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► To cite this version:

Marie Chambard, Mohamed Amine Ben Mlouka, Benjamin Lefranc, Jérôme Leprince, Azeddine Driouich, et al.. Exploring border cells by shotgun proteomic analyses - Research of new defence mechanisms deployed by Glycine Max (soybean) roots. Congrès de Spectrométrie de Masse et Analyse Protéomique 2019, Sep 2019, Strasbourg, France. hal-02346244

HAL Id: hal-02346244

<https://hal.science/hal-02346244v1>

Submitted on 4 Nov 2019

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Exploring border cells by shotgun proteomic analyses - Research of new defence mechanisms deployed by *Glycine Max* (soybean) roots

Marie Chambard^{1,2}, Mohamed Amine Ben Mlouka³, Benjamin Lefranc⁴, Jérôme Leprince⁴, Azeddine Driouch^{1,2}, Maité Vicré^{1,2}, Marie-Laure Follet-Gueye^{1,2}, Julie Hardouin³, Pascal Cosette³, Isabelle Boulogne^{1,2}

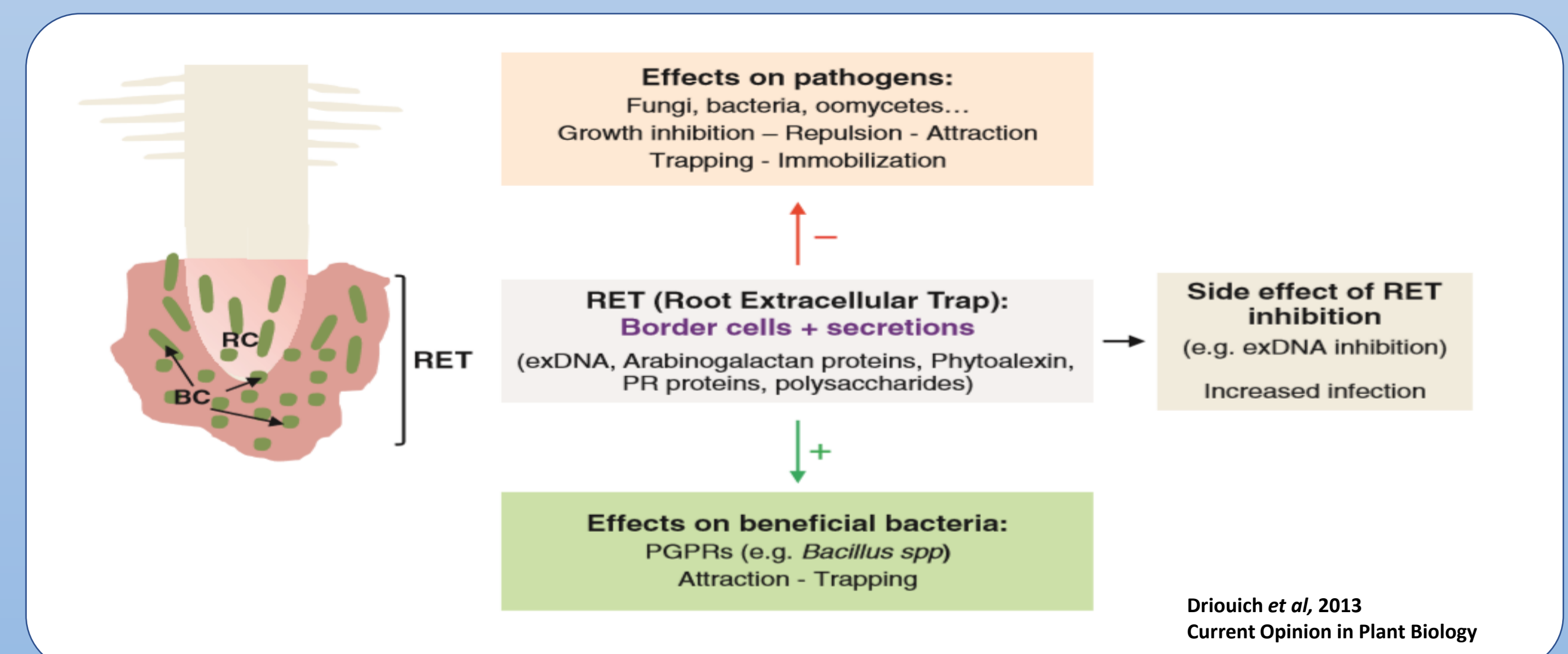
1 Laboratoire GlycoMEV EA 4358, Université de Rouen Normandie
 2 Fédération de recherche Normandie Végétal - FED 4277
 3 Plateforme Protéomique PISSARO, Université de Rouen
 4 PRIMACEN, Université de Rouen Normandie.

