

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

Hosted from Winnipeg, Canada

March 9th – 11th 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: Christof Rampitsch , Conference Chair; Jenny Renaut , INPPO President
14:10	14:40			Keynote Lecture: Dr. Jesús V. Jorrín-Novo , 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			Session 1: Chair, Dr. Jesús Jorrín-Novo
14:40	15:00			Talk 1.1: Luciana De Oliveira , INRAE, Gif-sur-Yvette, France. "SpecOMS, an open modification search approach challenging high-throughput single amino acid variations identification"
15:00	15:20			Talk 1.2: Ray Bacala , Canadian Grain Commission, Winnipeg MB, Canada. "New PTM observations raise questions on protein trafficking in developing wheat embryos"
15:20	15:40			Talk 1.3: Leonard Barnabas Ebinezer , University of Padova, Italy. "Effects of PFAS on growth, physiology and root proteome of hydroponically grown maize plants"
15:40	16:00			Invited talk 1: Dr. Jun Song , Agriculture & Agrifood Canada, Kentville NS, Canada. "Application of quantitative proteomics to maintain and improve eating quality of fruit"
16:00	17:00			Break
17:00	20:00			Poster Sessions 1 and 2

Tuesday March 9

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

GMT		My Time Zone		Poster	Presenter	Title
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			Plenary Lecture 1: "Closing the protein gap in plant chronobiology" Dr. Glen Uhrig , University of Alberta, Canada
14:30	16:00			Session 2: Chair, Dr. Jennifer Geddes-McAlister
14:30	14:50			Talk 2.1: Alessio Scarafoni , 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			Talk 2.2: Andrej Frolov , Leibnitz Inst. of Plant Biochem. Germany. "Glycation of plant proteins in the context of ontogenetic changes and ecological interactions"
15:10	15:30			Talk 2.3: Ramesh Katam , Florida A&M University. "Proteome and phospho proteome studies in heat tolerant and susceptible rice cultivars"
15:30	15:50			Invited talk 2: Dr. Stefanie Wienkoop , University of Vienna, Austria. "A plant core stress responsive proteome (CSRP) network is involved in moderate drought stress regulation"
15:50	16:00			COST Project update: Mélisande Blein-Nicholas
16:00	17:00			Break
17:00	20:00			Poster Sessions 3 and 4
20:00	21:00			INPPO Business Meeting (ALL WELCOME !)

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			Open for Questions		

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			Open for Questions		INPPO Business Meeting – All Welcome!
20:00	21:00			INPPO Meeting		

Thursday March 11

Symposium 3: Plant-Interactions

GMT		My Time Zone		
Start	End	Start	End	
13:55				Good Morning/Afternoon!
14:00	14:30			Plenary Lecture 2: “Identification of Effectors from the Phytopathogen <i>Fusarium graminearum</i> using BioID” Dr. Gopal Subramaniam , Agriculture and Agrifood Canada, Ottawa, Canada
14:30	15:40			Session 3 : Chair, Dr. Michel Zivy
14:30	14:50			Talk 3.1: Boyan Liu , University of Guelph, Canada. “Proteomics to decode the relationship between plant and fungal pathogen on a systems level”
14:50	15:10			Talk 3.2: Joana Figueiredo , University of Lisbon, Portugal. “Modulation of apoplast proteome by downy mildew in susceptible and tolerant grapevine cultivars”
15:10	15:30			Talk 3.3: Laurence Bindschedler , 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			Invited talk 3: Dr. Georgia Tanou , 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			Break
17:00	20:00			Poster Sessions 5, 6 and 7

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	Athanassios 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 [15]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 Agrobacterium tumefaciens and <i>Nicotiana benthamiana</i> with Quantitative Proteomics for Molecular Farming
19:40	19:50			Poster Prizes Announced	
19:50	20:00			Closing of INPPO2020	

ABSTRACTS

ORAL SESSIONS

POSTER SESSION 6

NITROGEN USE EFFICIENCY

POSTER#6.2

Proteomic changes in the roots of M4 grapevine rootstock in response to nitrate availability

Bhakti Prinsi, Muratore C, Espen L

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Nitrogen (N) is an essential macronutrient for plants, but very little is known about the biochemical roles played by roots in N acquisition in grapevine (*Vitis vinifera* L.), an important grafted perennial fruit crop. In recent years, the grapevine rootstock M4 [(*V. vinifera* × *V. berlandieri*) × *V. berlandieri*] was the subject of physiological, transcriptomic and proteomic analysis that highlighted its higher tolerance to drought and salinity stress in comparison with other rootstocks. However, little information is available about its metabolic responses to the availability of nitrate (NO₃⁻), the major form of N nutrient used by plants in agricultural soils. The aim of this study was to determine the metabolic events involved in NO₃⁻ acquisition in M4. In details, young M4 plants, grown in a hydroponic system, after a period of N starvation were maintained in the absence of N (control condition) or exposed to 10 mM NO₃⁻. Firstly, the changes of some biochemical parameters (such as NO₃⁻, sugar and amino acid contents) as well as the evaluation by Western blot analyses of the abundances of key enzymes (i.e. Nitrate Reductase and Glutamine Synthetase) were used to define the time course of the metabolic changes occurring in the first 30 h. Taken together, the results showed that root N metabolism significantly increased after 30 h of NO₃⁻ availability. To gain a better characterization, a proteomic analysis based on one-dimensional (1D) Gel Liquid Chromatography-Mass Spectrometry (GeLC-MS/MS) was conducted, comparing the root profiles in the control condition and after 30 h of NO₃⁻ induction. This approach allowed the identification of some hundreds of proteins, with high reliability and good reproducibility. Many of the proteins found to change in abundance were directly involved in NO₃⁻ uptake and assimilation, such as H⁺-ATPase, Nitrite Reductase and Glutamine Synthetase. According to the induction of N metabolism, some root enzymes involved in protein synthesis, folding and trafficking showed a relevant increment in abundances after 30 h of NO₃⁻ availability, while those involved in flavonoid metabolism generally showed a down-accumulation. Moreover, the results underlined the strict relationships between N nutrition, carbon metabolism and the metabolic pathways implicated in cell redox status. Overall, the proteomic analysis reveals that NO₃⁻ provision significantly affected the root proteome of M4 grapevine rootstocks, providing novel information about the biochemical pathways involved in N metabolism in this perennial plant. This study lays the bases for a better elucidation of the relations among N nutrition, rootstock/scion interactions and productivity in grapevine.

List of Participants

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