

Moulin

Comparative transcriptomics of the wheat response towards diverse partners of its microbiome

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Plants constantly live with a variety of microorganisms that can be beneficial or pathogenic. Although host-pathogen interactions are relatively well described at present in several models, those concerning the response of plants to beneficial and multiple interactions, remain poorly studied. In the MIC-CERES project (funded by Agropolis and Cariplo foundations), we analyzed the composition of the wheat microbiomes, and also the physiological and transcriptomic response of tender wheat (*Triticum aestivum* cv Chinese Spring) during its interaction with different actors of its phytobiome: two PGPR bacteria (one rhizospheric, *Azospirillum brasilense*; one endophyte, *Paraburkholderia graminis*), one mycorrhizal fungi (*Funneliformis mossae*), and a wheat pathogen, *Xanthomonas translucens* (Xt). In order to decipher the different responses of wheat to these microbes, we produced RNAseq data from wheat roots and leaves 50 days after inoculation (except Xt which was monitored at 1 dpi), in the same growth system for all interactions. The responses were analyzed at a global level, revealing clear difference between organs and types of interactions, and at gene-level, revealing specific gene networks linked to observed phenotype (Plant-growth promotion for bacteria, defense against Xt, plant biocontrol mechanisms induced by mycorrhiza against Xt).