

Figure S1. Phylogenetic analysis of blue light receptor proteins of *Medicago* and *Arabidopsis*. A phylogenetic tree was generated using the maximum likelihood method. FKF1 showed greater similarity to ZTL and LKP2 compared to the other four blue-light receptors (CRY1, CRY2, PHOT1, and PHOT2).

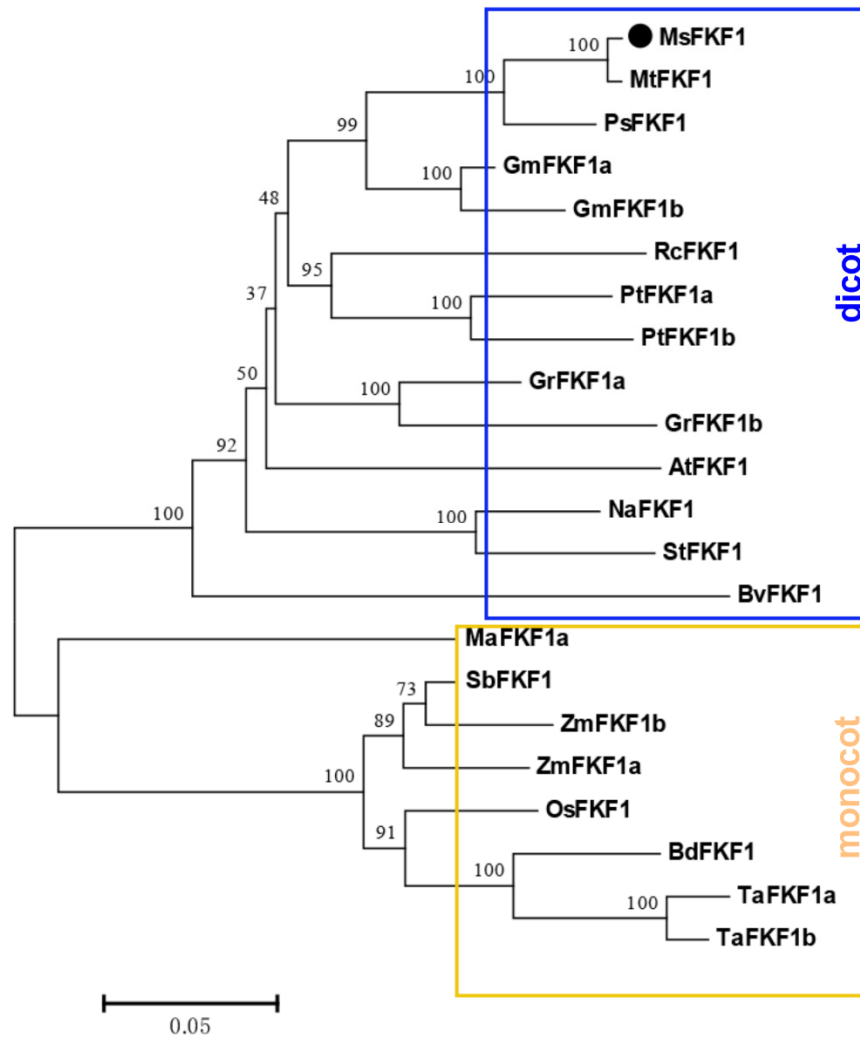


Figure S2. Phylogenetic analysis of MsFKF1 and its orthologs.

The phylogenetic tree was generated through the utilization of the neighbor-joining method, following sequence alignment conducted with the Clustal W program. The branch numbers present on the tree represent the percentage of replicates that provide support for each specific branch, as determined by implementing the bootstrap method with 1000 replicates. The scale bar depicted on the tree corresponds to a measurement of 0.05 amino acid substitutions per residue. The accession numbers of the proteins employed in constructing the phylogenetic tree can be found in Table S1.

