

Supplemental Material

Plant responses of maize to two formae speciales of *Sporisorium reilianum* support recent fungal host jump

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Figure S1

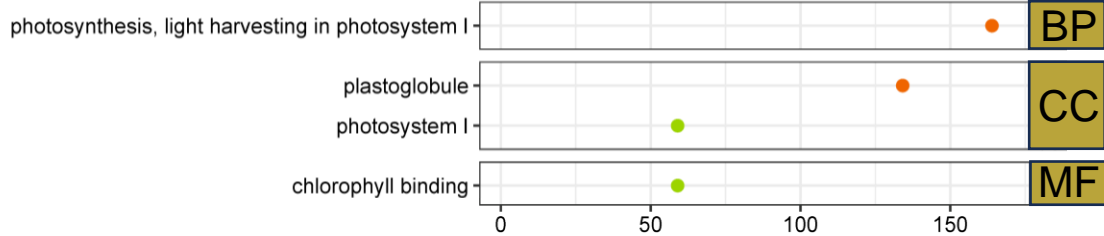
A up (298 genes only upregulated in Zm-SRS vs Zm-H2O)



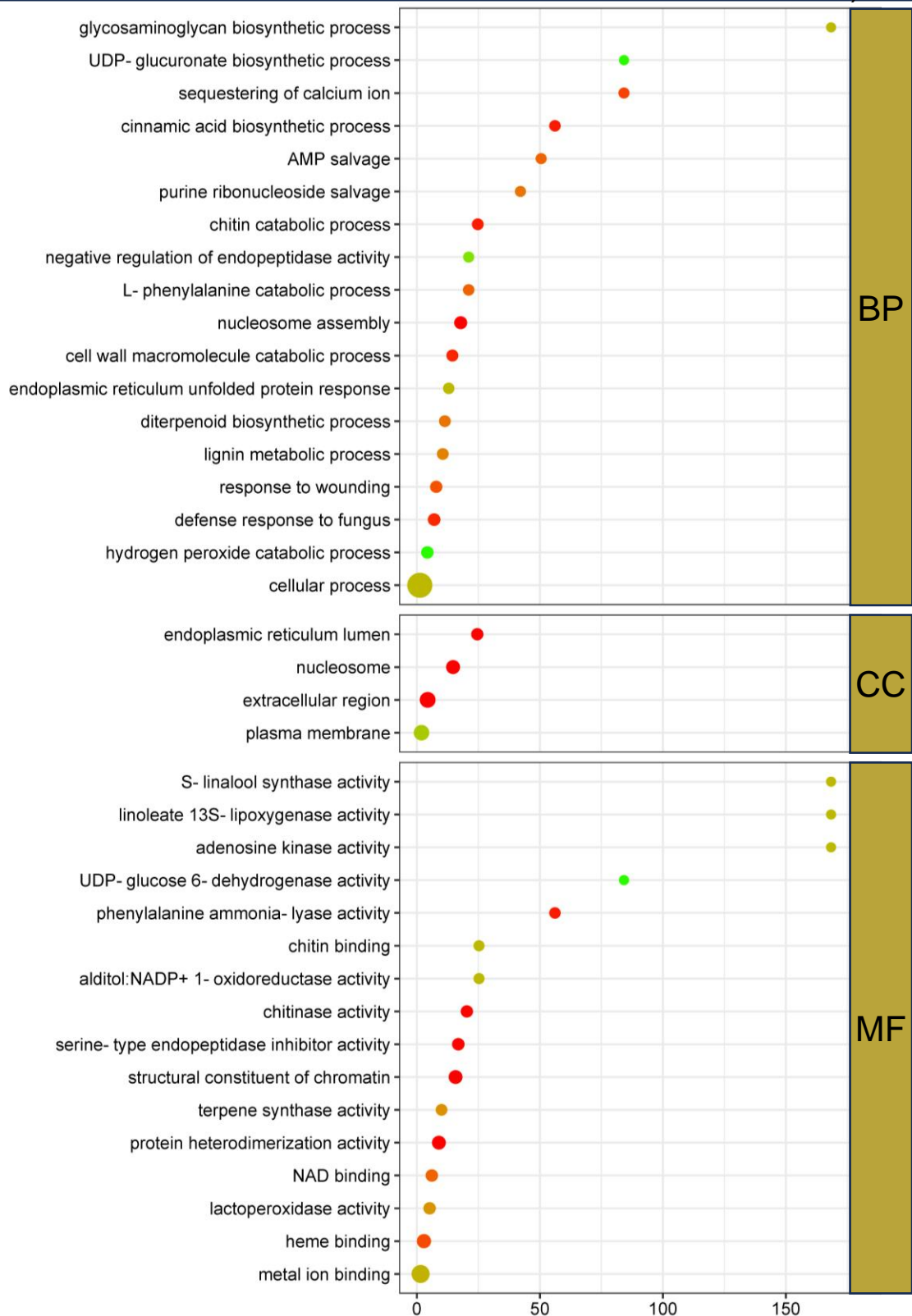
B up (528 genes only upregulated in Zm-SRZ vs Zm-H2O)



