

Genome-Wide Analyses Reveal the Roles of CCT Genes as Regulators of Abiotic Stress Responses in *Citrullus lanatus*

Table S1 Primer sequences used for quantitative real-time PCR analysis

| Name | Forward primer (5'→3') | Reverse primer (5'→3') |
|--------|--------------------------|---------------------------|
| CIACT | CCATGTATGTTGCCATCCAG | GGATAGCATGGGGTAGAGCA |
| CICCT0 | | |
| 1 | AACGCTCGGGCTCAGGCTAT | TTCTGCTTGCTGGACTGCTTAC |
| CICCT0 | | |
| 2 | ATTAGTGAGGTCTATGGGATGCG | GAGCTTTTCTTTGCGTTCTTCG |
| CICCT0 | | |
| 3 | CGATTTCATCTCCTCCCTCA | GGTGGCAGCAGCATTTCATCA |
| CICCT0 | | |
| 4 | TTTGTGCTTGTCTTGTGACCGAA | GAAATGGAGGCAGATGAGCTATG |
| CICCT0 | | |
| 5 | TCCACCCCTCAACCCACCTT | TACCCTGCGGACAGCCAAAC |
| CICCT0 | | |
| 6 | ATCTGATGCTGCTTGTGTTGTGC | CCTTACCGTGGAGGGTTGTG |
| CICCT0 | | |
| 7 | TGAAGCCCCTCTACTGCGACAC | TCTGAATAGCGACTTGCCACCT |
| CICCT0 | | |
| 8 | CAGAGGACGATTTGCGAGATACA | TTCTTCCTCTTCTCGCCCTTC |
| CICCT0 | ACTATGAAGAGGTTTTGGAAGCAT | |
| 9 | G | GGAGTCCTGAGTTGGGTCGTT |
| CICCT1 | | |
| 0 | ACGTCGCAGCCTGCCCTAAT | CGAGCATCCCCTTTCTGTTCTT |
| CICCT1 | | |
| 1 | ATGAGCGGAATGTTTTGAGACG | TGGGAGGGTTACCACTTGAATG |
| CICCT1 | | |
| 2 | AAGCCTTTACGGACAAATGAGC | TTCGTATTAGCATCACTTGGGTCT |
| CICCT1 | | |
| 3 | AAAAGCAGCCTTAGAAAGACCACT | CTGGATTGAGACATCAGGGAATG |
| CICCT1 | | |
| 4 | GTGAAGAACGGTGAAGTTGAGATG | TCGAGGTCGAGATTTGGTTCG |
| CICCT1 | | |
| 5 | CGACTGTGCGAAAGTTGTGGAATG | CCCCAGCAGCCAGTTGTAGATT |
| CICCT1 | | |
| 6 | AGGTTGCCTCCTGGCTTTTATC | GGTTGTTGACTGGATTTGGGTATT |
| CICCT1 | | |
| 7 | TGTGCTGCTGACGATGCTTTC | GGAGTTCTTGCCTTGCGAGTG |
| CICCT1 | | |
| 8 | GTGCGATTGGGACGCTCAT | TCTCGGATTCCCTCCAGTTTCTTAT |

| | | |
|--------|---------------------------|--------------------------|
| CICCT1 | | |
| 9 | AGAAGCCCGAGTCCTAAGGTACA | TTGGAGAATTTCCGGTCCAGT |
| CICCT2 | | |
| 0 | ACGCCCTGATTTTGACCCTC | CTCACCCCATATTCCCCACA |
| CICCT2 | | |
| 1 | TTCAAGTTGGGAGTCAGCACATAG | GACGCATTGCAGGTGTATTGTT |
| CICCT2 | | |
| 2 | CAACCCTGACGCCGTTTATG | GAAGATAGTTCGCAACCACCCA |
| CICCT2 | | |
| 3 | CCTTCCTATGCCTTGGCTGTG | TGTCGGAGTTGGAGGTGTCTG |
| CICCT2 | | |
| 4 | G TTCACATCTTCTAAACCCATCCA | CATCAGGTCCACGTCGCATC |
| CICCT2 | | |
| 5 | GTTCCGAGGGGAGGTTTACG | TCAATGAAGCAGCTCTTTGTGGT |
| CICCT2 | | |
| 6 | AAACAGGGGTGGAGGAGAAGTG | CCAATCATCTGCCGCCGTAC |
| CICCT2 | | |
| 7 | CTTTCGATTGGTGCCTGAG | CAGAATAGCGGGCGACCTT |
| CICCT2 | | |
| 8 | CCAATCGGCTTAGGGCTCA | AATCGCCACCAGTTTCCGT |
| CICCT2 | | AAGATGAAGAAACGCTATGGCTAA |
| 9 | GATGAATCCAATCCAGGAACAGA | G |

