

An Investigation of the JAZ family and the CwMYC2-like to reveal their regulation roles in the MeJA-induced biosynthesis of β -elemene in *Curcuma wenyujin*

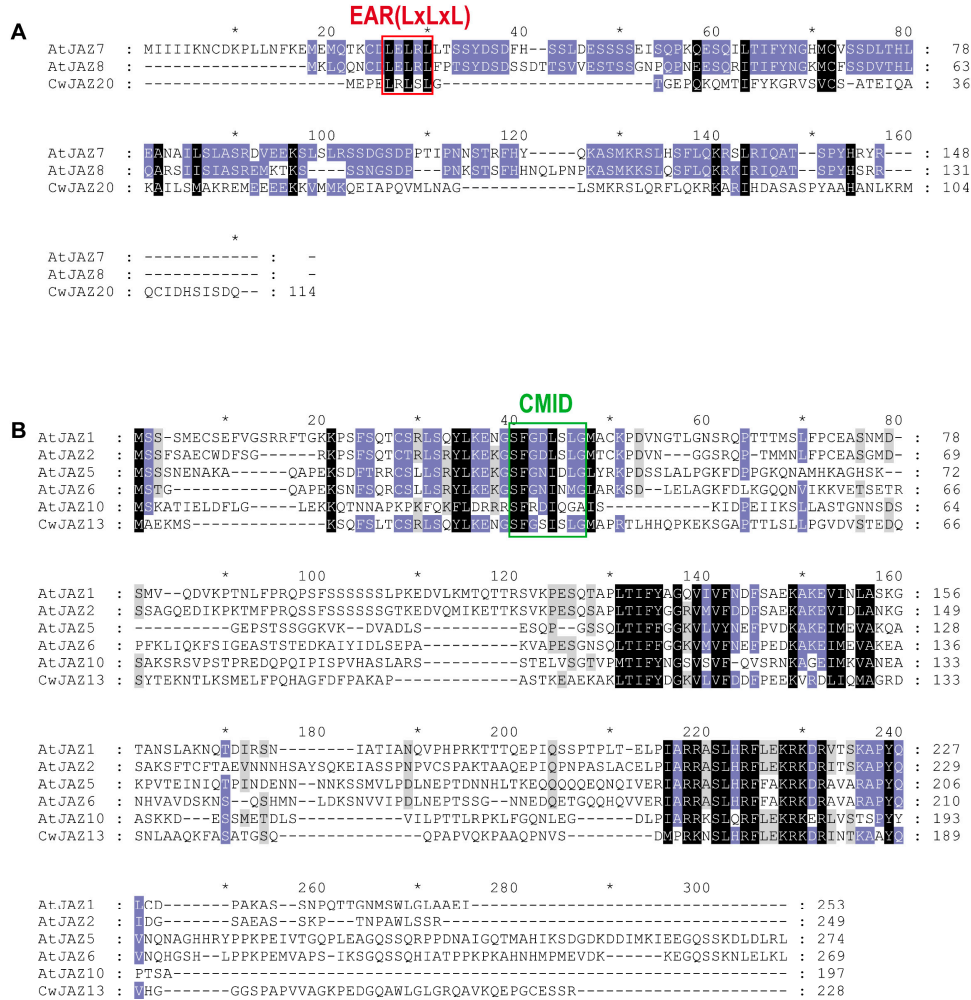


Fig.S1 Special motifs of CwJAZ13 and CwJAZ20.

