

# Construction of regulatory gene networks exploiting natural variability in *Arabidopsis thaliana*

## ACTIONS

Fifty-two ecotypes have been studied in these above described conditions (10 plants by ecotype). This represents a tremendous amount of work (2500 samples harvested) performed by the Pr Coruzzi, Dr Ruffel and Dr Krouk. Results are very encouraging since the ecotypes present a very important variation in their N content (Figure 2A) or development (Figure 2B) in response to fluctuating and heterogeneous conditions. These traits (among at least 21 other measured traits :Figure 1) will be mapped to the genome allelic variation. GWAM hits will map to genes. These genes will then be included in multidimensional networks ((Gutierrez et al., 2007; Gutierrez et al., 2008)). Transcriptomic analysis may be performed too for of subset of ecotypes that will well represent/spam across the natural variation of the studied traits. This will help to resolve the gene expression variation across the natural variation continuum. The expected networks may be one of a kind, since for the first time they may recapitulate natural variation and gene expression modulation.

## PERSPECTIVES

GWAM and network analysis will be performed in collaboration between Montpellier and New York labs.

**Responsable :**

**Date de démarrage :** 01/02/2012

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**Montant :**

