



## Seminar

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### Meta-analysis of transcriptomic responses to environmental stresses in tree fruit crops

RNA-Seq analysis is a strong tool to gain insight into the molecular responses to environmental stresses in crops. Transcriptomic studies are usually conducted in a singular time, they do not provide any repetition across different seasons and frequently they are performed in field conditions where environmental variability is high and disturbing factors are frequently present. The identification of up- or down-regulated genes in single transcriptomic experiments is often not enough to draw meaningful biological conclusions because it is hard to identify which gene plays a key role in specific signaling networks in host responses. This issue leads to high difficulties in deriving conclusive models for understanding molecular mechanisms involved in crop stress responses. Indeed, meta-analysis in transcriptomics represents a valid tool to identify key players in the complex regulative networks of quantitative traits such as drought resistance.

The identification of common genes between different biotic stress will allow to gain insight into these general responses and help the diagnosis of an early “stress state” of the plants. The objective of this work was to identify key players and features (genes, proteins, gene sets, pathways) linked to both abiotic (drought) and biotic stress resistances (bacteria, fungal pathogens and viruses) in *Malus domestica* through a meta-analysis of published transcriptomic data in this crop and other closely-related ones. Commonly regulated genes across species and different types of stress, belonging to key categories (transcription factors, stress signaling and signal transduction, hormone-related pathways etc..) were identified. These analyses will help in monitoring stressed plants to start early specific management procedures for each stress and develop more sustainable biotechnological strategies through a fine-tuning of crop physiological responses to abiotic and biotic stresses.

Room 6302 – Palazzo della ricerca e della conoscenza

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