Supplementary Material

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Data

Kinship and social structure

All data was extracted from the D-PLACE Ethnographic atlas github repository. Counts of the number of societies used for the signal and ancestral state analyses for each languages family are in table S1. Question and variable codes are displayed below in table S2. Due to the nature of the analysis, all variables are binary coded. The numbers in the value columns indicate the criteria for a society to have the terminology or social structure coded as present. For details on what each code indicates, refer to the Ethnographic Atlas codebook or the D-PLACE github repository.

Table S1: Count of societies in signal test and ancestral state analyses, by language family

	Count
Austronesian	85
Bantu	69
Uto-Aztecan	22

Table S2: Data coding taken from D-PLACE and Co-evolutionary analyses data counts

terminology	question	value	social question va	lue AN	BT	UA
~			structure	counts	counts	counts
Crow	27	1	matrilineal 43 3	85	69	
Crow	27	1	0 1 000 0	4,5,6 80		
Crow	27	1	1 0 00 0	3,4,5,6 80		
Crow	27	1	matri.anvunclocalresidenic	,	69	
Crow	27	1		5,8,9,10 84	69	
Eskimo	27	3	bi.linealdescent 43 2,	*		
Eskimo	27	3		3,4 85		
Eskimo	27	3	absenceofcousinmar25age1p	etilmiltäted 79		
Eskimo	27	3	absenceofcousinmar 23 age7p	seference 79		
Eskimo	27	3	monogamy 9 1	80		
Eskimo	27	3	neo.localresidence 10 6	84		
Eskimo	27	3	nuclear.families 8 1,2	2 83		
Hawaiian	27	4	bi.linealdescent 43 2,	5,7 85	69	23
Hawaiian	27	4	bi.localextendedfami&y 6,	7,8 83	69	22
Hawaiian	27	4	absenceofcousinmar25agelp	eringitated 79	66	19
Hawaiian	27	4	absenceofcousinmar23age7pt	seference 79	66	19
Hawaiian	27	4	bi.localresidence 10 2,	11,12 84	69	22
Iroquois	27	5	exogamy.unilineal.de5cen4	78	62	19
Iroquois	27	5	uni.linealdescent 43 1,	3,4 85	69	23
Iroquois	27	5	cross.cousinmarriag25perfq	it,9 ed 79	66	19
Iroquois	27	5	cross.cousinmarriag23prefe	2;8¢5,6,8,12 7,9 3,14	66	19
Iroquois	27	5	high.polygyny 9 3,4	4,5,6 80		22
Iroquois	27	5	polygyny 9 2,3	3,4,5,6 80		
Iroquois	27	5	matri.anvunclocalresidence	5,9 84	69	22
Iroquois	27	5	uni.localresidence 10 1,5	5,8,9,10 84	69	22
Omaha	27	6	patrilineal 43 1		69	
Omaha	27	6	matri.anvunclocalres0denk	5,9	69	
Omaha	27	6		5,8,9,10	69	

Table S3: hypotheses from earliest found source with quotes, references and page numbers

terminology	hypotheses	quote	justification	reference
Crow	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Crow	Matri-avunculocal residence	"Crow systems should occur more frequency in societies which are avunculocal"	terms. Avunculoval residence means married couples move to live with the husband's mother's brother and are spatially closer to maternal kin, meaning there is more pressure to specifically identify maternal kin, and paternal kin can be grouped together. With specific reference to Crow societies, it is likely that this also aligns with matrilateral cross-cousin marriage.	Eyde, D. B., & Postal, P. M. (1961). Avunculocal and Incest: The Development of Unilateral Cross-Cousin Marriage and Crow-Omaha Kinship Systems. American Anthropologist, 63(4), 747–771.
Crow	Matrilineal	"The tables show a strong correlation between Omaha terms and patrilineal unilineal descent groups and between Crow terms and matrilineal unilineal descent groups"	A matrilineal descent system imposes a higher social status (social differential) on maternal kin, and therefore the need to distinguish maternal kin over paternal. This allows the grouping of paternal kin.	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Crow	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.

Co-evolutionary hypotheses and references

Phylogenies

We tested hypotheses across three languages families, where data allowed. This was the Austronesian, Bantu, and Uto-Aztecan language phylogenies (@gray2009, @grollemund2015bantu, @Levinson_Greenhill_Gray_Dunn_2011). All language to phylogeny pairings were taken from decisions made in @kirby2016d. In Austronesian, we sub-sampled 1000 phylogenies from a posterior sample of 4199 phylogenies. Austronesian phylogenies were estimated through linguistic data and supported by genetic evidence, and archaeological records. Detailed methods can be found in @gray2009. Trees were pruned from the original sample of 400 languages, to 80 languages based on data availability. In Bantu, we sampled 1000 from a posterior sample of 2000 phylogenies developed in @grollemund2015bantu. These trees were built using linguistic data and calibrated using the archaeological record. Trees were pruned from the original sample of 425 languages, to 69 languages based on data availability. In Uto-Aztecan, we sampled 1000 phylogenies from a posterior of 10,000 phylogenies modeled by @Levinson_Greenhill_Gray_Dunn_2011. This posterior was built using linguistic data. Trees were pruned from the original sample of 34 languages, to 19 based on data availability. All branch lengths are standardized to have a mean length of 0.1, as per BayesTraits recommendations.

Signal tests

We performed 4 signal tests to assess the hypotheses that shared ancestry was a constraint on kinship diversity. The phylogenetic 'D' test uses simulation to determine whether the clustering of binary variables on a phylogeny follow patterns of Brownian motion (D = 0 indicates perfectly Brownian clusters and D < 0strong clustering) or random clustering (D=1 indicates complete randomness). To test whether geography may also predict the distribution of terminologies, we used Mantel tests. Mantel tests use random permutation and Pearson's correlation statistics to determine the correlation between two matrices. Here we compare log geographic distance, calculated with the Haversine formula, to a binary similarity matrix of each terminology present in each language family, each over the default setting of 999 permutations. To determine whether phylogenetic or geographic distances best determined the distribution of terminologies, we used partial Mantel tests. Partial Mantel tests control for a confounding third matrix, while comparing another two matrices. We perform a test between a terminology and geographic distance, controlling for phylogenetic distance, and another between terminology and phylogenetic distance, controlling for geographic distance. Phylogenetic distance is calculated using cophenetic distance, and the cophenetic function in R {stats} (R Core Team 2018). Table S3 shows the mean posterior result from 1000 phylogenies for all terminologies present within each language family. However, we only consider results viable if the terminology consists of more than 10% of the overall sample. All p-values are bonferonni corrected.

The code for all signal tests can be found in file analysis/signal-tests.R. This file comes with helper functions analysis/signal-functions and analysis/mantel-functions for the D-statistic and Mantel tests respectively.

Ancestral state

MCMC review

Ancestral state inference allows us to estimate the probability of a particular terminology at the root of each language phylogeny, as well as estimating the patterns of change between each state. We perform Bayesian reversible-jump MCMC ancestral state inference kinship terminologies using BayesTraits V 3.0 Multistate (Pagel and Meade 2017). Multistate uses a posterior of phylogenies to estimate the probability of each terminology present in the taxa at the phylogeny root, and an estimation of the rate (Q) matrix. The

Table S4: Signal tests for each terminology within each language family. Columns 2 and 3 indicate the presence and absence of a terminology. Columns 4 to 6 are outputs from the D-statistic test. Columns 7 to 21 are output from Mantel tests. P-values and bonferonni corrected values shown

