Inbreeding affects morphometrics and kinematic traits in stallion sperm: genomic evaluation using a chromosome-level modeling

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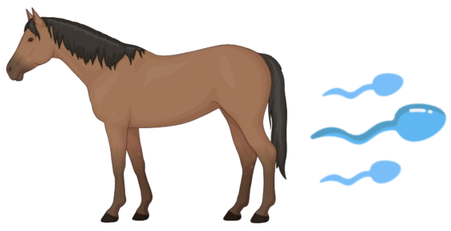
INTRODUCTION

Selective breeding programs aim to enhance specific traits in horses but often increase inbreeding coefficients, resulting in inbreeding depression that predominantly affects reproductive fitness. This phenomenon appears to be relevant in the case of stallions, where sperm motility and morphometry deficiencies are not uncommon.

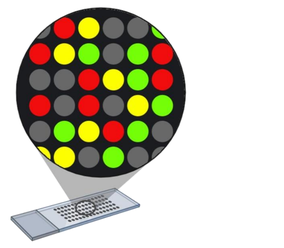
OBJECTIVE

Evaluate the influence of inbreeding levels across genome regions on sperm morphometry and motility in Polo Argentino (CPO) stallions.

MATERIALS AND METHODS



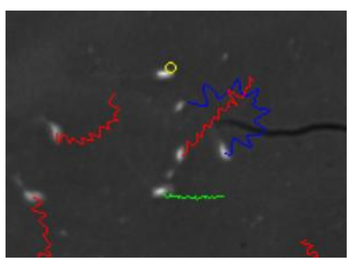
Semen samples from **67 CPO stallions**
100 spermatozoa per individual



GGP Equine Array
68,669 autosomal markers

SCA™ CASMA system

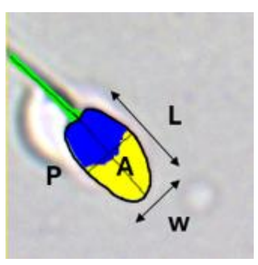
Motility



Time (min)
5, 60, 120, 180

Parameters
VCL= Curvilinear velocity
VSL= Straight line velocity
VAP= Mean path velocity
STR= Straightness
LIN= Linearity
WOB= Wobble
ALH= Amplitude of lateral head displacement

Morphometric



Parameters
L=Length
W=Width
A=Area
P=Perimeter
Elongation
p^2a

Analysis

PLINK 1.9 beta

R

METACRAN

ggplot2 tidyverse data.table MetBrewer

RESULTS

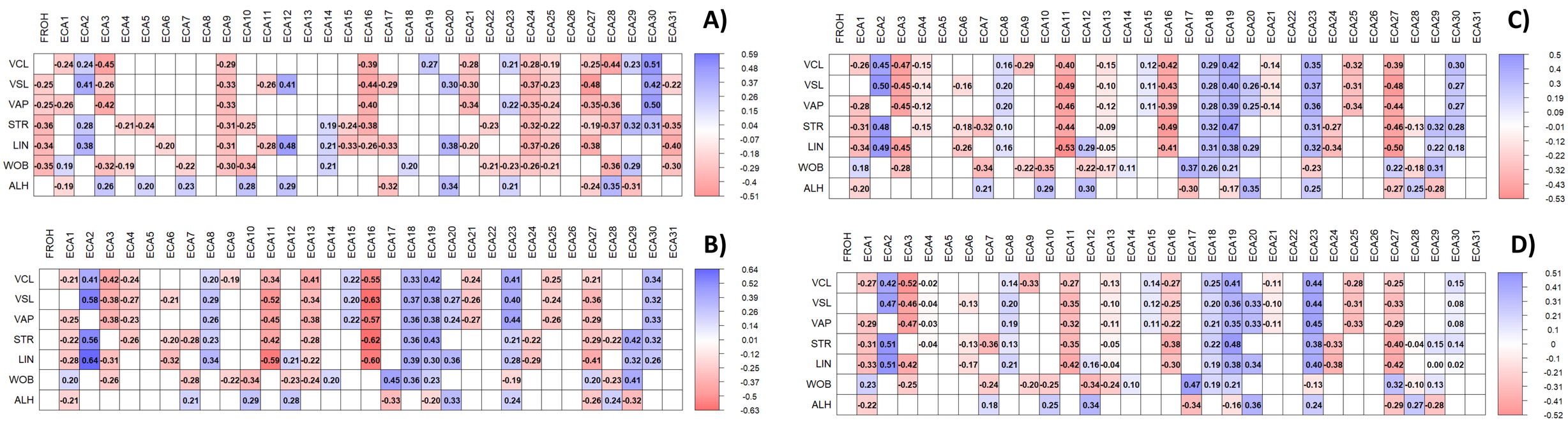


Figure 1. Correlation analysis between motility parameters and F_{ROH} per chromosomes: A (5min), B (60min), C (120min), D (180min). Values ($p < 0.05$).

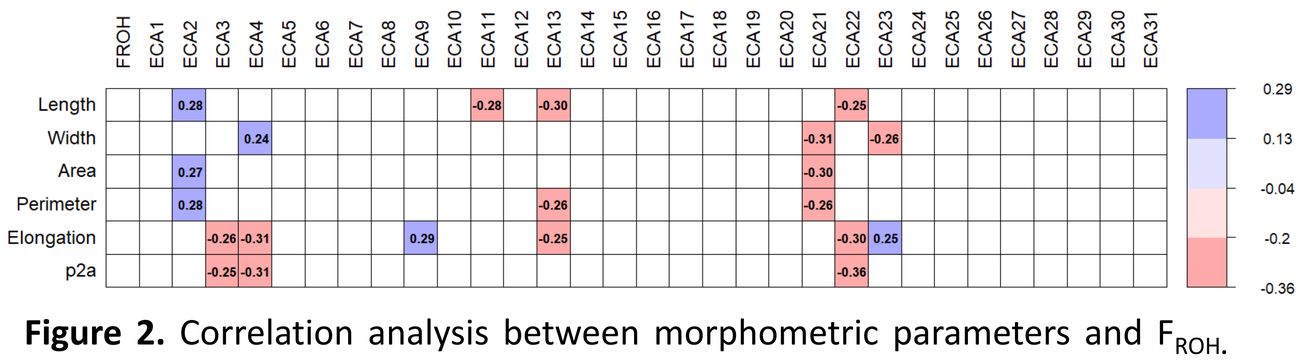


Figure 2. Correlation analysis between morphometric parameters and F_{ROH}. Values ($p < 0.05$).

	Most	Least
hc1	26	13
hc2	14	14
hc3	19	27
hc4	8	17

hc1: ↑ p^2a ↓ area
hc2: ↓ p^2a ↓ area
hc3: ↓ p^2a ↑ area
hc4: ↑ p^2a ↑ area

Figure 3. Morphometrics subpopulations. Most: n=67; Least: n=71 (n=71 due to individuals sharing identical minimum admixture proportions).

CONCLUSION

Our results identified specific chromosomal regions responsible for positive and negative variations in sperm morphometry, suggesting that inbreeding depression on sperm traits is highly localized, not a random, genome-wide event. Controlling inbreeding at specific genomic regions could become an interesting tool for accurately modeling and predicting negative effects in sperm traits, enhancing reproductive fitness in stallions.

Applied Animal Genomics and Citogenomics Lab

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