Genetics and Molecular Biology, 22, 2, 163-167 (1999)

GENETICAL-DEMOGRAPHIC DATA FROM TWO AMAZONIAN POPULATIONS COMPOSED OF DESCENDANTS OF AFRICAN SLAVES: PACOVAL AND CURIAU

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ABSTRACT

The Amazon region of Brazil includes communities founded by escaped slaves, some of which still remain relatively isolated. We studied two such Afro-Brazilian communities (Pacoval and Curiau), in the rural area of Alenquer, Pará, and in the metropolitan region of Macapá, Amapá, respectively. Among 12 blood loci, alleles considered as markers of African ancestry, such as *HBB**S*, *HBB**C*, *TF**D1*, *HP**2M*, *ABO**B*, *RH**D-*, and *CA2**2* were found at frequencies that are expected for populations with a predominantly African origin. Estimates of interethnic admixture indicated that the degree of the African component in Curiau (74%) is higher than that of Pacoval (44%); an Amerindian contribution was not detected in Curiau. Estimated values of African ancestry fit well with the degree of isolation and mobility of the communities. Pacoval exhibited a high proportion of immigrants among the parents and grandparents of the individuals studied, whereas persons living in Curiau exhibited a low level of mobility, despite its location in the metropolitan area of Macapá city, suggesting a relatively strong barrier against the interethnic admixture in this population. In addition, analysis of genetic data in a sub-sample consisting of individuals whose parents and grandparents were born in the study site, and that probably represents the populations two generations ago, indicated that gene flow from non-black people is not a recent event in both populations.

INTRODUCTION

The slave trade brought at least 53,000 black Africans to the Amazon region. They were imported directly from Africa by the General Company of Great Pará and Maranhão, private individuals, as well as indirectly through internal trade from other Brazilian regions such as Maranhão, Bahia, Pernambuco and Rio de Janeiro (Vergolino-Henry and Figueiredo, 1990). Historical records about the slave trade to the northern region indicate that most Africans were brought from Angola, Mozambique, Kenya and Tanzania, whereas a smaller number was brought from Guine-Bissau and Cape Verde. In addition, there are records of a small number of slaves from French Guyana and Surinam introduced to the region (State of Amapá and Marajó Archipelago). Some were victims of the illegal slave trade, while others came as fugitives (Curtin, 1969; Vergolino-Henry and Figueiredo, 1990).

Following the example of other Brazilian regions and South American countries, several communities named mocambos or quilombos were founded in the Amazon region by escaped slaves, particularly in the State of Pará, a point of entry of African slaves to the region. Many of these communities still remain relatively isolated, and much of their identity is preserved.

Several genetic studies have been performed in populations descended from Africans in the Amazon region of Brazil and Venezuela evaluating the level of isolation and mobility, and quantifying the gene contribution from non-blacks among them. In this study we report genetical (12 blood genetic systems), genetical-demographic (estimates of interethnic admixture) and demographic (migration) data from two populations of predominantly African ancestry in the Brazilian Amazon region.

MATERIAL AND METHODS

The mocambo of Pacoval, formed by fugitive slaves from farms of the neighboring municipality of Santarém, is located in the rural area of the county of Alenquer, along the right margin of the Curuá River, in the northwestern region of the State of Pará, at about 2°S, 55°W. Blood samples from 166 individuals were collected (63% females, ages varying from seven to 86 years).

Curiau is located in the metropolitan region of Macapá, capital of the State of Amapá, northern Brazil, at about 0°, 51°W. From 1770 Curiau constituted a point of convergence of escaped slaves from the region, including slaves from Suriname and French Guyana (Muggiati, 1971). One hundred and forty-five individuals (49% males, ages varying from four to 84 years) were sampled.

