mtDNA variability in SNCT produced cloned horses: Are they so identical genomically?

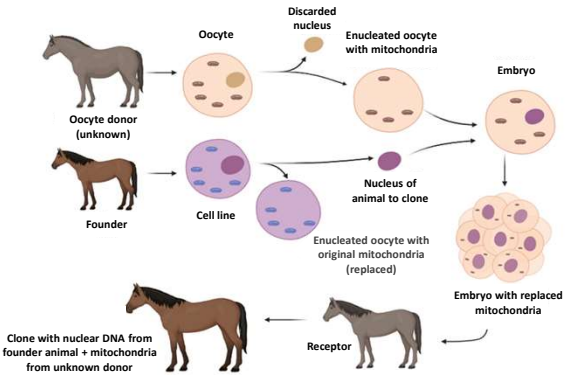
Ayelén Karlau[1,2], María Ángeles Vargas Pérez[3], Gabriel Anaya[3], Pablo Trigo[1,2], Florencia Azcona[3], María Yuzhi Arjona[3], Juan Pablo Sánchez Serrano[3], Antonio Molina[3], Sebastián Demyda Peyrás[3*]

1. Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina; 2. CONICET, La Plata, Buenos Aires, Argentina; 3. Departamento de Genética, Universidad de Córdoba, Córdoba, España.

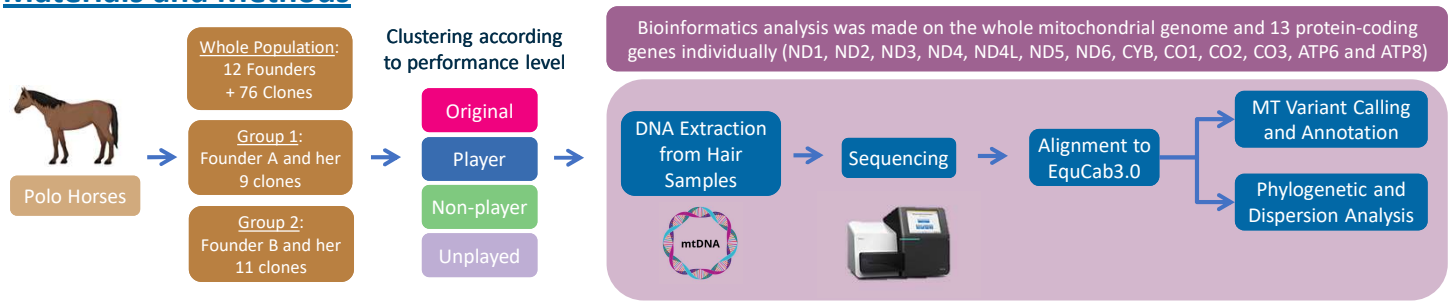
Introduction

Production of cloned animals using somatic cell nuclear transfer (SNCT) is a common practice with polo horses in Argentina. Clones receive the founder's nuclear DNA, but not the mitochondria, which is derived from an unknown oocyte donor. Mitochondria contains its own genome (mtDNA) comprising 37 genes, including 13 protein-coding genes that encode components of the mitochondrial respiratory chain, essential for cellular bioenergetics.

Differences in the mtDNA profile between founders and clones may have an impact on performance in polo horses



Materials and Methods



Results

Mean coverage = 144x

All Samples

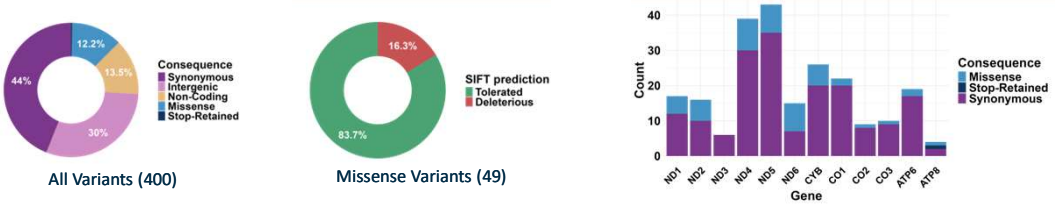
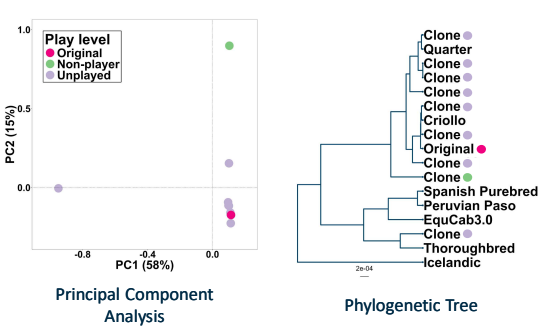
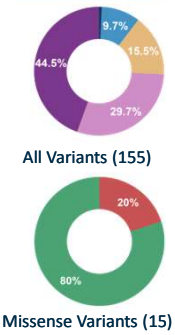


Figure 1. Variant consequences for all samples in whole mtDNA and per protein-coding gene. Variant consequences are depicted in purple (Synonymous), pink (Intergenic), beige (Non-Coding), light blue (Missense) and dark blue (Stop-Retained). Missense variants are further classified into tolerated (green) or deleterious (red). The number of variants detected on mitochondrial genes, classified according to their effect, is also shown.

Group 1 (Founder A and her 9 clones)





Group 2 (Founder B and her 11 clones)

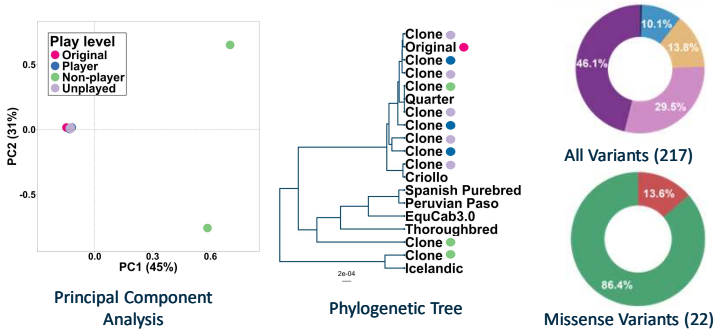


Figure 2. Principal component analysis, phylogenetic tree and variant consequences for groups 1 and 2. Samples are coloured according to their play level: Original (founders), **Player** (old clones that played polo), Non-player (old clones that never played polo) and Unplayed (young clones that do not have play yet). Variant consequences are depicted in purple (Synonymous), pink (Intergenic), beige (Non-Coding), light blue (Missense) and dark blue (Stop-Retained). Missense variants are further classified into tolerated (green) or deleterious (red). A UPGMA tree was built for each group, including EquCab3.0 (reference genome), Icelandic, Thoroughbred, Quarter, Peruvian Paso, Criollo and Spanish Purebred horses.

Conclusion

Our results show that there is considerable variability in the mitochondrial genome both at a genomic and gene level in polo horses, with clear differences between cloned and founder individuals. This suggests that the mitochondrial profile could have an influence on athletic performance.

equgenomics
@DemydaPeyrasLab
sebass@uco.es