FULL ARTICLE

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Genetic relationships of the Yucatan black hairless pig with Iberian breeds using single nucleotide polymorfisms

Relações genéticas de porcos pretos calvos de Yucatán com raças ibéricas usando Polimorfismo de nucleotídeos isolados

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ABSTRACT

To conduct *ex-situ* creole pig conservation programs, it is essential to determine which breeding animals will be used, preferentially those with a more significant Iberian genetic component to preserve their origin. This study used a Yucatan black hairless pigs (YBHP) subpopulation to estimate its genetic diversity and population structure. One hundred four adult pigs were selected for the absence of hair, black skin (without spots), black hoof, and straight snout. The porcine-GGP-50K chip was used for SNP genotyping in YBHP, and information on Iberian and Yucatán hairless pigs from the United States (USYU) was taken from databases. All analysis was performed using PLINK v1.9 and v2.1 software. Inbreeding and fixation index values were lower in YBHP, with high observed heterozygosity and allogamy index values, which agree with those obtained in the populations of Canarias and Chato Murciano. According to the clusters generated by the "Genome-Wide Identity by State" analysis, four groups were identified, one of which included pigs from Guadyerbas, USYU, and YBHP. Between populations, YBHP was closely related to the hairless pigs from Guadyerbas, USYU, and Canarias. Principal component analysis showed the same result. According to the results obtained from the runs of homozygosity investigation, aimed to get pools consensus of regions of overlapping, 119 SNPs associated with genes and biological processes were identified. The *BMP7* and *NSUN2* genes were associated with epithelial cell differentiation, morphogenesis, and epithelial development. For nutrient metabolism: energy, the *HADHA, PPARA, ADD1/SREBF1,* and *FAT1*genes were identified.

Keywords: Genetic diversity. Yucatan black hairless pig. Inbreeding. Single nucleotide polymorphism.

RESUMO

Para realizar programas de conservação *ex-situ* de suínos crioulos, é importante determinar quais animais serão criados, preferencialmente aqueles com maior componente de genética ibérica, para preservar sua origem. Uma subpopulação de porco preto calvo de Yucatán (YBHP) foi usada para estimar sua diversidade genética e estrutura populacional. Um total de 104 suínos adultos foram selecionados levando-se em consideração características como ausência de pelos, pele preta (sem manchas), casco preto e focinho reto. O painel GGP-50K foi utilizado para a genotipagem dos SNPs em animais YBHP, e informações de porcos sem pelos ibéricos e de Yucatán dos Estados Unidos (USYU) foram retiradas de bancos de dados. Todas as análises foram realizadas com o software PLINK v1.9 e v2.1. Os valores dos índices de endogamia e fixação foram menores em YBHP, com altos valores de índice de heterozigosidade e alogamia observados, que concordam com os obtidos nas populações de Canárias e Chato Murciano. De acordo com os clusters gerados pela análise "Genoma-Wide Identity By State", quatro grupos foram identificados, um dos quais incluiu porcos de Guadyerbas, USYU e YBHP. Entre as populações, YBHP estava intimamente relacionado com os porcos sem pelo de Guadyerbas, USYU e Canárias. A análise de componentes principais mostrou o mesmo resultado. De acordo com os resultados obtidos nas corridas de investigação de homozigose, visando obter consenso de pools de regiões de sobreposição, foram identificados 119 SNPs associados a genes e processos biológicos. Os genes BMP7 e NSUN2 foram associados à diferenciação de células epiteliais, morfogênese e desenvolvimento epitelial. Para metabolismo de nutrientes: energia, os genes HADHA, PPARA, ADD1/SREBF1 e FAT1 foram identificados.

Palavras-chave: Diversidade genética. Porco preto calvo mexicano. Consanguinidade. Polimorfismo de nucleotídeo único.

