

Table 1 Suppl. Primers of *PRX* genes in *Camellia sinensis*.

Name	Forward primers (5' - 3')	Reverse primers (5' - 3')
<i>CsPRX3</i>	ATGGGTTATTTTGAATTGTGA	TTAACTATTCACCACTGCACAA
<i>CsPRX4</i>	ATGGTGATTAATGTCACATTC	AGTTTCGTCATCATCATTAC
<i>CsPRX12</i>	ATGGCCTTCAATAATGCAGT	AAATCCAGACAAGGTCACCA
<i>CsPRX16</i>	ATGGAAAATCAAAGAAACAACC	CTAGTTGATAGCAGTGCAATCA
<i>CsPRX27</i>	ATGGCTAACACAAAGCTTCTCG	TCACCATTTGGACAAAAATACT
<i>CsPRX42</i>	ATGGGTTCCAAAGCTCTCTTCT	CTAGTGGTGCTTGTGGCAACA
<i>CsPRX43</i>	ATGGTACTAGTACTAGTGAATT	TCAATTGAAAGATCCACAAACA
<i>CsPRX47</i>	ATGGGGATTGCTAAGTTGGTTG	TCAGTTGACCTTACGACAATTT
<i>CsPRX55</i>	ATGGAGGCATGGAGAGGATT	TTACGAATTGAAGCTTGTGCAAT
<i>CsPRX72</i>	ATGGCTCATCAAACCATGAGCT	CTAAGAGTTTATTTTCTGCAA
<i>CsPRX73</i>	ATGGGTCAATTCATCAATCTTG	TCAATTAAACGCTCCACAATCG

Table 2 Suppl. Primers of *CsPRX* genes for reverse transcription quantitative PCR.

Name	Forward primers (5' - 3')	Reverse primers (5' - 3')
RT- <i>CsPRX3</i>	TCTATTGTTGTCACTGGAGG	GAAAATGATGAACAGTGGGC
RT- <i>CsPRX4</i>	TTCTCTCCTTCGCCTCCATTTT	GTTTTAGAATCCCTGCGTCCAA
RT- <i>CsPRX12</i>	TGACTGCTTTGTTCAAGGAT	TTTGTTGTTGCGAAGGTGAG
RT- <i>CsPRX16</i>	ACCCAACAACGCCTCAAACG	ACGGTGAATCTCTCCCTGGT
RT- <i>CsPRX27</i>	CTTGATGCTTGCTTTTTCTGTC	CAGAACCCTCACATCCCCTAAC
RT- <i>CsPRX42</i>	ACCCAGCAGGTCTTGTTATGAA	TTGAGTCCAGCAGTAGTGAAGC
RT- <i>CsPRX43</i>	GCAGAAGGGACTCTCAGACCAA	CCTCATCATCATAGAGCCTTGC
RT- <i>CsPRX47</i>	GGGATGTGATGCTTCAGTTTTG	ATGGTGATGAGTTGGGAGGTGT
RT- <i>CsPRX55</i>	GCCACACTTCGCTTATTCTT	AGCCAGGACTACAACATCTC
RT- <i>CsPRX72</i>	ACATTCCACCTCCAAACAACAC	CACAAAATCCAAGAAGAAGAGG
RT- <i>CsPRX73</i>	CAATCTTGTAATAGCCGTGTGG	TACTGAAGCATCACATCCCTGG

