

# Genetic diversity and structure of creole cattle (*Bos taurus*) from southern Peruvian Highlands

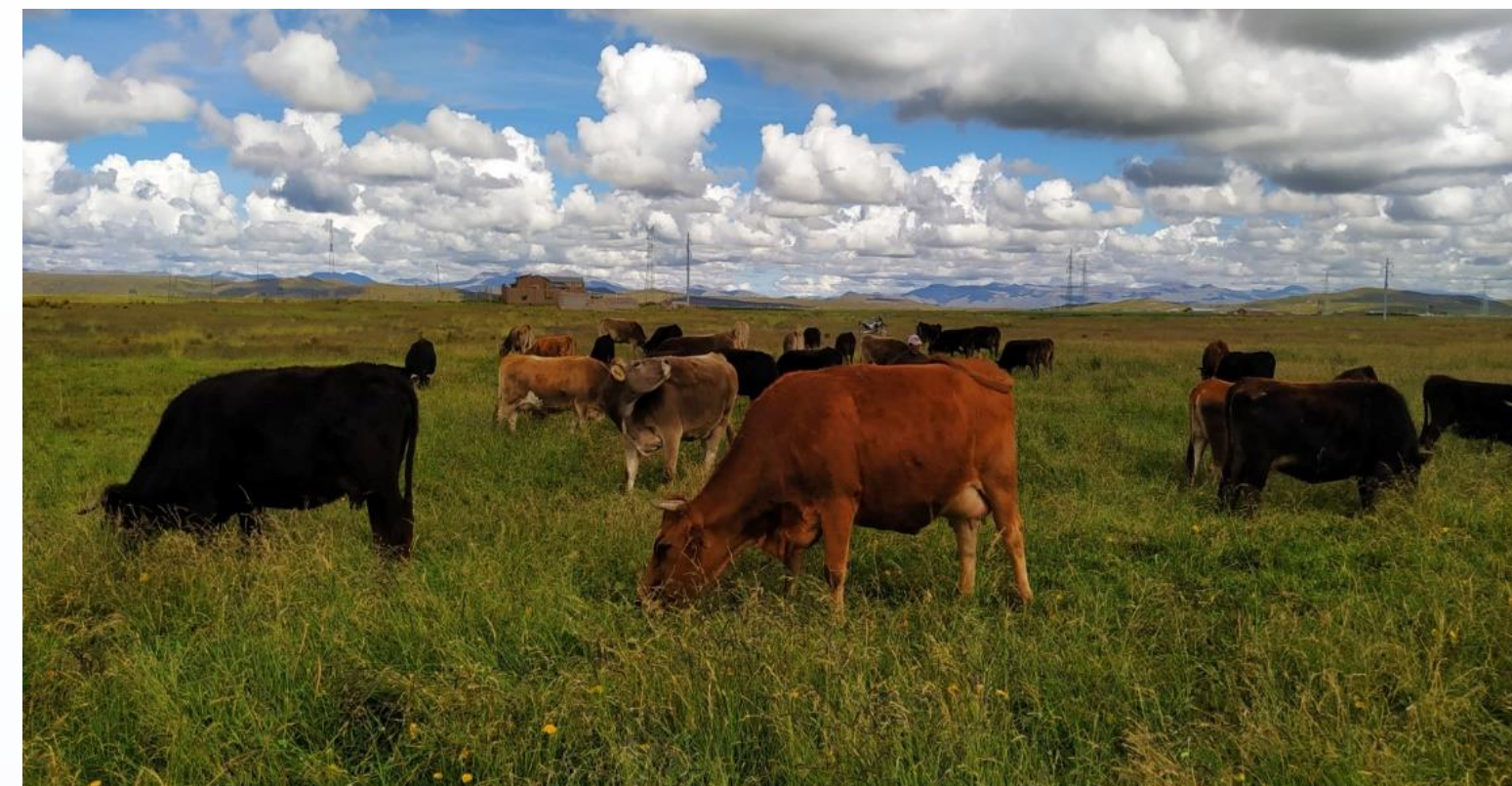
Deyanira Figueroa<sup>1</sup>, Carla L. Saldaña<sup>2</sup>, Flor-Anita Corredor<sup>1</sup>, Lizeth Heredia<sup>1</sup>, Rubén Mamani-Cato<sup>3</sup>, Gustavo Gutierrez<sup>4</sup>, Oscar Gomez-Quispe<sup>5</sup>, Aldo Ciprian<sup>6</sup>, Luis N. Murga<sup>2</sup>, Carlos I. Arbizu<sup>7</sup>

