

Phylogenetic relationships of Yucatan hairless pig with Asian and European breeds by mitochondrial DNA D-loop

Relaciones filogenéticas del cerdo pelón de Yucatán con razas asiáticas y europeas mediante el ADN mitocondrial

Relações filogenéticas do porco sem pelo de Yucatán com raças asiáticas e europeias através do DNA mitocondrial


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Abstract

In Mexico native pig genotypes exist whose populations face serious threats to survival. One of them is the Yucatan hairless pig (YUCMEX), for which limited information is available regarding its current conservation status. This study aimed to determine the phylogenetic relationship of YUCMEX with Iberian, wild pigs (WB), European, Asian, and commercial pigs using the mtDNA D-loop region. A total of 31 YUCMEX sequences and 77 mitochondrial haplotypes from GenBank were analyzed, aligned to reference sequence AJ002189. The study fragment, trimmed between positions 15435 and 15977, resulted in 543 base pairs. Genetic distances were calculated to compare YUCMEX with the other pig groups. Phylogenetic trees were constructed using the Neighbor-Joining method with Kimura's two-parameter distance and 1000 bootstrap replicates. Additionally, a principal component analysis (PCA) was performed based on evolutionary distances. Among the 108 sequences analyzed, 41 variable sites and 44 haplotypes were identified. YUCMEX individuals grouped into four haplogroups (HA, HB, HC, HD), showing lower D-loop diversity and genetic distance from the Duroc breed. European and Asian haplotypes formed seven phylogenetic groups, clearly separating both regions. The YUCMEX haplogroups clustered into three lineages close to WB from Portugal and Spain but were distinct from Asian pigs and Eastern European WB haplotypes. These findings confirm the European—specifically Iberian—origin of the Yucatan hairless pig.

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Resumen

En México existen genotipos de cerdos nativos cuyas poblaciones enfrentan serias amenazas para su supervivencia. Uno de ellos es el cerdo pelón de Yucatán (YUCMEX), para el cual se dispone de información limitada sobre su estado de conservación actual. Este estudio tuvo como objetivo determinar la relación filogenética de YUCMEX con cerdos ibéricos, jabalíes (WB), europeos, asiáticos y comerciales utilizando la región D-loop del ADNmt. Se analizaron un total de 31 secuencias de YUCMEX y 77 haplotipos mitocondriales de GenBank, alineados a la secuencia de referencia AJ002189. El fragmento de estudio, recortado entre las posiciones 15435 y 15977, resultó en 543 pares de bases. Se calcularon distancias genéticas para comparar YUCMEX con los otros grupos de cerdos. Los árboles filogenéticos se construyeron utilizando el método Neighbor-Joining con la distancia de dos parámetros de Kimura y 1000 réplicas bootstrap. Además, se realizó un análisis de componentes principales (ACP) basado en distancias evolutivas. Entre las 108 secuencias analizadas, se identificaron 41 sitios variables y 44 haplotipos. Los individuos YUCMEX se agruparon en cuatro haplogrupos (HA, HB, HC, HD), mostrando menor diversidad de bucle D y distancia genética con respecto a la raza Duroc. Los haplotipos europeos y asiáticos formaron siete grupos filogenéticos, separando claramente ambas regiones. Los haplogrupos YUCMEX se agruparon en tres linajes cercanos al WB de Portugal y España, pero distintos de los haplotipos WB de los cerdos asiáticos y de Europa del Este. Estos hallazgos confirman el origen europeo, específicamente ibérico, del cerdo pelón de Yucatán.

Palabras clave: genética, PCR, razas locales, haplotipos, linaje.

Resumo

No México existem genótipos nativos de suínos cujas populações enfrentam sérias ameaças à sua sobrevivência. Um deles é o porco sem pelo de Yucatán (YUCMEX), para o qual há informações limitadas disponíveis sobre seu status de conservação atual. Este estudo teve como objetivo determinar a relação filogenética de YUCMEX com suínos ibéricos, javalis (WB), europeus, asiáticos e comerciais usando a região D-loop do mtDNA. Um total de 31 sequências de YUCMEX e 77 haplótipos mitocondriais do GenBank foram analisados, alinhados à sequência de referência AJ002189. O fragmento de estudo, aparado entre as posições 15435 e 15977, resultou em 543 pares de bases. As distâncias genéticas foram calculadas para comparar YUCMEX com outros grupos de suínos. Árvores filogenéticas foram construídas usando o método Neighbor-Joining com a distância de dois parâmetros de Kimura e 1000 réplicas bootstrap. Além disso, uma análise de componentes principais (ACP) baseada em distâncias evolutivas foi realizada. Entre as 108 sequências analisadas, 41 sítios variáveis e 44 haplótipos foram identificados. Indivíduos YUCMEX agruparam-se em quatro haplótipos (HA, HB, HC, HD), mostrando menor diversidade de D-loop e distância genética em relação à raça Duroc. Haplótipos europeus e asiáticos formaram sete grupos filogenéticos, separando claramente ambas as regiões. Haplótipos YUCMEX agruparam-se em três linhagens próximas aos haplótipos WB de Portugal e Espanha, mas distintas dos haplótipos WB de suínos asiáticos e do Leste Europeu. Essas descobertas confirmam a origem europeia, especificamente ibérica, do porco sem pelo de Yucatán.

