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**BOOK OF
ABSTRACTS**

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Peroxisome-dependent transcription factors in plant response to stress

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Reactive oxygen species (ROS) act as secondary messengers that can be sensed by specific redox-sensitive proteins responsible for the activation of signal transduction culminating in altered gene expression. The chemical identity of ROS and their subcellular origin have a specific imprint on the transcriptional response of the plant. In recent years, several transcriptomic studies related to altered ROS metabolism in plant peroxisomes have been carried out. In this study, we made a meta-analysis of the changes in the transcriptional profiles to identify common footprints for plant peroxisomal-dependent signaling in response to stress both at early and later time points. These footprints highlight their putative regulatory role in various metabolic pathways involved in plant responses to several both abiotic and biotic stresses. Since transcription factors (TFs) are vital for gene expression regulation in most living organisms, further research was restricted to genes that had a function as TFs. Based on the meta-analysis in *Arabidopsis thaliana*, a search of the orthologs of these TFs in a crop of great agronomic importance, *Solanum lycopersicum* was carried out. The transcriptional regulation patterns of these orthologs under different biotic and abiotic stress conditions, support their involvement in diverse stress responses and point to a conserved functionality across distant plant species.