<sup>1</sup>Dirección de Desarrollo Tecnológico Agrario, Instituto Nacional de Innovación Agraria, Lima, Perú; <sup>2</sup>Instituto de Investigación en Ganadería y Biotecnología, Universidad Nacional Toribio Rodríguez de Mendoza, Amazonas, Perú; <sup>3</sup>Dirección de Desarrollo Tecnológico Agrario, Instituto Nacional de Innovación Agraria, Puno, Perú; <sup>4</sup>Facultad de Zootecnia, Universidad Nacional Agraria la Molina, Lima, Perú; <sup>5</sup>Universidad Nacional Micaela Bastidas de Apurímac, Apurímac, Perú; <sup>6</sup>Universidad Nacional San Cristóbal de Huamanga, Ayacucho, Perú; <sup>7</sup>Facultad de Ingeniería y Ciencias Agrarias, Universidad Nacional Toribio Rodríguez de Mendoza, Amazonas, Perú.

Corresponding author: D.F (deyanirafigueroa66@gmail.com), C.I.A. (carlos.arbizu@untrm.edu.pe)

## INTRODUCTION

The creole cattle was originated after the introduction of cattle into America 5 centuries ago. Currently, the production traits of Peruvian creole cattle is scarcely known. An important characteristic of the creole cattle is its adaptability to different extreme environments. However, to date, molecular studies in Peruvian creole cattle are still scarce.



Currently, due to the advances in molecular genetics, a new generation of molecular markers has been developed for the genetic characterization of livestock. Single nucleotide polymorphisms (SNP) have become a very popular tool for the genetic study of livestock populations. Genome-wide SNP chips were developed for multi-breed genetic studies in cattle.

