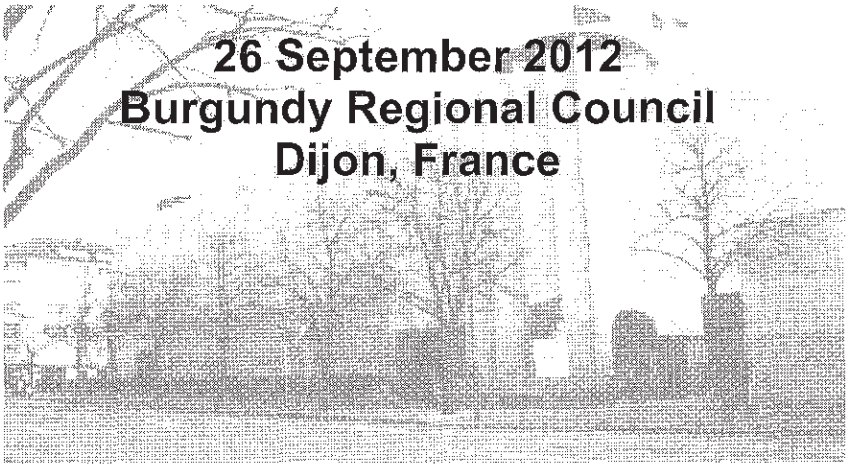
Label-free 1-DE-LC-MS/MS to identify arbuscular mycorrhiza related membrane proteins

Cosette C. Abdallah, Jenny Renaut, Benoît Valot, Michel Zivy, Ghislaine Recorbet, Daniel D. Wipf, Eliane Dumas Gaudot

Abstracts of the Third annual joint meeting on Plant Microbe Interactions



26 September 2012
Burgundy Regional Council
Dijon, France

Program:

8h20-8h30: Opening
Mr Daniel Wipf, UMR Agroécologie, Pôle IPM
Mr Jacques Rebillard - Representive of the Burgundy Regional Council

8h30-9h00
Mr. Christian Seebode, Generalkonsul der Bundesrepublik Deutschland
Wissen und Wissensmanagement

9h00-10h30 **session 1:**
Plant-Microbe Interactions: mechanisms and signaling

10h30-11h00 coffee break

11h00-12h30 **session 1:**
Plant-Microbe Interactions: mechanisms and signaling

12h30-14h00 lunch

14h00-15h30 **session 1:**
Plant-Microbe Interactions: mechanisms and signaling
session 2:
Fungal diversity in plant-microbe interactions

15h30-16h00 coffee break

16h00-18h00 **session 2:**
Fungal diversity in plant-microbe interactions
session 3:
Plant-Microbe Interactions: applied research

TALKS of 10 minutes+5 minutes for questions

Abstracts

SESSION 1; PLANT-MICROBE INTERACTIONS: MECHANISMS AND SIGNALING

9h00-9h15: Label-free 1-DE-LC-MS/MS to identify arbuscular mycorrhiza related membrane proteins.

Cosette Abdallah[1,2], Jenny Renaut[1], Benoît Valot[3], Michel Zivy[3], Ghislaine Recorbet[2], Daniel Wipf[2], Eliane Dumas-Gaudot[2].
[1]Centre de Recherche Public Gabriel Lippmann, Department of Environment and Agrobiotechnologies (EVA), Proteomics Platform, L-4422, Belvaux, Luxembourg, [2]UMR Agroécologie INRA 1347/Agrosup/Université de Bourgogne, Pôle Interactions Plantes Microorganismes ERL 6300 CNRS, BP 86510, 21065 Dijon Cedex, France
[3]Plateforme d'Analyse Protéomique de Paris Sud-Ouest (PAPPSO), Ferme du Moulon, 91190 Gif sur Yvette, France.

Deep changes in the shape and number of organelles, together with profound modifications in various membrane compartments, are induced within arbuscular mycorrhizal (AM) symbiosis. In this context, to investigate the membrane-associated proteins that are regulated in the model interaction *Medicago truncatula* – *Rhizophagus irregularis*, label-free 1DE-LC-MS/MS approach has been employed as alternative to two-dimensional gel electrophoresis. The existence of a correlation between protein abundance and peak areas or number of MS/MS spectra has widened the choice of label-free quantitative proteomics. The results highlighted microsomal protein candidates that could be involved in the symbiotic exchanges between plant and fungal cells.

9h15-9h30: Development of an artificial miRNA system for analyzing gene function in mycorrhizal *Medicago truncatula* roots using the endogenous miRNA159b precursor

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Max Planck Institute of Molecular Plant Physiology, 14476 Potsdam/Golm, Germany

It is a common strategy for the functional analysis of gene products to knock out the corresponding gene and to analyze the resulting phenotype. However, knock out mutants for the gene of interest, like T-DNA or transposon insertion as well as deletions produced by fast neutron bombardment are not always available. In these cases scientists make use of the RNA interference (RNAi) or viral induced gene silencing (VIGS) to produce knock-down mutants. No VIGS system has been established for *M. truncatula* so far, so only the RNAi system remains and is extensively used together with *Agrobacterium rhizogenes* mediated root transformation for functional gene analysis in labs working with *M. truncatula*. The RNAi is based on a hairpin construct with short inverted fragments of the gene of interest. The expressed RNA folds into a perfect matched double strand and is processed by the DCL proteins to short interfering RNAs (siRNAs). Sometimes this