		ı	D					-
							·'	J
Absent	Present	D	Prob. Brownian	Prob. Random	Z-stat	p-value	bonf-p	Z-st
1								
79	6	-0.115	0.603	0.036	1752616.53	0.039	0.233	3789.8
71	14	-0.494	0.806	0.000	4905208.29	0.219	1.000	8155.1
37	48	0.661	0.054	0.081	8021595.70	0.959	1.000	14388.1
70	15	0.097	0.468	0.007	4216334.11	0.032	0.190	8460.8
84	1	2.860	0.230	0.700	430380.25	0.376	1.000	702.3
84	1	-2.063	0.714	0.171	498098.38	0.260	1.000	709.8
				-		1		
65	4	1.105	0.129	0.525	348598.29	0.887	1.000	1823.4
68	1	2.941	0.066	0.881	93014.64	0.783	1.000	477.2
60	9	0.405	0.297	0.083	792380.62	0.524	1.000	3835.7
25	44	0.166	0.362	0.008	1636008.46	0.023	0.159	7853.2
68	1	-2.432	0.834	0.040	116322.82	0.320	1.000	500.4
61	8	0.767	0.140	0.274	733279.95	0.393	1.000	3484.3
67	2	1.051	0.287	0.459	169263.56	0.718	1.000	929.7
Uto-Aztecan								
21	1	0.243	0.419	0.462	13195.12	0.365	1.000	132.0
21	1	3.253	0.216	0.679	14128.24	0.818	1.000	133.0
6	16	-0.600	0.798	0.004	70096.07	0.259	0.980	606.5
18	4	-2.343	0.985	0.000	54649.14	0.881	1.000	457.4
	79 71 37 70 84 84 84 65 68 60 25 68 61 67	79 6 71 14 37 48 70 15 84 1 84 1 84 1 65 4 68 1 60 9 25 44 68 1 61 8 67 2 21 1 21 1 6 16	79 6 -0.115 71 14 -0.494 37 48 0.661 70 15 0.097 84 1 2.860 84 1 -2.063 65 4 1.105 68 1 2.941 60 9 0.405 25 44 0.166 68 1 -2.432 61 8 0.767 67 2 1.051 21 1 0.243 21 1 3.253 6 16 -0.600	Absent Present D Prob. Brownian 79 6 -0.115 0.603 71 14 -0.494 0.806 37 48 0.661 0.054 70 15 0.097 0.468 84 1 2.860 0.230 84 1 -2.063 0.714 65 4 1.105 0.129 68 1 2.941 0.066 60 9 0.405 0.297 25 44 0.166 0.362 68 1 -2.432 0.834 61 8 0.767 0.140 67 2 1.051 0.287 21 1 0.243 0.419 21 1 3.253 0.216 6 16 -0.600 0.798	79 6 -0.115 0.603 0.036 71 14 -0.494 0.806 0.000 37 48 0.661 0.054 0.081 70 15 0.097 0.468 0.007 84 1 2.860 0.230 0.700 84 1 -2.063 0.714 0.171 65 4 1.105 0.129 0.525 68 1 2.941 0.066 0.881 60 9 0.405 0.297 0.083 25 44 0.166 0.362 0.008 68 1 -2.432 0.834 0.040 61 8 0.767 0.140 0.274 67 2 1.051 0.287 0.459 21 1 0.243 0.216 0.679 6 16 -0.600 0.798 0.004	Absent Present D Prob. Brownian Prob. Random Z-stat 79 6 -0.115 0.603 0.036 1752616.53 71 14 -0.494 0.806 0.000 4905208.29 37 48 0.661 0.054 0.081 8021595.70 70 15 0.097 0.468 0.007 4216334.11 84 1 2.860 0.230 0.700 430380.25 84 1 -2.063 0.714 0.171 498098.38 65 4 1.105 0.129 0.525 348598.29 68 1 2.941 0.066 0.881 93014.64 60 9 0.405 0.297 0.083 792380.62 25 44 0.166 0.362 0.008 1636008.46 68 1 -2.432 0.834 0.040 116322.82 61 8 0.767 0.140 0.274 733279.95	Absent Present D Prob. Brownian Prob. Random Z-stat p-value 79 6 -0.115 0.603 0.036 1752616.53 0.039 71 14 -0.494 0.806 0.000 4905208.29 0.219 37 48 0.661 0.054 0.081 8021595.70 0.959 70 15 0.097 0.468 0.007 4216334.11 0.032 84 1 2.860 0.230 0.700 430380.25 0.376 84 1 -2.063 0.714 0.171 498098.38 0.260 65 4 1.105 0.129 0.525 348598.29 0.887 68 1 2.941 0.066 0.881 93014.64 0.783 60 9 0.405 0.297 0.083 792380.62 0.524 25 44 0.166 0.362 0.008 1636008.46 0.023 68 1 -2.43	Absent Present D Prob. Brownian Prob. Random Z-stat p-value bonf-p 79 6 -0.115 0.603 0.036 1752616.53 0.039 0.233 71 14 -0.494 0.806 0.000 4905208.29 0.219 1.000 37 48 0.661 0.054 0.081 8021595.70 0.959 1.000 70 15 0.097 0.468 0.007 4216334.11 0.032 0.190 84 1 2.860 0.230 0.700 430380.25 0.376 1.000 84 1 -2.063 0.714 0.171 498098.38 0.260 1.000 65 4 1.105 0.129 0.525 348598.29 0.887 1.000 68 1 2.941 0.066 0.881 93014.64 0.783 1.000 25 44 0.166 0.362 0.008 1636008.46 0.023 0.159

Table S5: Three MCMC chains for the austronesian language family

	Lh	Crow	Eskimo	Hawaiian	Iroquois	Omaha	Sudanese
1	-95.053	0.029	0.846	0.011	0.015	0.042	0.057
2	-95.037	0.029	0.846	0.010	0.015	0.042	0.058
3	-95.042	0.029	0.848	0.010	0.014	0.041	0.057
Mean	-95.044	0.029	0.847	0.010	0.015	0.042	0.057

Table S6: Three MCMC chains for the bantu language family

	Lh	Crow	Descriptive	Hawaiian	Iroquois	Omaha	Sudanese	Mixed
1	-81.151	0.089	0.078	0.157	0.393	0.101	0.082	0.099
2	-81.134	0.090	0.078	0.156	0.395	0.102	0.081	0.097
3	-81.141	0.089	0.078	0.156	0.397	0.101	0.081	0.098
Mean	-81.142	0.089	0.078	0.156	0.395	0.101	0.081	0.098

reversible-jump approach searches the model space for an optimal solution by dynamically setting some rate parameters (i.e. transitions from one state to another) to zero. This results in searching the model space where we are confident transition rates are non-zero. The Q matrix shows the likelihood of changing from any state to any other. MCMC chains were run for 10^9 iterations, sampling every 50,000 iterations with a burn-in of 10,000 iterations, to give a posterior sample of 20,000. Each analysis ran three times to test consistent MCMC convergence using the Gelman-Rubin diagnostic (Gelman and Rubin 1992). Due to uncertainty in the inference of the Bantu ancestral state, each terminology present in the phylogeny was 'fossilized' as the root to estimate likelihoods. Effectively, this forces the algorithm to build a model given a particular ancestral state and given the contemporary data. We can then compare the model fit across each constrained model. We calculate pairwise Bayes factors (BF) to assess the evidence for each response. BF < 3 indicates weak evidence, >3 positive evidence, and >10 very strong evidence. This is shown in section 3.1.1.

Fossilized Bantu

MCMC Review

We fossilize the ancestral state for each possible terminology within Bantu in an attempt to determine the most plausible ancestral state. Below are the marginal log-likelihoods for these models and the result with comparisons to the most likely ancestral state, Iroquoian.

Bayes factor model comparison

Bayes factor calculations show that there is some evidence for a Iroquoian root over a Hawaiian root (BF = 2.306). The table below shows comparisons to the fossilized Iroquois root to all other fossilized roots.

Fossilized Uto-Aztecan

MCMC Review

Table S7: Three MCMC chains for the utoaztecan language family

	Lh	Crow	Eskimo	Hawaiian	Iroquois
1	-19.279	0.232	0.226	0.310	0.232
2	-19.291	0.232	0.224	0.312	0.232
3	-19.282	0.232	0.225	0.311	0.232
Mean	-19.284	0.232	0.225	0.311	0.232

Table S8: Gelman-Rubin tests of MCMC convergence for each language family

	Point est.	Upper C.I.
austronesian	1	1
bantu	1	1
utoaztecan	1	1

Table S9: Marginal log-likelihood for each fossilized terminology in Bantu

terminology	MLL
Crow	91.683
Descriptive	90.914
Hawaiian	91.450
Iroquois	90.297
Mixed	91.819
Omaha	90.805
Sudanese	92.595

Table S10: Pariwise Bayes factor between Iroquois and all other possible states.

terminology	Bayes' Factor
Crow	2.772
Descriptive	1.235
Hawaiian	2.306
Iroquois	0.000
Mixed	3.043
Omaha	1.017
Sudanese	4.595

Table S12: Pariwise Bayes factor between Iroquois and all other possible states.

terminology	Bayes' Factor
Crow	-0.103
Eskimo	0.058
Hawaiian	0.000
Iroquois	0.852

Table S13: Ancestral state for PMP

	Probability
RecNode P(1)	0.020
RecNode P(3)	0.897
RecNode P(4)	0.004
RecNode P(5)	0.006
RecNode P(6)	0.026
RecNode P(7)	0.046

As with Bantu, we fossilize the ancestral state for each possible terminology within UtoAztecan to determine the most plausible ancestral state. Below are the marginal log-likelihoods for these models, followed by a BayesFactor comparisons between the most likely ancestral state & all other possible states.

```
## \begin{table}
##

## \caption{\label{tab:fossilized-uto}Table S11: Marginal log-likelihood for each fossilized terminolog
## \centering
## \begin{tabular}[t]{l|r}
## \hline
## terminology & MLL\\
## \hline
## Crow & 24.092\\
## \hline
## Eskimo & 24.173\\
## \hline
## Hawaiian & 24.144\\
## \hline
## Iroquois & 24.570\\
```

Bayes factor model comparison

Bayes factor calculations show that even when fossilizing to each possible root - there is no preference for a particular ancestral state.

PMP in Austronesia

\hline

\end{tabular}
\end{table}

Here we reconstruct the PMP state in Austronesian using the RecNode command in BayesTraits. All other settings remain the same as the Austronesian model.

Table S14: Transition rates between kin terminologies in the austronesian language family.

transition	parameterized	zero	percentage
Crow -> Hawaiian	9160	840	0.916
Eskimo -> Hawaiian	9080	920	0.908
Hawaiian -> Iroquois	8921	1079	0.892
Omaha -> Hawaiian	7260	2740	0.726
Sudanese -> Hawaiian	7114	2886	0.711
Iroquois -> Hawaiian	6993	3007	0.699
Omaha -> Crow	6919	3081	0.692
Crow -> Iroquois	6792	3208	0.679
Omaha -> Sudanese	6561	3439	0.656
Crow -> Omaha	6499	3501	0.650
Omaha -> Iroquois	6436	3564	0.644
Sudanese -> Crow	6305	3695	0.631
Iroquois -> Crow	6270	3730	0.627
Sudanese -> Omaha	6128	3872	0.613
Crow -> Sudanese	5964	4036	0.596
Sudanese -> Iroquois	5875	4125	0.588
Hawaiian -> Crow	5622	4378	0.562
Sudanese -> Eskimo	4980	5020	0.498
Omaha -> Eskimo	4876	5124	0.488
Iroquois -> Omaha	4191	5809	0.419
Crow -> Eskimo	3699	6301	0.370
Iroquois -> Sudanese	3229	6771	0.323
Eskimo -> Sudanese	2182	7818	0.218
Hawaiian -> Omaha	1851	8149	0.185
Hawaiian -> Sudanese	1279	8721	0.128
Eskimo -> Crow	1005	8995	0.101
Eskimo -> Omaha	953	9047	0.095
Iroquois -> Eskimo	846	9154	0.085
Eskimo -> Iroquois	410	9590	0.041
Hawaiian -> Eskimo	255	9745	0.025

Transition rates

RJ ancestral state analysis also estimates the rate of transition between kinship terminological types. The model constrains the number of parameters estimated, forcing some parameters to be zero, and then estimates and appropriate number of parameters for accurately represent the model. By looking at which parameters are set to zero across the MCMC chain, we can see which transition rates the model believes to be important. We consider transition rates to be important if they are estimated is more than 95% of models.

