GENETIC STRUCTURE AND BREED COMPOSITION OF THE MODERN CRIOLLO HORSE

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INTRODUCTION



The Criollo horse is recognized as Argentina's national horse and Cultural Heritage. Formally established in the early 20th century, it has been selectively bred for rusticity, cattle work, and breed-specific disciplines. The Criollo is bred in several countries, with separate studbooks allowing horse exchange among Federación Internacional de Criadores de Caballos Criollos (FICCC) members under specific conditions.

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This study aimed to assess the genetic structure of the Criollo horse based on breed composition

MATERIAL AND METHODS

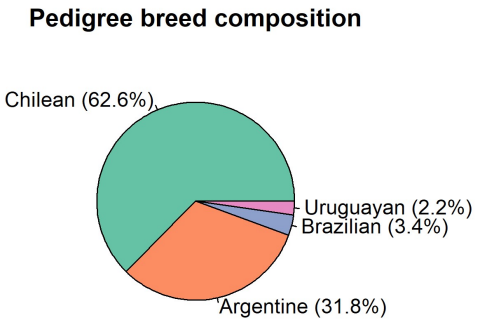
Criollo horses (n=132) sampled at FICCC exposition (Argentina) → Genotyping using EquineSNP70 Beadchip

Pedigree-based breed composition (Pedcom) estimation (optiSel R package), based on founder's country origin:

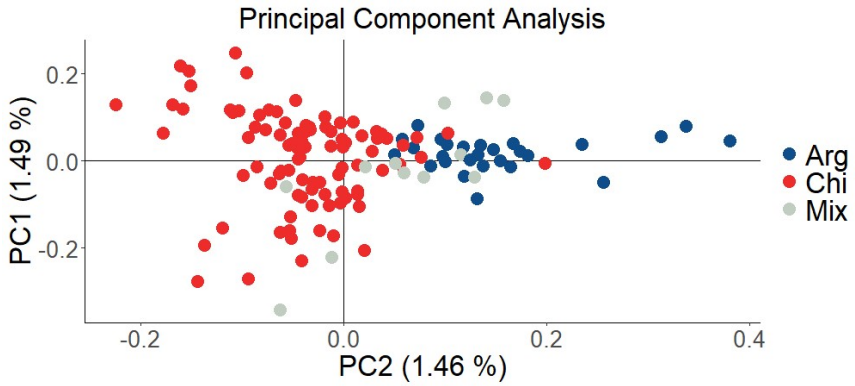
Argentina · Chile · Brazil · Uruguay

Horses grouped as **Chi** (>50% Chilean, n=93), **Arg** (>50% Argentine, n=27), and **Mix** (<50% assignment, n=12). Principal component analysis (PCA) and unsupervised ancestry analysis were conducted using Genesis R package and Admixture software.

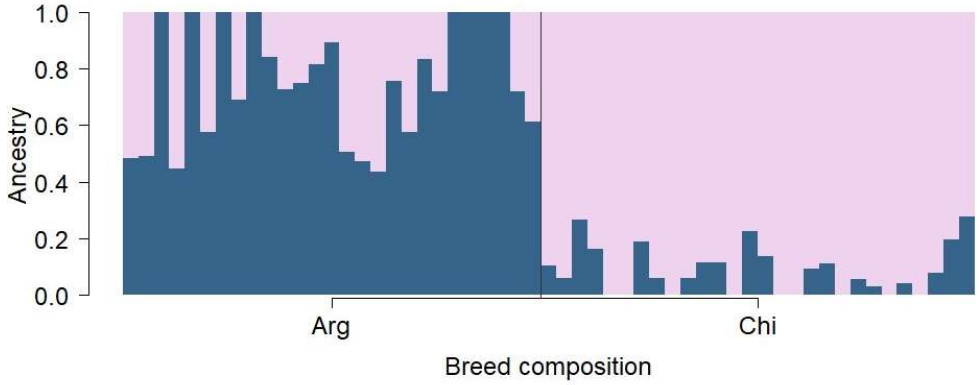
RESULTS



Horses had a high proportion of Chilean Pedcom, followed by Argentine, Brazilian, and Uruguayan.



Two main components of PCA account for 2.95% variability and showed a slight but clear distinction between Arg and Chi groups.



To balance sample sizes, ancestry analysis included the Arg group and a kinship-minimized Chi subset (n=28).

	Mean	
Group	K1	K2
Arg	0.754	0.246
Chi	0.084	0.916

K2 showed the lowest cross-validation error in ancestry analysis. Arg horses were mainly assigned to K1 and Chi to K2.

Strong correlations were found between K1 and Argentine Pedcom (0.87), and between K2 and Chilean Pedcom (0.88).

CONCLUSION

Criollo horse has a complex ancestry-based composition in both pedigree and genomic analysis. A slight genetic structuring was detected in the population analyzed according to the founder's origin, reflecting the magnitude of gene flow between populations from different countries. Further studies are needed to assess the phenotypic impact of genetic composition in the breed.

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