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Phenotypic trait variation in genetically distinct *Arabidopsis thaliana* populations from the Pyrenees Mountains highlight acclimation to environmental constraints.

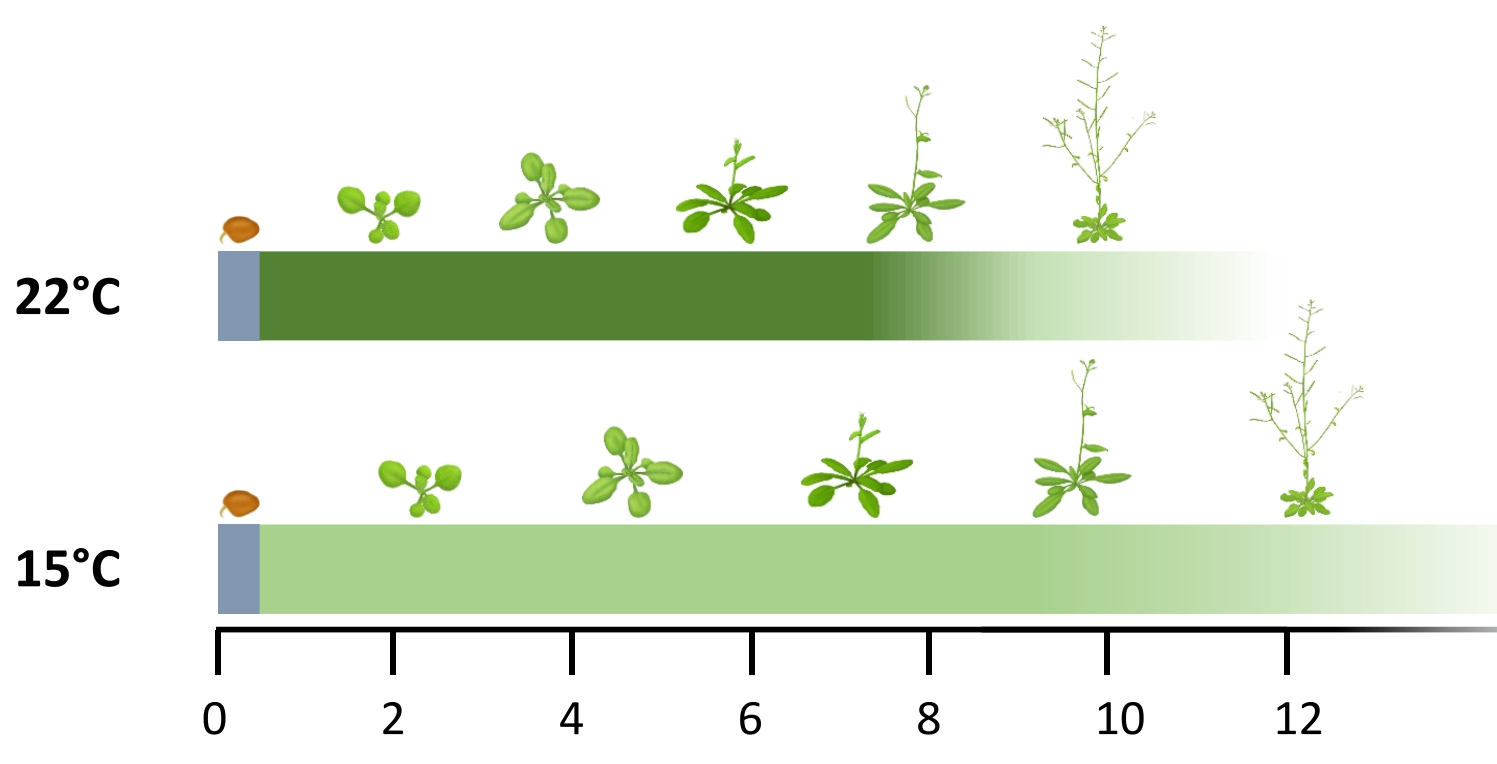
Harold Duruflé¹, Philippe Ranocha¹, Duchesse Lacour Mbadinga Mbadinga¹, Sébastien Déjean², Maxime Bonhomme¹, Hélène San Clemente¹, Nathalie Escaravage³, Monique Burrus³, Christophe Dunand¹