Guillon and Mace comparison

Previous research performed by Guillon and Mace, using similar methods, found support for a Hawaiian root, with some evidence of an Iroquoian root within the Bantu language family. The numerical results for this analysis are not available in the paper. This is the inverse of our result, which found most support for an Iroquoian root, with some support for Hawaiian. This discrepancy is concerning considering the terminological data for both analysis come from d-place. The primary difference between approaches is that here we use a more recently developed phylogeny, and secondarily, Guillon and Mace include missing data, where we exclude it. We re-analysed our data including missing data and found no change in our previous

Table S15: Transition rates between kin terminologies in the bantu language family.

transition	parameterized	zero	percentage
Iroquois -> Omaha	9163	837	0.916
Iroquois -> Hawaiian	8137	1863	0.814
Omaha -> Descriptive	7956	2044	0.796
Crow -> Sudanese	7449	2551	0.745
Omaha -> Iroquois	7339	2661	0.734
Sudanese -> Crow	6938	3062	0.694
Crow -> Hawaiian	6928	3072	0.693
Hawaiian -> Crow	6716	3284	0.672
Omaha -> Hawaiian	6447	3553	0.645
Crow -> Iroquois	6390	3610	0.639
Sudanese -> Hawaiian	6330	3670	0.633
Omaha -> Crow	6181	3819	0.618
Descriptive -> Omaha	6119	3881	0.612
Omaha -> Sudanese	5996	4004	0.600
Hawaiian -> Iroquois	5875	4125	0.588
Descriptive -> Hawaiian	5834	4166	0.583
Sudanese -> Omaha	5834	4166	0.583
Mixed -> Hawaiian	5722	4278	0.572
Sudanese -> Iroquois	5716	4284	0.572
Descriptive -> Crow	5576	4424	0.558
Crow -> Omaha	5546	4454	0.555
Mixed -> Omaha	5517	4483	0.552
Mixed -> Crow	5441	4559	0.544
Descriptive -> Mixed	5430	4570	0.543
Sudanese -> Mixed	5424	4576	0.542
Omaha -> Mixed	5417	4583	0.542
Mixed -> Iroquois	5411	4589	0.541
Crow -> Mixed	5362	4638	0.536
Descriptive -> Sudanese	5292	4708	0.529
Descriptive -> Iroquois	5280	4720	0.528
Sudanese -> Descriptive	5222	4778	0.522
Mixed -> Sudanese	5086	4914	0.509
Iroquois -> Crow	5075	4925	0.508
Mixed -> Descriptive	4959	5041	0.496
Crow -> Descriptive	4762	5238	0.476
Hawaiian -> Omaha	4197	5803	0.420
Hawaiian -> Sudanese	4080	5920	0.408
Hawaiian -> Mixed	3473	6527	0.347
Hawaiian -> Descriptive	2656	7344	0.266
Iroquois -> Sudanese	1774	8226	0.177
Iroquois -> Mixed	379	9621	0.038
Iroquois -> Descriptive	208	9792	0.021

Table S16: Transition rates between kin terminologies in the utoaztecan language family.

transition	parameterized	zero	percentage
Iroquois -> Hawaiian	9511	489	0.951
Crow -> Hawaiian	8658	1342	0.866
Eskimo -> Hawaiian	8393	1607	0.839
Hawaiian -> Iroquois	8036	1964	0.804
Eskimo -> Iroquois	7254	2746	0.725
Crow -> Iroquois	7220	2780	0.722
Crow -> Eskimo	6975	3025	0.698
Iroquois -> Eskimo	6877	3123	0.688
Eskimo -> Crow	6736	3264	0.674
Iroquois -> Crow	6240	3760	0.624
Hawaiian -> Crow	1380	8620	0.138
Hawaiian -> Eskimo	1336	8664	0.134

Table S17: Ancestral state of Bantu with missing data included

	probability
Crow	0.124
Descriptive	0.117
Hawaiian	0.139
Iroquois	0.259
Omaha	0.124
Sudanese	0.119
Mixed	0.118

conclusions. Suggesting that the improved phylogeny is driving the change in results. Efforts were made to contact the authors to make more direct comparisons, but with no response.

Co-evolution tests

MCMC settings

All co-evolutionary analyses was performed in BayesTraits v3.1 using Discrete models [@pagel2006bayesian]. For all models we used an Reversible Jump MCMC approach, and tested an independent and dependent model of evolution. In an independent model, a trait can change, regardless of the state of the other trait. In a dependent model, a trait change is dependent on the state of the second trait. If co-evolution has occurred, the data should fit a dependent model better than it fits an independent model. We test this using Bayes Factors and the same guides as described previously in the paper and SM. Analyses were run between 10,010,000 and 65,000,000 iterations, with burn-ins ranging between 10,000 and 55,000,000, and sampling every 1000 iterations. The results is a posterior of 10,000 iterations, approximately 10 iterations per tree per hypotheses. A stepping stone sampler was used to estimate the marginal likelihood. We used 100 stones sampled every 1,000 iterations. For details of the prior and other settings for each hypotheses, see the table below.

MCMC review and Bayes Factors

Here we show the results of MCMC chains and respective tests. The first table for each hypotheses is a review of the MCMC chains. Each row shows the marginal log-likelihood and averaged transition rates

Table S18: MCMC settings for both dependent and independent analyses

hypotheses	exponential mean	scaled branch length	iterations	samp
austronesian-crow-high.polygyny	10	Yes	10050000	1
austronesian-crow-matri.anvunclocalresidence	10	Yes	10050000	1
austronesian-crow-matrilineal	10	Yes	10050000	1
austronesian-crow-polygyny	10	Yes	10050000	1
austronesian-crow-matrilocal	10	Yes	10010000	1
austronesian-crow-matrilocal.strict	10	Yes	10010000	1
austronesian-crow-uni.localresidence	10	Yes	10010000	1
austronesian-eskimo-absenceofcousinmarriage.permitted	10	Yes	65000000	1
austronesian-eskimo-absenceofcousinmarriage.preference	10	Yes	65000000	1
austronesian-eskimo-bi.linealdescent	10	Yes	10010000	1
austronesian-eskimo-monogamy	10	Yes	10050000	1
austronesian-eskimo-neo.localresidence	10	Yes	65000000	1
austronesian-eskimo-nuclear.families	10	Yes	10010000	1
austronesian-eskimo-uni.linealdescent	10	Yes	10010000	1
austronesian-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10050000	1
austronesian-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1
austronesian-hawaiian-bi.linealdescent	10	Yes	10010000	1
austronesian-hawaiian-bi.localextendedfamily	10	Yes	10010000	1
austronesian-hawaiian-bi.localresidence	10	Yes	10050000	1
austronesian-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	1
austronesian-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1
austronesian-iroquois-exogamy.unilineal.descent	10	Yes	10010000	1
austronesian-iroquois-exogamy.ummiear.descent austronesian-iroquois-high.polygyny	10	Yes	10010000	1
austronesian-iroquois-mign.polygyny austronesian-iroquois-matri.anvunclocalresidence	10	Yes	10010000	1
	10	Yes	10010000	1
austronesian-iroquois-polygyny		Yes	10010000	1
austronesian-iroquois-uni.linealdescent	10	Yes		
austronesian-iroquois-uni.localresidence	10		10050000	1
bantu-crow-matri.anvunclocalresidence	10	Yes	10010000	1
bantu-crow-matrilineal	10	Yes	10010000	1
bantu-crow-matrilocal	10	Yes	10050000	1
bantu-crow-matrilocal.strict	10	Yes	10050000	1
bantu-crow-uni.localresidence	10	Yes	10010000	1
bantu-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	1
bantu-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1
bantu-hawaiian-bi.linealdescent	10	Yes	10010000	1
bantu-hawaiian-bi.localextendedfamily	10	Yes	10010000	1
bantu-hawaiian-bi.localresidence	10	Yes	10010000	1
bantu-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	1
bantu-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1
bantu-iroquois-exogamy.unilineal.descent	10	Yes	10010000	1
bantu-iroquois-matri.anvunclocalresidence	10	Yes	10010000	1
bantu-iroquois-uni.linealdescent	10	Yes	10010000	1
bantu-iroquois-uni.localresidence	10	Yes	10010000	1
bantu-omaha-matri.anvunclocalresidence	10	Yes	10010000	1
bantu-omaha-patrilineal	10	Yes	10010000	1
bantu-omaha-patrilocal	10	Yes	10010000	1
bantu-omaha-patrilocal.strict	10	Yes	10010000	1
bantu-omaha-uni.localresidence	10	Yes	10010000	1
uto-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	1
uto-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1
uto-hawaiian-bi.linealdescent	10	Yes	10010000	1
uto havrajian bi lacalertandadfamily	10	Yes	10010000	1
uto-hawaiian-bi.localresidence 12	10	Yes	10010000	1
	10	Yes	10010000	1
uto-iroquois-cross.cousinmarriage.permitted		Yes	10010000	1
uto-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1
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Table S19: Austronesian : Crow <-> High.polygyny

	Dependent										Iı	ndepende	nt	
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	58.486	2.537	1.219	17.085	2.878	23.205	4.089	7.454	6.586	59.016	1.68	21.444	2.778	1
2	58.607	2.521	1.259	16.807	2.979	23.77	4.074	7.654	6.568	58.942	1.704	21.656	2.777	1
3	58.54	2.546	1.236	17.188	2.985	23.439	4.042	7.67	6.556	59.1	1.688	21.731	2.827	1
Mean	58.544	2.535	1.238	17.027	2.947	23.471	4.068	7.593	6.57	59.019	1.691	21.61	2.794	1
BF	1.059													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

for the dependent and independent models for a single chain. There are three MCMC chains run for each hypotheses to ensure the model is reaching the same conclusion each time. The penultimate row shows the mean across the three runs. The final row tests which model was more appropriate for the data. We calculate a Bayes-factor, which compares the log marginal likelihood between the dependent and independent models, as explained in @pagel2006bayesian. A Bayes Factor greater than ten indicates strong support, greater than three positive support and less than three no support.