CsPRX3	MGYFGIVILAFVAF..LGSARAD.....	<u>IKMGEYDKSCFKAEKIVLDFVKEHIPNAPSIAAALIRM</u>	60
CsPRX4	MAFSSL.MVINVTFLMFVLLMGTSSAQ.....	<u>LSINBYFKTCFKLLSTVKSVNSAVSKEKRMGASLRL</u>	64
CsPRX12	MAFNNAVSLTSSMLVVFSSVLLSSCYFDISEAGDEPPVVKGLSWTFESSCKKLESIRKQKKVKDDIGQAAGLRL		80
CsPRX16	MENQRNNLLVSSFLVYVLLLTAAANAQ.....	<u>LRQDEYHNICFNVESLVRSAVTKFHQTFVTAFATRL</u>	66
CsPRX27	MANTKLLIPFFLHMLAFSVLDANAQ.....	<u>LKLGSKYKTSCKSAEHIVKEITKKFISRAPTLAAPLIRM</u>	65
CsPRX42	MGSKALFFFAIFSFLVTSFAFAENEENANDPAGLVNNEFKDSCQAEIDIEQVKLLYKRHNKNTAFSWIRN		71
CsPRX43	MVLVLVNLILILSCIVGISQSQ.....	<u>LQVGGADTCHDAESIVNGVVRDAFLSNSNTAFVLRL</u>	60
CsPRX47	MGIAKLVGVILVILSGMRNGAYG.....	<u>LSMSYIIMSCFLADLIVKNTVNRALRSDPTLAAGLIRM</u>	62
CsPRX55	MEAWRGLFLVMVMIVMEREGEQ.....	<u>LVENFSSSCNIVESIVNQVSTKFSQTFITAFATRL</u>	61
CsPRX72	MAHQTMFLIVVATLVFAPLC..FAHN.....	<u>LYFQGECHSCFKAEIVYSVVAQAVAEARMAASLRL</u>	63
CsPRX73	MGQFINLVIAVWSVSLCLSLASQA.....	<u>LRQNYHANVCNVENNVFNNAKQCFQQTFTVTPATRL</u>	62
Consensus		1 y cp z	
CsPRX3	<u>FHDC</u> EVRCGGGSILLNFTTASGNQTEKVAFFNLSVR..	<u>GESFIDRVKSLLEAE..CPGIVSCDIITLVTRISIVVTGG</u>	136
CsPRX4	<u>FHDC</u> EVNCGCGSILLDDTSS..FKGKTARPNNNGSVR.GYNVIDDIKSKVEKI..	<u>CPGIVSCDIITVAIAARISTVYLGG</u>	139
CsPRX12	<u>FHDC</u> EVRCGGGSVLLDGSAS..GPSBQEAFFNLSLRAEAFIINDLRRRVHKK..	<u>CGRVVSCDIITALAAADAVFLSGG</u>	156
CsPRX16	<u>FHDC</u> EVRCGGGSVILQNGG...KPEKDHDNLSLAGDGEDTVIKAKAAVSDPQCRNKVSCDILALATIRVIALAG		142
CsPRX27	<u>FHDC</u> EVRCGGGSVLLNSTKK..NQPEKDAFFNLSIR..	<u>GFQVIDAVKTALEKK..CPGIVSCDIITLALVQDAVSING</u>	139
CsPRX42	<u>FHDC</u> AVQSCDASLLDSTRR..SLSBKETDRSFGLR..NFRYLDITKEAVERE..	<u>CPGVVSCDIITLVLSGDDGVISLGG</u>	145
CsPRX43	<u>FHDC</u> EVRCGGGSILIDNGF...NPERHAFHQQGVG...GFEVIERTHAQLEAV..	<u>CPGVVSCDIITVAIAARDAIALANG</u>	132
