

How directional artificial selection has shaped the genome of Italian heavy pig breeds

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Introduction

In Italy, the main products derived from pigs are Italian dry-cured hams (e.g. Parma and San Daniele hams). High-quality hams are produced with a breeding system specifically designed for 'heavy pigs', involving the Italian Large White (ILW), Italian Duroc (ID), and Italian Landrace (IL) breeds. The breeding program for these breeds began in 1990, with the main objective of satisfying the needs of the Italian Protected Designation of Origin (PDO) ham industry.

This directional selection was based on several traits that substantially improved performance, reproduction and carcass traits of the three breeds while maintaining the meat quality for seasoning.

In this study, we monitored how over four decades this selection acted at the genomic level on Italian heavy pig breeds.

Material and Methods

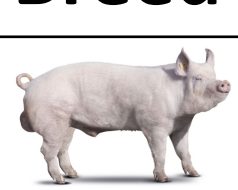
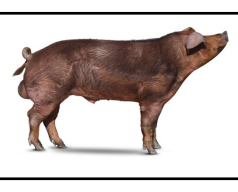
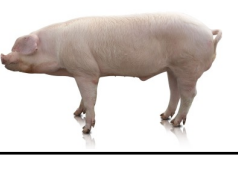
- 13,000 pigs were genotyped for the three breeds.
- Common SNPs from PorcineSNP60 v2 BeadChip array (~ 62,500 SNPs) and Illumina GGP Porcine HD Array (~ 68,500 SNPs) were obtained.

SNPs

- Quality control with PLINK:
 - Call rate < 0.1;
 - MAF < 0.05;
 - HWE < 0.001.

Haplotypes

- Phasing: *SHAPEIT2*, with the default parameters;
- Constructed: *GHap* package in R.

Breed	Pigs	SNPs	Haplotypes
	7,400	32,164	40,999
	1,929	28,608	34,597
	3,470	31,567	39,559

Evaluation of changes of allele frequencies over time

- glm analysis;**
- alpha corrected threshold (first 1% of P-values distribution and multiplied by total of analyzed DNA markers).

Top SNPs and Haplotypes

Check trend allele frequencies

- Δ MAF** in the most recent and in the oldest group of animals;
- percentile on the total DNA markers sorted in descending order.

