



# Genome-Wide Assessment of Signatures of Selection in the Pakistan Sahiwal Cattle

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## ABSTRACT

The Sahiwal breed of dairy cattle holds significant importance in Pakistan, mostly attributed to its ability to withstand high temperatures, resilience to diseases, and satisfactory performance when fed low-quality roughages. Domestication and breeding of mammals have exerted a consistent selection pressure on a wide range of characteristics in many domesticated species, resulting in discernible genetic modifications at the individual genome level. The study aimed to discover and analyze potential indicators of recent selection in Sahiwal cattle, specifically identifying the genes and quantitative trait loci associated with these selection indicators. The study utilized a sample size of 98 Sahiwal bulls. The genotyping of all animals was conducted using the BovineHD140k BeadChip. After undergoing quality control measures, 87 samples as well as 74,070 SNPs located throughout 29 autosomes were selected as well as included in the study. The selection signatures were examined using the iHS and the Tajima D approach. The result reveals the current positive selections on BTA 1, 2, 6, 11, 12, 15, 17, 21, and 27 with the iHS test, while for the Tajima D test, the current positive selections were detected on BTA 1, 2, 3, 4, 5, 6, 7, 9, 10, 14, 18, 20, 23, and 24. A total of 47 genes were detected within selection regions associated with vital economic traits. The QTL enrichment analysis has shown eight substantial QTLs in BTA19 and BTA20 linked with milk, production, as well as reproduction traits. Therefore, understanding the selection signatures and candidate genes that influence important economic traits can provide foundational knowledge that can be used effectively to gain insight into the underlying mechanisms controlling these traits in Sahiwal cattle.

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## Authors' Contribution

ARS and MSR designed the study, conducted the research, analyzed the data and wrote the drafted manuscript. FR and FSA assisted in interpreting the results and finalized the manuscript. All the authors reviewed the manuscript. All authors have read and agreed to the current version of the manuscript.

## Key words

Artificial selection, Candidate genes, Gene identification, Sahiwal cattle, Signature selection, SNP genotyping

## INTRODUCTION

The Sahiwal cattle breed originated in the central Punjab district of Pakistan. The breed is named after the Sahiwal district, part of its home track (Joshi *et al.*, 2001; Akram and Khan, 2011; Saeed *et al.*, 2020). They are members of a category of giant Zebu breeds known as dual purpose. Due to its higher milk production and growth capacity than other Zebu cattle breeds, it is primarily used for milk and meat production (Ilatsia *et al.*, 2011; Iqbal *et al.*, 2015). The Sahiwal breed of dairy cattle holds

significant importance in Pakistan, mostly attributed to its ability to withstand high temperatures, resilience to diseases, and satisfactory performance when fed low-quality roughages (Bhatti *et al.*, 2007; Zurwan *et al.*, 2017). Sahiwal cattle have been widely included in crossbreeding initiatives on a global scale due to their superior milk production attributes and remarkable resilience under adverse ecological conditions (Naskar *et al.*, 2012; Wilson, 2018; Silpa *et al.*, 2021). The use of selective breeding and genetic isolation contributes to the development of many breeds of cattle and aids in the preservation of genomic resources and the retention of adaptive traits adapted to specific local conditions (Alderson, 2018; Zhang *et al.*, 2018; Segelbacher *et al.*, 2022). Artificial selection has been shown to improve the prevalence of advantageous alleles associated with economic traits, facilitating the enhancement of production parameters (Kim *et al.*, 2015; Mei *et al.*, 2019). Domestication and breeding of mammals have exerted consistent selection pressure on a wide range of characteristics in many domesticated species, resulting in discernible genetic modifications at the individual

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genome level (Jensen, 2015; Jensen and Wright, 2022). The genomic regions under selection pressure shows a functional variation associated with the traits (Driscoll *et al.*, 2009; Stamps and Groothuis, 2010).

In Pakistan, researchers have been employing the progeny testing program as part of a selection effort to increase the milk production capacity of Sahiwal cattle for decades under the coordination of the Research Centre for Conservation of Indigenous Breeds (RCCIB), Jhang (Moaeeen-ud-Din *et al.*, 2014). The program involves registering and documenting institutional and private herds of Sahiwal cattle, recording for genetic evaluation, and identifying superior germplasm for genetic evaluation (McGill, 2015). However, applying for a conventional progeny testing program under Pakistani conditions appears to be difficult due to the small size of the herd, low awareness among the farmer community about pedigree and performance recording, resource limitations, and a lack of fundamental infrastructure (Shah *et al.*, 2008; Moaeeen-ud-Din *et al.*, 2014). Thus, the efficiency of the Sahiwal cattle has not improved much over the years (Moaeeen-ud-Din *et al.*, 2014; Zurwan *et al.*, 2017). The efficiency of the Sahiwal breed can be enhanced by improving nutrition and management practices, estimating genetic parameters, and identifying the genes as well as quantitative trait loci linked with vital economic traits and subsequent genomic selection for such genes (Meuwissen *et al.*, 2001; Rehman and Khan, 2012; Khan *et al.*, 2018). Thus, genomic areas of Sahiwal cattle will continue to experience intense selective pressures for an extended period as the quest to select the best animals with high milk production capability continues in the country (Haskell *et al.*, 2014; Illa *et al.*, 2021). The existing body of literature on the outcome of selection on the Pakistan Sahiwal cattle remains limited at present. Hence, it is imperative to investigate and explore the genomic signatures of selection in Sahiwal cattle to comprehend the molecular mechanisms that influence quantitative as well as other significant traits (Pedrosa *et al.*, 2021; Zhang *et al.*, 2022b; Rajawat *et al.*, 2023). Additionally, annotating the genes and quantitative trait loci (QTL) linked with economically vital traits is crucial (Illa *et al.*, 2021; Zhang *et al.*, 2022b).