A second table shows the results of a Gelman-Rubin diagnostic testing, to test for any significant differences between chains [@gelman1992single]. A value of 1 indicates no difference, and a rule of thumb suggests point-estimates of less than 1.1 indicate negligible differences between chains.

Some extra analyses are also shown here that are not seen in table 1. These are matrilocal and patrilocal hypotheses and matrilocal strict and patrilocal strict. The strict hypothesis exclude anything but societies classified as patrilocal or matrilocal. In the main text we discuss the differences between including virilocality and uxorilocality under each of these hypotheses, there are represented in the 'not strict' hypothesis.

Bantu node 70 state inference

Here we re-construct node 70 within the Bantu tree, to confirm the hypotheses that the presence of both Iroquois terminologies and a preference for cross-cousin marriage existed at this point.

Table 1 in the main text shows that the dependent model is already preferred, so here we only look at the dependent model. The figure below shows the likelihood of each possibility. Top left: Absence of both Iroquois terminology and a preference for cross-cousin marriage. Top right: Absence of cross-cousin marriage and the presence of cross-cousin marriage preference. Bottom right: Both Iroquoian terminologies and cross-cousin marriage preferences are present. Bottom left: presence of an Iroquoian terminology, and absence of a cross-cousin marriage preference.

Table S20: Austronesian : Crow <-> Matri.anvunclocalresidence

	Dependent										In	depender.	ıt
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	54.688	0.997	0.367	6.689	8.886	12.439	10.346	17.49	4.623	59.875	1.604	21.99	1.166
2	54.6	1.007	0.348	6.647	8.906	12.272	9.917	17.536	4.619	60.003	1.622	22.299	1.165
3	54.71	0.991	0.366	6.628	8.98	12.309	10.322	17.464	4.705	59.84	1.609	21.951	1.165
Mean	54.666	0.998	0.36	6.655	8.924	12.34	10.195	17.497	4.649	59.906	1.612	22.08	1.165
BF	10.374												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S21: Austronesian : Crow <-> Matrilineal

	Dependent										In	depender	ıt
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	55.963	0.755	0.324	5.045	8.59	12.393	11.438	17.922	8.894	61.187	1.573	21.589	1.01
2	56.018	0.765	0.318	5.079	8.606	12.566	11.038	17.838	8.997	61.205	1.575	21.477	1
3	56.128	0.751	0.322	5.082	8.556	12.417	11.061	17.805	8.803	61.206	1.574	21.449	1.003
Mean	56.036	0.757	0.321	5.069	8.584	12.459	11.179	17.855	8.898	61.199	1.574	21.505	1.004
BF	10.45												

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S22: Austronesian : Crow <-> Polygyny

				Γ		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	68.567	2.689	2.512	1.505	0.917	24.339	6.913	9.728	4.795	67.647	1.657	21.326	2.6	1.5
2	68.762	2.715	2.488	1.519	0.922	24.556	6.997	9.912	4.883	67.63	1.659	21.246	2.606	1.5
3	68.648	2.711	2.553	1.529	0.921	24.159	6.962	9.776	4.906	67.461	1.661	21.217	2.652	1.5
Mean	68.659	2.705	2.518	1.518	0.92	24.351	6.957	9.805	4.861	67.579	1.659	21.263	2.619	1.5
BF	-1.839													

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S23: Austronesian : Crow <-> Matrilocal

				Γ	epender		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	52.623	0.781	0.535	6.674	7.172	9.728	4.808	19.083	6.265	53.849	1.553	20.979	0.787	5.3
2	52.695	0.766	0.551	6.503	7.071	9.989	4.887	18.722	6.404	53.885	1.554	21.072	0.777	5.5
3	52.637	0.781	0.555	6.751	7.007	9.774	5.053	18.934	6.29	53.889	1.545	21.074	0.781	5.3
Mean	52.652	0.776	0.547	6.643	7.083	9.83	4.916	18.913	6.32	53.874	1.551	21.042	0.782	5.3
BF	2.452													

Gelman-Rubin MCMC chain diagnostic test

·	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S24: Austronesian : Crow <-> Matrilocal.strict

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	46.668	0.472	0.528	5.731	8.376	9.268	4.732	18.061	5.755	48.368	1.524	20.319	0.5	4.5
2	46.868	0.473	0.539	5.714	8.355	9.402	4.752	18.237	5.754	48.467	1.48	20.299	0.506	4.5
3	46.751	0.474	0.528	5.738	8.262	9.218	4.623	18.336	5.835	48.524	1.51	20.168	0.501	4.4
Mean	46.762	0.473	0.532	5.728	8.331	9.296	4.702	18.211	5.781	48.453	1.505	20.262	0.502	4.5
BF	3.401													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S25: Austronesian : Crow <-> Uni.local
residence

					Depende		Independent						
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	72.461	1.442	0.316	2.925	4.261	14.85	10.992	20.857	2.46	74.574	1.325	17.603	1.477
2	72.68	1.466	0.318	2.9	4.179	15.043	10.985	20.603	2.418	74.309	1.311	17.577	1.496
3	72.343	1.459	0.322	2.924	4.109	14.996	11.26	20.652	2.414	74.434	1.312	17.239	1.493
Mean	72.495	1.456	0.319	2.916	4.183	14.963	11.079	20.704	2.431	74.439	1.316	17.473	1.489
BF	4.228												

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S26: Austronesian : Eskimo <-> Absence
ofcousinmarriage.permitted

				$D\epsilon$		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	79.717	14.908	1.986	3.834	0.336	5.256	7.162	3.325	5.801	79.556	0.252	3.432	14.372	5.0
2	79.605	15.275	1.965	3.9	0.329	5.323	7.195	3.27	5.932	79.494	0.251	3.422	14.448	5.0
3	79.732	14.862	1.948	3.843	0.349	5.299	7.131	3.281	5.823	79.556	0.262	3.431	14.551	5.0
Mean	79.685	15.015	1.966	3.859	0.338	5.293	7.163	3.292	5.852	79.535	0.255	3.428	14.457	5.0
BF	-0.323													

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.002

Table S27: Austronesian : Eskimo <-> Absenceofcousin
marriage.preference

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	70.961	4.325	0.376	18.722	1.117	3.242	0.926	11.685	13.576	69.75	0.252	3.443	3.733	2
2	70.936	4.356	0.38	18.774	1.126	3.254	0.945	11.431	13.434	69.81	0.251	3.451	3.748	1
3	70.597	4.356	0.382	18.867	1.106	3.226	0.91	11.764	13.332	69.799	0.26	3.458	3.689	1
Mean	70.831	4.346	0.379	18.788	1.116	3.241	0.927	11.627	13.447	69.786	0.254	3.451	3.723	1
BF	-2.423													

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.000

Table S28: Austronesian : Eskimo <-> Bi.linealdescent

				D	ependen	t				Independent					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta	
1	92.099	4.625	0.685	5.322	0.5	3.896	1.499	5.741	9.434	91.281	0.165	3.213	2.651	4.33	
2	92.021	4.655	0.661	5.433	0.506	3.879	1.526	5.903	9.614	91.134	0.167	3.199	2.645	4.31	
3	91.91	4.65	0.666	5.415	0.495	3.879	1.521	5.832	9.371	91.503	0.161	3.183	2.619	4.30	
Mean	92.01	4.643	0.671	5.39	0.5	3.885	1.515	5.825	9.473	91.306	0.164	3.198	2.638	4.32	
BF	-1.634														

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S29: Austronesian : Eskimo <-> Monogamy

				D_{i}		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta
1	70.882	0.964	0.331	3.596	5.71	4.521	9.368	5.121	5.901	74.566	0.188	3.145	1.265	2.36
2	70.993	0.956	0.322	3.639	5.569	4.46	9.625	5.075	6.011	74.593	0.187	3.174	1.269	2.38
3	71.014	0.95	0.33	3.561	5.553	4.473	9.491	5.016	6.031	74.514	0.185	3.18	1.275	2.41
Mean	70.963	0.957	0.328	3.599	5.611	4.485	9.495	5.071	5.981	74.558	0.187	3.166	1.27	2.38
BF	7.368													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S30: Austronesian : Eskimo <-> Neo.local
residence

				I		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	52.993	0.19	0.207	8.934	10.115	3.249	4.742	6.91	11.153	56.985	0.166	3.223	0.619	7.
2	52.876	0.188	0.205	8.96	10.336	3.262	4.683	6.987	10.939	56.776	0.169	3.241	0.618	7.
3	52.852	0.189	0.202	8.97	10.232	3.233	4.714	6.961	11.16	56.722	0.165	3.214	0.619	7.
Mean	52.907	0.189	0.205	8.955	10.228	3.248	4.713	6.953	11.084	56.828	0.167	3.226	0.619	7.
BF	7.984													

