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)
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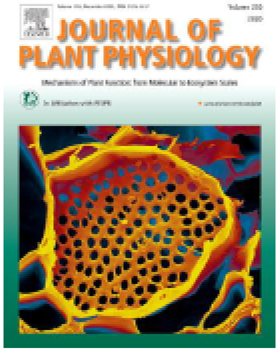
Special Issue



Journal of Plant Physiology

Plant Proteomics: from the Molecular Basis of Biological Processes to a Systems Biology Perspective

With the wealth of information and knowledge created in the past years by plant genomics research and international initiatives on sequencing of agronomically important genomes, the research environment is changing towards more widely applying this knowledge to study plant proteomes. At the same time, plant proteomics research has greatly evolved and, together with other experimental methodologies such as proteogenomics and metabolomics, it contributes to our understanding of plant functional networks from the systems biology perspective. Proteomics research provides valuable information, new understanding and discoveries about dynamic interactions between host and pathogens, plants with different genotypes and environment, about functional proteome organization and regulation by posttranslational modifications during plant defense responses associated with the development of diseases, biotic and abiotic stress responses, cold, drought and flooding resistance, investigation of crop growth and quality markers of agriculturally important proteins. The 4th Conference of the International Plant Proteomics Organization (INPPO2021) is the fourth in a series of biennial conferences and is a unique conference with a global reach that focuses entirely on Plant Proteomics.

This Special Issue features original research papers from INPPO2021 conference on recent advances in application of proteomics technology in plant and agricultural sciences, in cellular proteomics, physiology and metabolism, plant adaptation to the environment, abiotic and biotic stress, systems biology, as well as technical and methodological advances, and proteomics-specific bioinformatics. The aim of this Special Issue is to combine new insights that come from plant proteomics studies on increased understanding of the molecular basis of agriculturally important traits with observations on regulation of environmental stress perception and associated signaling via regulatory networks.

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 *Quercus ilex*"
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** (Stay and chat with speakers)
17:00	20:00			**Poster Sessions 1 and 2**

Tuesday March 9

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

GMT		My Time Zone		Poster	Presenter	Ttile
Start	End	Start	End			
16:50						Good Afternoon/Evening!
17:00	17:10			1.1	Sufia Farhat	Looking forward to *Cajanus cajan* 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 *Pinus nigra* 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 *Marchantia polymorpha* 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 (*Capsicum annuum* L.) fruit ripening: iTRAQ-based proteomic analysis
19:00	19:10			1.13	Salvador González-Gordo	Peroxisomes from sweet pepper (*Capsicum annuum* 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	
13:50				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** (Stay and chat with speakers)
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 (*Raphanus sativus* L.) in response to *Agrobacterium* 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 *Puccinia triticina*
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 *Populus × canescens* colonized with the ectomycorrhizal fungus *Paxillus involutus*, which limited plant host growth - a proteomic and metabolomic view
17:40	17:50			3.5	Aslihan Günel	Proteome profile of Endoplasmic Reticulum of *Pyrenophora teres* f.sp. *maculata*
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 (*Phaseolus vulgaris*)
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 *Phytophthora cinnamomi* in *Quercus ilex* 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 (*Pisum sativum* 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 *Ramonda serbica* leaves
19:20	19:30			4.6	Kjell Sergeant	The chloroplast of Craterostigma plantagineum 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 *Quercus ilex*
19:40	19:50			4.8	Madhiya Manzoor	Root proteomic analysis of Common bean (*Phaseolus vulgaris*) under Fe and P stress.
19:50	20:00			**Open for Questions**		
20:00	21:00			**INPPO Meeting**		INPPO Business Meeting – All Welcome!

Thursday March 11

Symposium 3: Plant-Interactions

GMT		My Time Zone		
Start	End	Start	End	
13:50				Good Morning/Afternoon!
14:00	14:30			**Plenary Lecture 2:** “Identification of Effectors from the Phytopathogen *Fusarium graminearum* 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**, Univeristy 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 *Blumeria graminis* to identify and validate host proteins required for susceptibility”
15:40	16:00			**Invited talk 3: Dr. Georgia Tanou,** Institute of Soil and Water Resources, ELGO-DEMETER, Greece. “Proteogenomics atlas in a perennial fruit trees: a sweet cherry case study”
16:00	16:10			INPPO 2022/3 Invitation. INPPO 2024/5?
16:10	17:00			**Break** (Stay and chat with speakers)
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 *Chlorella vulgaris*
17:20	17:30			5.3	Petra Peharec Štefanić	Effects of silver nanoparticles and silver nitrate on root proteins of tobacco (*Nicotiana tabacum*) 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. Natalia Bykova, Andrej Frolov)

17:50	18:00			6.1	Dristy Zaman	Transamination of L-asparagine in *Glycine max* 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 (*Zea mays* L.) roots in response to different availabilities of nitrate and ammonium
18:20	18:30			6.4	Yordan Muhovski	Comparative proteomic analyses of potato (*Solanum tuberosum* L.) cultivars grown in hydroponics and subjected to different dosses 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 *Arabidopsis* 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 *Halophila stipulacea* 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 (*Oryza sativa* 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 *Nicotiana benthamiana* with Quantitative Proteomics for Molecular Farming
19:40	19:50			**Poster Prizes Announced**		
19:50	20:00			**Closing of INPPO2020**		

