TWO MAIN GENETIC CLUSTERS WITH HIGH ADMIXTURE BETWEEN FOREST AND CULTIVATED CHESTNUT (*CASTANEA SATIVA* MILL.) IN FRANCE

ESM_8

ESM_8A CLASSIFICATION OF 529 EUROPEAN CHESTNUT GENOTYPES, IN RECONSTRUCTED PANMICTIC POPULATIONS (RPPS) WHEN K=2, BASED ON *18UNIK* DATA SET WITH SPANISH SAMPLES.

In green, French genotypes admixed (RPP1). In orange, genotypes from south-east of France (RPP2). Spanish genotypes are allocated in both RPPs.

Table of assignments of sampling regions in reconstructed panmictic populations (RPPs)

Sampling Region	RPP1 (qI≥50%)	RPP2 (qI≥50%)	Sum RPP1+RPP2	Admixed (qI≤80%)
CultArdech	30	19	49	28
CultAriege	1	34	35	9
CultAveyron		24	24	2
CultCorsica	32	6	38	16
CultHtPyr		25	25	5
CultLimousin		44	44	
CultSpain	6	3	9	8
CultVar	4		4	
ForAveyron		29	29	1
ForBasque		1	1	
ForCantal		22	22	1
ForCorsica	70	1	71	8
ForFinistere	1	96	97	4
ForGard	1	29	30	
ForGironde		5	5	3
ForHerault	4	12	16	11
ForVar	30		30	
Sum	179	350	529	96

Table of posterior probabilities of assignment of Spanish samples in reconstructed panmictic populations (RPPs)

Samples	Name	Cluster1 |RPP2	Cluster 2| RPP1
ref002	**Chamberga1**	0.684	0.316
ref003	**Negral**	0.711	0.289
ref004	**Pais**	**0.849**	0.151
ref005	**Parede**	0.31	0.69
ref006	**Porteliña**	0.372	0.628
ref007	**Puga**	0.727	0.273
ref008	**Raigona1**	0.664	0.336
ref009	**Rapada**	0.601	0.399
ref010	**Serodia**	0.366	0.634

Tables of pairwise Fst between RPPs using all individuals and strongly assigned individuals (ql≥ 80%)

RPPs	RPP1
RPP2	0.065 [0.049 ; 0.08]

RPPs (ql≥ 80%)	RPP1
RPP2	0.089 [0.069 ; 0.11]

ESM_8B CLASSIFICATION OF 1050 EUROPEAN CHESTNUT GENOTYPES. IN RECONSTRUCTED PANMICTIC POPULATIONS (RPPS) WHEN K=2 AND K=6

K=2

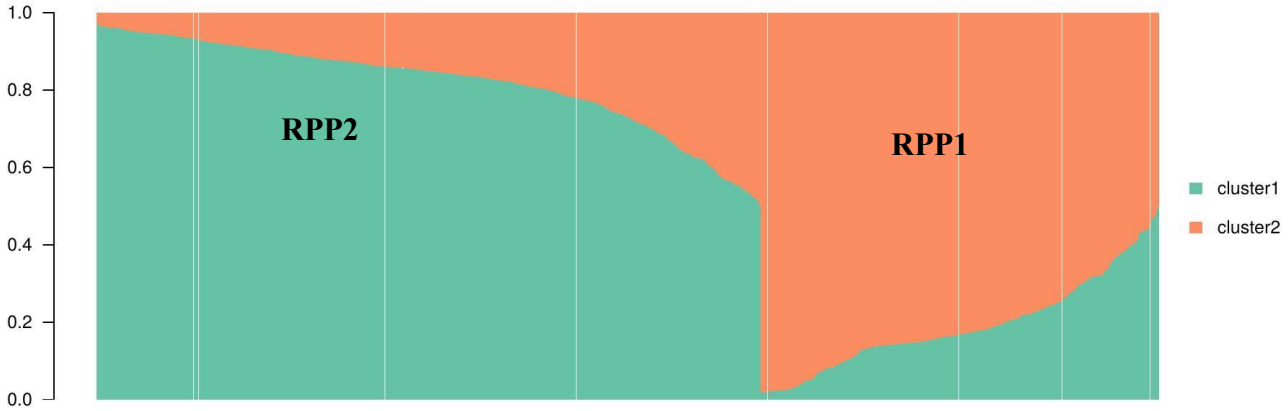

Table of assignments of sampling regions in reconstructed panmictic populations (RPPs) when K=2