CsPRX47	<u>FHDC</u> ELQCGDASVLIDSTKD..NTPEKDSFANLSIR..	<u>GVEIIDDAKQCLEQQ..CPGVVSCDIITVAIAARDAVFFAGG</u>	136
CsPRX55	<u>FHDC</u> EVRCGGGSIMISSPNG...DPBKDAFNDLSLAGDGEDTVIKAKAAVEAV..	<u>CPGVVSCDIITLAIASRDVVVLGG</u>	136
CsPRX72	<u>FHDC</u> EVRCGGGSLLDSSGS..IVSEKGSNPNRNSAR.GFEVLDAIKSALEKE..	<u>CENTVSCDIITLAAARISTVMTGG</u>	138
CsPRX73	<u>FHDC</u> EVRCGGGSVLISSGN..NKPEKDHDNLSLAGDGEDTVIKAKAAVDAIFSCRNKVSQDILAMATIRVVALSGG		140
Consensus	f h d c c s e c v s c d i l a m a t r d g		
CsPRX3	<u>FHWV</u> FTGRDGTIVSNATEALN.NIFAPTSNISTIQTKFAAKGLNLKDLVLISGAHTIGVAHSSFSNRLYNFTGVGDQD		215
CsPRX4	<u>FHWV</u> FKLGRDSTKASLAKANSQVIFPPTSLSNLIKREKARGLSAKMVLLVLSGSHITIGQARTSERNRINYNETH....		214
CsPRX12	<u>FHYD</u> VFLGRDGLIFATTNVTLANLGAESSNTITLLSSLATKKFEDATDVVALSGGHTIGISHCSSTIDRLYPQDIN....		232
CsPRX16	<u>FHSY</u> VELGRDGRISTIASVQH..KLSPNFSLDQINTMSSHGLTQSEMIALSGAHTIGFSHCFSRFSNRINYNFSPNRID		221
CsPRX27	<u>FHSW</u> VFTGRDGRISIAIDALN.NLSEPAFNIAQLKQSFASKGLSVKDLAVLSGGHTIGISHCFSEFVNRLYNFTGKGDIT		218
CsPRX42	<u>FVIL</u> PKTGRDGRKSRAEVLEQ.YLGDHNSMSVVLREFGSIGIDTPGVVAILGAHSVGRTHGVKLVHRLYPEVD....		219
CsPRX43	<u>FAYC</u> VFTGRDGSVSDVS.MAN.NMGGVSDSIEQLKAKFSQKGLSDQDLVLTAHTIGTTRCFMTDRLYNFFPFGSGSD		210
CsPRX47	<u>FVYE</u> IPRGRDGRISKIE..DTR.NLHFFFTNTSGLITMFAQHGFSAQEMVLLSGAHTIGVARCSSEKFRLSNFDSTHDT		214
CsPRX55	<u>FHSF</u> VELGRDGLVSGASDVAG.NLGEFSFNLQNTIIFAKNNLTQFEMIALSGAHTIGFSHCNRFANRLYFSSSSFVD		215
CsPRX72	<u>FSWE</u> VFLGRDPSKASLGSNN.NIFAPNNTFTQILTKEKLCGLDIVDLVALSGSHITIGNSRPTFSRQRLYNQSGNGLAD		217
CsPRX73	<u>FSYA</u> VELGRDGLSSTAASVNG.KLHCFGFNLQNLNSMFAAHGLSQTETIALSAPHTIGFSHCSREANRLYNFNRQNFVD		219
Consensus	p q r d p 1 h g c r		
CsPRX3	<u>FALD</u> SEYAAANFKARKPKTS...TDNTTLVEMDPGSFRTEFLDYITLVKRRGLFQSTESMRT.SSITKTYITQLLSGS..		289
