

The CaCA superfamily genes in *Saccharum*: comparative analysis and their functional implications in response to biotic and abiotic stress

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Fig. S1 General characteristic features of the CaCA superfamily proteins in *S. spontaneum*, R570, and *S. bicolor*. Red triangles filled with white represent outliers, black diamonds filled with white represent the average, and different colored dots filled with black represent specific values. The detailed information is shown in Supplemental Table S1 and Table S2.

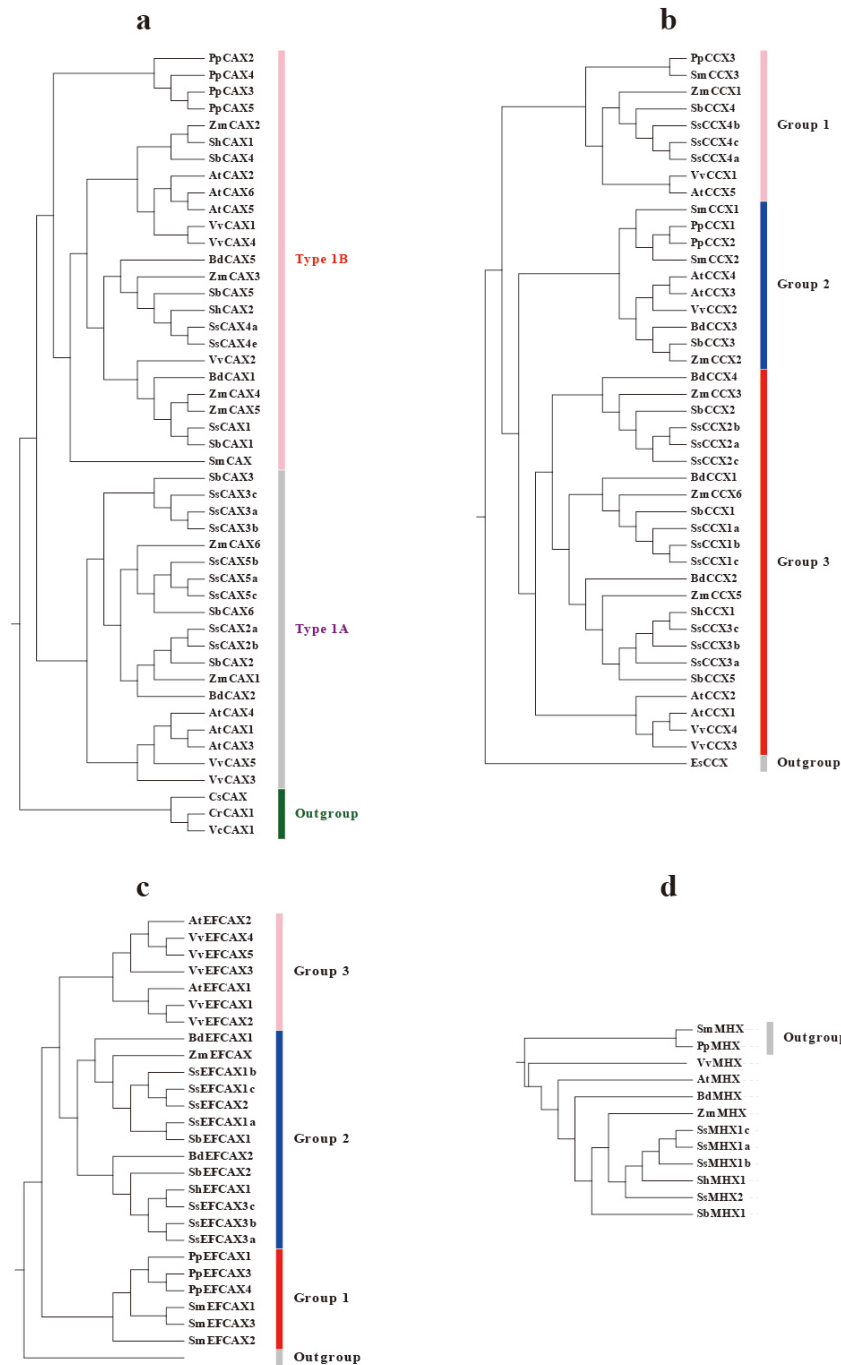


Fig. S2. Phylogenetic evolutionary tree of the CaCA superfamily members. (a) An ML phylogenetic tree was constructed using the full-length sequence alignments of 47 CAX proteins. (b) An ML phylogenetic tree was constructed using the full-length sequence alignments of 43 CCX proteins. (c) An ML phylogenetic tree was constructed using the full-length sequence alignments of 28 EFCAX proteins. (d) An ML phylogenetic tree was constructed using the full-length sequence alignments of 12 MHX proteins. All the corresponding reference numbers are listed in Supplemental Table S1 and Table S3.