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.001	1.002

Table S31: Austronesian : Eskimo <-> Nuclear.families

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	88.867	4.445	0.542	6.428	1.792	7.766	10.399	4.003	3.262	89.349	0.17	3.154	3.983	4.0
2	89.037	4.413	0.539	6.373	1.827	7.626	10.282	4.013	3.18	89.259	0.167	3.167	3.965	4.0
3	88.897	4.394	0.531	6.483	1.735	7.539	10.413	4.001	3.202	89.112	0.17	3.169	3.954	4.0
Mean	88.934	4.417	0.537	6.428	1.785	7.644	10.365	4.006	3.215	89.24	0.169	3.163	3.967	4.0
BF	0.963													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

Table S32: Austronesian : Eskimo <-> Uni.linealdescent

				I		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	86.068	2.3	0.518	3.44	0.558	3.108	1.524	11.284	10.553	85.802	0.179	3.218	1.437	3.4
2	86.834	2.335	0.507	3.427	0.553	3.098	1.531	11.294	10.388	85.815	0.188	3.228	1.443	3.4
3	86.23	2.326	0.515	3.428	0.562	3.142	1.5	11.261	10.464	85.894	0.178	3.249	1.489	3.4
Mean	86.377	2.32	0.513	3.432	0.558	3.116	1.518	11.28	10.468	85.837	0.182	3.232	1.456	3.4
BF	-0.532													

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S33: Austronesian : Hawaiian <-> Absenceofcousinmarriage.permitted

				D		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	102.542	4.757	4.315	2.359	8.871	4.497	15.427	7.638	4.567	102.648	6.738	6.067	14.573	5
2	102.493	4.618	4.2	2.318	8.747	4.58	15.457	7.478	4.706	102.624	6.728	6.057	14.533	5
3	102.484	4.928	4.295	2.318	8.716	4.681	15.472	7.413	4.679	102.653	6.714	6.118	14.56	5
Mean	102.506	4.768	4.27	2.332	8.778	4.586	15.452	7.51	4.651	102.642	6.727	6.081	14.555	5
BF	0.211													

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S34: Austronesian : Hawaiian <-> Absenceofcousinmarriage.preference

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	90.287	5.743	8.441	15.65	3.337	5.406	1.791	15.294	18.575	92.997	6.826	6.077	3.729	1
2	90.123	5.701	8.469	15.488	3.263	5.415	1.751	14.794	18.612	92.902	6.923	6.194	3.669	1
3	90.152	5.76	8.46	15.71	3.36	5.442	1.798	14.817	18.572	92.962	6.762	6.043	3.688	1
Mean	90.187	5.735	8.457	15.616	3.32	5.421	1.78	14.968	18.586	92.954	6.837	6.105	3.695	1
BF	5.421													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S35: Austronesian : Hawaiian <-> Bi.linealdescent

				De	pendent					Independent					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2		
1	111.998	4.097	10.549	13.825	8.256	16.902	3.161	2.369	3.754	117.348	7.679	6.872	2.454		
2	111.94	4.077	10.469	13.909	8.299	16.719	3.226	2.428	3.772	117.297	7.696	6.824	2.461		
3	111.932	4.107	10.525	13.756	8.355	16.86	3.097	2.39	3.732	117.44	7.782	6.855	2.451		
Mean	111.957	4.094	10.514	13.83	8.303	16.827	3.161	2.396	3.753	117.362	7.719	6.85	2.455		
BF	10.7														

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S36: Austronesian : Hawaiian <-> Bi.local
extended
family

				D	ependent		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	114.384	3.253	5.948	4.958	15.829	8.111	5.442	7.51	5.988	114.856	8.786	7.252	3.461	4
2	114.362	3.262	5.96	4.986	16.21	8.028	5.454	7.715	6.009	114.884	8.792	7.195	3.441	4
3	114.248	3.215	5.943	5.035	15.987	8.004	5.456	7.63	5.996	114.913	8.761	7.25	3.485	4
Mean	114.331	3.243	5.95	4.993	16.009	8.048	5.451	7.618	5.998	114.884	8.78	7.232	3.462	4
BF	0.945													

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.002

Table S37: Austronesian : Hawaiian <-> Bi.local
residence

				$D\epsilon$	ependent		Independent						
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	103.861	3.23	7.307	14.812	7.149	6.874	5.444	4.684	19.514	103.088	7.012	6.119	5.049
2	103.682	3.213	7.346	14.382	6.961	6.89	5.482	4.642	19.89	102.992	6.974	6.097	5.003
3	103.945	3.177	7.468	14.755	7.139	6.911	5.493	4.843	19.925	102.963	6.898	6.031	4.964
Mean	103.829	3.207	7.374	14.65	7.083	6.892	5.473	4.723	19.776	103.014	6.961	6.082	5.005
BF	-1.547			<u> </u>									

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S38: Austronesian : Iroquois <-> Cross.cousin
marriage.permitted

					ependent						-	1 1		_
				L		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	66.212	2.049	0.825	22.418	11.112	6.292	5.084	5.625	10.023	70.779	1.55	5.952	3.082	$\overline{2}$
2	66.078	2.035	0.809	22.079	11.321	6.317	5.223	5.484	10.178	70.666	1.526	5.964	3.063	$\overline{2}$
3	66.007	2.039	0.806	22.48	11.465	6.273	5.088	5.678	9.919	70.674	1.535	5.856	3.065	$\overline{2}$
Mean	66.099	2.041	0.813	22.326	11.299	6.294	5.132	5.596	10.04	70.706	1.537	5.924	3.07	$\overline{2}$
BF	9.135													П

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S39: Austronesian : Iroquois <-> Cross.cousin
marriage.preferred

				Γ		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	ŀ
1	89.481	7.937	0.769	14.233	3.791	10.733	12.362	6.278	2.794	94.373	1.526	5.851	9.951	1
2	89.475	7.963	0.792	14.414	3.715	10.917	12.374	6.15	2.8	94.259	1.524	5.854	10.026	1
3	89.216	7.93	0.795	14.286	3.696	10.931	12.209	6.159	2.797	94.269	1.509	5.798	10.106	1
Mean	89.391	7.943	0.785	14.311	3.734	10.86	12.315	6.196	2.797	94.3	1.52	5.834	10.028	1
BF	9.785													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S40: Austronesian : Iroquois <-> Exogamy.unilineal.descent

				D		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	53.48	0.896	1.035	16.672	8.804	5.495	2.883	5.831	15.25	53.582	1.143	5.231	1.199	18
2	53.262	0.876	1.037	16.762	8.615	5.446	2.896	5.71	15.16	53.591	1.131	5.157	1.189	18
3	53.163	0.882	1.019	16.582	8.725	5.46	2.866	5.695	14.919	53.578	1.122	5.166	1.193	18
Mean	53.302	0.885	1.03	16.672	8.715	5.467	2.882	5.745	15.11	53.584	1.132	5.185	1.194	18
BF	0.205													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S41: Austronesian : Iroquois <-> High.polygyny

				D_{i}		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	67.953	2.031	1.149	15.69	6.505	7.702	5.548	8.159	10.349	69.217	1.711	7.769	2.754	15
2	67.932	2.021	1.172	15.766	6.534	7.687	5.453	8.273	10.587	69.048	1.701	7.852	2.806	16
3	67.949	2.061	1.179	16.003	6.545	7.741	5.423	8.483	10.216	69.301	1.698	7.807	2.753	15
Mean	67.945	2.038	1.167	15.82	6.528	7.71	5.475	8.305	10.384	69.189	1.703	7.809	2.771	15
BF	2.528													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S42: Austronesian : Iroquois <-> Matri.anvunclocal
residence

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	73.872	1.383	0.844	7.123	3.16	4.147	1.605	11.378	8.102	72.25	1.045	4.985	1.153	5.6
2	73.796	1.4	0.841	7.184	3.167	4.198	1.606	11.468	8.018	72.407	1.055	5.016	1.166	5.73
3	73.704	1.39	0.856	7.093	3.163	4.189	1.608	11.213	8.029	72.18	1.049	4.976	1.16	5.6
Mean	73.791	1.391	0.847	7.133	3.163	4.178	1.606	11.353	8.05	72.279	1.05	4.992	1.16	5.6
BF	-3.243													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S43: Austronesian : Iroquois <-> Polygyny

						Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	78.608	1.915	1.063	1.325	2.521	11.089	11.082	9.884	3.903	77.895	1.695	7.788	2.586	1
2	78.508	1.919	1.061	1.331	2.566	10.846	11.184	10.011	3.916	77.924	1.708	7.843	2.628	1
3	78.393	1.914	1.078	1.328	2.6	10.918	11.112	10.047	3.865	77.762	1.69	7.83	2.611	1
Mean	78.503	1.916	1.067	1.328	2.562	10.951	11.126	9.981	3.895	77.86	1.698	7.82	2.608	1
BF	-1.425													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.001
Independent	1.000	1.000

Table S44: Austronesian : Iroquois <-> Uni.lineal descent

-				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	87.176	0.937	0.834	4.408	5.463	6.662	10.617	9.374	4.777	90.726	1.502	6.014	1.055	3.39
2	87.369	0.934	0.827	4.447	5.421	6.419	10.811	9.27	4.666	90.821	1.492	5.929	1.095	3.3
3	87.084	0.936	0.829	4.423	5.524	6.446	10.838	9.442	4.75	90.937	1.518	6	1.07	3.39
Mean	87.21	0.936	0.83	4.426	5.469	6.509	10.755	9.362	4.731	90.828	1.504	5.981	1.073	3.39
BF	7.101													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S45: Austronesian : Iroquois <-> Uni.local
residence

				D	ependen		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta
1	84.078	1.539	0.424	3.218	5.365	8.071	6.828	9.224	2.713	87.299	1.046	5.167	1.408	2.46
2	83.976	1.563	0.427	3.229	5.295	8.036	6.488	9.061	2.638	87.331	1.054	5.161	1.408	2.48
3	83.984	1.548	0.423	3.243	5.295	8.168	6.755	9.119	2.728	87.242	1.03	5.111	1.393	2.48
Mean	84.013	1.55	0.425	3.23	5.318	8.092	6.69	9.135	2.693	87.291	1.043	5.146	1.403	2.47
BF	6.441													

