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# Polymorphisms of Candidate Genes to Growth in Two Populations of Colombian Creole Sheep

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## Abstract

**Objective:** The study was to characterize the genetic polymorphism of 23 SNPs located in candidate growth genes in Colombian Creole hair (OPC). **Materials and Methods:** We used 106 individuals belonging to two OPC subpopulations located in the departments of Cesar (CS) and Córdoba (CB), these were genotyped using the OvineSNP50 Bead Chip of Illumina ®, were calculated frequencies genotypic, allelic, the Hetero zygosity observed (Ho) and expected (he), the Fixation Index (F), the Hardy-Weinberg equilibrium deviations (EHW) and a molecular variance analysis to estimate the values of FST, FIS and FIT. **Findings:** The minimum allelic frequency (MAF) varied from 0.042 to 0.491 in the entire OPC population, while in the CS subpopulation the values varied from 0.037 to 0.481 and in the subpopulation CB from 0.019 to 0.490. For this study four SNPs had MAF less than 10% in the subpopulation CS, while, for the subpopulation CB and OPC Just one. In addition, 47.8% of the loci showed MAF ≥ 0.10, 36.9% presented an MAF ≥ 0.20, 23.9% showed an MAF ≥ 0.30 and 8.6% of the evaluated loci presented an MAF ≥ 0.40%. Similar allelic and genotypic frequencies were found in both subpopulations. The average Ho found was 0.358 ± 0.02 and the average value was 0.378 ± 0.02, with greater diversity CB. The majority of the SNPs did not present significant diversions of EHW. **Application/Improvements:** Finally, the obtained results show that the studied loci have high genetic variability, which is necessary to preserve.

**Keywords:** Polymorphism, OPC, allelic frequencies, SNPs, genetic diversity.

## 1. Introduction

The majority of sheep production systems in Colombia are based on the Colombian creole sheep breed (OPC). The OPC presents important adaptive characteristics to the tropical climate, such as tolerance to heat, ecto parasites and capacity to consume pastures of low nutritional value[1] However, sheep production systems are considered secondary to livestock, since most of them are carried out in traditional and/or family systems, with low inputs in mixed production systems[2-3] with nutrition, reproduction, health, genetic progress, animal welfare, and business management problems, which are reflected in low productivity.[1-4] According to the Colombian agricultural institute (ICA) it can be affirmed that the exploitation of the ovine species in the country is low, there is a record of 1'449,705 specimens with the largest population in the departments

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of La Guajira (44.27%), Magdalena (7.41%), Boyacá (7.30%), Cesar (6.97%) and Córdoba (6.66%) which group 72.61%.[5] In spite of the above, the production of sheep meat has increased by 7.43% in the last two years.[5]

The development of genomics in Creole animals has introduced new methodologies and alternatives that can generate a global description of biological systems at the level of the expression of genes, proteins, and their interaction. To benefit from new approaches to advances, experimental methods are adapted to these new genomic technologies and important considerations must, therefore, be taken into account for the appropriate choice of technologies and methods of analysis.

Geneticists and sheep breeders are paying more attention to the growth of animals and traits associated with meat production.[7-8] In recent decades, a large number of loci have been found that affect quantitative traits (QTL) through the candidate gene approach and the genome scanning technology, 2129 QTLs or associations are currently reported of which 341 are in related parameters. With growth[9] (updated to September 1, 2018). However, the confidence interval of the QTLs is relatively long, and it is difficult to identify specific genes that influence the objective quantitative traits[7]. With the development of new genotyping technologies of high-throughput SNPs, full genome association studies (GWAS)[10] have been widely applied to detect and localize candidate genes for quantitative traits in different species, which increased efficiency of animal husbandry and selection.[7-11-12]

Genetic improvement schemes in the OPC breed are few, the crosses absorbent with breeds of temperate climates to take advantage of the hybrid vigor.[13] However, to increase the competitiveness of the sector, it is necessary to incorporate new technologies and/or management practices that generate competitive advantages through knowledge management systems that adapt to the conditions of primary production.[2-4-14] Logístico, Gompertz y Von Bertalanffy. Los parámetros de los modelos fueron estimados por medio del procedimiento NLIN de SAS. La selección de la curva que mejor describió el crecimiento se realizó considerando el Criterio de Información Aikaike (AIC. This is how molecular tools are used in animal genetic improvement programs, through molecular marker-assisted selection, a practice that improves accuracy and increases genetic progress, through the identification, mapping, and analysis of polymorphism of the genes involved in the main metabolic pathways related for example to animal growth.[15] Research on gene polymorphisms associated with growth in the OPC breed is limited. Therefore, the objective of this work was to characterize the genetic polymorphism of 23 SNPs located in candidate genes to grow the ovine of Colombian Creole hair.