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Context

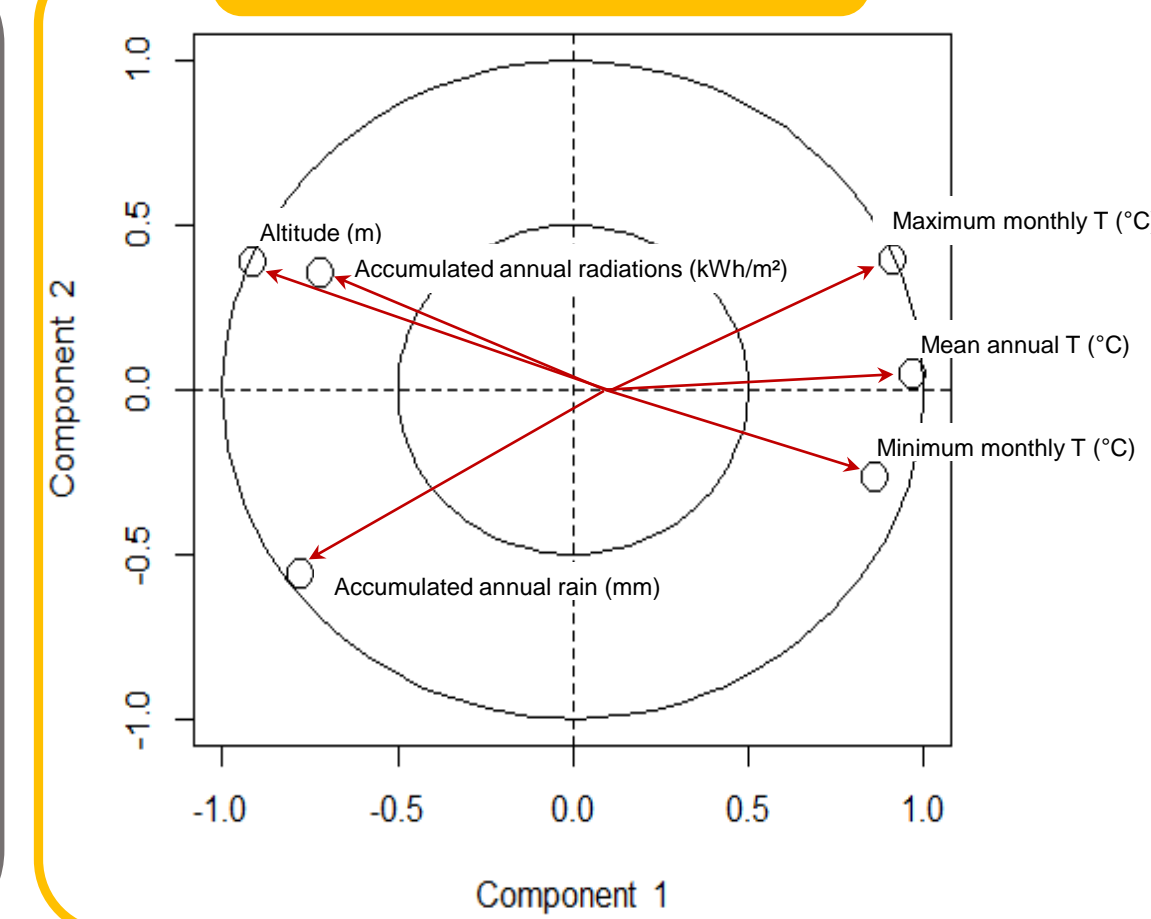
The natural diversity is a free reservoir of variation for studying morphological and developmental traits. Studying natural variation will help to identify genetic mechanisms of complex traits. Mountain habitats provide genuine environmental temperature gradients where plants need to adapt to multiple environments. Pyrenees Mountains constitute a physical barrier between Spain and France. In this study, 30 new natural populations of *Arabidopsis thaliana* were identified and collected between 200 and 1800 m above sea level. The genetic relationships between populations and also the phenotypic variability were analysed at sub-optimal temperature (22°C vs 15°C) to mimic natural environment.

Strategies & Objectives



- 1] Providing evidence of the genetic variation of *Arabidopsis thaliana* in the Pyrenees.
- 2] Phenotypic analysis at two growth temperatures.
- 3] Correlation between phenotypic traits, the climates and the genetic structure.