Table S2 Structures of the CCT proteins of *Arabidopsis*, bottle gourd and maize. The length and order of the domains represent their actual location within each protein.

| GeneID | CCT | BBX1 | BBX2 | REC | SubC |
|-----------|---------|-------|-------|-----|------|
| AT1G04500 | 288-331 | | | | CMF |
| AT1G05290 | 326-350 | | | | CMF |
| AT1G07050 | 151-194 | | | | CMF |
| AT1G25440 | 361-403 | 16-59 | | | COL |
| AT1G28050 | 385-428 | 8-51 | 51-91 | | COL |
| AT1G49130 | 278-321 | 27-68 | | | COL |
| AT1G51600 | 147-190 | | | | CMF |
| AT1G63820 | 192-235 | | | | CMF |
| AT1G68520 | 357-400 | 16-59 | | | COL |
| AT1G73870 | 345-387 | 22-65 | | | COL |
| AT2G24790 | 229-271 | 7-50 | 50-93 | | COL |
| AT2G32310 | 271-314 | | | | CMF |
| AT2G33350 | 311-354 | | | | CMF |
| AT2G33500 | 357-399 | 11-54 | 54-94 | | COL |
| AT2G46670 | 132-173 | | | | CMF |
| AT2G46790 | 229-271 | 7-50 | 50-93 | | COL |
| AT2G47890 | 287-329 | 12-55 | 55-96 | | COL |

| | | | | | |
|--------------|---------|-------|--------|--------|-----|
| AT3G02380 | 278-320 | 15-58 | 58-101 | | COL |
| AT3G07650 | 315-358 | 5-47 | 47-76 | | COL |
| AT3G12890 | 139-182 | | | | CMF |
| AT3G21175 | 143-186 | | | | CMF |
| AT3G21880 | 307-350 | 4-47 | 47-77 | | COL |
| AT4G15250 | 290-319 | 5-47 | | | COL |
| AT4G24470 | 146-189 | | | | CMF |
| AT4G25990 | 341-384 | | | | CMF |
| AT4G27900 | 214-257 | | | | CMF |
| AT5G02810 | 669-711 | | | 80-183 | PRR |
| AT5G14370 | 294-337 | | | | CMF |
| AT5G15840 | 306-349 | 19-62 | 62-105 | | COL |
| AT5G15850 | 286-329 | 11-54 | 54-97 | | COL |
| AT5G24470 | 509-551 | | | 52-155 | PRR |
| AT5G24930 | 295-337 | 5-48 | 49-91 | | COL |
| AT5G41380 | 215-258 | | | | CMF |
| AT5G48250 | 316-359 | 5-47 | 47-90 | | COL |
| AT5G53420 | 218-261 | | | | CMF |
| AT5G57180 | 383-419 | | | | CMF |
| AT5G57660 | 669-711 | | | 78-134 | PRR |
| AT5G59990 | 170-206 | | | | CMF |
| AT5G60100 | 442-484 | | | 66-169 | PRR |
| AT5G61380 | 533-575 | | | 21-124 | PRR |
| Lsi02G000880 | 535-577 | | | 34-137 | PRR |
| Lsi02G012400 | 105-146 | | | | CMF |
| Lsi02G013810 | 141-162 | | | | CMF |
| Lsi02G016150 | 276-319 | | | | CMF |
| Lsi02G028370 | 155-198 | | | | CMF |
| Lsi03G006960 | 180-223 | | | | CMF |
| Lsi04G002530 | 346-389 | 19-62 | | | COL |
| Lsi05G000970 | 195-238 | | | | CMF |
| Lsi06G011090 | 302-344 | 22-65 | 66-108 | | COL |
| Lsi06G013340 | 319-361 | 22-65 | | | COL |
| Lsi07G000030 | 442-485 | 13-56 | 56-99 | | COL |
| Lsi07G009830 | 284-326 | 23-66 | | | COL |
| Lsi08G004090 | 300-342 | 18-61 | | | COL |
| Lsi08G010150 | 94-135 | | | | CMF |
| Lsi08G010170 | 138-181 | | | | CMF |
| Lsi08G012660 | 276-318 | 5-48 | | | COL |
| Lsi09G000250 | 232-275 | | | | CMF |
| Lsi09G002360 | 233-276 | | | | CMF |
| Lsi09G011970 | 313-356 | | | | CMF |
| Lsi10G000330 | 360-403 | 5-47 | 47-91 | | COL |
| Lsi10G001560 | 353-396 | 4-47 | 48-73 | | COL |