Introduction

As part of the process of reducing pesticides, biocontrol agents are currently developed. They consist mainly of natural molecules or beneficial organisms allowing to improve plant defence mechanisms. The work presented here aims at a better understanding of the root extracellular trap (RET, see figure on the right), with an ultimate goal of the characterization of root defence under biocontrol agents exposure.

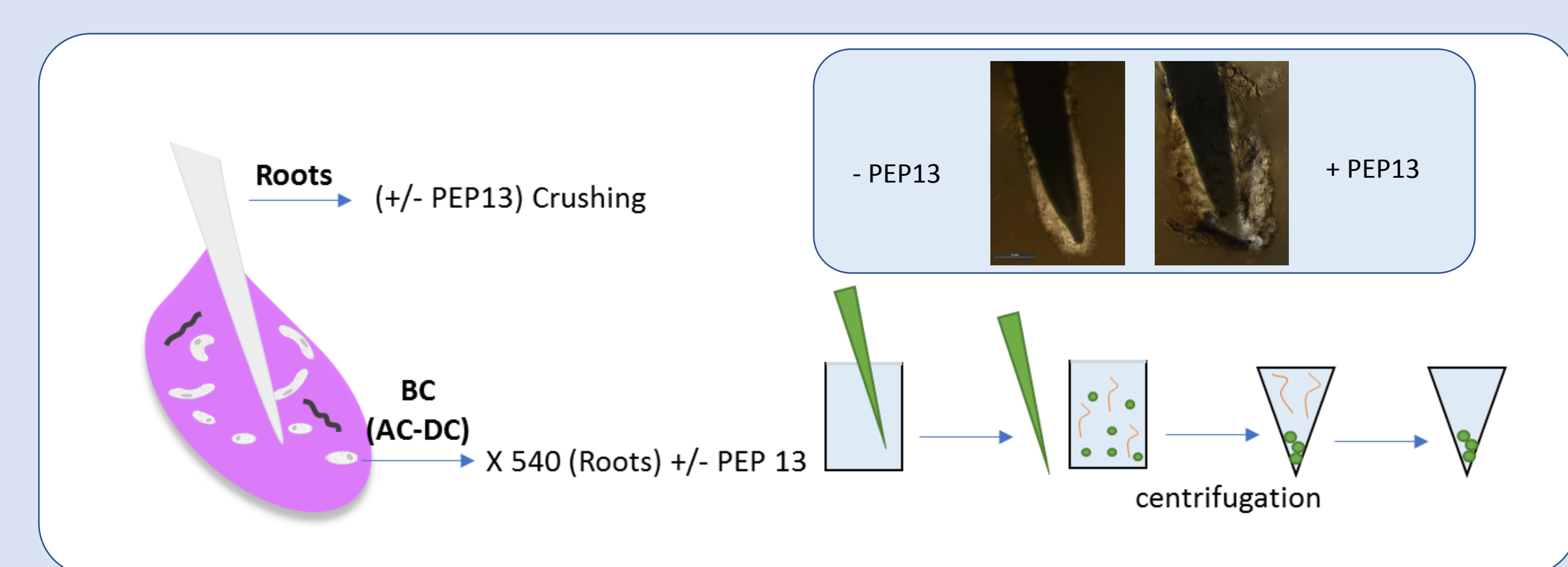
Objective

Notwithstanding their importance as regards the RET, no high throughput proteomic study on border cells is available yet. In this preliminary analysis, we compare *Glycine max* Roots and border cells (BC) by shot gun proteomic analysis exposed to a MAMP (PEP13) versus control conditions.



