AN ATTEMPT OF PHYLOGENETIC ANALYSIS OF THE LOCAL CATTLE OF GUADELOUPE

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SUMMARY

The purpose of this study is to determine the phylogenetic relationship between the local beef cattle of Guadeloupe ("créole" cattle) and some other cattle breeds of the world.

Polymorphism analysis of some biochemical markers have been performed on 204 "créole" cattle sampled in the population. Six protein loci, eleven blood group systems, and class I BoLA antigens, were studied. The data about other breeds, suspected to be more or less closely related to local cattle, were obtained from the literature available. The statistical analysis concerned Principal Component Analysis, computations of four genetic distances and their UPGMA presentation.

The results confirm the intermediate position of the local cattle, issued from several crosses occurred during the History, between the european taurines, mainly from iberican origins, and the african humped cattle. But the local population cannot be connected firmly to any of the groups studied. The "créole" beef cattle of Guadeloupe could therefore be classified with the sanga cattle.

INTRODUCTION

The analysis of former marker genes is an actual challenge for animal breeding and genetics. Populations characterization, gene mapping and markers studies could enhance improvement of livestock production, through a better knowledge of genetic diversity (a guideline to resources conservation), and genetics of particular traits (quantitative traits or disease resistance markers or genes).

On both points of view, the local beef cattle of Guadeloupe (French West Indies), called "créole" cattle, seems worth of interest. On the first hand, it seems a really original population, as a result of crossbreeding between diverse European taurines, African zebus and taurines, and Indian zebus, between the X VI° and the XIX° centuries (Maillard et al., 1993). Besides, "créole" cattle exhibits a good productivity in stressful environmental conditions (Naves and Vallee, 1991) and particularly a great resistance to diseases related to the tropical bont tick Amblyomma variegatum (Naves et al., 1993; Maillard et al., 1993).

The present study is an attempt to quantify the relationship between "créole" cattle of Guadeloupe and breeds of several origins throughout the World. The main objective is to elucidate the originality of this population, in comparison to well known breeds, within suspected ancestors or less related breeds.

MATERIALS AND METHODS

The local cattle population was sampled in the whole island, according to its spatial distribution. Biological material was taken on 204 animals, of both sexes and different ages, from 82 farms. Among them, 190 individuals were unrelated and used in the analysis. Whole blood samples were collected, and aliquotes of blood, serum, plasma, cells or DNA were sent immediately to the different laboratories or stored frozen for later analysis. 235 animals in half-sib families from a farm belonging to I.N.R.A. were also studied for blood groups transmission.

Eighteen polymorphic markers, among the more cited in the literature, were analysed. The concerned loci were:
- four blood proteins: Albumin (ALB: 189 samples), Haemoglobin (HBB: 188 samples), Transferrin (TF: 178 samples), Amylase-I (AMYI: 69 samples), studied by cellogel (ALB, HBB), polyacrylamide gel (TF) or starch gel (AMYI) electrophoresis;
- two milk proteins: Kappa Casein (CASK: 42 samples), β Lactoglobulin (LGB: 23 samples), studied by TaqI RFLP technique (CASK) or cellogel electrophoresis (LGB);
- class I Bovine Lymphocytes Antigens (BoLA-I) (167 samples), using the standard lymphocytotoxicity test.

In the later statistical analysis, four systems, linked with another one or less referenced in the litterature (A, M, R', T', LGB), were unused.

Alleles frequencies were calculated using the direct counting method (for codominant systems), the square-root method (for simple dominant systems) or the iterative method (for complex systems), as described by Neimann-Sorensen (1956). For the complex systems, simplification of the former alleles were used, based on the known map of the C blood group system (Guerin et al., 1981) or the alleles the most referenced in the litterature, for BoLA specificities and B and S systems. There were summarized according to the presence of some selected factors, as namely:

- B system: "B", "G", "K" and "null" alleles;
- C system: "C1", "C2", "C'1" and "C'2" alleles;
- S system: "H'", "U'", "U", "S" and "null" alleles

Data on the other breeds were found in about 200 references. A few breeds had enough informations on markers used in this study and could be included in the panel of comparison. For the proteins alleles frequencies, only data consistent with the review by Baker and Manwell (1980) were taken into account. For the blood groups, some alleles frequencies were calculated from phenotypic frequencies cited in the references, as also by grouping some detailed alleles. Finally, 36 alleles from 13 systems and referenced on 21 breeds, including the local cattle population of Guadeloupe, were retained. The breed groups represented concerns:

- Northern to southern Taurine breeds: Shorthorn; Holstein, Jersey, Guernsey, Normande, Bretonne Pie-Noire, Simmental; Charolais, Limousine; Alentejana, Retinta; Texas Longhorn, Cuban Criollo; African N'Dama;
- Indian zebus: Sahiwal, Tharparkar;
- African humped cattle: Bororo, Boran;
- Humped admixtures: Afrikander, Brahman, Guadeloupe "créole" cattle.

Statistical analysis of these data involved two main methods:
- Principal Component Analysis of the alleles frequencies
- and four distance matrix computations: Nei's Standard distance (Dq), Cavalli-Sforza distance (fD), Grégorius distance (Dg) and Khi² distance. These distances were summarized through UPGMA hierarchical classification procedure.

RESULTS

Only the main results obtained in the statistical analysis are presented here.

On the two first axes of the Principal Components Analysis, the differenciation between the main classes is clearly apparent: the taurine and the humped cattle are in an opposite position on the first axis, while the indian zebus are distinct from the taurine and the african humped cattle on both first axis. The third axis introduce a distinction between the taurine breeds, step-distributed along the second axis. The local breed of Guadeloupe is clearly in an intermediate position between the taurine and the african zebu breeds.
Several distance matrices were computed, due to the constraints of non-missing values and the number of degrees of freedom. In the comparison panel, only 8 systems representing 20 alleles were completely filled in. So, only 12 breeds could be used simultaneously in the classification based on these systems. Then, the other markers have been added in the computations, while the breeds with missing values had to be removed. A simple visual comparison of the different representations obtained had been done. Only some within these figures are presented. They concern a comparison of the phylogenetic trees computed on the Nei's Standard distance from four different sets of variables (Figure 2).

Figure 2: Comparison of dendrograms obtained from Nei's Standard Distance ($D_s$)
(numbers of breed/loci/alleles - loci studied)
In the different phylogenetic trees obtained, the clear distinction between taurine and zebu cattle can be observed. Indian zebus are quite apart from all breeds. Humped admixtures, as well as the Texas Longhorn shows a different branching pattern according to the trees considered.

For "Créole" cattle, the nearest breed is clearly the Cuban Criollo; when this breed is included, "créole" cattle is related to Iberian cattle and taurines. Then, the African humped cattle (Bororo, Boran) or Africander are quite close to the local breed of Guadeloupe. The N’Dama cattle does not seem closely related to "créole" cattle, but always clustered with European taurines.

**DISCUSSION**

This study gives us some precisions about the probable origins of the "créole" cattle of Guadeloupe. Its strong relationship with Cuban criollo reinforces the hypotheses of its Iberian origins, as reported by Rouse (1977) for all criollo cattle in the South America. But surprisingly, the Texas Longhorn, from the same origins (Kidd et al., 1980) seems quite different. We failed also in finding a precise relationship with one of the Iberian breeds, as Altarriba et al. found (1979) between Cuban Criollo and Retinta. These remarks can be explained by the deviations between breeds occurred during history, in different environments, but mainly by the importance of crossbreeds in the origins of the local population.

The contribution of African zebu seems quite important. This could be surprising as, within African cattle, missing data about west African breeds allowed us only to refer to breeds from the center and the east of this continent. But it is in agreement with observations of the shape of Y-chromosome of local cattle, described as acrocentric by Popescu et al. (1987). In contrast, from the data available here, the Indian zebu origin can be denied. The distinction between N’Dama and "créole" cattle is also surprising, as they were closely related in another study (Maillard et al., 1993) on some partial informations.

Our results shows the difficulty of inferring the origins of breeds from genetic data. In particular, we failed in founding sufficient informations about cattle from tropical countries, which could be closer to our population than others. The methods used here could also be discussed. Firstly, the choice of some others target markers, owing to the use of new technologies, could enhance the comparison. In another point of view, our interpretations based on distance matrices, which suppose a timed differentiation between breeds, are inadequate for crossbreeds relationships. The statistical interpretations could therefore be improved by the use of other methods recently described (Guyomard, 1993).

**REFERENCES**


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