Fig. S3 Phylogenetic relationship, architecture of conserved protein motifs, and structure of *CaCA* genes from *S. spontaneum*, R570, and *S. bicolor*. The phylogenetic tree was constructed based on the full-length sequences of CaCA proteins using MEGA X software. The motifs, numbers 1–10, are displayed in different colored boxes. The sequence information for each motif is provided in Supplemental Table S4. Green boxes indicate untranslated 5'- and 3'-regions, yellow boxes indicate exons, and black lines indicate introns. The length of the protein can be estimated using the scale at the bottom.

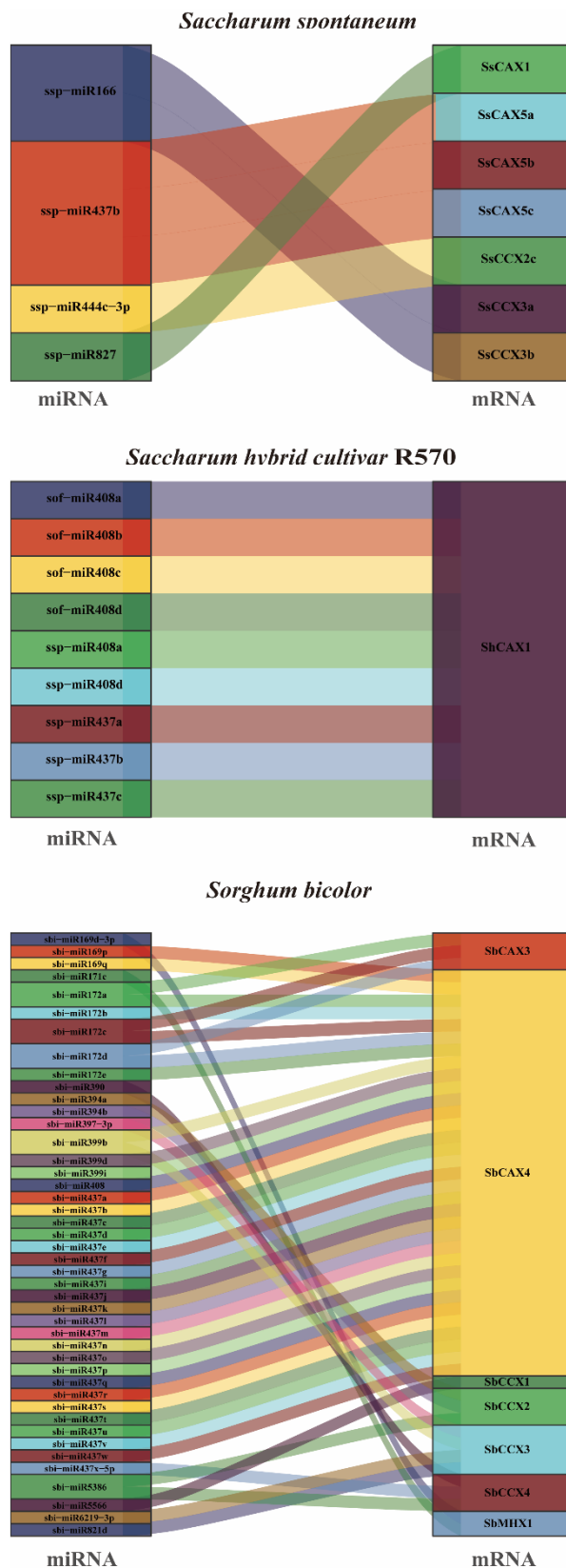


Fig. S4 Sankey diagram showing the miRNA–mRNA network. Each rectangle represents a gene, and the connection of each gene is visualized based on the size of the rectangle.

