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Comparative proteomics to reveal naturally occurring variability between *Arabidopsis thaliana* accessions

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Plant evolution to a specific ecosystem results in a genetic adaptation to environmental conditions. These non-genetically modified plants could be of great interest for physiologists and agronomists.

In this study, a comparative proteomics approach is used to evaluate genetic distances between 8 accessions of the model plant *Arabidopsis*, selected according to contrasted root architecture responses to phosphate starvation (1).

Accessions : Col-0, Cvi-0, Col-4, Ws-1, Be-0, LI-0, Rld-1, Ler-1

Growth : hydroponic culture, 42 days

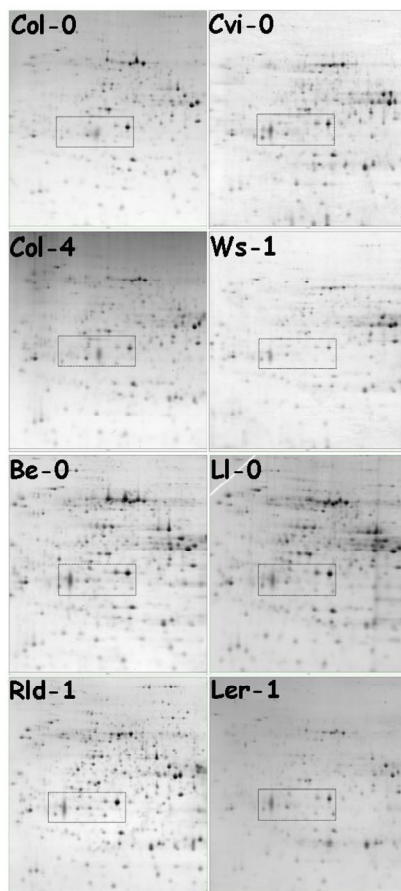
Samples : root soluble proteins, TCA/acetone extracted

1st D : 200 µg protein, 18 cm pH 4-7 strips (IPGPhor)

2nd D : 11% acrylamide SDS-PAGE (DALT system)

Staining : Colloidal Coomassie blue

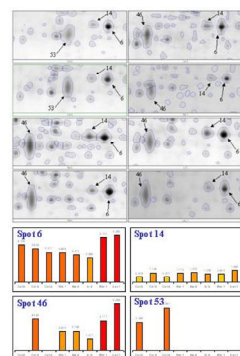
Gel analysis : Mean values of triplicates (Progenesis software)



2DE is performed on protein samples from the 8 *Arabidopsis* accessions.

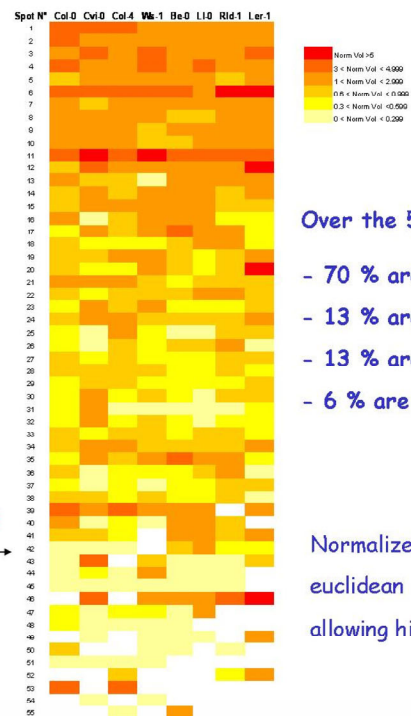
Intensity of the 24 most abundant spots of each is compared.

The normalized volume of the 24 more abundant spots for the 8 *Arabidopsis* accessions is compared using a colour code



Differential expression of spots between ecotypes :

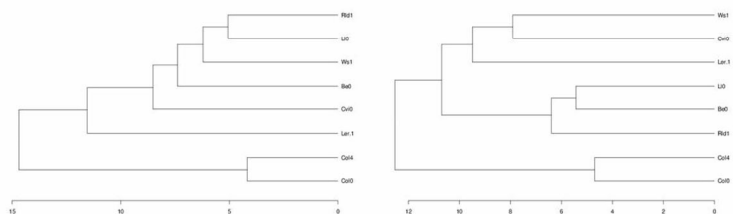
- spots 6 and 14 are conserved,
- spot 53 is specific to ecotypes Col-0 and Col-4,
- spot 46 is absent from ecotypes Col-0 and Col-4.



Over the 55 spots analysed :

- 70 % are common to all ecotypes
- 13 % are common to 7 ecotypes
- 13 % are common to 3 to 6 ecotypes
- 6 % are common to only 2 ecotypes.

Normalized volumes are used to calculate euclidean distance between accessions, allowing hierarchical clustering (Ward).



Clustering on the most abundant spots

Rld-1* ; LI-0* / Col-0
Ws-1 ; Be-0* / Col-4
Cvi-0 ; Ler-1

Clustering groups the 2 Col accessions

Clustering on the whole pattern

Ws-1 / LI-0* / Col-0
Cvi-0 / Be-0* / Col-0
Ler-1 / Rld-1* / Col-4

Clustering follows growth features.

* : accessions with contrasted root architecture responses to P-starvation

Results illustrate the usefulness of comparative proteomics in establishing genetic relationships between accessions. The next step will be the identification of proteins by MS.

Common, variable and specific protein among the different accessions will allow to point out pathways affected by environmental status and to give insights into the underlying adaptative processes.