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SUPPORTING INFORMATION

Climatically stable landscapes predict patterns of genetic structure and admixture in the Californian canyon live oak

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Appendix S1 Geographical location, allelic richness (A_R) and probability of population membership to each genetic cluster (C1, C2 and C3) inferred by STRUCTURE analyses for the studied populations of canyon live oak (*Quercus chrysolepis*) in California, USA.

Locality	Code	Latitude	Longitude	*n*	A_R	C1	C2	C3
1	Mad River	40.41838	−123.45644	1	−	0.031	0.603	0.069
2	Trinity National Forest	40.38203	−123.29874	5	2.73	0.049	0.526	0.069
3	Short Fork Eel River	40.21926	−123.81198	2	−	0.070	0.465	0.058
4	Redwood Highway	39.92774	−123.75834	5	2.72	0.046	0.629	0.057
5	Mount Diablo	37.88094	−121.92024	8	2.92	0.020	0.470	0.084
6	Stanislaus National Forest	37.81610	−119.94467	5	3.07	0.021	0.135	0.122
7	Yosemite-Sentinel Dome	37.73108	−119.60481	1	−	0.019	0.244	0.065
8	Yosemite-Big Oak Flat Road	37.71377	−119.72743	2	−	0.024	0.117	0.117
9	Yosemite-Incline	37.66518	−119.80762	2	−	0.020	0.064	0.205
10	Kings Canyon	36.74134	−119.03130	8	2.79	0.103	0.269	0.116
11	Sequoia National Forest	36.16261	−118.70589	1	−	0.017	0.100	0.102
12	San Gabriel Mountains–A	34.37137	−117.75443	14	2.87	0.149	0.130	0.121
13	San Gabriel Mountains−B	34.31516	−118.13680	2	−	0.042	0.014	0.766
14	San Gabriel Mountains−C	34.29850	−118.14864	2	−	0.185	0.272	0.087
15	San Gabriel Mountains−D	34.25204	−118.19614	2	−	0.049	0.098	0.179
16	San Gabriel Mountains−E	34.17832	−117.67668	1	−	0.306	0.078	0.200
17	San Gabriel Mountains−F	34.19299	−117.67851	1	−	0.190	0.454	0.069
18	San Bernardino Mountains−A	34.16885	−116.89307	3	−	0.063	0.153	0.157
19	San Bernardino Mountains−B	34.13028	−116.98250	2	−	0.169	0.184	0.107
20	San Bernardino Mountains−C	34.11334	−116.97994	10	2.85	0.144	0.194	0.117
21	San Bernardino Mountains−D	34.10532	−116.97227	6	2.83	0.200	0.147	0.142
22	San Bernardino Mountains−E	34.09975	−116.96264	1	−	0.120	0.100	0.131
23	San Jacinto Mountains−A	33.79186	−116.74465	3	−	0.121	0.117	0.057
24	San Jacinto Mountains−B	33.74875	−116.73753	1	−	0.765	0.060	0.049
25	San Jacinto Mountains−C	33.72830	−116.72005	5	2.49	0.507	0.075	0.150
26	San Jacinto Mountains−D	33.68201	−116.68956	10	2.84	0.102	0.281	0.081
27	Palomar Mountains−A	33.31366	−116.87095	2	−	0.078	0.029	0.111
28	Palomar Mountains−B	33.30513	−116.87831	14	2.95	0.032	0.060	0.059
29	Palomar Mountains−C	33.29343	−116.89023	11	2.68	0.328	0.054	0.048
30	Palomar Mountains−D	33.28688	−116.80194	3	−	0.303	0.111	0.098
31	Laguna Mountains−A	32.84524	−116.43885	12	2.79	0.123	0.277	0.278
32	Laguna Mountains−B	32.84954	−116.48535	10	2.56	0.790	0.029	0.066
33	Granite Mountains	34.78978	−115.67153	5	2.55	0.038	0.015	0.729

n, number of sampled individuals; A_R, standardized allelic richness. A_R was only calculated for localities with five or more genotyped individuals.

Appendix S2 Microsatellite loci used to genotype canyon live oaks (*Quercus chrysolepis*) in California (160 individuals from 33 localities): annealing temperature (T_a, in °C), number of alleles (A), expected heterozygosity (H_E), and observed heterozygosity (H_O) for each locus.

Locus	T_a	A	H_E	H_O	Primer origin
QpZAG1/5	55	15	0.72	0.50	Steinkellner *et al*., 1997
QpZAG9	55	26	0.89	0.78	Steinkellner *et al*., 1997
QpZAG15	50	24	0.90	0.83	Steinkellner *et al*., 1997
QpZAG36	50	13	0.75	0.54	Steinkellner *et al*., 1997
QpZAG46	53	15	0.85	0.80	Steinkellner *et al*., 1997
QpZAG110	55	39	0.94	0.93	Steinkellner *et al*., 1997
QrZAG11	50	53	0.94	0.83	Kampfer *et al*., 1998
QrZAG20	55	24	0.94	0.58	Kampfer *et al*., 1998
PIE020	50	8	0.57	0.50	Durant *et al*., 2010
PIE152	55	13	0.61	0.56	Durant *et al*., 2010
PIE242	55	6	0.44	0.53	Durant *et al*., 2010
PIE258	55	19	0.89	0.80	Durant *et al*., 2010
PIE271	55	6	0.64	0.60	Durant *et al*., 2010

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Appendix S3 Results of Bayesian clustering analyses in STRUCTURE for canyon live oaks (*Quercus chrysolepis*) in California (160 individuals from 33 localities). Plots show the mean (± SD) log probability of the data (ln Pr(X|*K*)) over 10 runs (left axis, black dots and error bars) for each value of *K*. The magnitude of Δ*K* as a function of *K* indicates the most likely number of genetic clusters (*K* = 3) (right axis, open dots).