



UNIVERSITY OF LIFE SCIENCES
"KING MIHAI I" FROM Timisoara
**Multidisciplinary Conference on
Sustainable Development**
25-26 May 2023



Assessing genomic inbreeding and homozygosity patterns in Hungarian Merino sheep and its relatives

George Wanjala^{1,2,3}, Putri Kusuma Astuti^{1,2}, Nelly Kichamu^{1,2,4}, Zoltán Bagi¹, Szilvia Kusza^{1*}

¹Centre for Agricultural Genomics and Biotechnology, Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, 4032 Debrecen Egyetem tér 1., Hungary.

²Doctoral School of Animal Science, University of Debrecen, 4032 Debrecen Böszörményi út 138., Hungary.

³Directorate of livestock production, Bungoma County, Box 437-50200, Bungoma Kenya.

⁴Ministry of agriculture livestock, fisheries, and cooperatives, State department of livestock development, Naivasha sheep and goats breeding station, Box 20117, Naivasha Kenya.

Abstract: Hungarian Merino had the second highest number of runs of homozygosity (ROH) class of 1-6 mbs after Rambouillet breed. The genomic inbreeding coefficient (FROH) of Hungarian Merinos was comparable to that of other studied breeds, while Spanish Merinos Cordoba had the highest. The results can be used to improve genomic management of Hungarian Merino sheep breed.

• Introduction

The objective of this study is to compare the genomic inbreeding coefficient (FROH) and patterns of runs of homozygosity (ROH) between the Hungarian Merino and other closely related Merino breeds.

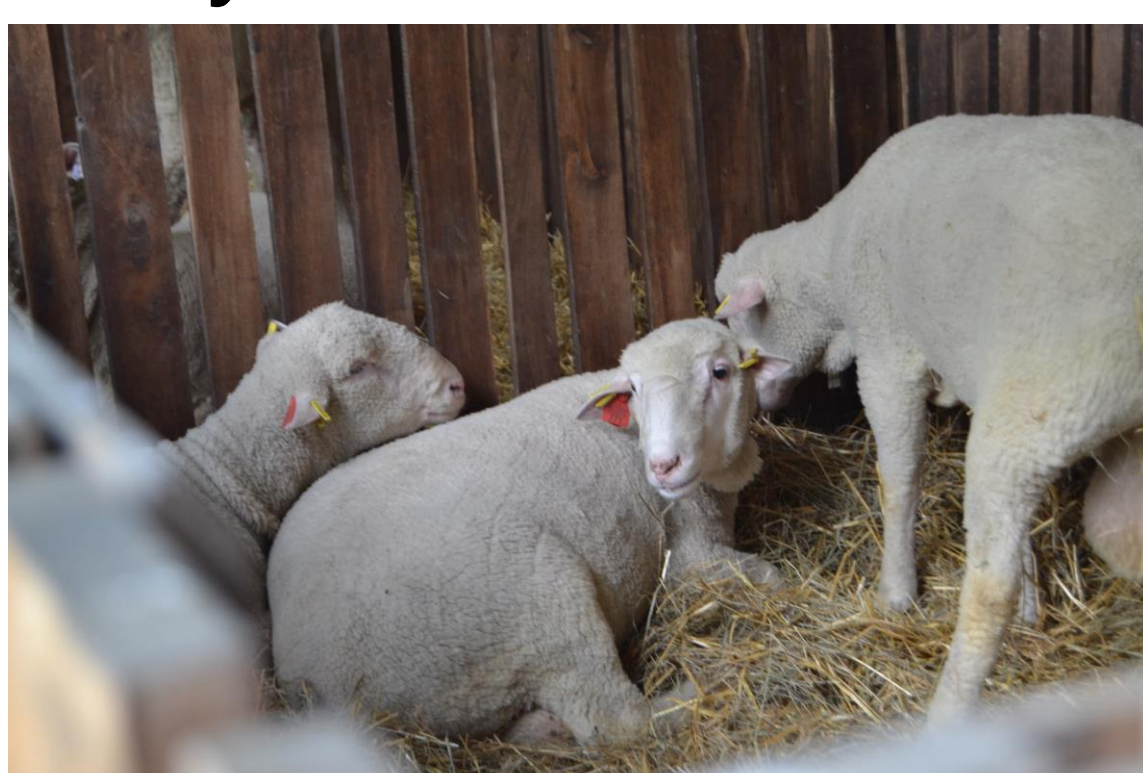


Fig 1: Hungarian Merino sheep

• Material and method

SNP data from Hungarian Merino ($n = 26$) were used in the study alongside other datasets retrieved from public repository and published in (1). The Hungarian Merino sheep breed relatives studied include Spanish Merino Cordoba ($n = 7$), Australian Merino ($n = 24$), Australian Industry Merino ($n = 24$), Chinese Merino ($n = 23$), and Rambouillet ($n = 24$).

Results and discussions

The Hungarian sheep breed had the second highest number of runs of between 1-6 mbs, trailing only the Rambouillet breed.

Hungarian Merino among others did not have ROH of > 48 mbs suggesting that they are less inbred (Table 1).

Table 1. Summary of runs of homozygosity and inbreeding levels per sheep breed.