Selection signatures refer to distinct genetic variations that occur at the DNA level as a result of deviations in the genomes of the chosen as well as neutral loci within a species that has experienced selection over time (Kreitman, 2000). Selection signatures are found in species subjected to selection during their evolution (Bamshad and Wooding, 2003; Laland *et al.*, 2010). Variants subjected to selection pressure can cause characteristic genomic patterns to emerge, including a change in the distribution of allele frequencies, an increase in the proportion of homozygous

genotypes, the prevalence of long haplotypes, and a significant degree of population substructure (Pritchard *et al.*, 2010; Zhang *et al.*, 2015). Modern cattle have undergone extensive selection over the centuries, resulting in dramatic phenotypic changes in the last 40 years (Pitt *et al.*, 2019; Frantz *et al.*, 2020; Brito *et al.*, 2021). The development of affordable genotyping techniques has allowed more individuals to genotype using different densities of single nucleotide polymorphism (SNP) arrays (Boichard *et al.*, 2012; Gorjanc *et al.*, 2015; Cortes *et al.*, 2022). New polymorphism data and the subsequent release of the bovine genome sequence have provided useful new resources for the search for evidence of recent selection in the bovine genome (Utsunomiya *et al.*, 2013; Xu *et al.*, 2015). This has improved precision and accuracy in identifying specific genomic areas in cattle (Hayes *et al.*, 2009; Meuwissen *et al.*, 2022). These advances have also contributed to identifying and analyzing genetic variations subject to natural selection in *Homo sapiens* as well as other animal species (Oleksyk *et al.*, 2010; Luikart *et al.*, 2019). When an allele experiences positive selection, it experiences a selective sweep when it becomes more common in the population (Moradi *et al.*, 2012; Booker *et al.*, 2017). Genetic hitch-hiking is the process through which closely related alleles increase frequency along with the positively chosen allele (Booker *et al.*, 2017). An area of the genome where the positively selected haplotype is more prevalent due to a strong selection sweep would have less haplotype diversity (Moradi *et al.*, 2012). Measuring LD or checking whether a haplotype is over-represented in a population are good ways to look for evidence of a selective sweep (Hayes, 2007; Zhang *et al.*, 2022a).

Several different statistical models have been created to identify signs of selection. Several studies have been performed to detect the signatures of selection using several statistical techniques, such as the integrated haplotype score (iHS) (Voight *et al.*, 2006), Tajima's D (Tajima, 1989), fixation index (FST) (Akey *et al.*, 2002), and the extended haplotype homozygosity (EHH) (Sabeti *et al.*, 2002). These studies use methods complementarity to improve statistical power (Illa *et al.*, 2021; Waineina *et al.*, 2022). The iHS and Tajima's D estimators are especially helpful among the numerous statistics used to recognize signs of positive selection from polymorphism data and would be the techniques of choice in this investigation (Zeng *et al.*, 2007; Chen *et al.*, 2010). The discovery of genomic areas under selection pressure has the potential to improve our comprehension of the underlying biology of certain phenotypes. This knowledge may be used to build techniques to improve selection efficiency (Moradian *et al.*, 2020). Therefore, the study aimed to discover and analyze potential indicators of recent selection in Sahiwal

cattle, specifically identifying the genes and quantitative trait loci (QTL) linked with these selection indicators.

## MATERIALS AND METHODS

### *Animal resources and SNP genotyping*

The study's sample size consisted of 98 Sahiwal cattle bulls, which were sourced from public as well as private livestock farms in the Punjab area of Pakistan. Blood samples were collected from all the 98 Sahiwal cattle bulls. The researchers employed a salting-out method to extract genomic DNA from blood samples, as described by Miller *et al.* (1988). The NanoDrop ND-1000 spectrophotometer, manufactured by NanoDrop Technologies in Wilmington, DE, was utilized to quantify the concentration of the isolated DNA. Good quality DNA samples were sent for genotyping utilizing the BovineHD140k Bead Chip (Illumina Inc. in San Diego, California, USA) following the standard operating procedure described by the manufacturer. Raw data was processed to generate ped files that provide genotypes and map files having a genomic location of markers.

### *Quality control*

The PLINK program (Purcell *et al.*, 2007) conducted quality control assessments on genotyping data. The research study opted for a call rate exceeding 95% for the collection of study data as well as subsequent analysis. The study employed SNPs with minor allele frequencies (MAFs) below 0.05. The analysis of the study included the examination of markers and animals, which did not exhibit a substantial divergence from Hardy-Weinberg proportions ( $P > 0.001$ , Bonferroni corrected). The analysis exclusively incorporated SNPs that were identified within autosomal chromosomes. Furthermore, samples that exhibited a missing genotyping rate exceeding 10% were excluded from the analysis. SNPs were subjected to a filtering process in order to exclude loci that were allocated to unmapped contigs and chromosomes associated with sexual determination. After undergoing quality control procedures, a total of 87 samples and 74,070 SNPs were deemed suitable for further analysis. These SNPs were distributed over the 29 autosomes.