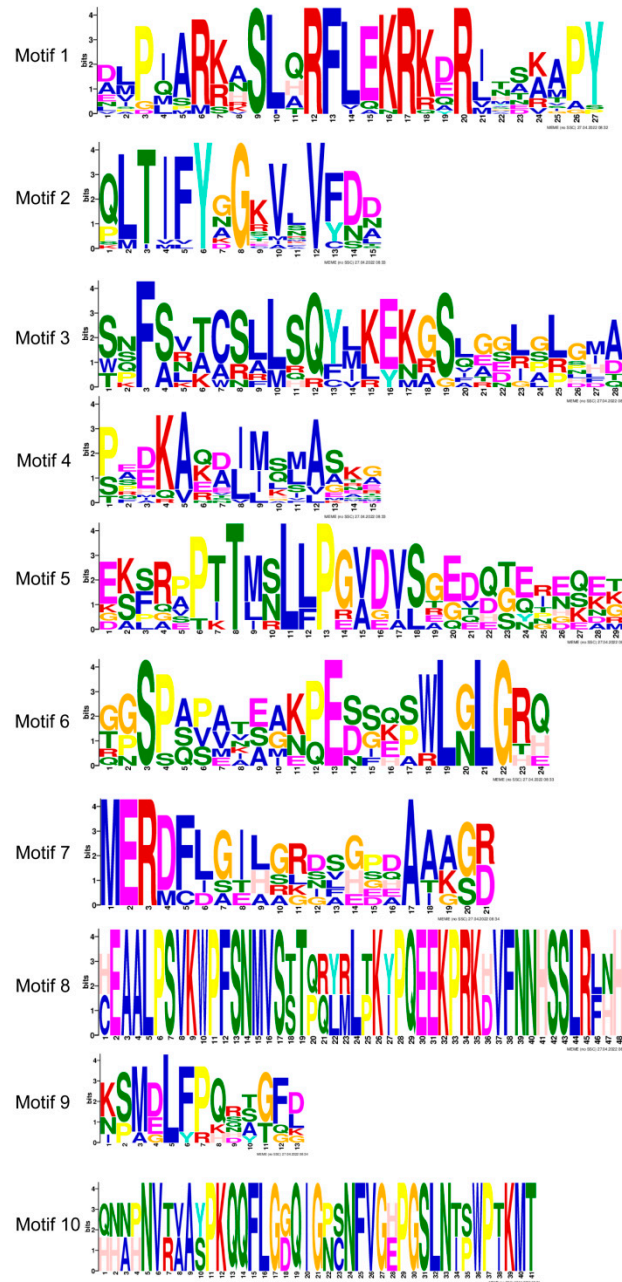


Fig.S2 Sequence logos of motifs 1-10 in JAZ proteins from *C. wenyujin*. Y axis indicates the content of the sequence and its conservation at the corresponding position. The picture was drawn with TB tools software.