CsPRX4	..IDSSFAKTRRR.SCPRAT.GSGDNNLAPLDLQTFTFFDNKYKYNLINQKGLLHSTQIHNN.GGSTDLSLVEKYSTNA..		287
CsPRX12	..MDRTFANNKLV.TCPA...LTDNTTVLDIRSPNKFEDNRYVVDLMNRQGLFTSQDYYT.DKRTDIVKSFVAVNE..		302
CsPRX16	<u>FTLN</u> SYALQLRQ.MOPIN...VDPRIANMDFTFTEFDNVYFQNLEQKGGLFTSETFT.DGRSKATVNLFSANN..		294
CsPRX27	<u>FTMD</u> QNYIAHLKS.KCKP...TDTTTFVNLSFRSTHKEFPNYITLVGKRRGLFQSDAPLIT.DSITTKAYIQLQAASK..		290
CsPRX42	<u>FVLN</u> PDHVEHMLH.KCPDSIFDPKAVQYVRNDRGTFMVLNNYRNILDNKGLLIVDHOAT.DKRTKPYVKKMAKSSQ..		295
CsPRX43	<u>FSIN</u> SEFLPELKS.MOPQN...GEVNVRIPIRSGSGQTFDNLQILNIRSGAAVLESAPRYD.DEATRSVVSYSFDALSP		285
CsPRX47	<u>FTLD</u> SNFAKILSK.TCSAG...DNAEQTFDARN...SFNDNYFNELTRSFGLVFSQTHYA.SARTRSIVNAYAMNQ..		284
CsPRX55	<u>FSLD</u> SSYAAQLMQ.ACPQN...VDPISAVMDPVTFTFENVYVYQNLIGGKGLFTSEVFT.NTASQSTVNDFAKNS..		288
CsPRX72	<u>MTLD</u> KSYAAQLRS.ROPRS...GGDQNLFFLDFVSFTKFDNYYFKNLASKGLINSQVFTKNQCTMELVKKYAENS..		291
CsPRX73	<u>FTLN</u> NFYAAQLQS.MCFRN...VDPRIANMDFNTFRTEDNMYFKNLQQGKGLFTSQVFT.DQRSKPTVNTWANN..		292
Consensus	c d l		
CsPRX3	..LQNIFYSEFALSMEKMGVRGVKTGSGAQIRKHCVAVNS.....		326
CsPRX4	..KTFYSDFAAAMIKMGDISPLTGSAGQIRKNCRKFN.....		322
CsPRX12	..TLFEKFLVLSMTKMGQLTVLTGTEGEIRANCSVRNSDNSYLAASVVGQEQEVVTLTG		358
CsPRX16	..SPFNQAFITAITKLGRVGVKTNQGEIHRDCTAIN.....		329
CsPRX27	..GSTFMKDFGESMVVMGQIGVLTGKSGEIRKQCNRIN.....		326
CsPRX42	..DYFKFEGRAITILSENNPLTGQGEIRLQONVANHH.....		333
CsPRX43	LFGPHFEITLWNSIVVMGQIDVKTGTQGEVRRVCGSFN.....		323
CsPRX47	..AFEFLEQQAMVKMGLLDVKEGSGNCEVRENCRRYN.....		319
CsPRX55	..NDENGAFATAMKKLGRVGVKTSQGGQIRIDOTSFNS.....		324
CsPRX72	..ELFFEQFAKSMIKMGNISPLIGSSGEIRKNCRKINS.....		327
CsPRX73	..PFQKAFVAAMTKLGRVGVKTSNGNIRIDCGAFN.....		327
Consensus	i d f f g g c n		

