

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 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 :

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Montant :

