

**Comparative transcriptome analysis reveals distinct gene expression profiles in
Brachypodium distachyon infected by two fungal pathogens**

Gengrui Zhu¹, Chengyu Gao¹, Chenyu Wu¹, Mu Li¹, Jin-Rong Xu², Huiquan Liu¹, Qinhu Wang^{1,*}

¹ State Key Laboratory of Crop Stress Biology for Arid Areas and College of Plant Protection, Northwest A&F University, Yangling, Shaanxi 712100, China.

² Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907, USA.

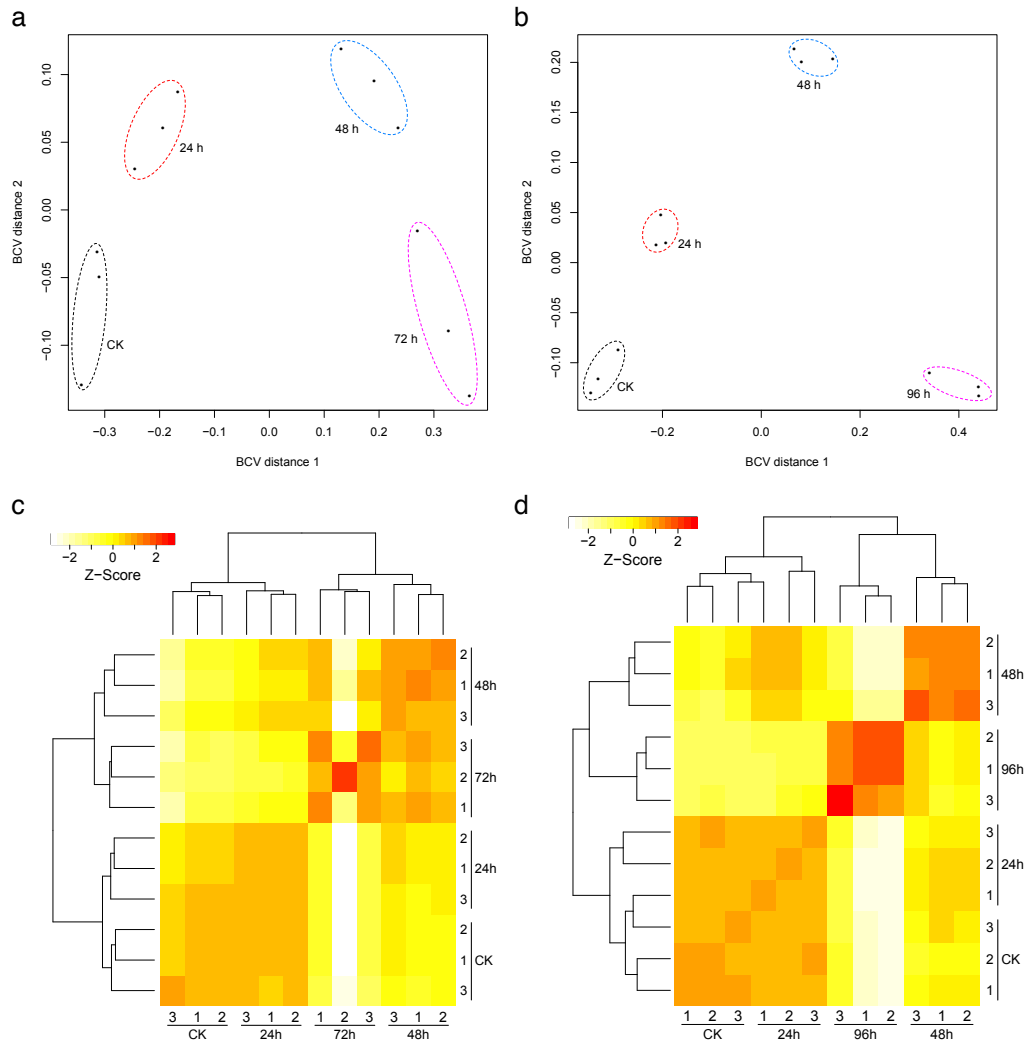


Figure S1. Global evaluation of the host transcriptomes. (a-b) Multi-dimensional scaling (MDS) plot of the gene expression in *Brachypodium* infected with *F. graminearum* (a) or *M. oryzae* (b), respectively. (c-d) Hierarchical clustering plot of the gene expression in *Brachypodium* infected with *F. graminearum* (c) or *M. oryzae* (d), respectively. Samples were clustered using the Pearson correlation distance measure.

