Animal 18 (2024) 101335

Contents lists available at ScienceDirect

Animal
The international journal of animal biosciences

Signatures of selection analyses reveal genomic differences among three heavy pig breeds that constitute the genetic backbone of a dry-cured ham production system

F. Bertolini [a,*], G. Schiavo [a], S. Bovo [a], A. Ribani [a], S. Dall'Olio [a], P. Zambonelli [a], M. Gallo [b], L. Fontanesi [a]

[a] Animal and Food Genomics Group, Division of Animal Sciences, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy
[b] Associazione Nazionale Allevatori Suini, Roma, Italy

ARTICLE INFO

Article history:
Received 16 May 2024
Revised 7 September 2024
Accepted 12 September 2024
Available online 19 September 2024

Keywords:
Duroc
Haplotype
Landrace
Large White
Runs of homozygosity

ABSTRACT

The Italian pig farming industry is unique in its focus on raising heavy pigs primarily for the production of high-quality dry-cured hams. These products require pigs to be slaughtered at a live weight of around 170 kg at 9 months of age. The primary breeds used in this system are Italian Duroc, Italian Landrace, and Italian Large White which are crossed to produce lines that meet standard requirements. Over the past four decades, selection and breeding programmes for these breeds have been subjected to distinct selective pressures to highlight the characteristics of each breed. In this study, we investigated the genome of these breeds by analysing high-density single nucleotide polymorphism data from over 9 000 pigs to scan for signatures of selection using four different methods, two within breeds and two across breeds. This allowed to identify the genomic regions that differentiate these breeds as well as any relevant genes and biological terms. On a global scale, we found that the Italian Duroc breed exhibited a higher genetic differentiation from the Italian Landrace and Italian Large White breeds, with a pairwise F_{ST} value of 0.20 compared with the 0.13 between Italian Landrace and Italian Large White. This may reflect either their different origins or the different breeding goals, which are more similar for the Italian Landrace and Italian Large White breeds. Despite these genetic differences at a global level, few signatures of selection regions reached complete fixation, possibly due to challenges in detecting selection linked to quantitative polygenic traits. The differences among the three breeds are confirmed by the low level of overlap in the regions detected. Genetic enrichment analyses of the three breeds revealed pathways and genes related to various productive traits associated with growth and fat deposition. This may indicate a common selection direction aimed at enhancing specific production traits, though different biological mechanisms are likely targeted by the same directional selection in these three breeds. Therefore, these genes may play a critical role in determining the distinctive characteristics of Italian Duroc, Italian Landrace, and Italian Large White, and potentially influence the traits in crossbred pigs derived from them. Overall, the insights gained from this study will contribute to understanding how directional selection has shaped the genome of these heavy pig breeds and to better address selection strategies aimed at enhancing the meat processing industry linked with dry-cured ham production chains.

Implications

This study provides insights into how directional selection has shaped the genome of Italian heavy pig breeds used in the dry-cured ham production industry. By analysing genotyping data from over 9 000 pigs, breed-specific signatures in genomic regions associated with growth and fat deposition have been identified. These findings have the potential to improve selective breeding strategies, ultimately supporting the sustainability of the Italian heavy pig farming industry, particularly in producing high-quality hams. The study highlights the genetic distinction among Italian Duroc, Landrace, and Large White breeds, which may guide future crossbreeding programmes aimed at maximising production traits through heterosis.

Introduction

Pig farming in most countries is primarily focused on raising animals for fresh meat production, with pigs typically being

* Corresponding author.
E-mail address: francesca.bertolini3@unibo.it (F. Bertolini).

https://doi.org/10.1016/j.animal.2024.101335
1751-7311/

slaughtered at an average live weight ranging from ~80 to 120 kg. The Italian pig production system stands out as an exception, as it is focused on raising heavy pigs, that are slaughtered at ~170 kg of live weight once the animals have reached at least 9 months of age. This exception is due to the main use of these pigs, which provide meat for curing and processing, as encoded by the specification rules of the typical value chains of several highly valued Protected Designation of Origin (**PDO**) products. The most important PDO products in terms of economic value and worldwide recognition are the Parma and San Daniele dry-cured hams, which annually produce a total of ~10 million of dry-cured legs (Consorzio del Prosciutto di Parma, 2024; Consorzio del Prosciutto di San Daniele, 2024). According to their production disciplinaries, fresh legs should be sourced from pigs that are born, raised, slaughtered and processed in specific production areas. The genetic types used are also strictly regulated to ensure that heavy pigs reach the required slaughtering weight at 9 months of age, with moderate daily growth, and carcass classification in the central classes of the European Union (EU) system for heavy (H) carcasses, therefore belonging to the classes U, R, and O of the SEUROP classification (Regulation (EU) No. 1308/2013, 2013). The pigs in this niche value chain are typically crossbred animals obtained from Italian Duroc, Italian Landrace, and Italian Large White breeds or related genetic lines. These breeds originated from the cosmopolitan Duroc, Landrace and Large White pigs that, at the end of the 1980s, constituted isolated Italian nuclei and underwent independent selection programmes (ANAS 2024). The selection programmes of these breeds have been designed to produce efficient animals with desiderable characteristics of the legs to meet the PDO specifications. These characteristics of the legs include the appropriate lean/fat ratio, fat coverage, fat unsaturation level, intermuscular fat content, weight, shape, and weight loss potential during the curing period (Bosi and Russo, 2004). Italian Large White and Landrace are typically crossed to produce hybrid sows and enhance maternal traits (maternal heterosis) such as prolificacy, maternal capacity, and longevity. Italian Duroc is the sire line used to produce the final three-way crossbred heavy pigs in the classical scheme of Italian Duroc × (Italian Large White × Italian Landrace). In compliance with PDO regulations, the specific crosses of these genetic components ensure the preservation of traditional production methods while meeting the standards for flavour, texture, and aroma of the hams (ANAS, 2024). The original genetic characteristics of the breeds, as well as the breeding and selection programmes conducted over the past four decades, have left distinct signatures of selection in the genomes of these three breeds (Bovo et al., 2020; Fontanesi et al., 2015; Schiavo et al., 2016).

Signatures of selection can be defined as the reduction, elimination or change of genetic variation in genomic regions that are adjacent to causative variants in response to natural or artificial selective pressures, which contribute to shaping the genetic characteristics of a breed or population (Qanbari and Simianer, 2014). The size of the chromosome regions reporting signatures of selection can vary depending on the strength and duration of the selection pressure, as well as the population size and other factors. For example, strong and recent selection pressures may result in larger signatures, as the selected alleles quickly rise in frequency. In contrast, ancestral signatures of selection that underwent frequent recombination events may lead to shorter regions (Ghildiyal et al., 2023). These regions may contain genetic variants that could influence breed-specific traits such as morphology, production, and adaptation to different production systems and environments (Keller and Taylor, 2008; Saravanan et al., 2020).

Livestock genomes can be studied using a variety of statistical genomic approaches designed to identify signatures of selection. Among the different methods proposed, the most commonly used approaches are based on the examination of (i) site frequency spectrum, such as runs of homozygosity (**ROH**) islands (McQuillan et al., 2008), (ii) linkage disequilibrium, like the integrated haplotype score (**iHS**) (Voight et al., 2006), (iii) reduced local variability, such as the Fixation index ($\mathbf{F_{ST}}$) (Karlsson et al., 2007), and (iv) haplotype-based differentiation, like cross-population extended haplotype homozygosity (**XP-EHH**) (Sabeti et al., 2002), among others (Klassmann and Gautier, 2022; Ma et al., 2015a; Ma et al., 2015b). It is therefore recommended to utilise more than one approach for capturing signatures within or across populations (Ma et al., 2015a).

Several efforts have already been made to detect signatures of selection in various pig breeds and identify regions harbouring genes involved in many different breed characteristics, such as body size, pigmentation, meat quality, behaviour and immune-related traits (e.g., Bovo et al., 2020; Ma et al., 2015b; Rubin et al., 2012; Wang et al., 2019; Wilkinson et al., 2013). These studies utilise and often combine various genomic methodologies to detect genetic features that contribute to breed-specific adaptations or to economically important traits that are linked to different breeding goals. We have recently begun evaluating the presence of signatures of selection in the genome of Italian pig breeds. This evaluation involves studying a limited number of animals through the identification of ROH islands (Schiavo et al., 2020) and using whole-genome resequencing using DNA pools (Bovo et al., 2020). Additionally, we have compared signatures of selection identified in both autochthonous and cosmopolitan Italian pig breeds with findings obtained in several other European autochthonous breeds (Bovo et al., 2020; Muñoz et al., 2019).

In this study, we further investigated the genomes of three Italian heavy pig breeds (Italian Duroc, Italian Landrace and Italian Large White) using high-density single nucleotide polymorphism (**SNP**) data from more than 9 000 pigs. The obtained results provided a comprehensive picture of signatures of selection in these breeds by combining and integrating results obtained from several approaches, such as ROH island, iHS, F_{ST} and XP-EHH.

Material and methods

Animals, genotyping datasets and filtering

A total of 9 089 pigs were included in this study. These animals belong to the three Italian heavy pig breeds: Italian Duroc (n. 1 210), Italian Landrace (n. 3 253) and Italian Large White (n. 4 626) sampled between the years 1987 and 2021, with the majority of animals (70.6%) from the years 2015 and 2019. All animals were derived from the sib-testing programmes managed by the National Association of Pig Breeders (ANAS). Blood samples were collected during routine monitoring procedures of the animals and reused for this study. No animal experiments were conducted specifically for this research. DNA was extracted from leukocytes following the method described by Muñoz et al. (2018). The pigs were genotyped with GGP Porcine HD Genomic Profiler (Neogen, Lansing, USA), interrogating 68 516 SNPs according to the manufacturer's instructions. The most recent version of the assembled pig genome (Sscrofa11.1, GCF_000003025.6) was used to map all SNPs, following a previously reported procedure (Bovo et al., 2021). SNP and animal filtering were carried out using the software PLINK v 1.9 (Chang et al., 2015): SNPs with a call rate < 0.90, a deviation from Hardy Weinberg Equilibrium with $P < 0.0001$ and those not mapped on autosomes, were excluded. Animals with individual call rates < 0.90 were also removed from the final dataset. For each breed, missing SNPs were imputed using Beagle v3.3.2 with default parameters (Browning and Browning, 2007).

Population genomic analyses

Population stratification was assessed using the software Admixture 1.3 (Alexander et al., 2009). Analyses were carried out by varying the number of subpopulations (K) from 1 to 20 and retaining the cross-validation error for each K, as outlined in the software manual. Genomic relationships among the genotyped pigs were visualised through multidimensional scaling (**MDS**) plots generated using the cluster function of PLINK v1.9 (Chang et al., 2015), with the function eigvals to retrieve the variance explained, and plotted with R4.1.0 (R core Team, 2013). Global pairwise F_{ST} values between breeds were also calculated using PLINK v1.9 (Chang et al., 2015).

