

Supporting Information

Figure S1

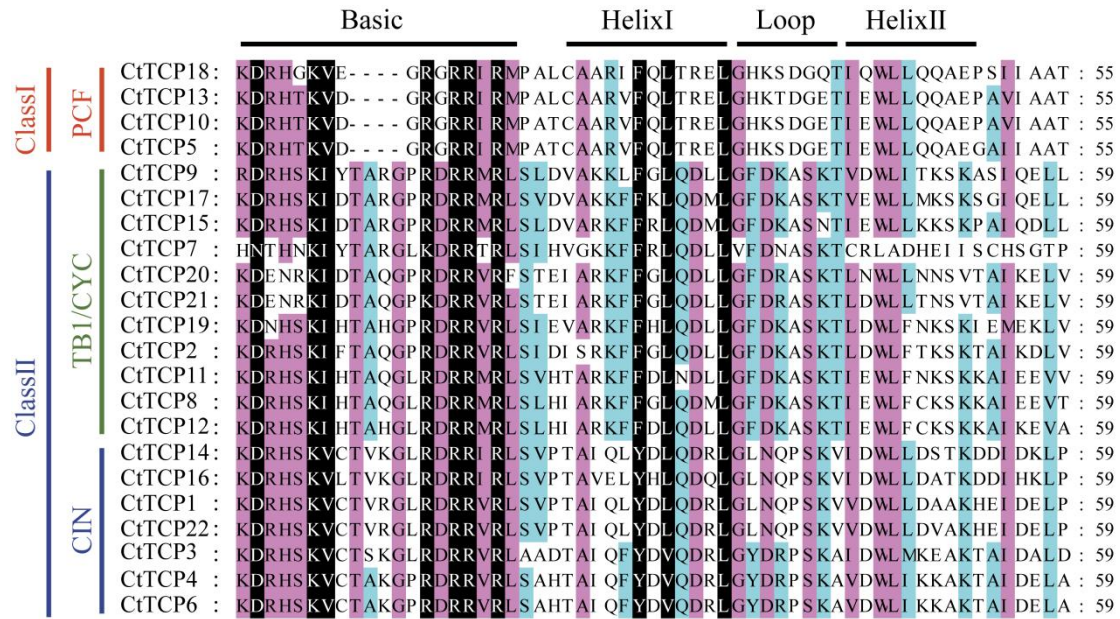


Fig. S1. Multiple sequence alignment of the TCP domain in *C. tinctorius*.

Table S1. Identification and physicochemical analysis of CtTCP family members

Gene name	Gene ID	Protein length (AA)	Molecular weight(kD)	Isoelectric point (pI)	Grand Average of Hydropathicity	Subcellular localization
<i>CtTCP1</i>	CtAH01T0018300.1	369	40980.13	6.37	-0.9	Nucleus
<i>CtTCP2</i>	CtAH01T0022800.1	391	43684.46	9.82	-0.752	Nucleus
<i>CtTCP3</i>	CtAH01T0210200.1	230	26489.27	5.33	-0.886	Nucleus
<i>CtTCP4</i>	CtAH03T0030200.1	347	38521.07	5.99	-0.995	Nucleus
<i>CtTCP5</i>	CtAH05T0066400.1	506	54326.49	6.7	-0.753	Nucleus
<i>CtTCP6</i>	CtAH05T0118200.1	543	59908.93	6.59	-0.886	Nucleus
<i>CtTCP7</i>	CtAH05T0251200.1	222	25371.11	9.91	-0.502	Nucleus
<i>CtTCP8</i>	CtAH06T0224200.1	396	44472.44	6.88	-0.914	Nucleus
<i>CtTCP9</i>	CtAH06T0310700.1	403	45730.35	6.79	-0.982	Nucleus
<i>CtTCP10</i>	CtAH07T0023000.1	356	37453.03	7.97	-0.619	Nucleus
<i>CtTCP11</i>	CtAH07T0053300.1	361	40475.22	7.8	-0.762	Nucleus
<i>CtTCP12</i>	CtAH07T0053500.1	338	38629.35	6.91	-0.79	Nucleus
<i>CtTCP13</i>	CtAH09T0063500.1	386	41267.33	6.46	-0.624	Nucleus
<i>CtTCP14</i>	CtAH09T0071100.1	343	38371.76	6.3	-0.757	Nucleus
<i>CtTCP15</i>	CtAH09T0075100.1	446	50604.14	8.92	-0.985	Nucleus
<i>CtTCP16</i>	CtAH09T0172100.1	408	45841.01	8.52	-0.495	Nucleus
<i>CtTCP17</i>	CtAH09T0177100.1	390	44317	6.81	-0.887	Nucleus
<i>CtTCP18</i>	CtAH11T0002600.1	186	19901.14	7.06	-0.579	Nucleus
<i>CtTCP19</i>	CtAH11T0044100.1	345	38908.57	7.75	-0.793	Nucleus

