

Effect of genomic selection on allele frequencies of QTL associated to number of teats in pigs

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• Number of teats ahead with progress in litter size



• Increase in litter size and in number of teats in the last five years





OBJECTIVE

Better understand the impact of GENOMIC SELECTION on NUMBER OF TEATS

by following the changes in allele frequency across generations on different QTL regions affecting NTE in two maternal lines.

Available information

- Number of teats on males and females.
- Phenotypes: 1,380,975 Landrace (Born 2006-2023)

1,893,122 Large White (Born 2006-2023)

- Genotypes: 375,610 Landrace (Born 2012-2022)
 346,420 Large White (Born 2012-2022)
- Genotyped on Illumina GeneSeek custom SNP chips (25K, 50K or 80K)
- Imputed to 660K in two steps (genotyped \rightarrow 50K \rightarrow 660K)



Line difference of 1.25 teats

Landrace 17.25 teats in average



Large White 16.02 teats in average

Topigs Norsvin

Phenotypic trend in teat numbers differs



More variation present in Landrace

	Landrace	Large White
Phenotypic	1.46 (0.02)	1.06 (0.01)
Genetic	0.57 (0.02)	0.36 (0.01)
Heritability	0.39 (0.01)	0.34 (0.01)

*Standard errors in parenthesis



Landrace



Chromosome

Opposite trend for VRTN allele increasing number of teats



Unexpected correlations with other trait



Chromosome

Landrace

16 17



2nd top QTL associated with NTE

Chromosome

10 11 12

Parameters for the SNPs in the 2 top QTL associated with NTE

Line	SSC	SNP	Position (Mb)	Freq.	Effect	Vg*	Vp*
L	12	AX-116444814	51	0.17	0.29	0.047	0.018
LW	12	AX-116758961	51	0.70	0.16	0.029	0.010





Discussion

- Less number of teats in Large White could be explained by less (genetic) variation.
- VRTN locus: the allele frequencies and their trend are the opposite in both lines.
 - Antagonist pleiotropy
 - Other QTLs contributes more to the overall genetic potential and selection space for NTE in Large White.





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LW	12	AX-116444814	51	0.01	NA	NA	NA
L	12	AX-116758961	51	0.23	0.13	0.011	0.004
LW	12	AX-116758961	51	0.70	0.16	0.029	0.010

*explained



Region in detail @

Allele frequency trend