Signatures of selection analyses

The analyses were based on four different approaches summarised in Fig. 1; two were based on allele frequency comparisons: one within breed (ROH island analyses) and one across breeds (F_{ST} analyses); the other two were based on haplotype comparisons: one within breed (iHS analyses) and one across breeds (XP-EHH analyses). The analyses between breeds were performed considering only common SNPs identified after the filtering steps previously described. For each analysis, two main thresholds were considered: a 99th percentile, used for comparative analyses across breeds and methods, and a more stringent 99.5th percentile, used for gene annotation and subsequent gene enrichment analyses, to capture meaningful biological common features.

(a) ROH island, defined as genomic regions where genetic diversity is lower and, as a result, homozygosity is higher around the selected locus in comparison to the rest of the genome (Pemberton et al., 2012; Peripolli et al., 2017). The analyses were performed within each breed using PLINK v1.9 (Chang et al., 2015) with the same parameters utilised in Schiavo et al. (2020). Briefly (i) the minimum number of consecutive homozygous SNPs included in the ROH was set at 15; (ii) the minimum length of a ROH was set at 1 Mb; (iii) the minimum density of SNPs in a genome window was set 1 every 100 kb; (iv) the maximum distance between consecutive SNPs was set at 1 000 kb; (v) the number of heterozygous SNP allowed in a ROH was set at zero. For each SNP, the percentage of animals having ROH including that SNP was calculated and the two thresholds (99th and 99.5th) were considered.

(b) F_{ST} for each SNP in the pairwise comparison was calculated using PLINK 1.9 (Chang et al., 2015) with the method of Weir and Cockerham (1984). Then, values were averaged over 350 kb overlapping chromosome windows (mF_{ST}) with an in-house script. The two thresholds based on the mF_{ST} values (99th and 99.5th) were then considered.

(c) iHS, which is based on extended haplotype homozygosity (EHH), was used to compare the integrated EHH profiles between two alleles at a given SNP in the same population (Voight et al., 2006).

(d) XP-EHH was used to compare the integrated EHH profiles between two populations at the same SNP (Sabeti et al., 2007).

Phasing of the animals needed to apply both iHS and XP-EHH approaches was performed with fastPHASEv1.4 (Scheet and Stephens, 2006). Both iHS and XP-EHH were calculated with the REHH package (Gautier and Vitalis, 2012). As ancestral alleles were unknown, the log ratio was considered for both iHS and XP-EHH. Based on the observations provided by Voight et al. (2006), selective sweeps typically result in clusters of SNPs with high scores concentrated within the sweep region, whereas under a neutral model, high scores are more evenly distributed throughout the genome. For this reason, only 350 kb overlapping chromosome windows that contained at least three SNPs in the top 99th and 99.5th percentile of the log ratio were retained for further analyses.

Comparison with previous genome-wide analyses on the same breeds

Previous works have investigated ROH island and other selection signatures in the three breeds utilising both the data retrieved from SNP chip and pooled Whole Genome resequencing (Bovo et al., 2020; Schiavo et al., 2020). Other works have reported Quantitative Trait Loci (**QTLs**) through genome−wide association studies (**GWASs**) in the Italian Duroc, Italian Landrace and Italian Large White pigs (Bertolini et al., 2018; Bovo et al., 2016, 2019, 2021; Fontanesi et al., 2012; Fontanesi et al., 2017a; Fontanesi et al., 2017b). These regions were retrieved from each work and, when based on the previous versions of the *Sus scrofa* genome, they were updated to meet the chromosomal coordinates of the latest version (Sscrofa11.1) utilised for our analyses. These data were collected in a unique file with chromosomal coordinates and matched with all the regions detected at a 99th percentile threshold with the four approaches (a total of 276 regions across the three breeds) with bedtools (Quinlan and Hall, 2010). The regions detected in adjacent positions were considered as one if they were close to each other for a maximum of 700 kb, based on consideration about the threshold in terms of window size utilised for our ROH analyses and works on Linkage Disequilibrium decay in various European commercial pig breeds (Amaral et al., 2008; Wang et al., 2013).

Annotation of chromosome regions and gene enrichment analyses

Candidate genes included in the genomic windows identified with the approaches mentioned above and considering the 99.5th percentile threshold were retrieved by mining the annota-

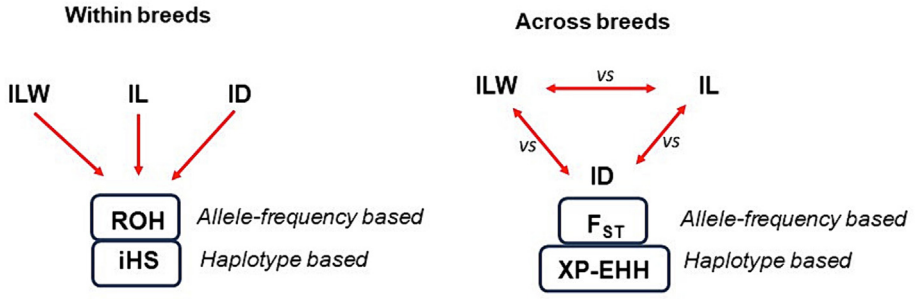

Fig. 1. Schematic representation of the signatures of selection analyses within pig breeds and across breeds. Abbreviations; ROH: Run of homozygosity; iHS: integrated haplotype score; FST: Fixation index; XP-EHH: cross-population extended haplotype homozygosity; ID: Italian Duroc; IL: Italian Landrace; ILW: Italian Large White.

tion available for the Sscrofa11.1 genome version (GCF_000003025.6) provided by NCBI using bedtools (Quinlan and Hall, 2010) and Ensembl using Ensembl Biomart tool (https://www.ensembl.org/biomart/martview/). Gene enrichment analyses were carried out with Enrichr (https://maayanlab.cloud/Enrichr/) combining the genes identified on the regions detected from different types of signatures of selection analyses (i.e. within breeds and between breeds). Analyses were run over the following human libraries: (i) Gene Ontology – Biological Process v. 2023; (ii) GWAS catalog v. 2023; (iii) Reactome v. 2022; (iv) WikiPathway v. 2023; and (v) BioCarta v. 2016. We considered statistically enriched terms having (i) at least two genes of the input set mapped to at least two different chromosomes and (ii) a P-value < 0.25 after Benjamini-Hochberg correction.

Results

Population genomic structures

The filtering steps retained 50 929 SNPs for the Italian Duroc, 47 533 SNPs for the Italian Landrace and 51 066 SNPs for the Italian Large White breeds. Among these SNPs, 42 841 were in common among all three pig breeds. No animals were discarded in the filtering process. Admixture analyses reported a steep decrease in cross-validation error with K = 3 (Fig. 2a). As expected, this number and the subpopulation clustered the breeds in three distinct groups (Fig. 2b). This distinction is confirmed even when the number of K increased, e.g. at K = 6 (Fig. 2c). Apart from this clear clusterisation, two additional features could be noted from this analysis: a potential ancestral common genetic background between Italian Landrace and Italian Large White breeds, visible in K = 3 and confirmed in K = 6 and a relatively mixed genetic background of Italian Large White pigs, especially when compared with Italian Duroc and Italian Landrace pigs (Fig. 2c), that may reflect the contribution of different genetic pools that have been used to originate the breed. Despite the higher similarities between Italian Landrace and Italian Large White breeds, the MDS plot showed a clear separation of the three breeds (Fig. 2d). The global pairwise F_{ST} confirmed a higher similarity between Italian Large White and Italian Landrace breeds with a value of 0.13. The comparison between Italian Duroc and the other two breeds produced in both analyses an F_{ST} value of 0.20.

A landscape of signatures of selection identified using within-breed analyses

ROH analyses considering the 99th percentile threshold detected four ROH islands [on *Sus scrofa* chromosomes (**SSCs**) 3, 9 and 15] in the Italian Duroc breed (Fig. 3 and Supplementary Table S1), 11 ROH islands (on SSC3, 4, 10, 11, 13, 14 and 17) in the Italian Landrace breed (Fig. 3 and Supplementary Table S1) and six ROH islands (on SSC1, 4, and 6) in the Italian Large White breed (Fig. 3 and Supplementary Table S1). The average ROH island length for the Italian Duroc breed was 5.75 ± 3.91 Mb with the longest ROH island (12.41 Mb) located on SSC9 (also confirmed in the 99.5th percentile) and the shortest (2.40 Mb) located on SSC3, not confirmed in the 99.5th percentile. The ROH islands detected in the Italian Landrace breed have an average length of 2.15 ± 1.08 Mb, with the longest ROH island on SSC11 (partially confirmed in the 99.5th percentile by two regions) and the shortest of 0.91 Mb (not confirmed in the 99.5th percentile) on SSC14. As for the Italian Large White breed, the average ROH island was 4.2 1 ± 2.19 Mb, with the longest island of 8.67 Mb located on SSC1 (confirmed also in the 99.5th threshold) and the shortest of 1.96 Mb located on SSC6 (not retained with the 99.5th threshold).

The iHS analyses detected a total of 32 regions in the Italian Duroc breed, 30 regions in the Italian Landrace breed and 31 regions in the Italian Large White breed (Fig. 3 and Supplementary Table S2). In the Italian Duroc breed, the average length of the iHS regions was 0.68 ± 0.45 Mb, with the longest one of 2.10 Mb on SSC6 (confirmed in the 99.5th percentile threshold) and several short regions of 0.35 Mb on different chromosomes (not always confirmed in the 99.5th percentile). The iHS regions detected in the Italian Landrace breed had an average length of 0.95 ± 0.89 M b, with the longest region of 3.85 Mb on SSC7 (partially confirmed by the 99.5th threshold) and several short regions of 0.35 Mb. Finally, the average length of iHS regions detected in the Italian Large White breed was 0.94 ± 1.77 Mb, with the longest region