Climate

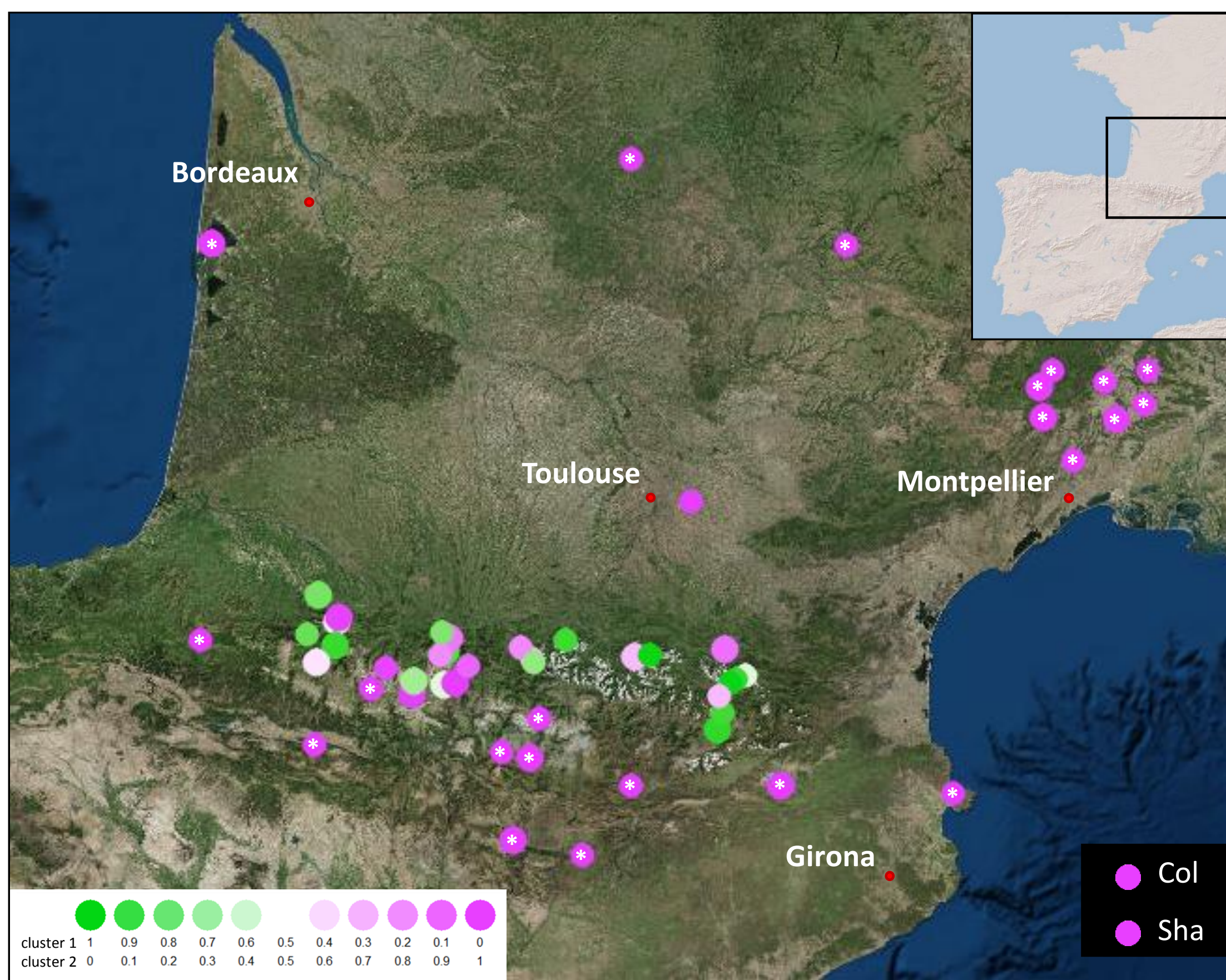


Principal component analysis (PCA) were used to quantify the climatic variance of 5 climate variables and the altitudes that describe the original conditions of the natural populations of *A. thaliana*.

The environmental characteristics of each population can be illustrated with climate PC1 value.

Population structure

5 class III peroxidases (Prx09, 25, 36, 48 and 62) genes were sequenced and used as polymorphic markers to evaluate genetic variation of 341 individuals of *A. thaliana* (representing 30 populations).

