

NEW TECHNOLOGIES FOR THE ANALYSIS OF REPRODUCTIVE EFFICIENCY IN IBERIAN SOWS

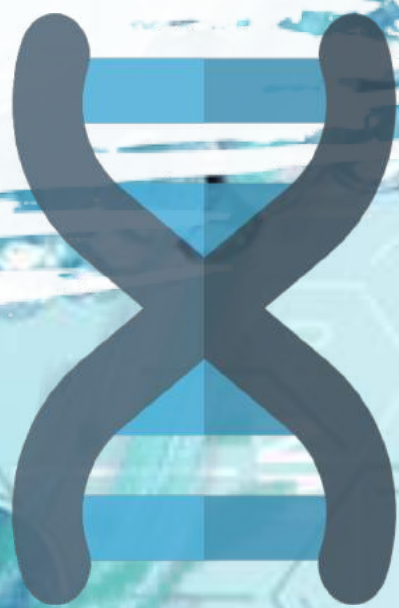
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INTRODUCTION AND OBJECTIVES

During the last decades, the vast advances in biotechnology and molecular biology have allowed the performance of genomic association studies that have served to identify a large number of markers linked with the characters of interest in animal production, among which are the reproductive traits.

However, fertility remains as a poorly understood trait at genetic level. With the aim of evaluating the inclusion of this character as a potential candidate for the selection and productive improvement of the Iberian breed, the present study attempted to clarify its additive genetic component, as well as locating the genome regions associated with this genetic variability.



MATERIAL AND METHODS

346 RETINTAS

330 ENTREPELADAS

1235
GENOTYPED
SOWS

PUREBRED

Inclusion of all phenotypic,
genotypic and genealogical data

BLUPs mixed linear model

Incorporation of genotypic values

Genome Wide Association Study

DISCUSSION AND CONCLUSIONS

This study obtained low heritability values, in line with those previously obtained in other pig breeds. However, despite its reduced additive component, it is important to keep in mind that there are genetic correlations between the reproductive traits, which could mean an alternative for indirect fertility selection.

On the other hand, the GWAs identified a high number of significant SNPs (859 in Entrepelado and 93 in Retinto) suggesting the presence of a large number of genes associated with the character, whose individual effect is small. Despite this remarkable numerical difference, common genomic regions associated with NCI were identified in both lines, which would indicate the sharing of the same conserved genetic mechanism.

In conclusion, the insemination cycle number (NCI) is considered as a poor candidate to be included in the Iberian improvement breeding programs, although future research is required to clarify possible mechanisms of indirect selection for this character in the Iberian breed.

RESULTS

Lineage	V_A		V_E		V_R		h^2	
	μ	S	μ	S	μ	S	μ	S
ENTREPELADO	0,068	0,029	0,435	0,104	1,248	0,105	0,039	0,016
RETINTO	0,069	0,032	0,434	0,101	1,538	0,140	0,034	0,015

Table 1. Analysis and decomposition of the phenotypic variance for the *insemination cycle number* (ICN) variable in each one of the lineages.