### *Calculation of the integrated haplotype score*

The rehh package (Gautier and Vitalis, 2012) in R Software was utilized to analyze the integrated haplotype score (iHS) test. The iHS score is derived from the assessment of extended haplotype homozygosity (EHH) linked to each allele. The computation of single-site iHS values was performed for each animal throughout the whole genome. These values were then averaged in non-

overlapping windows of 500 kb throughout the genome. The window size was adapted on the bases of the extent of LD as defined by Qanbari *et al.* (2011). The unstandardized iHS can be obtained by using the following calculation:

$$\text{Unstandardized } iHS = \ln \left( \frac{iHH_A}{iHH_D} \right) \dots (1)$$

Where  $iHH_A$  as well as  $iHH_D$  signify the integrated EHH score for ancestral as well as derived core alleles, separately. This value has been normalized such that the mean is 0 and the standard deviation is 1, and this is done regardless of the allele frequency at the core SNP (Voight *et al.*, 2006).

The standardized iHS was computed as follows:

$$iHS = \frac{\ln \left( \frac{iHH_A}{iHH_D} \right) - E \left[ \ln \left( \frac{iHH_A}{iHH_D} \right) \right]}{SD \left[ \ln \left( \frac{iHH_A}{iHH_D} \right) \right]} \dots (2)$$

In this context,  $iHH_A$  and  $iHH_D$  denote the integrated EHH score for ancestral (A) and derived (D) core alleles, while E and SD reflect the expectation and standard deviation of unstandardized iHS, respectively. To determine the P value at the genome level, the iHS scores for each single nucleotide polymorphism (SNP) were subjected to a subsequent transformation. This transformation involved calculating the  $p_{iHS} = -\log [1 - 2|\Phi(iHS) - 0.5|]$ . The function  $\Phi(x)$  denotes the Gaussian cumulative distribution function in the context of neutrality, whereas p iHS refers to the two-sided P-value linked to the neutral hypothesis (Gautier and Naves, 2011).

### *Tajima's D statistics*

Tajima's D statistics were also computed for each chromosome utilizing the vcfTools software (Danecek *et al.*, 2011). The Tajima D index was calculated using nonoverlapping sliding windows of 100 MB as a parameter (Tajima D 100). Within each bin, the p-values were calculated and given to each SNP. Zero was substituted for any missing values.

### *Identification of functional genes and QTL*

SNPs exhibiting statistically significant iHS and Tajima D values were analyzed utilizing the ARS-UCD1.2 assembly (Rosen *et al.*, 2018) as well as Ensembl Genome Browser (Zerbino *et al.*, 2018) databases. This analysis aimed to discover QTL genes or neighboring genes associated with these SNPs. The genes and QTLs were acquired from the ARS-UCD1.2 assembly (Rosen *et al.*, 2018) as well as the Animal QTL database (Hu *et al.*, 2016), respectively, in the gtf and gff formats. The study utilized Panther databases (Mi and Thomas, 2009) to document the molecular functions and biological processes associated with the discovered genes. The QTL animal database (available at <https://www.animalgenome.org>).

[org/cgi-bin/QTLdb/BT/index](http://org/cgi-bin/QTLdb/BT/index)) (Hu *et al.*, 2016) was utilized to ascertain the QTL reported in the literature for each specific candidate region. The gene as well as QTL annotations were conducted with the R package GALLO (Fonseca *et al.*, 2020). The enrichment analysis of QTLs was performed on all QTLs annotated using the chromosome-based technique, utilizing the GALLO program. Implementing a bootstrap approach involved conducting a correlation analysis between the observed as well as expected number of QTLs per characteristic, using data obtained from the cattle QTL database. The p-values derived from the enrichment analysis were adjusted utilizing the false discovery rate (FDR) approach. A significance threshold of less than 5% was used to accommodate for the numerous tests conducted. Gene ontology and pathway analyses were performed using the TOPGO and KEGGREST packages in R software.

## RESULTS

### Genome-wide distribution of *iHS*

The *iHS* distribution exhibited a close approximation to normality, as indicated by  $iHS \sim N(0, 1)$ . Consequently, it was possible to make comparisons between the markers and the chromosomes (Fig. 1). The unstandardized *iHS* within frequency bins (*iHS*-b) was used to identify the selection signatures in dairy cattle (Fig. 2). The *iHS*-b was calculated for each SNP within each frequency bin. The frequency bins were created by dividing the range of possible frequencies into equal intervals. The *iHS*-b was then calculated for each frequency bin. The SNPs with the highest *iHS*-b values were identified as signature SNPs.

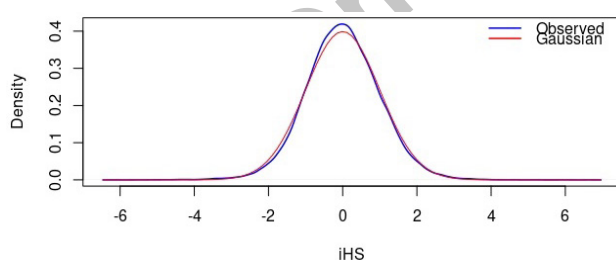


Fig. 1. Comparison between the distribution of standardized integrated haplotype scores (*iHS*) and the standard Gaussian distribution.

### Integrated haplotype score (*iHS*) test

Figure 3 shows the distribution of *iHS* by chromosome, while Figure 4 shows the alteration of analogous markers into *piHS*. The *iHS* statistic was plotted against the genomic location of the breed to visually represent the distribution of outlier signals across chromosomes. Since the *iHS* test

found many important signals, we used the maximum *iHS* and *piHS* values to assess genes in the target genomic regions. Considering the *iHS* values, the genomic regions under the recent signatures of selection were found on BTA 1, 2, 6, 11, 12, 15, 17, 21, and 27 (Table I). The most convincing evidence of selection in the Sahiwal cattle is on BTA6 with an *iHS* score of -5.23 as well as on BTA27 with an *iHS* score of -5.58.