| | | | | | |
|-----------------|---------|--------|-------|---------|-----|
| Lsi11G007470 | 246-289 | 58-98 | 17-58 | | COL |
| Lsi11G007920 | 372-415 | | | | CMF |
| Lsi11G013300 | 350-393 | 5-47 | 47-90 | | COL |
| Lsi11G016170 | 154-197 | | | | CMF |
| | 1166- | | | | |
| LsiUNG001570 | 1208 | | | 537-648 | PRR |
| Zm00001eb003210 | 281-323 | | | | CMF |
| Zm00001eb016800 | 329-372 | | | | CMF |
| Zm00001eb023220 | 232-256 | | | | CMF |
| Zm00001eb025830 | 134-177 | | | | CMF |
| Zm00001eb036970 | 445-487 | 15-58 | | | COL |
| Zm00001eb046390 | 320-363 | | | | CMF |
| Zm00001eb053170 | 138-178 | | | | CMF |
| Zm00001eb054810 | 382-409 | 17-62 | | | COL |
| Zm00001eb078490 | 242-284 | 61-104 | 21-61 | | COL |
| Zm00001eb081920 | 174-215 | | | | CMF |
| Zm00001eb092230 | 346-389 | | | | CMF |
| Zm00001eb103490 | 579-622 | | | 46-146 | PRR |
| Zm00001eb110960 | 364-407 | 15-57 | | | COL |
| Zm00001eb112080 | 759-801 | | | 168-271 | PRR |
| Zm00001eb148750 | 181-224 | | | | CMF |
| Zm00001eb156050 | 98-140 | | | | CMF |
| Zm00001eb163110 | 113-156 | | | | CMF |
| Zm00001eb170920 | 179-216 | 26-57 | | | COL |
| Zm00001eb173520 | 228-259 | | | | CMF |
| Zm00001eb184340 | 235-277 | 23-63 | | | COL |
| Zm00001eb184870 | 354-397 | | | 1-43 | PRR |
| Zm00001eb189080 | 349-392 | 4-47 | 47-90 | | COL |
| Zm00001eb198960 | 639-682 | | | 56-160 | PRR |
| Zm00001eb208040 | 405-435 | | | | CMF |
| Zm00001eb215440 | 103-146 | | | | CMF |
| Zm00001eb216410 | 327-369 | 20-62 | | | COL |
| Zm00001eb222170 | 335-378 | | | | CMF |
| Zm00001eb226740 | 174-217 | | | | CMF |
| Zm00001eb232250 | 216-259 | | | | CMF |
| Zm00001eb233790 | 283-322 | | | 85-188 | PRR |
| Zm00001eb247330 | 442-483 | | | 30-133 | PRR |
| Zm00001eb253150 | 372-393 | 4-47 | 47-90 | | COL |
| Zm00001eb253650 | 400-443 | 19-61 | | | COL |
| Zm00001eb261240 | 237-258 | 20-62 | | | COL |
| Zm00001eb280600 | 397-439 | 24-66 | | | COL |
| Zm00001eb297870 | 210-251 | | | | CMF |
| Zm00001eb319590 | 580-623 | | | 45-148 | PRR |
| Zm00001eb331630 | 611-653 | | | 53-156 | PRR |

| | | | | |
|-----------------|---------|--------|--------|-----|
| Zm00001eb345540 | 262-303 | | | CMF |
| Zm00001eb368200 | 173-216 | | | CMF |
| Zm00001eb368260 | 179-222 | | | CMF |
| Zm00001eb379680 | 184-226 | 8-47 | | COL |
| Zm00001eb379950 | 401-443 | 23-66 | | COL |
| Zm00001eb380460 | 313-356 | 31-74 | | COL |
| Zm00001eb380990 | 351-394 | 4-47 | 47-90 | COL |
| Zm00001eb389540 | 286-328 | 56-98 | 12-55 | COL |
| Zm00001eb391230 | 223-245 | | | CMF |
| Zm00001eb397240 | 711-754 | | 83-139 | PRR |
| Zm00001eb402810 | 291-334 | | | CMF |
| Zm00001eb418700 | 196-237 | | | CMF |
| Zm00001eb425790 | 236-278 | 61-104 | 21-61 | COL |

Table S3. The Ka/Ks ratios and divergence between paralogous ClCCT gene pairs.

| Paralogous pairs | Ka | Ks | Ka/Ks | Divergence-Time (MYA) |
|------------------|----------|----------|----------|-----------------------|
| CICCT02/CICCT13 | 0.324037 | 0.580626 | 0.558082 | 19.354 |
| CICCT07/CICCT27 | 0.991352 | 1.0288 | 0.963601 | 34.293 |
| CICCT08/CICCT10 | 0.935376 | 1.24232 | 0.752928 | 41.411 |
| CICCT14/CICCT17 | 0.559532 | 1.23031 | 0.454789 | 41.010 |
| CICCT14/CICCT20 | 0.992423 | 1.02146 | 0.97157 | 34.049 |
| CICCT21/CICCT22 | 1.02677 | 0.913329 | 1.1242 | 30.444 |