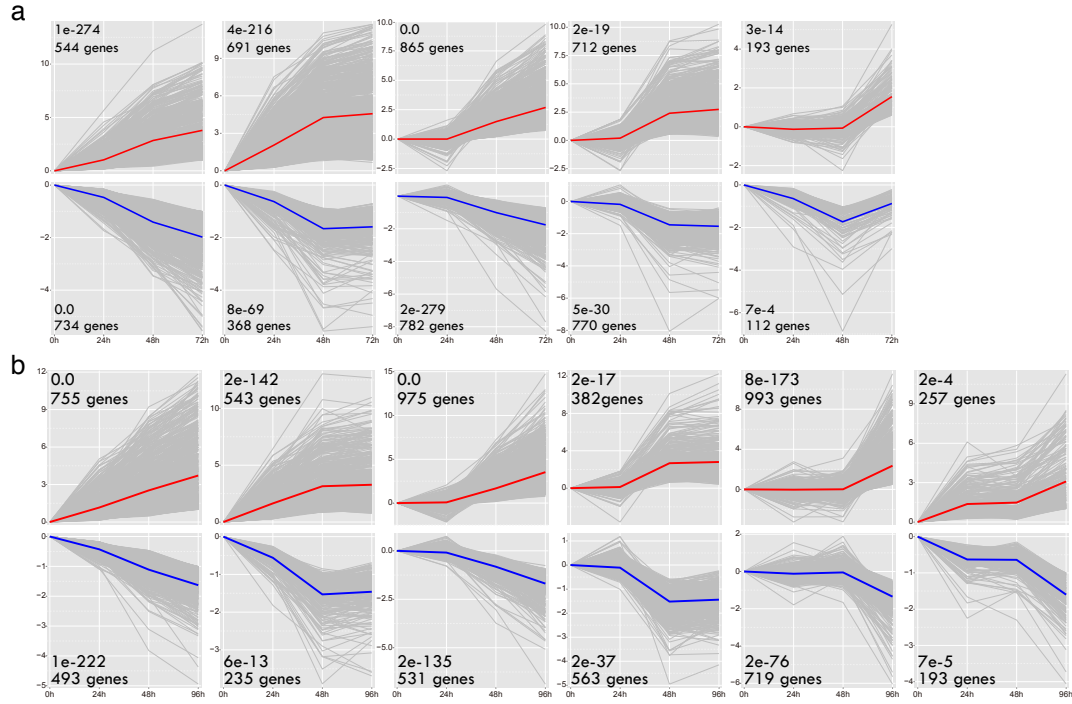


Figure S2. Profiles of the differentially expressed genes in *Brachypodium* infected with *F. graminearum* (a) or *M. oryzae* (b), respectively. The horizontal axis indicates different time points. The vertical axis shows the log₂ fold change. A gray line represents the expression pattern of a gene, and the bold red/blue line illustrates the average expression pattern of all genes in each cluster.