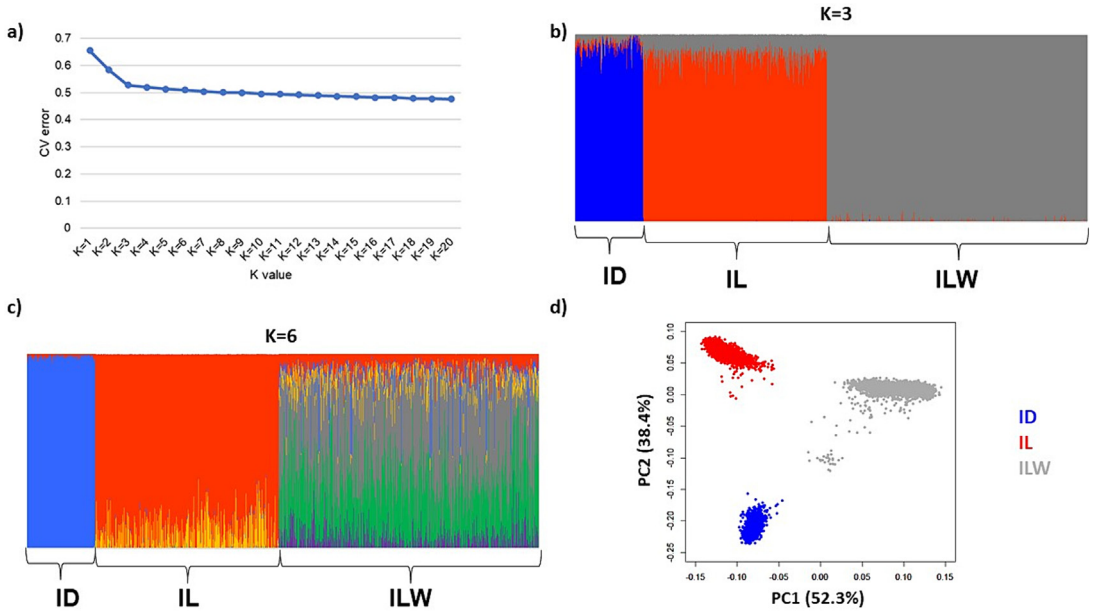

Fig. 2. Population structures based on genomic information for the Italian Duroc (ID), Italian Landrace (IL) and Italian Large White (ILW) breeds. a) Cross–validation (CV) error for different K (1–20) of the structure analyses for the three pig breeds. b) Population structures with K = 3. c) Population structures with K = 6. d) Multidimensional scaling plot that indicates in parenthesis the percentage of variance explained for each Principal Component (PC).

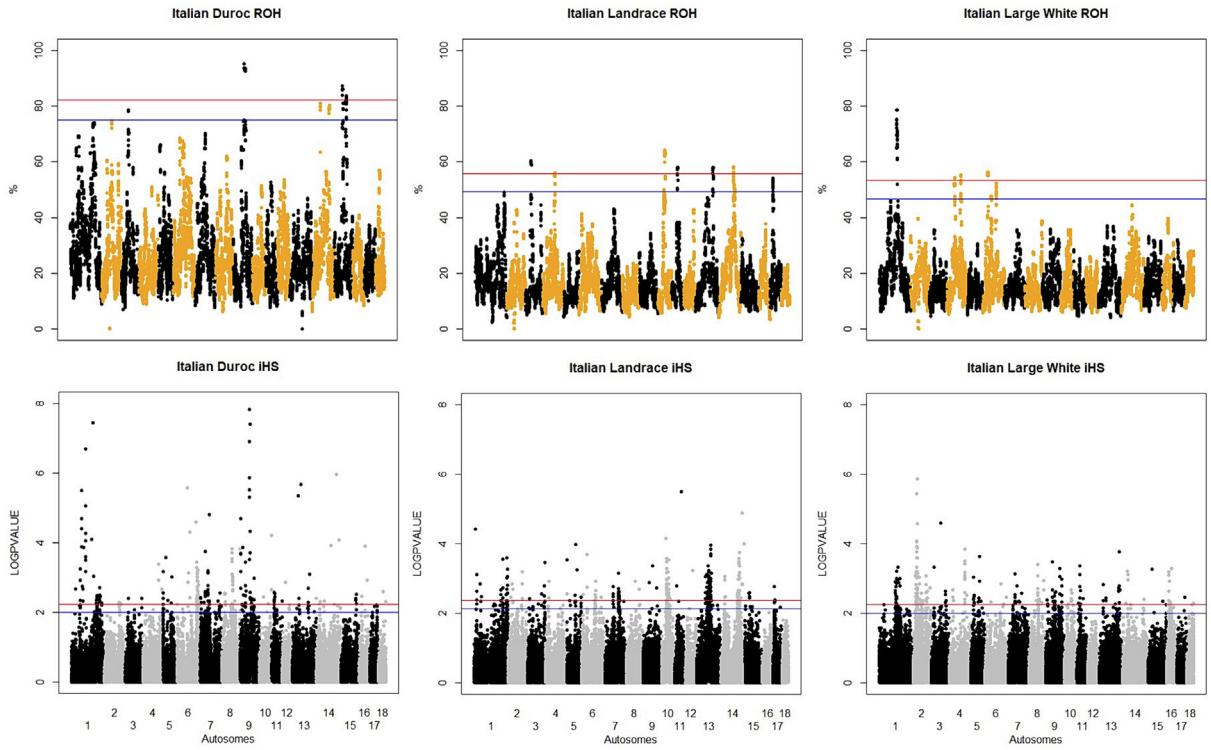

Fig. 3. Manhattan plots showing signatures of selection in the pig genome derived from within-pig breed analyses. The plots report genome-wide frequencies in percentage in Run of Homozygosity (ROH) island analysis in the upper part, and the log10-transformed value (LOGPVALUE) of the integrated Haplotype Score (iHS) in the lower part. The red lines indicate the 99.5th threshold, and the blue line indicates the 99th percentile threshold.

of 9.80 Mb on SSC10 (not confirmed in the 99.5th threshold) and several short regions of 0.35 Mb.

A landscape of signatures of selection detected using comparative analyses across breeds

The F_{ST} analyses (Fig. 4 and Supplementary Table S3) detected 32 regions with divergent mean F_{ST} value (mF_{ST}) in the Italian Duroc and Italian Landrace comparison, 22 regions for the Italian Duroc and Italian Large White comparison and 33 regions in the Italian Landrace and Italian Large White comparisons. The average length of the F_{ST} regions for the three breeds was relatively short. In the comparison of Italian Duroc vs Italian Landrace, the average length was 0.63 ± 0.59 Mb, with the longest region of 2.98 Mb detected on SSC11 (confirmed with the 99.5th percentile threshold). The comparison between Italian Duroc and Italian Large White breeds identified F_{ST} regions with an average length of 0.74 ± 0.74 Mb. The longest region was of 3.85 Mb on SSC15 partially confirmed in the 99.5th percentile threshold and several short 0.35 Mb regions. For the comparison between the Italian Landrace and the Italian Large White breeds, the average length of the F_{ST} regions was 0.62 ± 0.45 Mb (the shortest among all these comparisons), with the longest region of 2.1 Mb on SSC 2 confirmed in the 99.5th percentile and the majority of the regions (21 out of 33) with the minimum length of 0.35 Mb.

The XP-EHH analyses (Fig. 4 and Supplementary Table S4) detected 14 regions for the comparison between Italian Duroc and Italian Landrace breeds, 23 regions for the comparison between Italian Duroc and Italian Large White breeds and 22 regions for the comparison between Italian Landrace and Italian Large White breeds. The average length of the detected regions, higher compared to that reported in the F_{ST} analyses, was 2.20 ± 2.66 Mb for the Italian Duroc-Italian Landrace comparison, 1.44 ± 1.23 Mb for the Italian Duroc-Italian Large White comparison and 1.42 ± 1.17 for the Italian Landrace-Italian Large White comparison. Like the other analyses, all the longest regions were at least partially confirmed using the more stringent 99.5th threshold.

A few signatures of selection overlapped across breeds and methods

The regions detected in the two within-breed approaches (ROH islands and iHS analyses), either considering the 99th and the 99.5th percentile thresholds, are reported in Fig. 5a and Table 1. Within the same breeds, there were only a few chromosome regions where the results from the two approaches overlapped. A region on SSC9 (86.98–87.85 Mb) was detected with the 99.5th threshold for the ROH island approach and the 99th threshold for the iHS approach in the Italian Duroc breed. Four consistent regions were detected in Italian Landrace breed: on SSC10 (36.78–38.85 Mb) identified with the 99.5th threshold for both approaches; on SSC14 (100.45–102.07, 104.65–105.70 and 111.48–111.83 Mb). Two regions were detected with both approaches in Italian Large White breed: one on SSC1 (145.60–145.95 Mb) and a second on SSC4 (100.63–101.50 Mb). When we compared all the detected regions across breeds, only Italian Duroc and Italian Landrace breeds shared two regions detected by iHS on SSC1 (positions: 218.58–219.10 and 239.23–239.75 Mb).

The regions detected with the comparative analyses across breeds are reported in Fig. 5b and Table 1. Here, the overlapping among approaches was reported only for a region on SSC15 (54.60–55.83 Mb) in the contrast between the Italian Duroc and the Italian Landrace breeds using both across-breed approaches (F_{ST} and XP-EHH) and on SSC1 (143.33–143.68 Mb), SSC13

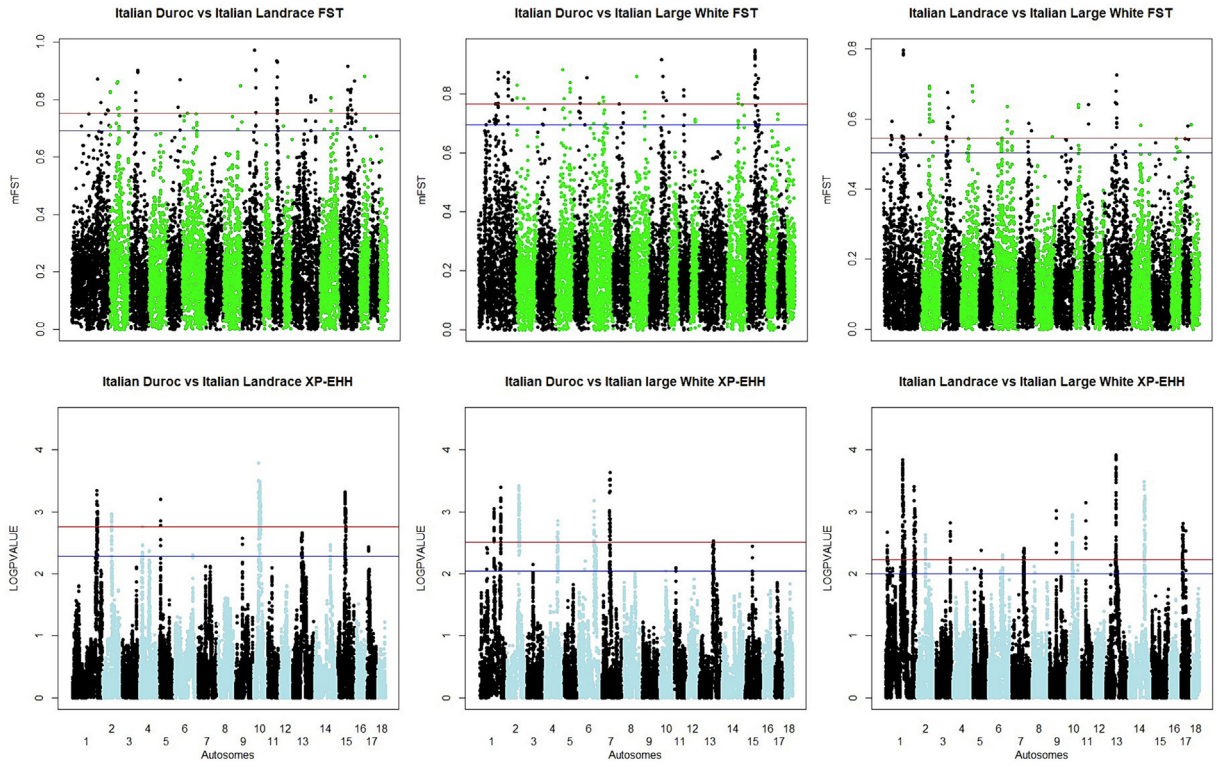

Fig. 4. Manhattan plots showing signatures of selection in the pig genome derived from across breed analyses. The plots report the average genome-wide average Fixation index (mF_{ST}) for F_{ST} in the upper part and the log10-transformed value (LOGPVALUE) for cross-population extended haplotype homozygosity (XP-EHH) in the lower part for the three pig breeds. The red lines indicate the 99.5th threshold, and the blue lines indicate the 99th percentile threshold.