Palavras-chave: genética, PCR, raças locais, haplótipos, linhagem.

Introduction

There is wide evidence, using molecular studies, that the wild pigs (*Sus scrofa*) distributed throughout Europe and Asia separated phylogeographically, indicating that Central Europe was a center of its early domestication (Giuffra *et al.*, 2000; van Asch *et al.*, 2012). The Iberian haplotypes are close to the European (other than Iberian pigs), but there is a second European group between Asians and Iberians from the region of Italy, considering that the divergence between Europeans and Asians has 600,000 years (Alves *et al.*, 2003). Similar studies with mitochondrial DNA analysis in wild boars introduced in the Ural region, indicate that the contribution of lineages originating in Eastern Europe was greater than expected than the proportions of European and Asian animals (Markov *et al.*, 2022). In native pigs, their ancestral origin is presumed and hybridization is assumed, so knowledge of their phylogeneia is necessary to know their identity. The study by Banayo *et al.* (2023) showed that the Philippine native pigs have originated from at least three *Sus scrofa* lineage and that they were not domesticated from the endemic wild pigs of the Philippines, indicating that the Philippine native pigs had other genetic origins; further analysis revealed its multiple ancestral origins, from East and Southeast Asia. The Iberian pigs exported during the colonization of America were ancestors of several breeds, which contributed to the origin of the Duroc in the United States and the hairless pig in Mexico (Jones, 1998; Burgos-Paz *et al.*, 2013; Lemus-Flores *et al.*, 2023). According to Alves *et al.* (2003), the characterization of genetic resources is needed to make clear their relationship and origin with other pig populations. It is documented that the hairless pig arrived in America on the second voyage of Christopher Columbus (Ogata, 2019). The entry of the Iberian pig into Mexico was along the Atlantic coast, reaching the Yucatan Peninsula (Ortega *et al.*, 2019), where it has remained under rural breeding and management, and local people have developed a gastronomy based on this pig (Hernández *et al.*, 2020; Ramos-Canché *et al.*, 2020). Other populations have been derived from the hairless pig populations, such as the one developed in Colorado, United States, patented as Yucatan minipig (Burgos-Paz *et al.*, 2013). There is no information on the flow of hairless pigs to the Yucatan Peninsula; however, the local culture, family exploitation system, and demography have allowed the conservation of the hairless pig (Hernández *et al.*, 2020; Ramos-Canché *et al.*, 2020). It is known that its phenotype and genetics are similar to Iberian hairless pigs (Lemus-Flores *et al.*, 2023), and that it shows a wide genetic diversity (Lemus-Flores *et al.*, 2020). For the conservation of the hairless pig in Yucatan, it is necessary to know its origin and genetic place concerning its ancestors. The objective of this study was to determine the phylogenetic relationship of the Yucatan hairless pig with the Iberian, wild European, Asian, and commercial pigs. The information here generated will be useful for the conservation programs carried out in Mexico, and for the identification of pigs that will be used for breeding. Another benefit is to give added value to their genetic identity in the promotion of their products in demand within the tourist gastronomy in the Yucatan Peninsula.

Materials and methods

Sample collection and isolation of mitochondrial DNA (mtDNA)

This project was registered at the Autonomous University of Nayarit-México, under number SIP18-076. Following animal management protocols NOM-051-ZOO-1995 (Secretary of

Agriculture, Livestock and Rural Development, 1998) and NOM-062-ZOO-1999 (Secretary of Agriculture, Livestock, Rural Development, Fisheries and Food, 2001), blood samples were collected from the jugular vein in Vacutainer EDTA K2 tubes (Becton Dickinson, Franklin Lakes, NJ, USA), from 31 unrelated hairless females from a group of hairless pig from different farms in Yucatan Mexico (YUCMEX). Total DNA was purified following the protocol established by Miller *et al.* (1989) in the Molecular Biotechnology laboratories of the Faculty of Veterinary Medicine at the National Autonomous University of Mexico.