Blood samples (10 ml) were collected with EDTA as an anticoagulant, and 12 genetic systems were analyzed: haptoglobin (HP), transferrin (TF), ceruloplasmin (CP), albumin (ALB), serum cholinesterase (loci 1 and 2), carbonic anhydrase (CA2), esterase D (ESD), glyoxalase (GLO), hemoglobin (HB), ABO and RH blood groups. Phenotypic determinations were made employing classical methods of horizontal and vertical electrophoresis and

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immunological tests that have been previously described or referenced (Santos *et al*., 1983; Schneider *et al*., 1987; Guerreiro *et al*., 1989).

Allele frequencies were estimated by the maximum likelihood method using the MAXLIK program developed by Reed and Schull (1968), and the degree of racial admixture was estimated through the maximum-likelihood method of Krieger *et al*. (1965), using the GENIOC program.

RESULTS AND DISCUSSION

Blood polymorphisms

All phenotype and allele frequencies were in Hardy-Weinberg equilibrium in Curiau, whereas in Pacoval the HP and CP loci showed significant deviations from equilibrium (Tables I and II). Some alleles considered to be markers of African ancestry (*HBB*S*, *HBB*C*, *TF*D1*, *HP*2M*, *ABO*B*, *RH*D-*, and *CA2*2*) were found at frequencies that are expected for populations with a predominantly African origin. Some unusual findings such as high frequencies of alleles *ABO*B* and *HBB*C* in Curiau, and allele *RH*D* in both populations, which are higher than average frequencies estimated for black African populations, may be attributed to microevolutionary factors (genetic drift and/or founder effect). In addition, the presence of the allele *HBB*C* in the Curiau sample (0.06) may also be attributed to the contribution of people from French Guyana to the formation of this population, since among the slaves brought to this country about 74% of them were from Senegambia and Guinea in West Africa (Curtin, 1969), where the *HBB*C* allele is relatively common. *HBB*C* was not found in Pacoval, nor in Trombetas or Cametá, two other communities of African descent in the Amazon region of Brazil (Schneider *et al*., 1987; Bortolini *et al*., 1992), but polymorphic frequencies were found in Curiepe and Panaquire, two Afro-Venezuelan populations (Bortolini *et al*., 1992; Castro de Guerra *et al*., 1996), and in various urban populations from the Brazilian Amazon characterized by a white + Amerindian + African contribution (Ayres *et al*., 1976; Santos *et al*., 1983, 1996; Cayres *et al*., 1991). Thus, these findings indicate that the contribution of people from West Africa to the formation of the Amazonian populations was heterogeneous.

Table I - Observed phenotype and allele frequencies in Pacoval and its native subsample[1].

Blood system and phenotype		Populations		Alleles	Populations	
		Native subsample	Total sample		Native subsample	Total sample
Haptoglobin	1-1	15	27	*HP*1*	0.500	0.468
	1-2	21	55	*HP*2*	0.472	0.500
	1-2M	3	8	*HP*2M*	0.028	0.032
	2-2	15	35			
Ceruloplasmin	BB	45	108	*CP*B*	0.933	0.943
	AB	7	14	*CP*A*	0.067	0.057
Transferrin	CC	64	161	*TF*C*	0.992	0.997
	CD	1	1	*TF*D1*	0.008	0.003
Serum cholinesterase (locus 1)	UU	66	166	*BCHE*U*	1.000	1.000
Serum cholinesterase (locus 2)	C5-	64	158	*CHE2*C5-*	0.985	0.985
	C5+	2	5	*CHE2*C5+*	0.015	0.015
Albumin	AA	66	165	*ALB*A*	1.000	1.000
Carbonic anhydrase	1-1	63	154	*CA2*1*	0.977	0.975
	1-2	3	8	*CA2*2*	0.023	0.025
ABO	O	31	94	*ABO*O*	0.700	0.757
	A	15	32	*ABO*A*	0.155	0.125
	AB	3	6	*ABO*B*	0.145	0.118
	B	14	30			
RH	RH+	58	150	*RH*D-*	0.718	0.728
	RH-	5	12	*RH*D-*	0.282	0.272
Esterase D	1-1	42	99	*ESD*1*	0.811	0.806
	1-2	23	55	*ESD*2*	0.189	0.194
	2-2	1	3			
Glyoxalase	1-1	2	9	*GLO*1*	0.356	0.368
	1-2	43	102	*GLO*2*	0.644	0.632
	2-2	21	52			
Hemoglobin	AA	60	154	*HBB*A*	0.954	0.964
	AS	6	12	*HBB*S*	0.046	0.036

[1] Native subsample: subjects whose parents and grandparents were born in the study site.