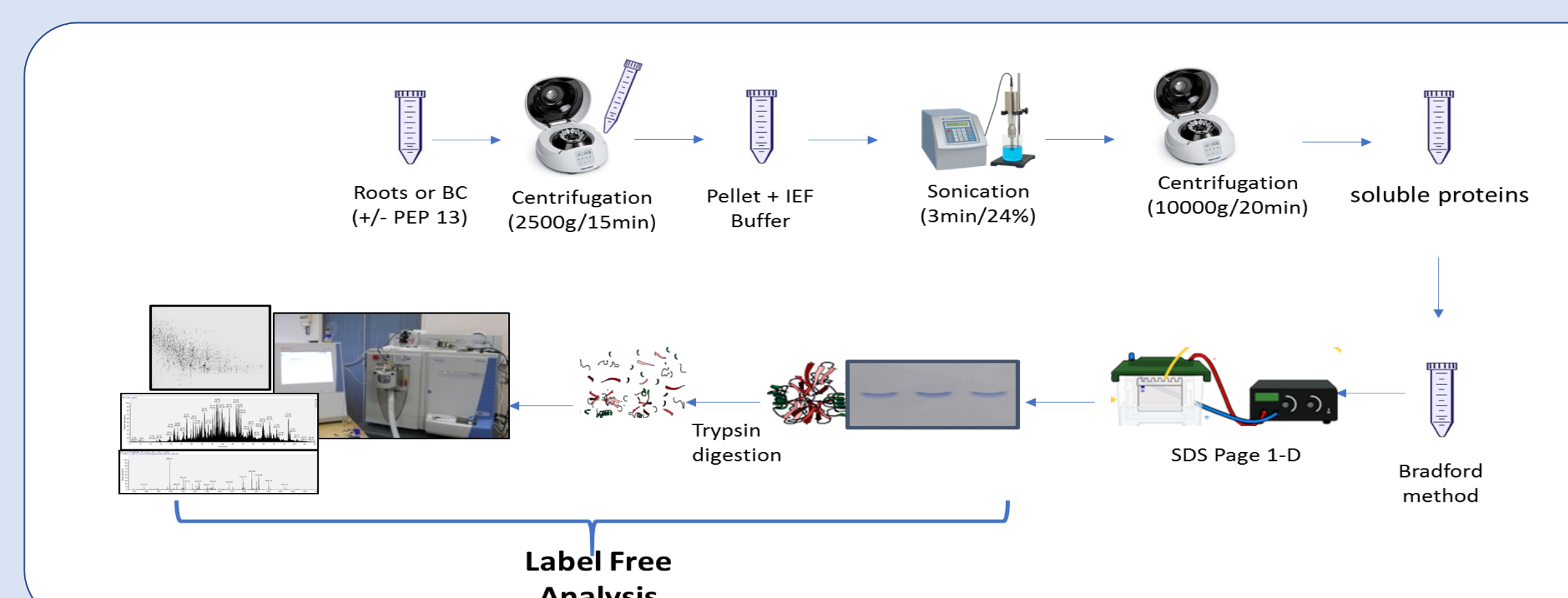
Driouch et al., 2013 Current Opinion in Plant Biology

The RET is a complex network consisting of border cells (BCs), glycomolecules and extracellular DNA