Top SNPs and haplotypes overlapped =
Best SNPs and haplotypes

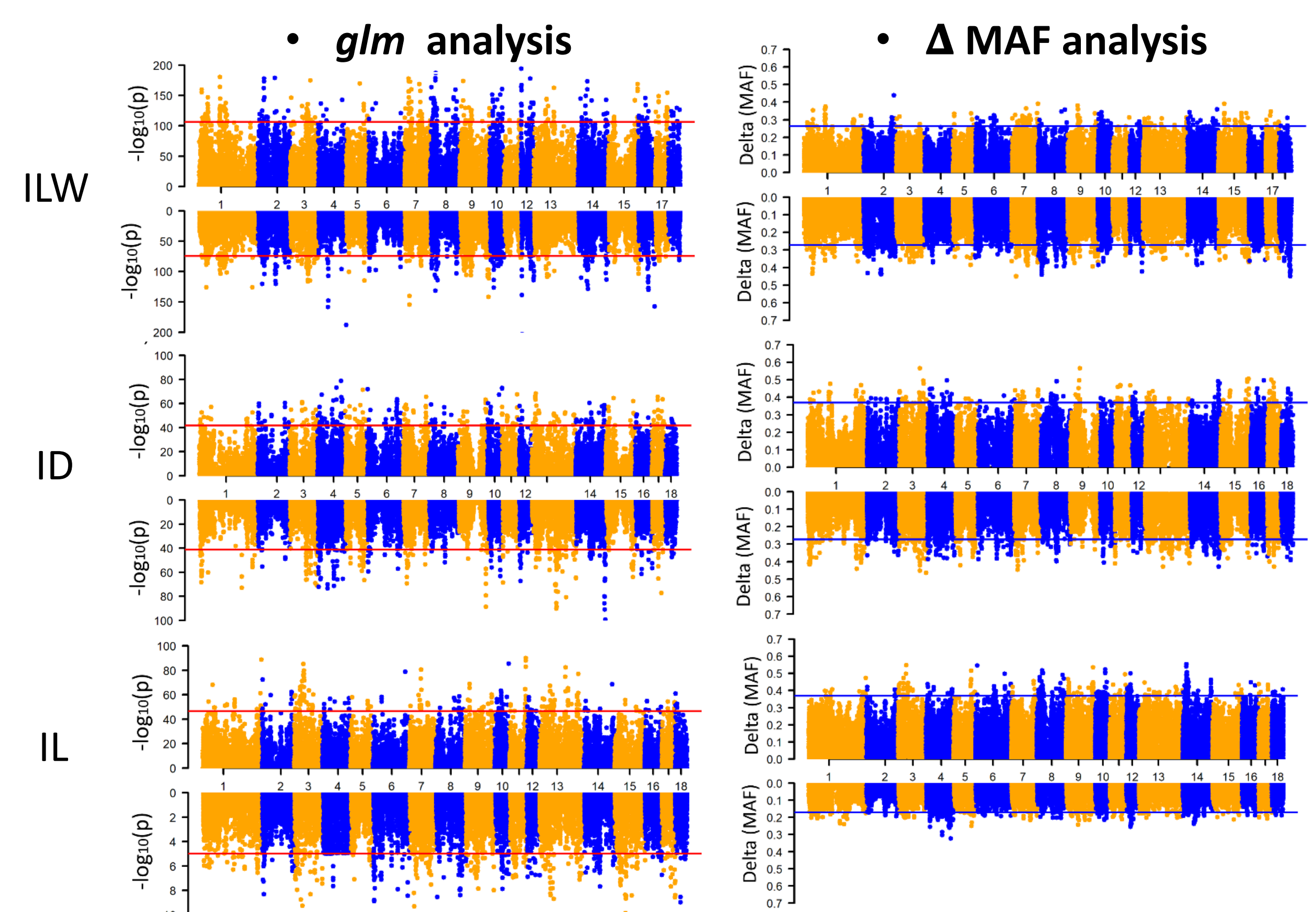
- Annotation genomic regions ± 500 kb from significant SNPs (Sscrofa 11.1 and databases used Ensembl Biomart and NCBI).

Acknowledgements:

Funded by Programma di Sviluppo Rurale Nazionale (PSRN) SUI5-2, co-funded by the European Agricultural Fund for Rural Development of the European Union and MASAF.

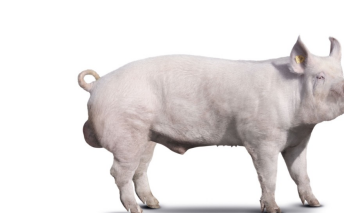
Results

Figure 1. Mirrored Manhattan plot of the different approaches for each breed. The upward section of each plot reports the SNPs, the downward sections is for haplotypes.



The table reports the number of regions that were significant in both single SNP and Haplotype approaches

Breed	Top SNPs	Top Haplotypes	Best SNPs and Haplotypes
ILW	61	193	25
ID	61	177	13
IL	76	22	/



SNPs (Mbp)	SSC	P-value	Gene
95.6	1	9.62E-129	<i>PSTPIP2</i>
40.8	1	1.65E-125	<i>GJA1</i>
53.1	9	1.11E-124	<i>CDON</i>
16.8	10	2.11E-124	<i>ZBTB18</i>

SNPs (Mbp)	SSC	P-value	Gene
135.3	14	1.38E-59	<i>ADAM12</i>
73.8	8	8.18E-58	<i>FRAS1</i>
89	13	1.80E-44	<i>AGTR1</i>

Some of the identified genes are involved in brain development and myogenesis in the embryo, having possible effects on maternity traits typical of the ILW breed. Other genes, such as *ADAM12*, *FRAS1* and *AGTR1* are known to regulate muscle development, a characteristic trait of the ID breed.

Conclusions

This study allowed to identify genomic regions that during these four decades of artificial selection contributed to improve the peculiar traits of the three breeds investigated. Finally, the study shows that artificial selection over four decades has favoured traits useful for the production of high-quality Italian hams.