Supporting Information

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SI Results

In general, results from multiple factor analysis (MFA) can be interpreted in a similar way as those from a principal component analysis (PCA). Table S8 gathers inertia (similar to the level of variance explained) from the separate and global analysis of these blocks of variables. In the separate analyses, the first eigenvalues are, respectively, 6.01 (phenotype), 3.30 (climate), and 2.99 (life-history traits). These different values illustrate the need to balance the influence of the sets using MFA. As for the global analysis, the first two dimensions together explain 65% of the total variance (Table S8).

Table S9 presents the correlations between variables and each global factor of the MFA analysis. This table shows that most of the variables that contribute to the first dimension are phenotypic, along with some climatic variables like temperature annual range, annual precipitation, and precipitation on the driest month. In addition, inbreeding and fertility life-history traits were correlated to the first dimension. This dimension represents mostly "head shape," along with some particular aspects of climate and life-history data. The variable contributing more to the second axis is annual mean temperature and temperature seasonality. The phenotypic dataset presents a high inertia in one direction, the first axis of the individual analysis, which is dominated by the nasal height, zygomatic breadth, and facial height measurements. In turn, these variables present a high correlation with the first dimension of the global analysis (Table S9).

The four active groups have close coordinates on the first dimension (Fig. S1), which means that their contribution to the first principal component is the same; it also means that the first principal component of the MFA is common to all of the groups. As for the second dimension, the cultural group has the highest coordinates, contributing the most to the second principal component, which depicts the evolution of traits inside the Jê-speaking clade.

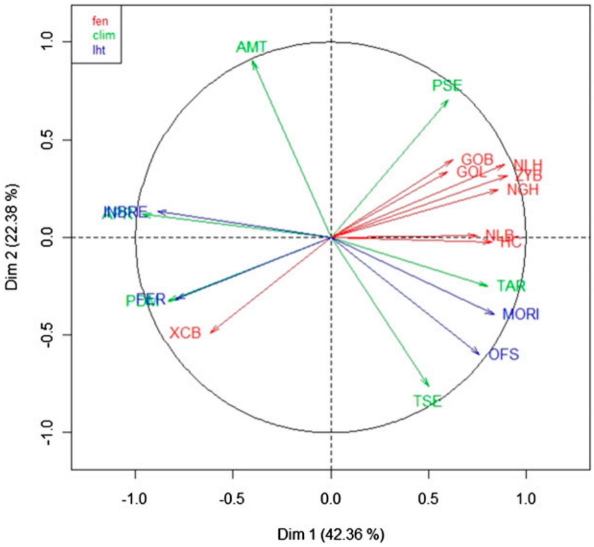

Fig. S1. Representation of the MFA variables map.

Table S1. Quantitative genetics parameters computed following refs. 1–3

Symbol	Measure	Biological meaning
W	Pooled within-groups variance/covariance matrix	The amount and pattern of variation and covariation within a group. W was computed twice, departing from data recorded on the six Central Plateau Brazilian groups and on a sample of 408 skulls belonging to 11 North South American samples.
G	The matrix of additive genetic variances (V) and covariances (CV)	The amount and pattern of genetic variation and covariation within the Hallstat population (4)
pmax	First principal component of the phenotypic W	The linear combination of traits accounting for the largest portion of phenotypic variance within a group; the phenotypic line of least resistance to evolutionary change (LLER). Pmax was computed on both versions of W, giving place to a pmax and a $\text{pmax}_{\text{Amerindian}}$.
gmax	First principal component of G	The linear combination of traits accounting for the largest portion of genetic variance within a group; the genetic LLER
Δz	Vector of differences in the averages of any two groups	Direction of the evolution
mA	Sum of the squared differences in the averages of morphological traits of any two groups	The amount of morphological differentiation between two groups
mP	mA divided by the branch length	The pace of morphological change between two groups
L	Between-groups variance/covariance matrix obtained from the V/CV among-groups means	The amount and pattern of divergence among populations
Total pmax	First principal component of L	The linear combination of traits accounting for the largest portion of phenotypic variance between groups
b-length	Branch length in the tribes' phylogenetic tree	Approximately the time between an ancestor and its immediate descendent

1. Schluter D, Price T, Mooers AØ, Ludwig D (1997) Likelihood of ancestor states in adaptive radiation. *Evolution* 51:1699–1711.
2. Schluter D (1996) Adaptive radiation along genetic lines of least resistance. *Evolution* 50:1766–1774.
3. Marroig G, Cheverud JM (2005) Size as a line of least evolutionary resistance: Diet and adaptive morphological radiation in New World monkeys. *Evolution* 59:1128–1142.
4. Martínez-Abadías N, et al. (2009) Heritability of human cranial dimensions: Comparing the evolvability of different cranial regions. *J Anat* 214:19–35.

