

# Welcome to the Fourth Conference of the International Plant Proteomics Organization

Hosted from Winnipeg, Canada

March 9<sup>th</sup> – 11<sup>th</sup> 2021

## PROGRAMME

On behalf of the Scientific and Organizing Committees, I would like to welcome you to INPPO2020 – being held virtually, and in 2021. I hope you have a productive and meaningful experience!

Christof Rampitsch, Conference Chair.

### Scientific Committee

Jenny Renaut, President (Luxemburg)  
Stefanie Wienkoop, VP (Austria)  
Dominique Job (France)  
Sabine Lüthje (Germany)  
Natalia Bykova (Canada)  
Silvia Mazzuca (Italy)  
Georgia Tanou (Greece)

### Local Organizing Committee

Jennifer Geddes-McAlister (Guelph, Canada)  
Joanne Ernest (Saskatoon, Canada)  
Ray Bacala (Winnipeg, Canada)  
Janette Champ (Toronto, Canada)

# Programme Overview

Tuesday March 9

## Symposium 1: Plant-Improvement

GMT		My Time Zone		
Start	End	Start	End	
14:00	14:10			Welcome Address: <b>Christof Rampitsch</b> , Conference Chair; <b>Jenny Renaut</b> , INPPO President
14:10	14:40			<b>Keynote Lecture: Dr. Jesús V. Jorrín-Novo</b> , University of Cordoba, Spain. "Past, present and future of plant proteomics: the view of the orphan and recalcitrant forest tree <i>Quercus ilex</i> "
14:40	16:00			<b>Session 1: Chair, Dr. Jesús Jorrín-Novo</b>
14:40	15:00			<b>Talk 1.1: Luciana De Oliveira</b> , INRAE, Gif-sur-Yvette, France. "SpecOMS, an open modification search approach challenging high-throughput single amino acid variations identification"
15:00	15:20			<b>Talk 1.2: Ray Bacala</b> , Canadian Grain Commission, Winnipeg MB, Canada. "New PTM observations raise questions on protein trafficking in developing wheat embryos"
15:20	15:40			<b>Talk 1.3: Leonard Barnabas Ebinezer</b> , University of Padova, Italy. "Effects of PFAS on growth, physiology and root proteome of hydroponically grown maize plants"
15:40	16:00			<b>Invited talk 1: Dr. Jun Song</b> , Agriculture & Agrifood Canada, Kentville NS, Canada. "Application of quantitative proteomics to maintain and improve eating quality of fruit"
16:00	17:00			<b>Break</b>
17:00	20:00			<b>Poster Sessions 1 and 2</b>

## Tuesday March 9

### POSTER SESSION 1: PLANT DEVELOPMENT & CROP IMPROVEMENT (Moderators Drs. Sabine Lüthje, Laurence Bindschedler)

GMT		My Time Zone		Poster	Presenter	Ttitle
Start	End	Start	End			
16:50						Good Afternoon/Evening!
17:00	17:10			1.1	Sufia Farhat	Looking forward to <i>Cajanus cajan</i> Proteome Atlas
17:10	17:20			1.2	Hua Bridget Bai	Unbiased RNA and protein co-expression networks identify key genes predictive of hybrid vigor in maize
17:20	17:30			1.3	Vanildo Silveira	Label-Free Quantitative Phosphoproteomics Reveals Signaling Dynamics Involved in Embryogenic Competence Acquisition in Sugarcane
17:30	17:40			1.4	Maxence James	Multi-omic analysis of 2 maize near- isogenic lines for cold tolerance QTLs
17:40	17:50			1.5	Ilaria Battisti	Label-free quantitative proteomic analysis of commercial soymilks
17:50	18:00			1.6	Emmanuelle Bancel	Proteomic and peptidomic tools to analyze in vitro gastrointestinal digestibility of bread wheat
18:00	18:10			1.7	Miroslav Perniš	The secretome of <i>Pinus nigra</i> Arn. embryogenic cell suspension culture
18:10	18:20			1.8	Ana Paulina Barba de la Rosa	Morphological, biochemical, and molecular characterization of wild and cultivated amaranth seeds
18:20	18:30			1.9	Ivan Takeshi Cerritos Castro	Amaranth calcium oxalate crystals as possible carbon pools
18:30	18:40			1.10	Hasan Kolkas	The <i>Marchantia polymorpha</i> cell wall proteome: to what extent is it conserved compared to that of higher plants?
18:40	18:50			1.11	Elisabeth Jamet	A core plant cell wall proteome could contribute to the maintenance of the basic cell wall functions
18:50	19:00			1.12	Salvador González-Gordo	Mitochondrial protein expression during sweet pepper ( <i>Capsicum annuum</i> L.) fruit ripening: iTRAQ-based proteomic analysis
19:00	19:10			1.13	Salvador González-Gordo	Peroxisomes from sweet pepper ( <i>Capsicum annuum</i> L.) fruit: iTRAQ proteomic analysis during ripening
19:10	19:20			Open for Questions		