Collection of border cells

Methods

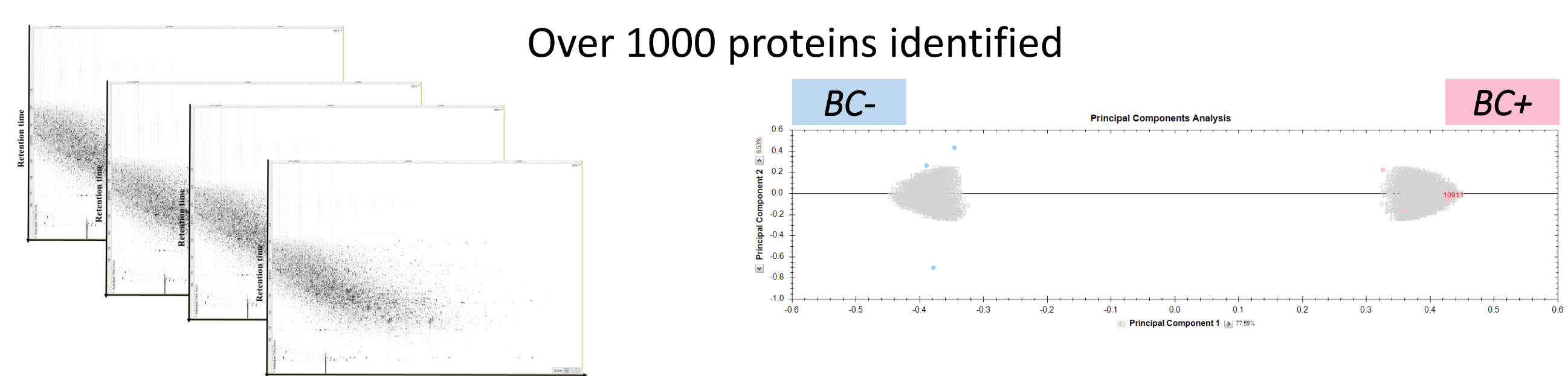


Protein extraction

Results

Impact of elicitation in BC

Over 1000 proteins identified

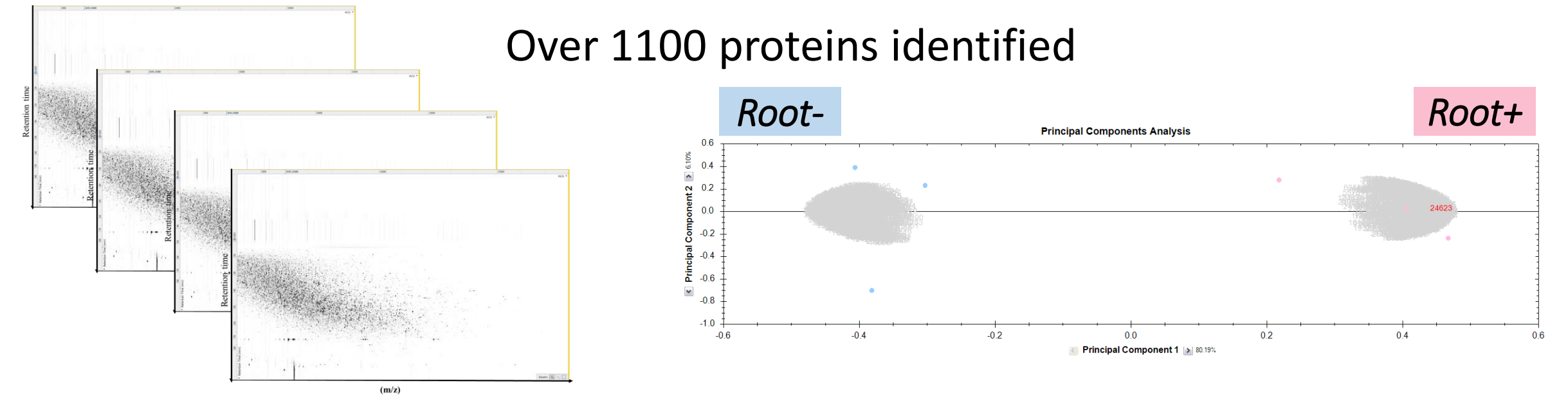


Exemples of proteins with differential abundance

BC (+/-PEP13) ➢ Phosphoenolpyruvate carboxylase: Response to stress
 ➢ Phospholipase D: Development & response to stress