Table S2. Analyses performed and corresponding symbols, how the analyses were performed, their biological meanings, and expectations

Symbol	Measure	Biological meaning/expectation
pmax-pmax	Vector correlation of the pmax of one group in relation to another group's pmax.	How similar two groups are in their LLER. Should be high for groups sharing the same orientation of the LLER and low for the reverse case.
gmax-pmax	Vector correlation of the gmax of one group in relation to another group's pmax.	How similar two groups are in their phenotypic and genetic LLER. Same as above.
Δz-gmax	Vector correlation between Δz and gmax.	How closely the direction of evolution follows the genetic LLER. Should be high if the genetic LLER influences the evolutionary path.
Δz-pmax	Vector correlation between Δz and pmax.	How closely the direction of evolution follows the phenotypic LLER. Should be high if the phenotypic LLER influences the evolutionary path.
Branch length × amount and pace measures	Pearson product moment correlation.	The association between time (branch length) and the amount and pace of evolution. Should be positive if longer time allows for more differentiation to accumulate; no a priori association expected in terms of the pace through time.
Branch length × Δz-pmax and Δz-gmax	Pearson product moment correlation.	The temporary nature of the effect of the LLER on evolution. A negative association is expected if the bias in the evolutionary trajectory imposed by the LLER is temporary.
Δz-pmax and Δz-gmax × amount and pace measures	Pearson product moment correlation.	Whether the amount and pace of evolutionary change is associated with how close to the LLER the direction of evolution was. Positive associations are expected, because when the evolutionary change occurs away from the LLER, genetic variance along those other dimensions are relatively low, reducing the amount and pace of evolutionary response.

Table S3. Vector correlations among phenotypic LLERs

	Pmax-XAV	Pmax-KAY	Pmax-BAN	Pmax-TIC	Pmax-KAI	Pmax-YAN	Pmax-OTO
Pmax-XAV	1.000	0.971	0.968	0.974	0.954	0.940	0.959
Pmax-KAY		1.000	0.995	0.997	0.992	0.987	0.993
Pmax-BAN			1.000	0.994	0.992	0.989	0.990
Pmax-TIC				1.000	0.988	0.981	0.988
Pmax-KAI					1.000	0.996	0.996
Pmax-YAN						1.000	0.986
Pmax-OTO							1.000

All vector correlations are significant. BAN, Baniwa; KAI, Kaingang; KAY, Kayapó; OTO, Otomí; TIC, Ticuna; XAV, Xavánte; YAN, Yanomami.

Table S4. Phenotypic LLER (pmax), (pmax and $\text{pmax}_{\text{Amerindian}}$) and vector correlations among tribes (pmax, gmax, and total pmax)

	Pmax XAV	Pmax KAY	Pmax BAN	Pmax TIC	Pmax KAI	Pmax YAN	Pmax OTO	Pmax total	$\text{Pmax}_{\text{Amerindian}}$
HC	−0.874	−0.925	−0.924	−0.910	−0.941	−0.964	−0.918	−0.720	−0.898
NGH	−0.215	−0.126	−0.072	−0.110	−0.062	−0.022	−0.108	−0.456	−0.028
NLH	−0.142	−0.033	−0.025	−0.011	0.030	0.024	0.002	−0.440	−0.028
NLB	−0.030	−0.033	−0.031	−0.014	−0.043	−0.026	−0.060	−0.040	−0.006
GOL	−0.374	−0.298	−0.305	−0.361	−0.245	−0.202	−0.260	−0.170	−0.281
XCB	−0.069	−0.165	−0.197	−0.135	−0.151	−0.143	−0.192	0.089	−0.296
ZYB	−0.044	−0.104	−0.049	−0.098	−0.133	−0.078	−0.171	−0.045	−0.157
GOB	−0.149	−0.021	−0.067	−0.032	−0.089	−0.049	−0.095	−0.199	−0.016
Eigenvalue	0.37	0.48	0.39	0.24	0.89	0.74	0.55	0.04	0.37
Percentage of variation	87.75	94.85	93.62	90.20	96.36	96.71	93.24	91.99	95.00
$g_{max} \times p_{max}$	0.94	0.96	0.96	0.96	0.97	0.95	0.98	0.74	0.97
Total $p_{max} \times p_{max}$ or g_{max}	0.88	0.78	0.76	0.77	0.75	0.73	0.76	n/a	0.70

All vector correlations are significant. Nodes according to Fig. 2. GOB, bigonial diameter; GOL, glabello-occipital length; HC, head circumference; n/a, not applicable; NGH, facial height; NLB, nasal breadth; NLH, nasal height; XCB, cranial breadth; ZYB, zygomatic breadth.