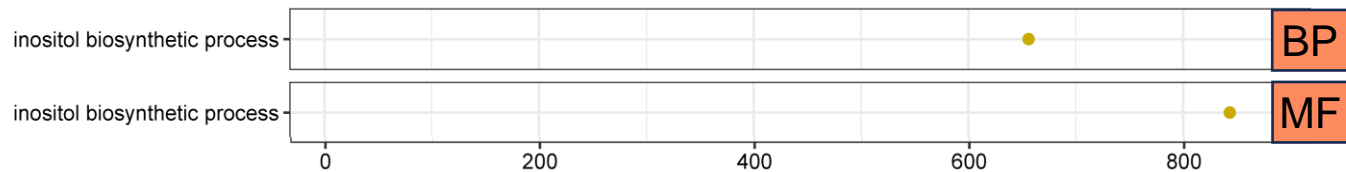
D down (45 genes in both Zm-SRZ vs ZmH2O and Zm-SRS vs Zm-H2O)



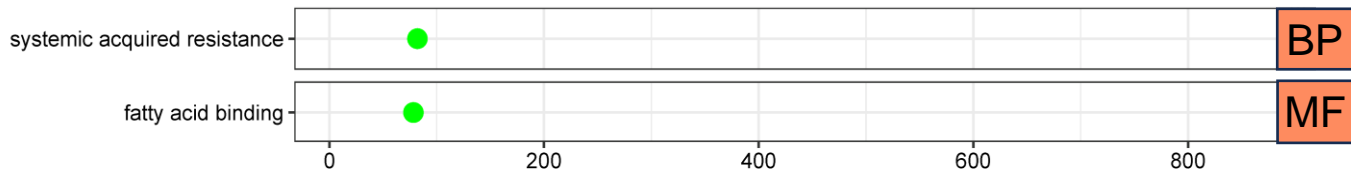
D up (520 genes in both Zm-SRZ vs ZmH2O and Zm-SRS vs Zm-H2O)



E down (15 genes in Zm-SRS vs Zm-H2O and Zm-SRS vs Zm-SRZ but not in Zm-SRZ vs Zm-H2O)



E up (77 genes in Zm-SRS vs Zm-H2O and Zm-SRS vs Zm-SRZ but not in Zm-SRZ vs Zm-H2O)



F up (152 genes in Zm-SRZ vs Zm-H2O and Zm-SRZ vs Zm-SRS but not in Zm-SRS vs Zm-H2O)

