Genetic Characterization of Mona Island Feral Goats and Pigs using Microsatellite Markers

Introduction

Feral goats (*Capra hircus*) and pigs (*Sus scrofa*) were introduced more than four centuries ago by Spanish settlers to Mona Island. They were set loose to reproduce and provide a source of fresh meat for travelers to Mona and other the Caribbean islands. Pigs and goats can be found in a wide range of habitats ranging from wet to dry ecosystems. Both species can also survive in harsh environments due to various physiological an behavioral adaptations. Because of their ability to adapt to different environments (Moran-Fehr et al., 2004) the goat, as well as the pigs are expected to show genetic responses to the range of environmental conditions they experience (Galal 2005).

The use of microsatellite markers is one of the most powerful means to study genetic diversity and differentiation among populations.

Microsatellite markers are highly polymorphic, randomly distributed throughout the genome and neutral with respect to selection (Agha et al., 2008). The characterization and of the genetic diversity of animals from Mona Island and other islands in the Caribbean will give us a better understanding on the ecological and evolutionary processes affecting the long term survival of the regionally adapted land races. The genetic characterization also provides us with data that can be used for more efficient management.

Objectives

Specific Questions:

1) What are the patterns of neutral genetic diversity in feral Mona goats and pigs, and how do these compare with other feral populations in the Caribbean, Europe and Africa?

2) Do feral goats and pigs of Mona Island represent unique landraces that may be useful for stock improvement of agricultural breeds?

3) What is the evolutionary and demographic history of the feral Mona goats and pigs of Mona Island?

Materials and Methods

Sample Collection

- 50 goat and 20 pig samples have been collected during hunting season in Mona (Figure 1).
- Samples consist of tissues collected during DNR sponsored culls and from fecal samples.
- Whole genomic DNA has been extracted using QiagenDNA easy kits for all pigs and goats samples.

Microsatellite primers

- A standardized set of 50 pig and 30 goat microsatellite markers proposed by the European-funded EconoGene project (Russell et al. 2003, SanCristóbal et al. 2006) are being used.
- The amplified loci are being genotyped on the ABI 3130 and analyzed in GeneMapper Software Version 4 (Figure 2).

Preliminary Results

- 30 goat microsatellite primers have been tested. 23 primers have successfully amplified and an additional 7 are currently being optimized.
- 9 out of the 23 successfully amplified goat loci showed no variation, in a samples of 20 individuals tested (Table 1 **).
- 14 out of the 23 successfully amplified goat loci are polymorphic with 7 of these having 3 or more alleles per locus.
- The entire sample of Mona Island goats is currently being characterized.
- Pig loci amplifications are in progress.

