

Table S1. Ka/Ks ratios of duplicated gene pairs of *CtJAZs*.

Sequence	Method	Ka	Ks	Ka_Ks	P-Value(Fisher)	Purifying Selection
CtZML1-CtZML2	YN	0.10	0.71	0.15	7.6626e-13	YES
CtJAZ4-CtJAZ5	YN	0.34	5.43	0.06	0.00000654	YES
CtJAZ4-CtJAZ7	YN	0.22	0.96	0.22	2.2644e-9	YES
CtJAZ5-CtJAZ7	YN	0.28	1.29	0.21	0.00003904	YES
CtJAZ6-CtJAZ8	YN	0.69	NaN	NaN	0.00169648	YES
CtJAZ8-CtJAZ9	YN	0.67	NaN	NaN	0.00053656	YES

Table S2. The primers used for qRT-PCR in this study.

Gene	Gene ID	Forwaed primer (5'-3')	Reverse primer (5'-3')	Length (bp)
CtJAZ1	CtAH01T0194	CAAGAAACACCCAGTGA	TGACGTCACAAATGCTA	109
	500.1	ATT	ACT	
CtJAZ2	CtAH01T0194	CAACAGCTAACGATTTTC	CCAGTTGGAGATGGTGA	167
	600.1	TATG	AGA	
CtJAZ3	CtAH02T0076	GCTTCTCAAGACCGCGAT	ACGTCGAAAACCGAGAC	207
	300.1	TGC	GCTT	
CtJAZ4	CtAH02T0137	CAATTTCTGCAACTTCAC	CAGTTGTAGACGGAAGA	207
	500.1	CAC	TTC	
CtJAZ5	CtAH04T0233	CAACAATCGTCACTCGAC	CTTGGCTAGAAAGGGTC	233
	400.1	TGA	TTG	
CtJAZ6	CtAH05T0002	AAGCAGATGATCTCCCTT	GCCTTGTCGGCTGGAAA	178
	300.1	TG	ATC	
CtJAZ7	CtAH07T0038	TGCAGTCCACTGGCCTCT	ATGGCTCGGTGGTTCCA	278
	000.1	GC	GCA	
CtJAZ8	CtAH09T0006	AATGCCAAATTTGATGCT	GTTGTGAGGCCTTTTGGC	118
	500.1	CCA	CTG	
CtJAZ9	CtAH12T0192	CAACGGCCACCATGAACC	CTTCATGATCTCCTTCAC	158
	200.1	TCTT	CTT	
CtTIFY1	CtAH06T0013	TGGCCAAAGAAACGATTT	CACCATCTCTTGATGAA	104
	400.1	TTC	CCCA	
CtTIFY2	CtAH11T0211	TGAAGGGGTGCCATTCTT	TGGTCGCAACTGGGGGA	133
	300.1	TGG	TACC	
CtZIM	CtAH10T0176	GTGCAAAAGGTGTTTTTA	TGGGATCTCATCTTGTGC	78
	300.1	CAT	TGC	
CtZML1	CtAH03T0096	GAGTTCGGTGAGATTCCG	GCGGCATTATGGCGAGG	199
	700.1	TCG	T	
CtZML2	CtAH05T0082	GAAGAGTCCATAGACAA	GTCCGGTACTGCATACA	156
	800.1	CCCT	AAGC	
Ct60s		CATCCATTATCCAACAAT	AAGAGTAATCAGTCTCC	
		C	A	

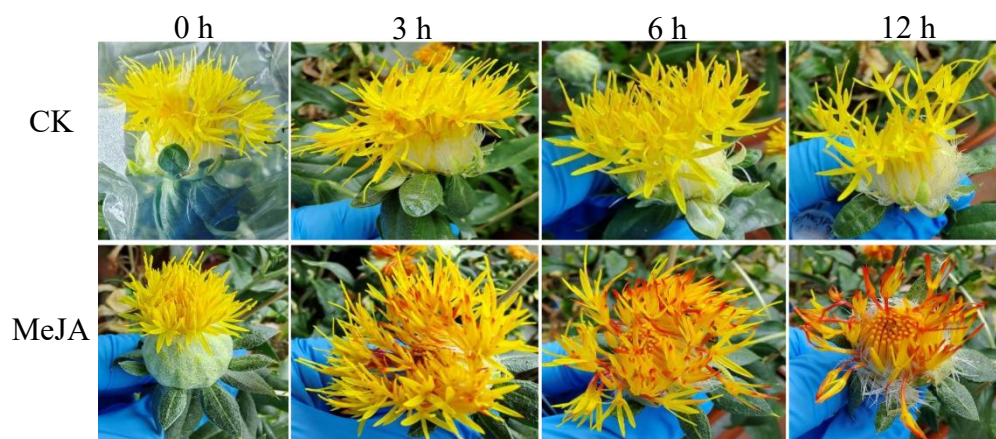


Figure S1. Phenotypic changes of safflower corollas under MeJA and 0.1% ethanol control at 0, 3, 6 and 12 h.