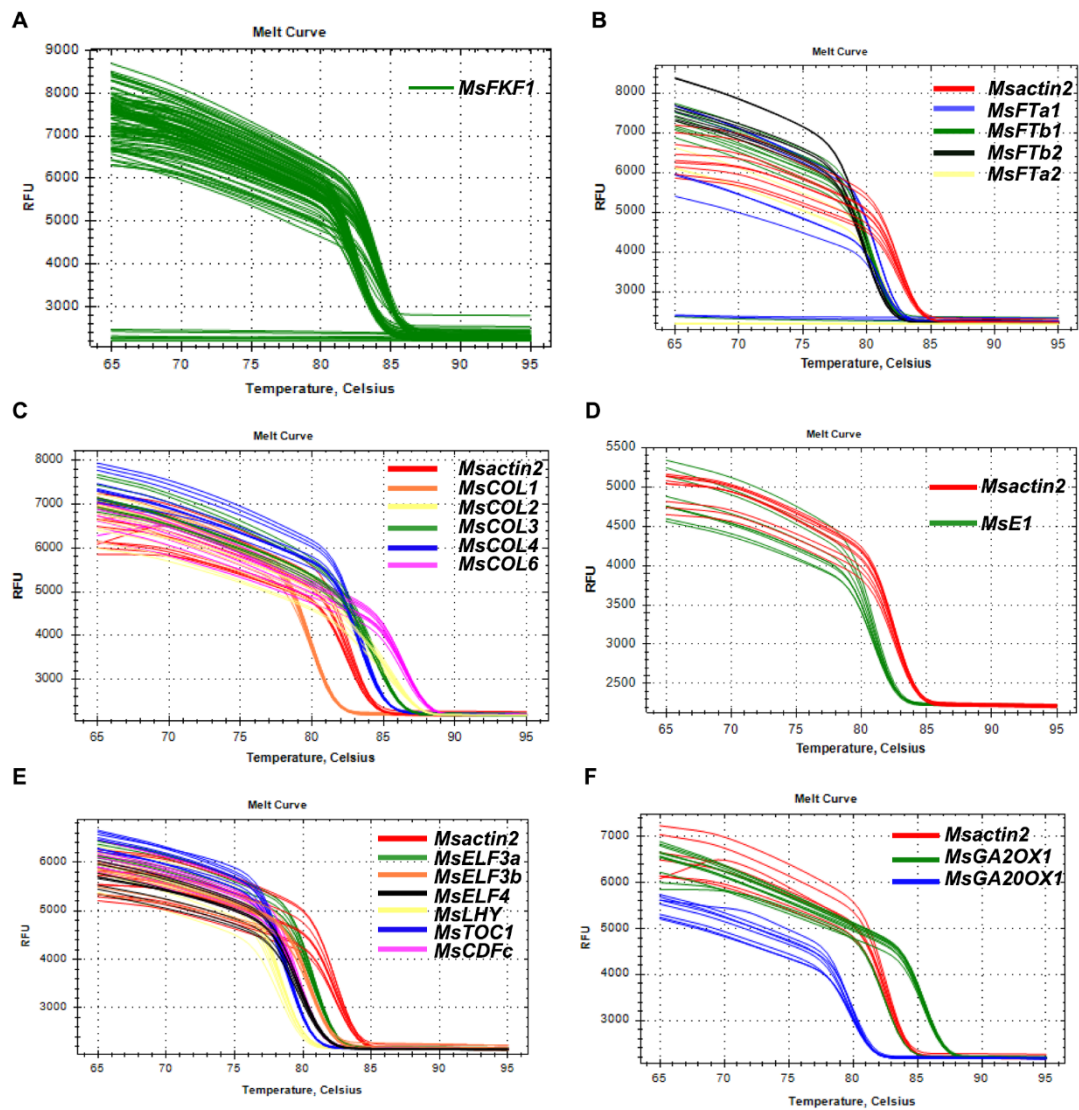


Figure S3. The melting curve diagram of RT-qPCR primers used in this study.

(A) The melting curve diagram of the MsFKF1 primer is used to analyze the effect of photoperiod on the expression level of MsFKF1. (B) The melting curve diagram of the RT-qPCR for alfalfa *flower locus T* gene primers. (C-E) The melting curve diagram of the RT-qPCR for Flowering time related genes primers. (F) the melting curve diagram of the RT-qPCR for GA biosynthesis related genes primers.

Table S1. Sequence homology of FKF1 proteins in the indicated species.

Gene	Homology matrix
MsFKF1	100%
MtFKF1	99.3% 100%
GmFKF1a	90.4% 90.2% 100%
AtFKF1	81.5% 81.5% 82.8% 100%
ZmAGO3	72.9% 72.7% 73.2% 71.2% 100%

Table S2. Comparison of the exon/intron composition of FKF1 in the indicated species.

Species	Gene symbol	Accession numbers	CDS (bp)	amino acid (a.a.)	extron 1 length (bp)	intron length (bp)	extron 2 length (bp)
<i>Medicago sativa</i>	MsFKF1	Msa0930760	1911	636	384	677	1942
<i>Medicago truncatula</i>	MtFKF1	MTR_8g105590	2328	635	384	677	1942
<i>Pisum sativum</i>	PsFKF1	Psat7g007600	2453	610	447	359	2004
<i>Glycine max</i>	GmFKF1a	Glyma05g239400	2400	620	517	992	1883
	GmFKF1b	Glyma08g046500	2252	647	377	1040	1875
<i>Rosa chinensis</i>	RcFKF1	RchiOBHm_Ch4g0442801	2354	631	464	822	1888
<i>Nicotiana attenuata</i>	NaFKF1	A4A49_16690	2307	634	326	4548	1981
<i>Gossypium raimondii</i>	GrFKF1a	B456_002G166800	2392	629	416	1892	1974
	GrFKF1b	B456_008G168500	2301	627	376	704	1923
<i>Arabidopsis thaliana</i>	AtFKF1	At1g68050.1	2168	619	369	100	1797
<i>Beta vulgaris</i>	BvFKF1	BVRB_6g154770	2322	633	490	5653	1832
<i>Populus trichocarpa</i>	PtFKF1a	Potri.010G105700.v4.1	2442	627	300	411	3240
	PtFKF1b	Potri.008G135200.v4.1	2532	637	454	1147	2076
<i>Solanum tuberosum</i>	StFKF1	PGSC0003DMT400051416	2239	634	343	2358	1896
<i>Sorghum bicolor</i>	SbFKF1	SORBI_3005G145300	2111	594	197	1785	1914
	ZmFKF1a	GRMZM2G107945	2582	629	494	8694	2086
<i>Zea mays</i>	ZmFKF1b	GRMZM2G106363	2367	618	422	743	1945
	TaFKF1a	TraesCS4A02G164000	2320	626	437	862	1883
<i>Triticum aestivum</i>	TaFKF1b	TraesCS4B02G157500	2191	620	300	843	1891
<i>Brachypodium distachyon</i>	BdFKF1	KQJ88263	2330	621	423	1529	1907
<i>Oryza sativa</i>	OsFKF1	Os11g34460	2190	630	397	2651	1791
<i>Musa acuminata</i>	MaFKF1a	Ma07_g10990	2358	616	519	1609	1839