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S46: Bantu : Crow <-> Matri.anvunclocal
residence

				I		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	63.233	3.683	0.933	8.457	2.134	16.453	7.622	14.886	7.657	62.465	1.269	17.921	4.049	8
2	63.222	3.759	0.931	8.619	2.118	15.965	7.62	14.76	7.5	62.369	1.267	17.875	4.082	8
3	63.23	3.744	0.936	8.622	2.106	16.082	7.723	14.656	7.519	62.411	1.308	18.338	4.028	8
Mean	63.228	3.729	0.933	8.566	2.119	16.167	7.655	14.767	7.559	62.415	1.281	18.045	4.053	8
BF	-1.536													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S47: Bantu : Crow <-> Matrilineal

				I		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	63.159	2.092	1.131	3.989	1.792	16.983	7.885	15.932	7.459	62.249	1.276	18.031	2.289	4
2	63.343	2.107	1.11	3.97	1.804	17.001	7.864	15.723	7.361	62.244	1.293	18.128	2.326	4
3	63.289	2.124	1.132	3.955	1.791	17.093	7.848	15.781	7.493	62.241	1.272	17.898	2.276	4
Mean	63.264	2.108	1.124	3.971	1.796	17.026	7.866	15.812	7.438	62.245	1.28	18.019	2.297	4
BF	-1.82													

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S48: Bantu : Crow <-> Matrilocal

				I		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	36.082	0.844	0.861	15.206	5.526	15.506	5.245	11.085	11.464	36.344	1.275	17.931	1.203
2	35.872	0.849	0.903	15.359	5.536	16.053	5.295	11.284	11.188	36.248	1.268	17.936	1.197
3	35.955	0.868	0.878	15.47	5.526	15.841	5.241	11.172	11.245	36.283	1.254	17.755	1.195
Mean	35.97	0.854	0.881	15.345	5.529	15.8	5.26	11.18	11.299	36.292	1.266	17.874	1.198
BF	0.523												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S49: Bantu : Crow <-> Matrilocal.strict

				I		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	36.041	0.86	0.861	15.297	5.524	15.811	5.204	11.074	11.242	36.417	1.258	17.746	1.198
2	35.908	0.861	0.862	15.371	5.578	15.86	5.285	11.54	11.216	36.355	1.271	17.976	1.18
3	36.16	0.897	0.875	15.562	5.606	15.799	5.05	11.536	11.234	36.312	1.255	18.041	1.191
Mean	36.036	0.873	0.866	15.41	5.569	15.823	5.18	11.383	11.231	36.361	1.261	17.921	1.19
BF	0.753												

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S50: Bantu : Crow <-> Uni.local
residence

				I		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	56.957	19.022	1.881	4.725	1.07	13.671	10.166	16.189	5.362	55.842	1.283	18.04	18.558
2	57.006	18.995	1.907	4.755	1.065	13.61	10.374	16.133	5.571	55.883	1.26	17.698	18.951
3	56.885	19.072	1.916	4.736	1.058	13.501	10.363	16.241	5.434	55.974	1.275	18.058	18.664
Mean	56.949	19.03	1.901	4.739	1.064	13.594	10.301	16.188	5.456	55.9	1.273	17.932	18.724
BF	-2.231												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S51: Bantu : Hawaiian <-> Absenceofcousinmarriage.permitted

				De		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	58.393	14.028	3.116	2.389	1.2	6.522	9.485	5.252	4.025	57.357	1.021	2.536	12.158	2.3
2	58.324	14.076	3.103	2.382	1.212	6.787	9.544	5.329	4.035	57.332	1.007	2.43	12.03	2.3
3	58.377	13.979	3.153	2.362	1.191	6.621	9.334	5.212	4.096	57.241	1.018	2.582	11.983	2.3
Mean	58.365	14.028	3.124	2.378	1.201	6.643	9.454	5.264	4.052	57.31	1.015	2.516	12.057	2.3
BF	-2.07													

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S52: Bantu : Hawaiian <-> Absenceofcousin
marriage.preference

				D		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	56.612	2.768	1.112	14.599	1.733	2.826	1.422	10.263	14.536	55.227	1.006	2.518	2.53	1
2	56.706	2.791	1.087	14.687	1.776	2.711	1.445	10.097	14.638	55.367	1.015	2.448	2.519	1
3	56.672	2.809	1.094	14.769	1.773	2.802	1.439	10.178	14.584	55.352	1.007	2.43	2.511	1
Mean	56.663	2.789	1.098	14.685	1.761	2.78	1.435	10.179	14.586	55.315	1.009	2.465	2.52	1
BF	-2.77													

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S53: Bantu : Hawaiian <-> Bi.linealdescent

				\mathbf{D}		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	60.055	3.092	1.279	18.826	3.927	7.162	4.153	8.473	11.61	59.335	1.391	6.346	3.362	18
2	60.145	3.111	1.267	18.837	3.904	7.084	4.184	8.717	11.652	59.389	1.377	6.284	3.402	18
3	59.917	3.097	1.263	18.648	3.827	7.109	4.065	8.385	11.312	59.293	1.376	6.261	3.316	18
Mean	60.039	3.1	1.27	18.77	3.886	7.118	4.134	8.525	11.525	59.339	1.381	6.297	3.36	18
BF	-1.44													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S54: Bantu : Hawaiian <-> Bi.localextendedfamily

				De	Independent									
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	71.5	6.828	1.406	20.283	2.408	7.765	5.858	7.939	9.5	70.622	1.388	6.392	7.039	19.
2	71.426	6.783	1.456	20.199	2.395	8.138	5.929	7.728	9.358	70.605	1.365	6.244	7.034	19.
3	71.384	6.853	1.426	20.222	2.376	7.822	5.895	7.779	9.483	70.642	1.369	6.021	7.05	19.
Mean	71.437	6.821	1.429	20.235	2.393	7.908	5.894	7.815	9.447	70.623	1.374	6.219	7.041	19.
BF	-1.756													

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S55: Bantu : Hawaiian <-> Bi.local
residence

				I		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	68.9	2.27	1.632	4.953	1.811	7.149	2.989	11.692	12.583	67.852	1.386	6.373	2.181	5.
2	69.01	2.262	1.661	4.806	1.82	7.435	2.975	11.673	12.592	67.97	1.397	6.322	2.182	5.
3	68.922	2.273	1.681	4.824	1.809	7.429	2.936	11.755	12.461	67.922	1.373	6.139	2.194	5.4
Mean	68.944	2.268	1.658	4.861	1.813	7.338	2.967	11.707	12.545	67.915	1.385	6.278	2.186	5.
BF	-2.097													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S56: Bantu : Iroquois <-> Cross.cousin
marriage.permitted

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	73.417	1.107	2.71	14.119	10.485	3.136	3.914	2.567	14.346	73.483	2.288	2.572	2.714	1
2	73.314	1.095	2.729	13.652	10.269	3.206	3.845	2.518	14.117	73.595	2.314	2.593	2.696	1
3	73.237	1.113	2.689	13.827	10.36	3.179	3.812	2.48	14.081	73.513	2.375	2.604	2.704	
Mean	73.323	1.105	2.709	13.866	10.371	3.174	3.857	2.522	14.181	73.53	2.326	2.59	2.705	
BF	0.132													

	Point est.	Upper C.I.
Dependent	1.001	1.001
Independent	1.000	1.000

Table S57: Bantu : Iroquois <-> Cross.cousin
marriage.preferred

				De		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	80.568	3.105	1.476	10.029	8.312	6.022	9.368	2.798	2.642	87.316	2.275	2.585	5.947	3.9
2	80.487	3.045	1.484	9.947	8.365	6.102	9.606	2.81	2.659	87.388	2.308	2.597	6.08	3.9
3	80.374	3.151	1.528	9.959	8.302	6.21	9.332	2.794	2.684	87.294	2.335	2.59	6.12	4.0
Mean	80.476	3.1	1.496	9.978	8.326	6.111	9.435	2.801	2.662	87.333	2.306	2.591	6.049	3.9
BF	13.494													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S58: Bantu : Iroquois <-> Exogamy.unilineal.descent

				D			In	depende	nt					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	70.066	3.594	2.12	16.39	7.682	2.787	2.428	4.407	13.797	69.06	2.257	2.65	3.112	16
2	70.024	3.645	2.124	16.476	7.545	2.803	2.456	4.317	13.538	69.042	2.223	2.598	3.108	16
3	70.061	3.636	2.106	16.683	7.722	2.771	2.395	4.41	13.785	69.048	2.239	2.61	3.118	16
Mean	70.05	3.625	2.117	16.516	7.65	2.787	2.426	4.378	13.707	69.05	2.24	2.619	3.113	16
BF	-2.012													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S59: Bantu : Iroquois <-> Matri.anvunclocal
residence

					1 .							1 1		
				D	ependent		89.474 2.703 2.685 4.125 8. 89.409 2.72 2.672 4.159 8.							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	87.245	1.606	2.689	11.907	11.656	3.573	6.588	2.854	8.986	89.474	2.703	2.685	4.125	8.
2	87.1	1.623	2.646	12.153	11.579	3.542	6.479	2.877	8.966	89.409	2.72	2.672	4.159	8.
3	87.178	1.621	2.619	11.977	11.772	3.553	6.522	2.868	8.984	89.459	2.654	2.667	4.134	8.
Mean	87.174	1.617	2.651	12.012	11.669	3.556	6.53	2.866	8.979	89.447	2.692	2.675	4.139	8.
BF	4.458													

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S60: Bantu : Iroquois <-> Uni.
linealdescent

