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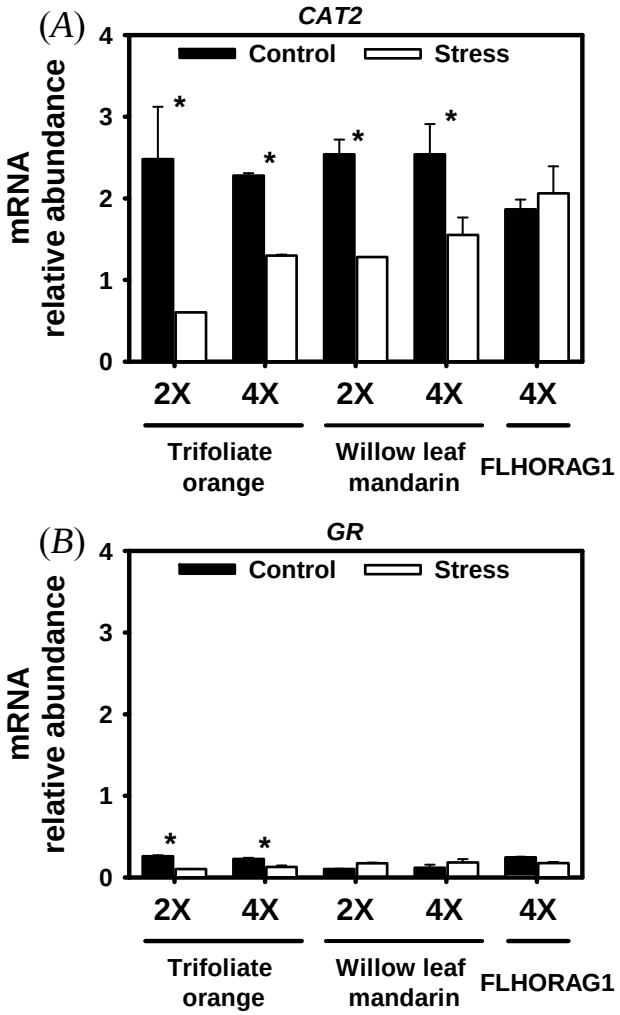

Fig. 1. Relative mRNA abundance coded by genes of (*A*) Catalase 2 (*CAT2*) and (*B*) Glutathion Reductase (*GR*). RNA were prepared from sampling harvested after 7 weeks of stress. Expression profiles were determined by qRT-PCR. Arbitrary units were assigned to mRNA level scales. Vertical bars indicate the mean value ± s.e. For each genotype, * indicates a significant change of gene expression (*t*-test) between control and stress condition ($P < 0.05$).

Table S1. Nuclear SSR markers used for the characterisation of allotetraploid FLHORAG1

Numbers in the table correspond to the band size obtained for each genotype. 4× trifoliate orange and 4× Willow leaf mandarin genotypes presented the same profiles than their respective 2×. Ta, annealing temperature

SSR markers			Genotypes		
Primer name	Primer sequence (5'-> 3')	Ta (°C)	Trifoliate orange	Willow leaf mandarin	FLHORAG1
Ci01C07	[19]	55	272	258/260	258/260/272
Ci02A04	[19]	55	180	184	180/184
Ci02B07	[19]	50	184	178/186	178/186/184
Ci02C09	[19]	50	253	269	253/269
Ci02F03	[19]	55	174	186	174/186
Ci07C07	[19]	50	225	243/255	225/243/255
Ci07D06	[18]	55	161	179/187	161/179/187
Ci07E06	[19]	55	256	244	244/256
mCrCIR01D06a	[19]	50	244	248/250	244/248/250
mCrCIR01F04a[B]	[19]	55	200/206	214/218	200/206/214/218
mCrCIR01F08a	[19]	50	32	136	132/136
mCrCIR02A01[A]	F : TAAATGGTGACTGGTGAG R : GCTTATGGATTGCGTT	55	312	304	312/304
mCrCIR02B11[A]	F : GTATTTGGCGTGATGAA R : CAAAGTAAATAGGGTGTGAG	55	247	256/264	247/256/264
mCrCIR02D03[A,B]	F : CAGACAACAGAAAACCAA R : GACCATTTTCCACTCAA	55	292/312	296/312	292/296/312
mCrCIR02D04b[A]	F : CTCTCTTTCCCCATTAGA R : AGCAAACCCCACAAC	50	211/213	215/244	211/213/215/244
mCrCIR02D11[A]	F : GAGTTGACCGAGAAGATT R : TGAGTTTCAGTAAGTGTATGAG	55	192	218/220	192/218/220
mCrCIR02E02a[A]	F : AGTGAGAAAGACTGGTGTG R : ACTTTCCCCATTTTGAT	50	220/222	210/220	210/220/222
mCrCIR02E08[A]	F : GGTTTGTGGGAGGTG R : TGATTAGCATGTTGCG	50	316	276/284	276/284/316
mCrCIR02G02[A]	F : CAATAAGAAAACGCAGG R : RTGGTAGAGAAACAGAGGTG	55	130/134	136/140	130/134/136/140
mCrCIR02G08[A]	F : CATGCAATGTTCCACTT R : AGGCAGTTGTTAGACCC	50	250	260	250/260
mCrCIR02G12[A,B]	F : AAACCGAAATACAAGAGTG R : TCCACAAACAATACAACG	55	278	266	266/278
mCrCIR03F09[A]	F : CGTCCATCTAAGTGACC R : TTTAACCTTCAGTAGAAACC	55	158	176	158/176
mCrCIR04H06[A]	F : GGACATAGTGAGAAGTTGG R : CAAAGTGGTGAAACCTG	55	202	208/214	202/208/214
mCrCIR05A05[A,B]	F : ATACCTGTGAGCGTGAG R : CCTCTTCCCTTCCATT	55	146/165	156/160	146/156/160/165
mCrCIR05D11[A]	F : TCAACATTCCTTACCAGA R : ATCATTCTCACTGCACC	55	268	248	248/268
mCrCIR06B05	[19]	55	0	222/244	222/244
mCrCIR07B05	[19]	50	216	222/266	216/222/266
mCrCIR07D07	[19]	55	216	222	216/222
mCrCIR07E05[B]	[19]	50	146/148	136/138	136/138/146/148
mCrCIR07G11	[19]	50	214/220	220/226	214/220/226
MEST0010	[20]	55	178	168/170	168/170/178
MEST0817	[20]	55	146	172/196	242/252/254

