**Supporting information**

**Soybean Calmodulin-binding Transcription Activators, GmCAMTAs, Negatively Coordinate the Circadian Regulation of Developmental Processes and Drought Stress Responses in Transgenic *Arabidopsis***

Dongwon Baek2,†, Hyun Min Cho1,†, Ye Jin Cha1,†, Byung Jun Jin3, Su Hyeon Lee1, Mi Suk Park2, Hyun Jin Chun3,\*, Min Chul Kim 1,2,3,\*

1 Division of Applied Life Science (BK21 Four), Gyeongsang National University, Jinju 52828, Republic of Korea; hmcho86@gnu.ac.kr (H.M.C.), cdw3280@naver.com (Y.J.C.), leesuhyeon86@gmail.com (S.H.L.)

2 Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 52828, Republic of Korea; dw100@hanmail.net (D.B.), misugip@hanmail.net (M.S.P.)

3 Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Republic of Korea; hj\_chun@hanmail.net (H.J.C.), scv5789@naver.com (B.J.J.)

† These authors contributed equally to this work

\* Correspondence: hj\_chun@hanmail.net (H.J.C.), Tel.: +82-55-772-1874 and [mckim@gnu.ac.kr](mailto:mckim@gnu.ac.kr) (M.C.K.), Tel.: +82-55-772-1874

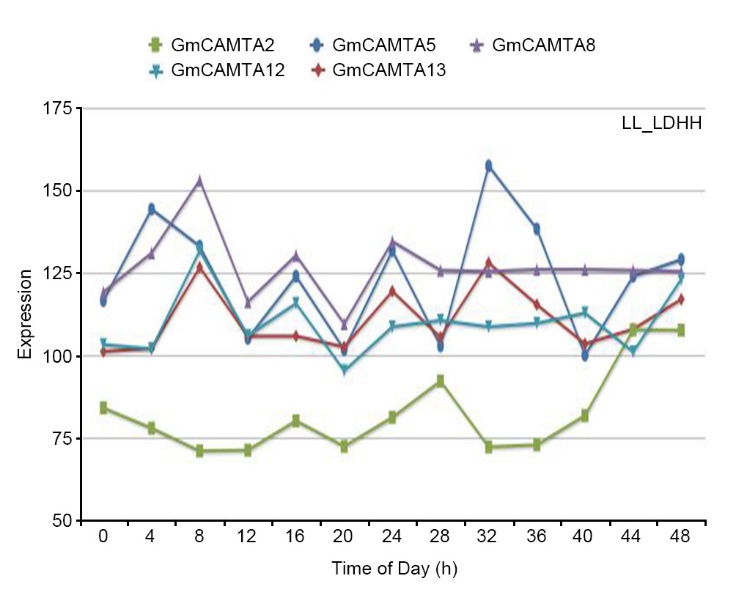
**Supplementary Materials:**

**Supplementary Figure S1.** Diurnal expression of *GmCAMTA*s in the Diurnal web database.

**Supplementary Figure S2.** RT-PCR analysis in *Arabidopsis* transgenic plants overexpressing *GmCAMTA2* and *GmCAMTA8*.

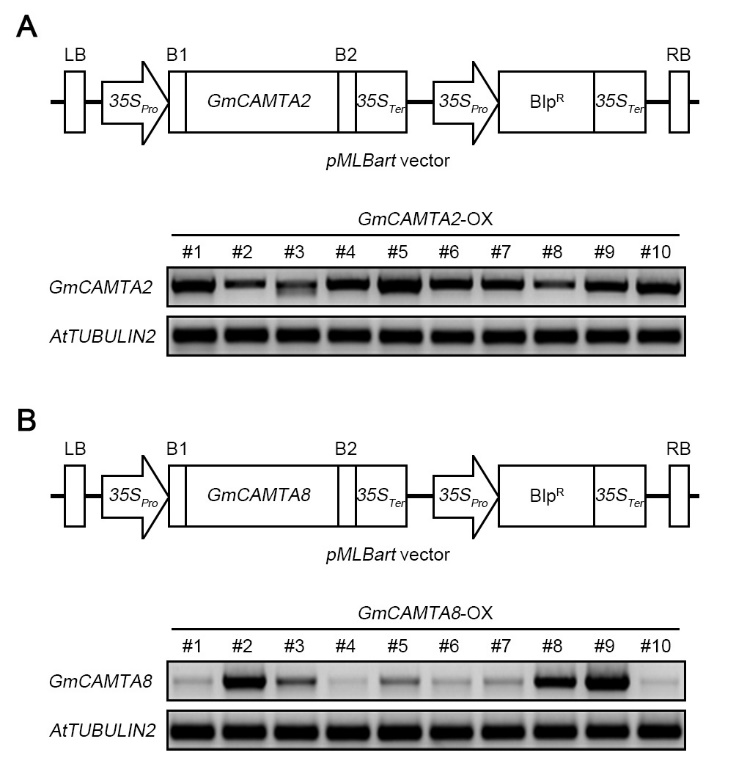
**Supplementary Table S1.** List of 15 *GmCAMTA* genes in Phytozome database