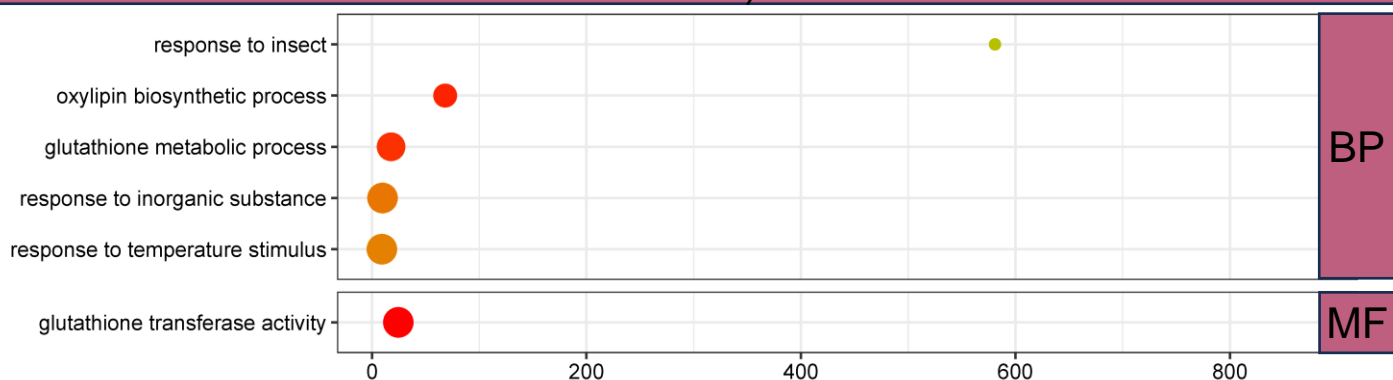


Figure Legend

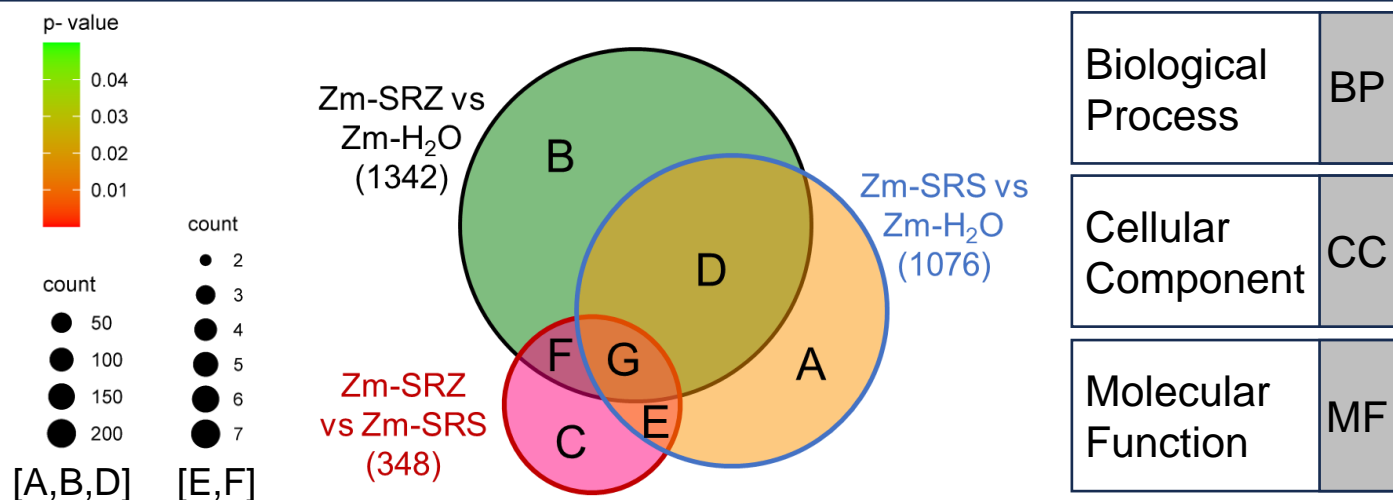


Figure S1. Enrichment analysis of GO terms associated with deregulated maize genes. Only GO terms with adjusted P-values below 0.05 are listed. Genes were analyzed in different sets (A, B, D, E, F) of deregulated genes according to the labeling in the Venn diagram below. For bubble plot size and color explanation see legend below. Bubbles are sorted according to fold enrichment of the specific GO term in the set of analyzed genes relative to in all genes. Missing entries indicate lack of significant GO terms.