Table II - Observed phenotype and allele frequencies in Curiau and its native subsample[1].

Blood system and phenotype		Populations		Alleles	Populations	
		Native subsample	Total sample		Native subsample	Total sample
Haptoglobin	1-1	28	3737	*HP*1*	0.536	0.547
	1-2	43	50	*HP*2*	0.443	0.432
	1-2M	4	5	*HP*2M*	0.021	0.021
	2-2	21	26			
Ceruloplasmin	BB	81	101	*CP*B*	0.870	0.879
	AB	19	23		0.130	0.121
Transferrin	AA	4	4	*CP*A*		
	CC	117	142	*TF*C*	0.992	0.990
	CD	2	3	*TF*D1*	0.008	0.010
Serum cholinesterase (locus 1)	UU	119	145	*BCHE*U*	1.000	1.000
Serum cholinesterase	C5-	116	142	*CHE2*C5-*	0.996	0.996
(locus 2)	C5+	1	1	*CHE2*C5+*	0.004	0.004
Albumin	AA	119	145	*ALB*A*	1.000	1.000
Carbonic anhydrase	1-1	103	124	*CA2*1*	0.933	0.928
	1-2	16	21	*CA2*2*	0.67	0.072
ABO	O	40	51	*ABO*O*	0.595	0.600
	A	35	39	*ABO*A*	0.197	0.187
	AB	7	10	*ABO*B*	0.208	0.213
	B	37	45			
RH	RH+	106	130	*RH*D-*	0.669	0.678
	RH-	13	15	*RH*D-*	0.331	0.322
Esterase D	1-1	89	112	*ESD*1*	0.857	0.869
	1-2	26	28	*ESD*2*	0.143	0.131
	2-2	4	5			
Glyoxalase	1-1	20	24	*GLO*1*	0.432	0.406
	1-2	55	61	*GLO*2*	0.568	0.594
	2-2	35	49			
Hemoglobin	AA	94	114	*HBB*A*	0.895	0.893
	AS	10	13	*HBB*S*	0.042	0.045
	AC	15	18	*HBB*C*	0.063	0.062

[1] Native subsample: subjects whose parents and grandparents were born in the study site.

Table III - Interethnic admixture in Afro-Brazilian populations from the Amazon region (%).

	Estimated admixture and standard error			
Population	Black	White	Amerindian	Reference
Trombetas[a]	56.4 ± 12.6	23.8 ± 11.0	19.8 ± 12.5	Bortolini *et al.* (1995)
Trombetas[b]	62.0 ± 5.0	27.0[c] ±	11.0 ± 4.0	Schneider *et al.* (1987)
Cametá[a]	48.0 ± 0.7	17.9 ± 0.6	34.1 ± 0.7	Bortolini *et al.* (1992)
Cametá[b]	49.6 ± 12.9	18.0 ± 11.5	32.3 ± 14.1	Bortolini *et al.* (1995)
Curiau[b]	73.6 ± 14.6	26.4 ± 14.6	0	Present study
Pacoval[b]	44.3 ± 11.7	27.4 ± 12.6	28.3 ± 11.7	Present study

[a]Method of Krieger *et al.* (1965). [b]Method of Long *et al.* (1991). [c]The authors did not furnish the standard error. Loci used for calculations: for Pacoval, CP, CA2, ABO, RH, ESD, GLO, HB; for Curiau, TF, CA2, ABO, RH, ESD, GLO, HB, HP.

