The Argentine-Patagonian Criollo cattle: A tale of genomic divergence after 70 years of natural selection and isolation

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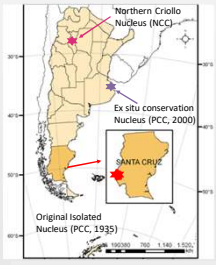
INTRODUCTION



The Argentine Patagonian (PCC) is a Criollo cattle population naturally selected over more than 70 years in isolation in Los Glaciares National Park, located in Santa Cruz, in the southern region of Argentina. Patagonian Criollos are distinguished by their rusticity, adaptability, and high fertility. Bred under harsh environments and natural selection, they have developed unique traits that support their survival and productivity in extensive systems.

Patagonian Criollos exhibit a smaller biotype compared with Northern Argentine Criollo (NCC), particularly in croup height and overall frame size. These characteristics reflect natural selection rather than artificial selection, making them a valuable model for studying adaptation and resilience in livestock.

This study aims to perform the first SNP-based genomic characterization of a large ex situ conserved Patagonian Criollo cattle population and to assess its genetic differentiation from Northern Argentine Criollo and a selected British cattle population.

MATERIAL AND METHODS

GGP 100K BY NEOGEN

PCA: Genesis Package

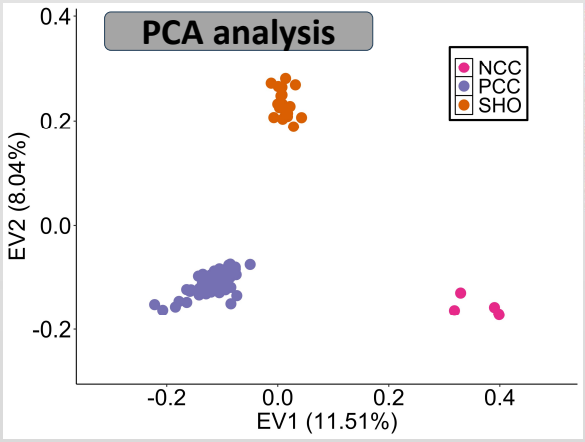
PLINK 1.90 beta

FST discrimination

Admixture Analysis

~ 45,000 SNP were included in this study after pruning (LD and CR)

RESULTS

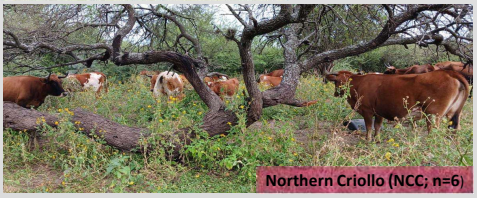


PCA components 1 and 2 explained 20% of the total variance and allowed a clear differentiation between groups.









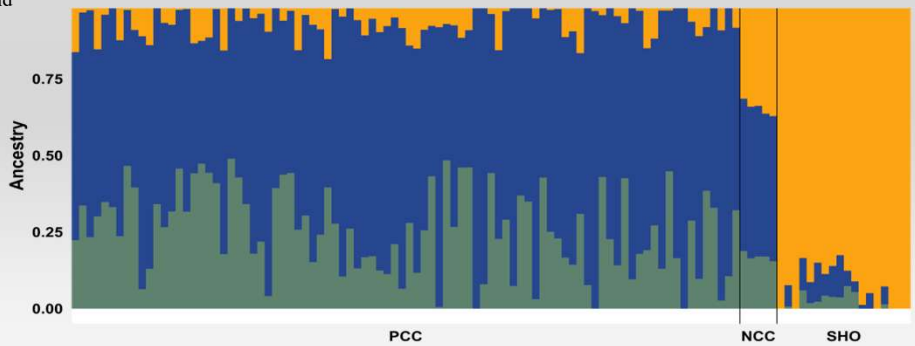


F_{ST} discriminant analysis

	SHO	PCC
NCC	0.176	0.101
PCC	0.140	

F_{ST} index differences among populations support the clear discrimination observed in PCA between breeds.

Coancestry analysis



K3 clustering was able to discriminate adequately most of the PCC individuals from NCC and SHO.

CONCLUSION

This is the first genomic characterization of a naturally selected Criollo cattle population from Patagonia. With minimal human intervention over 70 years, this population represents a unique reservoir of adaptive genetic diversity. The conservation and research efforts led by the University of Lomas de Zamora (UNLZ) are essential to preserve this valuable genetic resource for future generations.

ISAG 2025 CONFERENCE

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