Table S4. CCTsynteny gene pairs between *A. thaliana* (dicot), *O. sativa* (monocot), *Zea mays* L (monocot) and *Lsiceraria* (dicot) genomes

| Gene name | Chr | Gene name | Chr |
|-----------|-----|--------------|-----|
| CICCT02 | 1 | Lsi09G000250 | 9 |
| CICCT03 | 1 | Lsi09G002360 | 2 |
| CICCT28 | 11 | Lsi11G007920 | 11 |
| CICCT29 | 11 | Lsi11G007470 | 11 |
| CICCT05 | 2 | Lsi10G001560 | 10 |
| CICCT06 | 2 | Lsi10G000330 | 10 |
| CICCT04 | 2 | Lsi11G013300 | 11 |
| CICCT09 | 3 | Lsi02G012400 | 2 |
| CICCT10 | 3 | Lsi02G013810 | 2 |
| CICCT14 | 5 | Lsi04G002530 | 4 |
| CICCT13 | 5 | Lsi05G000970 | 5 |
| CICCT17 | 6 | Lsi06G013340 | 6 |
| CICCT16 | 6 | Lsi06G011090 | 6 |
| CICCT15 | 6 | Lsi09G011970 | 9 |
| CICCT18 | 7 | Lsi07G000030 | 7 |
| CICCT19 | 7 | Lsi07G009830 | 7 |

| | | | |
|---------|----|-----------------|----|
| CICCT20 | 8 | Lsi08G004090 | 8 |
| CICCT21 | 8 | Lsi08G010150 | 8 |
| CICCT22 | 8 | Lsi08G010170 | 8 |
| CICCT23 | 8 | Lsi08G012660 | 8 |
| CICCT26 | 9 | Lsi02G016150 | 2 |
| CICCT24 | 9 | Lsi02G028370 | 2 |
| CICCT25 | 9 | Lsi03G006960 | 3 |
| CICCT27 | 9 | Lsi11G016170 | 11 |
| CICCT15 | 6 | AT1G04500 | 1 |
| CICCT11 | 4 | Zm00001eb397240 | 9 |
| CICCT15 | 6 | Zm00001eb222170 | 5 |
| OsCCT01 | 1 | Zm00001eb148750 | 3 |
| OsCCT01 | 1 | Zm00001eb368200 | 8 |
| OsCCT34 | 10 | Zm00001eb046390 | 1 |
| OsCCT34 | 10 | Zm00001eb222170 | 5 |
| OsCCT38 | 11 | Zm00001eb092230 | 2 |
| OsCCT36 | 11 | Zm00001eb163110 | 3 |
| OsCCT39 | 12 | Zm00001eb163110 | 3 |
| OsCCT03 | 2 | Zm00001eb208040 | 4 |
| OsCCT06 | 2 | Zm00001eb184340 | 4 |
| OsCCT07 | 2 | Zm00001eb184870 | 4 |
| OsCCT07 | 2 | Zm00001eb247330 | 5 |
| OsCCT08 | 2 | Zm00001eb253150 | 5 |
| OsCCT05 | 2 | Zm00001eb233790 | 5 |
| OsCCT12 | 3 | Zm00001eb016800 | 1 |
| OsCCT10 | 3 | Zm00001eb003210 | 1 |
| OsCCT14 | 3 | Zm00001eb054810 | 1 |
| OsCCT13 | 3 | Zm00001eb053170 | 1 |
| OsCCT15 | 3 | Zm00001eb215440 | 5 |
| OsCCT14 | 3 | Zm00001eb216410 | 5 |
| OsCCT10 | 3 | Zm00001eb402810 | 9 |
| OsCCT16 | 4 | Zm00001eb425790 | 10 |
| OsCCT16 | 4 | Zm00001eb078490 | 2 |
| OsCCT24 | 6 | Zm00001eb226740 | 5 |
| OsCCT25 | 6 | Zm00001eb232250 | 5 |
| OsCCT23 | 6 | Zm00001eb389540 | 9 |
| OsCCT22 | 6 | Zm00001eb380990 | 9 |
| OsCCT27 | 7 | Zm00001eb110960 | 2 |
| OsCCT28 | 7 | Zm00001eb112080 | 2 |
| OsCCT28 | 7 | Zm00001eb331630 | 7 |
| OsCCT30 | 8 | Zm00001eb036970 | 1 |
| OsCCT42 | 8 | Zm00001eb173520 | 4 |
| OsCCT33 | 9 | Zm00001eb103490 | 2 |
| OsCCT33 | 9 | Zm00001eb319590 | 7 |