Sampling Regions	RPP2 (qI≥50%)	RPP1 (qI≥50%)	Sum RPP1+RPP2	Admixed (qI≤80%)
CultArdech	6	41	47	20
CultAriege	41	23	64	41
CultAveyron	51	19	70	31
CultCorsica	1	37	38	14
CultHtPyr	29	13	42	24
CultLimousin	59		59	5
CultVar	1	12	13	1
ForArdech	40	46	86	53
ForAveyron	135	5	140	29
ForBasque	22	2	24	13
ForCantal	22		22	2
ForCorsica	1	115	116	22
ForFinistere	232	16	248	69
ForGard	10	20	30	22
ForGironde	1	4	5	4
ForHerault	5	11	16	10
ForVar		30	30	
Sum	656	394	1050	360

Tables of pairwise Fst between RPPs using all individuals and strongly assigned individuals (qI≥ 80%)

RPPs	RPP1
RPP2	0.005 [0.029 ; 0.073]

RPPs (qI≥ 80%)	RPP1
RPP2	0.088 [0.054 ; 0.123]

K=6

- In green. main genotypes are from Corsica (Cluster 1, RPP1b).
- In orange. main genotypes are from many sampling regions (Cluster 2, RPP2c)
- In blue. main genotypes are from Var and Ardech (Cluster 3, RPP1a).
- In pink. main genotypes are from West of France (Cluster 4, RPP2a).
- In clear green. genotypes from Aveyron (Cluster 5, RPP2b)
- In yellow. main genotypes are from Pyrenees (Cluster 6, RPP2d)

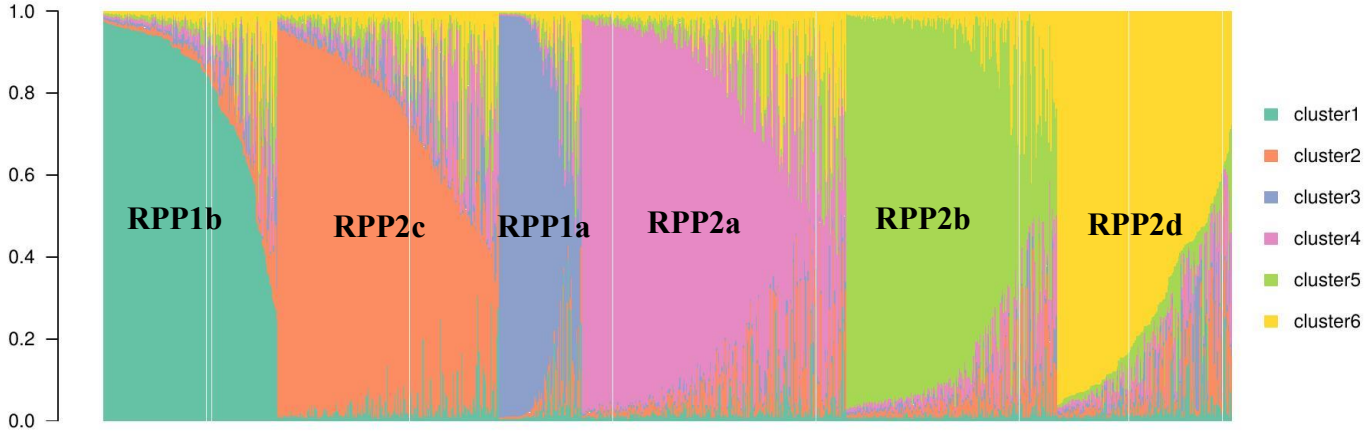

Table of assignement of sampling regions in reconstructed panmictic populations (RPPs) when K=6

