GENETIC RELATIONSHIPS AMONG CUBAN DONKEY POPULATIONS

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INTRODUCTION

- Putative centre of domestication
- Middle East migration
- European migration
- Columbus route

Fig. 1. Map of donkey domestication centres and main migrations.

Cuba

Donkeys were mainly used to breed mules in Cuba, which are used in mountainous regions. For this reason, donkeys are mostly found there, too.

However, it has changed in the last two decades (Fig. 2). A genetic improvement program in mule breeding, which affected donkeys and horses, has contributed.
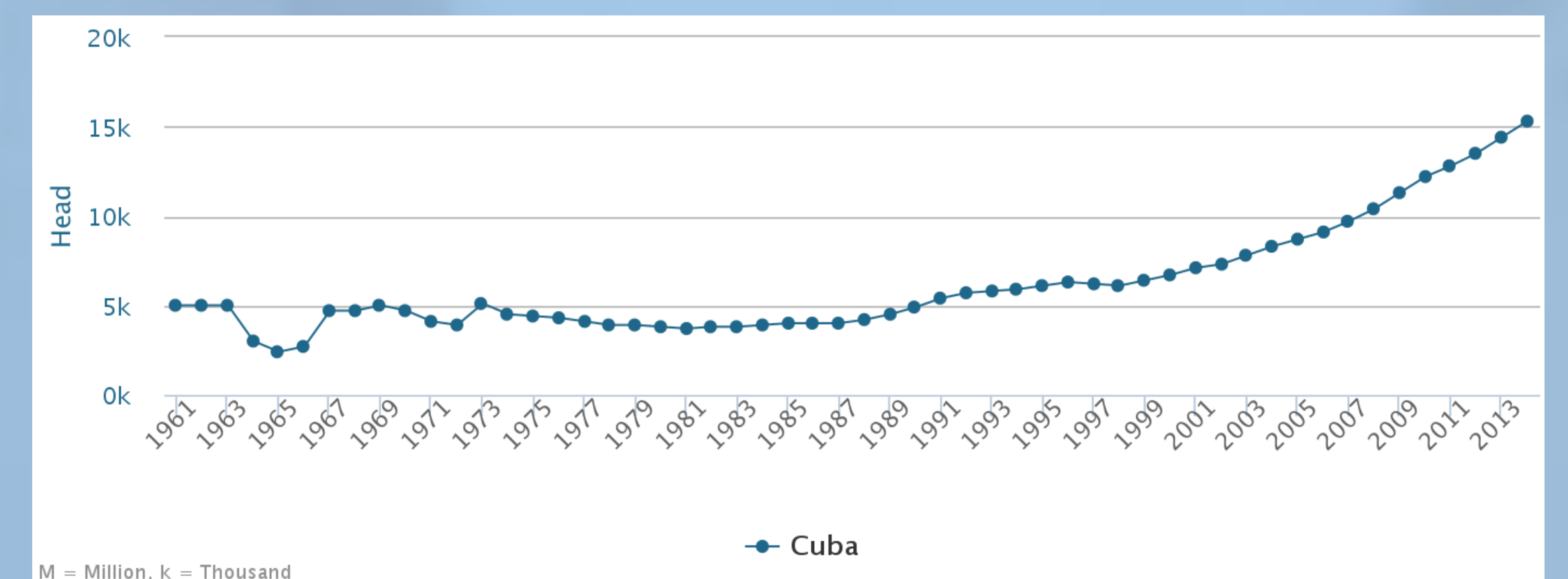

M = Million, k = Thousand

Fig. 2. Evolution of Cuban donkey census (1961-2014)[1].

OBJECTIVES

- Genetic characterization of Cuban donkey population and its subpopulations.

- Evaluation of population genetic structure, following geographic patterns.

MATERIAL AND METHODS

Genomic DNA isolation → Microsatellite loci amplification → Sequenciation → Sizing

Fig. 3. Cuba map with the cities (and provinces) where samples were taken from and the number of it in brackets.