Secretory_peroxidase
Plant_peroxidase_like_superfamily

Fig. 1 Suppl. The sequence alignment of 11 PRXs from *Camellia sinensis*; the conserved peroxidase domain is underlined. Different colors mean different levels of homology: dark blue - 100 %, pink - ≥ 75 %, dark green - ≥ 50 %.

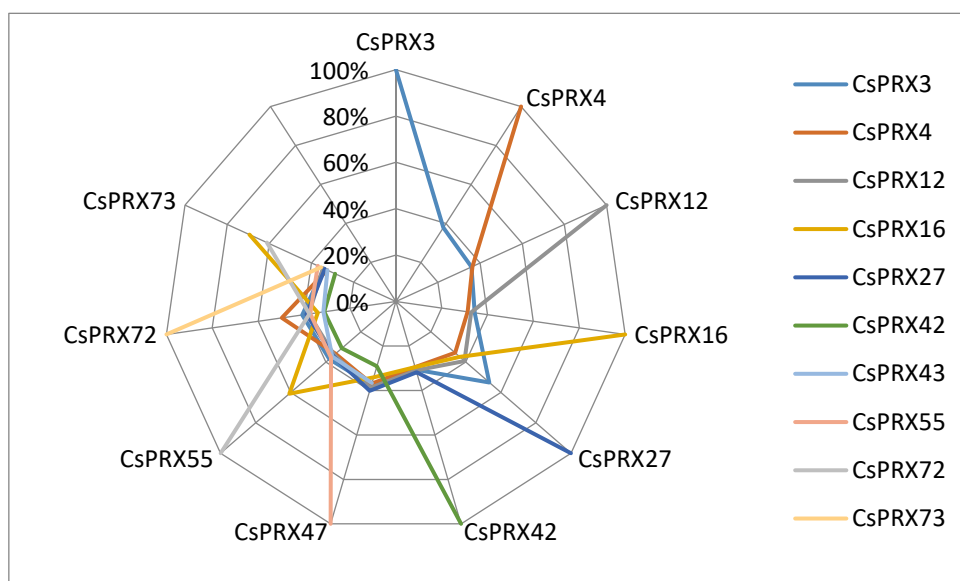


Fig. 2 Suppl. The radar map of two sequence similarities of CsPRXs.

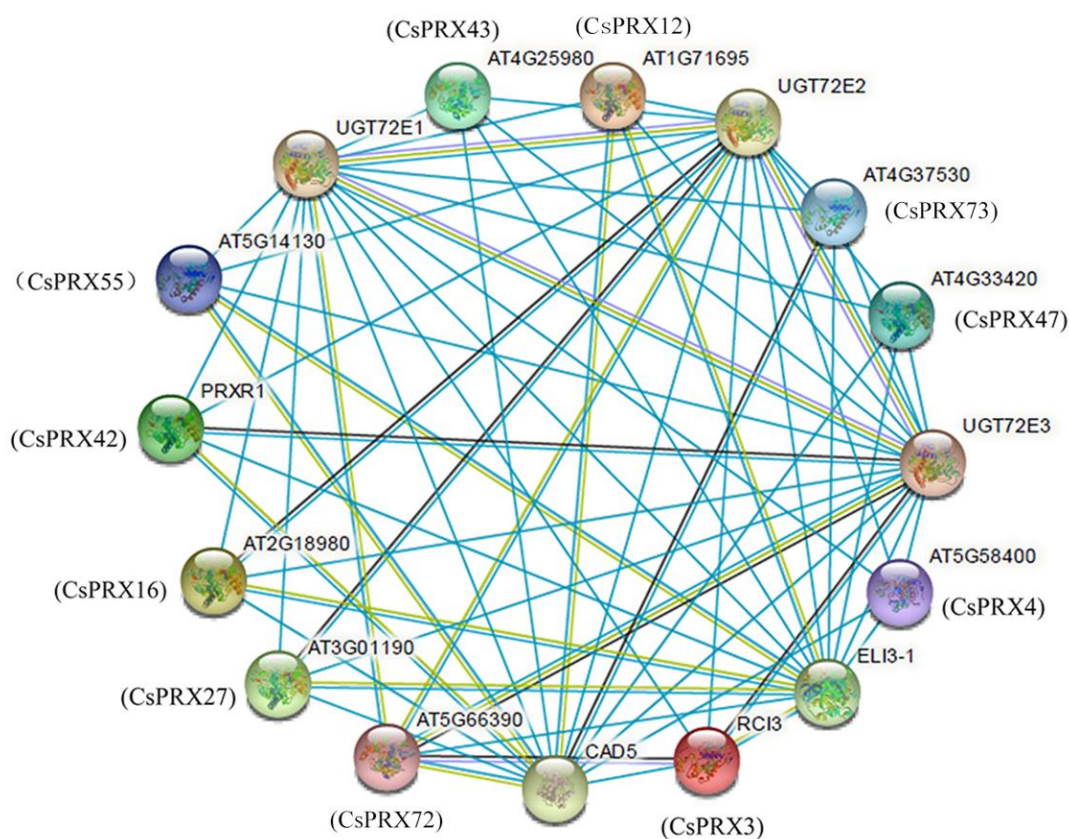


Fig. 3 Suppl. An orthologous protein interaction network map of PRXs based on the *Arabidopsis* and tea plants. Each *sphere* contains a known or predicted three-dimensional structure of proteins. Two proteins are connected by different lines, which represents the

relationship and different meanings between the two proteins. The *purple* lines represent co-expression between two proteins.