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Introduction

Iberian hairless pigs (IHP) were introduced to Latin America in the second Christopher Columbus voyage (1493). Since then, descendants of those IHP have been the source of protein and fat for the rural population of Latin America. Currently, Creole pigs are recognized in Mexico's rural tropical production systems (Ángel-Hernández et al., 2020; Ramos-Canché et al., 2020). The FAO (Food and Agriculture Organization, 2019) acknowledges that hairless pigs are in danger of extinction. Studies in Mexico show that they are genetically distant from commercial pig populations (Lemus-Flores et al., 2001, 2020). In addition, Latin-American hairless pigs and Iberian pigs are expected to maintain a close genetic relationship. Burgos-Paz et al. (2013) noted a genetic contribution of IHP from the Gulf and Pacific of Mexico of 0.49 and 0.99 in Yucatan hairless pigs from the United States (USYU). Burgos-Paz et al. (2013) suggest that the USYU population originated from pigs of Yucatan that have remained uncrossed, while the pigs from the Gulf and the Pacific of Mexico have been crossed to some degree with commercial breeds. Those authors also argue that the Duroc breed is the primary source of introgression in Mexican creole pigs. However, Lemus-Flores et al. (2020), exploring the amount of genetic diversity in a subpopulation of the Yucatan black hairless pig (YBHP), found it distant from Duroc. Still, this population, derived from the Mexican hairless pig (MHP), was not homogeneous and had subpopulations. To speak of YBHP pure breed is difficult because they show different phenotypic characteristics depending on the crossing system; nevertheless, YBHP retains a phenotypic like the Iberian hairless pig (Ángel-Hernández et al., 2018). Furthermore, according to an *ex-situ* conservation program initiated in 2005 in Yucatan (Sierra et al., 2005) and to current reports (Lemus-Flores et al., 2020), the hairless creole pigs of Yucatan are kept in rural communities, where they have gastronomic and economic importance. Consequently, to continue with that *ex-situ* conservation program, it is essential to determine which YBHP is genetically closer to the Iberian ones. A subpopulation of YBHP, classified phenotypically, was genotyped to study its genetic diversity, population structure, and genetic relationship with Iberian and USYU breeds using SNPs.

Materials and Methods

Animals and genotype analysis

A subpopulation of YBHP of the Central and Eastern regions of Yucatan-Mexico, consisting of 104 breeding adults of two to three years of age, localized in 49 farms, were evaluated (17 boars and 87 sows). Pigs were selected based on the absence of hair, black skin (without spots), black hoof, and straight snout. Information on the origin of the sows or boars was obtained to reduce kinship. Pigs of Iberian origin from the databases of Burgos-Paz et al. (2013) and Yang et al. (2017); Chato Murciano (ChM, n= 20), Manchado de Jabugo (MJ, n=7), hairless Canarias (CA, n=4), hairless La Serena (LS, n=20), hairless Guadyerbas (GUA, n =14) and Yucatán hairless pigs from the United States (USYU, n=10) were also evaluated. Blood samples from YBHP were obtained following the recommendations of the Official Mexican Standards NOM-051-ZOO-1995 (Secretaría de Agricultura, Ganadería y Desarrollo Rural , 1998) and NOM-062-ZOO-1999 (Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación, 2001) on the humane treatment of animals. The extraction and genotyping of genomic DNA from the blood were performed at NEOGEN (www.neogen.com). The porcine-GGP-50K (GeneSeek Genomic Profiler Porcine), which identifies a total of 50,967 SNPs, was used For SNP genotyping.

Quality control of SNPs

PLINK v1.9 (Purcell et al., 2007) was used for SNP data quality control. Excluded were SNPs with missing genotypes > 0.10 and with MAF (minor allele frequency) and < 0.0 (--missing --geno 0.10 --maf 0.01 –mind 0.1). We retained 29,589 SNPs and 179 pigs for further analysis of genetic diversity and population structure.

