Genome-wide analysis reveals the potential role of MYB transcription factors in floral scent formation in *Hedychium coronarium*

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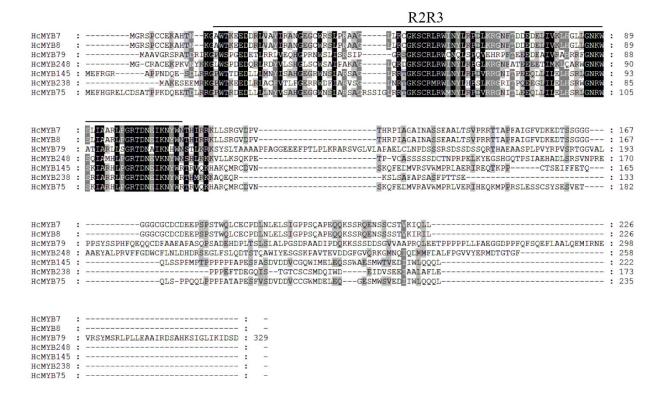
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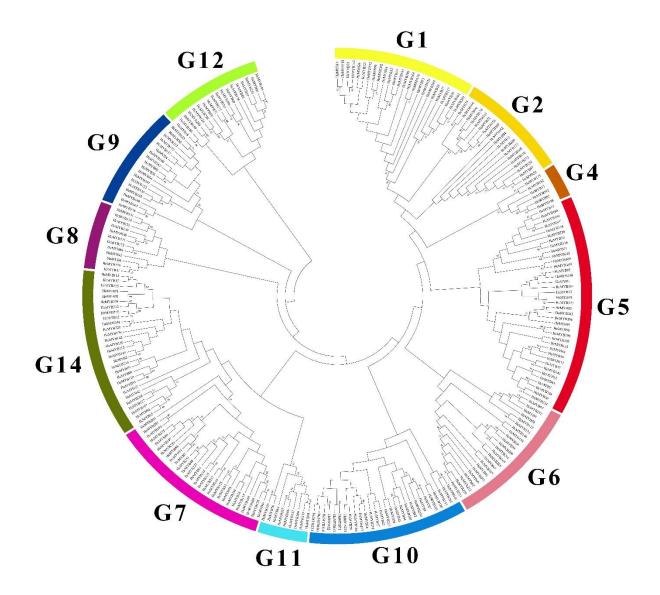
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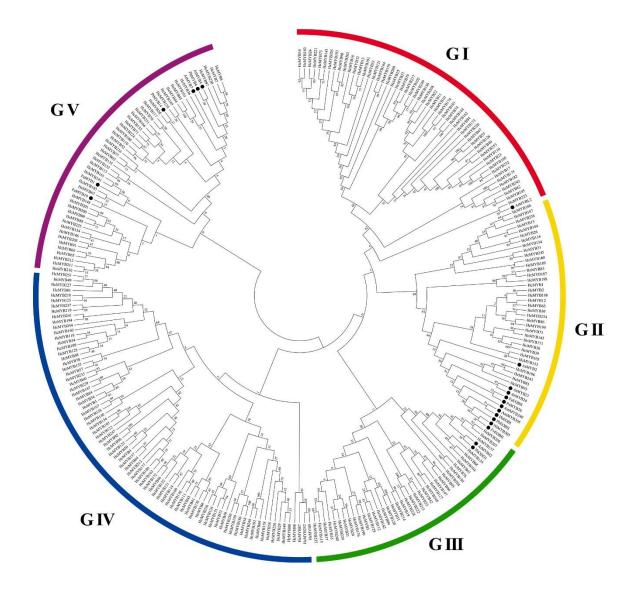
Supplementary data



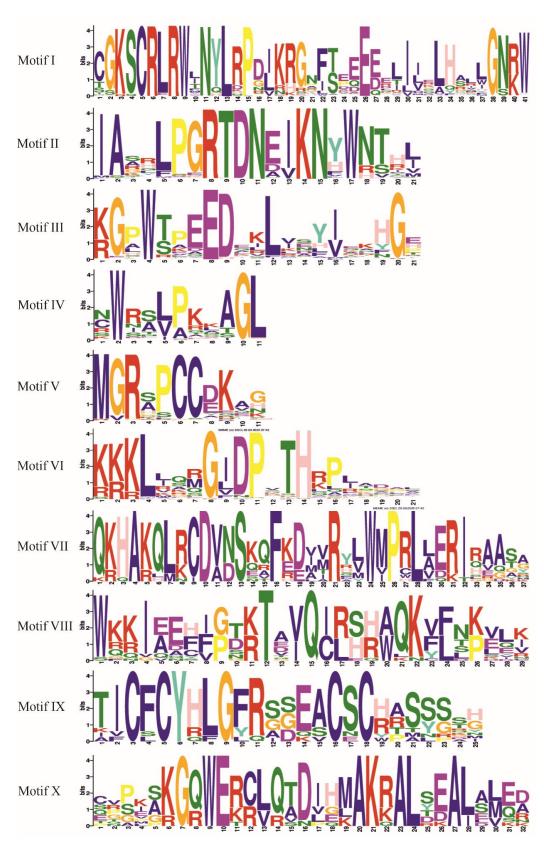
Supplementary Figure 1: Multiple sequences alignment of candidate *HcMYB* genes.



Supplementary Figure 2: Phylogenetic analysis of 253 HcMYB proteins.



