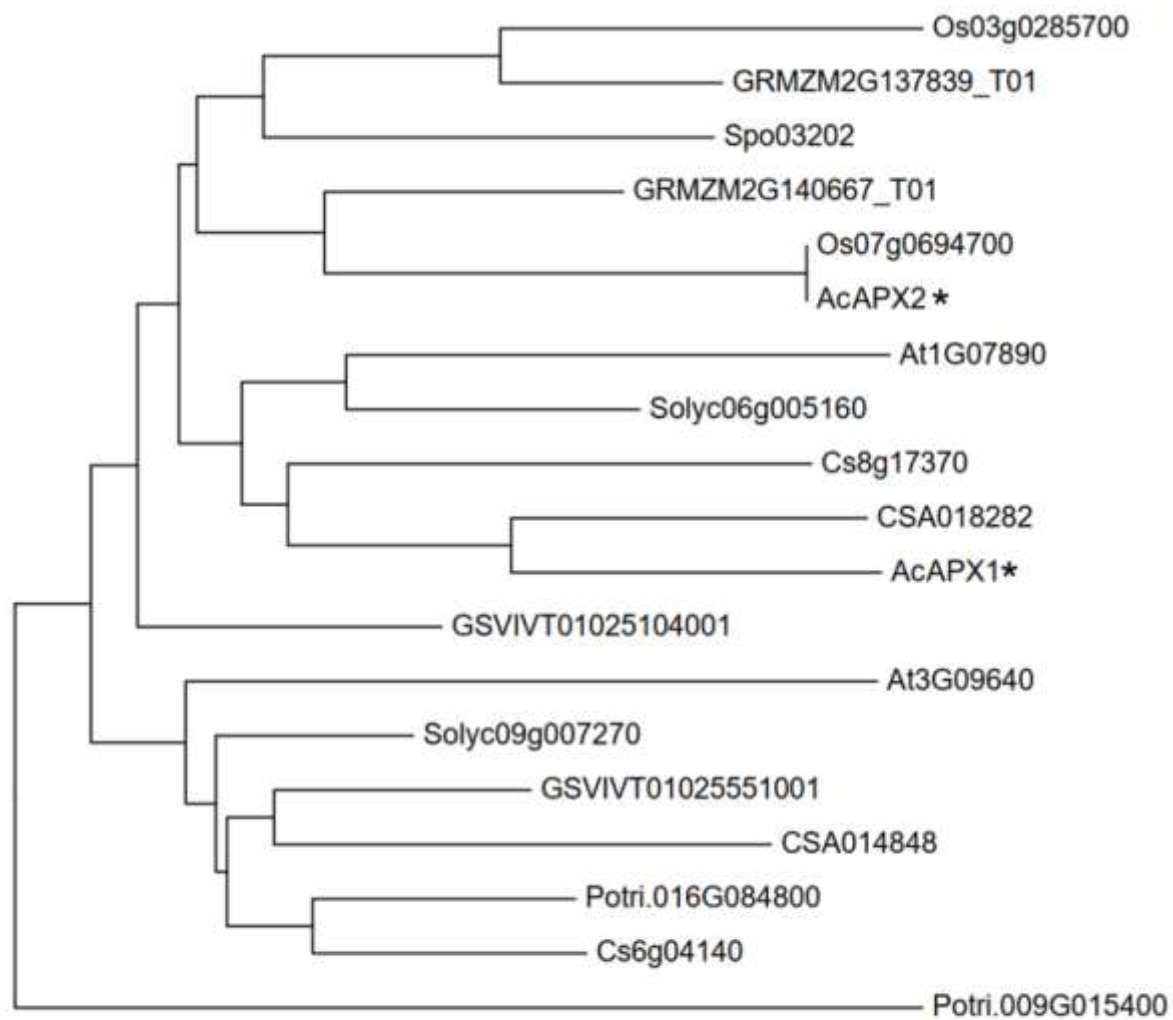


1 **Appendix A**Primer list.

