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Integrated miRNAome, transcriptome, and degradome analysis reveals miRNA-target modules governing floral florescence, development and senescence across early- and late-floweringphenotypes in Paeonia suffruticosa

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Abstract

As a candidate national flower of China, tree peony has extremely high ornamental, medicinal and oil value. However, the short florescence and rarity of early-flowering and late-flowering varieties restrict further improvement of the economic value of tree peony. Specific miRNAs and their target genes involved in tree peony floral florescence, development and senescence remain unknown. This report presents the integrated analysis of the miRNAome, transcriptome and degradome of tree peony petals collected from blooming, initial flowering, full blooming and decay stages in the early-flowering cultivar *Paeonia ostii* 'Fengdan', a mutant of early-flowering cultivar 'Fengdan' and late-flowering cultivar *Paeonia suffruticosa* 'Lianhe'. Transcriptome analysis revealed a transcript ('psu.G.00014095') which was annotated as a xyloglucan endotransglycosylase/hydrolase precursor XTH-25 and found to be differentially expressed across flower developmental stages in *Paeonia ostii* 'Fengdan' and *Paeonia suffruticosa* 'Lianhe'. The miRNA-mRNA modules were enriched in various pathways such as plant hormone signal transduction, indole alkaloid biosynthesis, arachidonic acid metabolism, folate biosynthesis, fatty acid elongation, and the MAPK signaling pathway. Multiple miRNA-mRNA-TF modules demonstrated the potential functions of MYB-related, bHLH, Trihelix, NAC, GRAS and HD−ZIP TF families in tree peony floral florescence , development , and senescence. Comparative spatio-temporal expression investigation of 8 floral-favored miRNA-target modules suggested that transcript 'psu.T.00024044' and microRNA mtr-miR166g-5p are involved in the floral florescence, development and senescence associated agronomic traits of tree peony. The results will facilitate the understanding of the potential molecular mechanisms underlying floral florescence, development and abscission, and provide guidance for tree peony breeding of varieties with later and longer florescence characteristics.

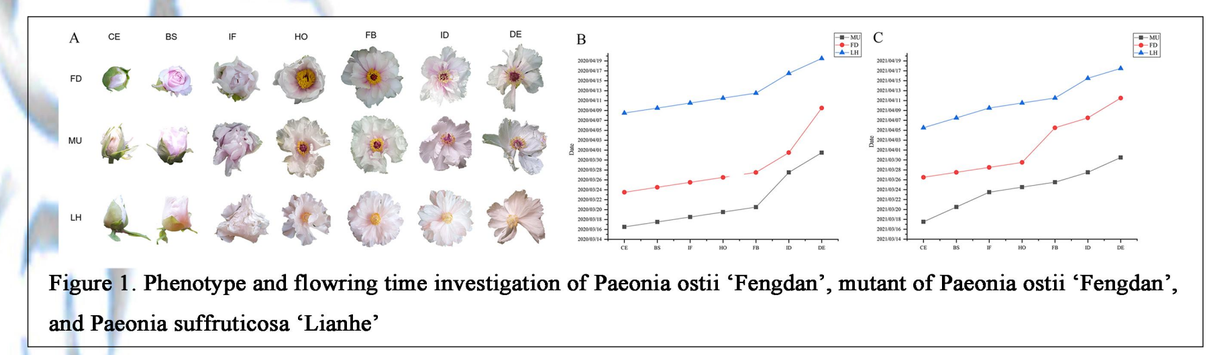

Figure 1. Phenotype and flowring time investigation of Paeonia ostii 'Fengdan', mutant of Paeonia ostii 'Fengdan', and Paeonia suffruticosa 'Lianhe'

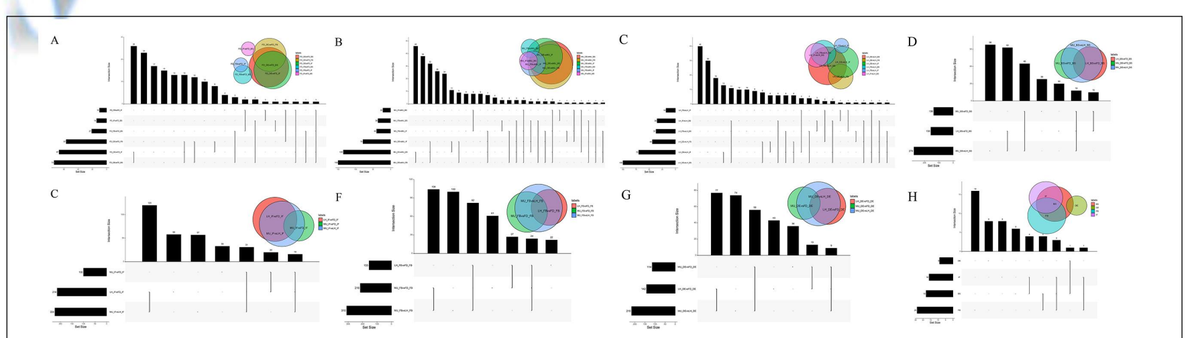

Figure 2. The distribution of DEMs across flower developmental stages and cultivars in Paeonia ostii 'Fengdan', mutant of Paeonia ostii 'Fengdan', and Paeonia suffruticosa 'Lianhe'

