

INTERINDIVIDUAL GENETIC RELATIONSHIPS IN AN AMAZONIAN INDIAN VILLAGE

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RESUMO - Uma das técnicas de estudo da estrutura genética de populações humanas é sua análise genealógica. Este trabalho descreve características da aldeia indígena Assurini de Kuatinemo (Amazônia brasileira) quanto ao parentesco genético entre seus membros, assim como alguns parâmetros demográficos de interesse genético. A genealogia da aldeia inclui 56 indivíduos. O coeficiente médio de co-ancestria (\bar{f}) foi $0,0076 \pm 0,0407$. Esta estimativa é relativamente baixa quando comparada à calculada para outras populações indígenas amazônicas. O maior coeficiente médio de co-ancestria "indivíduo-população" (definido como f_{ip}) foi 0,0204, observado em quatro irmãos, cujos elos de parentesco intra-aldeia envolveram 15 comparações ($f_{ij}=0,1875$). Não se verificou fecundidade diferencial significativa na população ($G = 3,925$; $p = 0,141$). Nossa hipótese é a de que as taxas reduzidas de co-ancestria calculadas entre os Assurini do Kuatinemo podem refletir limitações de dados genealógicos causadas pela grave depopulação sofrida por estes índios nas últimas gerações. Nesse sentido seria pertinente comparar resultados quantitativos genealógicos com a variabilidade genética bioquímica na aldeia.

PALAVRAS-CHAVE: Análise Genealógica, Co-Ancestria, Ameríndios, Assurini do Kuatinemo.

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ABSTRACT - One method to study the genetic variability of human populations is genealogical analysis. This work describes features of the Assurini of Kuatinemo Indian village (Brazilian Amazon) with respect to the genetic relationships among its members, as well as providing some demographic parameters of genetic interest. The village pedigree included 56 individuals. The average kinship coefficient (\bar{f}) was 0.0076 ± 0.0407 . This estimate is relatively low when compared with those obtained for other Amazonian Indian groups already investigated. The highest individual-population average kinship coefficient (here called f_{ip}) was 0.0204. This figure was observed among four sisters, involving 15 within-village comparisons ($f_{ij} = 0.1875$). Significant differential fertility was not observed among the members of the village ($G = 3.925$; $p = 0.141$). We suggest that the low kinship rates estimated for the Assurini of Kuatinemo may result from poor genealogical data due to the severe depopulation suffered by these Indians in the last generations. In this sense, it would likely be interesting to compare quantitative genealogical data with the village biochemical genetic variability.

KEY WORDS - Genealogical Analysis, Kinship, Amerindians, Assurini of Kuatinemo.

INTRODUCTION

From an anthropogenetic point of view, the two major techniques for the evaluation of population structure are the intergroup and the intragroup analyses. The former analysis estimates resemblance or distance between populations, while the later analysis allows one to estimate genic or phenetic variation on the basis of highly or moderately heritable markers. The purpose of both approaches is the same: to describe and to interpret the genetic structure of populations, as well as to explain evolutionary mechanisms under which such populations are submitted (Fix 1979).

In general, the within-group variation is studied by analysing mono or polygenic genetic systems. Such an analysis offers mathematical results capable to allow an approach of the group genetic profile (Wright 1951). A classic example of this approach relies on the calculation of mean per locus per individual heterozygosities (Nei 1987).

Pedigree analysis does constitute an alternative methodology to perform population biology investigations (Thompson 1986). Each individual living in a certain group may be related to others members of this group by several kinds of genetic linkage. We can therefore obtain measures of genetic closeness or genetic similarity. At the same time, general patterns of kinship, relationship

and inbreeding provide information on the within-group genetic structure. An adequate description of the genealogical system of interindividual relationships may reflect genetic diversity, since it estimates "concentration" or "dilution" of kinship among members of a population.

This article analyses briefly the available pedigree of the Assurini of Kuatinemo, an Amazonian Indian population located in the State of Pará, Brazil. The authors wish to carry out in the future the same kind of approach for other Amazonian groups in order to establish patterns of intervillage and intertribal genetic relationships.

MATERIAL AND METHODS

The Assurini village of Kuatinemo is located on the margins of the Xingu River (4° 12' S; 52° 26' W), Brazilian Amazonia, at a distance of about 100 km from the city of Altamira. Its population in 1984 was estimated in 53 subjects by Müller (1984/1985). The Assurini suffered severe depopulation in the last decades as a result of contacts with the Brazilian national society, of intertribal warfare, and of capture of their children by other groups (Aguiar 1991).