Cloning primers		Real-time quantitative PCR primers	
<i>AcAPX1-F</i>	ATGGGGAAGTGCTACCCGA	<i>AcAPX1-qF</i>	GAGGTACAAGGCTGAGCTAGGC
<i>AcAPX1-R</i>	TTAAGCTTCAGCAAACCCCAATTC	<i>AcAPX1-qR</i>	CCCTGGATGGAACGGAATG
<i>AcAPX2-F</i>	ATGGGCAGCAAGTCGTACC	<i>AcAPX2-qF</i>	GGGAAGATGCCACAAGGAG
<i>AcAPX2-R</i>	TTATTCCTCAGCAAATCCCAGT	<i>AcAPX2-qR</i>	GCTCGGTGAAGTAAGAGTTGTC
		<i>AcUCE2-qF</i>	TAGTGCTCCAAATCCAGACGAT
		<i>AcUCE2-qR</i>	TCCATTCCTTCGCTGTTTCA
		<i>AcPP2A-qF</i>	TCAAAAGACAGGGTACCTAACATC
		<i>AcPP2A-qR</i>	CTGCTCTACCACAGACTGGT
		<i>AtMDHAR1-qF</i>	TGGGAGGACATTGGAAGCC
		<i>AtMDHAR1-qR</i>	CAACAGCGTAAACATCTGGAACA
		<i>AtDHAR1-qF</i>	CCCAGTGGTTCTTGGACATTAGT
		<i>AtDHAR1-qR</i>	TCCGTCATTGGAGTCTTTGCT



0.02

4 **Appendix B. Phylogenetic tree of cytosolic APXs from kiwifruit and other species.** (A) A total of 19 cytosolic APXs from
5 *Zea mays*, *Citrus sinensis*, *Oryza sativa*, *Vitis vinifera*, *Arabidopsis thaliana*, *Actinidia chinensis*, *Populus trichocarpa*,
6 *Solanum lycopersicum*, *Camellia sinensis* and *Spinacia oleracea* were used to construct a Neighbor-Joining tree with 1000
7 bootstraps. AcAPX1 and AcAPX2 are marked with asterisks.

8

9 **Appendix C** Characterization of AcAPX1/2 proteins.

Protein name	Gene ID	Conserved Features/Sites			Deduced polypeptide				Genome location			Subcellular location
					Length (aa)	MW (kDa)	pI	Chr	Sequence position	Direction		
AcAPX1	Ach28g059971 / Acc32260.1 / NCBI accession no. MT074089	heme binding site	substrate binding site	K+ binding site		250	27.60046	5.65	Chr28	13029189-13034144	(-strand)	Cytosolic
AcAPX2	Unigene28335, Unigene22069 / NCBI accession no. MT074090	heme binding site	substrate binding site	K+ binding site		251	27.11756	5.18	-	-	-	Cytosolic
	Cys32	Arg38	Trp41	His42	Glu65	Asn71	Pro125	His163	Arg172	Phe175	Trp179	Asp208
AcAPX1	C	R	W	H	E	N	P	H	R	F	W	D
AcAPX2	C	R	W	H	E	N	P	H	R	F	W	D

11 **Appendix D** The *APX* family members in representative plant genomes.

Plant species	Gene ID
<i>Arabidopsis thaliana</i> ^[1]	AT1G07890
	AT1G77490
	AT3G09640
	AT4G08390
	AT4G09010
	AT4G32320
	AT4G35000
	AT4G35970
<i>Brachypodium distachyon</i> ^[1]	Bradi1g16510
	Bradi1g65820
	Bradi3g40330
	Bradi3g42340
	Bradi3g45700
	Bradi5g10490
	Bradi5g20670
<i>Brasica rapa</i> ^[1]	Brara.A00250
	Brara.A03521
	Brara.C02583
	Brara.G03518
	Brara.I02406
	Brara.I05334
	Brara.K00318
	Brara.K00699
<i>Cucumis sativus</i> ^[1]	Cucsa.060660
	Cucsa.162470
	Cucsa.213340
	Cucsa.311620
	Cucsa.370590
<i>Glycine max</i> ^[1]	Glyma.04G248300
	Glyma.06G068200
	Glyma.06G114400
	Glyma.11G078400
	Glyma.12G032300
	Glyma.12G073100
	Glyma.14G177200
<i>Zea mays</i> ^[1]	GRMZM2G004211
	GRMZM2G006791
	GRMZM2G047968
	GRMZM2G054300
	GRMZM2G120517
	GRMZM2G137839