(79.80–81.90 Mb) and SSC17 (16.80–17.15 Mb) for the same two approaches in the contrast between Italian Landrace and the Italian Large White breeds.

Combined signatures of selection and annotated genes

The overview of the chromosome regions where signatures of selection were detected with more than one approach (within and across breeds) is summarised in Table 1. For the Italian Duroc breed, nine regions were detected. Here, three regions on SSC1 (222.45–222.78 Mb and 239.05–240.28 Mb) and 15 (53.03–58.28 Mb) were detected using three and four comparisons respectively. These regions contain several genes, including IGF binding protein−like 1 (*IGFBPL1*), tropomodulin 1 (*TMOD1*) and XPA, DNA damage recognition and repair factor (*XPA*) on SSC1, and melanosomal transmembrane protein (*OCA2*) on SSC15. The Italian Landrace breed reported 17 overlapping regions. Among those, three regions were shared by three comparisons: two on SSC10 (23.80–26.08 Mb and 36.40–38.85 Mb), which contain, the importin 9 (*IPO9),* the leucine−rich repeat and Ig domain containing 2 (*LINGO2*) and the MOB kinase activator 3B (*MOB3B)* genes and a 2.45 Mb region on SSC13. For the Italian Large White breed, five regions have been reported. Among these, a region on SSC1 was shared by four approaches and contains the gene KLF transcription factor 13 (*KLF13*). Other three regions (two on SSC1 and one on SSC4) were shared by three approaches. Here, the region on SSC4 contains the gene phosphodiesterase 4D interacting protein (*PDE4DIP*).

Two genomic regions were shared by Italian Landrace and Italian Large White breeds. The first region was located on SSC14 (111.48–114.10 Mb) and was shared by Italian Landrace ROH island and iHS analyses and by Italian Large White ROH, as well as in the XP-EHH analysis. This region contains, among others, the Stearoyl-CoA desaturase Δ9 (*SCD*) gene. The second region was detected on SSC17 (16.42–17.33 Mb) and was detected by both Italian Landrace and Italian Large White ROH and overlapped with both F_{ST} and XP-EHH analyses.

Comparative analyses between signatures of selection and genome−wide association analyses in the same breeds

Previous studies that analysed ROH islands and the pooled heterozygosity in the same three breeds investigated in this study have identified a total of 58 and 36 genomic regions containing signatures of selection, respectively (Bovo et al., 2020; Schiavo et al., 2020). The overlap of the regions detected in our study with previous ROH and reduced heterozygosity analyses is presented in Supplementary Table S5. In this comparison, 47 regions overlap with regions detected in the previous studies. Apart from one region on SSC15, the rest of the overlapping regions align with the breeds analysed. This indicates that different approaches, whether within or across breeds, can be consistent in identifying a few regions as signatures of selection.

Additionally, GWAS studies have identified 606 genomic regions across all 18 autosomes, associated with a total of 38 traits, including productive traits, teat number, serum electrolytes and haematological parameters (Bovo et al., 2021; Bertolini et al., 2018; Bovo et al., 2016, 2019; Fontanesi et al., 2012; Fontanesi et al., 2017a; Fontanesi et al., 2017b) (Supplementary Table S6). Among the QTLs identified, 22 overlap with our sweeps. In nine regions, there is a match between the breed analysed in our study and the breed where the QTL was identified. In the remaining 12 regions, the breed analysed in our study differs from the breed where the QTL was found.

In silico functional enrichment

The enrichment analyses were performed considering the output of the genes retrieved by all analyses within and across breeds

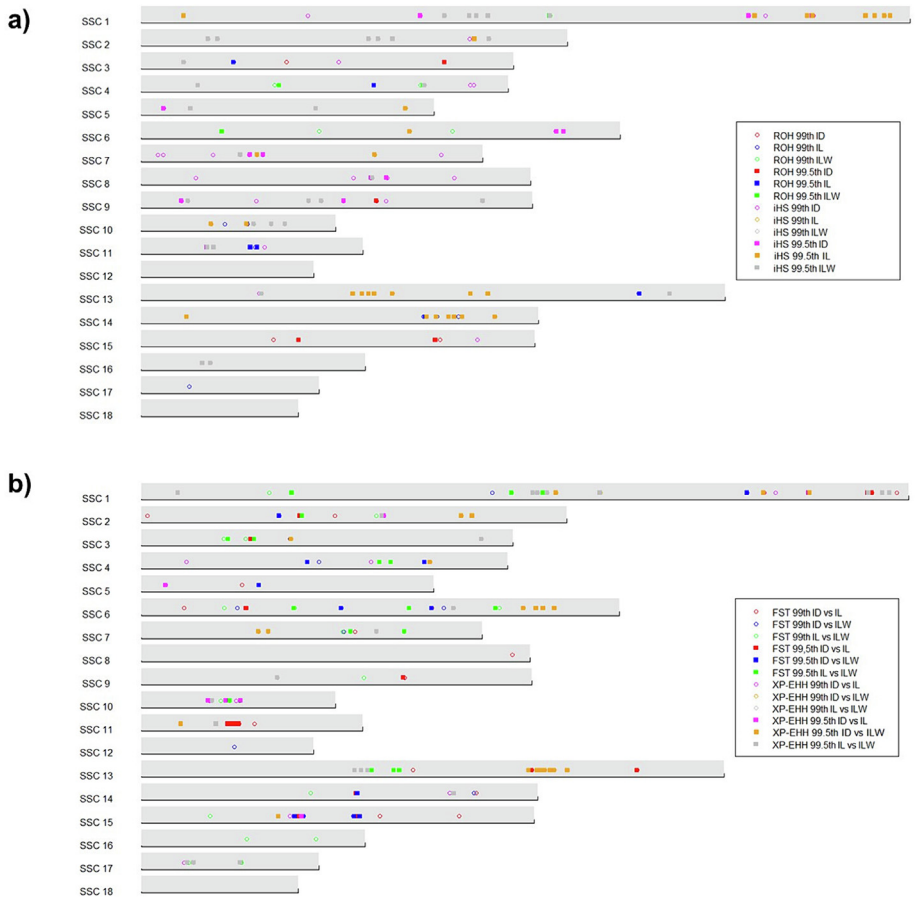

Fig. 5. Patterns of the signatures of selection identified on the pig genome derived from the three heavy pig breeds. a) Signatures of selection identified within breeds [i.e. Runs of homozygosity (ROH) islands and integrated haplotype score (iHS) analyses]. b) Signatures of selection identified across breeds [i.e. Fixation index (F_{ST}) and cross-population extended haplotype homozygosity (XP-EHH) analyses]. Abbreviations: ID = Italian Duroc; IL = Italian Landrace; ILW = Italian Large White; 99th = 99th percentile; 99.5th = 99.5th percentile.

using the 99.5th percentile threshold. Table 2 provides a summary of the most relevant terms obtained, while Supplementary Table S7 reports more detailed information. A high number of enriched terms were detected for hair and eye colour, encompassing 5 terms and 7 genes in total. The most recurrent genes were *OCA2* and *HECT* and *RLD* domain containing E3 ubiquitin protein ligase 2 (*HERC2*) genes. Other terms were related to growth, height and the immune system (interleukins). A total of 11 terms were related to growth (body mass index related) in Italian Landrace breed, along with infertility, while in Italian Large White breed, cholesterol and calcineurin-related pathways were the most represented.

The comparison between breeds confirmed some of the enriched pathways detected in the within-breed analyses. Among these, hair colour was previously detected for the Italian Duroc breed and also detected in the Italian Duroc vs Italian Landrace comparisons. Growth and fat deposition–related terms were found, even though not always in the same breeds (e.g. Body Mass Index and Regulation of Growth Hormone Receptor in Italian Duroc vs Italian Large White and IGF 1 levels in Italian Landrace vs Italian Large White).

Discussion

The identification of signatures of selection in the genomes of livestock breeds provides a landscape of regions that have been shaped by genetic events, contributing to the diversity of animal genetic resources over time. This is of particular relevance in the investigation of pig breeds, where crossbreeding practices are used to exploit the genetic diversity of different pig breeds and subsequently obtain heterosis to create lines/terminal animals that meet market demands (Sellier, 1976; Weaber, 2010). In the Italian production system, the terminal pigs should comply with the prescriptions of the PDO-dry cured ham consortia. Over the past decades, three key breeds (Italian Duroc, Italian Landrace and Italian Large White) have constituted the genetic backbone on the PDO dry-cured ham production system. These breeds have been the focus of specifically designed selection programmes aimed at maximising their specific characteristics. These characteristics will serve in the final crossbred combination to meet the requests of raw materials (i.e. the legs) for the processing and curing steps needed to produce PDO-dry cured hams. An investigation into the breed population structure, using both MDS and admixture approaches, revealed that the applied selection strategies have maintained three genetically distinct breeds, clearly showing three well-differentiated genetic pools.

The discovery of genomic regions influenced by artificial directional selection or that defined the original genetic background of the breeds is crucial for understanding the genetic foundations of these three economically relevant breeds. At the overall genetic level, pairwise F_{ST} revealed high genetic differences among the three breeds, with high genetic differences between the Italian Duroc breed (F_{ST} = 0.20) compared with other two breeds that were genetically closer to each other (F_{ST} = 0.13). It is well known that the Landrace and Large White cosmopolitan breed-groups share

Table 1
Genomic regions where signatures of selection were identified by more than one method in the three Italian pig breeds. Results are reported and divided by breed. For the comparative methods, only the opposite breed is reported.