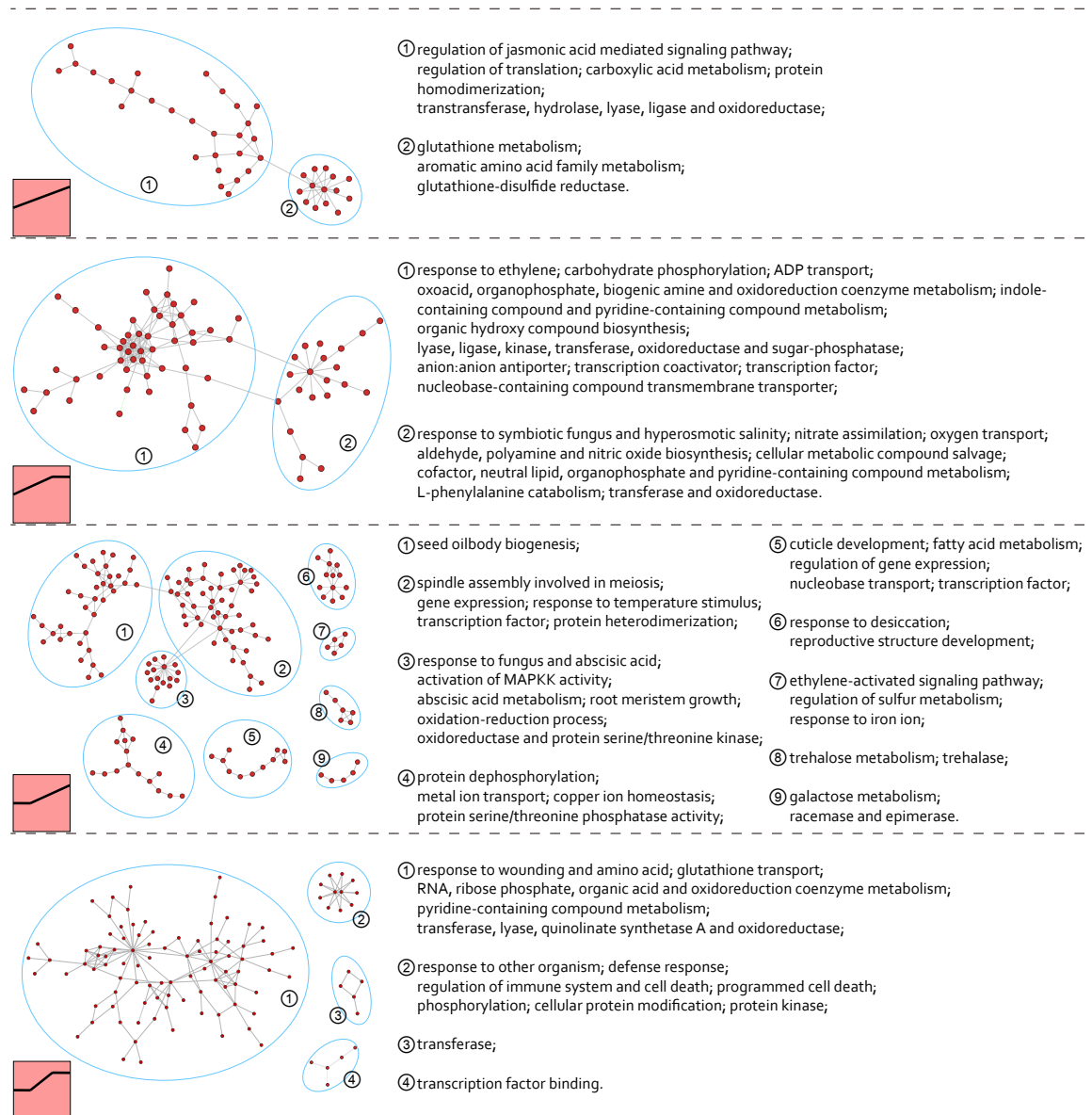


Figure S3. Protein-protein interaction networks of the up-regulated genes in *B. distachyon* infected by *F. graminearum*. The up-regulated genes in each profile were subjected to protein-protein interaction networks analysis. Gene Ontology annotation was used to reveal the function of each submodule of the networks (blue oval). Nodes and edges represent proteins and functional links, respectively.

