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Meta-analysis of RNA-seq data to gain insight into crop responses to environmental stresses

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RNA-Seq analysis is a strong tool to gain insight into the molecular responses to biotic stresses in plants. 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 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 disease symptomatology. For these reasons, more meta-analysis is needed to validate singular transcriptomic works with other similar studies performed with same research purposes. Meta-analysis of transcriptomic data identifies commonalities and differences between differentially regulated gene lists and allows screen which genes are key players in gene-gene and protein-protein interaction networks. These analyses allow delivering important information on how a specific environmental factor affects plant molecular responses and how plants activate general stress responses to environmental stresses. An early stress condition in plants is like the inflammatory response occurring in animals in response to pathogen-associated factors. The objective of this work is to identify specific and common molecular features (genes, proteins, gene sets and pathways) linked to both abiotic and biotic stress resistances among key crops. The identification of common genes between different biotic stress allow to gain insight into these general responses and help the diagnosis of an early “stress state” of the plants. These analyses help in monitoring stressed plants to start early specific management procedures for each disease or disorder.

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