

Supplementary Materials: Associations of Leaf Spectra with Genetic and Phylogenetic Variation in Oaks: Prospects for Remote Detection of Biodiversity

Jeannine Cavender-Bares, Jose Eduardo Meireles, John J. Couture, Matthew Kaproth, Clayton C. Kingdon, Aditya Singh, Shawn P. Serbin, Alyson Center, Esau Zuniga, George Pilz and Philip A. Townsend

Table S1. Analysis of variance for the *Quercus oleoides* experiment. Populations are treated as the main factor with each spectral PLS component as a response variable. F ratios indicate the variation in component scores among populations relative to variation within populations. Components are shown in bold if P values are less than 0.05, indicating a significant population effect.

Response	Df	Sum Sq	Mean Sq	F Value	p Value
Component 1	4	0.0604	0.0151	9.61	0.000
Component 2	4	0.00863	0.00216	4.00	0.003
Component 3	4	0.00133	0.000334	3.43	0.009
Component 4	4	0.00021	0.0000525	1.36	0.249
Component 5	4	0.000243	0.0000608	3.61	0.006
Component 6	4	0.0000786	0.0000197	1.24	0.292
Component 7	4	0.000208	0.000052	3.92	0.004
Component 8	4	0.000075	0.0000187	2.15	0.074
Component 9	4	0.0000219	0.00000546	1.03	0.391
Component 10	4	0.00000404	0.00000101	0.32	0.866
Component 11	4	0.00000668	0.00000167	0.72	0.576
Component 12	4	0.0000113	0.00000283	1.65	0.161
Component 13	4	0.000011	0.00000276	2.42	0.048
Component 14	4	0.0000106	0.00000265	4.27	0.002
Component 15	4	0.00000238	0.000000594	1.27	0.282
Component 16	4	0.00000123	0.000000307	0.77	0.543
Component 17	4	0.000000279	0.0000000699	0.23	0.921
Component 18	4	0.00000223	0.000000557	2.27	0.061
Component 19	4	0.00000666	0.00000166	10.17	0.000
Component 20	4	0.00000127	0.000000319	2.00	0.093

Table S2. Phylogenetic signal as given by Blomberg's K of components of the PCO analysis. Observed values of Blomberg's K are given relative to the mean and SD of the null model, computed using a tip shuffling algorithm. p values less than 0.05, shown in bold, indicate that the observed K value is significantly higher than expected by chance, such that the component shows significant phylogenetic signal. K values around 1 are consistent with a Brownian motion (BM) model of evolution, and the expected mean of the BM simulation is always 1.0. The SD of the expected K value with Brownian motion simulation is also shown for each component.

Principal Component	K	p Value	Null Mean	Null SD	BM SD
PCO 1	1.024	0.001	0.619	0.094	0.354
PCO 2	0.676	0.243	0.620	0.094	0.346
PCO 3	0.708	0.234	0.633	0.133	0.318
PCO 4	0.892	0.02	0.627	0.114	0.336
PCO 5	0.718	0.181	0.624	0.116	0.361
PCO 6	0.590	0.574	0.617	0.091	0.336
PCO 7	0.633	0.442	0.619	0.097	0.341
PCO 8	0.728	0.148	0.624	0.106	0.352