Table S3. Cis-element of the MsFKF1 promoter.

Name	Cis element	Number	Description
circadian	CAAAGATATC	1	circadian control
GT1-motif	GGTTAA	2	light responsiveness
G-box	CACGA/TC	3	light responsiveness
TCT-motif	TCTTAC	1	light responsiveness
ATCT-motif	AATCTAATCC	2	light responsiveness
Box 4	ATTAAT	1	light responsiveness
GATA-motif	GATAGGA	1	light responsiveness
ABRE	ACGTG	2	abscisic acid responsiveness
CGTCA-motif	CGTCA	3	MeJA-responsiveness
TGACG-motif	TGACG	3	MeJA-responsiveness
CAT-box	GCCACT	2	related to meristem expression

Note: The *MsFKF1* promoter sequence was extracted from 2000 bp upstream of the start codon (ATG) in the assembled genome of *Zhongmu*

No. 4.

Table S4. Primers used in this study.

Name	Popups	Forward (5' → 3')	Reverse (5' → 3')
MsFKF1	clone	GAAAATTATTGTACTCCACGG	CGGTTCAAGTTGATTTTCATAAGT
Homo-FKF1	Overexpression and GFP	CTCTAGAGTTAACCGGGCTCAG ATGTGTGGCATTCTCAGCT	CCTCAGAAATCAACTTTTGCTC CATGTCAGAGTCTTGTCG
BD-FKF1	Assemble clone to PGBKT7	atatggccatggaggccgaattcATGTGTGG CATTCTTCAGCT	aggtcgacggatccccgggaattTCACATG TCAGAGTCTT
qMsFKF1	qPCR	CAGGTCTTCATTACCGTCTC	ACTCATTCAAGCACCCATTCC
qMsFTa1	qPCR	TCAGAAACCTCAACACCCTAGTT A	CCTGGAATATCAGTCACCAACC AG
qMsFTa2	qPCR	ACCCAACAACCTTCTACACCCTG	AATCCCTAAATTGGGTCTGGCT
qMsFTb1	qPCR	GACTACAGGGACAACCTTCGGAG	GCCATCCAGGAGCTAATATAGTG A
qMsFTb2	qPCR	GGGGACAACGTTCCGGAC	CGCCATCCTGGAGCTAATATATT G
qMsE1	qPCR	TCTTGTGATGAAGCCTCTAC	TATCCCTTGTTGTCGTGT
qMsCOL1	qPCR	CTTGGGTTGGAGTTTGAGTC	TGTTCTTTTGGAGGTCTTG
qMsCOL2	qPCR	TCTCCAAACTCCTTCAAACC	TACAACTCCAACCTCCATCG
qMsCOL3	qPCR	GAATCCAACACTTCTCACTCTG	TCCTCTTCTCCCTATACCTCA
qMsCOL4	qPCR	GGTGTGAATAGTAACCAAGGGAT	CATAGATGAAGGAAGTGGGAGA
qMsCOL6	qPCR	TTCCCGTGTGACTATTGCG	AAAGATGAAGAGGTGGGGTT
qMsELF4	qPCR	AGTTTCAGGCAGGTTCACTCG	CTTCACCATATTATCAGGCATTCT
<i>qMsELF3a</i>	qPCR	AAAGGGATCTAAACAATCTGCG	TTGGCTTGCTTACTGAGGTGTC
<i>qMsELF3b</i>	qPCR	CCAGCGAGGCAAGCTAAGAA	CCATTGTAGTGTAAGGAGGC
<i>qMsLHY</i>	qPCR	GAGGAGCATAAAGATGAGGAAA G	CCGAAGATACAGATGAACAAGG
<i>qMsTOC1</i>	qPCR	AGCAAGAGTGGTGATGGATTCA	TGCCGTGCGGATTTTACAGA
qMsCDFc	qPCR	CTTCATCTCCCTCTTCTTCTCCA	AGGCTCCATCGTCTTGTGCT
qMsGA20ox1	qPCR	GAATGAGCCTTGGAGTTGG	TGGAATGCCATTGATCGTC
qMsGA20ox1	qPCR	TCCCTGCTTTTGGTAAAGAT	GGACAAGGGGGATAATGGTTG