Statistical analysis

Genetic Diversity

For each population, the observed heterozygosity (Ho), consanguinity (F), and the fixation index of individual pigs

within the subpopulations (Fis) were calculated with the PLINK v1.9 program (Purcell et al., 2007) (--het). The t (crossing rate or allogamy rate) was estimated according to Weir & Cockerham (1984). A one-way analysis of variance was used to compare the populations of YBHP, Iberian, and USYU pigs (Minitab, 2007).

Population structure analysis

Cluster, Similarity, Distances, and Principal Component Analyses (PCA) were conducted with the PLINK v2.1 software (Chang et al., 2015). (--assoc –adjust; --cluster--K 4; --pca approx). A plot with three eigenvectors of the PCA, generated based on genome-wide identity-by-state pairwise distances, was built using Minitab v15 (Minitab, 2007) to visualize the genetic and PCA distances among the YBHP, Iberian, and USYU pigs studied.

Candidate SNP regions

To obtain pools consensus regions of overlapping and potentially matching segments with 0.95 thresholds; runs of homozygosity with length (kb) 1000, SNPs (N) 50, density (kb/SNP) 50, and most significant gap (kb) 1000 (--homocyg-verbose --homocyg-kb 1000 – homocyg-window-snp 50 – homocyg-gap 1000 --homocyg- threshold 0.05 –homocyg-group) were generated using PLINK v1.9 (Purcell et al., 2007) for YBHP, Guadyerbas, Canarias, La Serena, and USYU pigs. Genetic annotations within the candidate regions were obtained using the preliminary genome assembly Sscrofa11.2 annotation provided by e-Ensembl (Groenen et al., 2012). The association of the SNPs identified with biological processes of the Gene Ontology (GO) categories was determined with the Gene Ontology database (Ashburner et al., 2000).

Results

Genetic diversity with SNP

F and Fis values were lower in YBHP, with high Ho and t values, which agree with those obtained in Canarias and Chato Murciano pigs. The populations of La Serena, Guadyerbas, and USYU showed higher F and Fis values, with low Ho and t values (Table 1; p<0.001).

Population structure

According to the pig clusters based on genome-wide IBS analysis, four groups were identified (Table 2). Pigs formed a group from Guadyerbas, USYU, and YBHP.

Within each population, YBHP were the least unrelated (0.73; Table 3), but between populations, YBHP is more like hairless pigs in Guadyerbas, USYU, and Canarias. Figure 1 shows a similar genetic relationship between pigs. The principal component analysis (PCA) was used in the multidimensional scaling analysis of the populations based on genome-wide identity-by-state pairwise distances.

SNP candidate regions

The homozygosity analysis between YBHP with IHP (Guadyerbas, Canarias, La Serena) and USYU reported 221 SNPs, of which 119 SNPs were related to genes and biological processes (Tables 4, 5). In addition, we found 18 genes associated with epithelial cell differentiation, morphogenesis, and epithelial development. Of the 13 genes for nutrient metabolism: energy, eight (*HADHA, PPARA, ACSS3, SLC25A17, VAC14, GHRb*, *ADD1-SREBF1,* and *FAT1*) were associated with fat metabolism.

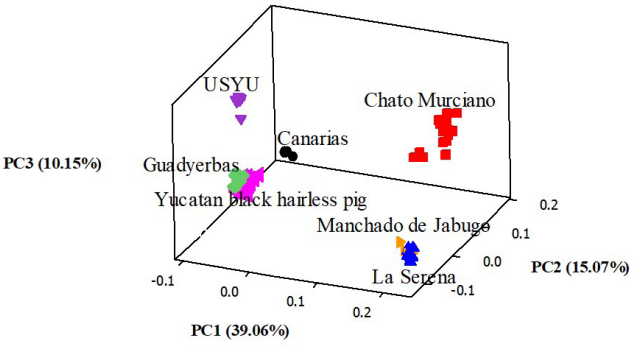

Figure 1 – Principal component analysis (PCA): Genetic structure of the porcine breeds.