PCR amplification and sequencing of mitochondrial DNA (mtDNA)

Considering the methodology used by van Asch *et al.* (2012), a 662 bp mtDNA fragment from the D-loop region was amplified. The whole D-loop was amplified using a package of PCR reagents, adding the amounts recommended by the manufacturer (Biogenica, S.A. of C.V), and under the following conditions: 1 cycle at 94 °C (5 min); 30 cycles at 94 °C (1 min), 56 °C (30 sec) and 72 °C (1 min); and a final cycle of 72 °C (5 min). mtDNA fragment was amplified by PCR using the primers SCMtF-CTAACTCCGCCATCAGCAC y SCMtR-CTGTGTTAGGGCCTTTGACG. Then, the amplified fragments were purified by the sodium iodide (NAI) plus silica pearls method and used in sequence reactions carried out with the commercial sequence kit ABIPRISM BigDye Terminator Cycle Sequencing v3.1 (Applied Biosystems Division, Perkin-Elmer, Foster City, CA, USA). The manufacturer's protocol was followed under the following conditions: 25 cycles at 96 °C (10 sec), 50 °C (5 sec), 60 °C (4 min). Then, the samples were filtered in columns of Sephadex G50 (SIGMA, St. Louis, MO, USA), and reading was performed with an automatic ABI prism 310 DNA Genetic Analyzer, (Applied Biosystems Division, Perkin-Elmer, Foster City, CA, USA). Two readings were obtained for all samples: one for each chain. The consensus sequences from both readings were obtained with the CHROMAS v.1.62 software (Technelyuim Pty. Ltd., Queensland, Australia). The amplified fragment was aligned to the GenBank AJ002189 sequence as a reference, trimming the studied fragment from position 15435 to 15977 with 543 bp (Alves *et al.*, 2003).

Mitochondrial DNA analysis

To identify the haplotypes, present in the 31 YUCMEX pigs sequences, 77 mitochondrial haplotype sequences (Alves *et al.* 2003; Alves *et al.*, 2010; van Asch *et al.*, 2012; Wu *et al.*, 2007), representative of European, Asian and commercial populations were used. The amplified fragments of YUCMEX pigs were aligned to the GenBank AJ002189 sequence as a reference, trimming the study fragment from position 15435 to 15977 with 543 bp (Alves *et al.*, 2003) using the MUSCLE tool in the MEGA software version 11 (Tamura *et al.*, 2021).

Phylogenetic analyses

Using haplotypes from the different pig populations, genetic distance analyses were carried out, comparing YUCMEX pigs with

commercial, European and Asian pigs. Phylogenetic trees were constructed with neighbor-joining (Saitou and Nei, 1987) incorporated in the MEGA 11 software (Tamura *et al.*, 2021). The differences in the composition bias among sequences were considered in evolutionary comparisons (Tamura and Kumar, 2002). All positions containing gaps and missing data were eliminated. Standard errors were computed with the bootstrap method using 1000 replicates (Tamura *et al.*, 2021). With the evolutionary distances, principal component analysis (PCA) was carried out with the Darwin program (Perrier *et al.*, 2003) and graphed with Minitab (2021).

Results and discussion

The analysis of 108 sequences identified 41 change sites grouped into 44 haplotypes (table 1). It should be noted that a greater number of haplotypes than change sites suggests high genetic diversity (Niedziałkowska *et al.*, 2021).

In the mitochondrial study within the YUCMEX population, four subsets (Haplotypes) were observed. The greatest amount corresponded to the HB and HD haplotypes (table 2) suggesting that the maternal line of descent associated with the HB haplotype is the most common haplotype in the YUCMEX population.

Table 2. Haplotypes identified in YUCMEX pigs according to the variable position of the mtDNA D-loop.

Haplotypes	15544	15558	15615	15714	15758	15878	n
HA	A	A	T	C	C	G	1
HB	G	A	T	C	C	G	22
HC	G	A	T	C	T	A	2
HD	G	T	C	C	C	A	6

n: Sample size, **HA**: haplogroup A, **HB**: haplogroup B, **HC**: haplogroup C, **HD**: haplogroup D.