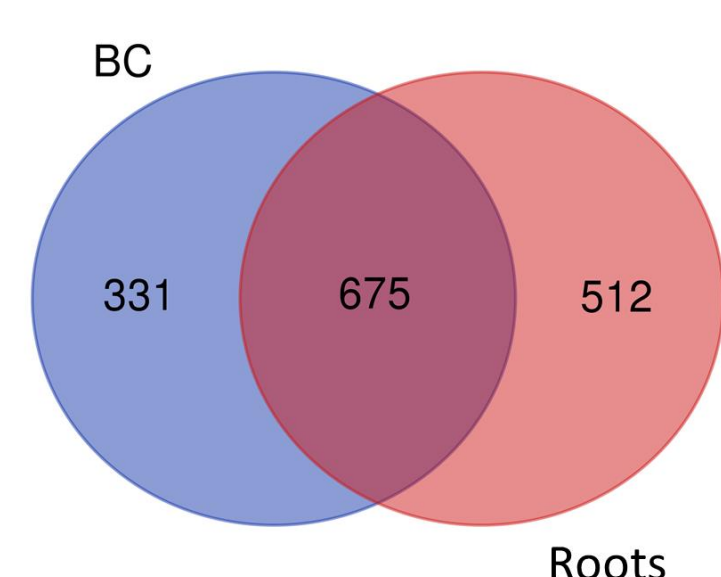
Impact of elicitation in Roots

Over 1100 proteins identified

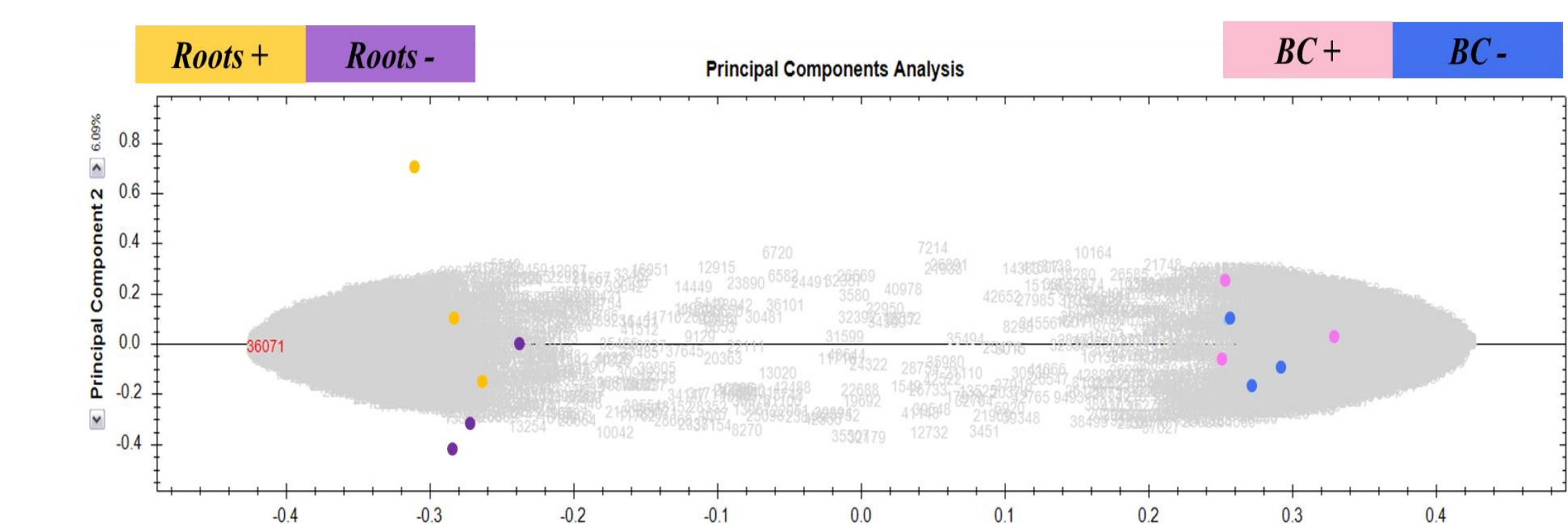


Roots (+/-PEP13) ➢ Lipoxygenase: Biotic and abiotic stress response
 ➢ Importin: Stress and resistance