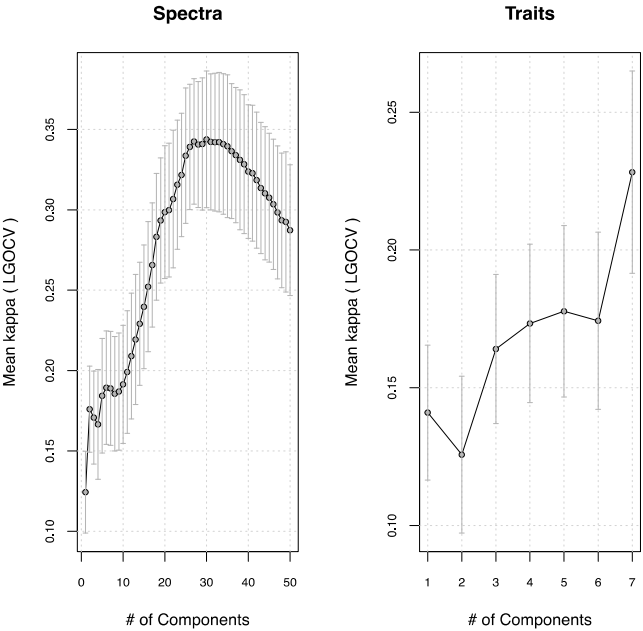
PCO 9	0.902	0.013	0.622	0.094	0.334
PCO 10	0.601	0.553	0.628	0.108	0.322
PCO 11	0.636	0.405	0.627	0.109	0.343
PCO 12	0.756	0.098	0.617	0.096	0.339
PCO 13	0.572	0.683	0.622	0.101	0.339
PCO 14	0.682	0.236	0.618	0.091	0.354
PCO 15	0.820	0.024	0.620	0.092	0.346
PCO 16	0.804	0.071	0.617	0.105	0.351
PCO 17	0.647	0.367	0.619	0.101	0.315
PCO 18	0.570	0.671	0.634	0.125	0.323
PCO 19	0.757	0.068	0.620	0.091	0.350
PCO 20	0.745	0.159	0.636	0.131	0.350

Table S3. Phylogenetic signal as given by Blomberg's K of traits predicted from spectral data. Headers are the same as in Table S2.

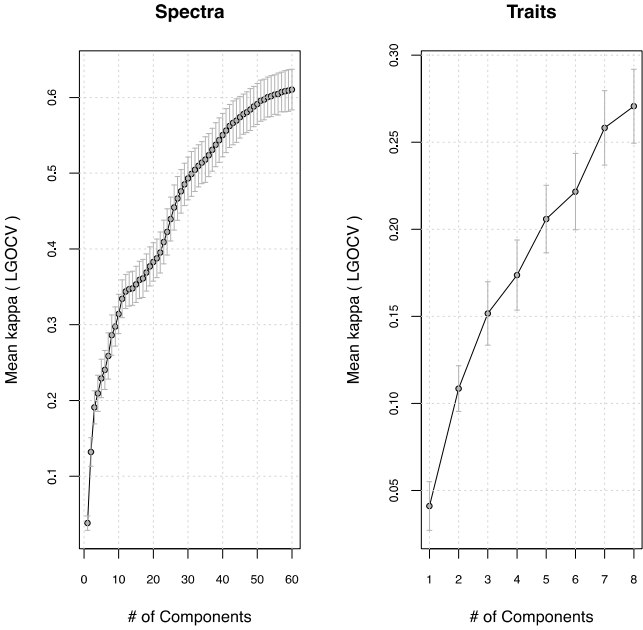
Trait	K	<i>p</i> Value	Null Mean	Null SD	BM SD
N	1.020	0.002	0.620	0.097	0.334
C	0.812	0.046	0.617	0.093	0.321
LMA	0.561	0.698	0.615	0.094	0.358
Fiber	0.933	0.006	0.622	0.098	0.322
Lignin	0.812	0.043	0.625	0.105	0.332
Cell	0.676	0.251	0.616	0.090	0.330
NDWI	1.084	0.001	0.617	0.090	0.332
Chl	0.765	0.084	0.620	0.094	0.362
PRI	0.584	0.606	0.620	0.111	0.337

Table S4. Analysis of variance for leaf type. Leaf type is treated as the main factor with each spectral PLS component as a response variable. F ratios indicate the variation in component scores among populations relative to variation within populations. Components are shown in bold if P values are less than 0.05, indicating a significant population effect.