## 2. Materials y Methods

### 2.1 Populations, blood collection, and DNA extraction

In the present investigation, 106 individuals belonging to two OPC subpopulations located in the departments of Cesar (CS, n=54) and Córdoba (CB, n=52) were used, blood samples were collected in Vacutainer® lid purple tubes (EDTA 7.2mg) taking into account for the procedures of sample collection, management, and conservation, the ethical, technical, scientific and administrative standards for animal research contained in Law 84 (National Congress of Colombia, 1989). The DNA was extracted using the QIAamp® DNA Mini Kit from QIAGEN, according to the manufacturer's instructions. The quantity and quality of the DNA were evaluated using a NanoDrop 2000™ (Thermo Fisher Scientific).

### 2.2 Genotyping, quality control of genotypes and selection of candidate SNPs.

Individuals were genotyped using the OvineSNP50 BeadChip from Illumina®, following the Infinium® Assay Super II Illumina® protocol and scanned using the HiScan™ SQ System. To visualize the images and guarantee the consistency of the data, the Genome Studio® and PLINK® (v1.07) programs were used, according.[16] Genotyping quality control excluded SNPs that had: a call rate of less than 90%, extreme deviation of the Hardy-Weinberg equilibrium ($p<0.001$), located in auto somal chromosomes that presented both homozygous genotypes, with unknown genomic position, located in sex chromosomes, mono morphic or if the frequency of the least common allele (MAF) was below 0.02. The 23 selected candidate SNPs (Table 1) were taken from a complete genome association study (GWAS) (unpublished data).

**Table 1.** Location in chromosome, alleles, ID Assemble and name of the gene in 23 SNPs evaluated

| SNP ID | Chromosome | Position | Alleles | ID Gen Ensamble | Name of the Gen |
|---|---|---|---|---|---|
| OAR1_189179554.1 | 1 | 175482796 | A/G | ENSOARG00000019298 | CD200 molecule (CD200) |
| OAR1_23734999.1 | 1 | 23651580 | A/G | ENSOARG00000004178 | LOC105605154 |
| s12060.1 | 1 | 75971485 | C/T | ENSOARG00000017670 | Phospholipid phosphatase related 4 (PLPPR4) |
| s25125.1 | 1 | 96847814 | C/T | ENSOARG00000020482 | Myomegalin (PDE4DIP) |
| OAR2_96008804.1 | 2 | 89509922 | A/G | ENSOARG00000014411 | S-methyl-5'-thioadenosine phosphorylase (MTAP) |
| OAR3_61737307.1 | 3 | 58315054 | C/T | ENSOARG00000020700 | Ring finger protein 103 (RFN103) |
| OAR3_89348294.1 | 3 | 84390370 | A/G | ENSOARG00000007947 | Transmembrane protein 178A (TMEM178A) |
| s62226.1 | 3 | 26419161 | A/G | ENSOARG00000016788 | Retinol dehydrogenase 14 (RDH14) |
| OAR5_107977075.1 | 5 | 99165665 | C/T | ENSOARG00000018405 | Peptidylglycine alpha-amidating monooxygenase (PAM) |
| OAR5_112451694.1 | 5 | 103304973 | C/T | ENSOARG00000018761 | Ephrin A5 (EFNA5) |
| s11274.1 | 5 | 71514994 | A/G | ENSOARG00000014001 | Gamma-aminobutyric acid type A receptor gamma2 subunit (GABRG2) |
| OAR6_27552838.1 | 6 | 24157625 | C/T | ENSOARG00000013694 | Endomucin (EMCN) |
| OAR6_77919148.1 | 6 | 71481367 | A/G | ENSOARG00000003002 | Centrosomal protein 135 (CEP135) |
| OAR7_85269064.1 | 7 | 85269064 | C/T | ENSOARG00000002286 | CLOCK-interacting pacemaker (CIPC) |
| OAR8_39977285.1 | 8 | 37211967 | A/G | ENSOARG00000011775 | PR/SET domain 13 (PRDM13) |
| OAR8_50320412.1 | 8 | 46840220 | C/T | ENSOARG00000012321 | Mitogen-activated protein kinase kinase kinase 7 (MAP3K7) |
| s33129.1 | 9 | 88576469 | A/C | ENSOARG00000011632 | Cyclic nucleotide-gated cation channel beta-3 (CNGB3) |
| OAR10_59207797.1 | 10 | 59207797 | C/T | ENSOARG00000017151 | SLIT and NTRK like family member 1 (SLITRK1) |
| OAR10_91128145.1 | 10 | 91128145 | A/G | ENSOARG00000009132 | Chromosome alignment maintaining phosphoprotein 1 (CHAMP1) |
| OAR12_20575087.1 | 12 | 17694724 | G/T | ENSOARG00000010714 | Usherin (USH2A) |
| s01263.1 | 14 | 58489098 | C/T | ENSOARG00000000628 | LOC101113879 |
| OAR23_49635171_X.1 | 23 | 46823961 | C/T | ENSOARG00000003371 | Protein inhibitor of activated STAT 2 (PIAS2) |
| DU261801_281.1 | 26 | 37119640 | C/G | ENSOARG00000004073 | Pleckstrin and Sec7 domain containing 3 (PSD3) |