Table 1 – Genetic diversity of the hairless black pig from Yucatan and Iberian breeds

	ChM	MJ	CA	LS	GUA	YBHP	USYU	SEM
N samples	20	7	4	20	14	104	10	
F	.114^{cd}	.147^{bc}	.069^{d}	**.207^{a}**	**.210^{a}**	.081^{d}	**.184^{ab}**	0.005
Ho	.294^{ab}	.268^{bc}	**.329^{a}**	.212^{d}	.209^{d}	**.319^{a}**	.235^{cd}	0.004
Fis	.218^{cd}	.289^{bc}	.124^{d}	**.437^{a}**	**.445^{a}**	.152^{d}	**.376^{ab}**	0.011
t	.652^{ab}	.558^{bc}	**.782^{a}**	.397^{d}	.388^{d}	**.749^{a}**	.456^{cd}	0.010

ChM= Chato Murciano; MJ= Manchado de Jabugo; CA= Canarias; LS= La Serena; GUA= Guadyerbas; YBHP= Yucatan black hairless pig; USYU= Yucatán hairless pigs from the United States; F: coefficient of inbreeding; Ho= Observed heterozygosity. Fis= subpopulation fixation index; t= Allogamy index; SEM= Standard error of the mean; Different letters by row indicate statistical differences between the subpopulations (Analysis of variance, p<0.001).

Table 2 – Groups of pig populations based on genome-wide identity-by-state (IBS) distance

Group	Population	N
1	Chato Murciano	20
2	La Serena	20
2	Manchado de Jabugo	7
3	Canarias	4
4	Guadyerbas	14
4	USYucatán	10
4	Yucatan black hairless pig	104

Discussion

Positive values of Fis indicate inbreeding values, which are low when it approaches zero. The genetic diversity in YBHP, Canarias, and Chato Murciano pigs was large. A population mates randomly when the value of t is close to 1; when t>1, it means an excess of heterozygotes, and when t=0, all pigs are homozygous (Weir & Cockerham, 1984). YBHP and Canarias populations, t were close to 1, lower than 1 for the

Table 3 – Similarities between pig populations based on genome-wide identity-by-state (IBS) distance

	ChM	MJ	CA	LS	GUA	YBHP	USYU
Chato Murciano	0.76	0.66	0.61	0.66	0.60	0.61	0.60
Manchado de Jabugo	0.66	0.81	0.61	0.74	0.62	0.61	0.61
Canarias	0.61	0.61	0.82	0.60	0.66	**0.66**	0.65
La Serena	0.66	0.74	0.60	0.79	0.64	0.61	0.60
Guadyerbas	0.60	0.62	0.66	0.64	0.79	**0.69**	0.70
Yucatan black hairless pig	0.61	0.61	0.66	0.61	0.69	0.73	0.68
USYU	0.60	0.61	0.65	0.60	0.70	**0.68**	0.84

ChM= Chato Murciano; MJ= Manchado de Jabugo; CA= Canarias; LS= La Serena; GUA= Guadyerbas; YBHP= Yucatan black hairless pig; USYU= Yucatán hairless pigs from the United States.

Table 4 – Number of SNPs identified on each chromosome (Chr) associated with biological processes

Chr	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	Total
nSNP	22	9	12	3	12	6	1	6	5	13	5	6	1	7	1	1	5	4	119

Table 5 – Biological processes, genes, and information from SNPs showed the greatest homozygosity pools consensus region between YBHP, IHP, and USYU pigs