Genetic diversity analyses
All diversity parameters, except from rarefacted allelic richness (rAR) - GENALEX v.6.502[2,3].

Genetic differentiation
Reynolds distance (D_R) matrix and the resulting genetic distance tree after 1000 bootstraps - POPULATIONS v.1.2.32[4].

Bayesian inference
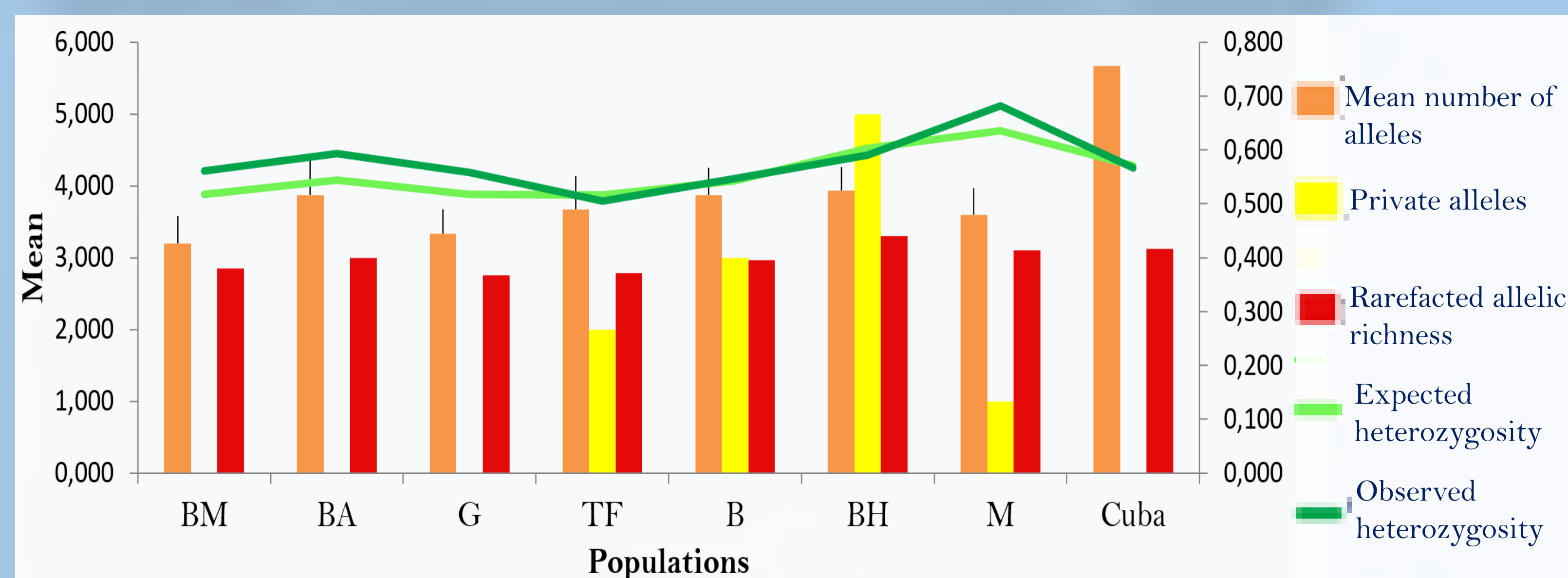Population clusters - STRUCTURE v.2.3.4[5].

RESULTS AND DISCUSSION

- Mean number of alleles
- Private alleles
- Rarefacted allelic richness
- Expected heterozygosity
- Observed heterozygosity

Fig. 4. Graphic of genetic diversity statistics for every population (represented by its initials) and Cuba.

- Genetic diversity of Cuban donkey was similar to American, but lower than the European and the Chinese one

- Different diversity between Cuban populations → migrations from Bahía Honda and Manicaragua to Granma

Origin centres retain higher diversity

- Manicaragua was a clearly differentiated population, probably because of USA and Canadian donkey importations to its breeding centres.