### 2.3 Analysis of data

The Arlequin programs see 3.5.2.2[17] and GENALEX see 6.5[18] were used to calculate the genotypic, allelic frequencies, the observed (Ho) and expected hetero zygosity (He), the fixation index (F), the deviations of the Hardy-Weinberg equilibrium (EHW) and a molecular variance analysis to estimate the $F_{ST}$, $F_{IS}$ y $F_{IT}$ values.

## 3. Results and Discussion

The SNPs evaluated, 21 were located in genes with known function and only two in proteins that have not been characterized; however, all the SNPs evaluated were polymorphic. The allele frequencies for each subpopulation and for the entire OPC are presented in Table 2. The minimum allelic frequency (MAF) varied from 0.042 to 0.491 in the entire OPC population, while in the CS subpopulation the MAF values varied from 0.037 to 0.481 and in the CB subpopulation from 0.019 to 0.490 (Table 2).

The power to detect the possible genetic effect of SNPs depends to a large extent on the MAF of the alleles under study. Specifically, loci with low MAF (<10%) have a significantly lower power to detect weak genotype-phenotype associations than loci with a high MAF value (> 40%).[19] Additionally, previous studies have shown that rare genotypes are more likely to generate illegitimate results due to a higher standard error within each test and a higher false-positive rate in multiple test procedures for many loci.[20]

In the present study, four SNPs had MAF less than 10% in the CS subpopulation (OAR3_89348294.1, s62226.1, OAR5_112451694.1, and OAR6_77919148.1), while only

