

## SUPPLEMENTARY DATA

TABLE S1. Genotypes used in this study

Group	Scientific name (Swingle)	Scientific name (Tanaka)	Cultivar	Ref.*
Mandarin	<i>C. reticulata</i> var. <i>austera</i>	<i>C. reshni</i> Hort. ex Tan.	Cleopatra	385I
Mandarin	<i>C. reticulata</i> Blanco	<i>C. deliciosa</i> Ten	Willow leaf	154I
Mandarin	<i>C. reticulata</i> Blanco	<i>C. reticulata</i> Blanco	Ponkan	482I
Mandarin	<i>C. reticulata</i> var. <i>austera</i>	<i>C. sunki</i> Hort. ex Tan.	Sunki	239I
Mandarin	<i>C. reticulata</i> Blanco	<i>C. tangerina</i> Hort. ex Tan.	Dancy	434I
Mandarin	<i>C. reticulata</i> Blanco	<i>C. unshiu</i> (Mak.) Marc.	Clausellina	19I
Mandarin	<i>C. reticulata</i> Blanco	<i>C. deliciosa</i> Ten	Avana apireno	189I
Pummelo	<i>C. maxima</i> (Burm.) Merr.	<i>C. maxima</i> (Burm.) Merr.	Chandler	207I
Pummelo	<i>C. maxima</i> (Burm.) Merr.	<i>C. maxima</i> (Burm.) Merr.	Pink	275I
Pummelo	<i>C. maxima</i> (Burm.) Merr.	<i>C. maxima</i> (Burm.) Merr.	Nam Roi	590I
Pummelo	<i>C. maxima</i> (Burm.) Merr.	<i>C. maxima</i> (Burm.) Merr.	Tahiti	727C
Pummelo	<i>C. maxima</i> (Burm.) Merr.	<i>C. maxima</i> (Burm.) Merr.	Sans Pepins	710C
Citron	<i>C. medica</i> L.	<i>C. medica</i> L.	Corsica	567I
Citron	<i>C. medica</i> L.	<i>C. medica</i> L.	Buddha's hand	202I
Citron	<i>C. medica</i> L.	<i>C. medica</i> L.	Diamante	560I
Citron	<i>C. medica</i> L.	<i>C. medica</i> L.	Arizona	169I
Citron	<i>C. medica</i> L.	<i>C. medica</i> L.	Poncire commun	701C
Papeda	<i>C. micrantha</i> Wester	<i>C. micrantha</i> Wester	Small flowered papeda	626I
Papeda	<i>C. hystrix</i> DC.	<i>C. hystrix</i> DC.	Mauritius papeda	178I
Papeda	<i>C. ichangensis</i> Swing.	<i>C. ichangensis</i> Swing.	Ichang papeda	358I
Papeda	<i>C. macroptera</i> Montr.	<i>C. macroptera</i> Montr.	Melanesian papeda	279I
Fortunella	<i>F. hindsii</i> (Champ.) Swing.	<i>F. hindsii</i> (Champ.) Swing.	Hong Kong kumkuat	281I
Fortunella	<i>Fortunella</i> hybrid	<i>F. crassifolia</i> Swing.	Meiwa kumkuat	280I
Fortunella	<i>F. japonica</i> (Thunb.) Swing.	<i>F. japonica</i> (Thunb.) Swing.	Round kumkuat	381I
Fortunella	<i>F. polyandra</i> (Ridl.) Tan	<i>F. polyandra</i> (Ridl.) Tan.	Malayan kumkuat	375I
Fortunella	<i>F. margarita</i> (Lour.) Swing.	<i>F. margarita</i> (Lour.) Swing.	Nagami kumkuat	38I
Microcitrus	<i>Microcitrus australasica</i> (F. Muell.) Swing.	<i>Microcitrus australasica</i> (F. Muell.) Swing.	Australian finger lime	150I
Microcitrus	<i>Microcitrus australis</i> (F. Muell.) Swing.	<i>Microcitrus australis</i> (F. Muell.) Swing.	Australian round lime	313I
Eremocitrus	<i>Eremocitrus glauca</i> (Lindl.)	<i>Eremocitrus glauca</i> (Lindl.)	Australian desert lime	346I
Poncirus	<i>Poncirus trifoliata</i> (L.) Raf.	<i>Poncirus trifoliata</i> (L.) Raf.	Pomeroy	374I
Poncirus	<i>Poncirus trifoliata</i> (L.) Raf.	<i>Poncirus trifoliata</i> (L.) Raf.	Rubidoux	217I
Poncirus	<i>Poncirus trifoliata</i> (L.) Raf.	<i>Poncirus trifoliata</i> (L.) Raf.	Flying dragon	537I
Haploid	<i>C. reticulata</i> Blanco	<i>C. clementina</i> Hort. ex Tan.	Haploid	HapClem
Clementine	<i>C. reticulata</i> Blanco	<i>C. clementina</i> Hort. ex Tan.	Clemenules	22I
Clementine	<i>C. reticulata</i> Blanco	<i>C. clementina</i> Hort. ex Tan.	Arrufatina	58I
Tangelo	<i>C. reticulata</i> x <i>C. paradisi</i>	<i>C. reticulata</i> x <i>C. paradisi</i>	Orlando	101I
Tangor	<i>C. reticulata</i> x <i>C. sinensis</i>	<i>C. nobilis</i> Lour.	King	477I
Sweet orange	<i>C. sinensis</i> (L.) Osb	<i>C. sinensis</i> (L.) Osb	Valencia Late Delta	363I
Sweet orange	<i>C. sinensis</i> (L.) Osb	<i>C. sinensis</i> (L.) Osb	Salustiana	125I
Grapefruit	<i>C. paradisi</i> Macf	<i>C. paradisi</i> Macf	Marsh	176I
Sour orange	<i>C. aurantium</i> L.	<i>C. aurantium</i> L.	Sevillano	117I
Sour orange	<i>C. aurantium</i> L.	<i>C. aurantium</i> L.	Bouquet de Fleurs	139I
Lime	<i>C. aurantifolia</i> (Christm.) Swing.	<i>C. aurantifolia</i> (Christm.) Swing.	Mexican	164I
Lemon	<i>C. limon</i> (L.) Burm	<i>C. limon</i> (L.) Burm	Eureka	297I
Severinia	<i>Severinia buxifolia</i> (Poir.) Tenore	<i>Severinia buxifolia</i> (Poir.) Tenore	Chinese box orange	147I