Breed	Runs of homozygosity classes					FROH
	1-6	6-12	12-24	24-48	>48	
1	670	86	28	9	-	0.053 ± 0.022
2	807	149	62	21	1	0.085 ± 0.052
3	591	106	33	11	-	0.055 ± 0.027
4	663	95	36	16	1	0.063 ± 0.046
5	1041	116	20	7	-	0.060 ± 0.024
6	1206	178	61	10	2	0.101 ± 0.052
7	318	187	115	41	7	0.347 ± 0.051

1 = Australian Industry Merino, 2 = Australian Merino, 3 = Australian Poll Merino, 4 = Chinese Merino,
5 = Hungarian Merino, 6 = Rambouillet, 7 = Spanish Merinos Cordoba.
FROH = Genomic inbreeding coefficient

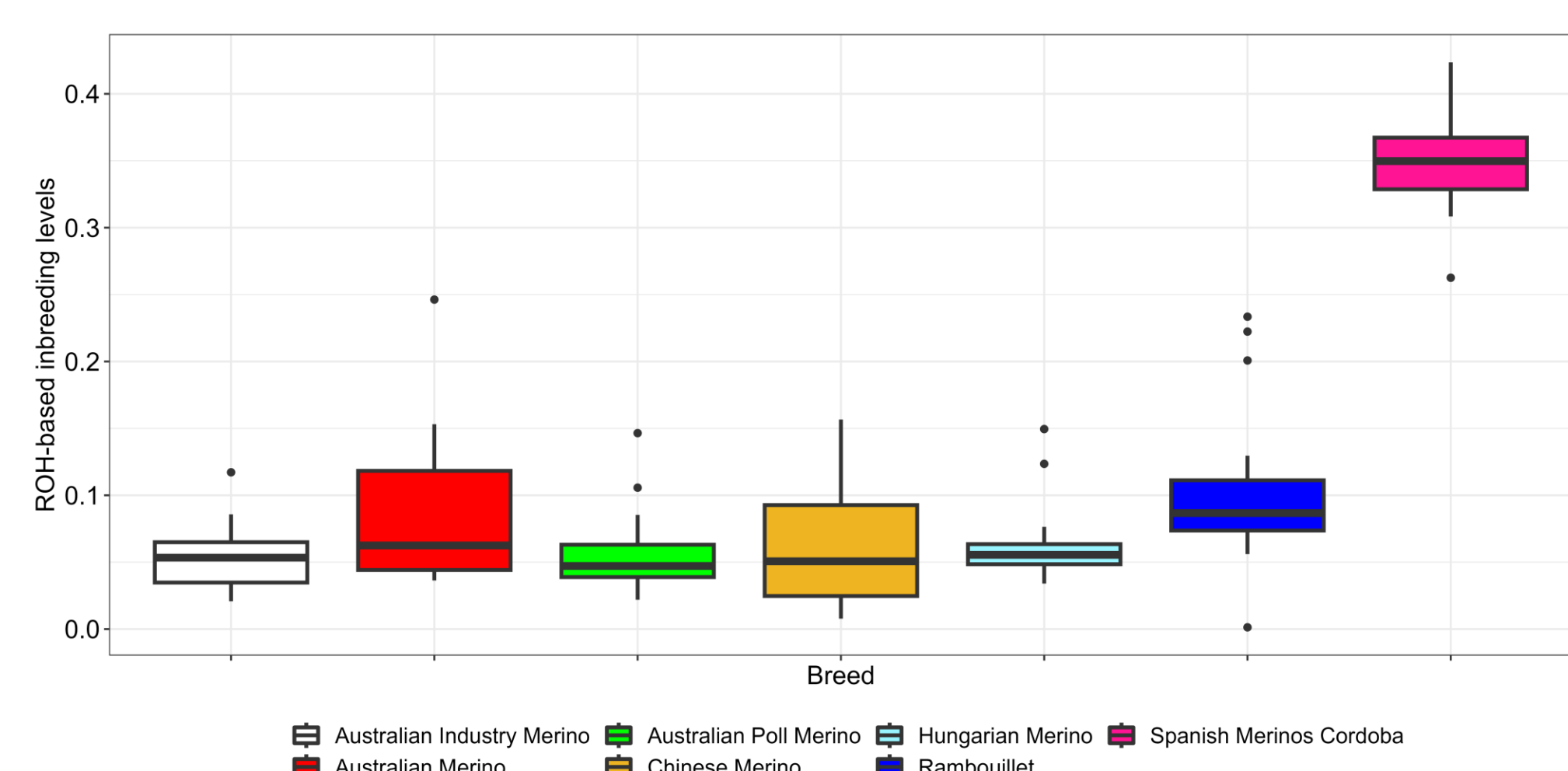


Fig 2: Average ROH-based inbreeding levels per sheep breed

The genomic inbreeding level of Hungarian Merino is comparable to other breeds studied while that of Spanish Merino Cordoba is higher than others (Fig 1).

• Conclusions

The presence of different classes of ROH indicates that Hungarian Merino has a distinct genetic resource as well as multiple ancestral backgrounds.

References: <https://doi.org/10.1186/s12711-015-0139-z>

Contact for more information
geog.wanjala@gmail.com

Acknowledgement: G.W, P.K.A and N.K acknowledges Stipendium Hungaricum scholarship program for supporting their PhD studies in Hungary, University of Debrecen.