## OBJECTIVES

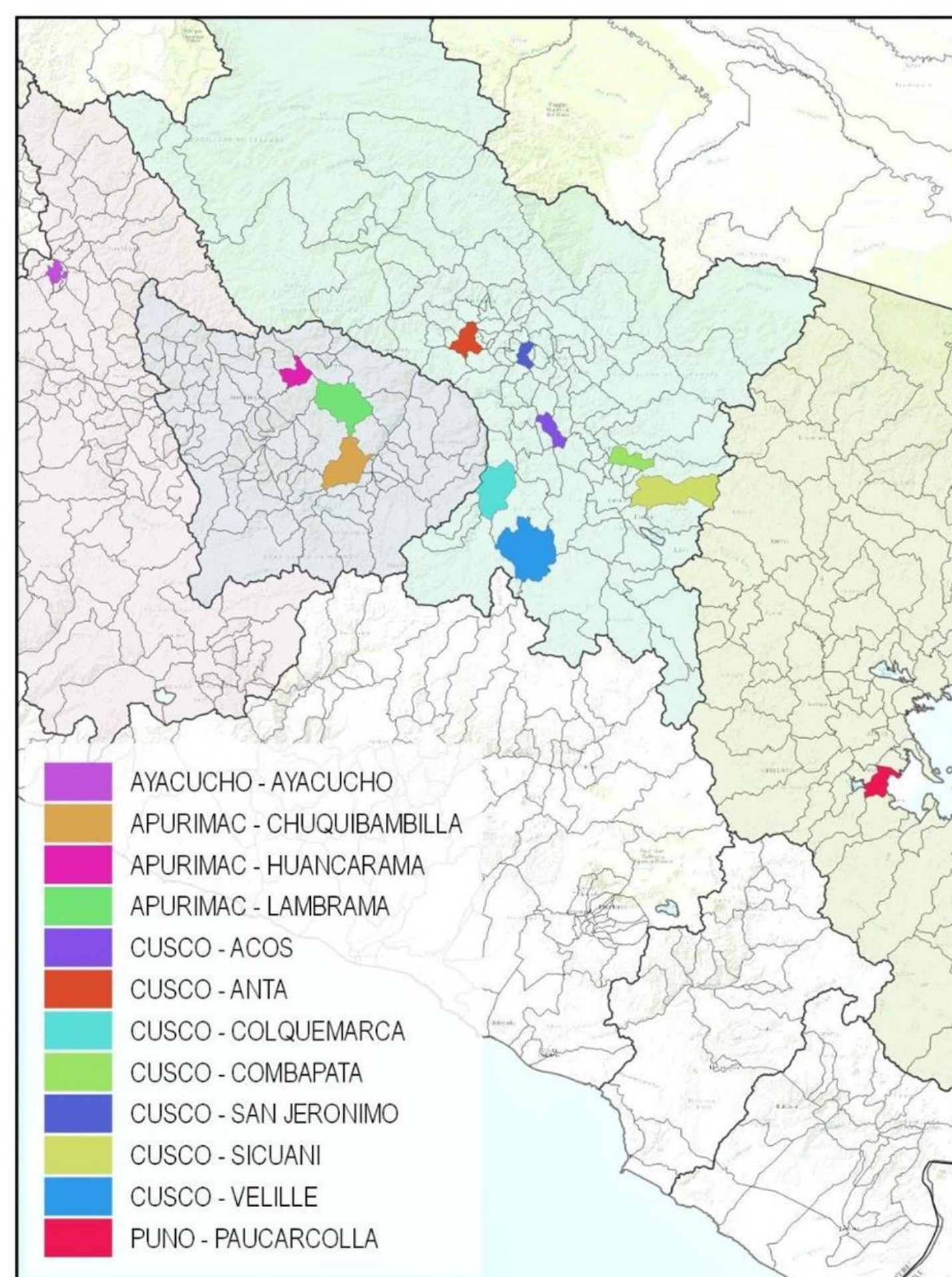
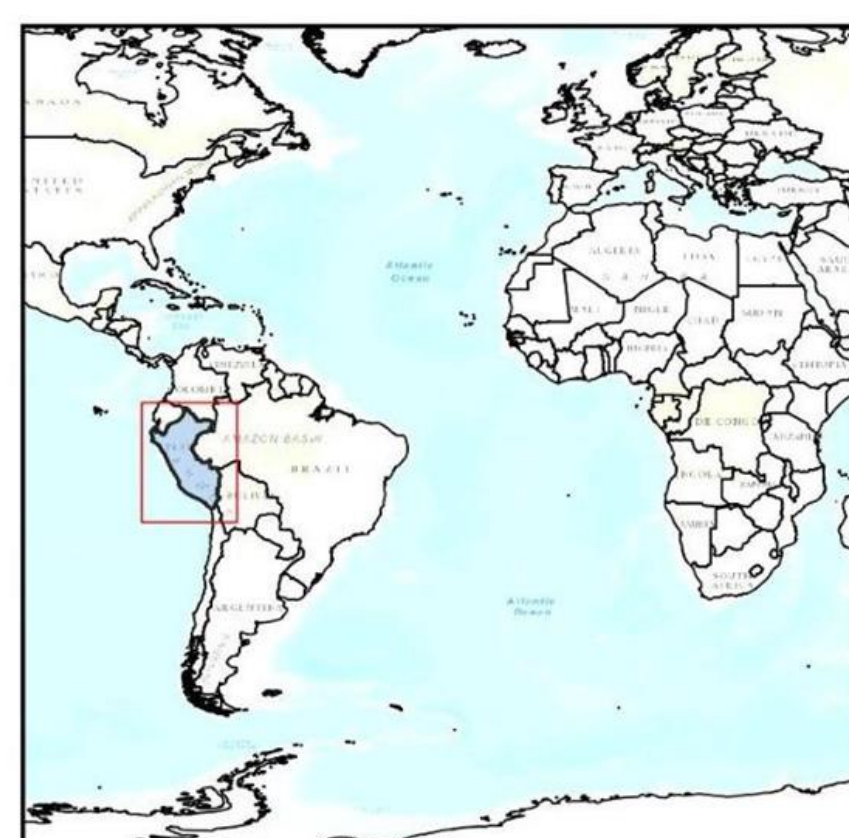
1. Estimate the genetic diversity and population structure of Peruvian creole cattle from four Southern regions of Peru (Apurímac, Ayacucho, Cusco and Puno).
2. Compare the Peruvian Creole cattle population structure with other breeds.