\*(I) IVIA germplasm; (C) INRA germplasm.

TABLE S2. New indel primers developed from polymorphisms found during sequencing of the candidate genes

Primer	GBA	Sequence	Length	T <sub>m</sub>	PCR	Product size (bp)
IDCHI2	DY263683	F:AATCAATTATTTCCACATT	20	48.91	50	94–96
		R:ATTACACGTAACGCAAGA	18	53.2		
IDFLS1	AB011796	F:GATCATCTCTCCACAGG	18	50.64	50	144–158
		R:GAAAATAAATTATTTATACATTTTGTTT	28	52.86		
IDFLS2	AB011796	F:AAACAAAATGTATAAATAATTTATTTTC	28	52.86	50	184–204
		R:AGCATGTACTCAATGTCG	18	49.76		
IDF3'H1	HQ634392	F:AAAGGCTCACCATCACCAAC	20	59.97	55	180–196
		R:AAAATGAACAACACAAAAGAAAGACC	25	55.2		
IDDFR1	DQ084722	F:CCACGCCTATGGACTTTGAG	20	60.65	55	181–192
		R:TCAATGTTATGCGGCTGTTC	20	59.69		
IDDFR2	DQ084722	F:ACTGTTCGCGATCCTGGT	18	59.21	55	140–156
		R:GCAACTCCAGCAAATGTTTC	20	58.35		
IDINVA1	AB074885	F:GAGCTCCCTTTTGCTTAAT	20	57.58	55	218–220
		R:AGTAGCTGAGCCAACATCAA	20	56.09		
IDINVA2	AB074885	F:CCTTCTGGTTCTTGCAGAT	19	55.35	55	233–237
		R:TATTGACATCATTTGCCTCA	20	55.01		
IDINVA3	AB074885	F:TTCTGAGGCAAATGATGTCAA	21	59.26	55	203–206
		R:CGAATGATCCACCTGCAAAT	20	60.86		
IDPEPC3	EF058158	F:TTTGTGATGTTCCACAAATG	20	55.3	55	130–133
		R:CTACCATTAGCCGATTGTTC	20	54.93		
IDPFK1	AF095520	F:AAAACCCTTTCAAATCGTC	20	55.85	55	246–248
		R:CCGATTTTCAACTTCTCATC	20	54.84		
IDPSY2	AB037975	F:TTGAGTCATGCCATTTTGC	20	59.67	55	347–364
		R:ATTGGGTTAAGGGTCCACTG	20	58.76		