Table S5 The cis-elements that have been identified in more than 9 ClCCTgenes.

| Cis -elements | Number of genes | Functions of the cis -elements | Cis -elements types |
|-----------------|-----------------|--|---------------------|
| CAAT-box | 29 | Common cis-acting element in promoter and enhancer regions | |
| TATA-box | 29 | Core promoter element around 230 of transcription start | |
| AAGAA-motif | 19 | Cis-acting element involved in the abscisic acid responsiveness | Hormone responsive |
| ABRE | 21 | Cis-acting element involved in the abscisic acid responsiveness | Hormone responsive |
| ARE | 22 | cis-acting regulatory element essential for the anaerobic induction | Stress responsive |
| Box 4 | 26 | part of a conserved DNA module involved in light responsiveness | Light responsive |
| CGTCA-motif | 15 | cis-acting regulatory element involved in the MeJA-responsiveness | Hormone responsive |
| G-Box | 21 | cis-acting regulatory element involved in light responsiveness | Light responsive |
| GT1-motif | 19 | light responsive element | Light responsive |
| LTR | 11 | cis-acting element involved in low-temperature responsiveness | Stress responsive |
| MBS | 9 | MYB binding site involved in drought-inducibility | Stress responsive |
| O2-site | 13 | cis-acting regulatory element involved in zein metabolism regulation | Stress responsive |
| TCA | 16 | cis-acting element involved in salicylic acid responsiveness | Stress responsive |
| TGACG-motif | 15 | cis-acting regulatory element involved in the MeJA-responsiveness | Hormone responsive |
| W-box | 13 | Wounding and pathogen responsievness | Stress responsive |
| WUN-motif | 11 | Wounding responsievness | Stress responsive |
| WRE3 | 11 | Wounding and defense responsievness | Stress responsive |
| TCT-motif | 13 | part of a light responsive element | Light responsive |
| TC-rich repeats | 11 | cis-acting element involved in defense and stress responsiveness | Stress responsive |