**Table 2.** Allele frequencies in the 23 SNPs evaluated in each subpopulation and for the entire OPC

| SNP | Allele | CS | CB | OPC | SNP | Allele | CS | CB | OPC |
|---|---|---|---|---|---|---|---|---|---|
| OAR1_189179554.1 | A | 0.343 | 0.346 | 0.344 | OAR6_77919148.1 | A | 0.074 | 0.346 | 0.208 |
| | G | 0.657 | 0.654 | 0.656 | | G | 0.926 | 0.654 | 0.792 |
| OAR1_23734999.1 | A | 0.343 | 0.644 | 0.491 | OAR7_85269064.1 | C | 0.583 | 0.808 | 0.693 |
| | G | 0.657 | 0.356 | 0.509 | | T | 0.417 | 0.192 | 0.307 |
| s12060.1 | C | 0.87 | 0.462 | 0.67 | OAR8_39977285.1 | A | 0.685 | 0.375 | 0.533 |
| | T | 0.13 | 0.538 | 0.33 | | G | 0.315 | 0.625 | 0.467 |
| s25125.1 | C | 0.806 | 0.75 | 0.778 | OAR8_50320412.1 | C | 0.861 | 0.712 | 0.788 |
| | T | 0.194 | 0.25 | 0.222 | | T | 0.139 | 0.288 | 0.212 |
| OAR2_96008804.1 | A | 0.102 | 0.404 | 0.250 | s33129.1 | A | 0.324 | 0.202 | 0.264 |
| | G | 0.898 | 0.596 | 0.750 | | C | 0.676 | 0.798 | 0.736 |
| OAR3_61737307.1 | C | 0.852 | 0.837 | 0.844 | OAR10_59207797.1 | C | 0.657 | 0.558 | 0.608 |
| | T | 0.148 | 0.163 | 0.156 | | T | 0.343 | 0.442 | 0.392 |
| OAR3_89348294.1 | A | 0.065 | 0.019 | 0.042 | OAR10_91128145.1 | A | 0.481 | 0.192 | 0.34 |
| | G | 0.935 | 0.981 | 0.958 | | G | 0.519 | 0.808 | 0.66 |
| s62226.1 | A | 0.046 | 0.308 | 0.175 | OAR12_20575087.1 | G | 0.194 | 0.115 | 0.156 |
| | G | 0.954 | 0.692 | 0.825 | | T | 0.806 | 0.885 | 0.844 |
| OAR5_107977075.1 | C | 0.843 | 0.817 | 0.830 | s01263.1 | C | 0.852 | 0.625 | 0.741 |
| | T | 0.157 | 0.183 | 0.170 | | T | 0.148 | 0.375 | 0.259 |
| OAR5_112451694.1 | C | 0.037 | 0.202 | 0.118 | OAR23_49635171_X.1 | C | 0.759 | 0.49 | 0.627 |
| | T | 0.963 | 0.798 | 0.882 | | T | 0.241 | 0.51 | 0.373 |
| s11274.1 | A | 0.62 | 0.663 | 0.642 | DU261801_281.1 | C | 0.556 | 0.308 | 0.434 |
| | G | 0.38 | 0.337 | 0.358 | | G | 0.444 | 0.692 | 0.566 |
| OAR6_27552838.1 | C | 0.593 | 0.288 | 0.443 | | | | | |
| | T | 0.407 | 0.712 | 0.557 | | | | | |

the OAR3_89348294.1 locus presented this characteristic in the CB subpopulation and for the entire OPC (Table 2).

Additionally, 47.8% of the *loci* showed MAF≥0.10, 36.9% had a MAF≥0.20, 23.9% showed a MAF≥0.30 and 8.6% of the *loci* evaluated had a MAF≥0.40%. The above suggests that the SNP set identified in the present study will probably have a high utility for the analysis of association in different populations to different characteristics of zoo technical interest. No significant difference was observed in the MAF value of sheep from different geographic regions (Asia, Europe, and South America).[20] However, it has been reported that Asian and African breeds have an excess of SNPs with low MAF (<0.10) compared to European populations.[21] This reflects the absence of any verification bias in the present study since the diversity panel was adequately represented.

The distribution of MAF values varied among the subpopulations evaluated, so that, in 26% of the SNPs investigated, not always the allele of lower frequency was the same in both subpopulations. This partly had an effect on the average values of MAF found (CS = 0.238, CB = 0.289) and for the entire Creole race (OPC = 0.283). Other average values of MAF in races present in America are 0.167 in Pampita, 0.218 in Corriedale and Junin[20] estimated from a panel of 39 SNPs. Mean MAF values of 0.28 in Corriedale, 0.29 in Merino and 0.20 in Argentine Criollo were reported using the OvineSNP50® BeadChip genotyping panel (Illumina, San Diego, CA).[22] Genotypic frequencies for each subpopulation and for the entire OPC are presented in Table 3. The AA genotype of the OAR3_89348294.1 *loci* and the AG genotype of the OAR10_91128145.1 *loci* were not found, in 56.5% of the SNPs evaluated, the three corresponding genotypes were found. Additionally, in 34.8% of the loci analyzed, the genotypes with the highest frequency were different in each subpopulation. The mean Ho found was 0.358±0.02 and the mean He value was 0.378±0.02, this heterozygote deficiency was not significant (p>0.05) (Table 4), although, the subpopulation level analysis showed an excess of hetero zygotes in the subpopulation of CS (Ho= 0.34± 0.03 and He= 0.325±0.02, p>0.05) and a deficit of hetero zygotes in the CB population (Ho= 0.374±0.02 and He= 0.383±0.02, p>0.05). In six races of America, He values are reported between 0.346[21] and 0.366,[20] values lower than the one presented here.

