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NOTA BREVE

MICROSATELLITE CHARACTERIZATION OF THE MOMIL, CORDOBA (COLOMBIA) DOMESTIC PIG

CARACTERIZACIÓN MEDIANTE MICROSATÉLITES DEL CERDO DOMÉSTICO EN MOMIL, CÓRDOBA

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ADDITIONAL KEYWORDS

Genetic variation. Hardy-Weinberg equilibrium. Probability of exclusion. *Sus scrofa domestica*.

PALABRAS CLAVE ADICIONALES

Variación genética. Equilibrio Hardy-Weinberg. Probabilidad de exclusión. *Sus scrofa domestica*.

SUMMARY

The genetic status of the domestic pig *(Sus scrofa domestica)* from Momil, Colombia, was studied on 45 samples using 20 microsatellites recommended by the FAO/ISAG for swine biodiversity studies. All microsatellites were polymorphic having from 2 (SW1067) to 13 (SW957) alleles. An average of 5.2 and a total of 104 alleles were detected. The average expected heterozygosity was 0.5376 and the observed was 0.5216. PIC values ranged between 0.1689 (SW1067) and 0.7352 (SW957), respectively. The population seems be genetically stable.

RESUMEN

Se estudió la situación genética del cerdo doméstico *(Sus scrofa domestica)* de Momil, Córdoba, Colombia sobre 45 muestras empleando 20 microsatélites de los recomendados por la FAO/ISAG para estudios de biodiversidad porcina. Todos los microsatélites resultaron polimórficos y se han detectado, entre 2 (SW1067) y 13 (SW957) alelos, con un número medio de 5,2 y un total de 104. La heterocigosidad media esperada ha sido 0,5376 y la observada 0,5216. El PIC osciló entre 0,1689 (SW1067) y 0,7352 (SW957). La población estudiada es genéticamente estable.

INTRODUCTION

In Córdoba (Colombia) the pig (mixtures of different races, ICA, 2013) production, is usually characterized by malnutrition, and bad health management. Animals usually remain on pasture, with free access to the farmers´ home. Their feeding in the growth phase (from 20 to 24 months age), is especially based on the intake of food scraps and leftover harvest (banana, yucca, yam, etc). For these reasons they grow weak, and vulnerable to several illnesses, resulting in a low weight. Taking into account that genetic information from samples of domestic pigs (*Sus scrofa domestica*) in the Caribbean countries, is low, it is necessary to generate studies in order to identify their genetic status. Although, the study of genetic characterization of domestic pigs in Momil, Cordoba is a major challenge from a scientific and strategic point of view, it is an outstanding opportunity to learn, and to have a better understanding of the reality of this species. This type of research will confirm the obligation of research to deepen the knowledge of these genetic resources, and their cultural and economic importance for the region. In this study, a sample of 45 domestic pigs in Momil (Córdoba) was genetically characterized using microsatellite markers in order to identify their genetic status.

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MATERIALS AND METHODS

Hair samples were collected in Momil, Cordoba (9 ° 14 '16 " N and 75 ° 36' 30" W), Colombia, from 45 specimens. As animals from family farms, there are no genealogy data available. Twenty microsatellites recommended by the FAO/ISAG for genetic diversity studies in pigs were used. For the analysis of fragments and allelic characterization, Genescan Analysis ® 3.1.2 and Genotyper ® 2.5.2 programs were used respectively. By using the Genetix v 4.02 program (Belkhir *et al.*, 2003), allele frequencies, heterozygosities and FIS value were calculated. The presence of the Hardy-Weinberg equilibrium (HW) was measured with the Genepop v. 3.1c program (Guo and Thompson, 1992). The polymorphic information content (PIC) was calculated with the Ben Hui Liu (1987) algorithm. The allelic richness and FIS values were obtained with the Fstat program.

Table I. *Categorized microsatellites, number of alleles detected (NA), motive of the repetition and allelic range (bp) of the Momil, Cordoba domestic pig.* (Microsatélites, número de alelos detectados (NA), repetición y rango alélico (pb) del cerdo doméstico en Momil, Córdoba).

Marker	NA	Repetition	Allelic range (bp)
SW489	5	$(GT)_{16}$	148 – 181
SW2519	9	$(CA)_{20}$	187 – 232
SW780	4	$(GT)_{11}(GA)_{9}$	115 – 170
SW2083	5	$(GT)_{10}$	143 – 167
SW2019	3	$(GT)_{14}AT(GT)_{4}$	127 – 147
SW2410	4	$(GT)_{15}$	103 – 137
S0215	7	$(CT)_{18}(CA)_{12}$	125 – 194
SW72	5	$(GT)_{15}$	97 – 119
SW911	4	$(CA)_{22}$	147 – 177
IFNG	5	$(GA)_{11}$	221 – 245
SW1041	3	$(CA)_{9}$	93 – 101
SWR345	4	$(CA)_{12}$	134 – 160
TNFB	8	$(CTG)_{20}$	142 – 203
S0385	5	$(CA)_{21}$	145 – 192
SW787	3	$(CA)_{19}$	144 – 164
S0090	5	$(CA)_{24}$	227 – 251
SW1083	4	$(GT)_{15}$	108 – 152
SW957	13	$(GT)_{28}$	112 – 157
SW2427	6	$(GT)_{13}$	116 – 146
SW1067	2	$(CT)_{20}(CA)_{22}$	137 – 175
Mean	5.2		