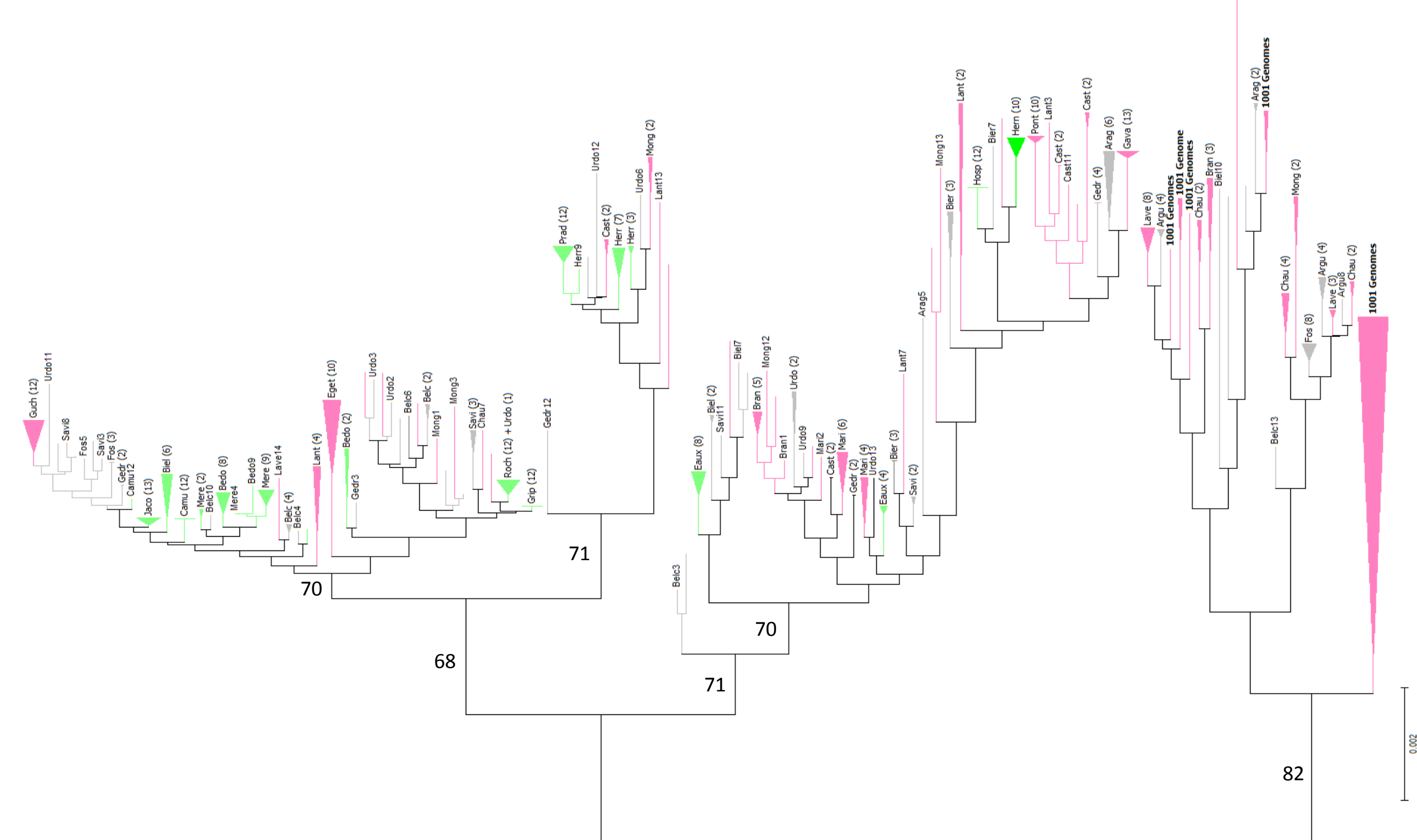


- Specific genetic cluster
- 11 homogeneous populations

Geographic location and genetic group assignment of 30 populations of *A. thaliana* in Pyrenees Mountains, 22 accessions of 1001 genomes and 3 out group populations Lant, Col and Sha. Relationships inferred with STRUCTURE^[1] are illustrated by colored circle. Each individual circle represents the populations allocation into their estimate membership proportions in each genetics cluster determined by STRUCTURE results (K=2). White stars stand for 1001 genomes populations.

Phylogeny

Illustration of the natural genetic diversity among of the *A. thaliana* populations collected in the Pyrenees by a phylogenetic analyses.