				D			In	depende	nt					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	79.123	14.122	5.772	3.675	3.359	6.596	17.602	2.675	3.188	78.33	2.712	2.702	17.789	3.
2	79.051	14.266	5.791	3.697	3.441	6.584	17.413	2.652	3.246	78.218	2.685	2.678	17.753	3.
3	79.209	14.273	5.842	3.684	3.468	6.728	17.444	2.662	3.203	78.202	2.676	2.669	17.646	3.
Mean	79.128	14.22	5.802	3.685	3.423	6.636	17.486	2.663	3.212	78.25	2.691	2.683	17.729	3.
BF	-1.586													

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S61: Bantu : Iroquois <-> Uni.local
residence

				D			In	depende	nt					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b€
1	84.198	14.459	7.409	3.398	3.372	3.4	18.168	3.191	5.269	82.955	2.689	2.672	18.782	4.9
2	84.14	14.678	7.317	3.396	3.275	3.449	18.311	3.193	5.265	82.853	2.67	2.674	18.834	5.0
3	83.9	14.514	7.441	3.334	3.324	3.462	18.109	3.176	5.303	82.932	2.635	2.638	18.933	4.
Mean	84.079	14.55	7.389	3.376	3.324	3.437	18.196	3.187	5.279	82.913	2.665	2.661	18.85	4.
BF	-2.486													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S62: Bantu : Omaha <-> Matri.anvunclocal
residence

					Depend ϵ	$_{ m ent}$					In	depender	nt
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	70.562	4.869	2.25	8.616	0.739	10.969	1.765	14.163	12.403	70.678	1.627	11.749	4.135
2	70.529	4.81	2.229	8.691	0.728	10.911	1.788	13.862	12.767	70.725	1.633	11.804	4.079
3	70.488	4.819	2.23	8.647	0.737	10.861	1.84	14.007	12.381	70.834	1.631	11.71	4.096
Mean	70.526	4.833	2.236	8.651	0.735	10.914	1.798	14.011	12.517	70.746	1.63	11.754	4.103
BF	0.232												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S63: Bantu : Omaha <-> Patrilineal

					Depende	ent					In	depender	ıt
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	72.936	3.622	0.717	5.773	3.123	14.209	10.119	10.375	2.417	74.604	1.657	11.807	3.241
2	72.797	3.602	0.727	5.734	3.163	13.75	10.183	10.545	2.411	74.537	1.646	11.773	3.189
3	72.935	3.602	0.72	5.709	3.126	13.724	10.447	10.376	2.363	74.607	1.611	11.609	3.195
Mean	72.889	3.609	0.721	5.739	3.137	13.894	10.25	10.432	2.397	74.583	1.638	11.73	3.208
BF	3.336												

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S64: Bantu : Omaha <-> Patrilocal

				I		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	69.489	19.426	0.871	8.128	1.91	13.444	13.605	10.198	1.899	69.161	1.632	11.707	19.964
2	69.45	19.311	0.915	8.118	1.952	13.63	13.447	10.14	1.902	69.128	1.631	11.667	19.949
3	69.387	19.431	0.884	8.182	1.954	13.6	13.468	10.218	1.925	69.101	1.625	11.573	20.107
Mean	69.442	19.389	0.89	8.143	1.939	13.558	13.507	10.185	1.909	69.13	1.629	11.649	20.007
BF	-0.655												

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S65: Bantu : Omaha <-> Patrilocal.strict

						Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	70.708	2.91	0.426	4.629	3.429	14.016	11.818	11.12	1.737	73.92	1.628	11.779	2.79
2	70.764	2.906	0.426	4.645	3.423	13.832	11.776	11.117	1.64	73.886	1.617	11.611	2.775
3	70.881	2.896	0.424	4.63	3.458	14.38	11.936	11.011	1.721	73.766	1.613	11.584	2.777
Mean	70.784	2.904	0.425	4.635	3.437	14.076	11.843	11.083	1.699	73.857	1.619	11.658	2.781
BF	6.424												

	Point est.	Upper C.I.
Dependent	1.001	1.003
Independent	1.001	1.002

Table S66: Bantu : Omaha <-> Uni.local
residence

				I		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	65.264	18.788	1.103	5.61	1.818	13.393	13.456	10.613	1.868	64.219	1.645	11.737	18.731
2	64.858	18.814	1.087	5.616	1.849	13.315	13.24	10.723	1.82	64.123	1.631	11.785	18.709
3	64.946	19.088	1.088	5.663	1.844	13.639	13.155	10.658	1.863	64.213	1.612	11.534	18.569
Mean	65.023	18.897	1.093	5.63	1.837	13.449	13.284	10.665	1.85	64.185	1.629	11.685	18.67
BF	-2.09												

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S67: Uto: Hawaiian <-> Absenceofcousinmarriage.permitted

				De			In	depende	nt					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	21.01	11.078	10.815	2.362	16.985	4.446	9.342	7.851	2.193	20.453	17.299	7.256	11.377	2
2	20.963	11.011	10.926	2.342	17.017	4.439	9.616	7.858	2.264	20.383	17.245	7.185	10.951	2
3	20.862	11.16	11.105	2.292	16.978	4.311	9.298	7.933	2.205	20.445	17.128	7.254	11.176	2
Mean	20.945	11.083	10.949	2.332	16.993	4.399	9.419	7.881	2.221	20.427	17.224	7.232	11.168	2
BF	-1.114													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

Table S68: Uto : Hawaiian <-> Absence of cousin marriage.preference

				De		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	20.186	2.033	17.534	11.31	9.369	7.466	1.974	5.066	17.712	19.37	17.279	7.291	1.785	1
2	20.141	2.068	17.475	11.169	9.319	7.557	1.95	4.952	17.707	19.334	17.13	7.251	1.757	1
3	20.17	2.014	17.439	10.877	9.037	7.476	1.919	4.849	17.433	19.29	17.197	7.234	1.804	1
Mean	20.166	2.038	17.483	11.119	9.242	7.5	1.948	4.956	17.617	19.331	17.202	7.259	1.782	1
BF	-1.632													П

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S69: Uto : Hawaiian <-> Bi.lineal descent

				D	ependen			In	depende	nt	$ \begin{array}{ccc} & 16 \\ & 319 & 16 \\ & 289 & 15 \end{array} $				
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be	
1	22.543	2.046	9.268	14.8	9.154	4.942	1.262	7.598	12.369	21.76	11.513	6.152	1.298	16	
2	22.443	2.077	9.259	14.794	9.165	4.871	1.297	7.56	12.528	21.79	11.527	6.142	1.319	16	
3	22.478	2.051	9.438	14.672	9.181	5.037	1.266	7.285	12.177	21.787	11.788	6.214	1.289	15	
Mean	22.488	2.058	9.322	14.755	9.167	4.95	1.275	7.481	12.358	21.779	11.609	6.169	1.302	16	
BF	-1.567														

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S70: Uto: Hawaiian <-> Bi.localextendedfamily

				Г		Independent								
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	30.775	8.311	9.53	10.87	11.001	4.341	5.867	9.315	13.714	30.626	12.774	7.016	7.521	1
2	30.651	8.501	9.562	11.08	11.166	4.404	5.834	9.123	13.545	30.642	12.927	7.046	7.587	1
3	30.579	8.401	9.297	10.802	11.189	4.185	5.732	8.967	13.385	30.671	12.829	7.013	7.597	1
Mean	30.668	8.404	9.463	10.917	11.119	4.31	5.811	9.135	13.548	30.646	12.843	7.025	7.568	1
BF	-0.298													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S71: Uto : Hawaiian <-> Bi.local residence

				D		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	26.281	1.668	11.853	13.363	10.441	7.761	5.103	3.591	16.547	26.196	12.714	6.925	3.791
2	26.359	1.651	11.773	13.286	10.512	7.803	5.12	3.708	16.532	26.136	12.713	6.921	3.755
3	26.44	1.744	11.523	13.638	10.217	7.639	4.985	3.719	16.345	26.158	12.578	6.891	3.777
Mean	26.36	1.688	11.716	13.429	10.39	7.734	5.069	3.673	16.475	26.163	12.668	6.912	3.774
BF	-0.171												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S72: Uto : Iroquois <-> Cross.cousinmarriage.permitted

				Γ	Dependen	-	Independent						
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	19.063	1.874	6.128	18.046	4.835	19.191	2.455	9.444	10.638	18.259	6.008	18.784	1.774
2	19.181	1.803	6.142	17.771	4.938	19.232	2.38	9.378	10.8	18.333	6.029	18.792	1.775
3	19.079	1.844	6.049	17.919	4.941	18.973	2.421	9.401	10.485	18.248	6.017	18.811	1.778
Mean	19.108	1.84	6.106	17.912	4.905	19.132	2.419	9.408	10.641	18.28	6.018	18.796	1.776
BF	-1.607												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S73: Uto : Iroquois <-> Cross.cousinmarriage.preferred

					D 1						т	1 1			
					Depende	ent				Independent					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2		
1	21.001	2.198	6.215	9.527	4.62	18.329	2.978	11.337	12.544	20.407	6.098	18.901	2.313		
2	21.062	2.199	6.212	9.481	4.489	18.401	2.981	11.133	12.646	20.484	6.016	18.785	2.346		
3	21.042	2.164	6.214	9.399	4.54	18.54	2.98	11.208	12.415	20.442	6.038	18.734	2.332		
Mean	21.035	2.187	6.214	9.469	4.55	18.423	2.98	11.226	12.535	20.444	6.051	18.807	2.33		
BF	-1.189														

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S74: Uto : Iroquois <-> Exogamy.unilineal.descent

