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JUNE 24th-26th, 2015

12th International Conference on Reactive Oxygen and Nitrogen Species in Plants: from model systems to field

Palazzo della Gran Guardia
Verona, Italy

PROGRAM&ABSTRACTS

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Program, Abstracts and List of Participants

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SIGNALLING PATHWAYS INDUCED BY ROS AND ABA IN LSD1/EDS1-RELATED REGULATION OF ARABIDOPSIS SEEDS GERMINATION

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It has recently been proposed that the theory of hormonal regulation of germination may also imply interactions between phytohormones and reactive oxygen species (ROS) signalling pathways, thus mediating important processes in seeds. In addition, rapid responses of seeds to environmental factors suggest that complex mechanisms other than just those involving regulation of gene expression are involved in the control of germination. Programmed cell death (PCD) occurs in various types of plant cells in response to environmental stimuli and during development including seed-related events. LESION SIMULATING DISEASE1 (LSD1) codes a protein which is an important negative regulator of PCD in Arabidopsis thaliana and it suppress ENHANCED DISEASE SUSCEPTIBILITY1 (EDS1) action, a positive PCD regulator. In spite of the fact that these regulators are expected to be involved in many processes in plants, knowledge about their function in seed biology is very limited. The present study has been specifically designed to address some biological questions with regards to possible PCD-ROS-ABA-related regulation of seeds germination. It is shown that after-ripened seeds of lsd1 null mutants placed in darkness germinated more slowly than Arabidopsis (Col) wild type and eds1 and the presence of light did not significantly improve lsd1 germination. Interestingly, in comparison to lsd1, eds1 seeds placed in light conditions germinated as well as the wild type but they germinated slower in darkness. The qRT-PCR analysis of transcript levels of genes involved in ROS and ABA signalling (i.e. MITOGEN-ACTIVATED PROTEIN KINASE, MAPK, GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA, AGB1, ABA INSENSITIVE, ABI; GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT APLHA-1, GPA1; HIGHLY ABA-INDUCED PP2C, HAI2; G-PROTEIN-COUPLED RECEPTOR 1, GCR1) indicated their role in LSD1/EDS1-related regulation of germination. These discoveries indicate the novel role of LSD1 positively regulating seed germination by modulation of hormonal and oxidative signalling pathways and suggest that it may act in a light-dependent manner.

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TRANSCRIPTIONAL RESPONSE TO HYDROGEN PEROXIDE IN GRAPEVINE BERRY SKIN AT THE BEGINNING OF RIPENING

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Fleshy fruit ripening represents the final stage of fruit development, when pulp and skin undergo many metabolic and phenotypic transformations to become attractive for seed dispersing animals. In grapevine, the beginning of ripening can be identified by the softening and coloring of the berries (véraison). The transition from mature green to ripening berries is controlled by many internal signals, such as hormones, transcription factors and metabolites, tuned to external stimuli, mainly light, temperature and water availability. Ripening onset is characterized by the gradual loss of photosynthetic activity and a transient shift to an aerobic fermentative metabolism (grapevine is a non climacteric plant) which are likely to favour an oxidative stress. We reported the transient accumulation of hydrogen peroxide (H_2O_2) and singlet oxygen ($^1O_2$) respectively in the cytosol and plastids of Pinot noir berry skin at the beginning of ripening. In order to ascertain the signaling function of H_2O_2, we treated pre-veraison berries with 1 mM H_2O_2 and analyzed the transcriptional response at the genome-wide level by RNA-seq. About 230 genes are modulated in green berries in response to H_2O_2 treatment: they are mainly involved in responses to stimuli and secondary metabolism and are mainly localized at the cell wall. To gain more insights into the function of these genes, a co-expression analysis has been undertaken, using an in-house built grapevine gene expression compendium, called Vitis Colombos. It considers most of the publicly available microarray and RNA-seq gene expression data of grapevine, and provides tools to analyze gene profiles and finding co-expressed genes. These in silico analyses suggest novel gene functional correlations that require experimental validation. The present study contributes new clues to the understanding of the regulatory role played by H_2O_2 at the beginning of ripening.