GBA: Gene Bank Accession.

T<sub>m</sub>: melting temperature

TABLE S3. Nucleotide diversity and divergence for each gene and taxa. Abbreviations: Mand, *C. reticulata*; Pum, *C. maxima*; Cit, *C. medica*; For, *Fortunella*; Pap, Papeda, wild citrus; Mic, *Microcitrus*; Ere, *Eremocitrus*; Pon, *Poncirus trifoliata*; AncTaxa, *C. reticulata*, *C. maxima*, *C. medica*, wild citrus; Pop, population; S, segregating sites;  $\pi_T$ , total nucleotide diversity;  $\pi_{sil}$ , nucleotide diversity silent sites;  $\pi_{syn}$ , nucleotide diversity synonymous sites;  $\pi_{nonsyn}$ , nucleotide diversity non-synonymous sites;  $\pi_{nonsyn/syn}$ , ratio of nucleotide diversity non-synonymous / synonymous sites;  $\pi_{nonsyn}/\pi_{sil}$ , ratio of nucleotide diversity non-synonymous/silent sites;  $D_{tajima}$ , Tajima's *D* neutrality test;  $N_h$ , number of haplotypes;  $H_e$ , haplotype diversity; s.d., standard deviation;  $F_{st}$ , Wright's differentiation index. See Table 1 in main text for locus abbreviations