POSTER#4.4

Plausible implications of chronic ionizing radiation stress for plant memory and immunity

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Most environmental pollutants, including radionuclides, are persistent; thus, they chronically influence plants. Ionizing radiation is a ubiquitous stress factor with unclear consequences of prolonged exposure to low doses. A comprehensive comparison of seed proteomes and photosynthetic indices of leaves between soybean (*Glycine max*) grown in a radionuclide-contaminated field, followed by a clean ground recovery season, allowed to formulate a hypothesis, explaining effects induced by chronic ionizing radiation [1]. Data indicated that during multigenerational growth in a contaminated environment of Chernobyl zone, detrimental heritable changes were accumulated. We suggested that low-quality seed provisioning caused a harmful effect persisting in the offspring generation. Energy flow was restricted at least partially because of suboptimal photosynthesis on the vegetative stage. Currently, we pursue follow-up experiments for direct functional testing of an idea about compromised immunity against phytopathogens in the field, but perhaps even primed in the clean ground. Additionally, we started a pilot study on post-translational modifications of proteins, particularly assays on oxidative stress-related carbonylations, to discover the mysterious nature of damaging factors in aquatic plant—common reed (*Phragmites australis*). From a practical perspective, our data can be used to develop biotechnological applications, targeting the engineering of crops for the phytoremediation of contaminated areas.

1. M. Pernis et al., J. Plant Physiol. 251, 153219 (2020)

POSTER#4.5

Twenty different late embryogenesis abundant proteins (LEAPs) accumulate in desiccated *Ramonda serbica* leaves

Marija Vidovic[1], Stevanovic S[1], Franchin C[2,3], Battisti I[2,3], Arrigoni G[2,3], Masi A[4], Veljovic-Jovanovic S[5]

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[2]Department of Biomedical Sciences, University of Padova, Padova, Italy
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Resurrection plant *Ramonda serbica* Panc. survives desiccation for a long period and fully recovers metabolic functions already within one day upon watering [1]. Besides osmotic stress, desiccation provokes the accelerated generation of reactive oxygen species. The aim of our study was obtaining more insight into the mechanisms of desiccation tolerance in *R. serbica* by TMT labelled comparative quantitative proteomics of hydrated (HL) and desiccated leaves (DL). After *de novo* transcriptome analysis, 189456 transcripts with 189003 unigenes were annotated with seven common databases. Proteomic analysis allowed for the relative quantification of 895 different protein groups, 321 with a statistically significant difference in abundance between FL and DL. Among them, 25% referred to chloroplast and almost the same percentage were associated with desiccation and oxidative stress. Almost all differentially abundant proteins related to photosynthetic processes were down-regulated in DL, while those required for protein translation were more abundant in HL. Within differentially abundant proteins involved in antioxidative defence, the levels of enzymes involved in ascorbate-glutathione cycle, peroxiredoxins, Fe and Mn superoxide dismutase (SOD) were all reduced in DL, while germin-like proteins, three Cu/Zn SOD isoforms and polyphenol oxidases were more abundant in DL compared with HL. The protein family with the highest number of members showing the greatest accumulation upon desiccation comprised twenty different late embryogenesis abundant proteins (LEAPs), similarly as found by differential transcriptomic analysis. Taken together, our results imply a key role of LEAPs and Cu/Zn SOD in protective mechanism against desiccation in *R. serbica*, that may have significant implications on drought-related studies of crops grown in arid areas.

This work was supported by the Science Fund of the Republic of Serbia (PROMIS project LEAPSyn-SCI, grant number 6039663). M.V. wishes to acknowledge the support of COST Action BM1405 for approving STSM in Padua during 2017 and 2018.

POSTER#4.6

The chloroplast of *Craterostigma plantagineum* during a complete dehydration/rehydration cycle.

Kjell Sergeant[1], Xu X[1], Legay S[1], Geurriero G[1], Charton S[1], Planchon S [1], Leclercq C[1], Giarola V[2], Bartels D[2], Hausman J-F[1], Renaut J[1]

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Water shortage and the occurrence of drought periods are predicted to increase in the next decades. The success of biotechnological programs aimed at improving drought tolerance of crops depends on the identification of the mechanisms by which plants withstand drought. While aimed at improving the drought resistance of crops, a group of plants, collectively called resurrection plants, is studied for their capacity to lose up to 98% of their water content and re-establish growth after rehydration. One species that is used as model resurrection plant is *Craterostigma plantagineum* [1]. Samples from this plant at different time-points during a dehydration/rehydration cycle were analysed by transcriptomics, proteomics and metabolomics. One of the processes occurring is the change of the composition, structure and thus functioning of the cell wall. During the dehydration cycle the flexibility of the cell wall increases, as such allowing the cell wall to fold, induced by changes in cell volume, without leading to rupture (Xu et al. submitted). Although the photosynthetic apparatus of *C. plantagineum* is maintained in a recoverable state during dehydration, accounting for the capacity to recover from dehydration within 24h of rewatering [2], all analyses result in significant changes in chloroplast localized molecular events.