Transcriptional responses of invasive and indigenous whiteflies to different host plants reveal their disparate capacity of adaptation

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Supplementary Dataset 1: Differently expressed genes between cotton-feeding and tobacco-feeding MEAM1.

Supplementary Dataset 2: Differently expressed genes between cotton-feeding and tobacco-feeding Asia II 3.

Supplementary Dataset 3: Comparison of DGE data and qRT-PCR results for 50 genes. Twenty-five DEGs from each comparison group (MT vs. MC and AT vs. AC) were selected for qRT-PCR analyses to validate the DGE data.

Supplementary Dataset 4: Carbohydrate and energy metabolism pathways enriched with DEGs in AT vs. AC.

Supplementary Dataset 5: DEGs in the ribosome pathway in AT vs. AC and MT vs. MC.

Supplementary Dataset 6: DEGs in proteasome, lysosome and protein digestion and absorption pathways in AT vs. AC and MT vs. MC.

Supplementary Dataset 7: Differently expressed detoxification genes in AT vs. AC and MT vs. MC.