	Df	Sum Sq	Mean Sq	F Value	<i>p</i> Value
Component 1	2	0.0975	0.0487	16.67	0.0000
Component 2	2	0.00161	0.000805	0.37	0.6879
Component 3	2	0.000652	0.000326	1.58	0.2073
Component 4	2	0.000449	0.000225	3.24	0.0399
Component 5	2	0.000291	0.000145	3.42	0.0337
Component 6	2	0.000259	0.00013	3.28	0.0385
Component 7	2	0.00016	0.0000801	3.87	0.0215
Component 8	2	0.0000881	0.0000441	2.85	0.0586
Component 9	2	0.0000286	0.0000143	1.50	0.2245
Component 10	2	0.0000145	0.00000727	1.29	0.2759
Component 11	2	0.0000136	0.00000681	1.47	0.2319
Component 12	2	0.0000605	0.0000303	10.01	0.0001
Component 13	2	0.00000631	0.00000315	0.14	0.8731
Component 14	2	0.00000712	0.00000356	1.92	0.1471
Component 15	2	0.0000106	0.00000532	4.03	0.0183
Component 16	2	0.000000144	0.000000072	0.07	0.9368
Component 17	2	0.00000586	0.00000293	3.61	0.0277
Component 18	2	0.00000212	0.00000106	1.47	0.2312
Component 19	2	0.0000123	0.00000617	12.24	0.0000
Component 20	2	0.000000541	0.000000271	0.72	0.4883



(A)



(B)

Figure S1. Cont.

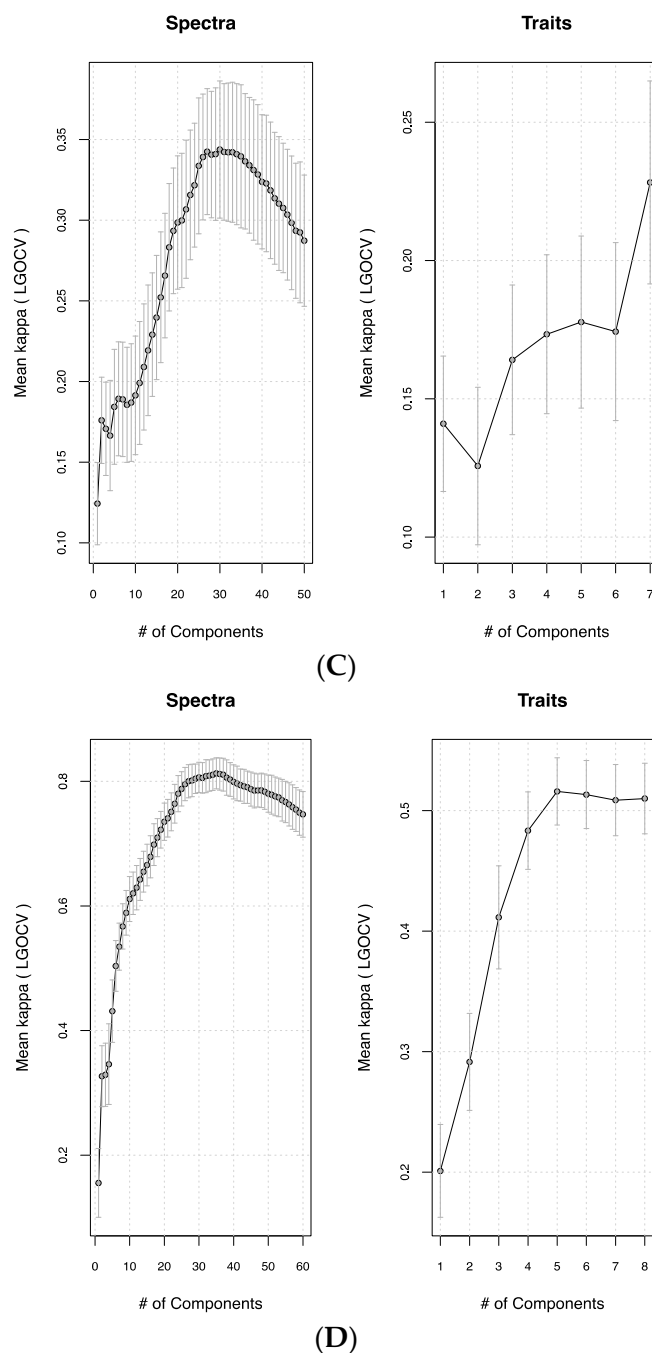


Figure S1. Kappa scores for PLS-DA model fit as a function of the number of components included in the validation model using full spectral data or traits for (A) population classification within *Quercus oleoides*; (B) oak species classification; (C) oak clade classification; and (D) leaf type classification. Shown are mean and $\pm 2SD$ of the kappa values for 300 model jackknife iterations (Leave group out cross validation, LGOCV) for each number of components.