	GRMZM2G156227
	GRMZM2G460406
<i>Sorghum bicolor</i> ^[2]	Sobic.001G410200
	Sobic.002G431100
	Sobic.004G175500
	Sobic.006G021100
	Sobic.006G084400
	Sobic.006G204000
	Sobic.007G177000
	Sobic.007G205600
	Sobic.008G057900
<i>Vitis vinifera</i> ^[1]	GSVIVG01008846001
	GSVIVG01009079001
	GSVIVG01024035001
	GSVIVG01025104001
	GSVIVG01025551001
	GSVIVG01035858001
<i>Oryza sativa</i> ^[1]	LOC_Os02g34810
	LOC_Os04g35520
	LOC_Os04g51300
	LOC_Os07g49400
	LOC_Os08g41090
	LOC_Os08g43560
<i>Prunus persica</i> ^[1]	ppa006270m
	ppa008008m
	ppa009582m
	ppa010413m
	ppa010426m
	ppa015878m
<i>Solanum lycopersicum</i> ^[1]	Solyc01g111510
	Solyc04g074640
	Solyc06g005150
	Solyc06g060260
	Solyc08g059760
	Solyc09g007270
	Solyc11g018550
<i>Actinidia chinensis</i> ‘Hongyang’ (V2.0)	Ach00g289741.2
	Ach04g123031.2
	Ach05g207061.2
	Ach07g340531.2
	Ach11g265461.2
	Ach11g265471.2
	Ach13g315041.2

	Ach21g117191.2
	Ach21g117211.2
	Ach23g082241.2
	Ach25g187071.2
	Ach28g059971.2
<i>A. chinensis</i> 'Hongyang' (V3.0)	Actinidia00816.t1
	Actinidia02628.t2
	Actinidia03760.t1
	Actinidia14603.t1
	Actinidia21310.t1
	Actinidia22955.t1
	Actinidia23590.t1
	Actinidia31250.t1
	Actinidia33123.t1
	Actinidia37285.t1
	Actinidia37405.t1
<i>A. chinensis</i> 'Red5'	Acc05061.1
	Acc07257.1
	Acc12171.1
	Acc14912.1
	Acc16308.1
	Acc16953.1
	Acc24386.1
	Acc24431.1
	Acc25912.1
	Acc25913.1
	Acc29186.1
Acc32260.1	
<i>A. eriantha</i> 'White'	DTZ79_02g05110
	DTZ79_04g07750
	DTZ79_07g00590
	DTZ79_11g03570
	DTZ79_13g11560
	DTZ79_14g12160
	DTZ79_21g08460
	DTZ79_21g12410
	DTZ79_23g05560
	DTZ79_25g10220
	DTZ79_28g09910
	DTZ79_28g09970

Based on Blast analyses, the Ascorbate Peroxidase (APX) family members in kiwifruit were identified from four different genome sequences, including *Actinidia chinensis* ‘Hongyang’ (V2.0), *Actinidia chinensis* ‘Hongyang’ (V3.0), *A. chinensis* ‘Red5’ and *A. eriantha*. All the genome sequences were downloaded from the kiwifruit genome database (kiwifruitgenome.org). The sequences of APXs from other representative plants were retrieved from Phytozome (phytozome.jgi.doe.gov).

