

STUDIES ON SERUM CHOLINESTERASE (*CHE1* AND *CHE2* LOCI) AMONG INDIANS FROM THE AMAZON REGION OF BRAZIL: MUNDURUKU AND PARAKANĀ TRIBES

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ABSTRACT

Serum cholinesterase polymorphism (*CHE1* and *CHE2* loci) was investigated among 196 Munduruku and 123 Parakanā Indians from the Amazon region, Brazil. The atypical variant was not found in either group, and the C5+ phenotype frequency was estimated at 11.3% in the Munduruku and was not found in the Parakanā group. These results are compared with those reported for other Amerindian population.

INTRODUCTION

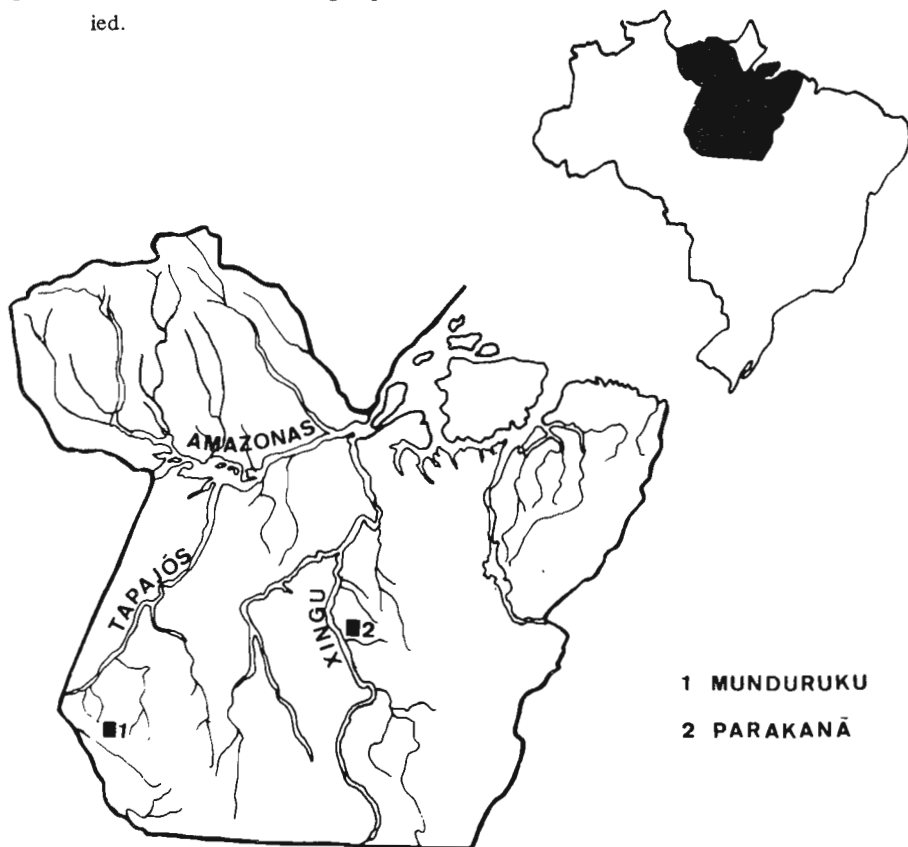
Serum cholinesterase is a liver esterase whose genetic determination is explained by two non-linked loci (*CHE1* and *CHE2*). The variants of the *CHE1* locus are responsible for different degrees of sensitivity to the muscle relaxant suxamethonium, and the most commonly found is the atypical one (*CHE1**A allele), which occurs at frequencies of 1 to 2% among European populations. In the majority of Indian populations this variant is rare or absent, but Vergnes and Quilici (1970) found a frequency of 0.038 for the atypical gene in one Mayan group, and Arends *et al.* (1970) observed a frequency of 0.031 for the same gene among the Makiritare.

The variant determined by the *CHE2* locus, called C5+, causes an increase in total serum cholinesterase activity and can be detected by various electrophoretic techniques. The distribution of the C5+ variant does not show a clear geographical or racial pattern, although with respect to average values the incidence seem to be higher in Caucasians (Steggmüller, 1975). Frequencies of the C5+ phenotype variant have been estimated for Indian groups and range from zero to 24.6% (Table I).

MATERIAL AND METHODS

The Munduruku Indians belong to the munduruku linguistic group and live in Pará State, on the right margin of the Tapajós River ($7^{\circ}41'S$; $57^{\circ}9'W$) near the village of Jacareacanga. The Parakanã belong to the tupi-guarani linguistic group, and also live in Pará State on the left margin of the Xingu River ($5^{\circ}34'S$; $52^{\circ}32'W$), not far from the town of São Felix do Xingu (Figure 1).