Sampling Regions	RPP1b | Cluster 1	RPP2c | Cluster 2	RPP1a| Cluster 3	RPP2a | Cluster 4	RPP2b| Cluster 5	RPP2d | Cluster 6	Sum	Admixed (qI≤80%)
CultArdech	2	15	22	1	3	4	47	41
CultAriege	3	4	2	1	6	48	64	35
CultAveyron		19	5	14	24	8	70	49
CultCorsica	34	1				3	38	23
CultHtPyr		3		1	1	37	42	17
CultLimousin		3		43	4	9	59	27
CultVar			12	1			13	2
ForArdech	2	75	4	4	1		86	34
ForAveyron		11		2	123	4	140	43
ForBasque	2	2		1		19	24	12
ForCantal		1		1	17	3	22	12
ForCorsica	110	4			1	1	116	26
ForFinistere	6	39	3	173	13	14	248	138
ForGard		26		1	3		30	11
ForGironde	2			1		2	5	3
ForHerault	1	2		2		11	16	9
ForVar		1	29				30	4
Sum	162	206	77	246	196	163	1050	486

Tables of pairwise Fst between RPPs using all individuals and strongly assigned individuals (ql≥ 80%)

RPPs	**RPP2c | cluster2**	**RPP1a | cluster3**	**RPP2a | cluster4**	**RPP2b | cluster5**	**RPP2d | cluster6**
RPP1b | cluster1	0.062 [0.045;0.081]	0.124 [0.071;0.193]	0.077 [0.049;0.114]	0.107 [0.082;0.13]	
RPP2c | cluster2		0.103 [0.071;0.137]	0.059 [0.035;0.085]	0.075 [0.047;0.106]	0.053 [0.031;0.081]
RPP1a | cluster3			0.153 [0.122;0.187]	0.165 [0.110;0.214]	0.142 [0.108;0.177]
RPP2a | cluster4				0.058 [0.033;0.082]	0.037 [0.022;0.052]
RPP2b | cluster5					0.047 [0.026;0.070]

RPPs (ql≥ 80%)	**RPP2c | cluster2**	**RPP1a | cluster3**	**RPP2a | cluster4**	**RPP2b | cluster5**	**RPP2d | cluster6**
RPP1b | cluster1	0.099 [0.073;0.129]	0.198 [0.115;0.286]	0.101 [0.066;0.143]	0.156 [0.116;0.192]	0.122 [0.082;0.162]
RPP2c | cluster2		0.158 [0.105;0.207]	0.096 [0.060;0.131]	0.117 [0.074;0.164]	0.097 [0.061;0.136]
RPP1a | cluster3			0.231 [0.18;0.286]	0.245 [0.163;0.316]	0.229 [0.177;0.282]
RPP2a | cluster4				0.088 [0.050;0.123]	0.073 [0.048;0.095]
RPP2b | cluster5					0.079 [0.045;0.117]

ESM_8C CLASSIFICATION OF 1060 EUROPEAN CHESTNUT GENOTYPES. IN RECONSTRUCTED PANMICTIC POPULATIONS (RPPS) WHEN K=2 AND K=6 WITH SPANISH SAMPLES

K=2

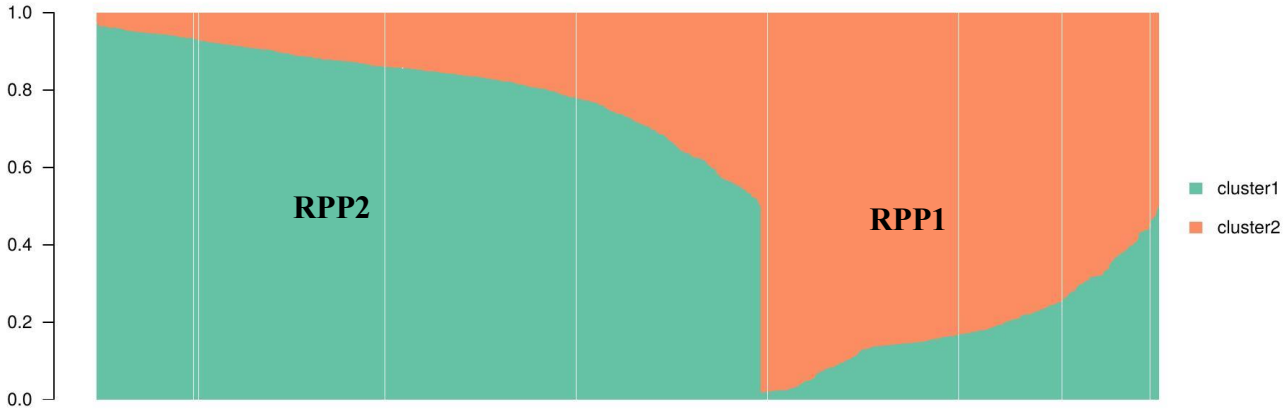

Table of assignments of sampling regions in reconstructed panmictic populations (RPPs) when K=2