Breed	Chromosome (position)[1]	Genes[2]
Italian Duroc		
iHS, ILW-F_{ST}*	1 (216 125 000–217 175 000)	*CD274, ERMP1, INSL6, JAK2, KIAA2026, MIR101-1, MLANA, PDCD1LG2, PLGRKT, RCL1, RIC1, RLN2*
iHS, ILW-XP-EHH, IL-XP-EHH	1 (222 425 000–222 775 000)	*APBA1, ENTREP1, FAM189A2, FXN, TJP2*
iHS*, ILW-XP-EHH*, IL-XP-EHH*	1 (239 050 000–240 275 000)	*ALDH1B1, ANP32B, CCDC180, CORO2A, FOXE1, GABBR2, HEMGN, IGFBPL1, NANS, TBC1D2, TDRD7, TMOD1, TRIM14, TRMO, TSTD2, XPA,*
iHS, ILW-XP-EHH*	2 (115 675 000–117 425 000)	*APC, CAMK4, DCP2, EPB41L4A, MCC, REEP5, SRP19, STARD4, TSLP, WDR36*
ROH, ILW-F_{ST}	3 (52 850 000–53 110 460)	*CNOT11, CREG2, RFX8, RNF149*
iHS*, IL-XP-EHH*	5 (8 400 000–8 750 000)	*ATF4, CACNA1I, ENTHD1, GRAP2, MIEF1, RPS19BP1*
iHS*, ILW-XP-EHH	6 (146 825 000–148 575 000)	*AK4, CACHD1, DNAJC6, JAK1, LEPR, LEPROT, MIR101-2, RAVER2, ROR1, UBE2U*
ROH*, iHS	9 (86 975 000–87 850 000)	*HDAC9, PRPS1L1, SNX13*
ROH*, ILW-F_{ST}*, IL-F_{ST}*, IL-XP-EHH*	15 (53 025 000–58 275 000)	*AMER3, ARHGEF4, CFC1B, DCTN6, DUSP4, ERI1, FAM168B, GPR148, GSR, GTF2E2, HERC2, LEPROTL1, MBOAT4, MFHAS1, NRG1, OCA2, PLEKHB2, PPP1R3B, PPP2CB, PURG, RBPMS, SARAF, SMIM18, TEX15, TNKS, UBXN8, WRN*
Italian Landrace		
iHS, ID-XP-EHH*	1 (237 300 000–237 650 000)	*MELK, PAX*
iHS, ILW-XP-EHH*	1 (264 250 000–265 300 000)	*ADGRD2, CRB2, DENND1A, LHX2, NEK6, NR5A1, PSMB7*
iHS, ILW-XP-EHH*	1 (266 700 000–267 400 000)	*LMX1B, MVB12B, ZBTB43*
iHS, ILW-F_{ST}*	6 (95 550 000–95 900 000)	*BMP8B, CAP1, MFSD2A, MYCL, PPIE, PPT1, TRIT1*
iHS*, ILW-XP-EHH	7 (83 475 000–84 525 000)	–
iHS,* ID-XP-EHH*, ILW-XP-EHH*	10 (23 800 000–26 075 000)	*AAED1, ADIPOR1, ARL8A, CDC14B, CSRP1, CTSV, CYB5R1, ELF3, FAM240B, GPR37L1, HABP4, HSD17B3, IPO9, KDM5B, KLHL12, LGR6, LMOD1, NAV1, PHLDA3, PPP1R12B, PRXL2C, PTPN7, RABIF, RNPEP, SHISA4, SLC35D2, SYT2, TIMM17A, TNNI1, UBE2T, ZNF367, ZNF510, ZNF782*
iHS,* ID-XP-EHH*, ROH*	10 (36 400 000–38 850 000)	*C10H9orf72, C9orf72, IFNK, LINGO2, MFSD14B, MIR876, MOB3B, ZNF658*
ROH*, ID-F_{ST}	11 (40 250 000–40 600 000)	–
ROH*, ID-F_{ST}	12 (176 925 000–177 275 000)	–
iHS,* ID-XP-EHH*, ILW-XP-EHH	13 (75 250 000–75 775 000)	*AMOTL2, ANAPC13, CEP63, KY, RYK*
iHS, ILW-XP-EHH	13 (78 575 000–78 750 000)	*SOX14*
ILW-F_{ST}*, ILW-XP-EHH*, iHS*	13 (79 800 000–81 900 000)	*CLSTN2, COPB2, MRPS22, NMNAT3, RBP1, RBP2, SLC25A36, SPSB4, TRIM42*
iHS*, ILW-F_{ST}*	13 (89 600 000–90 125 000)	*ANKUB1, COMMD2, RNF13, TM4SF1, TM4SF4, WWTR1*
ROH*, iHS*	14 (100 450 000–102 071 608)	*ACTA2, ANKRD22, CH25H, FAS, IFIT1, IFIT2, IFIT3, IFIT5, KIF20B, LIPA, LIPM, LIPN, MIR107, PANK1, RNLS, SLC16A12, STAMBPL1, ssc-mir-107*
ROH, iHS*	14 (104 650 000–105 700 000)	*CEP55, FFAR4, FRA10AC1, LGI1, MYOF, PDE6C, PLCE1, RBP4, SLC35G1*
iHS*, ILW-XP-EHH*	14 (109 375 000–109 900 000)	*CRTAC1, HPS1, HPSE2, LOXL4, PYROXD2, R3H, R3HCC1L*
IL-iHS,* ID-XP-EHH*	14 (109 550 000–109 900 000)	*HPS1, HPSE2, LOXL4, PYROXD2, R3H, R3HCC1L*
Italian Large White		
ROH*, IL-F_{ST}*, IL-XP-EHH*, ID-F_{ST}*	1 (142 975 000–143 850 000)	*KLF13, OTUD7A, TRPM1*
iHS, IL-XP-EHH*, ROH-*	1 (145 600 000–145 950 000)	*CTDP1, NFATC1, PCSK6, SNRPA1*
ROH*, ID-XP-EHH*	1 (146 650 000–149 625 000)	*CNDP1, CNDP2, DIPK1C, FAM69C, GALR1, MBP, PTGR3, TSHZ1, ZADH2, ZNF236, ZNF407, ZNF516*
ROH*, iHS*, ID-F_{ST}*	4 (100 625 000–101 500 000)	*ADAM30, HMGCS2, NOTCH2, PDE4DIP, PHGDH, REG4, SEC22B*
ROH*, IL-F_{ST}	6 (29 400 000–29 750 000)	*AMFR, GNAO1*
Multiple breeds		
IL_iHS*, IL-ILW_XP-EHH*, IL_ROH, ILW_ROH	14 (111 475 000–114 100 000)	*ACTR1A, ARL3, ARMH3, AS3MT, BORCS7, BTRC, C14H10orf76, CNNM2, CUEDC2, CYP17A1, DPCD, ELOVL3, FBXL15, FBXW4, FGF8, GBF1, HIF1AN, HPS6, KAZALD1, KCNIP2, LBX1, LDB1, LZTS2, MFSD13A, MGEA5, MIR146B, MRPL43, NDUFB8, NFKB2, NOLC1, NPM3, NT5C2, OGA, PAX2, PCGF6, PDZD7, PITX3, POLL, PPRC1, PSD, SCD, SEC31B, SEMA4G, SFXN2, SFXN3, SLF2, SUFU, TLX1, TRIM8, TWNK, WBP1L, WNT8B, ssc-mir-10382*
ILW_ROH, IL-ILW_XP-EHH*, IL-ILW_F_{ST}, IL_ROH	17 (16 422 085–17 325 000)	*TMX4, PLCB1, HAO1*

Abbreviations; ROH: Run of homozygosity; iHS: integrated haplotype score; F_{ST}: Fixation index; XP-EHH: cross-population extended haplotype homozygosity; ID: Italian Duroc; IL: Italian Landrace; ILW: Italian Large White.
* Regions identified at the 99.5th percentile threshold.
[1] Chromosomal coordinates (chromosome:start–end).
[2] List of genes included in the reported genomic region.

a close ancestral European origin, with both breeds developed in northern Europe (Landrace in Scandinavia and Large White in the UK; Porter, 1993). The Duroc breed-lineage, on the other hand, originated in the United States, with a distinct development path from that of the other European breeds (Porter, 1993; Rothschild and Ruvinsky, 2011). Moreover, both Landrace and Large White breeds have historically been developed with similar goals in mind, focusing on reproductive traits like fertility and litter size and meat quality. These common objectives could lead to greater genetic similarities between the two breeds compared to Duroc, which has been mainly selected for different traits, such as muscle growth and intermuscular fat (Bosi and Russo, 2004; Newcom et al., 2005; Rothschild and Ruvinsky, 2011).

Despite the differences at a global genomic level, only a few regions reached the level of almost complete fixation in our signature of selection analyses. Additionally, especially for the F_{ST} and iHS approaches, signatures of selection regions were relatively small. This may be due to the challenge of identifying regions of

Table 2
Summary of the gene enrichments obtained for the analyses within pig breeds and across breeds. Detailed terms are reported in Table S7.

Analyses	Library	Terms	N. of enriched terms	N. of genes
Within breed				
Italian Duroc	GWAS	Hair colour	3	7
	GWAS	Eye colour	2	4
	GWAS	Body Fat Distribution (Trunk Fat Ratio)	1	3
	GWAS	Monobrow	1	2
	GWAS	Height	1	45
	Reactome	Interleukins	6	2
	Reactome	Regulation Of Growth Hormone Receptor Signaling Pathway	1	2
Italian Landrace	GWAS	Body mass index related	11	10
	Wikipathway	Male infertility	1	5
Italian Large White	GWAS	Cholesterol	3	26
	Biological processes	Calcineurin	2	2
Across breeds				
Italian Duroc vs Italian Landrace	GWAS	Black Vs Blond Hair Colour	1	2
	GWAS	Immunoglobulin pathways	4	10
	GWAS	Facial Morphology	1	2
	GWAS	Bipolar Disorder or Major Depressive Disorder	1	4
	Biological processes	Myofibril components	2	6
	Biological processes	Wound	2	4
Italian Duroc vs Italian Large White	GWAS	Body Mass Index	1	18
	GWAS	Longevity	1	5
	Biological processes	Regulation of Growth Hormone Receptor	1	2
Italian Landrace vs Italian Large White	GWAS	IGF 1 Levels	1	12

Abbreviations: GWAS = GWAS catalog v. 2023; Reactome = Reactome v. 2022; WikiPathway = WikiPathway v. 2023; Biological processes = Biological Process v. 2023.

selection linked to quantitative polygenic traits, given the persistent variability at numerous loci influencing these traits (Pritchard et al., 2010). Consequently, the selection process for quantitative traits is often driven by polygenic adaptation, characterised by shifts in allele frequencies at numerous loci with minor effects on a trait, rather than fixation (Chevin and Hospital, 2008; Pritchard et al., 2010). Moreover, since strong and recent selection pressure can create larger genomic signatures due to rapidly increasing allele frequencies and older selection signatures that have undergone more recombination events may be smaller, what can be captured here may reflect the process that occurs at the beginning of the development of these breeds and that continued through the further differentiation when the Italian breeds begin to separate from the relative cosmopolitan breed stocks (Panigrahi et al., 2023; Stephan, 2019). This is confirmed by the analyses undergone in this study. For example, ROH islands typically reflect recent inbreeding events or selective sweeps within populations (Joaquim et al., 2019) and therefore may capture indicative of recent evolutionary events shaping the genome of the three breeds under investigation. These stretches of homozygosity arise due to mating between closely related individuals or intense selection pressures favouring specific genetic variants (Bosse et al., 2014). Conversely, iHS measures the extent of haplotype homozygosity surrounding a beneficial allele that has undergone positive selection (Voight et al., 2006). These regions, while impactful in terms of selective advantage, tend to be narrower and less extensive than ROH islands. This difference arises because selective sweeps affecting iHS regions occurred further back in evolutionary time, allowing the beneficial haplotype to spread and increase in frequency over shorter genomic distances (Sabeti et al., 2006).