-				Г		Independent							
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	19.857	1.932	5.193	18.951	5.548	16.727	2.342	8.695	10.838	19.197	5.327	16.263	1.785
2	19.857	1.97	5.198	19.098	5.449	16.791	2.344	8.594	11.127	19.085	5.349	16.39	1.775
3	19.869	1.956	5.278	19.102	5.306	16.811	2.363	8.67	11.019	19.138	5.398	16.558	1.769
Mean	19.861	1.953	5.223	19.05	5.434	16.776	2.35	8.653	10.995	19.14	5.358	16.404	1.776
BF	-1.319												

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S75: Uto: Iroquois <-> High.polygyny

				D	ependen	t				Independent					
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b	
1	23.396	2.502	2.665	15.353	9.714	15.527	6.503	9.305	7.858	24.323	4.802	17.655	3.476	1	
2	23.429	2.602	2.668	15.99	9.751	15.819	6.594	9.478	7.882	24.25	4.813	17.715	3.491	1	
3	23.556	2.538	2.711	15.703	9.558	15.598	6.439	9.431	7.899	24.22	4.716	17.393	3.481	1	
Mean	23.46	2.547	2.681	15.682	9.674	15.648	6.512	9.405	7.88	24.264	4.777	17.588	3.483	1	
BF	1.854														

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S76: Uto : Iroquois <-> Matri.anvunclocal
residence

	Dependent										Independent			
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	
1	23.743	3.709	5.2	15.888	3.246	16.871	2.763	11.271	11.102	23.108	4.764	17.368	3.48	
2	23.902	3.71	5.098	15.869	3.21	16.964	2.726	11.176	11.169	23.177	4.718	17.329	3.385	
3	23.767	3.705	5.025	16.002	3.288	16.726	2.778	11.181	11.147	23.197	4.748	17.52	3.417	
Mean	23.804	3.708	5.108	15.92	3.248	16.854	2.756	11.209	11.139	23.161	4.743	17.406	3.427	
BF	-1.269													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S77: Uto : Iroquois <-> Uni.lineal descent

	Dependent										Independent			
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	
1	21.561	2.016	1.526	13.847	12.606	15.418	14.468	7.107	4.671	26.413	4.466	17.233	4.945	
2	21.739	1.999	1.571	13.764	12.671	15.368	14.612	7.226	4.677	26.416	4.412	17.08	4.886	
3	21.82	2	1.549	13.637	13.198	15.486	14.877	7.239	4.588	26.461	4.447	17.223	4.862	
Mean	21.707	2.005	1.549	13.749	12.825	15.424	14.652	7.191	4.645	26.43	4.442	17.179	4.898	
BF	9.705													

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.000

Table S78: Uto : Iroquois <-> Uni.local
residence

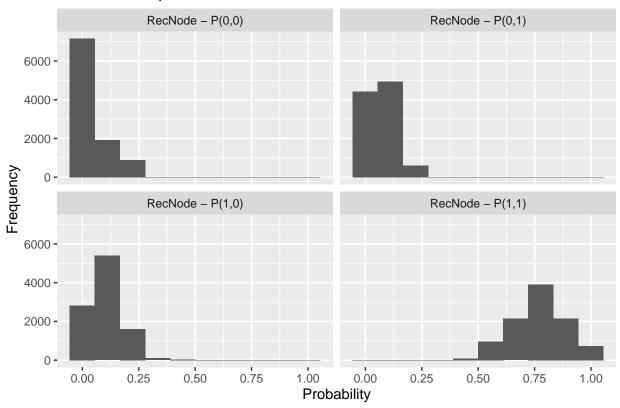
	Dependent									Independent			
run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	25.577	5.895	1.555	19.537	10.054	16.03	13.63	9.314	4.858	28.222	4.721	17.299	9.254
2	25.686	5.995	1.607	19.745	9.926	16.301	13.722	9.422	4.883	28.296	4.678	17.135	9.263
3	25.614	6.066	1.56	20.025	9.889	16.235	13.52	9.286	4.752	28.263	4.812	17.359	9.356
Mean	25.626	5.985	1.574	19.769	9.956	16.189	13.624	9.341	4.831	28.26	4.737	17.264	9.291
BF	5.29												

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

The graph clearly shows the presence of both traits being present here is the most likely option, with approximately 0.77 probability. This probability drops to around 0.5 on the ancestral node.

Bantu 70: Dependent model



Multiple comparisons

Since this study has numerous hypothesis tests, it is important we address the statistical problem of multiple comparisons. The multiple comparison problem says that the more hypotheses tested simultaneously, the more likely an erroneous error is to occur. There is strong debate in the literature on whether this is a problem here, but we argue that it is not.

The primary reason for this not being a problem is that all our hypotheses were set out *a priori*. They are not the result of comparing all social variables against all binary kinship terminologies, and make a tiny portion of those that are possible. All hypotheses are established in theory and many had been previously tested.

Phylogenetic Inertia

We were concerned that a prevalence of phylogenetic inertia was the primary reason for not finding many significant co-evolutionary relationships. That is, kinship terminologies and social organisation are so tightly tied, that we would not be able to detect a relationship using this approach. To assess how prevalent this was in our results we reviewed each hypothesis on 3 criteria; 1) What was the most likely independent ancestral state, 2) How likely was that ancestral state, and 3) How are the two variables distributed across the respective phylogenies. In an independent model (where each trait changes independent of the other) we would expect that if the ancestral state shows the presence of both traits, there is a possibility that both traits were been inherited over time, either by chance or due to a stable relationship. In both these cases, our phylogenetic approach would fail to pick up a relationship between these traits. The second criteria gives us a level of confidence in the first criteria, we assume a probability of above 0.7 indicates a high likelihood of the true ancestral state. The third criteria allows us to qualitatively review whether we think the methods are failing to detect a relationship, by visualizing the data on mirrored phylogenies. The first two criteria mean that it is plausible that two traits are ancestral, but unrelated, by looking at the distribution of traits on a tree, we can assess whether this is the case or not. Visualization also allows us to attest whether stable pairings occur later within a lineage. These plots can be found in the figures folder in the github repository. Using the three criteria above, we then decide if a hypothesis is likely to be influenced by phylogenetic inertia on a four point scale, ranging from highly likely to highly unlikely. The table below shows these judgments, and ancestral state criteria, for all hypotheses that we did not find support for. These decisions were independently decided on by each author and then conferred on the result.

References

Table S85: Judegments of phylogenetic inertia. The first columns shows our overall judgements. The second column shows the most likely ancestral state in an independent model of evolution, organised as [Kin terminology], [social structure]. The third column shows the probability of this state.

hypothesis	judgement	Most likely ancestral state	Probability of
austronesian-crow-high.polygyny	Highly unlikely	0,0	
austronesian-crow-polygyny	Unlikely	0,1	
austronesian-eskimo-absenceofcousinmarriage.permitted	Unlikely	1,1	
austronesian-eskimo-absenceofcousinmarriage.preference	Highly unlikely	1,0	
austronesian-eskimo-bi.linealdescent	Highly unlikely	1,0	
austronesian-eskimo-neo.localresidence	Highly unlikely	1,0	
austronesian-eskimo-nuclear.families	Likely	1,1	
austronesian-hawaiian-absenceofcousinmarriage.permitted	Unlikely	1,1	
austronesian-hawaiian-absenceofcousinmarriage.preference	Unlikely	1,0	
austronesian-hawaiian-bi.linealdescent	Unlikely	0,0	
austronesian-hawaiian-bi.localextendedfamily	Unlikely	1,1	
austronesian-hawaiian-bi.localresidence	Highly unlikely	1,0	
austronesian-iroquois-exogamy.unilineal.descent	Highly unlikely	0,0	
austronesian-iroquois-high.polygyny	Highly unlikely	0,0	
austronesian-iroquois-matri.anvunclocalresidence	Highly unlikely	0,0	
austronesian-iroquois-polygyny	Highly unlikely	0,1	
austronesian-iroquois-uni.linealdescent	Highly unlikely	0,0	
bantu-crow-matri.anvunclocalresidence	Highly unlikely	0,0	
bantu-crow-matrilineal	Highly unlikely	0,0	
bantu-crow-matrilocal	Highly unlikely	0,0	
bantu-crow-uni.localresidence	Highly unlikely	0,1	
bantu-hawaiian-absenceofcousinmarriage.permitted	Highly unlikely	0,1	
bantu-hawaiian-absenceofcousinmarriage.preference	Highly unlikely	0,0	
bantu-hawaiian-bi.linealdescent	Highly unlikely	0,0	
bantu-hawaiian-bi.localextendedfamily	Highly unlikely	0,0	
bantu-hawaiian-bi.localresidence	Highly unlikely	0,0	
bantu-iroquois-cross.cousinmarriage.preferred	Highly likely	1,1	
bantu-iroquois-exogamy.unilineal.descent	Highly unlikely	0,0	
bantu-iroquois-uni.linealdescent	Unlikely	1,1	
bantu-iroquois-uni.localresidence	Likely	1,1	
bantu-omaha-uni.localresidence	Highly unlikely	0,1	
uto-hawaii an-absence of cous in marriage. permitted	Unlikely	1,1	
uto-hawaiian-absenceofcousinmarriage.preference	Likely	1,0	
uto-hawaiian-bi.linealdescent	Highly unlikely	1,0	
uto-hawaiian-bi.localextendedfamily	Unlikely	1,0	
uto-hawaiian-bi.localresidence	Unlikely	1,0	
uto-iroquois-cross.cousinmarriage.permitted	Highly unlikely	0,0	
uto-iroquois-cross.cousinmarriage.preferred	Highly unlikely	0,0	
uto-iroquois-exogamy.unilineal.descent	Highly unlikely	0,0	
uto-iroquois-high.polygyny	Highly unlikely	0,0	
uto-iroquois-matri.anvunclocalresidence	Highly unlikely	0,0	
uto-iroquois-uni.linealdescent	Highly unlikely	0,0	
uto-iroquois-uni.localresidence	Highly unlikely	0,0	