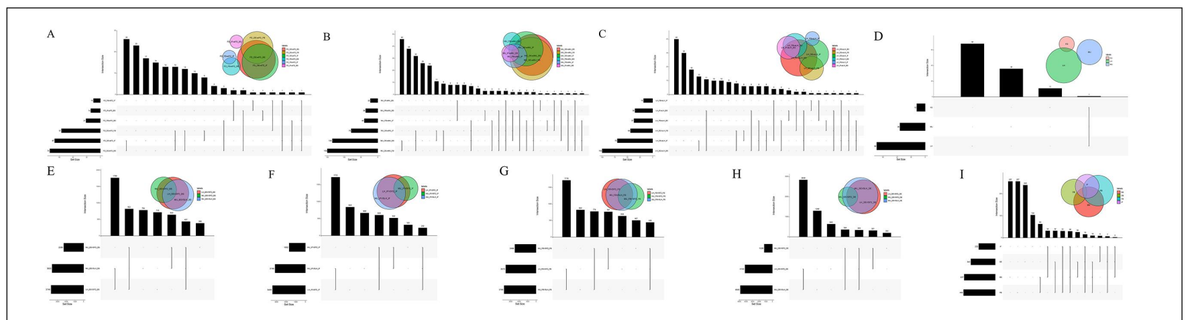

Figure 3. The distribution of DEGs across flower developmental stages and cultivars in Paeonia ostii 'Fengdan', mutant of Paeonia ostii 'Fengdan', and Paeonia suffruticosa 'Lianhe'.

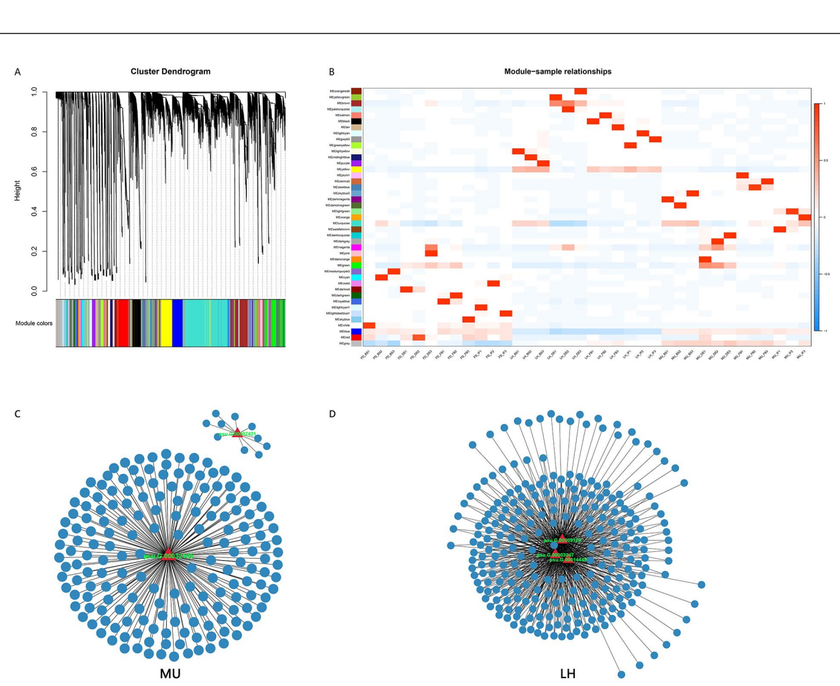

Figure 5 WGCNA analysis of differentially expressed genes regulating floral florescence, development and senescence