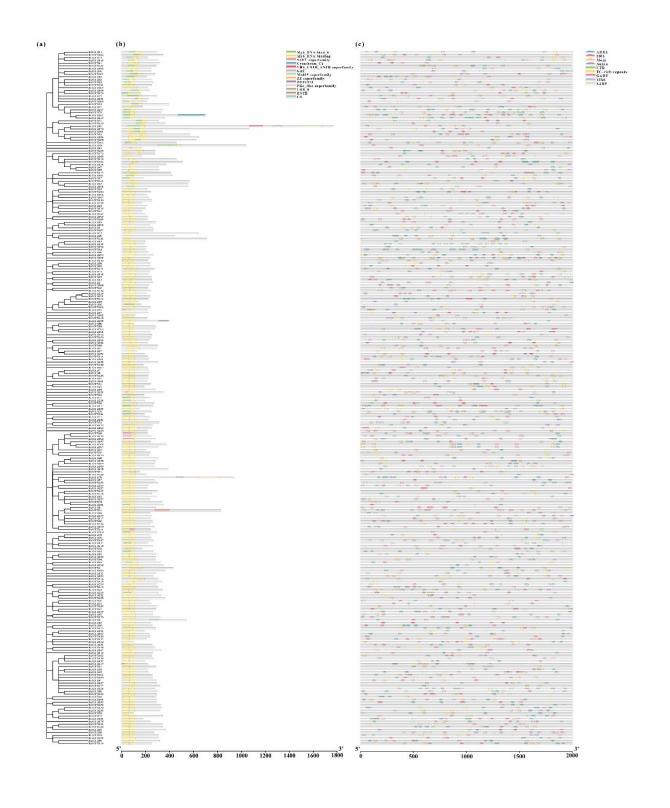
Supplementary Figure 3: Phylogenetic analysis of 253 HcMYB proteins with previously known scent-related MYBs.



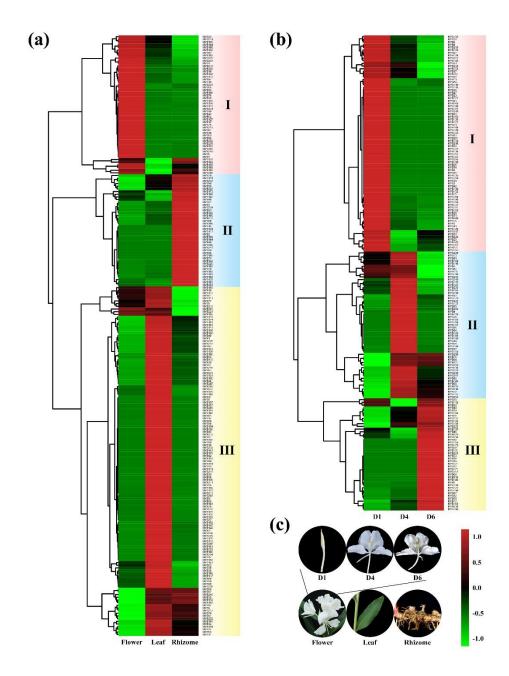
Supplementary Figure 4: The schematic representation of the individual motifs.



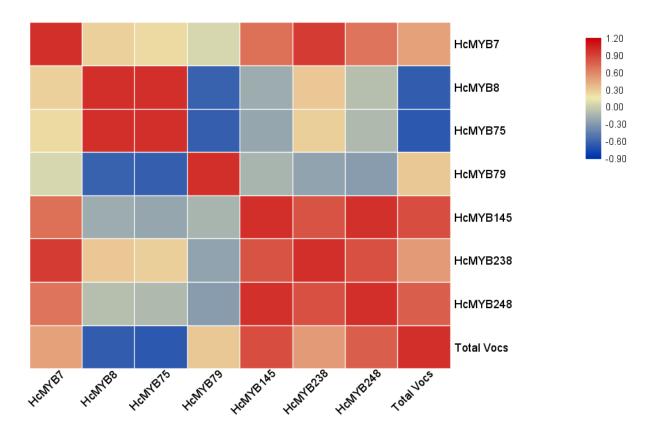
Supplementary Figure 5: Phylogenetic relationships, gene structure, and motif composition of HcMYBs



Supplementary Figure 6: Phylogenetic relationships (a), domain analysis (b), and (c) *cis*-regulatory elements in the promoters of 253 *HcMYB* genes.



Supplementary Figure 7: Tissue-specific expression profiles of *HcMYB* genes.



Supplementary Figure 8: The correlation analysis between the candidate *HcMYB* gene expression and total volatile compounds.

Supplementary Tables

Supplementary Table 1: Detailed characteristics of *HcMYB* genes in *H. coronarium*.

Supplementary Table 2: Primers used in the experiments.

Supplementary Table 3: The Ka/Ks ratios and estimated divergence time for segmentally and tandemly duplicated *HcMYB* genes.

Supplementary Table 4: The Ka/Ks ratios and estimated divergence time for orthologous HcMYB proteins between *H. coronarium* and *Arabidopsis thaliana*.

Supplementary Table 5: The Ka/Ks ratios and estimated divergence time for orthologous HcMYB proteins between *H. coronarium* and *Oryza sativa*.

Supplementary Table 6: The Ka/Ks ratios and estimated divergence time for orthologous HcMYB proteins between *H. coronarium* and *Ananas comosus*.

Supplementary Table 7: The Ka/Ks ratios and estimated divergence time for orthologous HcMYB proteins between *H. coronarium* and *Musa acuminata*.

Supplementary Table 8: Numbers of known stress-related elements in the promoter regions of *HcMYB* genes

Supplementary Table 9: List of *HcMYB* genes targeted by miRNAs were identified using psRNATarget.

Supplementary Table 10: MYB-core motifs in the promoters of bottom structural volatile biosynthesis genes.

Supplementary Table 11: Amino acid sequences of 253 HcMYBs

Supplementary Table 12: Coding sequences of 253 *HcMYBs*