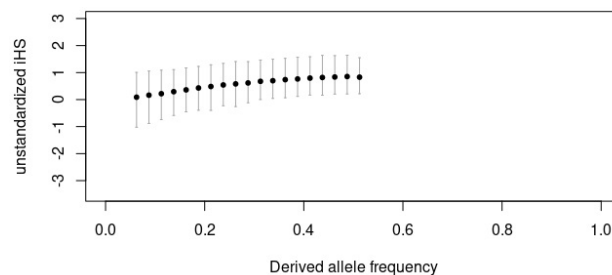


Fig. 2. Unstandardized integrated haplotype scores (*iHS*) within frequency bins.

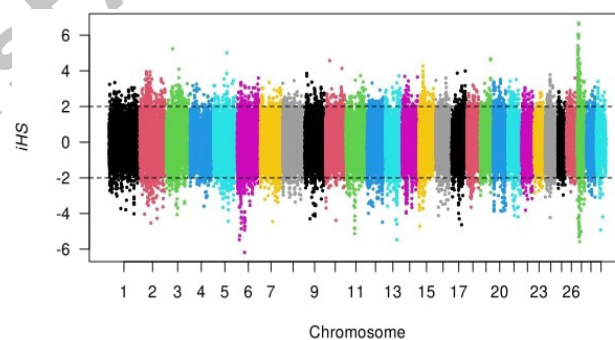


Fig. 3. Distribution of the integrated haplotype score (*iHS*) across the genome.

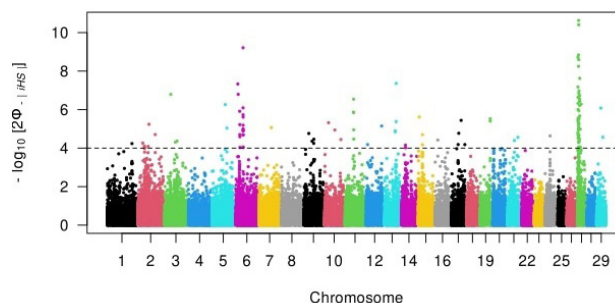


Fig. 4. Genome-wide distribution of the logarithmic transformed Integrated haplotype scores (*piHS*) of each SNP per chromosome.

**Table I. Genomic autosomal regions and potential**



**genes identified by the integrated haplotype score (iHS) test under the indication of the signature of selection in Sahiwal cattle.**

Chromosome	Position	Candidate gene	iHS	PiHS
1	132552990	PPP2R3A	-4.019491072	4.234152759
2	26259557	UBR3	-4.035439883	4.263602754
2	59837978	THSD7B	-4.533780388	5.237041985
2	92923678	PARD3B	-4.268678484	4.706340383
6	13502824	AP1AR	-5.238324881	6.790376077
6	21884446	CENPE	-4.852971281	5.914976041
6	22334879	MANBA	-4.526024536	5.221099479
6	22363715	MANBA	-4.26626077	4.70163512
6	22695313	SLC39A8	-4.210045351	4.59291613
11	45961342	CHCHD5	-4.824651776	5.853103064
11	45985907	CHCHD5	-4.829806865	5.864340963
11	47097519	EIF2AK3	-4.145736881	4.470155805
12	82530142	NALF1	-4.489584574	5.146531708
15	7365780	ATG13	-4.713396119	5.613283588
17	40308609	FAT4	-4.301386566	4.770234589
21	57523947	CHGA	-4.19035223	4.555140878
27	3658384	CSMD1	-4.272224754	4.713246396
27	13371357	TENM3	-4.738578572	5.667112173
27	13376444	TENM3	-5.581677719	7.623040968

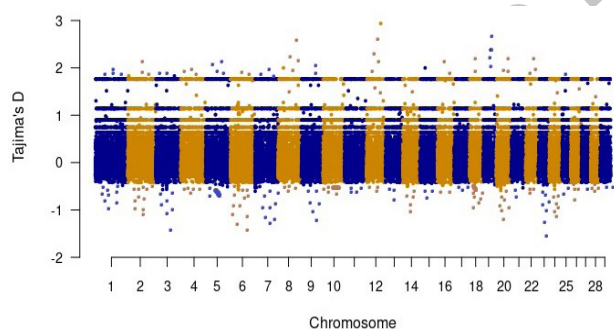


Fig. 5. Manhattan plot of Tajima's D values.

*Tajima's D statistics*

Most autosomes exhibited at least one significant signal of selection (Fig. 5), and high Tajima D values were found to be under positive selection in various contexts. The study only considered negative values representing current positive selection signals. Tajima's D test found significant selection signals in 51 genomic regions. Current signals of positive selection were detected on BTA 1, 2, 3, 4, 5, 6, 7, 9, 18, 20, 23, and 24. Tajima's D signals comprised 31 candidate genes (Table II). Furthermore, the 31 genes identified within the selection regions are linked with milk

composition traits like milk protein yield, milk alpha casein percentage, milk fat percentage, milk fat yield, milk alpha-lactalbumin percentage, milk protein percentage, as well as milk beta-casein percentage according to previous reports.