Investigating Roots and BC proteomes

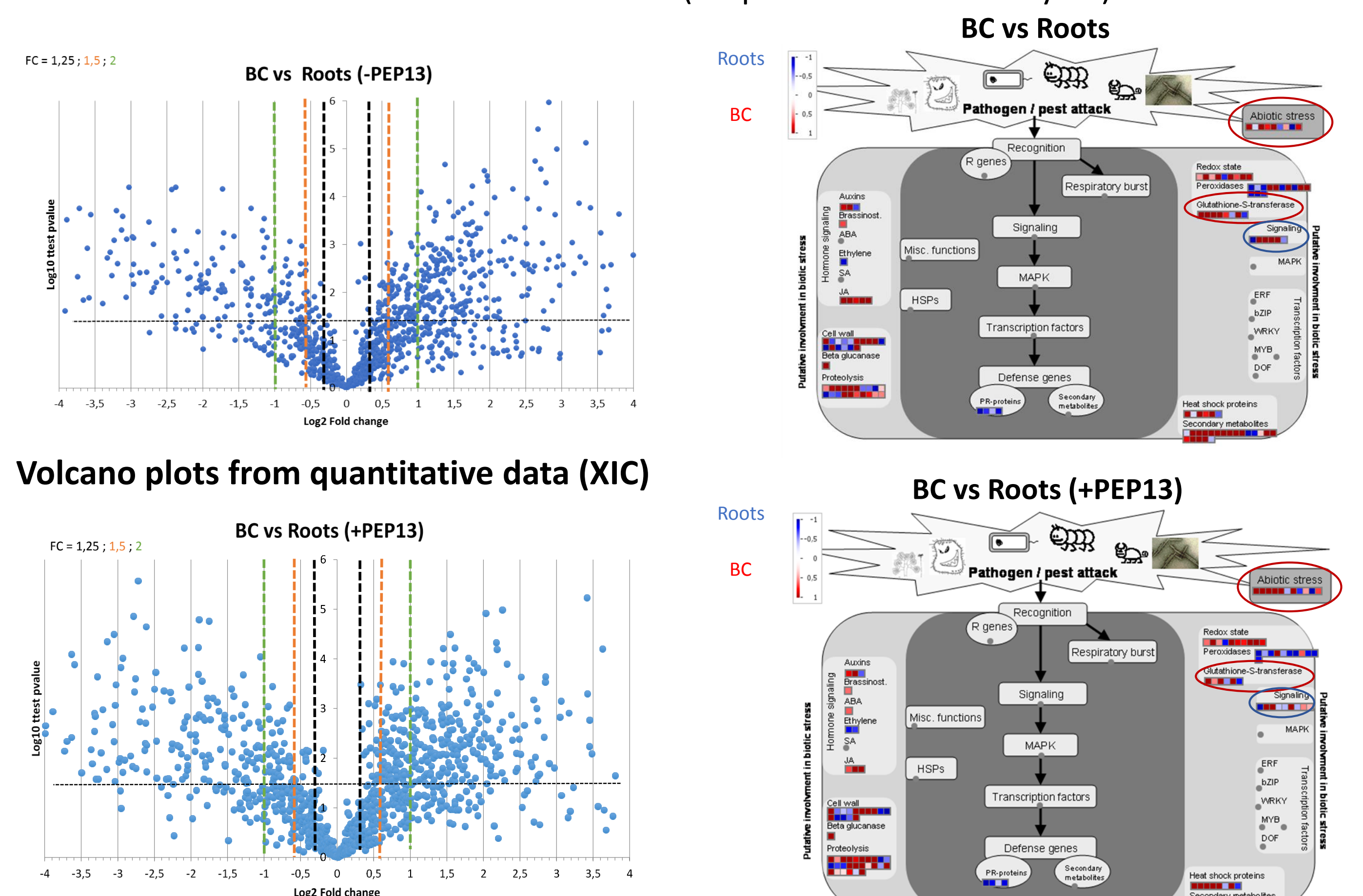


Venn Diagram from comparison of protein identification with Proteome Discoverer



ACP with the differential components between the 4 populations of cells : roots and border cells, with or without elicitation

Overexpression of proteins and stress pathways genes with or without elicitation (MapMan Software analysis)



Conclusion

- These results indicate that **BC proteome is highly specific** with regard to the root one. Thus, BC constitute a single tissue and is not a simple loss of cells from roots.
- **Elicitation with PEP13 highlight a specific set of proteins** which are currently under investigations. From our preliminary analysis, it appears that proteins implicated in response to stimulus or stress are importantly represented.

Acknowledgement

We are grateful to the Normandy Regional council and European Union for financial support. Europe gets involved in Normandie with the European Regional Development Fund (FEDER). We also thank the "Groupe Dauphinoise" for providing us the soybean seeds.