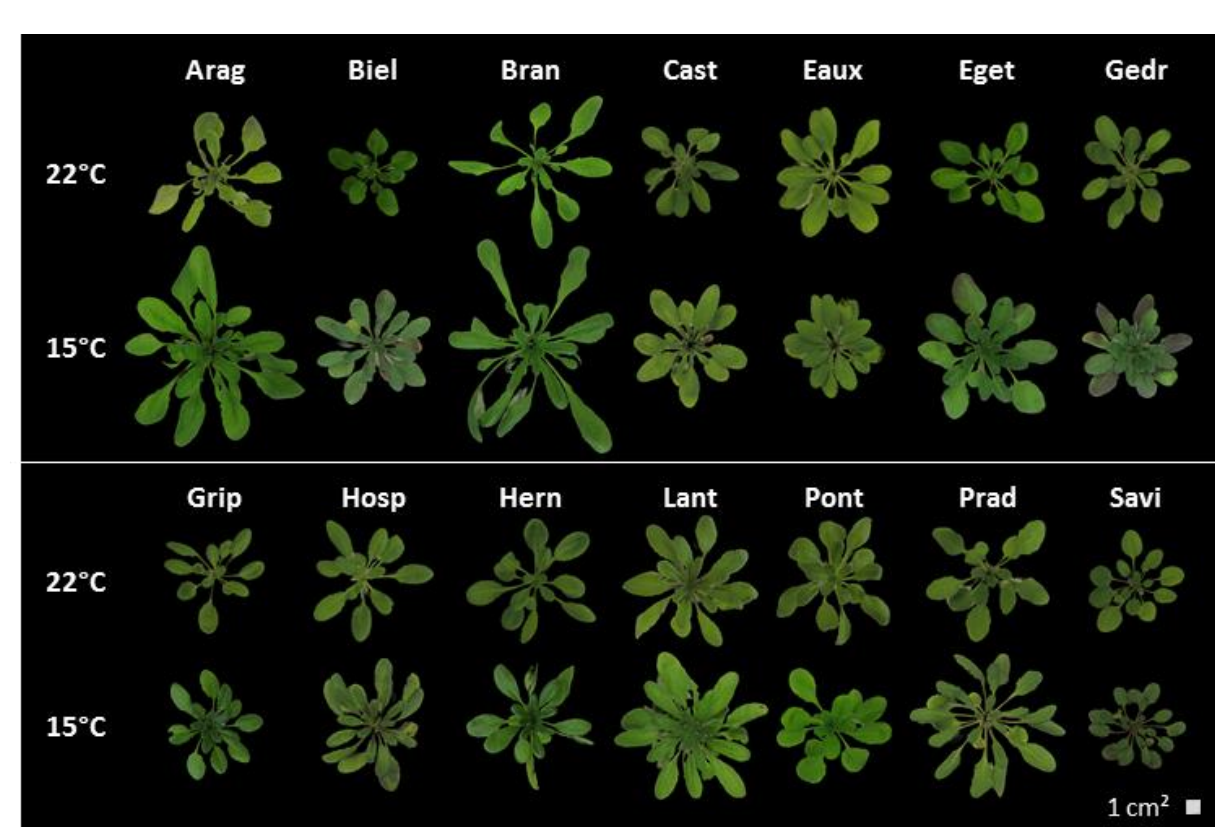


- Three major branches
- Description at fine-scale variation

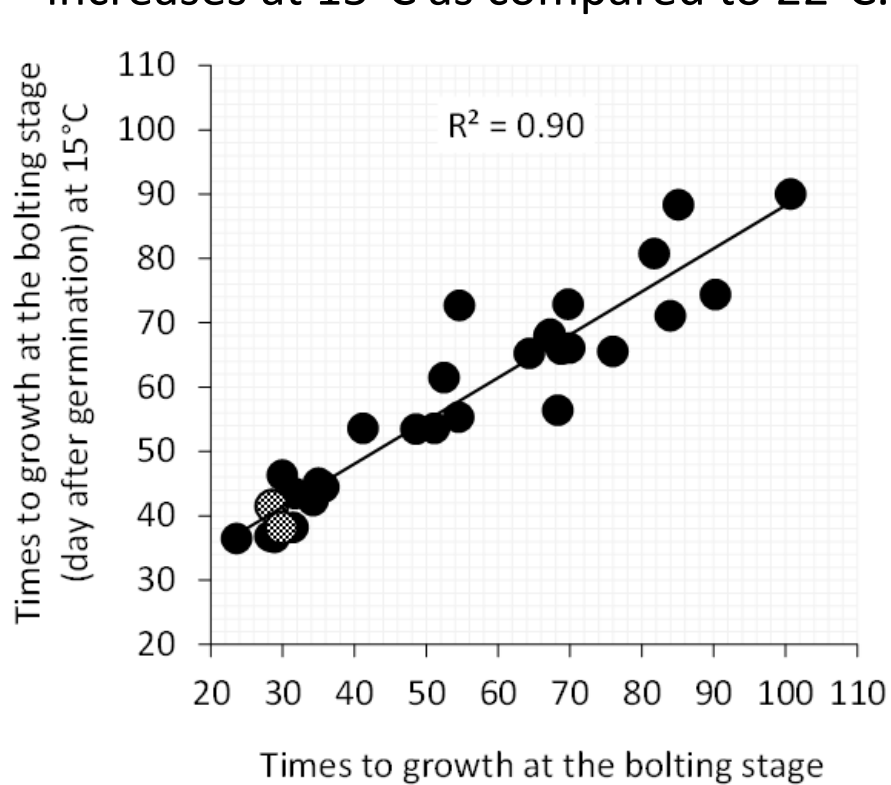
Phenotyping

Diversity of responses to the different temperature growth conditions

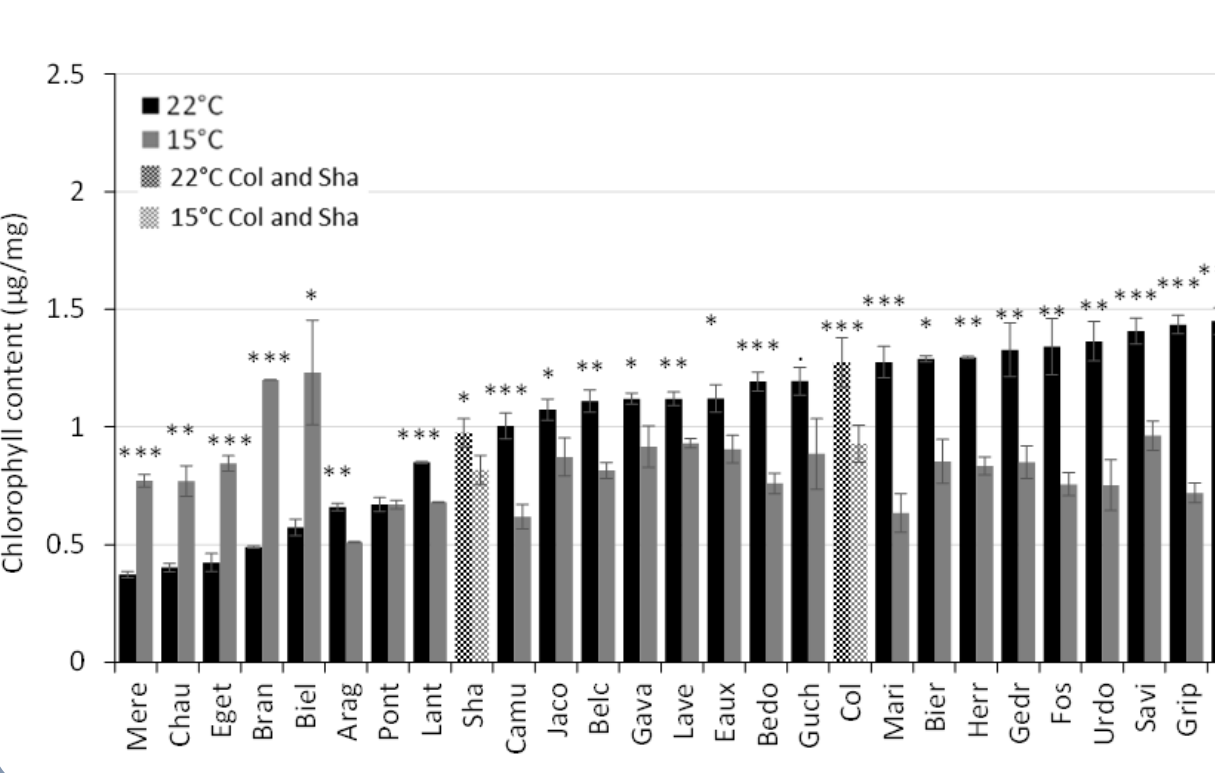
Examples of contrasted phenotype data :