**Table II. Genomic autosomal region and potential genes identified by Tajima's D test under the indication of a positive signature of selection in Sahiwal cattle.**

Chromosome	Start position	End position	Candidate gene	Trait
1	29105747	29418948	GBE1	Milk protein yield
1	1643680	1651038	ATP5PO	
1	3498977	3629442	HUNK	
1	20991748	21009134	LOC112447287	
1	4925473	4926072	LOC112446980	
1	57125817	57206343	CD200	
1	98873841	98873935	MIR551B	Milk alpha casein percentage
1	1.35E+08	1.35E+08	ANAPC13	
1	1.32E+08	1.32E+08	LOC112448286	
1	1.26E+08	1.26E+08	PAQR9	
1	1.56E+08	1.57E+08	KCNH8	Milk fat content
2	1.27E+08	1.27E+08	STMN1	Milk fat yield
2	47961935	48181188	LOC107132255	
2	44432998	44652244	NEB	
2	1.32E+08	1.32E+08	UBXN10	
2	1.04E+08	1.04E+08	SMARCAL1	
2	23404603	23571295	MAP3K20	
3	51855689	51880658	CDC7	Milk protein yield
3	30206039	30268283	LRIG2	Milk protein percentage
5	98993095	99048504	LOC101902742	Milk alpha lactalbumin percentage
6	55443414	55635282	ARAP2	Milk protein percentage
7	328408	329337	LOC107131408	Milk fat yield
7	23975396	24263996	CHSY3	Milk beta casein percentage
9	32590633	33013293	SLC35F1	Milk fat yield
14	22640320	22957122	XKR4	Milk fat percentage
18	43093119	43130616	ANKRD27	Milk fat yield
20	21798316	21799446	ACTBL2	
20	4596537	4709460	ERGIC1	
20	27974735	27974841	LOC112443073	
23	39178908	39266796	RNF144B	
24	27152147	27152251	LOC112444247	Milk fat content

*Analysis of QTL identification*

The study identified significant genomic regions consisting of 25.08% of milk-type QTLs in Sahiwal cattle as well as other QTLs associated with traits like meat as well as carcass, production, health, reproduction, as well as exterior, which were annotated and represented 21.54, 18.72, 13.85, 11.05, and 9.76%, respectively (Fig. 6). Milk-type QTLs included loci associated with milk protein yield, milk yield, milking speed, milk beta-casein content, milk energy yield, stearic acid content, milk oleic acid content, milk kappa-casein percentage, curd firming rate, milk caprylic acid content, milk caproic acid content, milk alpha-casein content, milk alpha-S2-casein percentage, milk casein content, milk color, milk kappa-casein content, milk protein content, milk odd-chain fatty acid percentage, milk palmitoleic acid content, milk saturated to unsaturated fatty acid ration, and milk whey protein content (Fig. 7).

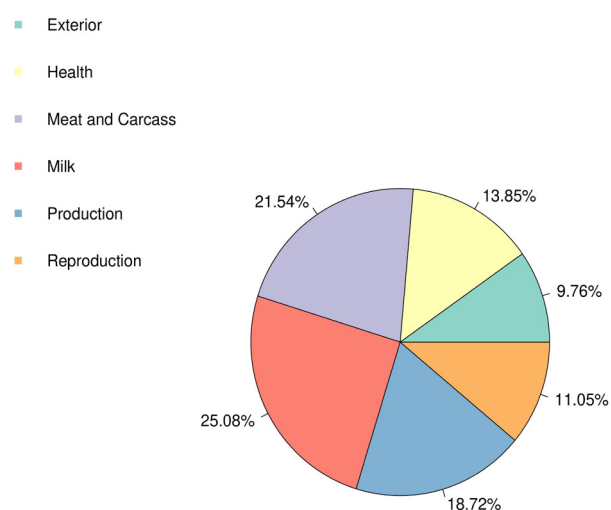


Fig. 6. Pie plot shows the part of six quantitative trait loci (QTL) classes annotated in the substantial genomic areas.

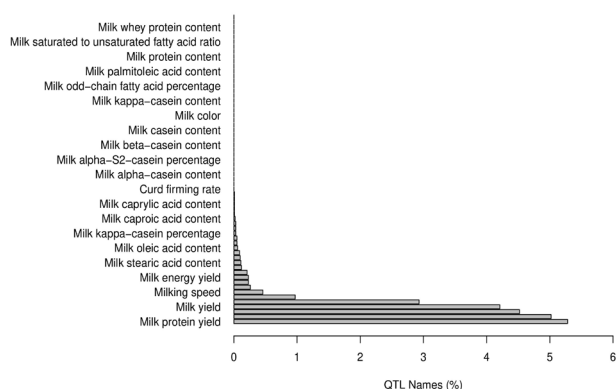


Fig. 7. Milk-type quantitative trait loci (QTL) component. *QTL enrichment analysis*

The QTL enrichment analysis was done to obtain unprejudiced data on the significant QTLs in the population instead of doing the QTL annotation. The QTL enrichment analysis has shown 8 substantial QTLs on BTA19 and BTA20, which are linked with milk, production, as well as reproduction traits (Table III). The utmost substantial QTLs were mapped on BTA19 and BTA20, linked with fat percentage, fertilization rate, milk fat yield, early embryonic survival, body depth, body weight, and average daily gain (Fig. 8). Intriguingly, the highest significant QTL identified on BTA19 was linked with milk fat yield as well as fat percentage.

Table III. The enriched QTLs were annotated in the assumed genomic areas.

Trait	Chromosome	Number of QTLs	Number of annotated QTLs	p-value
Milk	19	16	321	0.040234
	19	12	321	0.046226
Production	19	22	321	0.000171
	20	19	210	0.008069
	19	11	321	0.013937
	19	8	321	0.045253
Reproduction	19	12	321	0.009393
	19	10	321	0.020660



Fig. 8. Quantitative trait loci (QTL) enrichment analysis resolute the vital traits enriched in the substantial genomic areas.

#### Gene enrichment analysis for iHS

The gene ontology (GO) enrichment analysis of the significant genes of the iHS scores was categorized

into biological processes (Fig. 9A), molecular function (Fig. 9B), and cellular components (Fig. 9C). The GO enrichment analysis revealed 30 biological processes, 6

molecular functions, and 22 cellular components for the iHS test.