[A]SSR markers defined in the main paper.

[B]SSR markers used for analyzing the genetic conformity of the seedling.

Table S2. Chloroplastic and mitochondrial parental origins of the allotetraploid FLHORAG1

Three SSR markers (ccmp3, ccmp6′ and NTCP9′) were used for chloroplastic analysis and three PCR markers (*nad*7/1–2 and *nad*5/2–1) were used for mitochondrial analysis. Numbers in the table correspond to the PCR product size obtained for each genotype

	SSRs chloroplastic markers			Mitochondrial markers	
Genotypes	ccmp3	ccmp6′	NTCP9′	*nad*7/1–2	*nad*5/2–1
Willow leaf mandarin	104	127	255	152	220
Trifoliate orange	103	139	254	132	210
FLHORAG1	103	139	254	152	220

Table S3. Sequences of the primers used to monitor by qRT-PCR the expression of candidate genes

Name	Protein encoded by the targeted gene	Sequence of the forward primer (5′ -> 3′)	Sequence of the reverse primer (5′ -> 3′)	mRNA origin	Accession number	Size of the product of amplification (bp)	Tm
PAM1	Protein Arginine N-MethylTransferase	GATATGCTCTCCGACCGTGT	TTCAACGGCATAAACCTTCC	*Arabidopsis thaliana*	AJ007582	161	55
RZFP	Ring H_2-Zinc Finger Protein	AGCCACTTCTCCAAGCACAC	GTTGAGGAGTTCCGAAACCA	*Poncirus rubidoux*	aCL198Contig1	170	56
MYB8	MYB8 transcription factor	GAAGTGGATCGGATCAAAGG	GTGCTCGACTTGAGGTGACA	*Citrus sinensis*	aCL891Contig1	174	56
SOS3	Calcium protein sensor	TCTTTCCAGGCTCTTGCTTC	GGACCATGGGGTTTTTATGA	*Oryza sativa*	DQ201198	173	54
cNHX1	Antiport vacuolaire Na^+/H^+	GCGGGAAAACGCTATTATGA	AGTGGCTGCGACAGAGATTT	*Citrus paradisi*	AY028416	171	54
SOS1	Antiport membranaire Na^+/H^+	TCTTTCCAGGCTCTTGCTTC	GGACCATGGGGTTTTTATGA	*Citrus clementina*	aIC0AAA94AC03RM1_c	173	52
CCC12Ac	Transporteur de Cl^-	GTAGGGATGGTGAAGATGC	AAGCTACCACCAATAACGAG	*Arabidopsis thaliana*	NM_001036913	183	53
CMO	Choline MonoOxygenase	GCAACTGGAAGGTTTTCTGC	CAAGGCGATGGGTATCATCT	*Citrus reticulata × C. temple*	aC32201B02EF_c	180	55
cLEA5	Group 5 Late Embryogenesis Abundant	ACCCTTGGGGACCATATCTC	CTCTCGAAGCTCTGCTGGAT	*Citrus unshiu*	aCL9Contig8	166	57
P5CS	Delta 1 Pyrolline 5 Carboxylate Synthetase	ATGTGCGTGCTGCTATTGAC	AGTCCAAATCGTGCTCCATC	*Citrus sinensis*	aCL174Contig2	166	55
NCED1	9 Cis Epoxycarotenoid Dioxygenase	GACCAGCAAGTGGTGTTCAA	AGAGGTGGAAACAGGAGCAA	*Citrus cv.* Shiranuhi	aCL1933Contig1	163	55
CAT2	Catalase 2	ACCGTCTAGGGCCGAACTAT	TTTCAGGAGGAGTTGGATGC	*Citrus sinensis*	aCL63Contig2	174	53
GR	Glutathione Reductase cytosolique	GGAGGAGCTACCAAAACGTG	TGCTGGATTTCAGATGCTTG	*Oryza sativa*	NM_001055020	179	55