Mitochondrial study between Yucatan hairless pigs and commercial breeds

When the mitochondrial sequences of YUCMEX pigs with commercial populations were analyzed to measure the average distances in each population, it was observed that the genetic distance of the YUCMEX population concerning the Duroc (0.06 ± 0.03) and Landraces (0.03 ± 0.02) breeds was the smallest. These small distances indicate lower diversity according to the haplotypes used in each population and also suggests that they are genetically more similar to these breeds than to other populations. It appears that the YUCMEX population and the Duroc and Landrace breeds have either a shared genetic origin or a closely related recent evolutionary history.

With other populations was higher: Hampshire 0.48 ± 0.25 , Pietrain 0.44 ± 0.19 , Large White 0.21 ± 0.09 and among YUCMEX 0.03 ± 0.02 .

The short genetic distance in the YUCMEX pig reflects the conservation of the hairless variant in that region of the Yucatán

Table 1. Change sites according to the variable position of the DNAmT D-loop, AJ002189 sequence as a reference.

1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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Peninsula, supported by local breeding programs (Hernández *et al.*, 2020), without using crossbreeding with commercial pigs (Lemus-Flores *et al.*, 2020).

In the grouping with commercial pigs, a greater closeness of the YUCMEX pigs to the Duroc breed is identified in the four haplotypes (figure 1). The close relationship to the Duroc breed in all four haplotypes indicates that the maternal lines of descent of YUCMEX pigs are genetically very similar to those of the Duroc breed. This reinforces the idea of a common origin or significant crossbreeding between the two populations. Likewise, it is seen through the principal component analyses (figure 2) that the YUCMEX haplotypes are grouped closely meaning that the pigs are genetically very similar to each other in their maternal ancestry, and corroborates a lower diversity in the D-loop mtDNA, but close to the Duroc population revealing evidence of genetic conservation rather than genetic erosion.



Figure 1. Haplotypes groups in the DLoop del DNAm region.

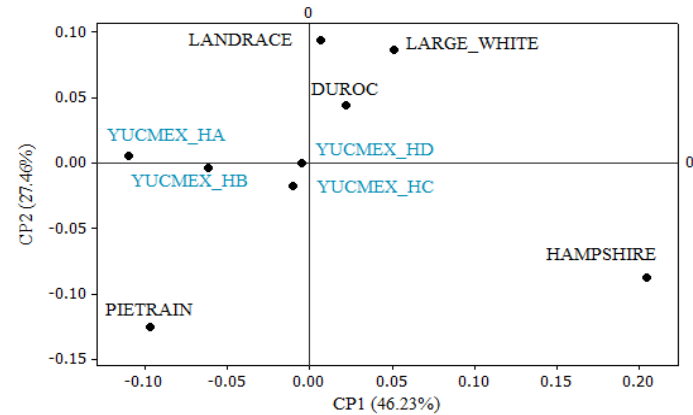


Figure 2. Principal component analysis of commercial pig populations and YUCMEX haplotypes.

The phylogenetic and principal component analysis reveals a smaller distance with commercial pigs of the Duroc breed, because they have a similar ancestral origin with Iberian pigs (Jones, 1998) since there is no evidence of interbreeding of hairless pigs with this commercial breed in Yucatan. The loss of diversity in local

or locally adapted pigs, such as YUCMEX, is more common than in commercial pigs, as pointed out by Zhang *et al.* (2016). In this work, introgression of commercial breeds cannot be attributed, to the distance observed because the phenotypic appearance of YUCMEX pigs is distant from the white and spotted colors, retaining the black and hairless color (Lemus-Flores *et al.*, 2023). However, evidence of interspecific hybridization is common in local pigs, such as that found in Philippine pigs (Banayo *et al.*, 2023).

Mitochondrial study among hairless pigs from Yucatan and European and Asian racial groups.

The grouping of the haplotypes of European and Asian populations identified seven groups in the phylogenetic analysis (table 3).

Table 3. Average distance within the populations of pigs.

Group	Population	Distance	Standard Error
A	Asian	0.1525	0.0489
B	French WB, Italian WB	0.2744	0.0896
C	Portuguese WB	0.1154	0.0582
D	Spanish WB, Iberian with hair, Bisaro, Malhado	0.0499	0.0214
E	Spanish WB, Portuguese WB, Hairless Iberian	0.0227	0.0103
F	Red Iberian, French WB, Italian WB, Portuguese WB	0.0075	0.0077
G	Mangalica, Croatian WB, Austrian WB	0.0488	0.0272
YUCMEX	México	0.0300	0.0200

The greatest distance within each group is identified in groups B (French WB Italian WB), A (Asians) and C (Portuguese WB); and the smallest distance in the YUCMEX and Iberian haplotypes indicates strong genetic homogeneity and close kinship confirming the historical theory that American Creole pigs, like the Yucatán pig, descend from pigs that arrived from the Iberian Peninsula during colonization.

