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Interplay between ubiquitination, phosphorylation and acetylation regulates aquaporin function under osmotic stress

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Journées du PROTÉOME VERT

9 et 10 Juin 2022

IDEEV, Université Paris-Saclay
Gif-sur-Yvette

Résumés / Abstracts

Programme

Jeudi 9 juin

- 14h-14h45 **Anne Goelzer** - MaIAGE INRAE-Jouy en Josas
Towards a multi-scale resource allocation model of Arabidopsis
- 14h45-15h05 **Hakim Mireau** - IJPB INRAE-Versailles
Méthodes de marquage de proximité pour l'analyse des interactions protéine-protéine
- 15h05-15-25 **Véronique Santoni** – IPSiM Montpellier
Interplay between phosphorylation and ubiquitination to regulate aquaporin function under osmotic stress
- 15h25-15h45 **Emmanuel Baudouin** - IBPS UPMC Paris
Remodelage du phosphoprotéome des graines d'Arabidopsis au cours de la germination

15h45-16h05 Pause

- 16h05-16h25 **Nathalie Berger** - IPSiM Montpellier
Identification of client proteins of the chloroplastic iron-sulfur transfer protein NFU2 in Arabidopsis thaliana.
- 16h25-16h45 **Harold Duruflé** - BioForA INRAE Orléans
Protéome du Douglas : une nouvelle ressource pour la recherche génomique
- 16h45-17h05 **Titouan Bonnot** - Agroéco INRAE Dijon
Des potentiels régulateurs des réponses au stress hydrique et à la carence en soufre identifiés grâce à une analyse multi-omiques chez le pois
- 17h05-17h25 **Mélanie Blein-Nicolas** GQE-PAPPSO, Le Moulon
Développements vers la protéomique végétale à haut-débit

Vendredi 10 Juin

- 9h30-10h15 **Laurence Lejay** - IPSiM Montpellier
Post-translational regulation of the root nitrate transporter NRT2.1 in Arabidopsis thaliana
- 10h15-10h35 **Annick Moing** - BFP INRAE Bordeaux
Combining phenotypic, metabolome and proteome data to study maize response to a mild nitrogen deficit
- 10h35-10h55 **Sylvie Coursol** - IJPB INRAE Versailles
titre à venir
- 10h55-11h15 **Yacine Djabali** - GQE Le Moulon
Rôles des variations structurales dans la construction des caractères moléculaires et phénotypiques

11h15-11h30 Pause

- 11h30-11h50 **Maxence James** - UGSF Lille
Multi-omic analysis of 2 maize near- isogenic lines for cold tolerance QTLs
- 11h50-12h35 **Michel Zivy** - GQE-PAPPSO Le Moulon
Variation génétique de la réponse des plantes aux variations environnementales : que peut nous dire la protéomique ?

Interplay between phosphorylation and ubiquitination to regulate aquaporin function under osmotic stress

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Maintaining water balance in plant cells and organs involves control of water fluxes, and hence, a tight regulation of water channels (also called aquaporins) in plant cell membranes [1, 2]. In *Arabidopsis*, 35 homologs comprised in four homology subclasses have been identified. The plasma membrane intrinsic proteins (PIPs; with 13 isoforms further subdivided in the PIP1 and PIP2 subgroups) are the most abundant aquaporins in the plasma membrane. An excellent mechanism for fine-tuning the function of channels can be provided by post-translational modifications (PTMs). PTMs are central to regulate protein structure and function and thereby to modulate and control protein catalytic activity, subcellular localization, stability, and interaction with other partners. We showed that a short-term osmotic treatment induces a maximal root hydraulic conductivity inhibition by 60% that could be accounted for a decrease in PIPs function [3] and not in PIPs degradation since their cellular abundance remains stable [4]. By contrast, such treatment induced PIP2;1 internalization [5]. Using proteomics, we described PIPs as being modifiable by phosphorylation, acetylation, methylation, deamidation and ubiquitination [3, 4, 6, 7]. The MS quantification of phosphorylation and ubiquitination provided evidences for an interplay between phosphorylation and ubiquitination at the C-terminus of a major aquaporin (PIP2;1) [4]. We hypothesize that such interplay governs PIP2;1 internalization under osmotic stress. Perspectives will be discussed in terms of characterization of modifying enzymes involved in PIP2;1 internalization.

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