Table S5. Genetic LLER (gmax), phenotypic LLER (pmax) and vector correlations among node-specific pmax, gmax, and total pmax

	Gmax	Pmax13	Pmax8	Pmax11	Pmax9	Pmax12	Pmax10
HC	−0.852	−0.957	−0.921	−0.837	−0.919	−0.944	−0.944
NGH	−0.033	−0.032	−0.169	−0.274	−0.164	−0.007	−0.007
NLH	−0.057	0.012	−0.109	−0.190	−0.102	0.000	0.000
NLB	−0.009	−0.030	−0.050	−0.032	−0.050	−0.052	−0.052
GOL	−0.341	−0.222	−0.283	−0.370	−0.292	−0.267	−0.267
XCB	−0.198	−0.155	−0.099	−0.058	−0.100	−0.152	−0.152
ZYB	−0.293	−0.074	−0.116	−0.125	−0.124	−0.104	−0.104
GOB	−0.166	−0.052	−0.080	−0.178	−0.078	−0.016	−0.016
Eigenvalue	6.46	0.61	0.86	0.85	0.86	0.45	0.77
Percentage of variation	80.83	95.55	93.81	92.81	94.16	93.54	94.03
$g_{max} \times p_{max}$	n/a	0.95	0.96	0.94	0.96	0.96	0.96
Total $p_{max} \times p_{max}$ or g_{max}	0.74	0.74	0.85	0.91	0.84	0.72	0.72

All vector correlations are significant. Nodes according to Fig. 2.

Table S6. Quantitative genetics parameters

Group-ancestor	Pmax-pmax	Δz-Pmax	Δz-pmax$_{Amer}$	Δz-Gmax	Branch length	mA	mP
8-OTO	**0.986**	**0.801**	0.308	0.282	0.006	0.072	12.55
8–9	**1.000**	**0.800**	0.308	0.281	0.006	0.072	12.51
9–10	**0.978**	0.323	0.102	0.170	0.015	0.064	4.28
10-KAI	**0.995**	**0.601**	**0.908**	**0.940**	0.060	0.667	11.07
10–11	**0.917**	**0.805**	**0.627**	**0.584**	0.023	0.157	6.69
11-KAY	**0.952**	**0.972**	**0.733**	**0.777**	0.012	0.170	14.78
11-XAV	**0.993**	**0.926**	**0.683**	**0.783**	0.108	6.074	56.47
9–12	**0.978**	**0.925**	0.467	0.464	0.016	0.287	18.43
12–13	**0.997**	**0.811**	0.227	0.238	0.012	0.099	8.58
13-BAN	**0.993**	**0.605**	0.158	0.146	0.074	0.508	6.85
13-YAN	**1.000**	**0.736**	0.211	0.230	0.021	0.208	10.10
12-TIC	**0.989**	**0.851**	**0.868**	**0.833**	0.126	2.054	16.32

For each pair of ancestor-descendent the vector correlations between pmax values, the divergence vector Δz, and the genetic (gmax) and phenotypic (pmax and pmax$_{Amer}$) axes of maximum variance, branch lengths, and morphological amount and pace of evolutionary change are shown. Ancestor descendant numbers refer to the nodes in Fig. 2. Significant vector correlations are shown in bold. mA, morphological amount; mP, morphological pace.

Table S7. Sample composition, sample sizes, geographic location, and linguistic affiliation of the analyzed groups

Population (code)	Village	Sample size (males/females)	Linguistic affiliation	Geographic location
Xavánte (XAV)		113 (57/56)	Jê, central branch	
	Simões Lopes	84 (42/42)		13°20′S–51°40′W
	São Domingo	29 (15/14)		13°20′S–51°40′W
Kayapó (KAY)		235 (105/130)	Jê, northern branch	
	Mekranoti	49 (18/31)		08° 40′ S 54° W
	Kuben-Kran-Kegn	112 (51/61)		08°10′ S 58°8′ W
	Txukahamae	74 (36/38)		10° 20′ S 53° 5′ W
Baniwa (BAN)	Jandu Cachoeira	64 (33/31)	Arawak/Eastern Nawiki subbranch	01° N 67° 50′ W
Ticuna (TIC)		456 (235/221)	Ticuna/language isolate	3° 53′° S 70°W
	Vendaval	178 (89/89)		
	Nova Italia	63 (30/33)		
	Campo Alegre	132 (70/62)		
	Belém	83 (46/37)		
Kaingang (KAI)		181 (92/89)	Jê, southern branch	27–28° S 51–54° W
	Ligeiro	55 (27/28)		
	Guarita	65 (32/33)		
	Nonoai	28 (16/12)		
	Cacique Doble	33 (17/16)		
Yanomama (YAN)	Surucucu/Toototobi/Auaris	154 (77/77)	Yanomami/Yanomaman/ language isolate	02°30′–04°30′ N 64° W
Otomí (OTO)*		60 (28/32)	Otomanguean/Otomí	20°28′ N–99°13′ W
	Banganto	20 (11/9)		
	El Maye	7 (3/4)		
	San Antonio	16 (7/9)		
	Tamaleros	17 (7/10)		
Total		1263 (627/636)		

*Considered only as an "outgroup" on the computation of quantitative genetics parameters. Morphological data obtained from Jaén et al. (1).