The relationship between signatures of selection and QTL detected with GWAS in livestock revolves around understanding how selection pressures shape the genetic landscape of animal populations. While the results of GWAS link genetic variations with phenotypic variations, they differ from signatures of selection, which instead look for a reduction in genetic variability at a specific locus. Therefore, we expect a reduced level of overlap between the signals detected by our analyses and the QTL detected with GWAS. This was confirmed by the low number of regions that overlap between the two types of investigations, GWAS and our analyses of signatures of selection. Moreover, all the regions that overlap with the QTL did not reach complete fixation. Another interesting observation is related to the overlap between signatures of selection and GWAS in different breeds. This may indicate that while selection may improve common traits to a certain degree, the biological bases of these traits across breeds may differ.

A higher degree of overlapping was detected when we compared the signals detected in our study with those already detected on the same breeds. As expected, the overlapping was not complete for two main reasons: the utilisation of a single approach and the number of animals, that was reduced compared to the dataset used in this study. Therefore, the utilisation of multiple approaches and the large dataset we investigated provided additional hints on signatures of selection in the Italian heavy pig breeds.

The enrichment analyses conducted across the different signals have identified relevant pathways and genes that may be associated with important traits that characterise the three breeds. For example, in the Italian Duroc breed, two genes (*OCA2* and *HERC2*) were relevant in defining the enrichment within the hair and eye colour pathways. These genes are known to have a significant genetic impact on pigmentation and eye colour variation in humans (Liu et al., 2013; Sturm and Larsson, 2009). *OCA2* is responsible for regulating melanin production, while *HERC2* controls *OCA2* expression and influences pigmentation levels (Liu et al., 2013; Sturm and Larsson, 2009). We have recently suggested that *OCA2* may play a crucial role in determining coat colour in Duroc pigs (Bovo et al., 2020). Additionally, both genes were identified in ROH islands in the same breed (Schiavo et al., 2020), further supporting their importance in the phenotypic characteristics of Italian Duroc pigs. Other relevant enriched processes detected within this breed are related to growth, height and the immune system. The latest term may be due to the fact that the Duroc breed is the most rustic among the three breeds considered (Fontanesi et al 2012; Utrilla et al., 2010).

One important objective that distinguishes the selection of heavy pigs is to maintain a constant backfat thickness to meet the fat covering requirements for ham set by the rules of dry-cured ham consortia. Insufficient fat covering on the legs can lead to increased seasoning loss and a decrease in the organoleptic characteristics of dry-cured ham (Bosi and Russo, 2004). In our analyses, some enriched growth-related terms were similar across breeds, despite originating from different chromosomal regions and genes, while some others were enriched in the comparison across breeds, underlying that some of the growth−related traits may be divergent across breeds. This suggests that despite a shared selection focus on increasing growth and fat deposition parameters in all breeds, these breeds target different biological mechanisms through the same directional selection. It is interesting to note that Italian Landrace breed had 11 growth-related terms, as well as the infertility term, while Italian Large White breed showed a functional enrichment focused on cholesterol and calcineurin-related pathways, which are also linked to oxidative fibre conversion and the regulation of myosin heavy chain genes and, ultimately, meat quality (Park et al., 2009).

In this work, we have utilised various approaches to capture multiple signals across the pig genome. The analyses conducted revealed a low degree of overlap among the different methods employed, reinforcing the use of applying several approaches to provide a more complete picture of the landscape of signatures of selection in the three breeds. However, when a genomic region is pointed by several approaches, this may strengthen the potential importance of that region (Ma et al., 2015a). In addition to the cluster on SSC15 containing the *OCA2* gene discussed earlier, a cluster of four relevant genes for the Duroc breed was identified in another window on SSC1 through iHS and both XP-EHH comparisons. This region includes *IGFBPL1, TMOD1* and *XPA. IGFBPL1* belongs to the insulin-growth factor gene family, which includes genes involved in muscle development and growth in various farm animal species, including pigs (Mohammadabadi et al., 2021). While the *IGFBPL1* gene has not been as extensively studied as other family members, differences in expression in embryos of breeds with varying muscularity levels (i.e. Pietrain and Duroc) suggest a potential role in myogenic differentiation (Muráni et al., 2007). This highlights *IGFBPL1* as a possible driver of distinguishing factors between Italian Duroc and the other breeds analysed. Another gene linked with muscle development is *TMOD1* which is a member of the tropomodulin family that is involved in the architecture of the sarcomere in muscle cells and the membrane skeleton in non−muscle cells (Gregorio et al., 1995). This porcine gene has been associated with different loin muscle, backfat thickness and ham pH (Wu et al., 2009). In our study, this gene was also enriched for the terms Myofibres Assembly and Actomyosin Structure Organization in the Italian Duroc vs Italian Landrace comparison and Striated Muscle Cell Development in the Italian Duroc vs Italian Large White comparison. The *XPA* gene provides instructions for making a protein that is involved in repairing damaged DNA and was found as part of ROH in differentiating two Duroc lines (Canadian and American) (X. Wang et al., 2022).

Relevant genes for the Italian Landrace breed have been previously associated with growth, fat and muscle development. In our study, the genes *IPO9* and *LINGO2* were identified in several enriched terms related to adipose tissue development and growth. *IPO9* showed differential expression in breeds with different meat quality traits, such as Pietrain, Landrace and Pulawska (Ropka-Molik et al., 2015). *LINGO2*, reported to be highly expressed in the central nervous system, has been associated with body mass in elderly humans (Rask-Andersen et al., 2015). While there is no direct association with pigs yet, this gene has been identified to be present in a QTL region for body size in Simmental beef cattle (An et al., 2020). *MOB3B* did not appear in any enrichment term but has been found to be significantly associated with intramuscular fat and residual feed intake in cattle (Higgins et al., 2019) as well as with backfat thickness and predicted lean meat percentage in Duroc pigs (Ruan et al., 2021).

In the case of the Italian Large White breed, the *KLF13* gene was detected in five out of the six analyses performed. This gene was found to be present in the enriched pathways for High−Density Lipoprotein Cholesterol Levels and HDL Cholesterol. KLF13 acts as a positive regulator of adipogenesis and is linked to the fatty acid composition in pigs through the interaction of a miRNA (Du et al., 2018; Raza et al., 2022). Another gene, *PDE4DIP* was detected in the ROH and iHS analyses and in the F_{ST} comparison against the Italian Duroc breed. This gene was associated with average daily gain (Li et al., 2011). Another gene of relevance, that was not present in any enriched pathway but was in a region detected with multiple approaches was the *SCD* gene. A marker close to this gene has been associated with palmitoleic:palmitic ratio in Italian Large White pigs, and this gene is involved in fatty acid desaturation and elongation, an important pathway linked to meat quality parameters (Zappaterra et al., 2018; Catillo et al., 2020).

Conclusions

The identification of signatures of selection in the genomes of the three key Italian pig breeds (Italian Duroc, Italian Landrace, and Italian Large White) provides insights into the genetic events that shaped these important breeds that are specifically raised for the Italian PDO dry-cured ham production system. The identified gene clusters and enriched pathways across Italian Duroc, Italian Landrace, and Italian Large White pigs highlight the distinctive biological processes that define each breed's characteristics. Additionally, the observed genetic differentiation among breeds aligns with their distinct developmental paths and selection goals, reinforcing the importance of maintaining genetic diversity within livestock populations for robust and resilient breeding practices. The focus on specific traits like muscle growth, fat development, and body mass reflects the shared selective breeding targets of the Italian meat processing industry that are crucial for meeting dry-cured ham consortia requirements. The study reveals that while different breeds share a common selection focus on growth and fat deposition, they may achieve these goals through the involvement of different genes. The findings of this study underline the complexity of the effect of the selection programmes in different breeds and emphasise the need for a refined approach to identify and understand the resulting signatures of selection. Furthermore, these results highlight the importance of exploring multiple genomic approaches to uncover genomic regions showing signatures of selection, offering valuable guidance for future investigations in this field. Overall, the insights gained from this study will contribute to understanding how directional selection has shaped the genome of these heavy pig breeds and to better address selection strategies aimed at enhancing the sustainability of the Italian dry-cured production chain.

Supplementary material

Supplementary material to this article can be found online at https://doi.org/10.1016/j.animal.2024.101335.

Ethics approval

Not applicable.

Data and model availability statement

The datasets generated and/or analysed during the current study are not publicly available due owned by a third party but are available from the corresponding author on reasonable request.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) did not use any AI and AI-assisted technologies.

Author ORCIDs

F. Bertolini: https://orcid.org/0000-0003-4181-3895.
G. Schiavo: https://orcid.org/0000-0002-3497-1337.
S. Bovo: https://orcid.org/0000-0002-5712-8211.
A. Ribani: https://orcid.org/0000-0001-6778-1938.
S. Dall'Olio: https://orcid.org/0000-0003-1384-3771.
P. Zambonelli: https://orcid.org/0000-0002-2532-5528.
L. Fontanesi: https://orcid.org/0000-0001-7050-3760.

CRediT authorship contribution statement

F. Bertolini: Writing – review & editing, Writing – original draft, Software, Methodology, Funding acquisition, Formal analysis, Conceptualization. **G. Schiavo:** Writing – review & editing, Funding acquisition, Data curation. **S. Bovo:** Writing – review & editing, Data curation. **A. Ribani:** Writing – review & editing, Data curation. **S. Dall'Olio:** Writing – review & editing. **P. Zambonelli:** Writing – review & editing. **M. Gallo:** Writing – review & editing, Resources. **L. Fontanesi:** Writing – review & editing, Writing – original draft, Funding acquisition, Conceptualization.

Declaration of interest

None.

Acknowledgements

We acknowledge Associazione Nazionale Allevatori Suini (ANAS) for providing the biological samples.