## MATERIALS & METHODS

### Animal sampling

74 animals  
(46 females,  
29 males)

Puno (n=24)  
Cusco (n=20)  
Apurímac (n=18)  
Ayacucho (n=12)



### Genotyping and SNP quality control

- Samples were genotyped by using the Illumina GGP Bovine 100K DNA array at the Neogen laboratory (Neogen, Geneseek, NL, USA).
- Quality control was performed using PLINK v1.9. Samples and SNPs with a genotyping rate  $\geq 90\%$  and minor allele frequency (MAF) higher than 0.05 were retained. Linkage disequilibrium pruning was done, using the PLINK parameter --indep 5 0.5.

### Diversity Analysis

- We used:
- PLINK v1.9 to determine:
- Observed heterozygosity (Ho)
  - Expected heterozygosity (He)
  - Index of fixation (FIS, inbreeding coefficient)
  - Minor allele frequency (MAF)
- ARLEQUIN v.3.5.2 to estimate:
- Pairwise  $F_{ST}$  values
  - Reynold's genetic distances among different populations

### Population Structure

- We used:
- R v.4.3.2 to determine:
- PCoA with ade4 v.1.7-22 package.
  - AMOVA and phylogenetic UPGMA tree with poppr package v.2.9.4
- STRUCTURE software v.2.3.4 to estimate:
- Population structure and individual membership.

## RESULTS

After quality control a data set of 24,200 SNPs and 69 individuals, were left.

### - Genetic diversity parameters

Table 1. Genetic diversity parameters among Peruvian creole bovine populations from four regions of southern Peru.

	n	HO	HE	FIS	MAF
CUSCO	17	0.4 $\pm$ 0.027	0.401 $\pm$ 0.0	0.001	0.314 $\pm$ 0.126
APURIMAC	18	0.399 $\pm$ 0.023	0.402 $\pm$ 0.0	0.01	0.316 $\pm$ 0.125
PUNO	23	0.414 $\pm$ 0.022	0.391 $\pm$ 0.0	-0.057	0.303 $\pm$ 0.13
AYACUCHO	11	0.418 $\pm$ 0.017	0.402 $\pm$ 0.0	-0.041	0.313 $\pm$ 0.127

### - Population structure

Table 2. Analysis of molecular variance (AMOVA) for four Peruvian creole bovine populations

Source of variation	df	SS	MS	Est. Var.	%
Between populations	3	22395,02	7465,01	172,41	3,65
Within populations	65	295850,52	4551,55	4551,55	96,35
Total	68	318245,54	4680,08	4723,96	100,00