Sampling Regions	cluster1 |RPP2	cluster2 | RPP1	Sum	Admixed (qI≤80%)
CultArdech	6	41	47	20
CultAriege	42	22	64	42
CultAveyron	51	19	70	31
CultCorsica	1	37	38	14
CultHtPyr	30	12	42	26
CultLimousin	59		59	5
CultVar	1	12	13	1
CultSpain	3	7	10	5
ForArdech	39	47	86	54
ForAveyron	134	6	140	25
ForBasque	20	4	24	15
ForCantal	22		22	3
ForCorsica	1	115	116	19
ForFinistere	230	18	248	73
ForGard	10	20	30	23
ForGironde	1	4	5	4
ForHerault	5	11	16	10
ForVar		30	30	
Sum	655	405	1060	370

Tables of pairwise Fst between RPPs using all individuals and strongly assigned individuals (ql ≥ 80%)

RPPs	RPP1
RPP2	0.005 [0.029 ; 0.072]

RPPs strongly assigned	RPP1
RPP2	0.089 [0.054 ; 0.124]

Table of posterior probabilities of assignment of Spanish samples

Samples	**Name**	**Cluster1 | RPP2**	**Cluster2 | RPP1**
ref001	**Luguesa**	0.058	**0.942**
ref002	**Chamberga1**	0.6703	0.3297
ref003	**Negral**	0.4955	0.5045
ref004	**Pais**	0.1407	**0.8593**
ref005	**Parede**	**0.8618**	0.1382
ref006	**Porteliña**	0.4929	0.5071
ref007	**Puga**	0.1974	**0.8026**
ref008	**Raigona1**	0.1474	**0.8526**
ref009	**Rapada**	0.2068	0.7932
ref010	**Serodia**	0.6479	0.3521

K=6

- In green. main genotypes are from many sampling regions (Cluster 1, RPP2c).
- In orange. main genotypes are from Var and Ardech (Cluster 2, RPP1a)
- In blue. main genotypes are from Aveyron (Cluster 3, RPP2b).
- In pink. main genotypes are from north west of France (Cluster 4, RPP2a).
- In clear green. genotypes from Corsica (Cluster 5, RPP1b)
- In yellow. main genotypes are from Pyrenees (Cluster 6, RPP2d)

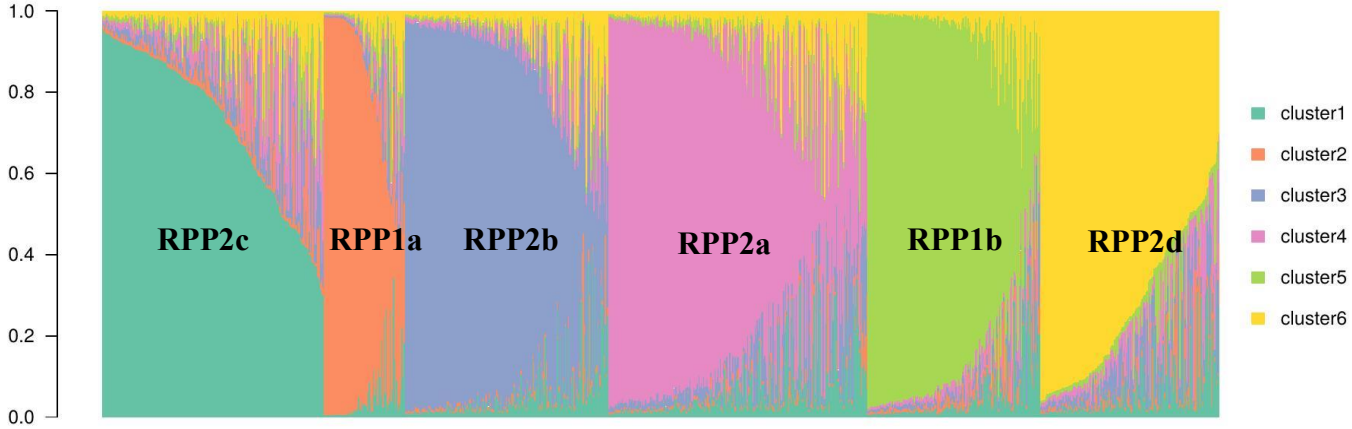

Table of assignement of sampling regions in reconstructed panmictic populations (RPPs)