RESULTS AND DISCUSSION

The results show a high degree of polymorphism for all microsatellites, detecting a total of 104 alleles, ranging from 2 (SW1067) and 13 (SW957) alleles per locus **(table I)** and a number of alleles found in the sample of 5.2 **(table I)**. Other studies of genetic diversity in pigs reported higher and lower values between 2.3 ((Nidup *et al.*, 2011) and 13.31 alleles (Chang *et al.*, 2009). The obtained polymorphic information content **(table II)** varied between 0,1689 (SW1067) and 0.7352 (SW957). These values correspond to the markers that showed the lowest and the highest number of alleles respectively. Only 16 markers can be considered very informative (PIC>0.7), making them very revealing in detecting the genetic variation in this sample. One marker was moderately informative (PIC>0.25) and 3 not very informative (PIC <0.25). Compared with previously published data, we found that the average value of PIC was lower than that reported by Vicente *et al.* (2008), and similar to those reported by Castro *et al.* (2007). Sixteen out of the 20 microsatellites analyzed were found in the Hardy-Weinberg equilibrium, therefore, we can say that the sample is genetically stable **(table II)**. This could show that intra-population mating occurred randomly (with respect to the markers considered) or, if new animals have recently joined this sample, they have come from samples with the same gene pool of the analyzed sample in this study Four loci showed a significant deviation from the Hardy-Weinberg equilibrium (SW2019, SW1041, SW180 and SW1067), revealing an excess of homozygotes. Excess of homozygotes in a sample could be the result

Table II. *Microsatellites established, expected heterozygosity (He), observed heterozygosity (Ho), PIC, HW equilibrium deviation (p-value) and F_{IS} index of the Momil, Cordoba domestic pig.* (Microsatélites tipificados, heterocigosidad esperada (He), heterocigosidad observada (Ho), PIC, valores deprobabilidad por dseviación del equilibrio de Hardy-Weinberg e índice de fijación F_{IS} del cerdo doméstico de Momil, Córdoba).

Marker	He	Ho	PIC	H-W (p-value)	F_{IS}
SW489	0.5211	0.6239	0.5177	0.5223 NS	-0.312
SW2519	0.7323	0.8418	0.7226	0.1232 NS	-0.222
SW780	0.3143	0.2296	0.3121	0.0082*	0.211
SW2083	0.5314	0.4765	0.5287	0.6843 NS	-0.032
SW2019	0.3494	0.2643	0.5290	0.0054*	0.333
SW2410	0.6503	0.3544	0.2345	0.7577 NS	0.027
S0215	0.5987	0.5865	0.5007	0.3446 NS	0.102
SW72	0.2871	0.7576	0.7008	0.2343 NS	-0.411
SW911	0.6567	0.7154	0.5858	0.6361 NS	-0.434
IFNG	0.5672	0.5581	0.5121	0.8742 NS	0.045
SW1041	0.7361	0.2487	0.5473	0.0234*	0.306
SWR345	0.5430	0.6227	0.2433	0.0789 NS	-0.254
TNFB	0.2659	0.2665	0.5221	0.0765 NS	0.056
S0385	0.6138	0.7156	0.7012	0.7297 NS	0.019
SW787	0.5466	0.7111	0.5565	0.1544 NS	0.033
S0090	0.6344	0.6111	0.5676	0.3456 NS	0.076
SW1083	0.5650	0.4332	0.5247	0.5577 NS	-0.028
SW957	0.8383	0.7141	0.7352	0.1319 NS	-0.187
SW2427	0.7454	0.7006	0.6083	0.7433 NS	0.014
SW1067	0.0564	0.0021	0.1689	0.0176*	0.447
Mean	0.5376	0.5216	0.5159		-0.010

NS: Not significant. *Markers that are not in the Hardy-Weinberg equilibrium ($p<0.05$).

of inbreeding events within the sample (Allendorf and Luikart, 2007). However, inbreeding equally affects the entire genome, then, as it is expected, all used markers would show an excess of homozygotes, which did not occur in this case. On the other hand, there might be a genetic structure by subdivision (Wahlund effect). If this is true, it would mean that there are marked differences between close domestic pig samples to the markers SW2019, SW1041, SW180 and SW1067, but not for the other markers. If the differences for these markers were not removed it is because the gene flow between near samples is limited (aspect not shown for the other markers). These differences may also indicate that the markers SW2019, SW1041, SW180 and SW1067, are linked to genes under natural selection, which acts differentially at the micro or macro spatial. Another possibility is the presence of null alleles at these loci, frequent event in much of microsatellite studies (Dakin and Avise, 2004). Null alleles can be caused by high mutation rate that exhibit these types of markers, causing an alteration of the sequence between slightly distant populations, or due to technical problems during PCR. Levels of observed heterozygosity and expected heterozygosity found in the sample studied **(table II)** show low genetic variability, perhaps due to consanguineous mating, something often carried out by animal owners. The percentage of heterozygotic individuals was above 50 %, reaching values of 52.16 % for the mean observed heterozygosity and 53.76 % for the expected average heterozygosity. These values are higher than those reported by Oslinger *et al*. (2006) in Colombia and above those reported in India, Thailand and Spain (Nidup *et al*., 2011). The mean number of alleles per locus and allelic richness indicate that this sample exhibits a certain degree of variability. The FIS value found demonstrates a homogeneous sample in its genetic characteristics.

CONCLUSIONS

The chosen microsatellites contribute to the genetic characterization of this sample. High polymorphism, low genetic variability, and high PIC values were observed, resulting in very informative and useful markers to measure the genetic diversity. The usefulness of this study will increase when analyzing other populations using phylogenetic mating, especially to contrast and clarify genetic relationships with the Momil pigs.

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