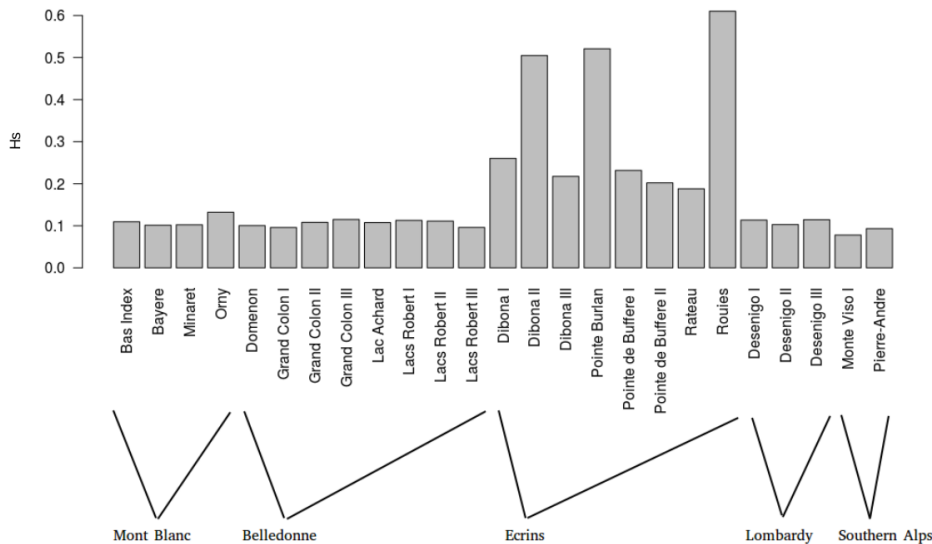


Fig 3. Genetic diversity (expected heterozygosity metric) of different populations that we intend to use for coalescent modeling. Localities Dibona II, Pointe Burlan and Rouies have the highest genetic variability and are thus the most likely to be glacial refugial.

### Production scientifique (articles scientifiques, actes de congrès...)

Smyčka J., Roquet C., Lavergne S., 2016. Patterns of endemism and species diversification in the Alps, International Conference on Ecological Sciences SFE, Marseille (talk)

Smyčka J., Roquet C., Lavergne S., 2017. Patterns of endemism and species diversification in the Alps, XIV MEDECOS & XIII AEET meeting, Sevilla, Spain (talk)

Smyčka J., Roquet C., Lavergne S., 2017. Disentangling drivers of plant endemism and diversification in the Alps – a phylogenetic and spatially explicit approach, Carpathian Biogeography Conference, Cluj-Napoca, Romania (talk)

### Bilan financier succinct (avec suivant les cas : co-financements éventuels, équipements achetés, missions, recrutements divers, fonctionnements divers...)

#### Dépenses réalisées au 2 février 2018

	Postes
Fournitures & petit matériel	270,55 €
Missions (location voitures)	2284,77 €
Missions (frais)	5709,17 €
Sous-traitance (séquençage)	4392 €
<b>Total</b>	<b>12656,49 €</b>