Sampling Regions	RPP2c | Cluster 1	RPP1a | Cluster 2	RPP2b| Cluster 3	RPP2a | Cluster 4	RPP1b| Cluster 5	RPP2d | Cluster 6	Sum	Admixed (qI≤80%)
CultArdech	15	22	3	1	2	4	47	41
CultAriege	4	2	6	1	3	48	64	36
CultAveyron	19	5	21	18		7	70	49
CultCorsica	1				34	3	38	24
CultHtPyr	3		1	1		37	42	18
CultLimousin	4		4	42		9	59	27
CultVar		12		1			13	2
CultSpain	1			4	2	3	10	9
ForArdech	77	4	1	2	2		86	33
ForAveyron	11		123	2		4	140	43
ForBasque	2			1	2	19	24	12
ForCantal	1		17	1		3	22	11
ForCorsica	4		1		110	1	116	26
ForFinistere	39	3	13	168	6	19	248	140
ForGard	26		3	1			30	11
ForGironde				1	2	2	5	4
ForHerault	2			2	1	11	16	9
ForVar	1	29					30	4
Sum	210	77	193	246	164	170	1060	499

Tables of pairwise Fst between RPPs using all individuals and strongly assigned individuals (ql ≥ 80%)

RPPs	cluster2	cluster3	cluster4	cluster5	cluster6
cluster1	0.103 [0.072;0.135]	0.075 [0.049;0.104]	0.060 [0.036;0.085]	0.061 [0.045;0.079]	0.050[0.030;0.076]
cluster2		0.166 [0.110;0.214]	0.153 [0.121;0.185]	0.123 [0.072;0.19]	0.140 [0.105;0.172]
cluster3			0.059 [0.035;0.085]	0.107 [0.082;0.13]	0.048 [0.027;0.072]
cluster4				0.077 [0.048;0.112]	0.037 [0.023;0.053]
cluster5					0.071 [0.046;0.096]

RPPs (ql≥ 80%)	cluster2	cluster3	cluster4	cluster5	cluster6
cluster1	0.157 [0.104;0.207]	0.118 [0.076;0.162]	0.097 [0.06;0.135]	0.100 [0.075;0.128]	0.096 [0.063;0.135]
cluster2		0.245 [0.163;0.316]	0.232 [0.181;0.286]	0.199 [0.119;0.287]	0.231 [0.181;0.281]
cluster3			0.088 [0.053;0.123]	0.157 [0.116;0.194]	0.082 [0.045;0.120]
cluster4				0.101 [0.066;0.143]	0.071 [0.047;0.093]
cluster5					0.121 [0.080;0.161]

Table of posterior probabilities of assignment of Spanish samples

Samples	Name	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6
ref001	**Luguesa**	0.3809	0.2989	0.007	0.007	0.275	0.0312
ref002	**Chamberga1**	0.0223	0.0052	0.0101	0.0414	0.036	**0.8849**
ref003	**Negral**	0.0216	0.0103	0.0192	0.4945	0.4108	0.0436
ref004	**Pais**	0.0289	0.0525	0.0137	0.0334	0.7942	0.0773
ref005	**Parede**	0.0161	0.0149	0.0769	0.7942	0.0648	0.0332
ref006	**Porteliña**	0.0367	0.0101	0.0088	0.5012	0.1989	0.2442
ref007	**Puga**	0.0093	0.0617	0.01	0.0267	0.2627	0.6296
ref008	**Raigona1**	0.0213	0.314	0.0083	0.0317	0.1454	0.4792
ref009	**Rapada**	0.0353	0.049	0.048	0.0543	0.5119	0.3014
ref010	**Serodia**	0.0132	0.0062	0.0131	0.6748	0.2157	0.077