**Supplementary Table S2.** List of primers in this study



**Supplementary Figure S1.** Diurnal expression of *GmCAMTA*s in the Diurnal web database.

The diurnal expression of *GmCAMTA2*, *GmCAMTA5*, *GmCAMTA8*, *GmCAMTA12*, and *GmCAMTA13* under LL\_LDHH condition using Diurnal database tool (http://diurnal.mocklerlab.org/). The diurnal expression data of other *GmCAMTAs* were not available in the Diurnal web database. The “LL\_LDHH” means a constant light for 24 h (LL), light 12h/dark 12h conditions (LD), and a constant hot temperature (31 °C; HH).



**Supplementary Figure S2.** RT-PCR analysis in *Arabidopsis* transgenic plants overexpressing *GmCAMTA2* and *GmCAMTA8*.

Upper panels in (A) and (B); Schematic representation of the *pMLBart* binary vectors used for generating *Arabidopsis* transgenic plants overexpressing *GmCAMTA2* (A) and *GmCAMTA8* (B). Bottom panels in (A) and (B); Analysis of RT-PCR. Total RNAs isolated from each 10-day-old seedlings of *Arabidopsis* T1 transgenic plants overexpressing *GmCAMTA2* (A) and *GmCAMTA8* (B). The analysis of RT-PCR was performed with each *GmCAMTAs*-specific primer (Supplementary Table S2). The *AtTUBULIN2* in *Arabidopsis* was used as an internal control.

**Supplementary Table S1.** List of 15 *GmCAMTA* genes in Phytozome database

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene Name | Locus No. | Chromosome No. | Genome Length (bp) | Transcript Length (bp) | CDS Length (bp) | Protein Length (aa) |
| *GmCAMTA1* | *Glyma.05G178200* | 5 | 8,069 | 3,889 | 3,369 | 1,123 |
| *GmCAMTA2* | *Glyma.08G135200* | 8 | 8,007 | 3,872 | 3,309 | 1,103 |
| *GmCAMTA3* | *Glyma.15G053600* | 15 | 11,253 | 3,830 | 3,267 | 1,089 |
| *GmCAMTA4* | *Glyma.08G072100* | 8 | 11,294 | 3,813 | 3,240 | 1,080 |
| *GmCAMTA5* | *Glyma.05G117000* | 5 | 10,456 | 3,791 | 3,267 | 1,089 |
| *GmCAMTA6* | *Glyma.08G178900* | 8 | 11,604 | 3,947 | 3,246 | 1,082 |
| *GmCAMTA7* | *Glyma.17G038800* | 17 | 8,414 | 3,665 | 3,000 | 1,000 |
| *GmCAMTA8* | *Glyma.15G143400* | 15 | 9,976 | 3,274 | 2,736 | 912 |
| *GmCAMTA9* | *Glyma.09G038300* | 9 | 10,333 | 3,378 | 2,736 | 912 |
| *GmCAMTA10* | *Glyma.05G148300* | 5 | 10,592 | 3,637 | 2,952 | 984 |
| *GmCAMTA11* | *Glyma.18G005100* | 18 | 9,037 | 3,570 | 2,889 | 963 |
| *GmCAMTA12* | *Glyma.17G031900* | 17 | 8,109 | 3,606 | 2,769 | 923 |
| *GmCAMTA13* | *Glyma.07G242000* | 7 | 8,858 | 3,425 | 2,766 | 922 |
| *GmCAMTA14* | *Glyma.11G251900* | 11 | 8,300 | 3,196 | 2,733 | 911 |
| *GmCAMTA15* | *Glyma.08G105200* | 8 | 8,020 | 3,220 | 2,898 | 966 |