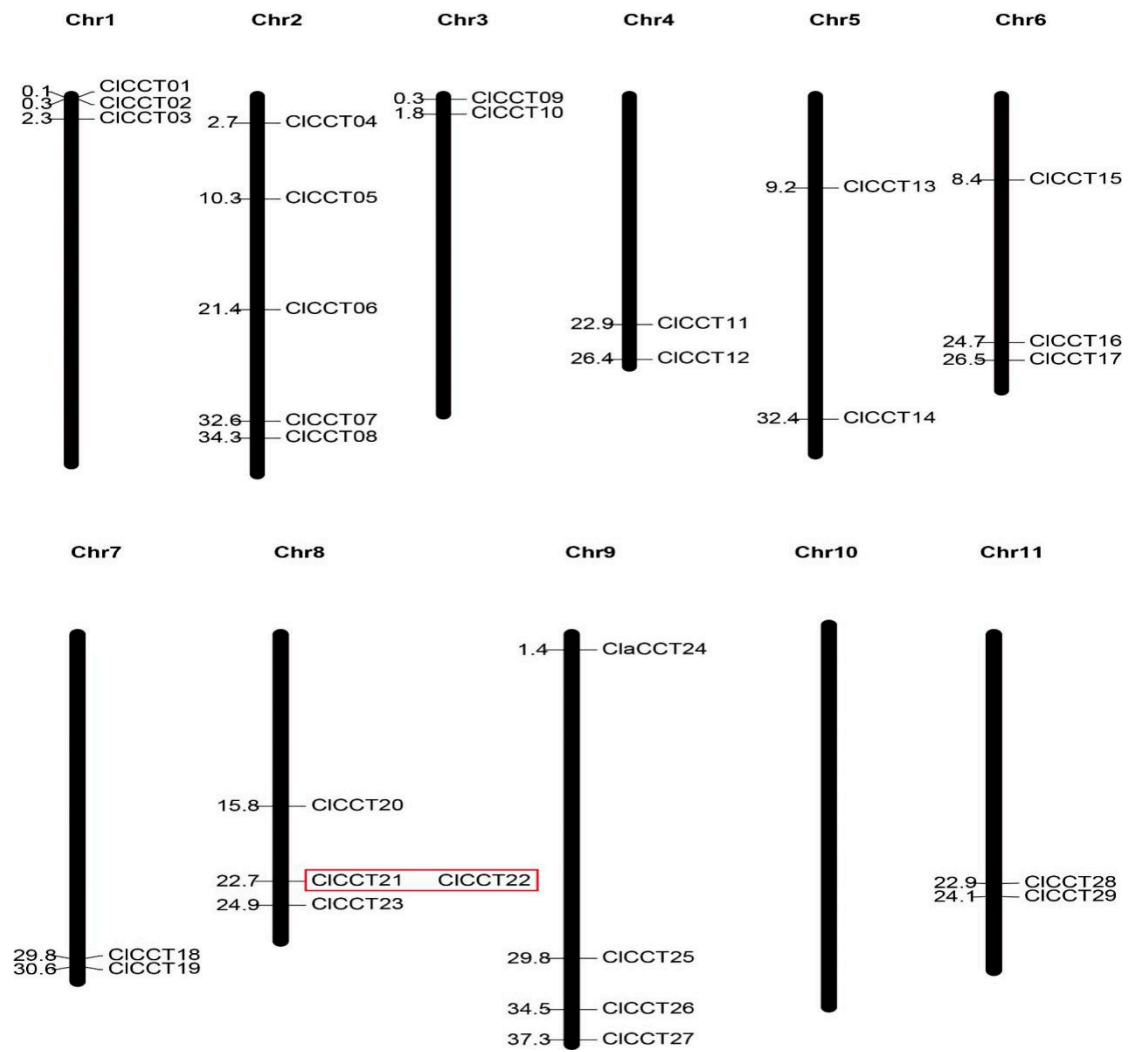


Figure S1. Distribution of *Citrullus lanatus* CCT genes on 11 chromosomes. The left number represented the position of CCT genes, and the right information represented the name of CCT.

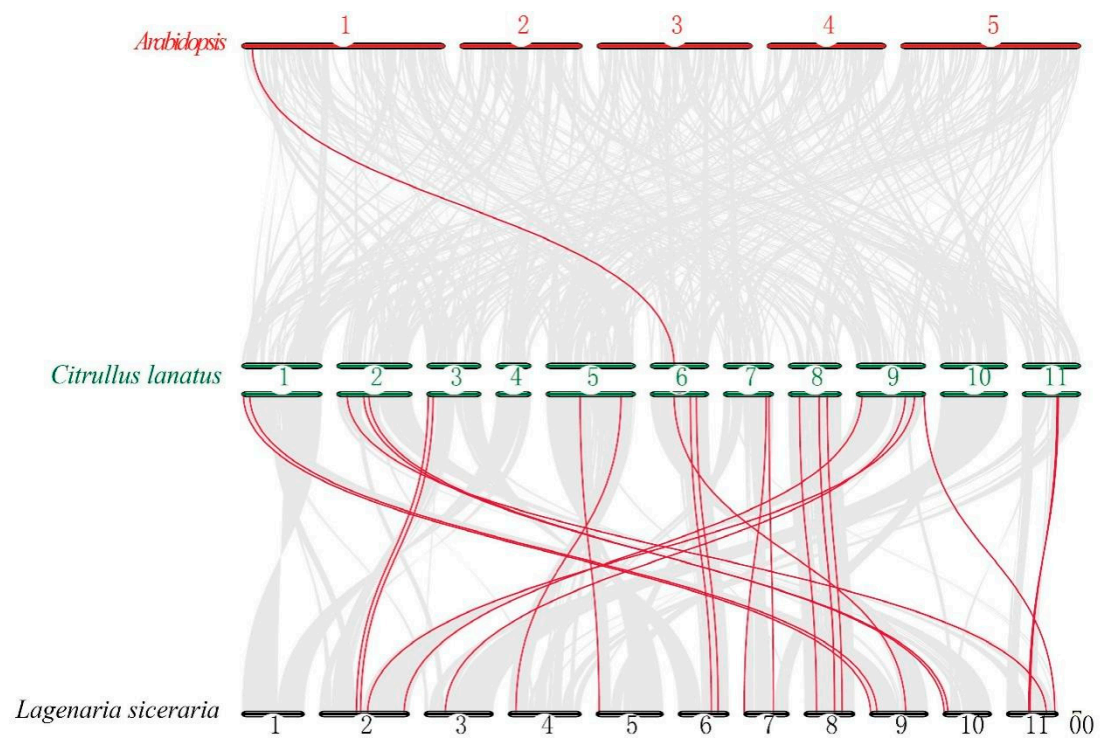


Figure S2. Collinearity analysis of ClCCT genes between *C. lanatus* and *A. thaliana*/*Lsiceraria*. Gray lines: the collinear blocks within *C. lanatus* and *A. thaliana*/*Lsiceraria*; the red lines: the syntenic ClCCT gene pairs.