1. Jaén M, Serrano C, Comas J (1976) *Data Antropométrica de Algunas Poblaciones Indígenas Mexicanas* (UNAM, Mexico).

Table S8. Eigenvalues (= inertia) and percentage of variance explained by the axes from separate PCA and from MFA (global) analysis

	PHEN		CLIM		LHT		MFA	
Axes	Eigenvalue	%	Eigenvalue	%	Eigenvalue	%	Eigenvalue	%
1	6.01	75.11	3.30	55.07	2.99	74.85	3.46	42.36
2	1.08	13.47	2.20	36.72	0.79	19.76	1.83	22.38
3	0.77	9.64	0.31	5.23	0.21	5.24	1.11	13.57
4	0.11	1.39	0.15	2.55	0.01	0.15	0.94	11.45
5	0.03	0.39	0.03	0.43			0.84	10.23

CLIM, climatic; LHT, life-history traits; MFA, multiple factor, analysis; PHEN, phenotypic.

Table S9. Correlations between variables and each global factor of MFA analysis

Variable	Dim.1	Dim.2
HC	0.82	−0.02
NGH	0.86	0.24
NLH	0.89	0.37
NLB	0.75	0.01
GOL	0.60	0.34
XCB	−0.62	−0.49
ZYB	0.90	0.32
GOB	0.62	0.40
AMT	−0.40	0.90
TSE	0.50	−0.76
TAR	0.80	−0.25
APR	−0.97	0.12
PDM	−0.83	−0.33
PSE	0.60	0.71
INBRE	−0.89	0.13
FER	−0.79	−0.32
MORI	0.84	−0.40
OFS	0.76	−0.60

AMT, annual mean temperature (°C × 10); APR, annual precipitation (mm); FER, fertility (mean of offspring per woman); GOB, bigonial diameter; GOL, giabello-occipital length; HC, head circumference; INBRE, inbreeding coefficient (10 × 4); MORI, infant mortality (%); NGH, facial height; NLB, nasal breadth; NLH, nasal height; OFS, opportunity for selection (maximum rate at which the fitness of a population can change); PDM, precipitation of driest month (mm); PSE, precipitation seasonality (coefficient of variation); TAR, temperature annual range (maximum temperature of warmest month − minmum temperature of coldest month); TSE, temperature seasonality (SD × 100); XCB, cranial breadth; ZYB, zygomatic breadth.

Dataset S1. Phenotypic averages, climatic, sociocultural, and life-history traits data belonging to the six Brazilian tribes studied

Dataset S1 (XLSX)

References to the Sociocultural Information: 12 and 32–41 (reference numbering continues from main text).

12. Coimbra CEA, Flowers NM, Salzano FM, Santos RV (2002) *The Xavante in Transition. Health, Ecology, and Bioanthropology in Central Brazil* (University of Michigan Press, Ann Arbor).
32. Burton ML, Moore CC, Whiting JW, Romney AK (1996) Regions based on social structure. *Curr Anthropol* 37:87–123.
33. Carneiro-da-Cunha M (1998) *History of Brazilian Indians.* (FAPESP, São Paulo) (Portuguese).
34. Fox R (1967) *Kinship and Marriage: An Anthropological Perspective* (Penguin, Baltimore).
35. Keesing RM (1975) *Kin Groups and Social Structure* (Holt, Rinehart and Winston, New York).
36. Murdock GP (1949) *Social Structure* (Macmillan, New York).
37. Murdock GP, White DR (1969) Standard cross-cultural sample. *Ethnology* 8:329–369.
38. Murphy DM (2001) *A Kinship Glossary: Symbols, Terms and Concepts* (Department of Anthropology, College of Arts and Sciences, The University of Alabama; http://www.as.ua.edu/ant/Faculty/murphy/436/kinship.htm). Accessed January 12, 2009.
39. Parkin R (1997) *Kinship: An Introduction to Basic Concepts* (Blackwell Publishers, Oxford).
40. Posey DA (2002) *Kayapó Ethnoecology and Culture* (Taylor and Francis Books Ltd., London).
41. Schusky EL (1965) *Manual for Kinship Analysis* (Holt, Rinehart and Winston, New York).

Dataset S2. Haplotype relative frequencies obtained from sequence data and used to calculate F_{st} distances and Neighbor-Joining tree (*Upper* table) and nucleotide sequence defining each haplotype (*Lower* list)

Dataset S2 (XLSX)

See Dataset S2 for references.