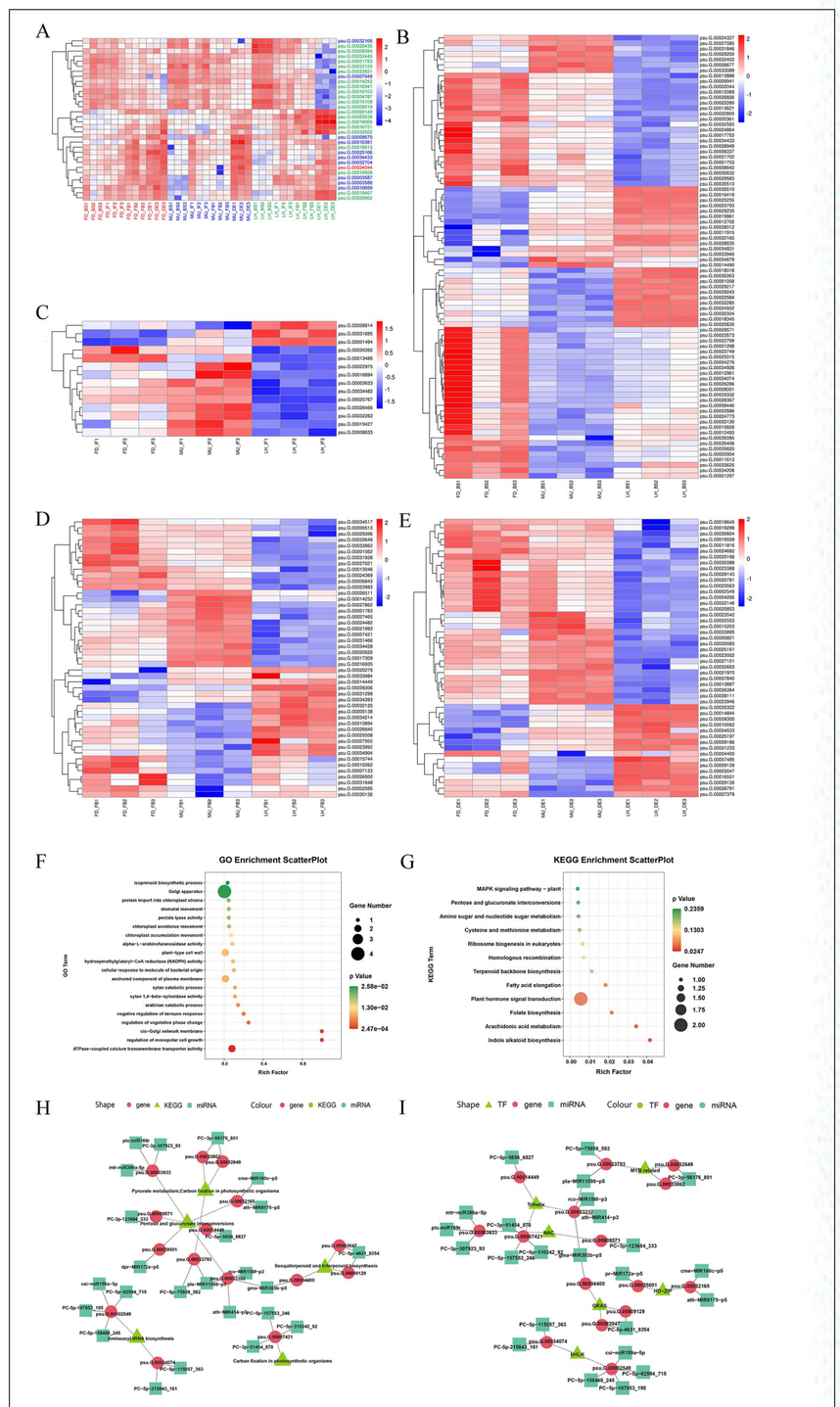

Figure 4 Integrated analysis of miRNA targets specific to flower developmental stages and cultivars by miRNAome, transcriptome and degradome in tree peony

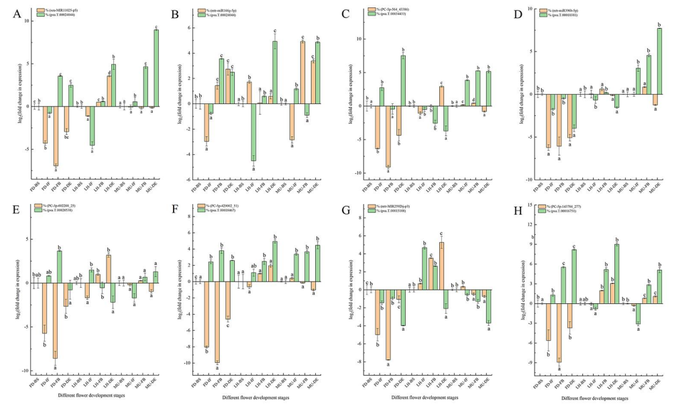

Figure 6 RT-qPCR analysis of miRNA-mRNA pairs