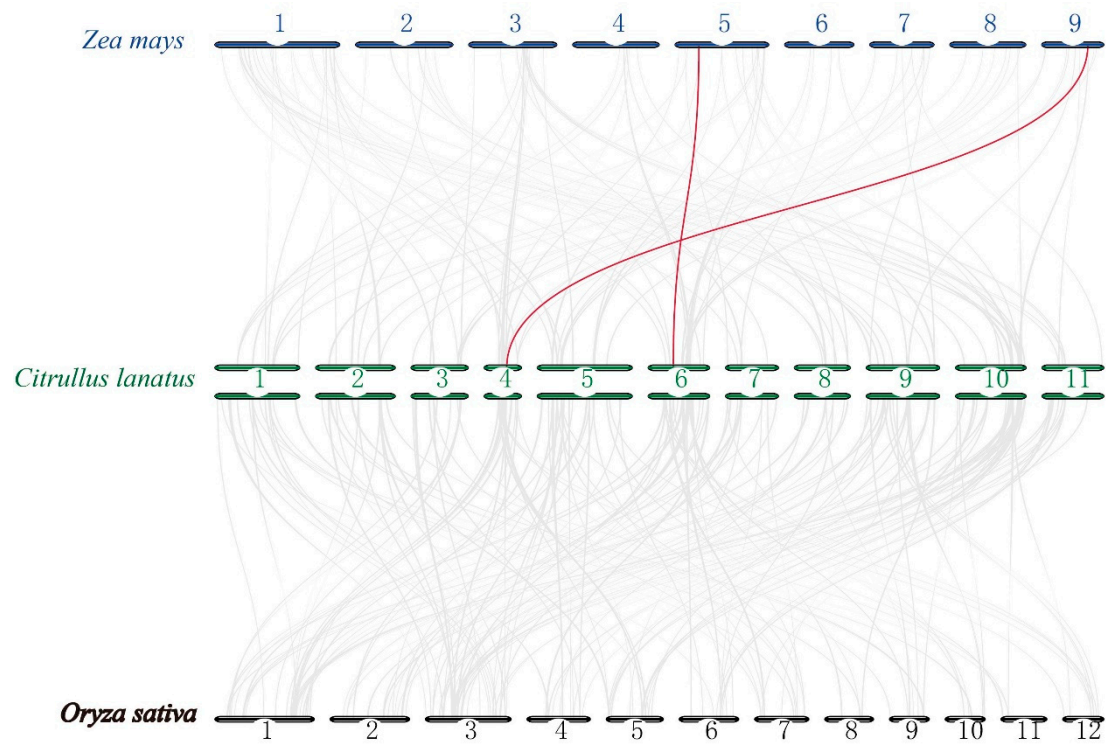


Figure S3. Collinearity analysis of ClCCT genes between *C. lanatus* and *O. sativa*/ *Zea mays* L. Gray lines: the collinear blocks within *C. lanatus* and *O. sativa*/ *Zea mays* L; the red lines: the syntenic ClCCT gene pairs.