Locus	Taxa	S	Polymorphism						Haplotype diversity				
			$\pi_T$	$\pi_{sil}$	$\pi_{syn}$	$\pi_{nonsyn}$	$\pi_{nonsyn}/\pi_{syn}$	$\pi_{nonsyn}/\pi_{sil}$	$D_{tajima}$	$N_h$	$H_e$	s.d.	$F_{st}$
CHI	Mand	20	0.009	0.010	0.011	0.006	0.522	0.541		7	0.833	0.072	0.757
	Pum	6	0.003	0.002	0.000	0.007	-	3.036		5	0.756	0.130	
	Cit	21	0.013	0.017	0.007	0.002	0.320	0.136		3	0.622	0.138	
	For	12	0.007	0.007	0.000	0.006	-	0.848		5	0.667	0.163	
	Pap	22	0.014	0.016	0.000	0.007	-	0.425		5	0.933	0.122	
	Mic	8	0.008	0.010	0.000	0.004	-	0.448		2	0.667	0.204	
	Ere	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	Pon	1	0.001	0.001	0.000	0.000	-	0.000		2	0.600	0.129	
	AncTaxa	73	0.026	0.032	0.008	0.011	1.381	0.361	-0.300	28	0.959	0.010	
	Whole Pop	76	0.024	0.030	0.008	0.010	1.377	0.350	-0.407	34	0.958	0.008	
s.d.			0.001										
CHS	Mand	1	0.001	0.003	0.003	0.000	0.000	0.000		2	0.440	0.112	0.698
	Pum	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	Cit	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	For	4	0.001	0.005	0.005	0.000	0.096	0.096		3	0.378	0.181	
	Pap	5	0.004	0.009	0.009	0.002	0.207	0.207		5	0.933	0.122	
	Mic	4	0.003	0.008	0.008	0.002	0.289	0.289		2	0.500	0.265	
	Ere	1	0.002	0.008	0.008	0.000	0.000	0.000		2	1.000	0.500	
	Pon	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	AncTaxa	20	0.004	0.016	0.016	0.001	0.079	0.079	-1.256	14	0.885	0.015	
	Whole Pop	20	0.004	0.015	0.014	0.001	0.065	0.064	-1.258	15	0.857	0.018	
s.d.			0.000										
FLS	Mand	14	0.008	0.015	0.019	0.002	0.442	0.145		7	0.817	0.073	0.608
	Pum	4	0.004	0.007	0.005	0.003	0.567	0.372		5	0.844	0.080	
	Cit	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	For	7	0.007	0.017	0.018	0.003	0.151	0.167		6	0.889	0.075	
	Pap	14	0.014	0.040	0.033	0.004	0.137	0.113		6	1.000	0.096	
	Mic	8	0.010	0.025	0.030	0.004	0.121	0.142		4	1.000	0.177	
	Ere	10	0.022	0.046	0.064	0.012	0.191	0.267		2	1.000	0.500	
	Pon	4	0.004	0.008	0.011	0.003	0.240	0.332		5	0.933	0.122	
	AncTaxa	45	0.021	0.055	0.059	0.007	0.122	0.131	-0.329	34	0.958	0.014	
	Whole Pop	47	0.020	0.055	0.062	0.007	0.120	0.135	-0.211	48	0.960	0.011	
s.d.			0.001										
F3'H	Mand	10	0.004	0.003	0.003	0.005	1.767	1.714		6	0.747	0.111	0.574
	Pum	4	0.002	0.001	0.000	0.004	-	6.066		4	0.733	0.101	
	Cit	6	0.003	0.005	0.000	0.002	-	0.383		4	0.778	0.091	
	For	21	0.012	0.011	0.013	0.014	1.048	1.312		7	0.933	0.062	
	Pap	10	0.006	0.005	0.010	0.006	0.619	1.136		6	1.000	0.096	
	Mic	10	0.007	0.012	0.019	0.006	0.327	0.534		3	0.833	0.222	
	Ere	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	Pon	1	0.001	0.002	0.000	0.000	-	0.000		2	0.600	0.129	
	AncTaxa	55	0.010	0.013	0.016	0.008	0.515	0.612	-1.285	33	0.970	0.009	
	Whole Pop	60	0.009	0.012	0.014	0.008	0.554	0.643	-1.474	36	0.949	0.013	
s.d.			0.001										
DFR	Mand	1	0.000	0.000	0.000	0.001	-	-		2	0.143	0.119	0.675
	Pum	1	0.000	0.001	0.000	0.000	-	0.000		2	0.200	0.154	
	Cit	4	0.004	0.006	0.025	0.000	0.000	0.000		5	0.822	0.097	
	For	7	0.007	0.010	0.006	0.000	0.000	0.000		6	0.867	0.085	
	Pap	7	0.008	0.012	0.009	0.000	0.000	0.000		5	0.933	0.122	
	Mic	4	0.005	0.008	0.000	0.000	-	0.000		3	0.833	0.222	
	Ere	4	0.010	0.011	0.000	0.007	-	0.660		2	1.000	0.500	
	Pon	3	0.004	0.005	0.000	0.000	-	0.000		3	0.733	0.155	
	AncTaxa	32	0.013	0.017	0.024	0.005	0.194	0.280	-0.893	26	0.928	0.020	
	Whole Pop	32	0.011	0.015	0.019	0.005	0.248	0.308	-0.949	34	0.898	0.026	
s.d.			0.001										
EMA	Mand	3	0.004	0.005	0.000	0.000	-	0.000		3	0.667	0.075	
	Pum	1	0.000	0.001	0.000	0.000	-	0.000		2	0.200	0.154	
	Cit	1	0.001	0.002	0.000	0.000	-	0.000		2	0.533	0.095	
	For	10	0.007	0.008	0.006	0.002	0.308	0.246		7	0.911	0.077	
	Pap	2	0.007	0.000	0.011	0.003	0.255	-		3	0.733	0.155	
	Mic	8	0.010	0.013	0.016	0.000	0.000	0.000		3	0.833	0.222	
Ere	3	0.007	0.010	0.032	0.000	0.000	0.000		2	1.000	0.500		