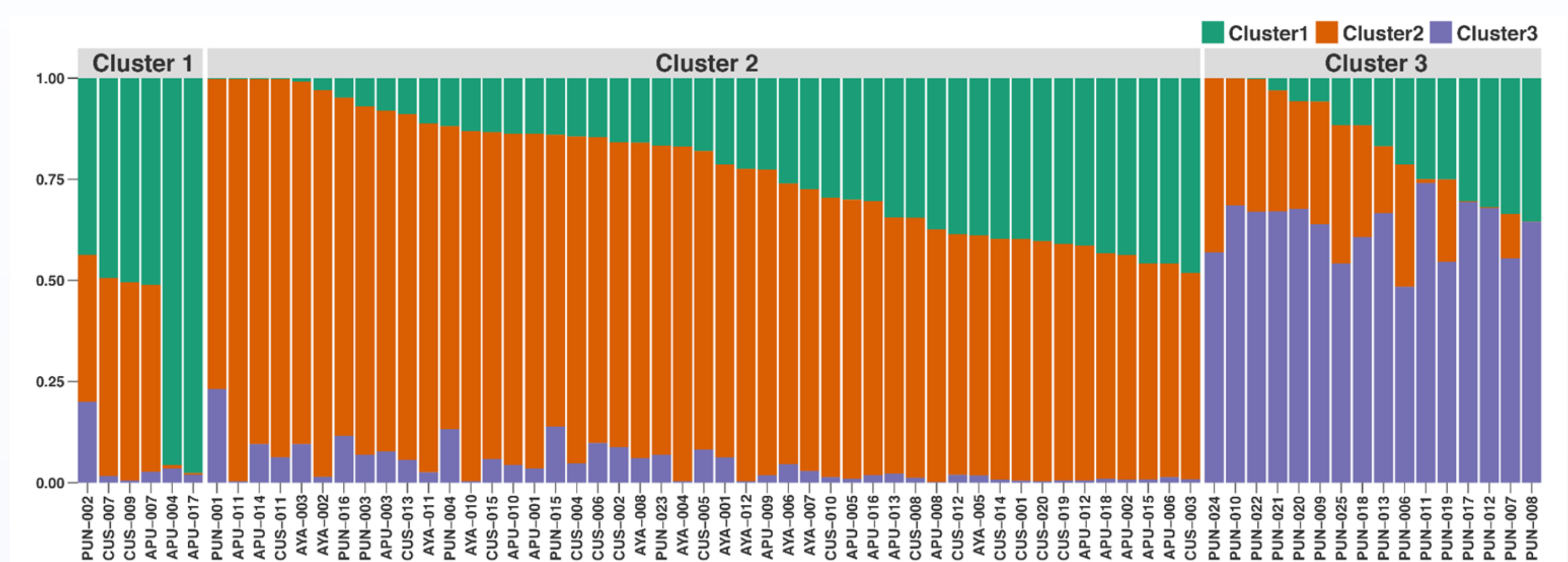


Figure 1. Population structure of four creole bovine populations.