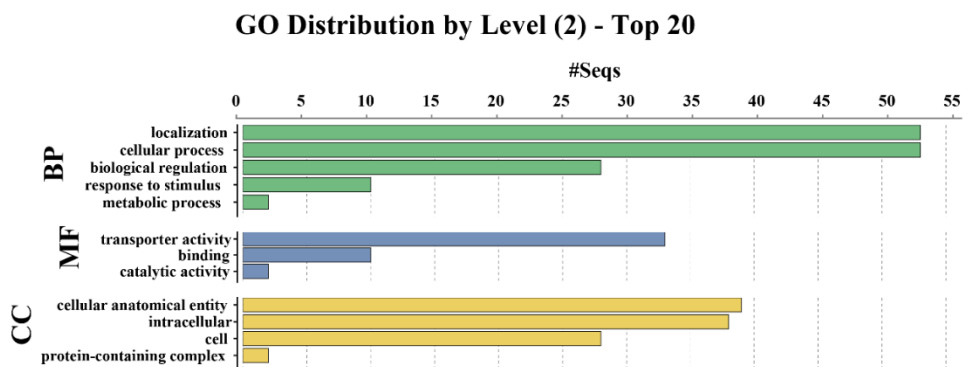


Fig. S5 Functional annotation of identified *CaCA* genes. The enrichment gene ontology analysis of *CaCAs* shows significantly enriched GO terms involved in biological processes (BP), molecular functions (MF), and cellular components (CC).

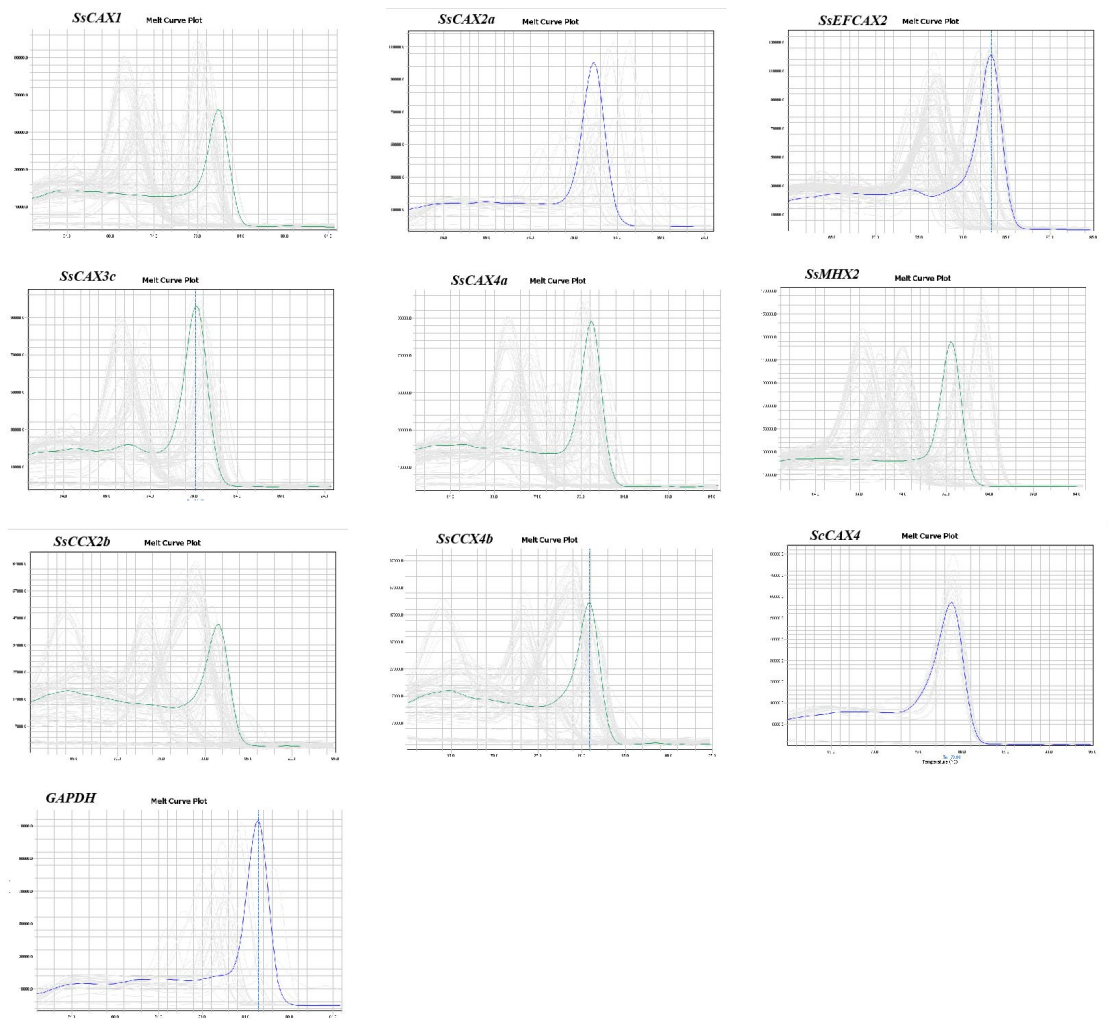


Fig. S6 The melt curve plots of primers in this study.