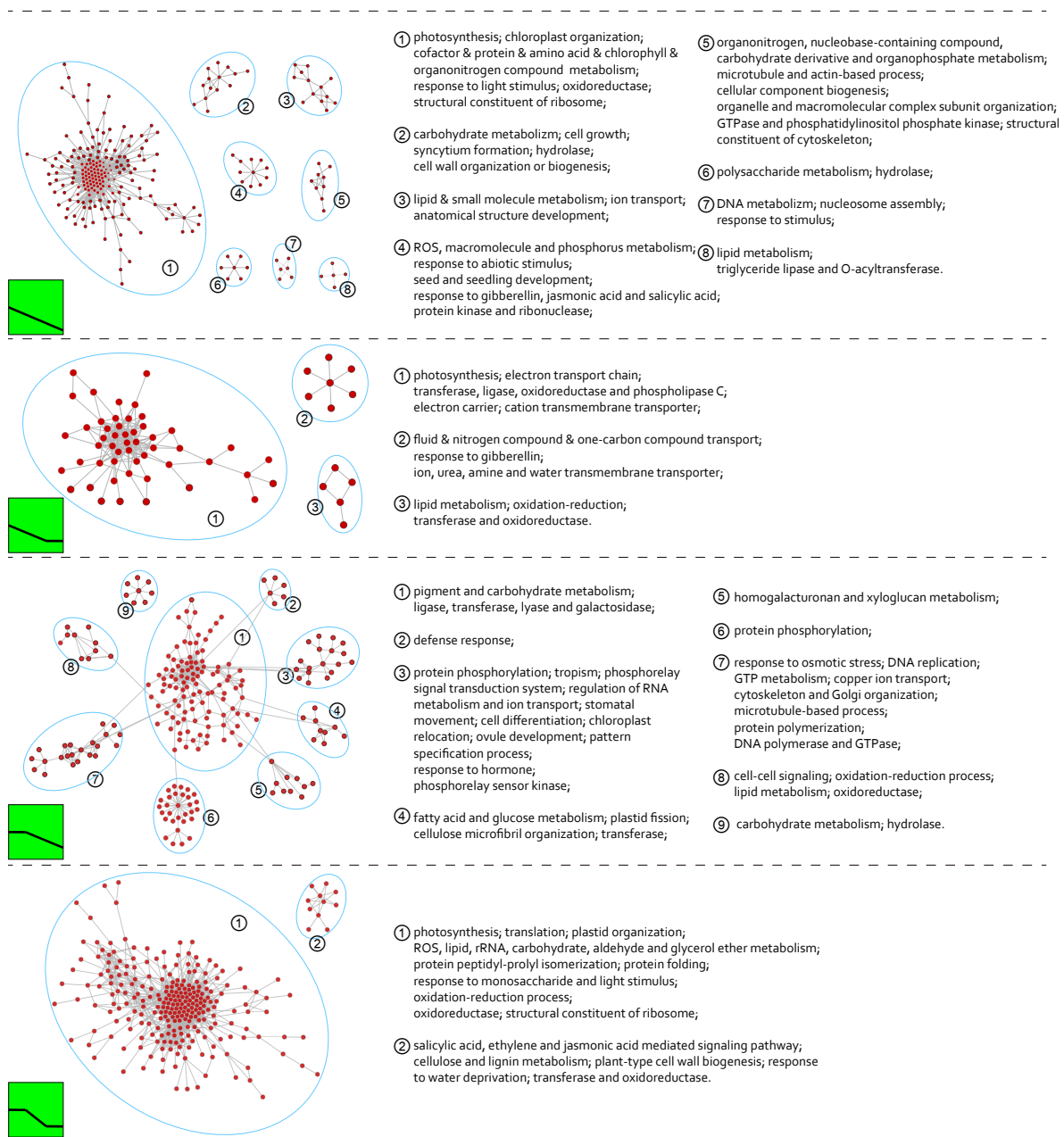


Figure S4. Protein-protein interaction networks of the down-regulated genes in *B. distachyon* infected by *F. graminearum*. The down-regulated genes in each profile were subjected to protein-protein interaction networks analysis. Gene Ontology annotation was used to reveal the function of each submodule of the networks (blue oval). Nodes and edges represent proteins and functional links, respectively.