Biological process	Chr	Variants	Identified genes
Cell and cellular processes	1	rs81353442, rs80957361, rs80932895, rs81313556, rs81349911, rs81348144	*L3MBTL3, RSPO3, NKAIN2, NKAIN2, RPS6KA2, SCAF8*
	2	rs81365713, rs81320209	*FSTL4, ABTB2*
		rs81255511	*JAKMIP2*
	3	rs81370451, rs81376315	*CUX1, OTOF*
		rs81225677, rs81374478	*SDK1, TMEM178A*
	5	rs81374478	*DIP2B*
	6	rs81353143, rs81299172	*PARD6G, PIK3C3*
	10	rs81302281, rs81422589	*WAC, ERCC6L2*
		rs81424783, rs81477625	*RSU1, ANKRD16*
	11	rs80874261, rs80834643	*ATP7B, GPC6*
	12	rs81437481, rs81432821	*MYH13, CALCOCO2*
Epithelial cell differentiation, morphogenesis and epithelial development	1	rs81351524, rs81351497	*SMOC2, SMOC2*
		rs81313812	*COL5A1*
	2	rs81363045, rs81339178	*MCC, VDAC1*
		rs81315377	*VDAC1*
	3	rs81238759	*LRATD1-FAM84A*
	4	rs81374478	*COL22A1*
	9	rs81267672	*SYTL2*
	10	rs81426164, rs81330805	*PARD3, FRMD4A*
		rs81425214, rs81288871	*FRMD4A, PTCH1*
		rs81244777, rs326112956	*PARD3, PTCH1*
	13	rs81298415	*COL8A1*
	14	rs80998591	*PDZD8*
	15	rs81478868	*CLASP1*
	16	rs81326497	*NSUN2*
	17	rs80786641	*BMP7*
	18	rs81288498	*HIPK2*
Inmunidad	17	rs81465715	*POLR3F*

Table 5 – Continued...

Biological process	Chr	Variants	Identified genes
Muscle, skeletal and embryonic development	3	rs81299746	*EIF2AK2*
	4	rs80883848	*DNAI3*
	5	rs346188763	*PLEKHA5*
	6	rs81353174, rs81320314	*ADNP2, GLG1*
	8	rs81294321	*DMP1*
	10	rs81318702	*KDM5B*
	11	rs80887667, rs80946169	*ARHGEF7, RXFP2*
	12	rs81432645	*SP6*
	14	rs80812359	*PDZD8*
Nervous system	1	rs81296777, rs81354275	*ADGRG6, ORC3*
	2	rs81346169	*SHANK2*
	5	rs81387482, rs80868031	*SYN3, LIN7A*
	9	rs322515279	*ADAM22*
	14	rs80824784, rs80896578	*GFRA1, GFRA1*
	17	rs328574890	*PCSK2*
Nutrient metabolism: energy	1	rs80847091	*HMGN3*
	3	rs81376431	*HADHA*
		rs81235728	*PRKRIP1*
	5	rs81232818	*PPARA*
		rs80812768	*ACSS3*
		rs81284021	*SLC2A13*
		rs81275045	*SLC25A17*
	6	rs81390532	*VAC14*
		rs80939886	*GHRb*
	8	rs81332349	*ADD1-SREBF1*
	10	rs81477511	*ITIH5*
	11	rs81430254	*ESD*
	17	rs80877048	*FAT1*
Nutrient metabolism: minerals	3	rs81374637	*PRKD3*
	8	rs81303957	*HTT*
	12	rs81434419	*TSPOAP1*
	18	rs81472416	*CALU*
Nutrient metabolism: proteins	1	rs81355084, rs81331204	*TULP4, RGS3*
			UST, PTPRK
		rs81349440, rs80990751	*PTPRK, RABGAP1*
		rs81353520, rs80900725	*NCOA7, PTPRK*
		rs80978606, rs80949040	*HINT3, TTLL11*
		rs81353564, rs319558321	
	2	rs81356596, rs55618343	*FBXO3, ASRGL1*
	3	rs343472475, rs81258584	*RMDN2, PPM1G-ZNF513*
	7	rs80945706	*PPP4R3A*
	8	rs81403665, rs81400803 rs81401003	*TBCK, RGS12 MSANTD1*
	9	rs81477403, rs81408738	*CNTNAP2, CNTN5*
	10	rs81423925	*WAC*
	12	rs80951900	*MPO*
	14	rs80952995, rs80909629	*ADAMTS14, TTC13*
		rs80996847	*ATE1-FGFR2*
	17	rs81291556	*DCUN1D2*
	18	rs81467529, rs339556787	*GRM8, CHRM2*
Nutrient transport	3	rs81475079	*SFXN5*
	4	rs80868835	*KCNQ3*
	5	rs81387478, rs80790531	*SYN3, GRIN2B*
		rs81384304, rs81271990	*GRIN2B, ASIC1-SMARCD1*
	9	rs81408589	*MAML2*
	12	rs81432653	*COPZ2*