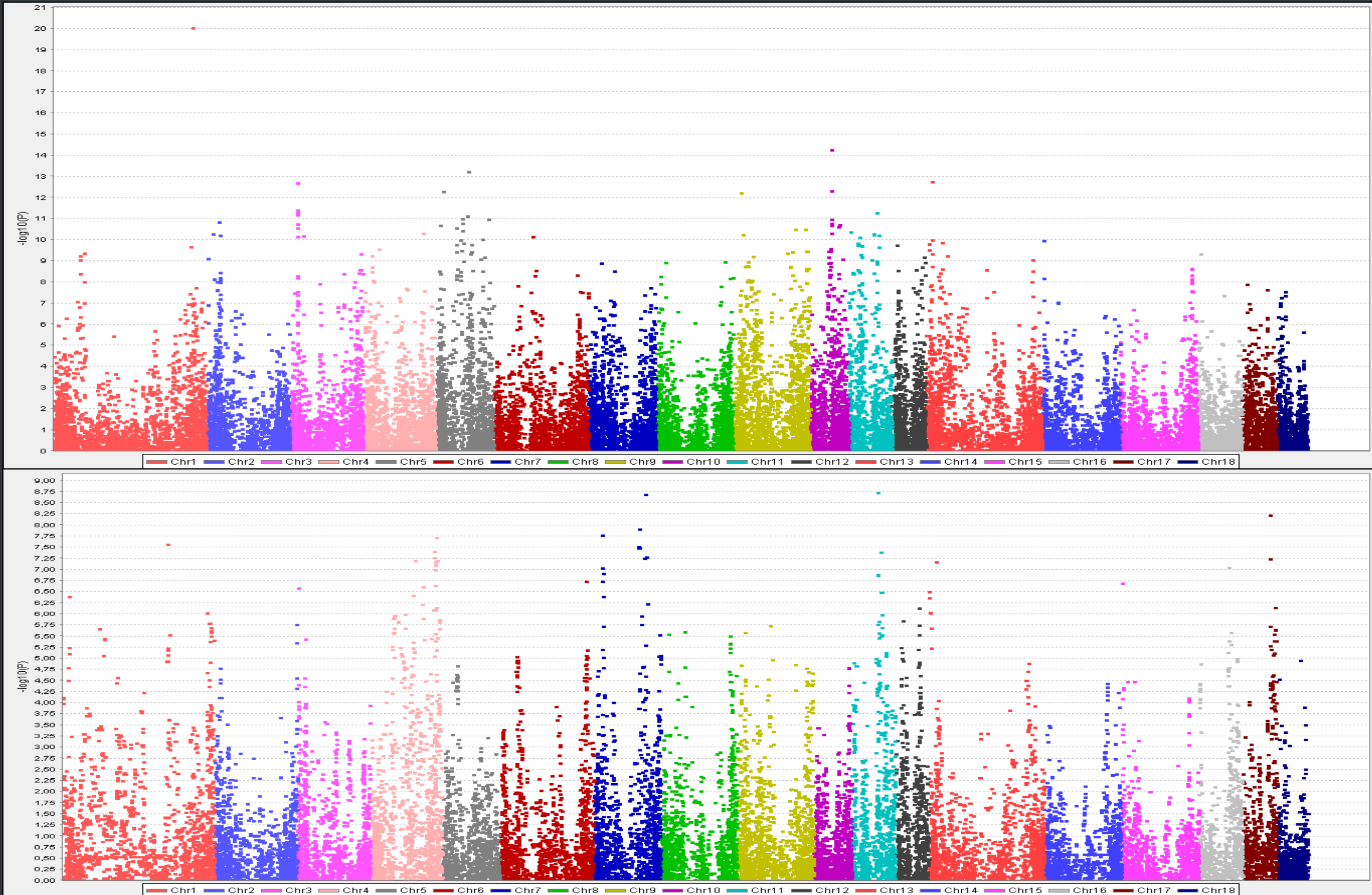


Figure 1. Manhattan plots for the ICN character in the Entrepelado (above) and Retinto (below) lineages.

Lineage	Chr	SNP	Position	A1	A2	FA1	b	se	p value
ENTREPELADO	1	rs336169801	265589331	G	A	0,33	-0,04	0,01	2,48E-07
	1	rs80828129	265619998	A	G	0,33	-0,04	0,01	2,13E-07
	1	rs337517599	265836097	G	A	0,16	-0,06	0,01	1,74E-07
	1	rs331813955	266807652	G	A	0,18	-0,06	0,01	9,12E-08
	1	rs80943535	267786964	A	C	0,40	-0,04	0,01	1,37E-06
	4	rs81272123	77503038	G	A	0,42	0,04	0,01	1,90E-08
	11	rs333034346	52016277	G	A	0,13	-0,07	0,01	3,03E-08
	11	rs342533143	52354280	G	A	0,43	0,04	0,01	1,20E-06
	11	rs80838262	54696699	A	G	0,04	-0,12	0,02	1,67E-07
	11	rs80804675	54737728	G	A	0,07	-0,12	0,02	6,11E-11
RETINTO	11	rs81431399	55152688	A	C	0,08	-0,08	0,02	1,10E-07
	11	rs81431400	55180420	G	A	0,08	-0,08	0,02	1,10E-07
	11	rs81431403	55209417	G	A	0,11	-0,09	0,01	2,20E-10
	1	rs344359566	262231222	A	C	0,16	0,05	0,01	9,40E-07
	1	rs81340206	266193966	G	A	0,22	0,04	0,01	1,62E-06
	1	rs337015601	266215776	G	A	0,22	0,04	0,01	1,62E-06
	1	rs324919029	266271241	A	G	0,22	0,04	0,01	1,62E-06
	1	rs340225835	266514922	G	A	0,22	0,04	0,01	1,62E-06
	1	rs81474352	266639949	A	G	0,22	0,04	0,01	1,62E-06
	4	rs81272123	77503038	G	A	0,25	-0,04	0,01	3,79E-07
COMMON	11	rs321975288	52276151	A	G	0,50	-0,04	0,01	4,06E-08
	11	rs80920041	52558999	G	A	0,25	0,04	0,01	3,20E-07
	11	rs81341149	52562607	A	C	0,25	0,04	0,01	3,20E-07
	11	rs80841480	54445816	A	C	0,25	0,04	0,01	3,20E-07
	11	rs336342341	55121472	A	G	0,26	0,04	0,01	1,05E-06

Table 2. Significant SNPs for the ICN character located in common chromosomal regions in both Entrepelado and Retinto lineages.

