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# Production and treatment of heterogeneous omics data in order to study the cell wall plasticity in various Pyrenean altitudinal *A. thaliana* ecotypes

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# Context

Molecular actors of **plant adaptation to climate changes** are not well known. Plant cell walls constitute an external barrier which is modified upon environmental changes and their structures and compositions can change<sup>1</sup>. By providing and combining omics data, **the WallOmics project** aims at understanding the **plant cell wall adaptation to global warming**<sup>2</sup>. Production of large sets of heterogeneous data will require the development of the existing mixOmics<sup>3</sup> package in order to perform the integrative approach required for a **global analysis**.

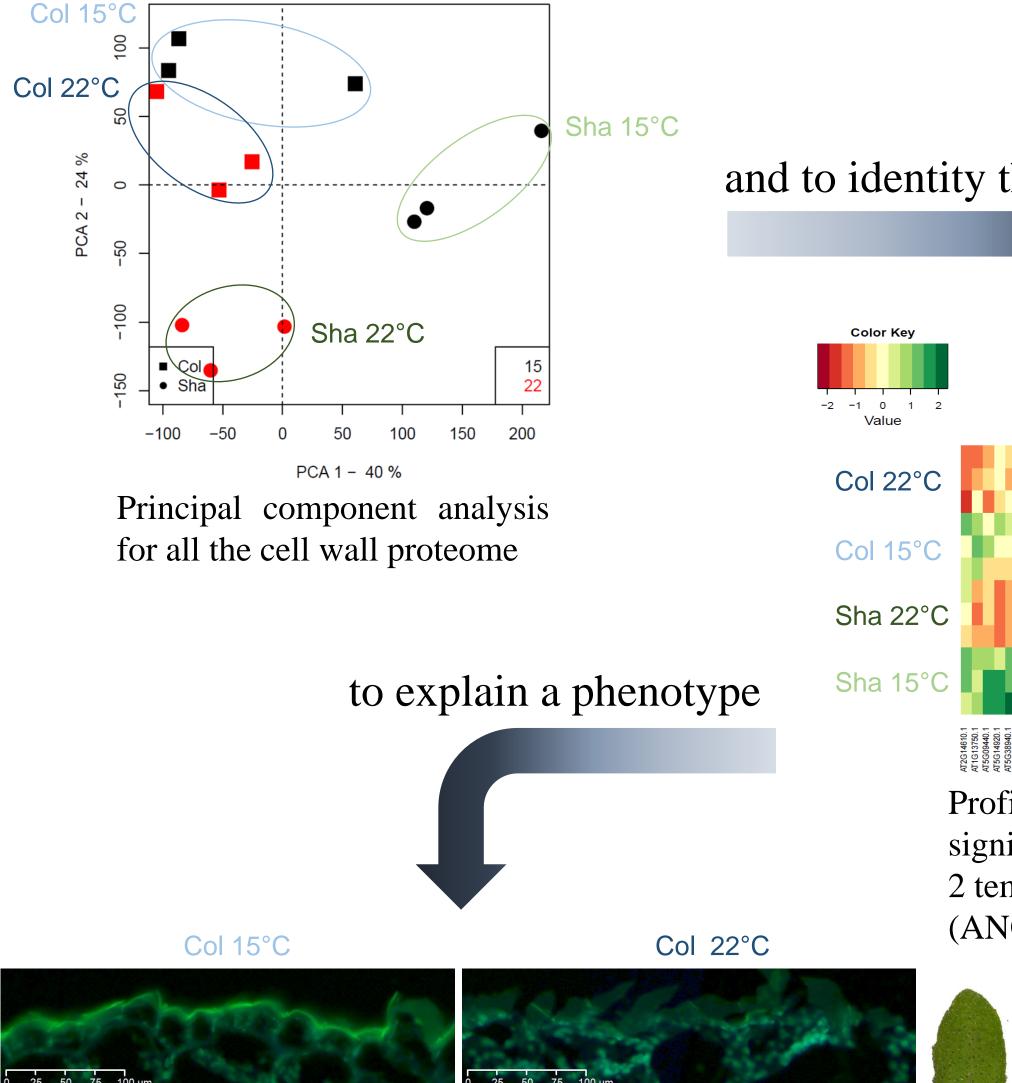
## First study in two contrasted ecotypes