In the phylogenetic analysis and principal component analysis (figure 3), the YUCMEX HA and HB haplotypes are located close to group C (Portuguese WB), the HC haplotype with D (WB from Spain, Iberian with hair, Bisaro, Malhado) and E (Spanish WB, Portuguese WB, Iberian hairless), the HD haplotype near group F (Iberian red, French WB, Italian WB, and Portuguese). Groups A, B and G (Mangalica, WB from Croatia, Austrian WB) are more distant from the YUCMEX haplotypes.

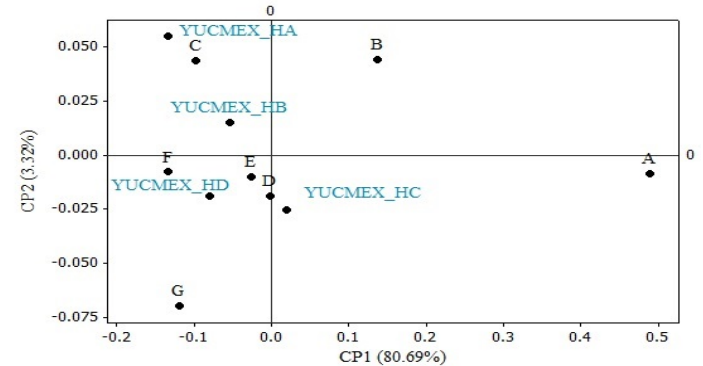


Figure 3. Principle component analysis (PCA) of haplotypes of European, Asian wild and YUCMEX pigs.

A separation is observed between Asian (A) and European groups, where group B (French and Italian WB) was closer to the Asian pigs. The four YUCMEX haplotypes (HA, HB, HC and HD) clustered within clusters from Portugal and Spain pigs, indicating a European origin.

The presence of only four haplogroups in YUCMEX pigs suggest little genetic variability, compared to that of Iberian pigs, in which 14 haplogroups were identified (Alves *et al.*, 2003), six to 11 haplotypes in Indian pigs (Laxmivandana *et al.*, 2022). Asian groups retain a distinct lineage from Europeans, which has been mentioned in several papers using mtDNA D-loop analysis (Giuffra *et al.*, 2000; van Asch *et al.*, 2012; Alves *et al.*, 2010) and with SNP analysis (Ramírez *et al.*, 2015). Ishihara *et al.* (2023) detected 50 haplotypes from Vietnamese native pigs, with 27 novel haplotypes and no European haplotypes found.

Concerning YUCMEX pigs the four haplogroups were grouped into three lineages, within the Portuguese WB and Iberian pigs, away from the Asian pigs, and groups formed by haplotypes from Eastern Europe with French WB, Italian WB, Mangalica, WB from Croatia, and Austrian WB; confirming their European origin from the Iberian Peninsula from where they were originally left for America. Alves *et al.* (2010) suggest that the Iberian Peninsula was a refuge for the pig (*Sus scrofa*) during the ice age and that there is no evidence of Asian mtDNA introgression. Analysis by Vergara *et al.* (2021) indicates that Ecuadorian Creole pigs probably diverged from the Asian pig population and that, like the YUCMEX pigs, they appear to be genetically influenced by European and Iberian populations raised in Spain.

In the Yucatan hairless pig, little diversity was quantified with four haplotypes that distance them from white commercial pigs (Landrace and Large White) and spotted pigs (Pietrain), but close to Duroc. There was a greater phylogenetic relationship of the Yucatan hairless pig with Iberian and European wild pigs from the Iberian Peninsula, far from Asian and wild pigs from Eastern Europe. Like the Iberian pigs, the hairless pigs of Yucatan are distanced from the Asian pigs.

Conclusions

Four YUCMEX haplogroups were grouped into three lineages close to the WB from Portugal and Spain, distant from the Asian pigs and the groups formed by WB haplotypes from Eastern Europe. The European origin, from the Iberian Peninsula of the YUCMEX pig is confirmed.

This information could contribute to a better understanding of the origin of the Yucatan hairless pig and to assess its conservation. Further exploration is needed through complete mitochondrial DNA sequencing and analysis.

Acknowledgments

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