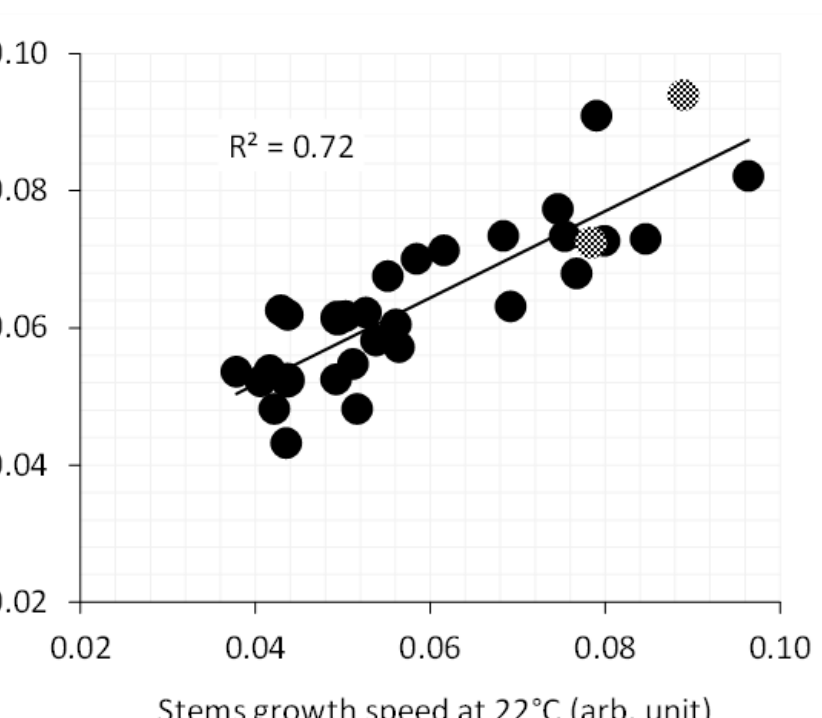
The time to growth at the bolting stage increases at 15°C as compared to 22°C.



Chlorophyll content is more stable in rosettes of different population grown at 15°C.