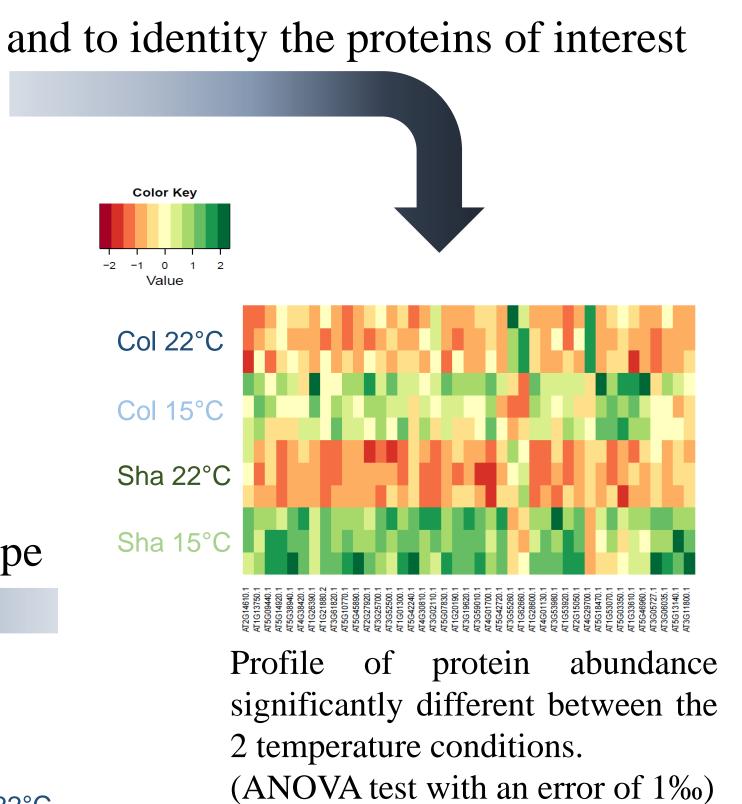
Two contrasted ecotypes from Poland (Col) and Tajikistan (Sha) were grown at two different conditions (15 vs 22°C):

## Selection of population

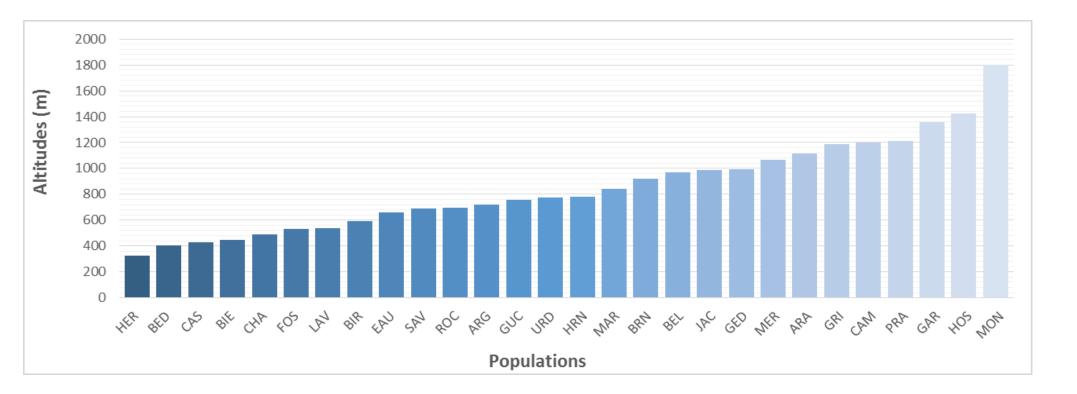
29 natural populations of the annual plant *Arabidopsis thaliana* (L.) were collected at different altitudinal levels that cover all the Pyrenean mountains:

