



Figure S1. Multiple sequence alignment of subgroup 1-6 of CsLAC gene family. Sequence alignment among CsLACs showed the highest identity of 80.99% in group I, identity of 80.44%, 80.25%, 71.41% and 71.16% respectively in group III, group V, group II and group VI. There was the lowest similarity in laccase protein sequences from group IV, sharing an identity of 59.25%.

Table S1. The gene ID used for phylogenetic analysis.

Gene	Resource	Locus number
AtLAC1	<i>Arabidopsis thaliana</i>	At1g18140
AtLAC2	<i>Arabidopsis thaliana</i>	At2g29130
AtLAC3	<i>Arabidopsis thaliana</i>	At2g30210
AtLAC4	<i>Arabidopsis thaliana</i>	At2g38080
AtLAC5	<i>Arabidopsis thaliana</i>	At2g40370
AtLAC6	<i>Arabidopsis thaliana</i>	At2g46570
AtLAC7	<i>Arabidopsis thaliana</i>	At3g09220
AtLAC8	<i>Arabidopsis thaliana</i>	At5g01040
AtLAC9	<i>Arabidopsis thaliana</i>	At5g01050
AtLAC10	<i>Arabidopsis thaliana</i>	At5g01190
AtLAC11	<i>Arabidopsis thaliana</i>	At5g03260
AtLAC12	<i>Arabidopsis thaliana</i>	At5g05390
AtLAC13	<i>Arabidopsis thaliana</i>	At5g07130
AtLAC14	<i>Arabidopsis thaliana</i>	At5g09360
AtLAC15	<i>Arabidopsis thaliana</i>	At5g48100
AtLAC16	<i>Arabidopsis thaliana</i>	At5g58910
AtLAC17	<i>Arabidopsis thaliana</i>	At5g60020

Table S2. Primers used for cloning laccase genes in *Camellia sinensis*.

Primers	Purpose	Primer Sequence (5'→3')
1-1RACE3-1	5'-RACE	GCGGCAAGTGTGTTGGTATTAGCAGGGG
1-1RACE3-2	5'-RACE	AGGGATGACGAAATGGGTAAGGGACA
1-2RACE5-1	5'-RACE	GTGGTATTCGAGGATTGCGGCGGTAG
1-2RACE5-2	5'-RACE	CTCGGCGGATTGCCCCTGTAGTTGA
1-2RACE3-1	3'-RACE	GTGGTTGAAGCGGACGCAATCTAT
1-2RACE3-2	3'-RACE	ACCACTGATTTTCCAGCGAACCCG
1-3RACE5-1	5'-RACE	TTCTCCGCCCCAAAATACTGGTATCCT
1-3RACE5-2	5'-RACE	TGGACAGTTTTAGGGACCTTATTGGCAG
1-4RACE3-1	3'-RACE	ATTGAAAAGCCTCGCATCCCCTAAA
1-4RACE3-2	3'-RACE	CGCCGAACAACACGATGGTGAGTAA
1-5RACE5-1	5'-RACE	CACTCTCCAAAGATGATGGGAACCT
1-5RACE5-2	5'-RACE	GCCAGTTTGTATGGGGCATTGAGTT
1-5RACE3-1	3'-RACE	TGGTCCTATAATCATCCGTCCCAAACA
1-5RACE3-2	3'-RACE	GGAGGTTCCCATCATCTTTGGAGAGTG
1-6RACE3-1	3'-RACE	GGTGGCATTTCATGGGAGTTATCGT
1-6RACE3-2	3'-RACE	TTCCTCAACCAGCACTTGCCACGG
1-7RACE5-1	5'-RACE	TGGGGGACATTGGCAGGGTATTGAGC
1-7RACE5-2	5'-RACE	TGGCAAGGCTGAGTGAAGAAGTGGTG
1-7RACE3-1	3'-RACE	GACCGACACGCTTCTCATTACTCCCG
1-7RACE3-2	3'-RACE	GTGCCACATTCTTGATGATTGCCAGG
2-1RACE5-1	5'-RACE	TTGCCATTGTCCACCAAGAATGCCATC
2-1RACE5-2	5'-RACE	CCATCTTTAGTCCCCATGATGTGTGCA
2-2RACE3-1	3'-RACE	ACCCCGCCTCCTAAAAACGCCACCCCAG
2-2RACE3-2	3'-RACE	GAGTTCCGTCTGGAGGATGGACTGCTAT
2-3RACE5-1	5'-RACE	CCACCGCCACCACACTGTCCATAAA
2-3RACE5-2	5'-RACE	CTGGCGGTTAGGAGGGCATTGTGG
2-3RACE3-1	3'-RACE	AGACCACAAATGCCCTCCTAACCGC
2-3RACE3-2	3'-RACE	CTTTATGGACAGTGTGGTGGCGGTG
2-4RACE5-1	5'-RACE	AAGTCACTGGAGGGCGGTCTGGG
2-4RACE5-2	5'-RACE	TGGTGTGCCAGCGATGGCGAAG
2-5RACE5-1	5'-RACE	GTGGTCCTGGTTTCCCATTGATTGT
2-5RACE5-2	5'-RACE	TTTGGAATGGCACAGCCTGCTCACA
2-5RACE3-1	3'-RACE	TTCTTTCTTGCCACACTAACGCTGC
2-5RACE3-2	3'-RACE	TGTTCTACTGGCGGTTGGACTGCTA
2-6RACE5-1	5'-RACE	CCCTGGGAACATCCCATTCACTGTCA
2-6RACE5-2	5'-RACE	TGCTCACATTCTTCACTTGTATCTGA
2-6RACE3-1	3'-RACE	ACAAGTGAAGAATGTGAGCAGATTGTG
2-6RACE3-2	3'-RACE	TGACAGTGAATGGGATGTTCCCAGGGC
3-1RACE5-1	5'-RACE	GGATTGAAGTTTCCAAAGCCCTGTGCGA
3-1RACE5-2	5'-RACE	CTGCCCCAGTTCTTGTAGCCTGCCTCAC
3-2-F	Clone	CTTGGGTTGTAGTAGTTTC
3-2-R	Clone	AACCAAAACCAAAACCACCC
3-3RACE3-1	3'-RACE	CCCCAGCCTTGCTCTATTTGCTCTCAT
3-3RACE3-2	3'-RACE	AGACAGAGGGGAACGCCGTGGGCAGAC
3-4RACE5-1	5'-RACE	CCCTGGATTATCAGCGACAAACCG
3-4RACE5-2	5'-RACE	TGCCCATCCACCAACAGGGACATC
4-1RACE5-1	5'-RACE	GGAACACGAAAGGTATTCACTTGCGG
4-1RACE5-2	5'-RACE	GCAGGACATTGCTTTCTTGGAACACT