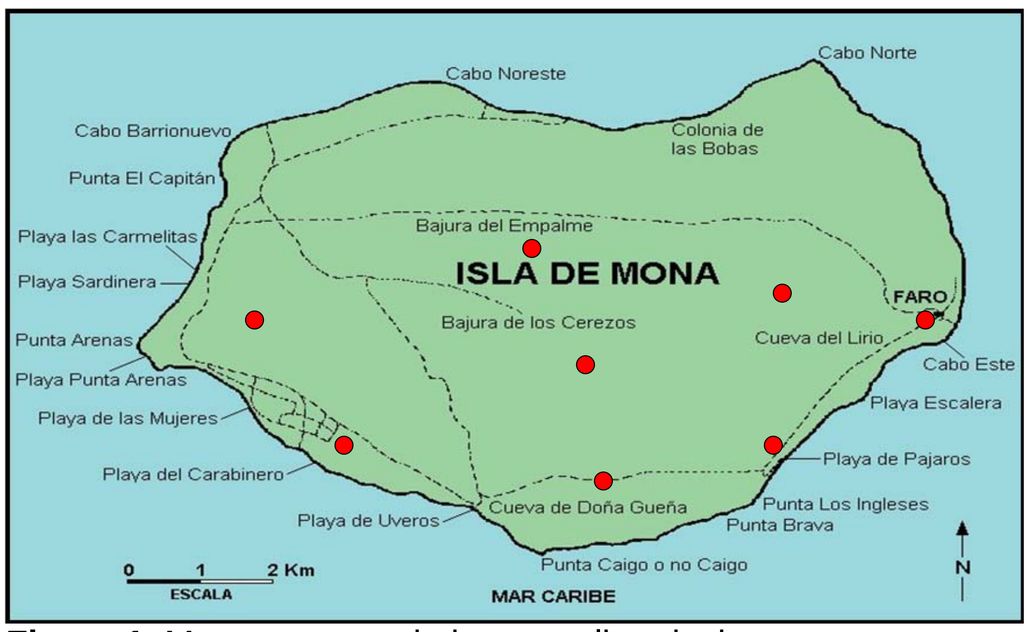

Figure 1. Mona goats and pigs sampling design.

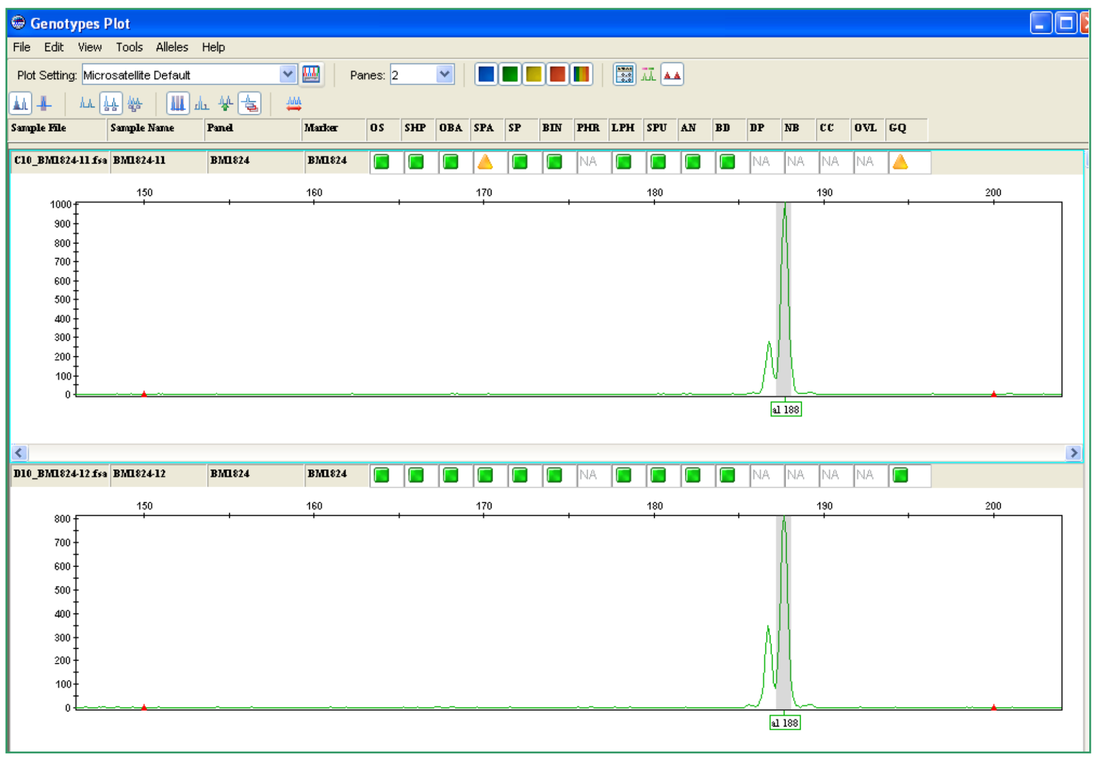

Figure 2. Analysis for the microsatellite locus BM1824 using GeneMapper Software Version 4. An example of two homozygous individuals.

Table 1. Genetic variability in the Mona goat (*Capra hircus*)

Locus	Num. of alleles
BM1818**	1
BM1824**	1
CSRM60	5
CSSM663	4
ETH104	4
ETH152	5
ETH185	3
ETH225**	2
HAUT24**	1
HAUT27**	2
HEL1**	2
ILSTS005**	1
ILSTS006**	2
ILSTS0113**	2
ILSTS030**	1
ILSTS0332**	2
ILSTS0344**	2
ILSTS0541**	1
INRA0052	3
INRA023**	1
INRA035**	1
INRA063**	1
MM12	4

Literature Cited

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