**Table 3.** Genotypic frequencies in the 23 SNPs evaluated in each subpopulation and for the entire OPC

| Genotype | CS | CB | OPC | Genotype | CS | CB | OPC |
|---|---|---|---|---|---|---|---|
| | OAR1_189179554.1 | | | | OAR6_77919148.1 | | |
| AA | 0.130 | 0.058 | 0.094±0.05 | AA | 0.019 | 0.154 | 0.085±0.09 |
| AG | 0.426 | 0.577 | 0.500±0.10 | AG | 0.111 | 0.385 | 0.245±0.19 |
| GG | 0.444 | 0.365 | 0.406±0.05 | GG | 0.870 | 0.462 | 0.670±0.28 |
| | OAR1_23734999.1 | | | | OAR7_85269064.1 | | |
| AA | 0.148 | 0.462 | 0.302±0.22 | CC | 0.352 | 0.615 | 0.481±0.18 |
| AG | 0.389 | 0.365 | 0.377±0.01 | CT | 0.463 | 0.385 | 0.425±0.05 |
| GG | 0.463 | 0.173 | 0.321±0.20 | TT | 0.185 | ---- | 0.094±0.13 |
| | s12060.1 | | | | OAR8_39977285.1 | | |
| CC | 0.741 | 0.231 | 0.491±0.36 | AA | 0.500 | 0.558 | 0.528±0.04 |
| CT | 0.259 | 0.462 | 0.358±0.14 | AG | 0.370 | 0.346 | 0.358±0.01 |
| TT | ---- | 0.308 | 0.151±0.21 | GG | 0.130 | ---- | 0.066±0.09 |
| | s25125.1 | | | | OAR8_50320412.1 | | |
| CC | 0.611 | 0.615 | 0.613±0.01 | CC | 0.778 | 0.442 | 0.613±0.23 |
| CT | 0.389 | 0.269 | 0.330±0.08 | CT | 0.167 | 0.538 | 0.349±0.26 |
| TT | ---- | 0.115 | 0.057±0.08 | TT | 0.056 | 0.019 | 0.038±0.26 |
| | OAR2_96008804.1 | | | | s33129.1 | | |
| AA | 0.019 | 0.173 | 0.094±0.10 | AA | 0.111 | 0.058 | 0.085±0.03 |
| AG | 0.167 | 0.462 | 0.311±0.20 | AC | 0.426 | 0.288 | 0.358±0.09 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| GG | 0.815 | 0.365 | 0.594±0.31 | CC | 0.463 | 0.654 | 0.557±0.13 |
| | OAR3_61737307.1 | | | | OAR10_59207797.1 | | |
| CC | 0.704 | 0.692 | 0.698±0.01 | CC | 0.407 | 0.327 | 0.368±0.05 |
| CT | 0.296 | 0.288 | 0.292±0.06 | CT | 0.500 | 0.462 | 0.481±0.02 |
| TT | ---- | 0.019 | 0.009±0.01 | TT | 0.093 | 0.212 | 0.151±0.08 |
| | OAR3_89348294.1 | | | | OAR10_91128145.1 | | |
| AA | ---- | ---- | ---- | AA | 0.111 | 0.019 | 0.066±0.06 |
| AG | 0.130 | 0.038 | 0.085±0.06 | AG | 0.444 | 0.346 | 0.396±0.07 |
| GG | 0.870 | 0.962 | 0.915±0.06 | GG | 0.444 | 0.635 | 0.538±0.13 |
| | s62226.1 | | | | OAR12_20575087.1 | | |
| AA | ---- | 0.096 | 0.047±0.06 | GG | ---- | ---- | ---- |
| AG | 0.093 | 0.423 | 0.255±0.23 | GT | 0.389 | 0.231 | 0.311±0.11 |
| GG | 0.907 | 0.481 | 0.698±0.30 | TT | 0.611 | 0.769 | 0.689±0.11 |
| | OAR5_107977075.1 | | | | s01263.1 | | |
| CC | 0.685 | 0.654 | 0.670±0.02 | CC | 0.722 | 0.462 | 0.594±0.18 |
| CT | 0.315 | 0.327 | 0.321±0.01 | CT | 0.259 | 0.327 | 0.292±0.04 |
| TT | ---- | 0.019 | 0.009±0.01 | TT | 0.019 | 0.212 | 0.113±0.11 |
| | OAR5_112451694.1 | | | | OAR23_49635171_X.1 | | |
| CC | ---- | 0.077 | 0.038±0.04 | CC | 0.537 | 0.288 | 0.415±0.17 |
| CT | 0.074 | 0.250 | 0.160±0.12 | CT | 0.444 | 0.404 | 0.425±0.02 |
| TT | 0.926 | 0.673 | 0.802±0.17 | TT | 0.019 | 0.308 | 0.160±0.20 |
| | s11274.1 | | | | DU261801_281.1 | | |
| AA | 0.370 | 0.404 | 0.387±0.02 | CC | 0.278 | 0.115 | 0.198±0.11 |
| AG | 0.500 | 0.519 | 0.509±0.01 | CG | 0.556 | 0.385 | 0.472±0.12 |
| GG | 0.130 | 0.077 | 0.104±0.03 | GG | 0.167 | 0.500 | 0.330±0.23 |
| | OAR6_27552838.1 | | | | | | |
| CC | 0.296 | 0.115 | 0.208±0.12 | | | | |
| CT | 0.593 | 0.288 | 0.443±0.21 | | | | |
| TT | 0.111 | 0.596 | 0.349±0.34 | | | | |