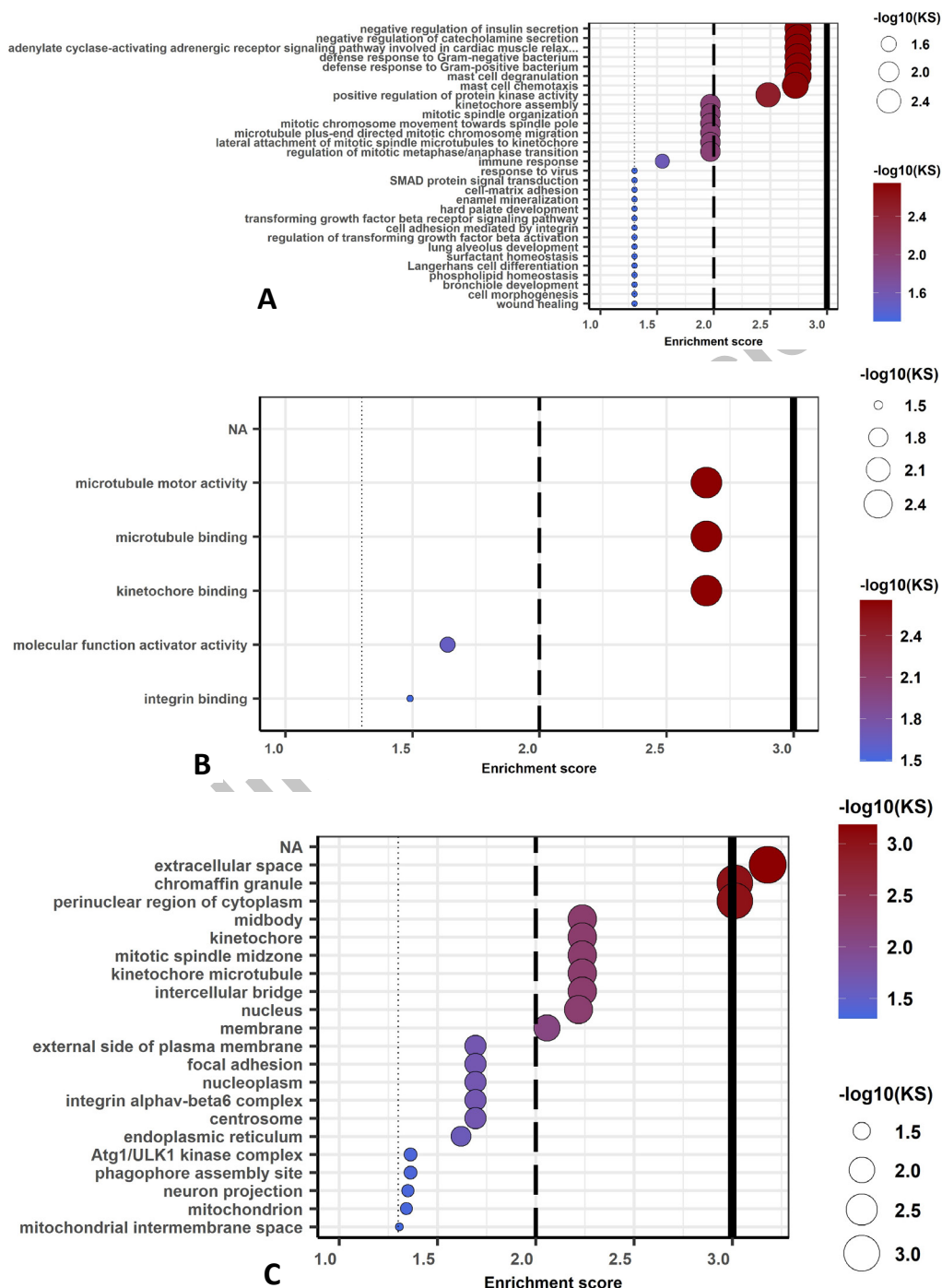


Fig. 9. Biological process (A), molecular function (B) and cellular component (C) of gene network computed for the iHS significant potential genes. The cut off lines drawn at equivalents of  $p=0.05$ ,  $p=0.01$ , and  $p=0.001$ . KS means the  $p$ -value of Kolmogorov-Smirnov test implemented in the R package 'topGO'.

