

Brief Exchanges on Selection of Genomic Regions and Genes Related to Adaptation and Fertility Traits of Two Colombian Creole Cattle Breeds

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ABSTRACT

Natural selection and domestication in livestock species are one of the main evolutive changes resulting in phenotypic adaptations; these patterns create genetic signatures within the genome. To discovery signatures and genes involved in adaptation and fertility traits in two Colombian creole cattle breeds *Blanco orejinegro* (BON) and *Sanmartinero* (SM) in the present study it was detected selected genomic regions by comparing differences in regional linkage disequilibrium (LD) using 58,868 single nucleotide polymorphisms (SNPs) from BON and 57482 SNPs from SM. Also was estimated the variation of genome-wide LD between populations using the VARLD program. The top 0.1 and 0.01th percentiles of standardized VarLD scores were used as a criterion for all comparisons. Ten regions were detected on chromosomes 3, 5, 11, 15, 18, 21, 22, 23, 25 and 29 and genes in it such as *CTDSP2*, *CES1*, *CFAP161*, *CLEC14A*, *HIPK1*, *RBM4*, *KDMID*, *OLFML3*, *ATP23*, *LRRTM1*, *SLC6A2*, *DEK*, *SYT6*, *KDMID* involved in adaptation and fertility traits. These findings open the prospect to develop new studies in other cattle breeds and other livestock species which will serve as support in genetic improvement and conservation programs.

Keywords: Creole breeds; SNPs; Adaptability indexes; LD variation

DESCRIPTION

Many studies developed in livestock species based on Genome wide association study (GWAS) and other, have led to the discovery of genomics regions and genes involved in the expression of adaptability and fertility traits widely used in selection and conservation programs [1]. Therefore, new selection methods as provided in this study, became essential for the progress in this field, so, the selection signatures and genes found in the genome appears promising with most statically power than the other methods applied in selection programme [2].

Blanco orejinegro (BON) and *Sanmartinero* (SM) Colombian creole cattle breeds have been genetically characterized by Martínez et al. with limited impact because lacked assessing in depth the variation and genetic differences of these two breeds [3]. Genetic differences can be measured through determination of selection signatures what are genomic regions fixed in the genome as a result of artificial or natural selection for reasons such as adaptability or productivity.

Linkage disequilibrium (LD) was studied in ROMO an BON Colombian creole cattle breed by Bejarano, reporting increasing LD from 0.3 ($r^2 > 0.3$) in both breeds, similar finding was reported by Li et al., and Pérez O'Brien et al., who also reported LD breaks down rapidly in absence of selection [4-6]. In other *Bos taurus* breeds, to milk and meat production, have been reported $r^2 \geq 0.3$ at distances less than or equal to 30 Kb (Figure 1 and Table 1) [7,8].

Genes identified in these selected regions consistent with other research work, are involved in the various biological processes from production, reproduction and adaptation and can be used in selection and conservation programs of these Colombian Creole breeds. This study helps to explain the genetic architecture conformed for productive, reproductive and adaptation processes. Different genes identified in these selected regions consistent with other research work, are involved in the various biological processes from production, reproduction and adaptation and can be used in selection and conservation programs of these Colombian Creole breeds.

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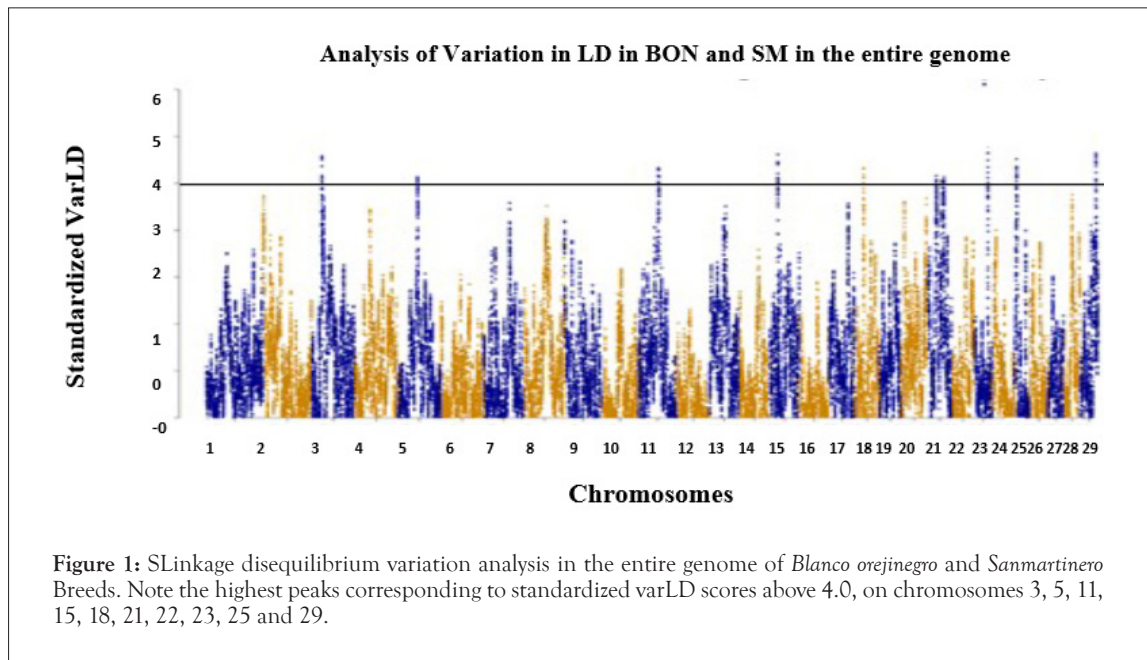


Table 1: Genomic regions in base pairs (bp) on chromosomes 3, 5, 11, 15, 18, 21, 23, 29. Linkage disequilibrium variations and standardized varLD scores, on percentiles 0.001 and 0.1 and genes found in these regions.

Chr/Percentiles	Regions (bp)	varLD	Standardized varLD scores	Genes
Chr3				
P 0.01	29.224.886	21.7	4.58	
P 0.1	29.285.827	21.6	4.54	
Chr5				
P 0.01	55.085.241	20.3	4.13	<i>ATP23, CTDSP2</i>
P 0.1	55.582.528	20.2	4.10	
Chr11				
P 0.01	55.683.407	20.9	4.33	<i>LRRM1</i>
P 0.1	55.443.099	20.8	4.30	
Chr15				
P 0.01	24.184.623	21.8	4.61	<i>ZW10 24.284.251-24.319.569</i>
P 0.1	24.186.798	21.3	4.45	
Chr18				
P 0.01	23.903.882	20.9	4.32	<i>SLC6A2, CES1</i>
P 0.1	23.955.588	20.8	4.30	
Chr21				
P 0.01	26.990.623	20.3	4.15	<i>CFAP161</i>
P 0.1	26.929.649	19.9	4.02	
P 0.01	48.369.157	20.2	4.12	<i>SSTR1</i>
P 0.1	48.313.773	19.9	4.01	
Chr23				
P 0.01	39.339.694	23.9	5.24	<i>DEK: 39.355.962-39.387.656</i>
P 0.1	39.354.709	23.9	5.22	<i>KDM1B: 39.389.854-39.432.004</i>
Chr29				
P 0.01	44.796.094	21.9	4.64	<i>SPTBN2,RBM4B</i>
P 0.1	44.707.685	21.8	4.59	

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