Table S1. List of samples analyzed in the present study including cultivar full name and individual genotype codes employed in the different visualization schemes.

sample (genotype) no	cultivar full name (transliterated in Latin)	genotype code		number of independent genotypes per cultivar
		in similarity dendrogram (Figure 1) and CBT (Figure 3)	in “Structure” (appears within parentheses; Figure 2)	
1	Adramytini	ADRA1	1	2
2		ADRA2	1	
3	Aggouromanakolia	AGOU1	2	3
4		AGOU2	2	
5		AGOU3	2	
6	Amfissis	AMFI1	3	2
7		AMFI2	3	
8	Arbequina	ARBE1	4	1
9	Arbosana	ARBO1	5	2
10		ARBO2	5	
11	Asprolia Alexandroupolis	ASAL1	6	1
12	Asprolia Lefkados	ASLE1	7	2
13	Asprolia Lefkados	ASLE2	7	
14	Chalkidikis	CHAL1	8	1
15	Chondrolia Chalkidikis	CHHO1	9	1
16	Dafnelia	DAFN1	10	1
17	Dopia Zakynthou	DOZA1	11	1
18	Frantoio Rodou	FRRO1	12	1
19	Frantoio	FRAN1	13	1
20	Gaidourelia	GAID1	14	1
21	Galatistas	GALA1	15	1
22	Gordal	GORD1	16	1
23	O. e. subsp. cuspidata	CUSPI	17	1
24	Kalamon	KALA1	18	2
25		KALA2	18	
26	Kalokairida	KALO1	19	2
27		KALO2	19	
28	Karydolia	KARI1	20	2
29		KARI2	20	
30	Kolybada	KOLI1	21	2
31		KOLY1	21	
32	Koroneiki	KORO1	22	6
33		KORO2	22	
34		KORO3	22	

35		KORO4	22	
36		KORO5	22	
37		KORO6	22	
38	Kothreiki	KOTR1	23	2
39		KOTR2	23	
40	Koutsourelia	KUTS1	24	2
41		KUTS2	24	
42	Leccino	LECI1	25	1
43	Lefkolia Serron	LESE1	26	1
44	Lianolia Kerkyras	LIAK1	27	2
45		LIAK2	27	
46	Lianomanako Tyrou	LIAT1	28	1
47	Makris	MAKR1	29	1
48	Manzanilla	MANZ1	30	3
49		MANZ2	30	
50		MANZ3	30	
51	Mastoidis	MAST1	31	2
52		MAST2	31	
53	Matolia	MATO1	32	2
54		MATO2	32	
55	Megareitiki	MEGA1	33	2
56		MEGA2	33	
57	Myrtolia	MYRT1	34	2
58		MYRT2	34	
59	Nev. Blanco	NEBL1	35	1
60	Nev. Negro	NENE1	36	1
61	Oblonga	OBLO1	37	1
62	Petrolia	PETR1	38	2
63		PETR2	38	
64	Picual	PICU1	39	2
65		PICU2	39	
66	Pierias	PIERI1	40	2
67		PIERI2	40	
68	Pikrolia	PIKR1	41	2
69		PIKR2	41	
70	Picholine Marocaine	PIMA1	42	1
71	Rahati	RAHA1	43	2
72		RAHA2	43	
73	San Augustino	SANA1	44	1
74	San Francesco	SANF1	45	1
75	Singoise	SING1	46	1
76	Stroggylolia	STRO1	47	1
77	Thiaki	TIAK1	48	3

78		TIAK2	48	
79		TIAK3	48	
80	Tragolia	TRAG1	49	2
81		TRAG2	49	
82	Throuboelia	TROUB1	50	3
83		TROUB2	50	
84		TROUB3	50	
85	Throuba Thassou	TRTHA1	51	1
86	Valanolia	VALA1	52	2
87		VALA2	52	
88	Vasilikada	VASI1	53	2
89		VASI2	53	
90	Dopia Zakynthou	ZAKI1	54	1

Table S2. Pairwise relatedness summary according to the LRM estimator.

Genotype	Genotype	LRM
CHAL1	CHHO1	0.857
FRAN1	OBLO1	0.601
GAID1	GALA1	0.526
KALO1	KALO2	0.569
AMFI1	KOLI1	0.584
ADRA1	DAFN1	0.354
ADRA2	MYRT2	0.543
KOTR1	PIERI2	0.528
KUTS2	RAHA2	0.582
AMFI2	KALA2	0.372
ADRA1	KORO6	0.357
ADRA1	KOTR1	0.404
DAFN1	KOTR1	0.483
DAFN1	KOTR2	0.351
KORO3	KUTS2	0.373
KORO6	KUTS2	0.368
KARI2	LIAT1	0.403
KOLI1	MANZ1	0.351
KUTS2	MAST2	0.352
AGOU3	MEGA1	0.437
LIAT1	MEGA2	0.381
LESE1	PETR2	0.419
MEGA2	PIERI1	0.370
KOTR2	PIERI2	0.437
LIAK2	PIKR2	0.410
KUTS1	RAHA2	0.379
GORD1	SING1	0.369
MAKR1	TIAK2	0.397
CHAL1	TROUB1	0.404
TIAK2	TRTHA1	0.380
PIKR1	VASI2	0.416

