

System-level transcriptomics of wheat responses to FHB identifies gene regulatory networks and conserved master regulators as key susceptibility genes

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February 23, 2023

Abstract

Plant diseases are driven by an intricate set of defense mechanisms counterbalanced by the expression of host susceptibility factors promoted through the action of pathogen effectors. In spite of their central role in the establishment of the pathology, the primary components of plant susceptibility are still poorly understood and challenging to trace. Focusing on Fusarium head blight (FHB) in bread wheat and integrating plant transcriptomics responses from a susceptible cultivar facing *Fusarium graminearum* strains of different aggressiveness, we described unexpected differential expression of a conserved set of transcription factors and an original subset of master regulators were evidenced using a regulation network approach. The dual-integration with the expression data of pathogen effector genes combined with database mining, demonstrated robust connections with the plant molecular regulators and identified relevant candidate genes involved in plant immunity, mostly able to suppress plant defense mechanisms. Furthermore, taking advantage of wheat cultivars of contrasting susceptibility levels, a refined list of 142 conserved susceptibility gene candidates were proposed to be necessary host's determinants for the establishment of a compatible interaction. In this respect, our findings provide new clues for improving FHB control in wheat and also could conceivably leverage further original researches dealing with a broader spectrum of plant pathogens.

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