

the different modes of regulation of hormone-induced defense responses, we performed high-resolution RNA-seq time series analyses of hormone-treated *Arabidopsis* plants. Together with input of publicly available DAP-seq data and other RNA-seq data, we built dynamic gene regulatory network (GRN) models and inferred novel regulators of the individual and combinatorial hormone-induced responses. The significance of these novel regulatory components was validated by molecular and genetic analyses and by bioassays using pathogens and insects.

#### S-07.4-1

##### Study of spatial responses in combination with network analysis reveals mechanisms of plant resistance to viruses

Š. Baebler, T. Lukan, A. Coll, M. Križnik, Ž. Ramšak, M. Zagorščak, M. Pompe Novak, M. Petek, A. Blejec, **K. Gruden**  
National Institute of Biology, Ljubljana, Slovenia

Infection of a plant by a pathogen initiates a complex interaction between both players involved, leading to changes in the complex signalling network, which result in gene activity changes and reprogramming of the cell metabolism. A systems biology approach was adopted to understand the mechanisms and dynamics involved in potato plant defense following the infection with potato virus Y. We collected multi-layered omics datasets with spatiotemporal resolution. A qualitative model of potato plant immune signalling network was constructed describing the biosynthesis and signal transduction pathways for three crucial phytohormones involved in plant defence: salicylic acid, jasmonic acid and ethylene. The prior knowledge from literature was expanded with information on the viral and plant component interactions, protein-protein interactions and protein-DNA interactions in plant *Arabidopsis* and translated to potato. Additionally, potato smallRNA regulatory network and gene regulatory networks were constructed from experimental data and overlaid with prior knowledge network. The resulting robust qualitative model offers new insights into the plant-virus interaction by expanding the knowledge on critical properties of plant defence signalling, thus producing novel hypotheses to be tested in the wet lab. Examples of two tested and confirmed hypothesis will be given.

#### ShT-07.4-2

##### Omic insights into the molecular response of *Sargassum vulgare* to acidification at volcanic CO<sub>2</sub> vents

S. Nonnis<sup>1,2</sup>, A. Kumar<sup>3</sup>, I. Castellano<sup>4</sup>, H. AbdElgawad<sup>5</sup>, G.T. Beemster<sup>6</sup>, M.C. Buia<sup>3</sup>, G. Tedeschi<sup>1,2</sup>, A. Palumbo<sup>4</sup>  
<sup>1</sup>Dipartimento di Medicina Veterinaria, DIMEVET, Università degli Studi di Milano, Lodi, Italy, <sup>2</sup>CRC "Innovation for well-being and environment" (I-WE), Università degli Studi di Milano, Milan, Italy, <sup>3</sup>Stazione Zoologica Anton Dohrn, Department of Integrative Marine Ecology, Marine Research Center, Ischia, Naples, Italy, <sup>4</sup>Stazione Zoologica Anton Dohrn, Department of Biology and Evolution of Marine Organisms, Naples, Italy, <sup>5</sup>Department of Botany, Faculty of Science, Beni-Suef University, Beni-Suef, Egypt, <sup>6</sup>University of Antwerp, Department of Biology, Integrated Molecular Plant Physiology Research Group, Antwerp, Belgium

Ocean acidification is impacting marine life all over the world. Understanding how species are able to cope with the changes of

seawater carbonate chemistry represents a challenging issue. We addressed this topic using underwater CO<sub>2</sub> vents that naturally acidify some marine areas occurring off the island of Ischia. In the most acidified area of the vents, the biomass is dominated by the brown alga *Sargassum vulgare*. In the present study, we performed the characterization of the *S. vulgare* proteome, by a label-free quantification MS-based shot-gun proteomic approach, together with metabolites analyses to identify the key proteins, metabolites and pathways affected by ocean acidification. Several differentially expressed proteins were involved in a wide range of cellular and metabolic processes such as protein synthesis and folding, transport, photosynthesis and oxidation-reduction. Analyses of other metabolites revealed variations in the levels of some fatty acids and phenols. Overall, the results obtained by proteins and metabolites analysis, integrated with previous transcriptomic (1), physiological and biochemical studies, have allowed to delineate the molecular strategies adopted by *S. vulgare* to grow in future acidified environments. 1. Previously published in: Kumar A et al. (2017) Molecular Ecology 26

#### ShT-07.4-1

##### How is salicylic acid perceived in potato?

Š. Tomaz<sup>1,2</sup>, A. Coll<sup>1</sup>, T. Stare<sup>1</sup>, T. Lukan<sup>1</sup>, K. Pogačar<sup>1</sup>, R. Vollmeier<sup>1</sup>, K. Gruden<sup>1</sup>

<sup>1</sup>National Institute of Biology, Ljubljana, Slovenia, <sup>2</sup>Jozef Stefan International Postgraduate School, Ljubljana, Slovenia

Potato (*Solanum tuberosum*) is one of the most important crops of our time, produced, processed and consumed by countries all around the globe. At the same time, it is exposed to a number of plant pathogens, causing high loss in yield and lower product quality. Plants respond to pathogen infections with a complex network of signalling cascades, which are orchestrated by hormones and ultimately affect the expression of defence genes. One of the main hormonal pathways in plant immunity is the salicylic acid pathway, which is also a key component of potato defence response to potato virus Y (PVY), the most dangerous virus infecting potato. The salicylic acid pathway has been extensively studied in *Arabidopsis thaliana*, where it regulates the expression of *PR-1* defence gene through NPR transcription cofactors and TGA transcription factors. Although this pathway has also been investigated in some economically important crops, the transcription regulation during potato PVY infection is mostly unknown and data on similar mechanisms in potato are scarce. We have selected three potato TGA transcription factors involved in potato defence response, investigated the chromosomal arrangement of their genes, classified them phylogenetically and analysed their protein sequences and domains *in silico*. We determined the localization of all three TGAs in plant cells and studied the protein-protein interactions among them, their interactions with potato NPR cofactors and proteins from other signalling pathways using the yeast two-hybrid assay. As we found several positive interactions between investigated proteins in yeast, we continued with their confirmation *in planta* with co-immunoprecipitation experiments, currently in progress. The results of our study provide new insights into salicylic acid mediated transcription regulation of defence genes and will help us to better understand the potato immune response on a molecular basis.