### POSTER SESSION 2: SIGNALLING (Moderators: Drs. Laurence Bindschedler, Sabine Lüthje)

19:20	19:30			2.1	Wendy Lyzenga	Identification and characterization of ubiquitination components in cucumber phloem which function as long-distance signaling agents in phosphorus homeostasis
19:30	19:40			2.2	Ascensión Martínez-Márquez	Proteomics-driven discovery of an ABC transporter b family member (VvABC-B) in elicited grapevine cells: functional analysis as a trans-resveratrol transporter
19:40	19:50			2.3	Véronique Santoni	Root ubiquitinome under osmotic stress
19:50	20:00			Open for Questions		

## Wednesday March 10

### Symposium 2: Plant-Signals

GMT		My Time Zone		
Start	End	Start	End	
13:55				Good Morning/Afternoon!
14:00	14:30			<b>Plenary Lecture 1:</b> "Closing the protein gap in plant chronobiology" <b>Dr. Glen Uhrig</b> , University of Alberta, Canada
14:30	16:00			<b>Session 2: Chair, Dr. Jennifer Geddes-McAlister</b>
14:30	14:50			<b>Talk 2.1: Alessio Scarafoni</b> , University of Milan, Italy. "Extracellular vesicles of the apoplast of germinating lupin seeds: proteomic analysis and mechanism of release from the cells"
14:50	15:10			<b>Talk 2.2: Andrej Frolov</b> , Leibnitz Inst. of Plant Biochem. Germany. "Glycation of plant proteins in the context of ontogenetic changes and ecological interactions"
15:10	15:30			<b>Talk 2.3: Ramesh Katam</b> , Florida A&M University. "Proteome and phospho proteome studies in heat tolerant and susceptible rice cultivars"
15:30	15:50			<b>Invited talk 2: Dr. Stefanie Wienkoop</b> , University of Vienna, Austria. "A plant core stress responsive proteome (CSR) network is involved in moderate drought stress regulation"
15:50	16:00			COST Project update: <b>Mélisande Blein-Nicholas</b>
16:00	17:00			<b>Break</b>
17:00	20:00			<b>Poster Sessions 3 and 4</b>
20:00	21:00			<b>INPPO Business Meeting ( ALL WELCOME ! )</b>

## Wednesday March 10

### SESSION 3: BITOIC INTERACTIONS AND STRESS (Moderator: Drs. Jenny Renaut, Stefanie Wienkoop)

16:50						Good Afternoon/Evening!
17:00	17:10			3.1	Nadezhda Frolova	Changes in the proteome of radish ( <i>Raphanus sativus</i> L.) in response to <i>Agrobacterium</i> infection
17:10	17:20			3.2	Natalia V. Bykova	Profiling the total and nuclear proteomes of host-pathogen interactions of the wheat Thatcher near-isogenic line for Lr2a resistance gene with virulent and avirulent races of <i>Puccinia triticina</i>
17:20	17:30			3.3	Leonor Guerra-Guimarães	Proteomic Analysis of three Coffee Leaf Rust races with different pathogenic behavior
17:30	17:40			3.4	Agnieszka Szuba	Molecular adjustments in <i>Populus × canescens</i> colonized with the ectomycorrhizal fungus <i>Paxillus involutus</i> , which limited plant host growth - a proteomic and metabolomic view
17:40	17:50			3.5	Aslihan Günel	Proteome profile of Endoplasmic Reticulum of <i>Pyrenophora teres</i> f.sp. <i>maculata</i>
17:50	18:00			3.6	Rita B. Santos	Grapevine – downy mildew proteomics of the first hours of an incompatible interaction
18:00	18:10			3.7	Ahyoung Kim	Characterization of age-related proteome changes in common beans ( <i>Phaseolus vulgaris</i> )
18:10	18:20			3.8	María-Dolores Rey	A shotgun proteomics approach for the study of the effect and responses to combined drought and <i>Phytophthora cinnamomi</i> in <i>Quercus ilex</i> seedlings from two contrasting Andalusian populations
18:20	18:30			<b>Open for Questions</b>		

