

## Genetic Diversity and Variation of ESR, RBP4 and FUT1 Genes in Mexican Creole and Yorkshire Pig Populations

<sup>1</sup>C. Lemus-Flores, <sup>1</sup>K. Mejía-Martínez, <sup>1</sup>J.G. Rodríguez-Carpina,

<sup>2</sup>A. Barreras-Serrano, <sup>1</sup>J.G. Herrera-Haro and <sup>1</sup>R. Alonso-Morales

<sup>1</sup>Postgraduate of Biological and Veterinarian Sciences, Autonomous University of Nayarit, City of Culture Amado Nervo, Tepic, Nayarit, CP 63190, México

<sup>2</sup>Instituto de Ciencias Veterinarias, Autonomous University of Baja California,

<sup>3</sup>Programa de Ganadería, Colegio de Posgraduados,

<sup>4</sup>Laboratory of Molecular Genetics, Faculty of Veterinary Medicine, National Autonomous University of Mexico D.F., México

**Abstract:** The ESR, RBP4 and FUT1 candidate genes were studied in 103 pigs from the commercial breed Yorkshire and Mexican Creole. Pelón and Cuino animals, for establishing genic and genotypic differences, unbiased diversity and genetic distances by employing standard distances and phylogenetic tree build up by the Neighbor-joining technique. Polymorphism was determined by PCR-RFLP methods using established procedures from other investigations. For ESR gene there were no homozygote BB animals in Pelón and Cuino; the allele B and A were more frequent in Yorkshire (0.38) and Cuino (0.84). Genetic distance was greater in Yorkshire and Cuino as compared to Pelón, with greatest heterozygosity for Yorkshire (3.47%) followed by Pelón (0.390) and Cuino (0.275). The BB genotype for RBP4 gene was not detected in any breed examined; there was no dependence of genic and genotypic frequencies in any breed. Allele A frequency was similar in Yorkshire, Pelón and Cuino pigs (0.74, 0.74 and 0.75), in similitude of frequency of AA and AB genotypes in all breeds. Genetic distances and heterozygosity were similar in the three breeds (Yorkshire, 0.390; Pelón, 0.390 and Cuino, 0.382). For FUT1 gene a major frequency of allele G and genotype GG was found in Yorkshire (0.60 and 0.45) and Pelón (0.64 and 0.39) animals. The allele A was more frequent in Cuino pigs (0.55). There was a greater genetic distance between Yorkshire and Cuino animals. Cuino pigs showing a greater heterozygosity (0.503) as compared to Pelón (0.465) and Yorkshire (0.448) which in turn were no different between them.

**Key words:** Mexican creole pigs, genetic biodiversity, candidate genes

### INTRODUCTION

Pig meat is the major protein source for human beings; this assumption is directly derived from World production (FAO, 2000). In this context, it is worth to mention that only a small number of pig breeds have been selected in an intensive manner as breeds of high commercial exploitation, with efficient levels of meat production. This factor has been decisive in the decrease of local breeds, which have been replaced by others through programs of assisted selection (Ramos *et al.*, 2003). According to a FAO (2007) report, during the last seven years a breed of domestic livestock has made extinct every month (<http://www.fao.org>). Besides, among pig breeds of high yield which are more utilized (Large White, Duroc and Landrace), genetic

diversity has been menaced by the use of reduced number of boars for improvement purposes.

Disappearance of creole breeds would be a non replaceable lost of the unique genetic heritability. This is the reason why of the importance of preservation of these local genotypes is essential, since they warrant the genetic variability contained in these breeds for future generations. In Mexico, in recent time an important impulse has been done for the study of animal genetic resources, since it has been understood the relevance of these generic variants which are so abundant, but at the same time so poorly characterized and even more when creole or local populations are concerned (Ramos *et al.*, 2003; Sierra *et al.*, 2005; Canal *et al.*, 2005). The Mexican creole pig, which has been reported by FAO as an animal in danger of extinction (FAO, 2000), is a poorly evaluated

**Corresponding Author:** Clemmie Lemus Flores, Postgraduate of Biological and Veterinarian Sciences,

Autonomous University of Nayarit, City of Culture Amado Nervo, Tepic, Nayarit, CP 63190, México  
878