

Supplementary Materials

Figure S1. Pathway enrichment analysis of significantly upregulated (A) and downregulated (B) DEGs in Root vs Stem comparisons, and significantly upregulated (C) and downregulated (D) DEGs in Seed vs Stem comparisons.

Figure S2. Scale-free topology and mean connectivity as functions of soft-thresholding power (β) in WGCNA analysis of metabolomic (A) and transcriptomic (B) data from *S. moorcroftiana*. Left panels display scale-free topology model fit (signed R^2) against β , with red points labeled by power values and a red horizontal line at $R^2 = 0.8$ indicating the threshold for scale-free topology. Right panels show mean connectivity (average network connectivity) versus β , with a red horizontal reference line at mean connectivity = 100 illustrating the decline in connectivity as β increases.

Figure S3. Networks illustrating co-accumulation between L-lysine (yellow module) (A), sophoridine (brown module) (B), oxysophocarpine (magenta module) (C), and the top 30 hub metabolites within their respective metabolomic modules. Plots were generated using Cytoscape v3.10.3.

Table S1. Mapping and annotation statistics for pre-processing of *S. moorcroftiana* transcriptomic data

Table S2. Secondary metabolites uniquely enriched in each tissue (root, stem, leaf, seed) of *S. moorcroftiana*

Table S3. Genes from integrated analysis showing significant correlation with matrine and sophoridine abundance within the transcriptomic turquoise module, and genes significantly correlated with (-)-sparteine and lupinine abundance within the transcriptomic yellow module

Table S4. AME motif enrichment in 1-kb promoters. AME results for promoters (–1 kb upstream of TSS) of gene candidates associated with Sophoridine, (–)-Sparteine, Lupinine and Matrine. The table lists motif identities, consensus sequences, significance and hit statistics comparing primary sequences to shuffled controls, ordered by gene families and adjusted significance. For each TF, we also annotate the putative stress-response pathways and secondary-metabolite biosynthetic pathways in which it may participate.