

Supplementary caption

Supplementary results

The GO and KEGG analysis of DEGs of both *U. esculenta* and *Z. latifolia*

Supplementary Figures Captions

Figure S1. Pearson correlation coefficient heatmap of all gene expression between the two stages (–10 d before and 0 d) of stem gall formation. A. *U. esculenta*. B. *Z. latifolia*

Figure S2. Functional annotation of DEGs between the two stages (–10 d before and 0 d) of stem gall formation based on the *U. esculenta* genome. A. GO enrichment of DEGs. B. KEGG enrichment of DEGs

Figure S3. Functional annotation of DEGs between the two stages (–10 d before and 0 d) of stem gall formation based on the *U. esculenta* genome. A. GO classification. Each DEG was classified into at least one GO term and grouped into three categories: biological process, cellular component and molecular function. B. Pathway assignment based on KEGG. DEGs were grouped into cellular processes, environmental information processing, genetic information processing, metabolism, and organismal systems

Figure S4. Functional annotation of DEGs between the two stages (–10 d before and 0 d) of stem gall formation based on the *Z. latifolia* genome. A. GO enrichment of DEGs. B. KEGG enrichment of DEGs

Figure S5. Functional annotation of DEGs between the two stages (–10 d before and 0 d) of stem gall formation based on the *Z. latifolia* genome. A. GO classification of DEGs. B. Pathway assignment based on KEGG of DEGs

Figure S6. DEGs of PR genes in the initial stage of stem gall formation

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Figure S8. Structural analysis of the C2H2 zinc finger proteins family.

Supplementary Tables Captions

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Table S2. GO enrichment analysis of DEGs of *U. esculenta* in the initial stage of stem gall formation

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