**Supplementary Table S2.** List of primers in this study

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Primer | Direction | Sequence (5’→3’) | Purpose |
| *GmCAMTA1*  (*Glyma.05G178200*) | MG-2943 | Forward | GAAAAGGTAGTGGTTTGCGTG | Analysis of qRT-PCR or RT-PCR |
| MG-2944 | Reverse | CTTTGCTCTGTTTGCTTCCTG |
| *GmCAMTA2*  (*Glyma.08G135200*) | MG-2931 | Forward | AAGGCTGGAAGTGTGGATG |
| MG-2932 | Reverse | TTGGTTCCCTTCACTTGTCG |
| *GmCAMTA3*  (*Glyma.15G053600*) | MG-2957 | Forward | AGGGACGGAAACAAAAGGAAG |
| MG-2958 | Reverse | ACCCTTGTTAGATGCCTTGG |
| *GmCAMTA4*  (*Glyma.08G072100*) | MG-2947 | Forward | GTTCAGTATCCAGAGGCACG |
| MG-2948 | Reverse | TCCCTTGGTTTGACGGAAG |
| *GmCAMTA5*  (*Glyma.05G117000*) | MG-2963 | Forward | GTTCAGTATCCAGAGGCACG |
| MG-2964 | Reverse | CACCATCAACTGTCTCTTCCG |
| *GmCAMTA6*  (*Glyma.08G178900*) | MG-2951 | Forward | AGGGACGGAAACAAAAGGAAG |
| MG-2952 | Reverse | AACCCTCGTTAGATGCCTTG |
| *GmCAMTA7*  (*Glyma.17G038800*) | MG-2959 | Forward | CAGATCCACCTGTTATGCCTC |
| MG-2960 | Reverse | GCTTCTCTTACAGTCTTCCCATC |
| *GmCAMTA8*  (*Glyma.15G143400*) | MG-2933 | Forward | CTGCGTTGGCGTTTAAAGAG |
| MG-2934 | Reverse | AATCACTTTCCTGCGTCTCC |
| *GmCAMTA9*  (*Glyma.09G038300*) | MG-2953 | Forward | GTAGTCCTTTATCTTCGGGTGG |
| MG-2954 | Reverse | GTTCATCCATGTTCCAAAGCTG |
| *GmCAMTA10*  (*Glyma.05G148300*) | MG-2941 | Forward | TGACATCAATGGGTGGACTG |
| MG-2942 | Reverse | GGTTGGATCTTGTGCATTTGG |
| *GmCAMTA11*  (*Glyma.18G005100*) | MG-2961 | Forward | TGGGCAGTTGGAATCTTGG |
| MG-2962 | Reverse | CGGAACACGCTGAGAAAATC |
| *GmCAMTA12*  (*Glyma.17G031900*) | MG-2935 | Forward | CTCGCATACAGTGTACATACCG |
| MG-2936 | Reverse | ACGACACCAACAGACCAAAG |
| *GmCAMTA13*  (*Glyma.07G242000*) | MG-2945 | Forward | TCTTTGGTCTGTTGGTGTGG |
| MG-2946 | Reverse | ATCGACAGTTTTGACCTGGAG |
| *GmCAMTA14*  (*Glyma.11G251900*) | MG-2955 | Forward | ATTTCTCTGCCATGACTCGG |
| MG-2956 | Reverse | ATGCCGTCCTGAATTATCTCTG |
| *GmCAMTA15*  (*Glyma.08G105200*) | MG-2949 | Forward | GTCTTTTCTCTGTCATCCCTCG |
| MG-2950 | Reverse | TGCACAGAGTAACCTTTCCAG |
| *GmTUBULIN*  (*Glyma.17G258300*) | MG-2937 | Forward | TGGCCGTTACCTGACAGCAT |
| MG-2938 | Reverse | CTCGGAGGGATGTCACACAC |
| *AtRD29A*  (*AT5G52310*) | MG-2000 | Forward | CCTGAAGTGATCGATGCACCAG |
| MG-2001 | Reverse | TGGTGTAATCGGAAGACACGAC |
| *AtRD29B*  (*AT5G52300*) | MG-2002 | Forward | GTGAAGATGACTATCTCGGTGG |
| MG-2003 | Reverse | CACCACTGAGATAATCCGATCC |
| *AtP5CS2*  (*AT3G55610*) | MG-2018 | Forward | AGCAGCCTGTAATGCGATGG |
| MG-2019 | Reverse | AAGTGACGCCTTTGGTTTGC |
| *AtKIN1*  (*AT5G15960*) | MG-2016 | Forward | CCAACAAGAATGCCTTCCAAGC |
| MG-2017 | Reverse | GCTGCCGCATCCGATACACT |
| *AtTUBULIN2*  (*AT5G62690*) | MG4028 | Forward | TGGCATCAACTTTCATTGGA |
| MG-4029 | Reverse | ATGTTGCTCTCCGCTTCTGT |
| *GmCAMTA2*  (*Glyma.08G135200*) | MG-1523 | Forward | CCATGGCTGAGGCCAGACTCTAC | Gene cloning |
| MG-1281 | Reverse | CTCAGCTGTGAAATTCTAAATCACCCC |
| *GmCAMTA8*  (*Glyma.15G143400*) | MG-1530 | Forward | CATCCCAAATATGGGGAAACCTTGTTC |
| MG-1531 | Reverse | CATCCCAAATATGGGGAAACCTTGTTC |