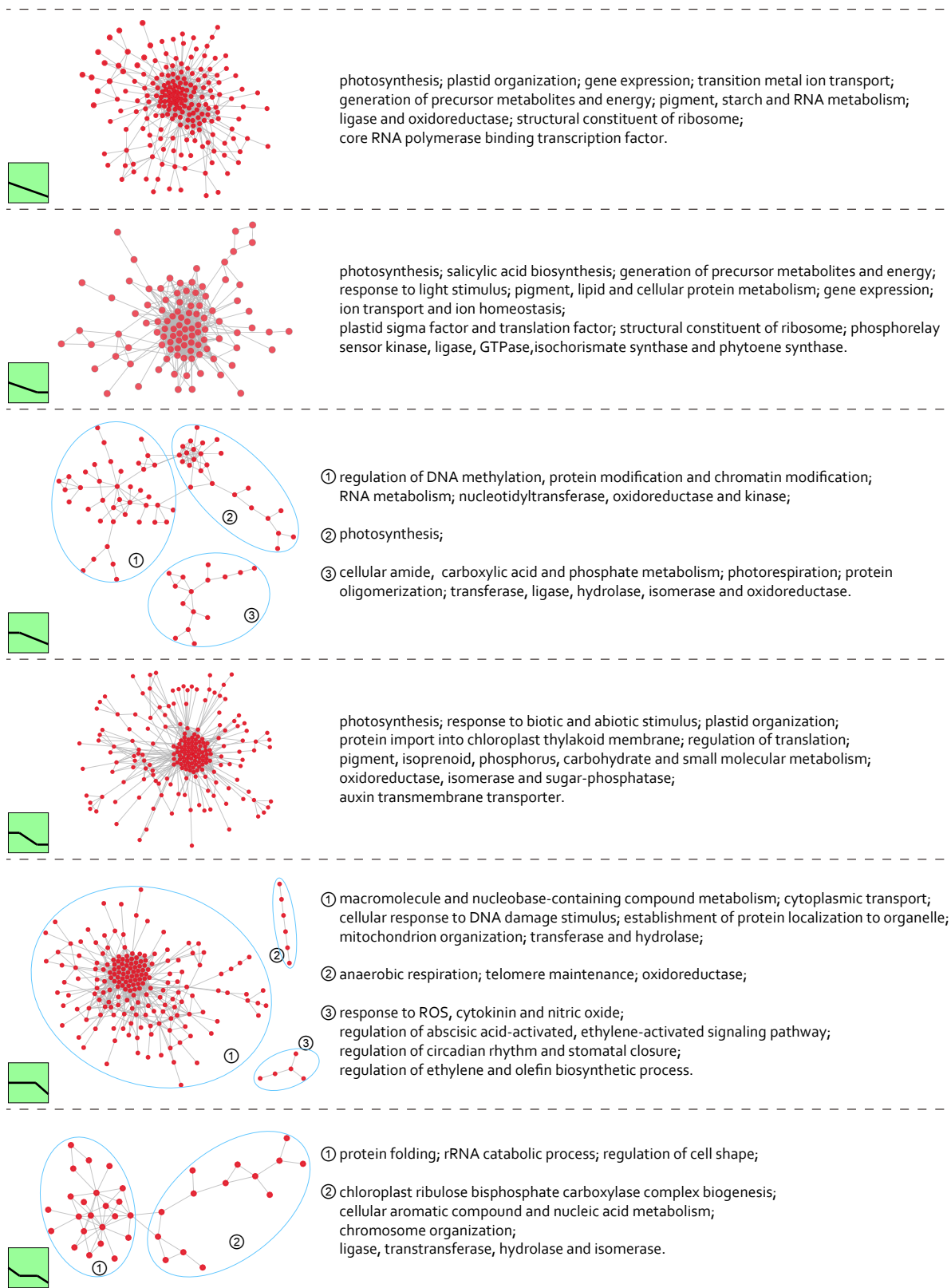


Figure S5. Protein-protein interaction networks of the down-regulated genes in *B. distachyon* infected by *M. oryzae*. The down-regulated genes in each profile were subjected to protein-protein interaction networks analysis. Gene Ontology annotation was used to

reveal the function of each submodule of the networks (blue oval). Nodes and edges represent proteins and functional links, respectively.