We have obtained genealogical data from FUNAI's ("Fundação Nacional do Índio") informants and by interviewing native members of the village, which did allow cross reference of data. The Kuatinemo genealogy involved 56 individuals. The accuracy of data was improved after the field work by excluding 11 individuals of their supposed families on the basis of HLA haplotypes. Furthermore, it is necessary to mention that some Kuatinemo Indians do not belong to any family group in the pedigree, since their biological ancestry is unknown.

The pedigree analysis was performed by the SAGEN ("Sistema de Análise Genealógica", System for Genealogical Analysis, version 1.0), a software created by researchers of the Museu Paraense Emílio Goeldi (Aguiar & Souza-Junior 1992). We calculated interindividual, average within-sample and individual-population kinship coefficients (f). This coefficient is defined as the probability that two genes randomly chosen in the same locus of two individuals, are identical by common ancestry (Kempthorne 1963; Malecôt 1966; Falconer 1986). The shorter the path connecting two individuals to their common ancestors the higher this measure.

Quantitative results of the work were analysed by non-parametric statistics.

RESULTS AND DISCUSSION

Generally speaking, the distance between two individuals and their common ancestors (number of steps or length of paths) is negatively correlated with their kinship coefficient. For instance, when we submitted Kuatinemo Indians to this treatment, we obtained a Spearman's rank correlation of -0.399 ($p < 0.05$). Such an approach is essentially probabilistic. The observed relationships may be distinct from that expected as a result of factors producing inter-generation variability (e.g., crossing-over).

The average kinship coefficient for all Indians studied (\bar{f}) was relatively low (0.0076 ± 0.0407). The analysis involved 1540 different interindividual comparisons ($f_i - f_j$) within the village. A fraction of 95.1% of the comparisons provided $f_{ij} = 0$; 2.5%, $f_{ij} = 0.25$; 1.0%, $f_{ij} = 0.125$; and 0.2%, $f_{ij} = 0.0625$. An explanation for the low average kinship among the Kuatinemo is that there is poor information on the ancestry of some individuals, although we had analysed four generations.

The calculation of the average kinship coefficient between each individual and the remaining population (\bar{f}_{ip}) is a reliable method to identify genetically referential individuals within a population. There was a high rank correlation between \bar{f}_{ip} and number of sibs (Spearman = 0.732; $p < 0.01$). Although seemingly obvious, this correlation is not necessarily observed in other human groups, because it suffers influence from variant genealogical structures, number of generations, family size, etc.

The highest figure of \bar{f}_{ip} in Kuatinemo (0.0204) was observed among four sisters, involving 15 interindividual comparisons ($f_{ij} = 0.1875$). There were detected isolated cases of polygyny among the Kuatinemo, including of the sororal type. However, taking into account the available genealogical data, there is no significant differential fertility within the village (G-test = 3.925; 2 d.f.; $p = 0.141$). The average offspring size for males (1.62) was not significantly different from that of females (1.44) (G-test = 0.288; 1 d.f.; $p = 0.592$). The parameter \bar{f}_{ip} for polygynous males was also not significantly greater than that of the remaining population. The distribution of offspring size (for fathers and mothers) can be observed in Table 1. The statistical analysis did not reveal excess or deficit of descendants for individuals with offspring (G-test/Mothers = 0.91, $p = 0.339$; G-test/Fathers = 2.32, $p = 0.314$). Significant correlation between parental age and offspring size was not observed, either for fathers ($r = 0.36$, $p > 0.100$) and mothers (a surprisingly

negative correlation of -0.232) or for both sexes ($r = 0.15$, $p > 0.100$). It is interesting to remark that there is also no statistical association between fip and offspring size (Spearman = 0.096; $p > 0.200$), to the contrary of the result verified for sibs.

We suggest that the low kinship rates among the Assurini of Kuatinemo may result from poor genealogical data due to the severe depopulation suffered by these Indians in the last generations. In this sense, it would likely be interesting to compare quantitative genealogical data with the village biochemical genetic variability.

Table 1 - Offspring sizes for fathers and mothers in the Assurini of Kuatinemo village.

Offspring size	Nr. of fathers	Nr. of mothers	Nr. of descendantes
1	4	5	9
2	3	4	14
3	1	-	3
Total	8	9	26

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