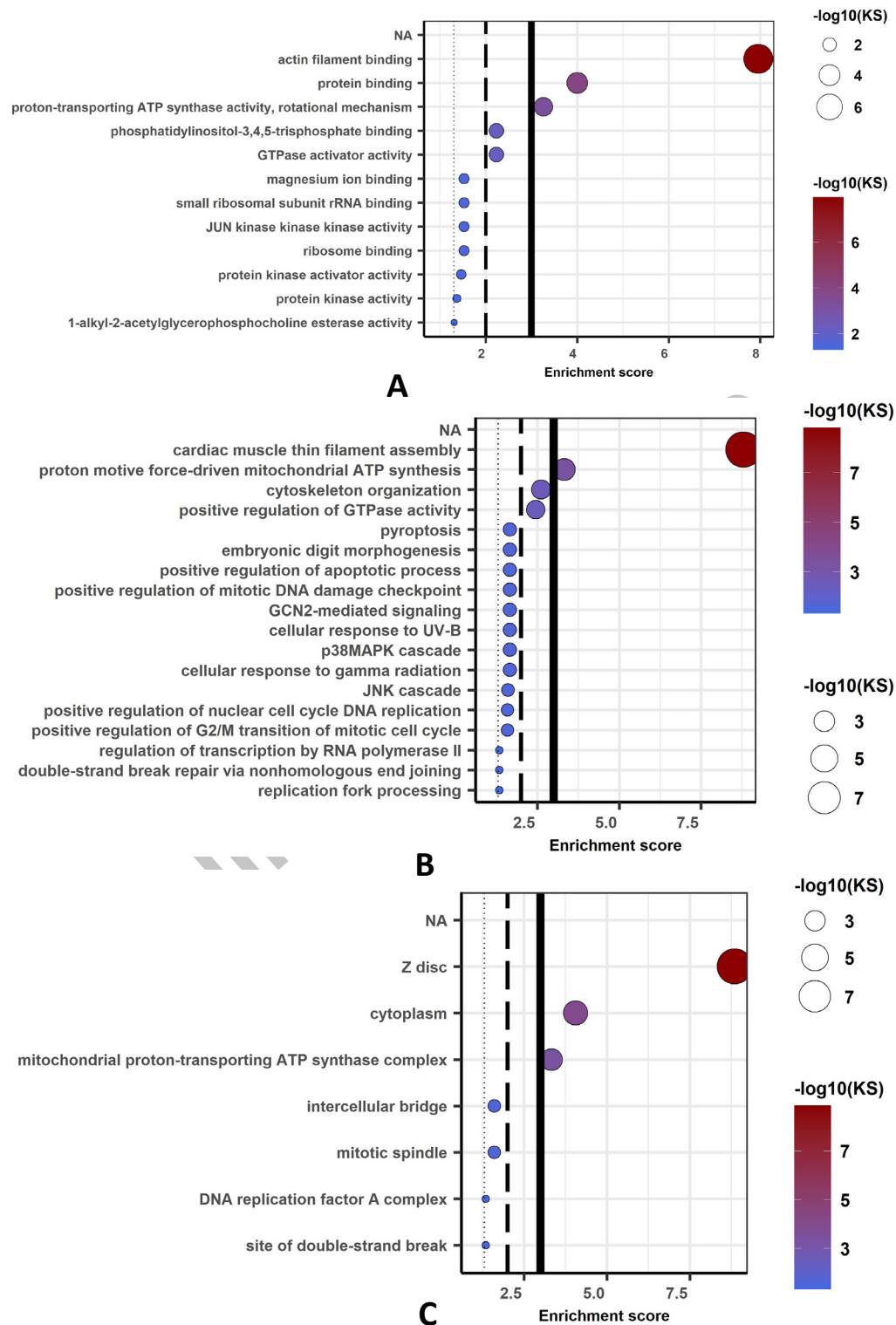


Fig. 10. Biological process (A), molecular function (B) and cellular component (C) of gene network computed for the Tajima's D significant potential genes. The cut off lines drawn at equivalents of  $p=0.05$ ,  $p=0.01$ , and  $p=0.001$ . KS means the p-value of Kolmogorov-Smirnov test implemented in the R package 'topGO'.



### Gene enrichment analysis for Tajima D

The gene ontology (GO) enrichment analysis of the significant genes of the Tajima's D test was categorized into biological processes (Fig. 10A), molecular function (Fig. 10B), and cellular components (Fig. 10C). The GO enrichment analysis revealed 19 biological processes, 13 molecular functions, and 8 cellular components for Tajima's D test.

## DISCUSSION

The study investigated the signature of selection in the genomes of Sahiwal cattle utilizing two methods (iHS and Tajima D). Considering iHS values, the regions on BTA 1, 2, 6, 11, 12, 15, 17, 21, and 27 are under the recent signatures of selection (Table I). The study observed recent signatures of selection on BTA 1, 2, 3, 4, 5, 6, 7, 9, 14, 18, 20, 23, and 24 with Tajima's D test (Table II). This study also noticed results that were similar to those observed by other researchers. In Thai dairy cattle, Buaban *et al.* (2022) found that regions associated with milk production traits were located on BTA 1, 2, 3, 4, 5, 6, 7, 9, 11, 12, 13, 14, 15, 16, 20, 21, 26, 27, and 29. Kolbehdari *et al.* (2009) performed a whole genome scan on Canadian Holstein bulls to identify QTL for milk production characteristics and somatic cell score. Their research identified map QTL significantly associated with protein yield in six SNP at the genome level, and nine at the chromosome level on BTA 1, 4, 7, 8, 9, 11, 14, 18, 21, 23, 26 and 28; 13 SNP significantly related to fat yield at the genome level, and 7 at the chromosome level on BTA 1, 4, 5, 7, 10, 11, 14, 21, 23, 24 and 28; 6 and 12 SNP that were significantly associated with the fat percentage in the genome were found on BTA 3, 6, 9, 10, 14, 17, 21, 23, and 26; and one SNP at genomic and 9 SNPs at the chromosome level were found on BTA 3, 4, 5, 10, 13, 17, 22, and 23 for the percentage of protein. In a whole genome evaluation of recent selection signatures in Sarabi cattle from Iran, Moradian *et al.* (2020) identified statistically significant SNPs on BTA5, BTA7, BTA10, BTA14, and BTA17. Kadri *et al.* (2015) found potential genes on BTA20 that are related to milk production, percentage of proteins, and resistance to mastitis.