4-2RACE5-1	5'-RACE	TTGTCTCTGGTGTCCCGCCATCTCTT
4-2RACE5-2	5'-RACE	TTCCTGCGTCCAACACATTAGTCCCT
4-2RACE3-1	3'-RACE	GCCTGAATACATCACACAATGCGGAA
4-2RACE3-2	3'-RACE	CAAGGGACTAATGTGTTGGACGCAGG
4-3RACE5-1	5'-RACE	GACCCCAACAGTGTTCAACTCAGGTG
4-3RACE5-2	5'-RACE	GACCCAACGACATAAAAACTGAACCC
4-3RACE3-1	3'-RACE	GGGTTTCAGTTTTTATGTCGTTGGGTC
4-3RACE3-2	3'-RACE	TCCACCTGAGTTGAACACTGTTGGGG
4-4RACE5-1	5'-RACE	TGAAAAAATAAAGGTGGTTGACTCGGAA
4-4RACE5-2	5'-RACE	TCACCATTGGGTCCATCACAAGAAGT
4-5RACE5-1	5'-RACE	TGATGATTTGCGATGGAGAAAAAGAGAA
4-5RACE5-2	5'-RACE	GCCACCATAGGGTTCCTTCCTCTGTTGA
4-6RACE5-1	5'-RACE	GGATTGGGCACTGGGTAATGTAGGAA
4-6RACE5-2	5'-RACE	GGTGGCATTGTAGGGAGATTGTTGG
4-7RACE3-1	3'-RACE	CTCCGCCAAGCCCATCCCTACCA
4-7RACE3-2	3'-RACE	GGTTCGTACGGAACTAAATACACACG
4-8RACE5-1	5'-RACE	GACCCAAGCCAGTATTCCTCGTGTGAC
4-8RACE5-2	5'-RACE	CATCATTGTCTGTGAAAGCCTGGAAAGA
4-8RACE3-1	3'-RACE	CAACAATCTTTCCAGGCTTTCACGACA
4-8RACE3-2	3'-RACE	ACCGATTTTCATCCTCCACAAGGTTTCAT
5-1RACE5-1	5'-RACE	TGACATTGTTGACAAAGGCTTCCATCA
5-1RACE5-2	5'-RACE	ATAGAAGTTGTGGGCTGTTGGTGTGTC
5-1RACE3-1	3'-RACE	ATGACACACCAACAGCCCAAGTTCT
5-1RACE3-2	3'-RACE	CCCATGCGAAGCAGGTTCCAACTGTAG
5-2RACE5-1	5'-RACE	CGGGAGCAATAACAATGAAGTCGGTGA
5-2RACE5-2	5'-RACE	TTGGAAGTGTAGGAGCACCACCGC
5-2RACE3-1	3'-RACE	TCTCCAACGACTATGCCGCAATCAA
5-2RACE3-2	3'-RACE	ACCGACTTCATTGTTATTGCTCCCG
5-3-F	Clone	CGATCTCATCGTTGTATGAAATAC
5-3-R	Clone	AGCAATACGGGAAAAATGTTAG
5-4RACE3-1	3'-RACE	TTCGTACCCATTCCCAAAACCGCA
5-4RACE3-2	3'-RACE	TGCCACTCCATCAACCCACAGA
6-1RACE5-1	5'-RACE	GATTAGGACCCGACCCGCTTTTCAC
6-1RACE5-2	5'-RACE	CCGTTGAGTCAGGCACTTGATTCCG
6-1RACE3-1	3'-RACE	GAATCAAGTGCCTGACTCAACGGG
6-1RACE3-2	3'-RACE	GGGACAAGGCTTTTGGAGGTGAAC