	Pon	5	0.005	0.007	0.000	0.000	-	0.000		3	0.600	0.215	
	AncTaxa	34	0.014	0.017	0.003	0.005	1.511	0.289	-0.732	21	0.921	0.018	0.677
	Whole Pop	34	0.013	0.016	0.002	0.005	2.273	0.323	-0.622	27	0.914	(0.016)	
	s.d.		0.001										
<b>MDH</b>	Mand	6	0.002	0.004	0.004	0.001	0.179	0.179		3	0.908	0.115	
	Pum	2	0.002	0.000	0.000	0.002	-	-		2	0.538	0.075	
	Cit	0	0.000	0.000	0.000	0.000	-	-		1	0.556	0.000	
	For	10	0.005	0.011	0.011	0.004	0.338	0.338		7	0.000	0.077	
	Pap	6	0.004	0.007	0.007	0.003	0.418	0.418		4	0.867	0.129	
	Mic	5	0.004	0.011	0.011	0.002	0.235	0.235		3	0.821	0.222	
	Ere	4	0.006	0.000	0.000	0.007	-	-		2	0.833	0.500	
	Pon	1	0.001	0.000	0.000	0.001	-	-		2	1.000	0.129	
	AncTaxa	31	0.007	0.014	0.014	0.005	0.356	0.356	-0.768	21	0.929	0.015	0.677
	Whole Pop	31	0.006	0.012	0.012	0.005	1.065	0.394	-0.835	23	0.600	0.014	
	s.d.		0.000										
<b>ACO</b>	Mand	3	0.001	0.001	0.000	0.001	-	0.778		3	0.473	0.136	
	Pum	9	0.007	0.010	0.008	0.000	0.000	0.000		2	0.556	0.075	
	Cit	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	For	7	0.004	0.005	0.000	0.000	-	0.000		7	0.911	0.077	
	Pap	6	0.004	0.006	0.000	0.000	-	0.000		3	0.733	0.155	
	Mic	14	0.012	0.016	0.018	0.000	0.000	0.000		4	0.031	0.177	
	Ere	6	0.009	0.012	0.031	0.000	0.000	0.000		2	1.000	0.500	
	Pon	4	0.003	0.004	0.000	0.000	-	0.000		4	0.867	0.129	
	AncTaxa	44	0.009	0.012	0.006	0.000	0.030	0.014	-1.184	26	0.935	0.016	0.554
	Whole Pop	45	0.008	0.011	0.005	0.000	0.024	0.010	-1.173	30	0.908	0.019	
	s.d.		0.001										
<b>TRPA</b>	Mand	14	0.005	0.008	0.011	0.003	0.286	0.423		3	0.385	0.149	
	Pum	5	0.001	0.002	0.003	0.001	0.327	0.414		3	0.378	0.181	
	Cit	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	For	8	0.003	0.005	0.002	0.002	0.779	0.341		7	0.911	0.077	
	Pap	10	0.005	0.017	0.014	0.006	0.430	0.355		5	0.933	0.122	
	Mic	15	0.010	0.012	0.017	0.008	0.486	0.682		4	1.000	0.177	
	Ere	7	0.009	0.013	0.025	0.006	0.242	0.469		2	1.000	0.500	
	Pon	4	0.002	0.006	0.004	0.000	0.000	0.000		3	0.733	0.155	
	AncTaxa	56	0.014	0.020	0.025	0.010	0.411	0.514	-0.705	26	0.918	0.019	0.688
	Whole Pop	57	0.012	0.018	0.022	0.009	0.430	0.518	-0.745	32	0.883	0.022	
	s.d.		0.001										
<b>INVA</b>	Mand	22	0.008	0.010	0.022	0.004	0.190	0.401		8	0.867	0.060	
	Pum	11	0.004	0.004	0.010	0.004	0.397	0.848		6	0.778	0.137	
	Cit	6	0.002	0.003	0.003	0.002	0.614	0.656		3	0.622	0.138	
	For	9	0.004	0.006	0.015	0.001	0.091	0.226		5	0.800	0.100	
	Pap	22	0.012	0.019	0.028	0.004	0.148	0.219		6	1.000	0.096	