The common genomic region identified by both tests (iHS and Tajima's D) was on BTA 1, 2, and 6. Pitt *et al.* (2019) identified positive selection in Creole cattle breeds on BTA1 that harbored genes associated with Polled, milk production, and reproduction. Alshawi *et al.* (2019) found the most compelling evidence of selection in Jenoubi cattle in BTA1 with an iHS score of -5.40 as well as in BTA26 with an iHS score of -5.0. Iraqi Rustaqi cattle notice a clear selection indication at BTA1 with an iHS score of -5.60 as well as BTA18 with an iHS score of -5.03. Hayes *et al.*

(2008) used an LD-based iHS technique and found many QTLs associated with milk production traits. They found selection signatures present on BTA6 in Norwegian red cattle. In a study on selection signatures employing ROH patterns in four different cattle breeds, Szmatoła *et al.* (2016) discovered that a homozygous area under selection on BTA2 was related to QTL for the muscling trait in the Limousin breed. At least three QTLs that influence milk traits are located on BTA6 (Khatkar *et al.*, 2004; Ogorevc *et al.*, 2009), and it has been hypothesized that dairy breeders are selecting these areas to improve milk production (Schwarzenbacher *et al.*, 2012). Using iHS, FST, as well as XP-EHH methods, Maiorano *et al.* (2018) demonstrated the existence of QTLs that impact milk as well as meat quality traits in dual-purpose Gir cattle populations on BTA6. Lee *et al.* (2016) also found a gene on BTA6 that was under selection and related to milk production parameters like milk yield, fat composition, as well as protein yield in Holstein dairy cattle.

These genomic regions identified by both tests in the study harbor candidate genes linked with milk, production and reproduction. PARD3B identified on BTA2 in the study has been found to be linked with bovine development and neural development in red Angus beef cattle (Smith *et al.*, 2022). The gene has also been found to be linked with fat percentage in Danish Holstein cattle (Buitenhuys *et al.*, 2014). PARD3B in red Angus beef cattle has been found to be associated with bovine tuberculosis traits (Raphaka *et al.*, 2017). The PARD3B gene has also been identified in pigs as a candidate gene for body weight (Xu *et al.*, 2020). The CENPE identified on BTA6 in the study has been found to be a candidate gene linked with milk composition traits in Holstein cattle (Jiang *et al.*, 2016). The CENPE gene has also been identified in cattle to be linked with residual feed intake (Rathert *et al.*, 2020). CSMD1 and TENM3 have also been detected on BTA27 in the study. Gonzalez *et al.* (2020) found CSMD1 to be associated with the rear udder height trait in Holstein cows. In the context of Hanwoo cattle, it was observed that CSMD1 exhibited higher expression levels in muscle samples derived from animals with elevated carcass weight, particularly in relation to intramuscular fat content and eye muscle area (Lee *et al.*, 2011). Hoff *et al.* (2019) identified a region in the CSMD1 gene that regulates the complement system that controls inflammatory responses in Holstein cattle. CSMD1 has also been identified in goats as associated with goat fertility (Li *et al.*, 2022). TENM3 has been found to be a candidate gene within the most significant QTL, which is associated with wither height or stature in beef cattle (Doyle *et al.*, 2020). TENM3 has also been identified in sheep as associated with milk production traits (Sutera *et al.*, 2019). TENM3, among others, affects the metabolic pathways of cell differentiation

and proliferation and is linked with the regulation of the immune system in goats (Krivoruchko *et al.*, 2022).

The identification of QTLs in the study discovered that significant genomic areas consist of 25.08% of milk-type QTLs in Sahiwal cattle as well as other types like meat as well as carcass, production, health, reproduction, as well as exterior, which were annotated and represented 21.54, 18.72, 13.85, 11.05, and 9.76%, respectively (Fig. 6). The study revealed a low percentage of milk-type QTLs in Pakistani Sahiwal cattle compared to Indian Sahiwal cattle, where Illa *et al.* (2021) observed 54.6% milk-type QTLs. This may suggest that Pakistani Sahiwal cattle have not been subjected to intense selection for milk production traits. The QTL enrichment analysis has shown 8 substantial QTLs on chromosomes BTA 19 and BTA20, associated with milk, production, as well as reproduction traits. The utmost significant QTLs were assigned to BTA19 and BTA20, associated with milk fat yield, fat percentage, fertilization rate, early embryonic survival, body weight, body depth, and average daily gain (Fig. 8). Illa *et al.* (2021) conducted signature selection in Indian Sahiwal cattle, and the QTL enrichment analysis painted 14 substantial locations in BTA 1, 3, 6, 11, 20, as well as 21. They found that the top most three enriched QTLs were in BTA 6, 20, as well as 23, linked to the exterior, milk production, health, as well as reproduction traits. They obtained a more significant region, which may be due to Indian Sahiwal cattle being under intense selection for milk yield; they have a milk-type QTL of 54.6% as compared to the Pakistani Sahiwal cattle, which have just 25.08% milk-type QTLs.

## CONCLUSION

The study findings revealed many genomic regions and several novel genes that exhibited positive selection in the Sahiwal cattle for both the test (iHS and Tajima's D) used in the study. Considering iHS values, the regions on BTA 1, 2, 6, 11, 12, 15, 17, 21, and 27 are under the recent signatures of selection. While genomic regions on BTA 1, 2, 3, 4, 5, 6, 7, 9, 14, 18, 20, 23, and 24 are under recent signatures of selection with Tajima's D test. The common genomic region identified by both tests under positive selection signatures was BTA 1, 2, and 6. These genomic regions harbor candidate genes linked with milk composition traits. The study also observed that the Sahiwal cattle population has low milk-type QTLs of 25.08%, indicating that the population is not under intense selection for milk production traits. Therefore, understanding the selection signatures and candidate genes that influence important economic traits can provide foundational knowledge that can be used effectively to

gain insight into the underlying mechanisms controlling these traits in Sahiwal cattle. Additionally, the results might serve as a basis for further investigation of economically vital traits linked to milk production in Sahiwal cattle.

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## Ethical approval

Ethical approval was given by the Ethics Committee of University Agriculture Faisalabad, Pakistan.

## Statement of conflict of interest

The authors have declared no conflict of interest.

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