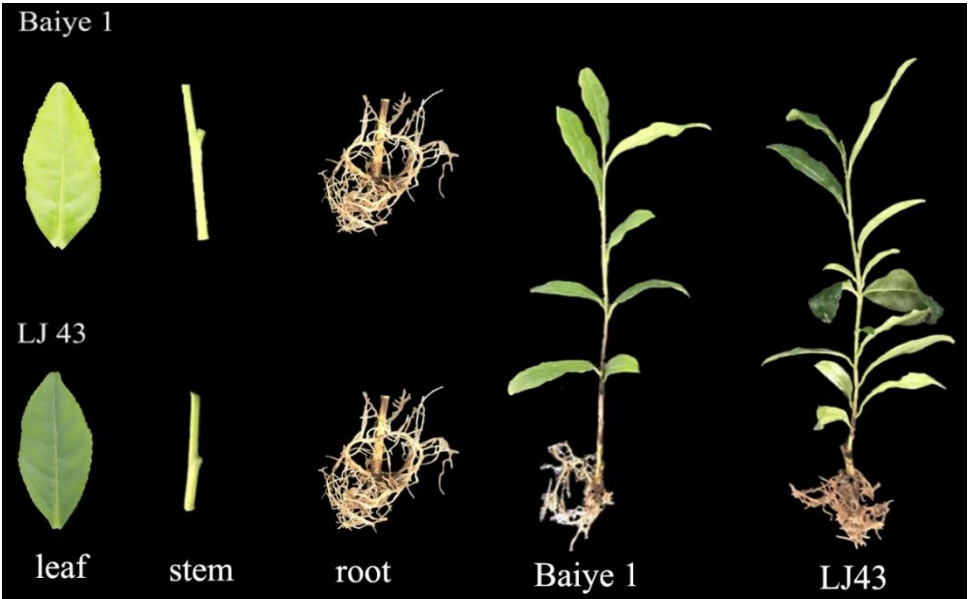


Fig. 4 Suppl. The photo of whole plants and their parts.

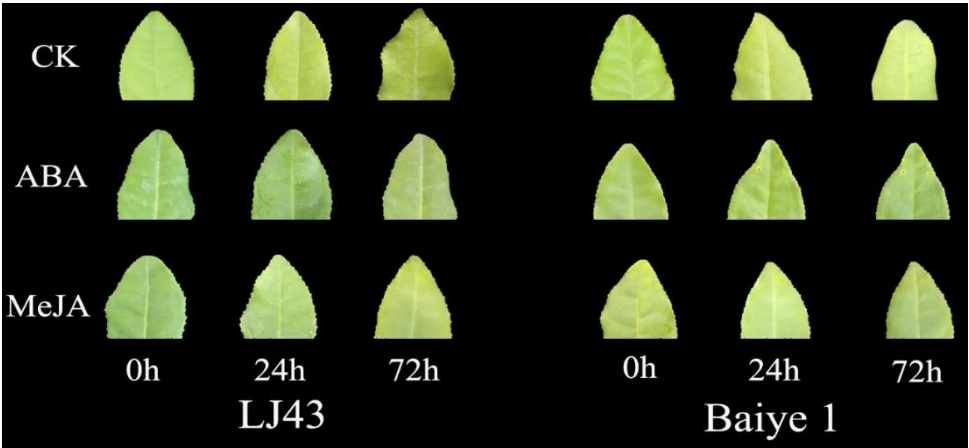


Fig. 5 Suppl. The picture of treated tea plant leaves.