Table S3. Primers used for *q*RT-PCR.

Name	Forward primer (5'→3')	Reverse primer (5'→3')
LAC1-2	AGACGTGTCAAGGACCCAAC	ATGGAGATGCAAAGGGTGAG
LAC1-3	ACAAGTGTCTCCTCCAGTC	GTTAGGTGGTGTCCCGGTAT
LAC1-4	CTCAAAACCAAACCGCATTT	GGACGTTTGCTGGGAATTTA
LAC1-5	ACAAGATTGTGCCACACCAA	ATATGGGCATGCCAAAAGAG
LAC1-6	GGACAGACCACAAACGTCCT	ATTGGCAGGGTATTGAGCAC
LAC2-1	GCCACGGTTCAACTTGTTTT	ATGTGTGCACCTCCAAATGA
LAC2-2	CCTCGGTGTCAATCCTTGTT	TTCAGGGGCTATCATTCCAG
LAC2-5	CCACACTAACGCTGCATTGA	CCCGGGAACATTCCATTAC
LAC2-6	TCCATTGGCATGACTTGAAA	GTGTGCATGCCACCATAAAG
LAC3-1	GCACCTGTCAAGGTCCAAAT	AGTGACCGGCTCACATTACC
LAC3-2	CCCTTCACCACCTCAGTCAT	GGCTTTTCATGGGGTATCTGA
LAC3-3	TCCTTCCAATGTCTGAAGTCC	AAGGTAGGTTGCCACAATGC

LAC3-4	TCCCGAGAAGGAAAAGGAAT	GACCCTGGAACCAAACCTTCA
LAC4-1	CGGCAAAGAACACCCTGTAT	TTCGCATTGACTCTTGTTC
LAC4-3	TATCACTGCAAGCGACCAAG	AATCTGATGACTGCCCAACC
LAC4-5	TGCATGTTTACAAGGGTGAT	CCATGGATTTCTTGGTTGCT
LAC4-6	ACCCAGGAGTGTGGCTTATG	TGGAGGCAGCAGTTTTTCTT
LAC4-7	GGGACAGTTACCACCGAGAA	CAAGTTCAAATTGGCGGTTT
LAC4-8	TGGCTTTGCTCTTGAATGTG	TGCTCTACTCCATGCCAGTG
LAC5-2	TGACCTTCGTTTCTTTGGCTCT	CAACATCAGCGGAGGTGAGT
LAC5-3	GTTGAAAACCGACCAGCCAC	CCCAATGAGGCGCATTTACG
LAC5-4	TTATGAATGGGCCTCACTGG	TTGCACCTAATCGTTGCTTG
LAC6-1	CTTGCTGCCAGGAACACAAC	CTCCTGTGATTGGGCACTGT

Table S4. Sequence information of the reference genes used under different treatments.

NO	Treatments		Reference genes for each treatment	GeneBank Accession Number	Primer sequence (5'–3') forward/reverse
	Names	Organs			
1	tea leaves at different stages of maturity	1st leaves	<i>CsTBP</i>	AT1G55520	GGCGGATCAAGTGTGGAAGGGAG
		2nd leaves			
		3rd leaves			ACGCTTGGGATTGTATTCGGCATT
		4th leaves			
2	<i>T. aurantii</i> infestation	2nd leaves	<i>CsACTIN1</i>	KA280216.1	TGGGCCAGAAAGATGCTTATGTAGG ATGCCAGATCTTTTCCATGTCATCC
3	<i>E. grisea</i> infestation	2nd leaves	<i>CsGAPDH1</i>	KA295375.1	TTTTTGGCCTTAGGAACCCAGAGG GGGCAGCAGCCTTATCCTTATCAGT
4	JA treatment	2nd leaves	<i>CsGAPDH1</i>	KA295375.1	TTTTTGGCCTTAGGAACCCAGAGG GGGCAGCAGCCTTATCCTTATCAGT
5	SA treatment	2nd leaves	<i>CsTBP</i>	AT1G55520	GGCGGATCAAGTGTGGAAGGGAG ACGCTTGGGATTGTATTCGGCATT