References

1. Akbudak MA, Filiz E, Vatansever R, Kontbay K. 2018. Genome-wide identification and expression profiling of ascorbate peroxidase (APX) and glutathione peroxidase (GPX) genes under drought stress in sorghum (*Sorghum bicolor* L.). *Journal of Plant Growth Regulation*, **37**, 925 - 936.
2. Ozyigit II, Filiz E, Vatansever R, Kurtoglu KY, Koc I, Ozturk MX, Anjum NA. 2016. Identification and comparative analysis of H₂O₂-scavenging enzymes (ascorbate peroxidase and glutathione peroxidase) in selected plants employing bioinformatics approaches. *Frontiers in Plant Science*, **7**, 301.

AchAPX1 MGKCYPTVSD⁵⁰EYK⁵¹K⁵²LDKAKR⁵³KLRG⁵⁴FIADKNCAPLMRLRLAWHSAGTYDVITK⁵⁵TGGPF⁵⁶GTMR⁵⁷YK⁵⁸AE⁵⁹LGHAAN⁶⁰GLEI⁶¹AVRLL⁶²EP⁶³IK⁶⁴Q⁶⁵FP⁶⁶IL⁶⁷S⁶⁸FG⁶⁹DFY⁷⁰QL 99
 AchAPX2 MGS⁷¹KSYPTVSD⁷²EYLA⁷³AVGKAKR⁷⁴KLRG⁷⁵LI⁷⁶AEKNCAPLMRLRLAWHSAGTFD⁷⁷VSS⁷⁸R⁷⁹TGGPF⁸⁰GTMR⁸¹NP⁸²GE⁸³QSHAAN⁸⁴AGL⁸⁵I⁸⁶AVRLL⁸⁷EP⁸⁸IK⁸⁹Q⁹⁰FP⁹¹IL⁹²SY⁹³ADF⁹⁴Y⁹⁵QL 100
 Consensus mg k yptvs ey a kakrklrg ia kncaplmrlrlawhsagt dv tggpfgtm e haan gl iavrll pik q pils dfyql

Heme binding site

AchAPX1 AGVVAVEITGGEDIPFHPGREDKPEPELEGRLPDATQGS¹⁹⁹DHLR²⁰⁰DFVEV²⁰¹KEMGL²⁰²DKDIVALS²⁰³GGHTLGRCHKERSGFEG²⁰⁴WTINPLIFD²⁰⁵NSY²⁰⁶HT²⁰⁷EL²⁰⁸VS²⁰⁹G²¹⁰EK 199
 AchAPX2 AGVVAVEITGGEVIPFHPGRQDKPEPELEGRLPDATQGS¹⁹⁹DHLR²⁰⁰DFVSA²⁰¹QMGL²⁰²DKDIVALS²⁰³GGHTLGRCHKERSGFEG²⁰⁴WTSNPLIFD²⁰⁵NSY²⁰⁶HT²⁰⁷EL²⁰⁸VS²⁰⁹G²¹⁰EK 200
 Consensus agvvave tggp pfhpgr dkpepp egrlpdatqgsdhlr vf mgl dkdivalsggghtlgrchkersgfeg wt nplifd²⁰⁵nsyf el gek

Substrate binding site

K⁺ binding site

AchAPX1 DGLLQLE²⁴⁹DK²⁵⁰VL²⁵¹AD²⁵²SAFRPLVEKYAAED²⁵³VF²⁵⁴FADYAEAH²⁵⁵KLSELGFAE 249
 AchAPX2 EGLLQLES²⁴⁹DK²⁵⁰FL²⁵¹AD²⁵²SAFRPLVEKYAAED²⁵³VF²⁵⁴FADYAEAH²⁵⁵KLSELGFAE 250
 Consensus gllqlp dk l ad afrplvekyaaed ffadyaeah klselgfae

- 13 Appendix E. Sequence comparison of AcAPX1/2 proteins. Amino acid residues
 14 that are completely conserved are in dark blue, and those that share >50%
 15 homology are in cyan. Heme binding site, substrate binding site and K⁺
 16 binding site are designated with red, yellow and green lines.
 17
 18
 19