- There was a genetic structure among Cuban populations, which followed a geographic pattern, although some close populations were unrelated, such as Granma populations.
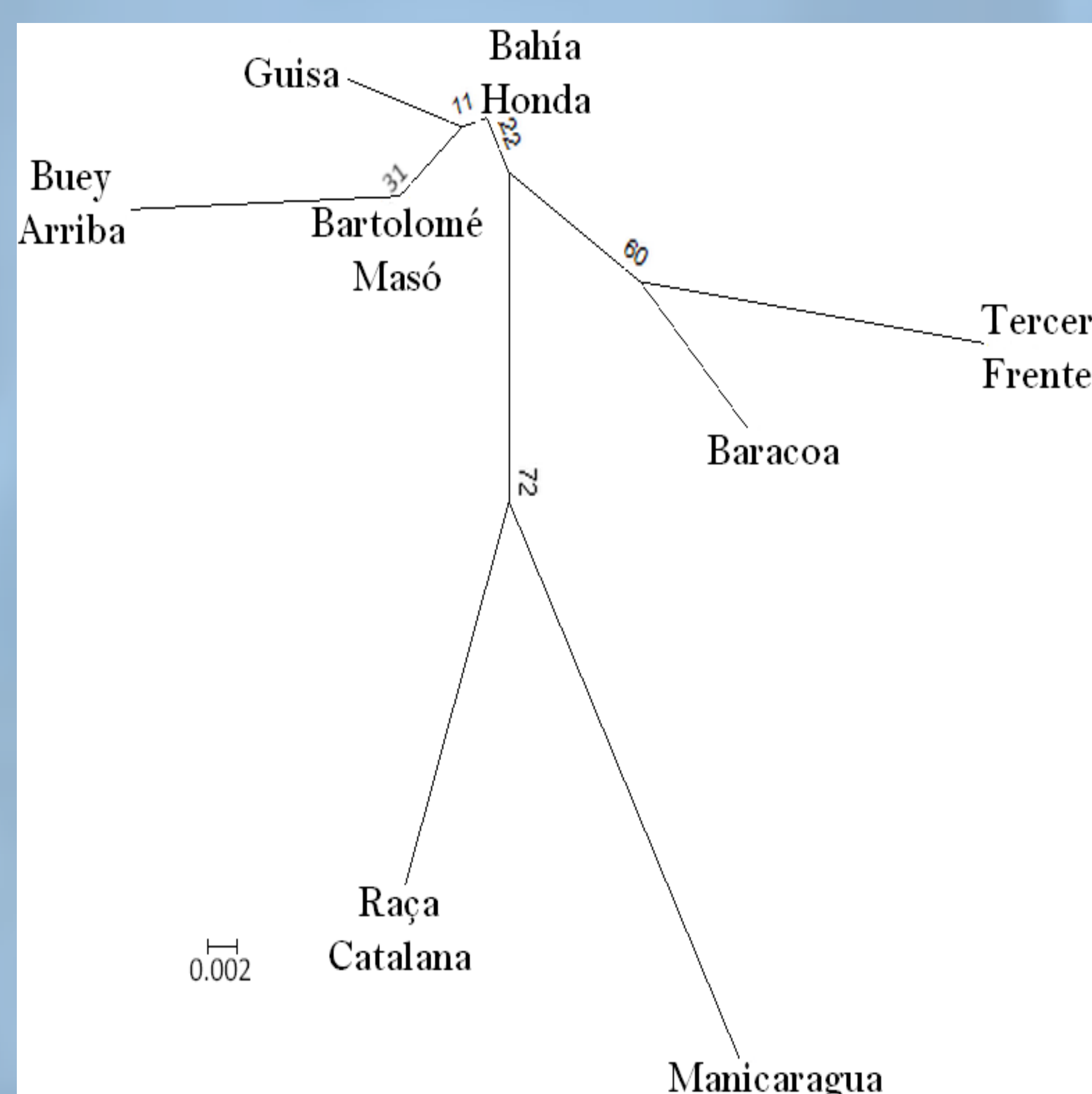