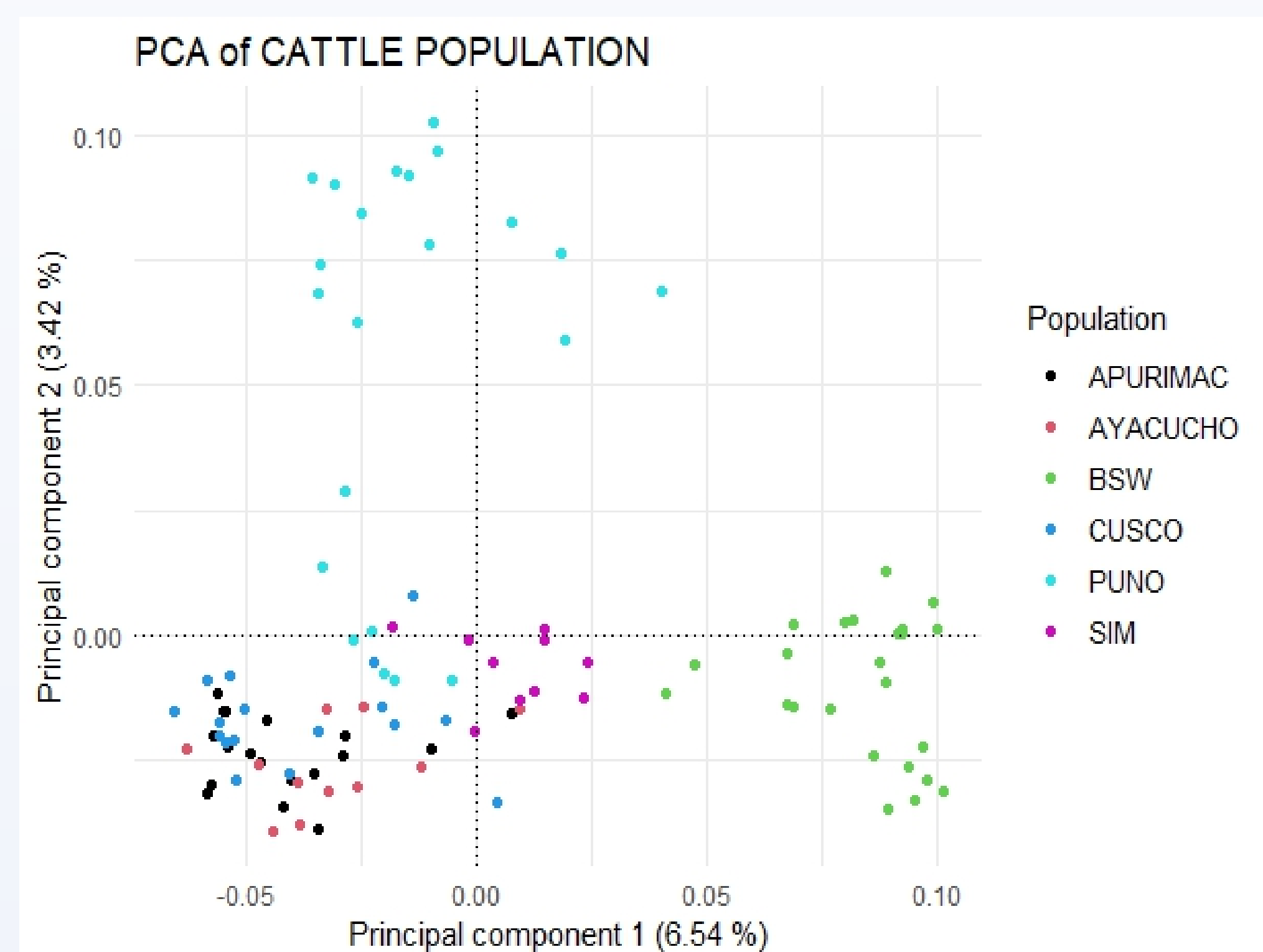


Figure 2. PCoA of four creole bovine populations and two breeds (Brown Swiss (BSW) and Simmental (SIM)).

## CONCLUSIONS

We estimate for the first time the genetic diversity and population structure of southern Peruvian creole cattle from Peru using SNPs. Individuals from Apurímac and Ayacucho showed higher genetic diversity than other regions. The AMOVA results revealed that the partitioning of the genetic variation was largest among individuals within populations (96.35%) and lower genetic differentiation among populations from Southern Creoles bovines. Similar pattern has been seen in other studies of creole bovines, all above 90% of variation within populations. A total of three clusters were identified, interestingly, most of the individuals from Puno region were placed in a single cluster.

The PCoA analysis supports what was found in the structure analysis, that some individuals from the Puno region are clearly separated from the rest of the Southern Creole cattle. On the other hand, Brown Swiss cattle seems to be separated from the Southern Creole cattle, while Simmental is closer. We hope that this work will help in decision making for national cattle breeding programs in Peru.

## ACKNOWLEDGMENTS

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