other populations. The decrease in genetic diversity in pigs from La Serena, Guadyerbas, and USYU indicates some within-population selection with non-random mating, which could have increased inbreeding and depression. Inbreeding has been reported in small populations of Iberian pigs (Saura et al., 2015). Esteve-Codina et al. (2013) report that the genetic variability is lower in Guadyerbas than in other Iberian pigs, which are genetically distant from commercial and Latin American Creole pigs from Guatemala (Ramírez et al., 2015). In addition, the values of F (0.39 to 0.80) reported in Guadyerbas pigs (Esteve-Codina et al., 2011; Saura et al., 2015) are higher than that obtained here, which increases by 0.09% per year, under a conservation program (Toro et al., 2000).

In Entrepelados Iberian pigs, an F of 0.25 was obtained, which is higher than that reported for YBHP and Canarian pigs, which also revealed a negative genetic trend due to inbreeding depression. However, it had a lower F than Retinto pigs, reducing 0.25 the number of piglets born per litter in inbred sows (Casellas et al., 2019). In modern breeds, the levels of genetic diversity are stable, like those from Chinese species and populations under conservation (Faria et al., 2019). Furthermore, F levels in most commercial populations are low (Faria et al., 2019), with Ho values for Yorkshire, Landrace, and Duroc of 0.375, 0.397, and 0.372, respectively. In another study, an F of 0.079 and a Ho of 0.30 were also observed in Duroc (Lemus-Flores et al., 2020). These values, with higher Ho (YBHP and Canarias), agree with those reported here. Muñoz et al. (2019) found that several local European breeds have low genetic diversity with low Ho, which shows the need to establish conservation strategies. However, in a population of YBHP, due to the random mating (males were frequently replaced and females were not kept in the herd for many parities), genetic diversity was high (Ángel-Hernández et al., 2020), as has been reported in other studies (Lemus-Flores et al., 2001, 2020). Another reason for genetic diversity is that YBHP is commonly found in rural communities, geographically distant from one another (Ángel-Hernández et al., 2020), which reduces the risk of using inbred boars. It has been observed that within the same geographic region of Yucatan, there are different subpopulations of YBHP (Lemus-Flores et al., 2020). Some traditional producers opt for crossbreeding with modern breeds, integrating hybrid pigs into the production systems, resulting in greater genetic diversity because of hybridism but a loss of Iberian pig genes.

Entrepelados, Retinto and Torbiscal Iberian pigs maintain close genetic similarities (Alonso et al., 2020). Fabuel et al. (2004) studied five Iberian pig biotypes (Entrepelado, Retinto, Lampiño, Torbiscal, and Guadyerbas); the Guadyerbas population had the most significant genetic distance from the other populations. We found a similar result in the present study, obtaining a greater distance between Guadyerbas pigs and other Iberian pigs, but they were close to YBHP and USYU (Figure 1). Since 1945, the conservation program of Guadyerbas pigs has isolated that germplasm, an older line of Iberian pigs (Toro et al., 2000; Esteve-Codina et al., 2011), the proximity with YBHP and USYU pigs is significant. Previous studies confirm that Latin American pigs are of Iberian origin, but this origin is not predominant, except for the creole pigs from Mexico, Peru, and Colombian (Burgos-Paz et al., 2013). It has been noted that the most significant ancestry component was like the IHP, consistent with a primeval origin from the Iberian Peninsula (Burgos-Paz et al., 2013; Yang et al., 2017).