### SESSION 4: ABITOIC STRESS (Moderators: Dr. Stefanie Wienkoop, Jenny Renaut)

18:30	18:40			4.1	Klára Kosová	Potential utilization of dehydrin proteins as indicators of cereal (wheat, barley) tolerance to environmental stresses
18:40	18:50			4.2	Daria Gorbach	Protein glycation and drought response of pea ( <i>Pisum sativum</i> L.) root nodule proteome: a proteomics approach
18:50	19:00			4.3	Maryke Labuschagne	Proteomic analysis of durum glutenin protein under heat and drought stress
19:00	19:10			4.4	Maksym Danchenko	Plausible implications of chronic ionizing radiation stress for plant memory and immunity
19:10	19:20			4.5	Marija Vidovic	Twenty different late embryogenesis abundant proteins (LEAPs) accumulate in desiccated <i>Ramonda serbica</i> leaves
19:20	19:30			4.6	Kjell Sergeant	The chloroplast of <i>Craterostigma plantagineum</i> during a complete dehydration/rehydration cycle.
19:30	19:40			4.7	María-Ángeles Castillejo	Targeted post-acquisition proteomics as an approach for the search of proteins and peptides to be used as markers of tolerance to drought in <i>Quercus ilex</i>
19:40	19:50			4.8	Madhiya Manzoor	Root proteomic analysis of Common bean ( <i>Phaseolus vulgaris</i> ) under Fe and P stress.
19:50	20:00			<b>Open for Questions</b>		INPPO Business Meeting – All Welcome!
20:00	21:00			<b>INPPO Meeting</b>		

## Thursday March 11

### Symposium 3: Plant-Interactions

GMT		My Time Zone		
Start	End	Start	End	
13:55				Good Morning/Afternoon!
14:00	14:30			<b>Plenary Lecture 2:</b> "Identification of Effectors from the Phytopathogen <i>Fusarium graminearum</i> using BioID" <b>Dr. Gopal Subramaniam</b> , Agriculture and Agrifood Canada, Ottawa, Canada
14:30	15:40			<b>Session 3 : Chair, Dr. Michel Zivy</b>
14:30	14:50			<b>Talk 3.1: Boyan Liu</b> , Univeristy of Guelph, Canada. "Proteomics to decode the relationship between plant and fungal pathogen on a systems level"
14:50	15:10			<b>Talk 3.2: Joana Figueiredo</b> , University of Lisbon, Portugal. "Modulation of apoplast proteome by downy mildew in susceptible and tolerant grapevine cultivars"
15:10	15:30			<b>Talk 3.3: Laurence Bindschedler</b> , Royal Holloway, London, UK. "Investigating the barley powdery mildew extra-haustorial proteome during infection by the biotrophic fungus <i>Blumeria graminis</i> to identify and validate host proteins required for susceptibility"
15:40	16:00			<b>Invited talk 3: Dr. Georgia Tanou</b> , University of Thessaloniki, Greece. "Proteogenomics atlas in a perennial fruit trees: a sweet cherry case study"
16:00	16:30			INPPO 2022/3 Invitation. INPPO 2024/5?
16:30	17:00			<b>Break</b>
17:00	20:00			<b>Poster Sessions 5, 6 and 7</b>

## Thursday March 11

### SESSION 5: ENVIRONMENTAL PROTEOMICS (Moderator Drs. Antonio Masi, Christof Rampitsch)

16:50						Good Afternoon/Evening!
17:00	17:10			5.1	Nasser Mahna	Response of soybean to graphene oxide nanostructures stress at proteomic level
17:10	17:20			5.2	Bruno Komazec	The effects of silver nanoparticles and ions on <i>Chlorella vulgaris</i>
17:20	17:30			5.3	Petra Peharec Štefanić	Effects of silver nanoparticles and silver nitrate on root proteins of tobacco ( <i>Nicotiana tabacum</i> ) plants
17:30	17:40			5.4	Karla Košpić	Changes in activities and isoform patterns of antioxidant enzymes in tobacco plants upon exposure to silver nanoparticles and silver nitrate
17:40	17:50			5.5	Athanasios Molassiotis	Proteo-metabolomic study of olive (cv. 'Chondrolia Chalkidikis') drupe development and maturation

### SESSION 6: NITROGEN USE EFFICIENCY (Moderator: Drs. Natlaia Bykova, Andrej Frolov)

17:50	18:00			6.1	Dristy Zaman	Transamination of L-asparagine in <i>Glycine max</i> leaf tissue
18:00	18:10			6.2	Bhakti Prinsi	Proteomic changes in the roots of M4 grapevine rootstock in response to nitrate availability
18:10	18:20			6.3	Chiara Muratore	Comparative proteomics of organelles in maize ( <i>Zea mays</i> L.) roots in response to different availabilities of nitrate and ammonium
18:20	18:30			6.4	Yordan Muhovski	Comparative proteomic analyses of potato ( <i>Solanum tuberosum</i> L.) cultivars grown in hydroponics and subjected to different doses of nitrate