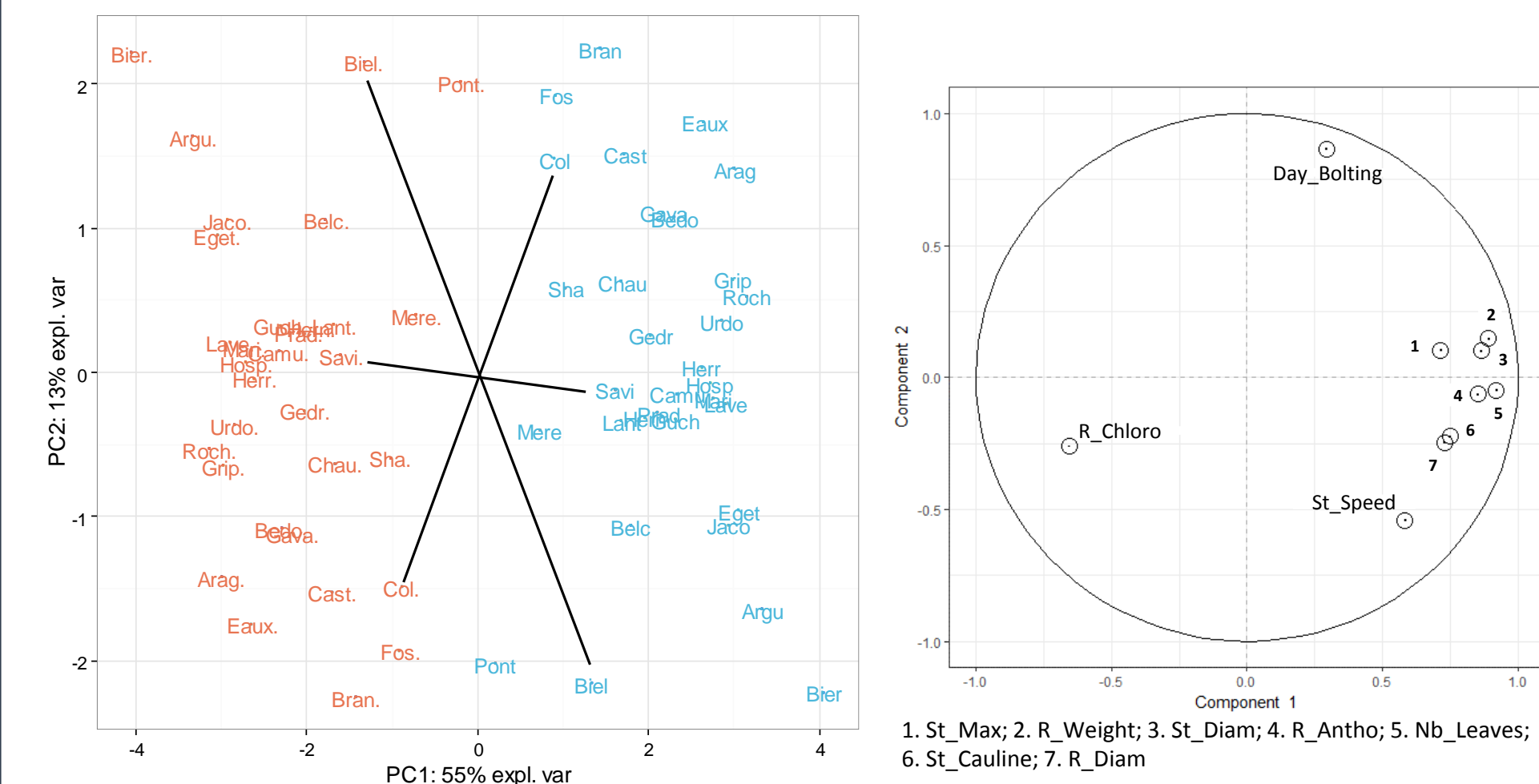


The stems growth speed depend to the environmental condition

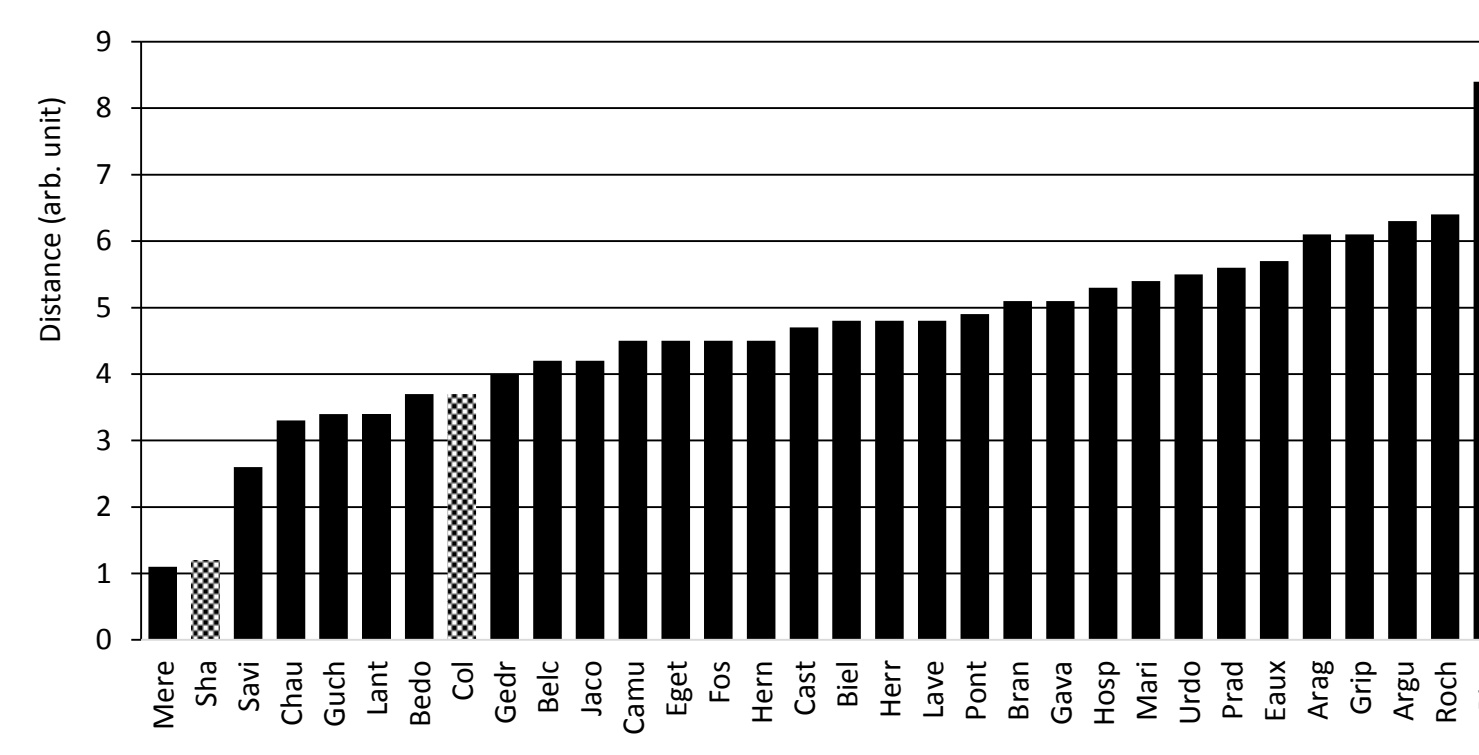


Multivariate analysis

Multilevel PCA was used to investigate the underlying variation between population,