Morphologically, alopecia is an important characteristic for the identification of YBHP. However, the present research results disagree with other studies, where genes related to hair follicle development, epithelial cell differentiation, morphogenesis, and epithelium development were identified. Esteve-Codina et al. (2013) reported the *NSDHL, FOXP1, IGF1R, HNF1B, PTEN, AXIN2, KRT81, KRT83, KRT84, KRT85, KTR86, PRKD1* and *AC0210066.1* genes in a pool of Iberian pigs. Lemus-Flores et al. (2020), on the other hand, report the *EHF, DST, PDE8A, FOXA1,* and *VCL* genes in YBHP compared to the Duroc breed. Su et al. (2014) note that *RB1* and *BAMBI* genes are associated with the lack of hair in USYU and Mexico hairless pigs. Jiang et al. (2019) report the *MAP2* (HR) and *FOXI3* genes as candidate markers, considering that hair follicle morphogenesis occurs at an early stage of embryo development, like in humans and mice. In addition, those authors consider that the genes responsible for alopecia are in chromosome 15. In the present study, the *CLASP1* gene was also located in that chromosome. Schiavo et al. (2018) reported the *ARHGEF10* gene and considered the *FOXN3* gene a plausible candidate for this chromosome region, like the forkhead box (FOX) family genes responsible for alopecia in humans.

Only now is there a conclusive report, since there is not a unian amazing cadence, existing several candidate genes that could have interactions yet to be reported. The *BAMBI* gene written by Su et al. (2014), as well as the *BMP7* gene reported here, are candidates' genes since they are related to type I receptors of the transforming growth factor-beta (TGF-beta) family, whose members play essential roles in the transduction of signals in many pathological and developmental processes (GeneCards, 2022). Another gene reported in the present paper is the *NSUN2* gene associated

with alopecia in mice and defective differentiation of germ cells (Chi & Delgado-Olguín, 2013). According to Blanco et al. (2011), the nucleolar protein MISU/NSUN2 (Myc-induced SUNdomain-containing protein) is the direct target gene of c-Myc, associated with partial alopecia in mice, observed which the Misu protein gives origin to the nervous system and the epidermis.

Another essential and distinctive characteristic of YBHP is fatness. Here are seven reported genes associated with fat metabolism. According to Miklas et al. (2019), the *HADHA* gene is required for fatty acid beta-oxidation. The *PPARA* (peroxisome proliferator-activated receptor-α) gene encodes a nuclear receptor that plays a crucial role in fatty acid catabolism by transcriptional regulation of genes involved in fatty acid oxidation and could be considered as a candidate gene for fatness traits in pigs (Stachowiak et al., 2014). Adipocyte determination and differentiation factor-1/sterol regulatory element-binding protein-1c (*ADD1/SREBF1*), trans-factors for regulating fatty acid synthase promoter in adipocytes, plays a significant role in the quality of meat in Meishan pigs (Li et al., 2006). *FAT1* catalyzes the conversion of internal oleic acid to linoleic acid in pigs by delta-12 desaturase encoded by this gene, further promoting the synthesis of n-3 PUFAs from n-6 analogs (Tang et al., 2019).

The information generated in this study provides valuable information to continue with a conservation program, applying the available methodology and considering the identified candidate genes.

Conclusion

The YBHP, Canarias, and Chato Murciano have high genetic diversity. A cluster formed by pigs from Guadyerbas, USYU, and YBHP was found. 119 SNPs were associated with genes and biological processes. The *BMP7* and *NSUN2* genes related to epithelial cell differentiation, morphogenesis, and epithelial development were identified. The HADHA, PPARA, ADD1/SREBF1, and FAT1 genes were associated with fat metabolism. Using SNPs to identify YBHP with a significant Iberian genetic component, *ex-situ* conservation programs are possible.

Conflict of Interest

No potential conflict of interest relevant to this article was reported.

Ethics Statement

This research was approved by the Secretariat for Research and Postgraduate Studies of the Autonomous University of Nayarit SIP18-076. This research is not against the animal rights, the official Mexican standards were followed.

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