Financial support statement

This work was financially supported by (1) the Horizon Europe Re-Livestock project that has received funding from: the European Union's Horizon Europe research and innovation programme under the grant agreement No. 01059609 (for the elaboration and analysis of the data); (2) the Italian PRIN2022 project FEEDTHEPIG, Funded by the European Union - NextGenerationEU under the National Recovery and Resilience Plan (PNRR) - Mission 4 Education and research - Component 2 From research to business - Investment 1.1 Notice PRIN 2022 PNRR (DD N. 1409 del 14/09/2022), proposal code P2022FZMJ9 - CUP J53D23018310001 (for the analysis of part of the data); (3) the Italian PRIN2022 HamCapture, funded by the European Union - NextGenerationEU under the National Recovery and Resilience Plan (PNRR) - Mission 4 Education and research - Component 2 From research to business - Investment 1.1 Notice Prin 2022 - DD N. 104 del 2/2/2022, proposal code 202238NP9N – CUP J53D23009570001 (for the analysis of part of the data); (4) the Programma di Sviluppo Rurale Nazionale (PSRN) SUIS-2, co-funded by the European Agricultural Fund for Rural Development of the European Union and by the MASAF (for pig genotyping data); (5) and was carried out within the Agritech National Research Center (Agritech Spoke 1) and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022) - This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

References

Alexander, D.H., Novembre, J., Lange, K., 2009. Fast model-based estimation of ancestry in unrelated individuals. Genome Research 19, 1655–16564.
Amaral, A.J., Megens, H.J., Crooijmans, R.P., Heuven, H.C., Groenen, M.A., 2008. Linkage disequilibrium decay and haplotype block structure in the pig. Genetics 179, 569–579.
An, B., Xu, L., Xia, J., Wang, X., Miao, J., Chang, T., Song, M., Ni, J., Xu, L., Zhang, L., Li, J., Gao, H., 2020. Multiple association analysis of loci and candidate genes that regulate body size at three growth stages in Simmental beef cattle. BMC Genetics 21, 32.
ANAS, 2024. National Pig Breeders Association. Retrieved on 2 May 2024 from: https://www.anas.it/files/circolari/202200001.PDF.
Bertolini, F., Schiavo, G., Galimberti, G., Bovo, S., D'Andrea, M., Gallo, M., Buttazzoni, L., Rothschild, M.F., Fontanesi, L., 2018. Genome-wide association studies for seven production traits highlight genomic regions useful to dissect dry-cured ham quality and production traits in Duroc heavy pigs. Animal 12, 1777–1784.
Bosi, P., Russo, V., 2004. The production of the heavy pig for high quality processed products. Italian Journal of Animal Science 3, 309–321.
Bosse, M., Megens, H.J., Frantz, L.A., Madsen, O., Larson, G., Paudel, Y., Duijvesteijn, N., Harlizius, B., Hagemeijer, Y., Crooijmans, R.P., Groenen, M.A., 2014. Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. Nature Communication 5, 4392.
Bovo, S., Schiavo, G., Mazzoni, G., Dall'Olio, S., Galimberti, G., Calò, D.G., Scotti, E., Bertolini, F., Buttazzoni, L., Samorè, A.B., Fontanesi, L., 2016. Genome-wide association study for the level of serum electrolytes in Italian Large White pigs. Animal Genetics 47, 597–602.
Bovo, S., Mazzoni, G., Bertolini, F., Schiavo, G., Galimberti, G., Gallo, M., Dall'Olio, S., Fontanesi, L., 2019. Genome-wide association studies for 30 haematological and blood clinical-biochemical traits in Large White pigs reveal genomic regions affecting intermediate phenotypes. Scientific Reports 9, 7003.
Bovo, S., Ribani, A., Muñoz, M., Alves, E., Araujo, J.P., Bozzi, R., Čandek-Potokar, M., Charneca, R., Di Palma, F., Etherington, G., Fernandez, A.I., García, F., García-Casco, J., Karolyi, D., Gallo, M., Margeta, V., Martins, J.M., Mercat, M.J., Moscatelli, G., Fontanesi, L., 2020. Whole-genome sequencing of European autochthonous and commercial pig breeds allows the detection of signatures of selection for adaptation of genetic resources to different breeding and production systems. Genetics Selection Evolution 52, 1–19.
Bovo, S., Ballan, M., Schiavo, G., Ribani, A., Tinarelli, S., Utzeri, V.J., Dall'Olio, S., Gallo, M., Fontanesi, L., 2021. Single-marker and haplotype-based genome-wide association studies for the number of teats in two heavy pig breeds. Animal Genetics 52, 440–450.
Browning, S.R., Browning, B.L., 2007. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. American Journal of Human Genetics 81, 1084–1097.
Catillo, G., Zappaterra, M., Zambonelli, P., Buttazzoni, L., Steri, R., Minelli, G., Davoli, R., 2020. Genome-wide association study identifies quantitative trait loci regions involved in muscle acidic profile in Large White heavy pigs. Animal 14, 1342–1350.
Chang, C. C., Chow, C. C., Tellier, L. C. A. M., Vattikuti, S., Purcell, S. M., Lee, J. J., 2015. Second-generation PLINK, Rising to the challenge of larger and richer datasets. *GigaScience* 4, s13742-015.
Chevin, L.M., Hospital, F., 2008. Selective sweep at a quantitative trait locus in the presence of background genetic variation. Genetics 180, 1645–1660.
Consorzio del prosciutto di Parma 2024. Piano di Regolazione dell'Offerta 2024 – 2026. Retrieved on 2 May 2024 from: https://www.prosciuttodiparma.com/wp-content/uploads/2024/01/Piano-di-Regolazione-dellOfferta-2024-2026-29-gennaio.pdf.
Consorzio del prosciutto di San Daniele 2024. Prosciutto di San Daniele DOP: i dati di mercato del 2023. Retrieved on 2 May 2024 from: https://prosciuttosandaniele.it/2024/02/prosciutto-di-san-daniele-dop-i-dati-di-mercato-del-2023.
Du, J., Xu, Y., Zhang, P., Zhao, X., Gan, M., Li, Q., Ma, J., Tang, G., Jiang, Y., Wang, J., Li, X., Zhang, S., Zhu, L., 2018. MicroRNA-125a-5p affects adipocytes proliferation, differentiation and fatty acid composition of porcine intramuscular fat. International Journal of Molecular Sciences 19, 501.
Fontanesi, L., Schiavo, G., Galimberti, G., Calò, D.G., Scotti, E., Martelli, P.L., Buttazzoni, L., Casadio, R., Russo, V., 2012. A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. BMC Genomics 13, 1–9.

