

Genetic diversity and population structure of a Creole sheep flock from Uruguay

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Electronic Supplementary Material (ESM)

Table S1. Sex and category of individuals sampled per population

Table S2. ROH counts per size class and population

Figure S1. Frequency of ROH per size class and population

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Table S1. Sex and category of individuals sampled per population

Code	Population	Source	N	Sex		Category		
				Male	Female	Rams	Ewes	Lambs
CSM	San Miguel National Park Creole	this study	139	34	105	21	43	75
CLB	INIA Las Brujas Creole	this study	139	51	88	7	34	98
COM	Commercial breeders Creole	this study	35	12	23	8	20	7
COR	Corriedale breed	this study	139	45	94	45	0	94
MER	Merilin breed	this study	43	45	0	45	0	0
BCS	Brazilian Creole	Sempere et al. (2015)	23	not available				
SOA	Soay breed	Sempere et al. (2015)	110	not available				

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

Table S2. ROH counts per size class and population

ROH length (Mb)	BCS	CLB	COM	COR	CSM	MER	SOA
0–2 Mb	726	7 402	1 655	4 061	8 383	1 359	10 190
2–4 Mb	880	6 512	2 069	2 909	9 608	1 200	9 125
4–8 Mb	438	2 403	1 074	684	4 083	381	2 241
8–16 Mb	95	444	230	57	699	47	123
>16 Mb	1	1	2			1	
Total	2 140	16 762	5 030	7 711	22 773	2 988	21 679

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; ROH = runs of homozygosity; SOA = Soay

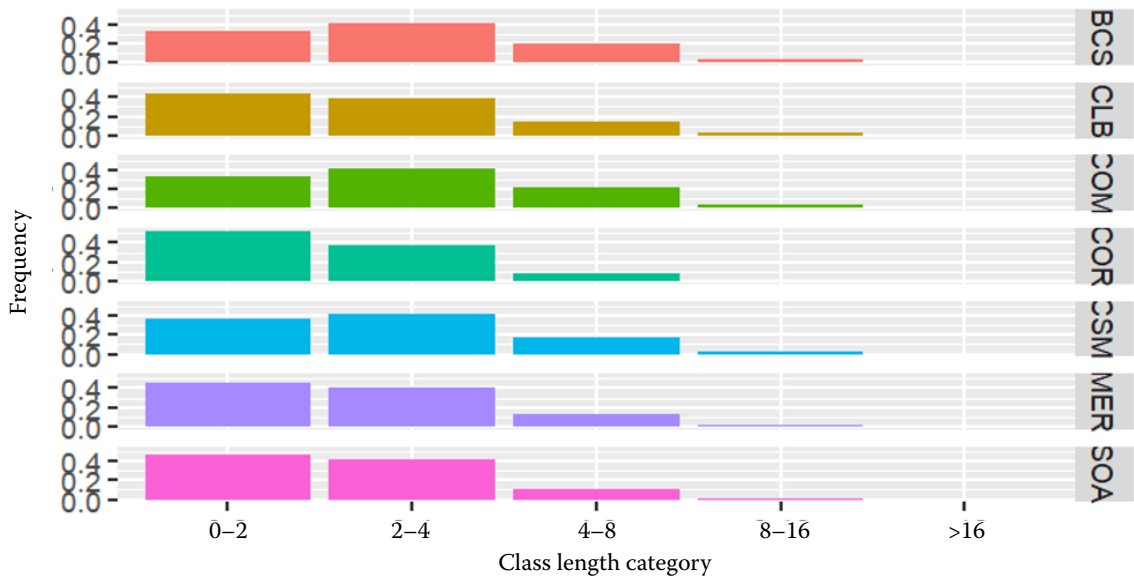


Figure S1. Frequency of ROH per size class and population

ROH = runs of homozygosity

Reference: Sempere G, Moazami-Goudarzi K, Eggen A, Laloe D, Gautier M, Flori L. WIDDE: A Web-Interfaced next generation database for genetic diversity exploration, with a first application in cattle. BMC Genomics. 2015 Nov 14;16:940.