**Table 4.** Indices of genetic diversity in the 23 SNPs evaluated in each subpopulation and for the entire OPC

| SNP | CS | | CB | | OPC | |
|---|---|---|---|---|---|---|
| | He | F | He | F | He | F |
| OAR1_189179554.1 | 0,450 | 0,054 | 0,453 | -0,275 | 0,452 | -0,107 |
| OAR1_23734999.1 | 0,450 | 0,137 | 0,458 | 0,203 | 0,500 | 0,245 |
| s12060.1 | 0,226 | -0,149 | 0,497 | 0,071 | 0,442 | 0,190 |
| s25125.1 | 0,313 | -0,241 | 0,375 | 0,282 | 0,345 | 0,043 |
| OAR2_96008804.1 | 0,183 | 0,089 | 0,482 | 0,041 | 0,375 | 0,170 |
| OAR3_61737307.1 | 0,252 | -0,174 | 0,273 | -0,055 | 0,263 | -0,113 |
| OAR3_89348294.1 | 0,121 | -0,069 | 0,038 | -0,020 | 0,081 | -0,044 |
| s62226.1 | 0,088 | -0,049 | 0,426 | 0,007 | 0,288 | 0,116 |

| | | | | | | |
|---|---|---|---|---|---|---|
| OAR5_107977075.1 | 0,265 | -0,187 | 0,299 | -0,095 | 0,282 | -0,138 |
| OAR5_112451694.1 | 0,071 | -0,038 | 0,322 | 0,224 | 0,208 | 0,229 |
| s11274.1 | 0,471 | -0,062 | 0,447 | -0,163 | 0,460 | -0,108 |
| OAR6_27552838.1 | 0,483 | -0,227 | 0,384 | 0,250 | 0,490 | 0,095 |
| OAR6_77919148.1 | 0,137 | 0,190 | 0,447 | 0,096 | 0,323 | 0,212 |
| OAR7_85269064.1 | 0,486 | 0,048 | 0,311 | -0,238 | 0,425 | 0,002 |
| OAR8_39977285.1 | 0,431 | 0,141 | 0,469 | -0,190 | 0,498 | 0,071 |
| OAR8_50320412.1 | 0,239 | 0,303 | 0,411 | -0,312 | 0,334 | -0,044 |
| s33129.1 | 0,438 | 0,028 | 0,322 | 0,105 | 0,389 | 0,078 |
| OAR10_59207797.1 | 0,450 | -0,110 | 0,493 | 0,064 | 0,476 | -0,010 |
| OAR10_91128145.1 | 0,499 | -0,113 | 0,311 | -0,114 | 0,449 | -0,010 |
| OAR12_20575087.1 | 0,313 | -0,241 | 0,204 | -0,130 | 0,263 | -0,184 |
| s01263.1 | 0,252 | -0,027 | 0,469 | 0,303 | 0,384 | 0,239 |
| OAR23_49635171_X.1 | 0,366 | -0,216 | 0,500 | 0,192 | 0,468 | 0,092 |
| DU261801_281.1 | 0,494 | -0,125 | 0,426 | 0,097 | 0,491 | 0,040 |
| Mean | 0.325±0.02 | -0.045±0.03 | 0.383±0.02 | 0.182±0.03 | 0.378±0.02 | 0.129±0.02 |