The cell wall proteomics analysis allowed to discriminate the four samples:



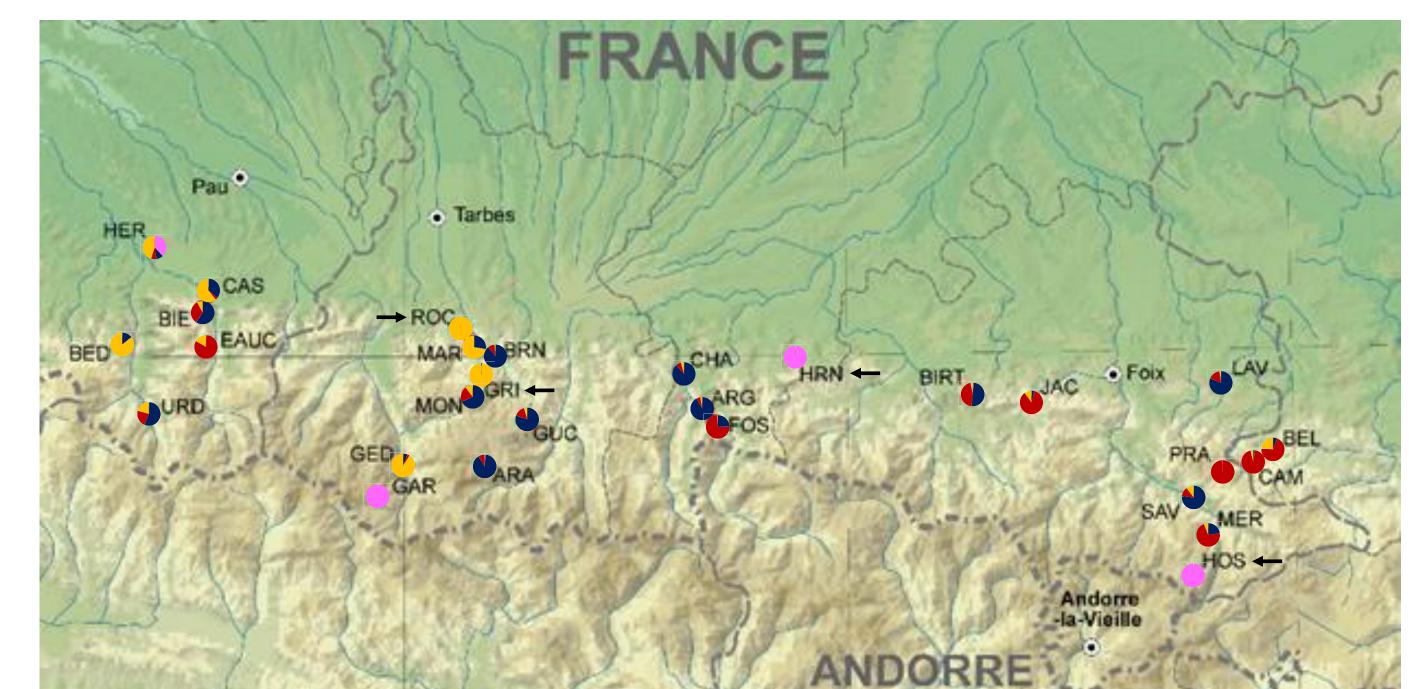


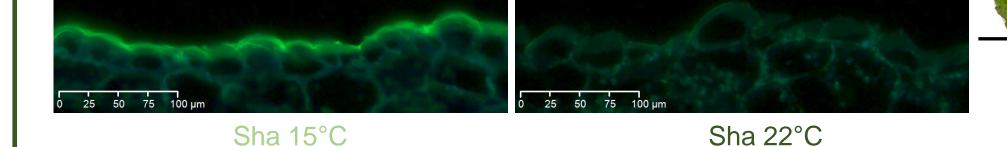
The leaf petioles (transverse cut) are more lipophilic at 15°C (Auramine O staining).