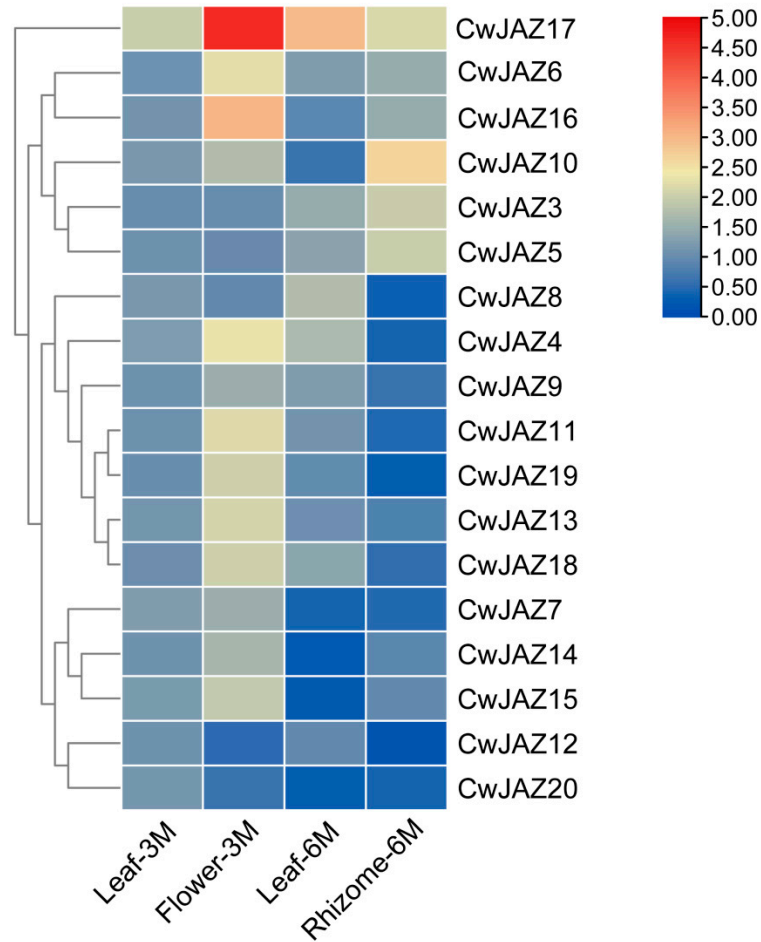


Fig.S3 Expression heatmaps of 20 *CwJAZ* genes in different organizations of *C. wenyujin*. The values were determined via qRT-PCR from three biological replicates. The “Leave-3M, Flower-3M, Leave-6M, Rhizome-6M” heatmaps below indicate leaves, flowers, and rhizomes obtained from 3-month-old and 6-month-old *C. wenyujin* plants, respectively. The expression of “Leave-3M” was considered as the control. All expression levels were calculated using the $2^{-\Delta\Delta C_t}$ method and displayed by the colored boxes. Blue and red represent the two extremes of high and low expression levels.

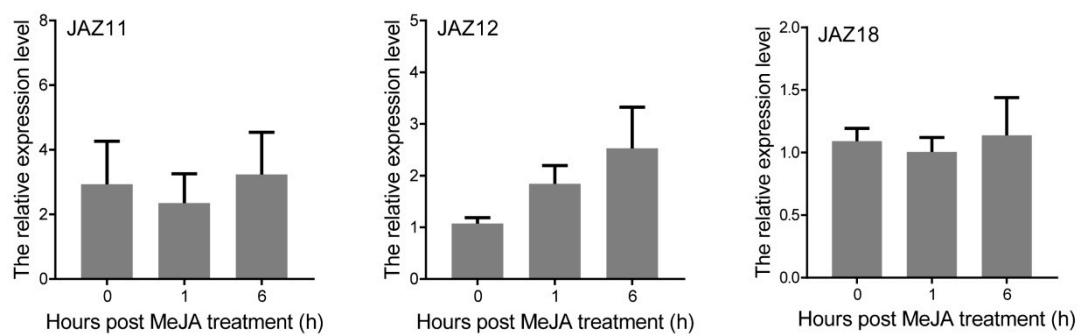


Fig.S4 Expression levels of *CwJAZ* genes under MeJA treatments. Three biological replicates were performed. Vertical bars refer to \pm SE (n = 3).

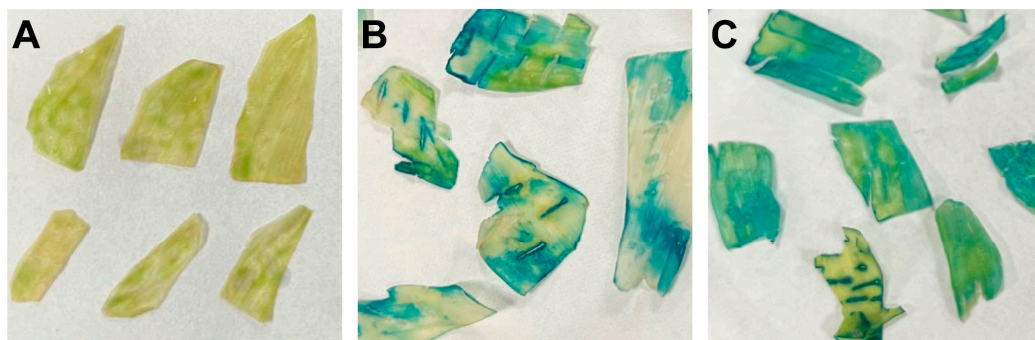


Fig.S5 Gus staining of *C. wenyujin* leaves. (A) Leaves infected with *A. tumefaciens* GV3101. (B) Leaves infected with GV3101 carrying pBI121-GUS empty plasmid. (C) Leaves infected with GV3101 carrying pBI121-CwMYC2-like-GUS recombinant plasmid.