Interethnic admixture

Estimates of interethnic admixture obtained for the two populations (Table III) indicate that the degree of black component in Curiau is significantly higher than in Pacoval. These results fit well with the apparent morphological classification of the individuals sample, which indicated 14% individuals with mixed ancestry in Curiau, and 49% in Pacoval. Interethnic admixture values are also in accordance with the level of isolation and mobility of the two populations. The proportion of immigrants among the parents and grandparents of the individuals sampled in Pacoval is high, whereas Curiau, despite its location in the metropolitan area of Macapá city, exhibits a low level of mobility (Table IV), suggesting a relatively strong barrier against interethnic admixture in this population. The

Table IV - Birthplace distribution (in %) of the individuals studied in Pacoval and Curiau and that of their ancestors.

	Subjects tested		Their parents		Their grandparents	
Birthplaces	Pacoval N = 166	Curiau N = 140	Pacoval N = 327	Curiau N = 260	Pacoval N = 649	Curiau N = 516
At the study site	96.4	93.6	76.2	96.9	70.1	96.9
Outside the study site:						
In the same county	3.0	5.7	13.8	2.7	17.6	2.7
In the same state	0.6	-	7.0	-	8.3	-
In the north	-	0.7	0.9	0.4	0.6	0.4
In the northeast	-	-	1.8	-	2.8	-
Abroad	-	-	0.3	-	0.5	-

proportion of African ancestry obtained for Curiau is the highest reported among communities composed of descendants of black Africans thus far studied in the Amazon region (Table III). In addition, Curiau is the first Amazonian population where an Amerindian contribution was not detected.

In order to evaluate whether admixture with Caucasians and Amerindians has occurred in the last two generations, a subsample of subjects whose parents and grandparents were born in the study site was analyzed. There where no significant differences (Tables I and II) with respect to the total sample (Pacoval: $\chi^2 = 5.95$, d.f. = 12, P = 0.91; Curiau: $\chi^2 = 1.00$, d.f. = 12, P = 1.00), indicating that admixture with non-blacks is not a recent event in both communities.

In summary, the genetic variability observed in Pacoval and Curiau is consistent with the African origin of the populations, with some degrees of local differentiation and admixture with people of Caucasian and/or Amerindian ancestry. In addition, the presence of people from West Africa among the African slaves brought to the Amazon region was well characterized by the occurrence of the allele *HBB*C* in Curiau.

RESUMO

A região amazônica brasileira abriga diversas comunidades formadas por descendentes de escravos africanos, algumas das quais ainda relativamente isoladas. Nós estudamos duas dessas comunidades (Pacoval e Curiau), localizadas na área rural do município de Alenquer, Pará, e na região metropolitana de Macapá, Amapá, respectivamente. Entre os 12 loci investigados, alelos considerados como marcadores de ancestralidade africana, tais como *HBB*S*, *HBB*C*, *TF*D1*, *HP*2M*, *ABO*B*, *RH*D-* e *CA2*2*, foram encontrados com freqüências elevadas, de acordo com o esperado para populações com origem predominantemente africana. As estimativas de mistura racial indicaram que o percentual de contribuição africana em Curiau (74%) é maior do que em Pacoval (44%) e que em Curiau não foi detectada mistura com indígenas. As estimativas de ancestralidade africana estão de acordo com o grau de isolamento e com a mobilidade das comunidade estudadas. Pacoval apresenta um elevado percentual de imigrantes entre os pais e avós dos individuos estudados, enquanto que a comunidade de Curiau, apesar de situada na região metropolitana de Macapá, apresenta uma pequena proporção de imigrantes, sugerindo a existência de uma barreira relativamente forte contra a mistura interétnica. A análise dos dados genéticos foi também efetuada em sub-amostras constituídas apenas por indivíduos cujos pais e avós nasceram na localidade em estudo e que provavelmente representam essas populações duas gerações atrás. Os resultados indicaram que a mistura com não-negros nas duas populações não é um evento recente.

AKNOWLEDGMENTS

We are grateful to the communities studied for their collaboration, and to Roberto A.N. Madeiro, Vilson C. Monteiro, Edson S. Abrahim Filho and Hailton O. Monteiro for assistance with the blood sample collection. This work was supported by UFPA and CNPq.

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(Received April 6, 1998)