#### Population structure after having been analyzed by STRUCTURE<sup>4</sup> software:

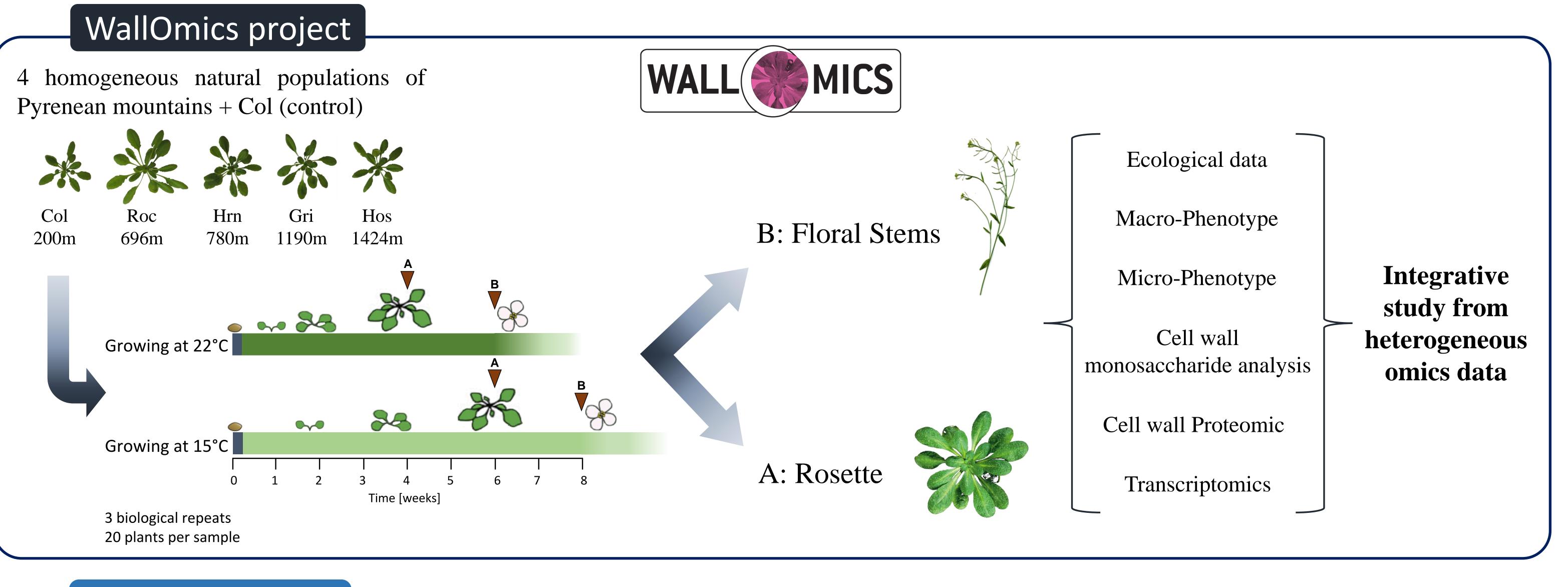




Determine a workflow and analyses for preparing the WallOmics project

### Results of STRUCTURE software with 5 neutral genes

4 homogenous populations at different altitudinal levels were selected for the WallOmics project



## Expected results

The integrative analysis with mixOmics (statistical integrative package developed by the Mathematics Institute of Toulouse) should allow us to draw a model regarding adaptation to climate changes and to identify proteins, genes or metabolic pathways potentially involved in cell wall plasticity in response to environmental changes.

References: [1] Frankovà & Fry, J Exp Bot. 2013; 64(12):3519-3550; [2] Sasidharan et al., Critical Reviews in Plant Sciences. 2011; 30:548-562; [3] Dejean et al., Genetics. 2000; 155:945-959