### SESSION 7: TECHNOLOGIES (Moderator: Drs. Andrej Frolov, Natalia Bykova)

18:30	18:40			7.1	Tatiana Bilova	Ageing stimulated protein glycation process in <i>Arabidopsis</i> plants
18:40	18:50			7.2	Willy Bienvenut	Sub optimal [ <sup>15</sup> N] metabolic labelling in plant to determine protein turnovers: A new look at the isotopic distribution
18:50	19:00			7.3	Ascensión Martínez-Márquez	Application of MRM for grapevine organelle abundance profiling analysis in cell-suspension culture
19:00	19:10			7.4	Amalia Piro	Fine-tuned procedure to extract high purified proteins from the seagrass <i>Halophila stipulacea</i> and proteins identification by means of several seagrass genomic resources
19:10	19:20			7.5	Tatiana Leonova	Validation of a filter aided sample preparation (FASP)-based label-free quantification approach for proteomics analysis of plant tissues
19:20	19:30			7.6	Zachary Provost	Known and novel proteins identified in mature rice ( <i>Oryza sativa</i> L.) starch grain revealed by three diverse granule preparation methods
19:30	19:40			7.7	Nick Prudhomme	Profiling the Infectome of <i>Agrobacterium tumefaciens</i> and <i>Nicotiana benthamiana</i> with Quantitative Proteomics for Molecular Farming
19:40	19:50			<b>Poster Prizes Announced</b>		
19:50	20:00			<b>Closing of INPPO2020</b>		

# ABSTRACTS ORAL SESSIONS

## POSTER SESSION 6

### NITROGEN USE EFFICIENCY

POSTER#6.3

#### **Comparative proteomics of organelles in maize (*Zea mays* L.) roots in response to different availabilities of nitrate and ammonium**

Chiara Muratore C, Galli G, Espen L, Prinsi B.

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Nitrogen (N) is one of the main factors limiting agricultural productivity, especially in cereals such as maize (*Zea mays* L.), and nitrate ( $\text{NO}_3^-$ ) and ammonium ( $\text{NH}_4^+$ ) represent the predominant forms of N in agricultural soils. Plants are differently affected by the availability of these two N forms at morphological, physiological and metabolic levels, especially during the early stages of development. In particular, roots responses to different N availabilities involve the modulation of distinct metabolic pathways, the regulation of ion compartmentation and the balancing of cellular homeostasis. In this context, the strict coordination between the biochemical activities of cell organelles, among which mitochondria, plastids and vacuole, is crucial. Hence, subcellular proteomics represents a powerful method to study these metabolic interactions. The aim of this research was to study the roles of organelles in the adaptation to different N availabilities in maize roots, through the combination of physiological, metabolic and proteomic analyses. The research was conducted in roots of three-day-old maize plants, grown by hydroponic system, and exposed to different N availabilities: absence of N, 2.5 mM  $\text{NO}_3^-$ , 2.5 mM  $\text{NH}_4^+$ , 1.25 mM  $\text{NO}_3^-$  + 1.25 mM  $\text{NH}_4^+$ . This experimental design allowed to appreciate differences in plant growth and metabolic status, with variations in plant biomass accumulation and in the shoot/root ratios, in the contents of  $\text{NO}_3^-$  and  $\text{NH}_4^+$  and metabolites, such as sugars and amino acids, and in the abundance of key enzymes in N assimilation (i.e. Nitrate Reductase and Glutamine Synthetase). Root organelles were enriched by differential centrifugation techniques and the sub-proteomic profiles were analysed by means of one-dimensional (1D) Gel Liquid Chromatography-Mass Spectrometry (1D GeLC-MS/MS). This approach allowed to identify and quantify a total of 365 proteins, showing, by means of bioinformatic analysis, a good degree of enrichment of the target proteomes (77.7%), and revealing that the 33% of the proteins were differently accumulated in the four conditions (one-way ANOVA,  $p \leq 0.01$ ). The results showed that the N forms induced different changes in abundance of proteins involved in the assimilation of N at the plastid level, in protein synthesis, in respiratory metabolism, and in the exchange of metabolites between organelles. Interestingly, some classes of mitochondrial carrier proteins, such as Mitochondrial dicarboxylate/tricarboxylate transporter (DTC), Mitochondrial phosphate carrier protein 3 and ADP/ATP carrier protein showed the highest abundance in  $\text{NH}_4^+$ -fed plants, highlighting a specific involvement of mitochondrion metabolism in root adaptations to this nutrient. Differently, the availability of  $\text{NO}_3^-$  affected the accumulation of some tonoplast proteins, such as aquaporins (TIP) and V-type proton ATPase subunits, and of some proteins involved in cell calcium network, providing new hints about the role of this nutrient both as osmolyte and metabolic signal. Overall, this research confirms the fundamental roles of roots in N acquisition and provides novel information about the responses induced by the different N nutrients in multiple sub-cellular compartments in young maize plants.



## List of Participants

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