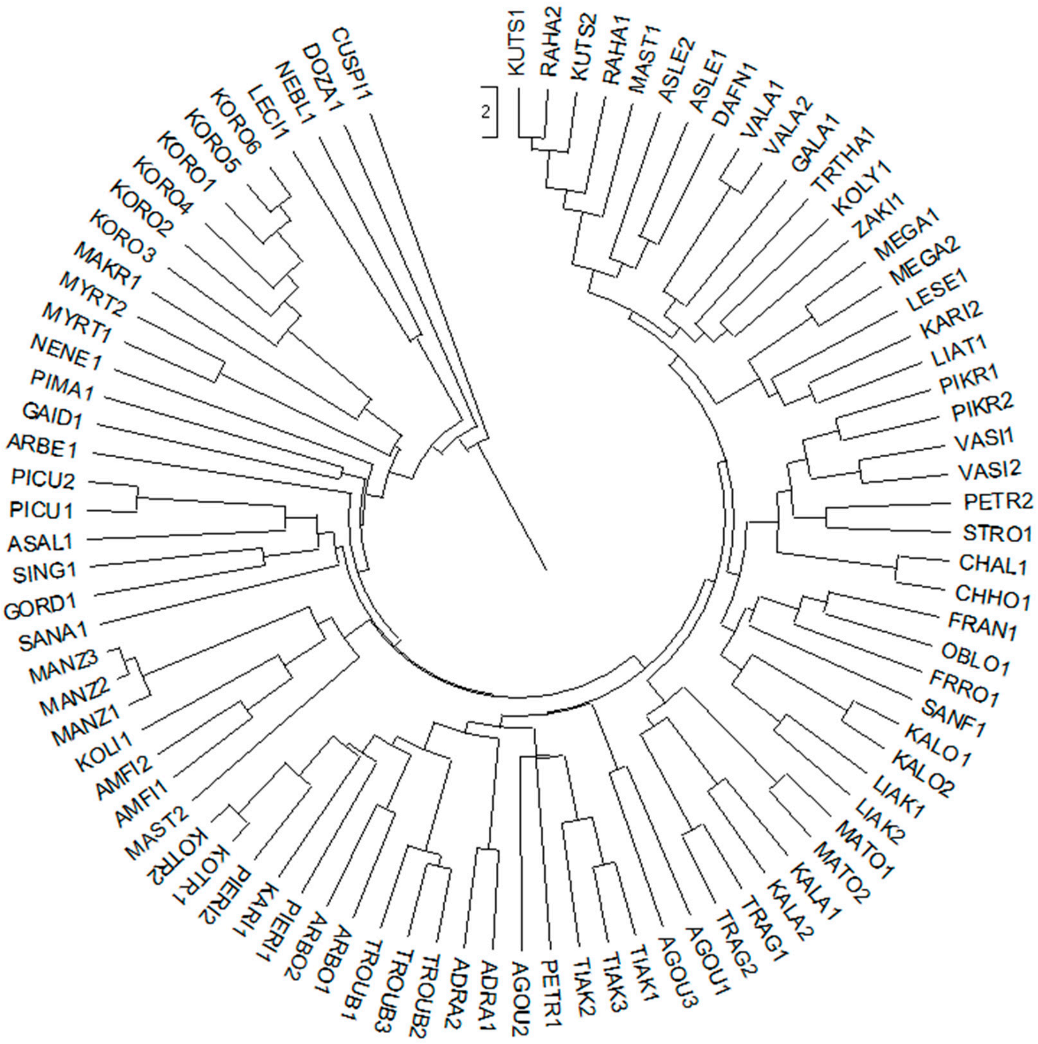

Figure S1. Dendrogram based on unweighted pair group method with arithmetic mean (UPGMA) algorithm (Sneath and Sokal, 1973) using the MEGA X software (Kumar et al., 2018).

Table S3. The number of splits in which an allele participates and the proportional reduction in error it confers to the tree.

Alleles	**∑(Proportional reduction of error)**	**# of splits**
DCA16_2	0.11	10
DCA5_1	0.088	8
DCA9_2	0.088	8
EMO9__2	0.077	7
DCA14_2	0.066	6
DCA5_2	0.066	6
GAPU101_2	0.066	6
DCA14_1	0.055	5
UDO043_1	0.055	5
DCA16_1	0.044	4
DCA18_1	0.044	4
DCA18_2	0.044	4
GAPU71B_1	0.044	4
GAPU71B_2	0.044	4
EMO90_1	0.033	3
DCA3_1	0.011	1
DCA3_2	0.011	1
UDO043_2	0.011	1