Fontanesi, L., Schiavo, G., Scotti, E., Galimberti, G., Calò, D.G., Samorè, A.B., Gallo, M., Russo, V., Buttazzoni, L., 2015. A retrospective analysis of allele frequency changes of major genes during 20 years of selection in the Italian Large White pig breed. Journal of Animal Breeding and Genetics 132, 239–246.
Fontanesi, L., Schiavo, G., Galimberti, G., Bovo, S., Russo, V., Gallo, M., Buttazzoni, L., 2017a. A genome-wide association study for a proxy of intermuscular fat level in the Italian Large White breed identifies genomic regions affecting an important quality parameter for dry-cured hams. Animal Genetics 48, 459–465.
Fontanesi, L., Schiavo, G., Gallo, M., Baiocco, C., Galimberti, G., Bovo, S., Russo, V., Buttazzoni, L., 2017b. Genome-wide association study for ham weight loss at first salting in Italian Large White pigs, towards the genetic dissection of a key trait for dry-cured ham production. Animal Genetics 48, 103–107.
Gautier, M., Vitalis, R., 2012. Rehh an R package to detect footprints of selection in genome-wide SNP data from haplotype structure. Bioinformatics 28, 1176–1177.
Ghildiyal, K., Panigrahi, M., Kumar, H., Rajawat, D., Nayak, S.S., Lei, C., Bhushan, B., Dutt, T., 2023. Selection signatures for fiber production in commercial species, A review. Animal Genetics 54, 3–23.
Gregorio, C.C., Weber, A., Bondad, M., Pennise, C.R., Fowler, V.M., 1995. Requirement of pointed-end capping by tropomodulin to maintain actin filament length in embryonic chick cardiac myocytes. Nature 377, 83–86.
Higgins, M.G., Kenny, D.A., Fitzsimons, C., Blackshields, G., Coyle, S., McKenna, C., McGee, M., Morris, D.W., Waters, S.M., 2019. The effect of breed and diet type on the global transcriptome of hepatic tissue in beef cattle divergent for feed efficiency. BMC Genomics 20, 1–11.
Joaquim, L.B., Chud, T.C.S., Marchesi, J.A.P., Savegnago, R.P., Buzanskas, M.E., Zanella, R., Cantão, M.E., Peixoto, J.O., Ledur, M.C., Irgang, R., Munari, D.P., 2019. Genomic structure of a crossbred Landrace pig population. PLoS One 14, e0212266.
Karlsson, E.K., Baranowska, I., Wade, C.M., Salmon Hillbertz, N.H.C., Zody, M.C., Anderson, N., Biagi, T.M., Patterson, N., Pielberg, G.R., Kulbokas, E.J., Comstock, K. E., Keller, E.T., Mesirov, J.P., Von Euler, H., Kämpe, O., Hedhammar, Å., Lander, E. S., Andersson, G., Andersson, L., Lindblad-Toh, K., 2007. Efficient mapping of mendelian traits in dogs through genome-wide association. Nature Genetics 39, 1321–1328.
Keller, S.R., Taylor, D.R., 2008. History, chance and adaptation during biological invasion, separating stochastic phenotypic evolution from response to selection. Ecology Letters 11, 852–866.
Klassmann, A., Gautier, M., 2022. Detecting selection using extended haplotype homozygosity, EHH-based statistics in unphased or unpolarized data. PLoS ONE 17, e0262024.
Li, X., Kim, S.W., Do, K.T., Ha, Y.K., Lee, Y.M., Yoon, S.H., Kim, H.B., Kim, J.J., Choi, B.H., Kim, K.S., 2011. Analyses of porcine public SNPs in coding-gene regions by re-sequencing and phenotypic association studies. Molecular Biology Reports 38, 3805–3820.
Liu, F., Wen, B., Kayser, M., 2013. Colourful DNA polymorphisms in humans. Seminars in Cell and Developmental Biology 24, 562–575.
Ma, Y., Ding, X., Qanbari, S., Weigend, S., Zhang, Q., Simianer, H., 2015a. Properties of different selection signature statistics and a new strategy for combining them. Heredity 115, 426–436.
Ma, Y., Wei, J., Zhang, Q., Chen, L., Wang, J., Liu, J., Ding, X., 2015b. A genome scan for selection signatures in pigs. PLoS ONE 10, e0116850.
McQuillan, R., Leutenegger, A.L., Abdel-Rahman, R., Franklin, C.S., Pericic, M., Barac-Lauc, L., Smolej-Narancic, N., Janicijevic, B., Polasek, O., Tenesa, A., MacLeod, A. K., Farrington, S.M., Rudan, P., Hayward, C., Vitart, V., Rudan, I., Wild, S.H., Dunlop, M.G., Wright, A.F., Wilson, J.F., 2008. Runs of homozygosity in European populations. American Journal of Human Genetics 83, 359–372.
Mohammadabadi, M., Bordbar, F., Jensen, J., Du, M., Guo, W., 2021. Key genes regulating skeletal muscle development and growth in farm animals. Animals 11, 835.
Muñoz, M., Bozzi, R., García, F., Núñez, Y., Geraci, C., Crovetti, A., García-Casco, J., Alves, E., Škrlep, M., Charneca, R., Martins, J.M., Quintanilla, R., Tibau, J., Kušec, G., Djurkin-Kušec, I., Mercat, M.J., Riquet, J., Estellé, J., Zimmer, C., Óvilo, C., 2018. Diversity across major and candidate genes in European local pig breeds. PLoS ONE 13, e0207475.
Muñoz, M., Bozzi, R., García-Casco, J., Núñez, Y., Ribani, A., Franci, O., García, F., Škrlep, M., Schiavo, G., Bovo, S., Utzeri, V.J., Charneca, R., Martins, J.M., Quintanilla, R., Tibau, J., Margeta, V., Djurkin-Kušec, I., Mercat, M.J., Riquet, J., Óvilo, C., 2019. Genomic diversity, linkage disequilibrium and selection signatures in European local pig breeds assessed with a high density SNP chip. Scientific Reports 9, 13546.
Murání, E., Murániová, M., Ponsuksili, S., Schellander, K., Wimmers, K., 2007. Identification of genes differentially expressed during prenatal development of skeletal muscle in two pig breeds differing in muscularity. BMC Developmental Biology 7, 1–16.
Newcom, D.W., Baas, T.J., Stalder, K.J., Schwab, C.R., 2005. Comparison of three models to estimate breeding values for percentage of loin intramuscular fat in Duroc swine. Journal of Animal Science 83, 750–756.
Panigrahi, M., Rajawat, D., Nayak, S.S., Ghildiyal, K., Sharma, A., Jain, K., Lei, C., Bhushan, B., Mishra, B.P., Dutt, T., 2023. Landmarks in the history of selective sweeps. Animal Genetics 54, 667–688.
Park, S.K., Gunawan, A.M., Scheffler, T.L., Grant, A.L., Gerrard, D.E., 2009. Myosin heavy chain isoform content and energy metabolism can be uncoupled in pig skeletal muscle. Journal of Animal Science 87, 522–531.
Pemberton, T., Absher, D., Feldman, M., Myers, R.M., Rosenberg, N.A., Li, J.Z., 2012. Genomic patterns of homozygosity in worldwide human populations. American Journal of Human Genetics 91, 275–292.
Peripolli, E., Munari, D.P., Silva, M.V.G.B., Lima, A.L.F., Irgang, R., Baldi, F., 2017. Runs of homozygosity, current knowledge and applications in livestock. Animal Genetics 48, 255–271.
Porter, V., 1993. Pigs. A Handbook to the Breeds of the World. Helm Information Ltd, Mountfield, UK.
Pritchard, J.K., Pickrell, J.K., Coop, G., 2010. The genetics of human adaptation, hard sweeps, soft sweeps, and polygenic adaptation. Current Biology 20, R208–R215.
Qanbari, S., Simianer, H., 2014. Mapping signatures of positive selection in the genome of livestock. Livestock Science 166, 133–143.
Quinlan, A.R., Hall, I.M., 2010. BEDTools, A flexible suite of utilities for comparing genomic features. Bioinformatics 26, 841–842.
R Core Team, 2013. R, A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.
Rask-Andersen, M., Almén, M.S., Lind, L., Schiöth, H.B., 2015. Association of the LINGO2-related SNP rs10968576 with body mass in a cohort of elderly Swedes. Molecular Genetics and Genomics 290, 1485–1491.
Raza, S.H.A., Pant, S.D., Wani, A.K., Mohamed, H.H., Khalifa, N.E., Almohaimeed, H.M., Alshanwani, A.R., Assiri, R., Aggad, W.S., Noreldin, A.E., Abdelnour, S.A., Wang, Z., Zan, L., 2022. Krüppel-like factors family regulation of adipogenic markers genes in bovine cattle adipogenesis. Molecular and Cellular Probes 65, 101850.
Regulation (EU) No. 1308/2013 of the European Parliament and of the Council of 17 December 2013. Retrieved on 2 May 2024 from: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX%3A32013R1308.
Ropka-Molik, K., Zukowski, K., Eckert, R., Piórkowska, K., Oczkowicz, M., Gurgul, A., Szmatoła, T., 2015. Whole transcriptome analysis of the porcine muscle tissue of breeds differing in muscularity and meat quality traits. Livestock Science 182, 93–100.
Rothschild, M.F., Ruvinsky, A., 2011. The genetics of the pig. CABI, Wallingford, UK.
Ruan, D., Zhuang, Z., Ding, R., Qiu, Y., Zhou, S., Wu, J., Xu, C., Hong, L., Huang, S., Zheng, E., Cai, G., Wu, Z., Yang, J., 2021. Weighted single-step GWAS identified candidate genes associated with growth traits in a duroc pig population. Genes 12, 117.
Rubin, C.J., Megens, H.J., Barrio, A.M., Maqbool, K., Sayyab, S., Schwochow, D., Wang, C., Carlborg, Ö., Jern, P., Jørgensen, C.B., Archibald, A.L., Fredholm, M., Groenen, M.A.M., Andersson, L., 2012. Strong signatures of selection in the domestic pig genome. Proceedings of the National Academy of Sciences of the United States of America 109, 19529–19536.
Sabeti, P.C., Reich, D.E., Higgins, J.M., Levine, H.Z.P., Richter, D.J., Schaffner, S.F., Gabriel, S.B., Platko, J.V., Patterson, N.J., McDonald, G.J., Ackerman, H.C., Campbell, S.J., Altshuler, D., Cooper, R., Kwiatkowski, D., Ward, R., Lander, E.S., 2002. Detecting recent positive selection in the human genome from haplotype structure. Nature 419, 832–837.
Sabeti, P.C., Schaffner, S.F., Fry, B., Lohmueller, J., Varilly, P., Shamovsky, O., Palma, A., Mikkelsen, T.S., Altshuler, D., Lander, E.S., 2006. Positive natural selection in the human lineage. Science 312, 1614–1620.
Sabeti, P.C., Varilly, P., Fry, B., Lohmueller, J., Hostetter, E., Cotsapas, C., Xie, X., Byrne, E.H., McCarroll, S.A., Gaudet, R., Schaffner, S.F., Lander, E.S., Frazer, K.A., Ballinger, D.G., Cox, D.R., Hinds, D.A., Stuve, L.L., Gibbs, R.A., Belmont, J.W., Stewart, J., 2007. Genome-wide detection and characterization of positive selection in human populations. Nature 449, 913–918.
Saravanan, K.A., Panigrahi, M., Kumar, H., Bhushan, B., Dutt, T., Mishra, B.P., 2020. Selection signatures in livestock genome, a review of concepts, approaches and applications. Livestock Science 241, 104257.
Scheet, P., Stephens, M., 2006. A fast and flexible statistical model for large-scale population genotype data, applications to inferring missing genotypes and haplotypic phase. The American Journal of Human Genetics 78 (4), 629–644.
Schiavo, G., Galimberti, G., Calò, D.G., Samorè, A.B., Bertolini, F., Russo, V., Gallo, M., Buttazzoni, L., Fontanesi, L., 2016. Twenty years of artificial directional selection have shaped the genome of the Italian Large White pig breed. Animal Genetics 47, 181–191.
Schiavo, G., Bovo, S., Bertolini, F., Dall'Olio, S., Nanni Costa, L., Tinarelli, S., Gallo, M., Fontanesi, L., 2020. Runs of homozygosity islands in Italian cosmopolitan and autochthonous pig breeds identify selection signatures in the porcine genome. Livestock Science 240, 104219.
Sellier, P., 1976. The basis of crossbreeding in pigs; a review. Livestock Production Science 3, 203–226.
Stephan, W., 2019. Selective sweeps. Genetics 211, 5–13.
Sturm, R.A., Larsson, M., 2009. Genetics of human iris colour and patterns. Pigment Cell and Melanoma Research 22, 544–562.
Utrilla, M.C., Soriano, A., Ruiz, A.G., 2010. Quality attributes of pork loin with different levels of marbling from Duroc and Iberian cross. Journal of Food Quality 33, 802–820.
Voight, B.F., Kudaravalli, S., Wen, X., Pritchard, J.K., 2006. A map of recent positive selection in the human genome. PLoS Biology 4, e72.
Wang, X., Li, G., Ruan, D., Zhuang, Z., Ding, R., Quan, J., Wang, S., Jiang, Y., Huang, J., Gu, T., Hong, L., Zheng, E., Li, Z., Cai, G., Wu, Z., Yang, J., 2022. Runs of homozygosity uncover potential functional-altering mutation associated with body weight and length in two duroc pig lines. Frontiers in Veterinary Science 9, 832633.

Wang, L., Sørensen, P., Janss, L., Ostersen, T., Edwards, D., 2013. Genome-wide and local pattern of linkage disequilibrium and persistence of phase for 3 Danish pig breeds. BMC Genetics 14, 1–11.
Wang, Z., Sun, H., Chen, Q., Zhang, X., Wang, Q., Pan, Y., 2019. A genome scan for selection signatures in Taihu pig breeds using next-generation sequencing. Animal 13, 683–693.
Weaber, B., 2010. Crossbreeding for commercial beef production. In: Nielsen, M.K. (Ed.), Beef Sire Selection Manual. National Beef Cattle Evaluation Consortium, Ames, IA, USA, pp. 50–57.
Weir, B.S., Cockerham, C.C., 1984. Estimating F-statistics for the analysis of population structure. Evolution 38, 1358–1370.
Wilkinson, S., Lu, Z.H., Megens, H.J., Archibald, A.L., Haley, C., Jackson, I.J., Groenen, M.A.M., Crooijmans, R.P.M.A., Ogden, R., Wiener, P., 2013. Signatures of diversifying selection in European pig breeds. PLoS Genetics 9, e1003453.
Wu, H., Zhao, S., Liu, B., Yu, M., Zhu, M., Li, C., Fan, B., 2009. Tropomodulin 1, TMOD1 is associated with lean meat growth and meat quality in the pig, brief report. Archives Animal Breeding 52, 108–110.
Zappaterra, M., Ros-Freixedes, R., Estany, J., Davoli, R., 2018. Association study highlights the influence of ELOVL fatty acid elongase 6 gene region on backfat fatty acid composition in Large White pig breed. Animal 12, 2443–2452.