Fig. 5. Unrooted Neighbor-Joining distance tree with the weighted D_R after 1000 bootstraps using Catalan breed as an outgroup.
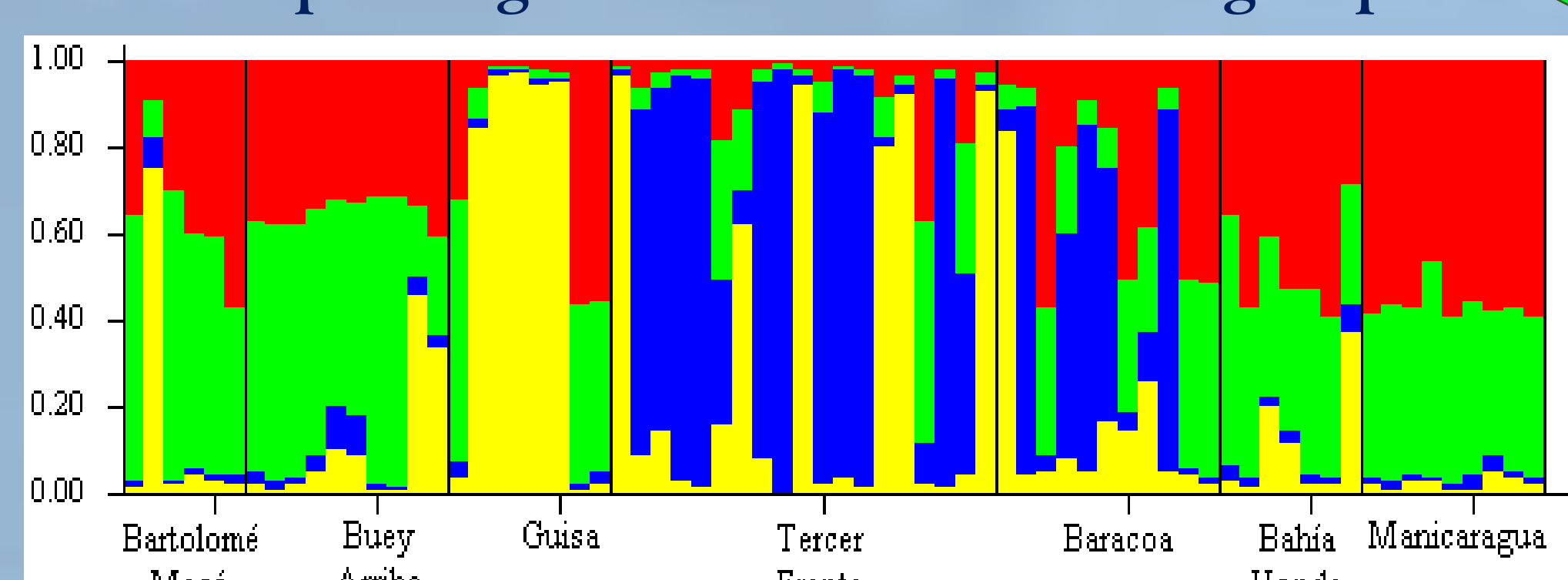

Fig. 6. Summary of Q estimations for the most probable K (K=4). Every vertical fragmented line represents an individual. It is divided in K colours, according to its probability of belonging to that cluster.

CONCLUSIONS

- Genetic diversity in Cuban donkey population was similar to other American, but lower than the European and the Chinese one.

- Occidental and central populations tended to a higher genetic diversity.

- Population genetic structure was demonstrated in Cuba, which mostly followed geographic pattern.

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