Figure 1 - Location of the Indian groups studied.



The samples studied consisted of 196 Munduruku (52.0% male), varying in age from 1 to 75 years, and 123 Parakanã Indians (52.0% males), age range from 1 to 75 years. Serum samples were collected and stored at $-20^{\circ}C$ for a short period of time during transportation to the Human Genetics Laboratory of the Federal University of Pará, Belém.

Serum cholinesterase phenotype (*CHE1* locus) was determined by the method of Morrow and Motulsky (1968). The C5+ variant (*CHE2* locus) was detected by the acid agar gel electrophoresis technique described by Van Ros and Vervoort (1973), as modified by Boman and Habib (1983). The gels consisted of 1% Bacteriological Technical agar (Difco) instead of Bacto or Noble agar.

RESULTS AND DISCUSSION

None of the Munduruku or Parakanã Indians showed the atypical variant and all can be classified as homozygotes for the usual allele (*CHE1*U/CHE1*U*), even though the method of Morrow and Motulsky (1968) does not detect the heterozygotes for the fluoride resistant gene (*CHE1*U/CHE1*F*) nor the heterozygotes for the silent gene (*CHE*U/CHE1*S*), which are classified as homozygotes for the usual allele. However, since these genotypes are very rare, the Munduruku and Parakanã Indians can be considered to have only the usual genotype.

Since at present we do not know the exact physiological function of serum cholinesterase, the rarity of this allele in most Indian populations could be ascribed to the absence or very low frequency of the atypical allele in the ancestors of present-day Amerindians, as suggested by Lisker *et al.* (1967). On the other hand, the low frequencies of the atypical gene reported for some Indian groups could be attributed to Caucasian admixture. Nevertheless, in the Mayan group and in the Makiritare, the Caucasian admixture alone cannot explain the high frequencies reported, because they exceed the highest levels observed among European populations. Thus, it seems more reasonable to consider that, even with Caucasian admixture, these findings may be better explained by the action of genetic drift or founder effects, since the Indian communities are exposed to these evolutive factors because of their small size.

In the Munduruku group the C5 band was observed in 22 samples (11.3%), and the frequencies obtained for men (10.9%) and for women (11.8%) were similar ($\chi^2_1 = 0.0004$; $P = 0.98$). Among the Parakanã, the C5+ phenotype was not found (Table I).

The heterogeneous distribution of the C5 variant has been observed not only among Indian populations, but in other human groups, with the exception of "pure" Black populations, where the C5+ variant frequencies are consistently rare (Stegmüller, 1975). The reason for this relatively wide heterogeneity is obscure, but we may assume again that it is due to genetic drift or founder effects. The alternative explanation, selective factors, is difficult to test, since, as for the atypical gene, the biological function of this enzyme is still not definitively known.

Table I - Incidence of the C5+ variant in South American Indian populations.

Population	Place	N	Frequency (%)	Authors
Makiritare	Venezuela	418	11.5	Arends <i>et al.</i> (1970)
Motilon	Venezuela	70	1.4	Arends <i>et al.</i> (1967)
Warrau	Venezuela	131	0.0	Arends <i>et al.</i> (1967)
Sirionó	Bolivia	65	0.0	Vergnes <i>et al.</i> (1976)
Wayana-Apalai	Brazil	127	7.9	Guerreiro <i>et al.</i> (1985)
Mura	Brazil	112	1.8	Primo-Parmo <i>et al.</i> (1986)
Tenharim	Brazil	23	8.7	Primo-Parmo <i>et al.</i> (1986)
Sateré-Mawé	Brazil	188	0.0	Primo-Parmo <i>et al.</i> (1986)
Pacaás-Novos	Brazil	219	15.1	Primo-Parmo <i>et al.</i> (1986)
Krahó	Brazil	94	8.5	Primo-Parmo <i>et al.</i> (1986)
Kaingang and Guarani	Brazil	27	0.0	Primo-Parmo <i>et al.</i> (1986)
Kaingang	Brazil	57	24.6	Primo-Parmo <i>et al.</i> (1986)
Munduruku	Brazil	194	11.3	Present study
Parakanã	Brazil	123	0.0	Present study

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RESUMO

O polimorfismo da colinesterase do soro (locos *CHE1* e *CHE2*) foi investigado em 196 índios Munduruku e 123 índios Parakanã, da Amazônia brasileira. A variante atípica não foi detectada nos dois grupos, e a frequência do genótipo C5+ foi estimada em 11.3% entre os Munduruku, estando ausente entre os Parakanã. Estes resultados são comparados com os descritos para outras populações ameríndias.

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