<i>CtTCP20</i>	CtAH11T0044400.1	318	36197.48	6.22	-0.829	Nucleus
<i>CtTCP21</i>	CtAH11T0044700.1	309	35138.39	6.13	-0.754	Nucleus
<i>CtTCP22</i>	CtAH11T0052400.1	316	35237.22	6.62	-0.869	Nucleus

Table S2. Ka/Ks ratios of duplicated gene pairs of *CtTCPs*

Sequence	Method	Ka	Ks	Ka/Ks	P-Value(Fisher)	Purifying Selection
CtTCP1-CtTCP14	YN	0.509626	4.09447	0.124467	1.68299e-033	Yes
CtTCP1-CtTCP16	YN	0.542005	3.8114	0.142206	7.26932e-030	Yes
CtTCP1-CtTCP22	YN	0.208347	1.87714	0.110992	4.08436e-031	Yes
CtTCP2-CtTCP11	YN	0.755744	3.98959	0.189429	2.15812e-035	Yes
CtTCP2-CtTCP15	YN	0.755598	4.04236	0.18692	1.38782e-026	Yes
CtTCP2-CtTCP19	YN	0.555395	1.55317	0.357587	9.28034e-012	Yes
CtTCP4-CtTCP6	YN	1.21452	4.44907	0.272982	4.79921e-010	Yes
CtTCP9-CtTCP15	YN	1.077	4.13009	0.260771	8.64789e-012	Yes
CtTCP9-CtTCP17	YN	0.963288	3.96661	0.242849	1.37002e-023	Yes
CtTCP10-CtTCP13	YN	0.402922	2.37332	0.169771	1.33694e-027	Yes
CtTCP14-CtTCP16	YN	0.370345	1.84566	0.200657	5.96448e-021	Yes
CtTCP14-CtTCP22	YN	0.520985	3.98785	0.130643	6.53318e-024	Yes
CtTCP15-CtTCP17	YN	0.501253	2.65154	0.189043	3.59397e-021	Yes

Table S3. The primer sequences used in this study

Gene name	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Function
<i>qCtTCP1</i>	CCCAAAGGATGGAAGAGGC	GAAGAAATTACCGGGTTGAACA	qRT-PCR
<i>qCtTCP3</i>	ACAAACGTGATGAAAACCCG	ACAAAACCTTCGTAGCCCTG	
<i>qCtTCP5</i>	CATATCTTGACCGCCGACC	CCAACCGTTACCTCCCCTT	
<i>qCtTCP10</i>	GCTGGCAATAACCACCACAAT	ACTCCCCAAACCTCCTCCTCT	
<i>qCtTCP11</i>	TTGTTCTTGACAGTTCCCTTCA	CCCACACCTCTTCTTCCCTTA	
<i>qCtTCP16</i>	AGTTCTGACTGTAAAAGGGTTGC	GAGAGGTGGGAGTTTGTGGAT	
<i>qCtTCP21</i>	CGAAACTAAGCGAAAACACGA	ACTTCAGACTCCAACAGCCAC	
<i>qCtTCP22</i>	TACCGTGAGAGGGTTGAGGG	ATCTGGAGAGGGGGGAGTTC	
<i>Ct60S</i>	TGGAGCTCATCAAGAAGGG	GGTAAGGACCACAAGACCGTA	Gene amplification
<i>CtTCP1</i>	ATGAATATTTCAAATCTAAGAGAAGCCG	TCATTTGTCTGATTGATCATGTCCG	
<i>CtTCP3</i>	ATGAGGCAAAATCGGGCACC	CTAGCTCTCTTGCTGATCTTCATAA	
<i>CtTCP22</i>	ATGAATATTTCGAATTTAAGAGAATCGGA	TCAATTTCCCTTTATTGGTTTCATCTTCT	
GFP- <i>CtTCP1</i>	CAAATCGACTCTAGAAAGCTTATGAATATTT	GCCCTTGCTCACCATGGTACCTTTGTCTGA	Subcellular localization
	CAAATCTAAGAGAAGCCG	TTGATCATGTCCG	
GFP- <i>CtTCP3</i>	CAAATCGACTCTAGAAAGCTTATGAGGCAA	GCCCTTGCTCACCATGGTACCGCTCTCTTG	
	AATCGGGCACC	CTGATCTTCATAA	
GFP- <i>CtTCP22</i>	CAAATCGACTCTAGAAAGCTTATGAATATTT	GCCCTTGCTCACCATGGTACCATTTCTTTA	
	CGAATTTAAGAGAATCGGA	TTTGGTTTCATCTTCT	