The *locus* OAR10_91128145.1 showed the highest value of He in the subpopulation CS with a negative value of F and the OAR23_49635171_X.1 in the subpopulation CB with a positive value of F. The positive values of F indicate a deficit of heterozygous individuals and negative values indicate the opposite.[23] On the other hand, the SNPs that contributed least to genetic diversity were OAR5_112451694.1 in CS, OAR3_89348294.1 in CB as well as for the entire OPC. Regarding its functions, the *locus* OAR10_91128145.1 located within the gene (CHAMP1) is associated with the formation of bonds between nucleic acids and the *locus* OAR23_49635171_X.1 (PIAS2) aids in the regulation and transcription of DNA and RNA, similarly the SNPs of lower genetic diversity OAR5_112451694.1 (EFNA5) is involved in the process of stimulating the cellular response of hormones such as FSH, and OAR3_89348294.1 (TMEM178A) acts as a negative regulator in the differentiation of osteo clasts in inflammatory processes.[24]

Each of the genes associated with the different loci under study encodes, according to their biological function, immunological and growth processes in terms of muscle, bone and other tissue formation.[24] This is confirmed by studies conducted in humans where they evaluate different genes associated with the immune system.[25] Only the SNPs OAR8_50320412.1 (F= 0.303) in the CS subpopulation and the *loci* OAR1_189179554.1 (F= -0.275), s25125.1 (F= 0.282), OAR8_50320412.1 (F= -0.312) and s01263.1 (F= 0.303) in the CB subpopulation showed significant deviations of the EHW. However, in analysis at the level of the entire OPC, the SNPs with significant deviations of EHW are OAR1_23734999.1 (F= 0.190), OAR5_112451694.1 (F= 0.229), OAR6_77919148.1 (F= 0.212) and s01263.1 (F= 0.239) (Table 4). This indicates that most of the SNPs did not present deviations from the theoretical proportions of the EHW, indicating the lack of genetic improvement plans in the OPC.

In 15 SNPs in CS, 10 in CB and 9 in all the OPC, they presented negative F values that on average were not statistically significant ($p>0.05$). The analysis of molecular variance showed three possible sources of variation (Table 5), of which, variation within individuals is the largest contributor to diversity, followed by a variation between subpopulations. On the other hand, the values of FST, FIS and FIT were 0.141 ($p<0.05$), 0.006 ($p>0.05$) and 0.146 ($p<0.05$), respectively. The variation found among the subpopulations is confirmed by the calculated $F_{ST}$ value, this indicates a moderate population structure with a low gene flow between the subpopulations,[13] in addition, and the positive $F_{IS}$ and $F_{IT}$ values could be explained by the origin different and distant from the subpopulations evaluated[26] and through cross-breeding programs.[22] In 74 breeds from different parts of the world and using 50,000 SNPs with high levels of genetic diversity, low values of genetic differentiation have been found.[21] In 22 races of different origin higher values of $F_{ST}$ (0.213) and similar

values were found to those presented here for $F_{IS}$ and $F_{IT}$ (20)". Moderate values of FST have also been reported in Creole cattle in Latin America.[27]

**Table 5.** Molecular variance analysis for two OPC populations from the allele frequencies found

| Source of Variation | LG | MC | % |
|---|---|---|---|
| Among Subpopulations | 1 | 118.474 | 14% |
| Between Individuals | 104 | 6.497 | 1% |
| Within Individuals | 106 | 6.415 | 85% |
| Total | 211 | | 100% |

## 4. Conclusions

The results obtained show that the loci studied present high genetic variability, which is necessary to conserve. Additionally, the MAF found are considerably high, which is why they could be used for future gene-assisted selection programs, in order to increase productivity in sheep systems by managing the OPC as the genetic basis for its exploitation.

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