

Ad hoc support : EcoNet

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

ABSTRACT

EcoNet program aims at identifying regulatory modules in gene networks that have evolved in *Arabidopsis thaliana* natural ecotypes in order to adapt NO₃⁻ nutrition to fluctuating environment. The use of natural variation is now extensively used to decipher gene functions through Genome Wide Association Mapping (GWAM) (for details see : (Weigel, 2012)). Here we decided to probe a subset of the Norborg ecotype collection (a core collection of *Arabidopsis* ecotype fully sequenced: (Atwell et al., 2010)) for NO₃⁻ heterogeneity response ((Ruffel et al., 2011)). The Pr Coruzzi has been personally involved in the experiments described below and benefited from Sandrine Ruffel and Gabriel Krouk expertise on the experimental set-up and 15N measurement. An experimental set-up has been used as described in Ruffel et al 2010. In brief plants are grown in vertical Petri dishes. After 10 days the primary root is cut in order to let 2 lateral root grow. Then, these lateral roots are treated with different N sources. This help to reveal after 5 days how roots adapt to heterogeneous conditions of the soil. The expected response is that root in contact with NO₃⁻ rich zone are able to preferentially grow in order to compensate for the N deprivation perceived by the -N root (Figure 1). Here the NO₃⁻ provided to plants was labeled with 15N. The 2 parts of the root system, and the plant shoots have been analyzed by mass spectrometry thanks to Pascal Tillard (IR INRA). This set-up was built to decipher if 15N allocation can differs across ecotypes. Interestingly, since all the accessions used in this work have been fully sequenced we expect to identify genes being strongly associated with N allocation variation, and root development response upon NO₃⁻ treatment.

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Project leader : Gabriel Krouk

Project leader's institution : CNRS

Project leader's RU : BPMP

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Funding : Labex

ACTION

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.