	Mic	13	0.008	0.011	0.017	0.003	0.177	0.268		4	1.000	0.177	
	Ere	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	Ponc	2	0.001	0.001	0.004	0.002	0.345	1.462		2	0.733	0.155	
	AncTaxa	69	0.014	0.017	0.039	0.008	0.197	0.449	-0.640	34	0.970	0.009	0.593
	Whole Pop	72	0.014	0.019	0.031	0.007	0.226	0.368	-0.514	49	0.975	0.006	
	s.d.		0.000										
<b>PEPC</b>	Mand	3	0.001	0.002	0.000	0.000	-	0.000		3	0.001	0.138	
	Pum	3	0.001	0.002	0.000	0.000	-	0.000		4	0.001	0.152	
	Cit	1	0.001	0.001	0.000	0.000	-	0.000		2	0.001	0.095	
	For	12	0.006	0.006	0.000	0.000	-	0.000		4	0.006	0.101	
	Pap	5	0.003	0.004	0.000	0.000	-	0.000		4	0.800	0.172	
	Mic	10	0.008	0.008	0.033	0.000	0.000	0.000		3	0.833	0.222	
	Ere	4	0.006	0.006	0.066	0.000	0.000	0.000		2	1.000	0.500	
	Ponc	5	0.004	0.004	0.000	0.000	-	0.000		3	0.733	0.155	
	AncTaxa	52	0.014	0.015	0.016	0.000	0.000	0.000	-0.821	25	0.945	0.013	0.714
	Whole Pop	53	0.013	0.014	0.012	0.000	0.000	0.000	-0.757	33	0.950	0.011	
	s.d.		0.000										
<b>PKF</b>	Mand	9	0.003	0.004	0.003	0.003	0.914	0.681		4	0.659	0.120	
	Pum	1	0.000	0.000	0.000	0.000	-	0.000		2	0.200	0.154	
	Cit	2	0.001	0.000	0.000	0.002	-	-		2	0.356	0.159	
	For	6	0.002	0.003	0.000	0.000	-	0.000		3	0.378	0.181	
	Pap	12	0.008	0.010	0.000	0.005	-	0.517		4	0.867	0.129	
	Mic	2	0.002	0.000	0.000	0.004	-	-		3	0.833	0.222	
	Ere	4	0.005	0.007	0.000	0.003	-	0.492		2	1.000	0.500	
	Pon	0	0.000	0.000	0.000	0.000	-	-		1	0.000	0.000	
	AncTaxa	38	0.009	0.012	0.005	0.006	1.072	0.491	-0.855	21	0.925	0.014	0.647
	Whole Pop	44	0.009	0.011	0.006	0.006	0.883	0.514	-1.058	27	0.937	0.010	
	s.d.		0.000										
<b>DXS</b>	Mand	14	0.006	0.009	0.009	0.002	0.227	0.228		6	0.767	0.084	
	Pum	4	0.003	0.004	0.007	0.000	0.000	0.000		4	0.733	0.101	
	Cit	2	0.001	0.001	0.006	0.001	0.235	1.219		3	0.689	0.104	
	For	7	0.004	0.006	0.005	0.001	0.301	0.230		7	0.911	0.077	
	Pap	17	0.012	0.016	0.015	0.007	0.466	0.434		6	1.000	0.096	
	Mic	4	0.003	0.004	0.006	0.002	0.304	0.534		3	0.833	0.222	
	Ere	7	0.010	0.013	0.026	0.004	0.153	0.296		2	1.000	0.500	
	Pon	4	0.003	0.005	0.000	0.000	-	0.000		2	0.533	0.172	
	AncTaxa	51	0.015	0.021	0.018	0.006	0.348	0.289	-0.321	32	0.967	0.009	0.659





FIG. S1. Neighbor-Joining tree with all the SNP markers in the whole population studied, ancestral *Citrus* species, relatives, secondary species and interspecific hybrids (1000 bootstraps performed). Branch support over 50% represented.