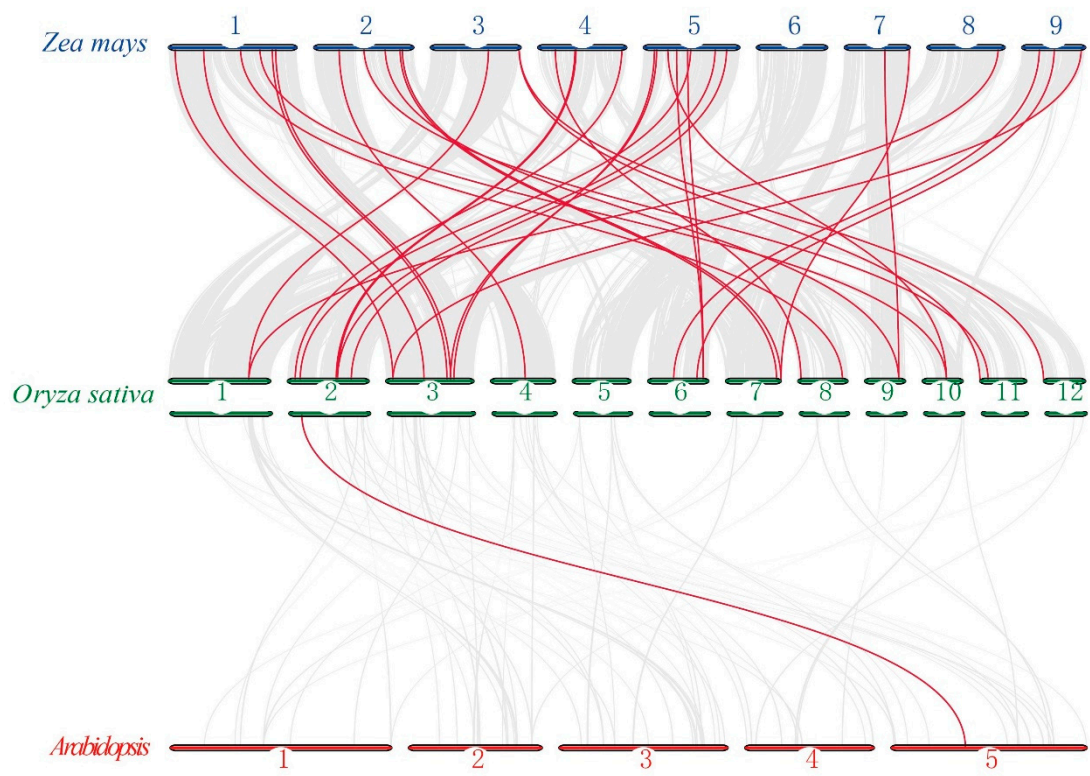


Figure S4 Synteny analysis of ClCCT genes between *O. sativa* and *A. thaliana*/*Zea mays* L. Gray lines in the background indicate the collinear blocks within *O. sativa* and *A. thaliana*/*Zea mays* L, and the red lines highlight the syntenic ClCCT gene pairs.

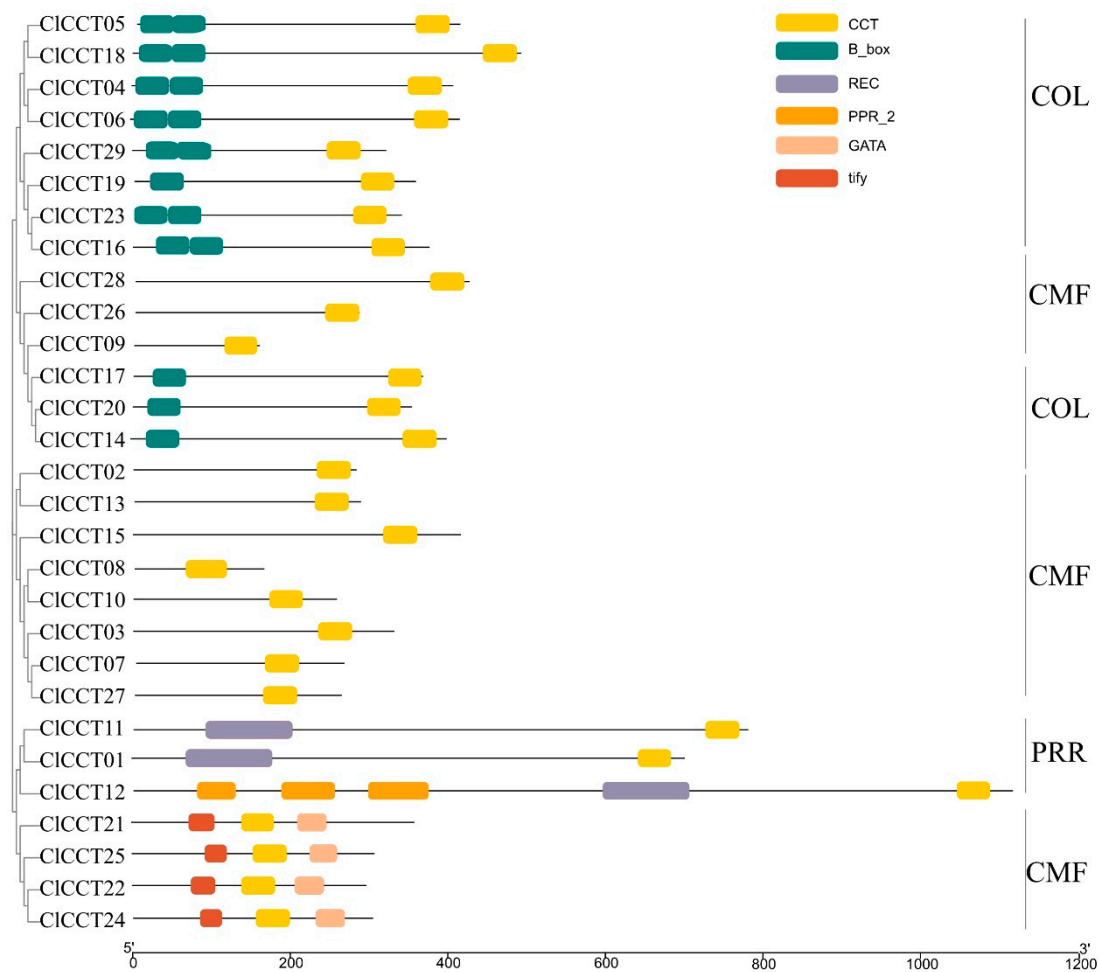


Figure S7. The main conserved domain of CCT family genes in *Citrullus lanatus*.