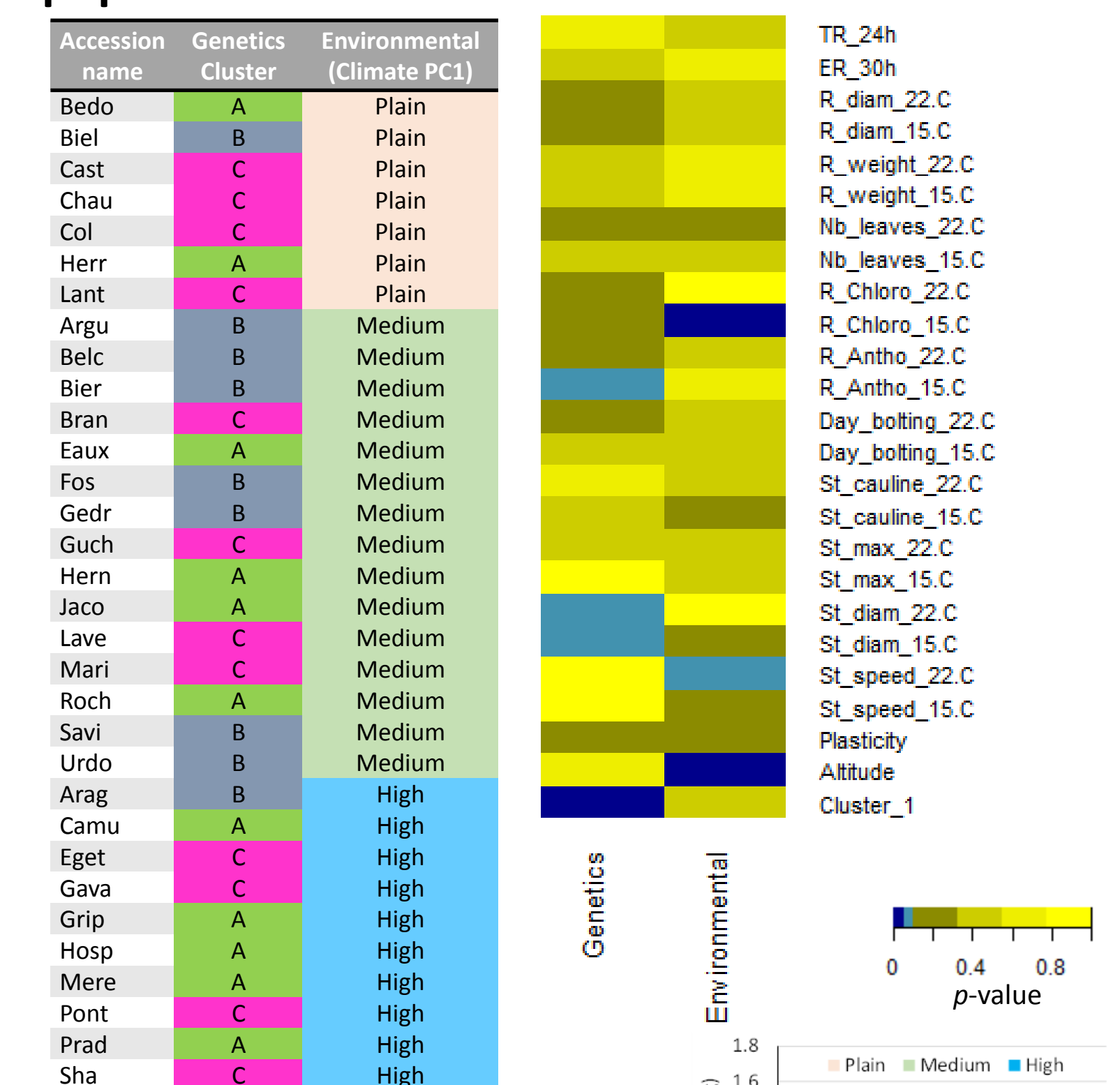
... and reveal different phenotype diversity of plasticity



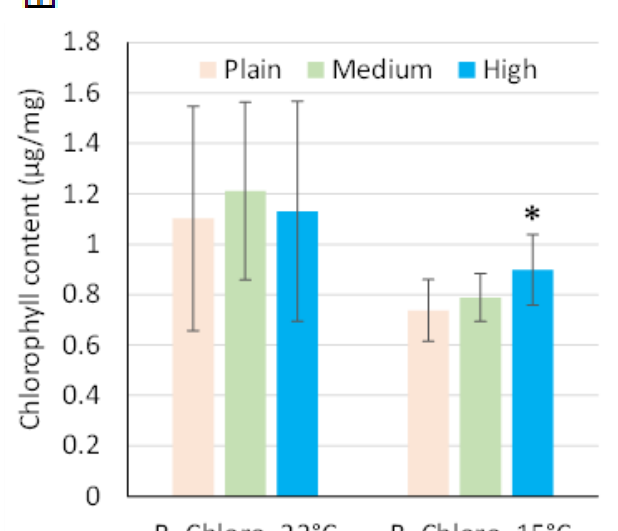
Distance separating the populations according to the temperature in the scaled PCA multilevel.

Integrative study

Relationships between phenotypic data, genetic and environmental classification of the populations were observed



Example: Population living in high altitude show significantly accumulation of chlorophyll content at 15°C compare to the other populations.



Conclusion & Perspectives

In conclusion, genetic structure as well as inter- and intra-population variation emphasized the unexpected variability found in this region. This study also revealed phenotypic variation in acclimation of *A. thaliana* across abiotic gradient characterized here by the temperature. Some of them are correlated with identified genetic clusters or with environmental data. These analyses contribute to enrich knowledge on abiotic stress acclimation in natural plant populations.

References: [1] Pritchard et al., Genetics. 2000; 155:945-959