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# Comparative analysis of milk composition in Swedish Mountain Cattle and modern dairy breeds (Swedish Red and Swedish Holstein)

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## ABSTRACT

This study compared the milk composition of Swedish Mountain Cattle (SMC) with modern dairy breeds, Swedish Red (SRB) and Swedish Holstein (SH). SRB milk had significantly higher fat and saturated fatty acid contents ( $p < 0.001$ ), whilst SH milk demonstrated the lowest levels of most solids. SMC milk exhibited a higher lactose and a favourable casein profile with elevated  $\alpha$ 1-casein, total  $\beta$ -casein, and  $\beta$ -casein A1 concentrations ( $p = 0.001$ ,  $p < 0.001$ ,  $p = 0.006$ ), indicating good potential for cheese-making. However, SMC milk also contained reduced  $\kappa$ -casein levels and a significantly higher pH ( $p < 0.001$ ), compared to the modern breeds. Principal Component Analysis revealed a homogeneous and compositionally stable profile in SMC milk, distinct from SRB and SH, underscoring its value in traditional dairy production. These findings support the preservation and targeted use of native breeds in diversified dairy systems.

## ARTICLE HISTORY

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Swedish Mountain Cattle; Fjällko; native cattle breeds; artisan cheese-making; milk composition; casein fractions; coagulation; milk protein profile

## Introduction

On December 3 2024, UNESCO inscribed the summer pasture (*fäbod*) culture of Sweden and Norway on the Representative List of the Intangible Cultural Heritage of Humanity (UNESCO; FAO, [n.d.](#)). Summer pasture farming is a traditional Nordic practice that has supported resource-efficient food production for centuries. Indeed, this system has shaped species-rich grasslands and biodiverse pastures, whilst also contributing to vibrant rural communities and a unique cultural heritage. In addition to its ecological and cultural value, summer pasture farming also holds relevance from a food security and resilience perspective, as it preserves knowledge of low-input food production under constrained conditions.

At the heart of summer pasture culture are indigenous Swedish Mountain Cattle (SMC), or *Fjällko*, a native breed uniquely adapted to thrive on poor mountain soils. Without this breed, traditional summer pasture milk production would not have been possible. SMC can efficiently convert low-quality forage into milk during the growing season, and they are known to outperform commercial breeds under hay-based feeding regimes – an advantage in scenarios where there is a limited access to concentrates and imported inputs. Moreover, SMC exhibit strong foraging skills and efficient utilisation of fibrous feed, which allows them to graze in forests and on semi-natural pastures whilst maintaining milk production (NordGen, [n.d.](#)). Current discussions highlight how this breed is positioned within agricultural discourse, primarily as suitable for small-scale farming systems, summer pasture farming, and artisanal or on-farm food production.

Historical records from 1296, describe white and grey polled cattle that resemble today's SMC (Hallander, 1994). The breed's significance increased in the late nineteenth century, when a formal breeding programme was initiated (Swedish Mountain cattle, 2022). At its peak, the SMC population exceeded 400,000. However, due to the introduction of high-yielding modern breeds, numbers had drastically declined by the late twentieth century (MÖTET: Issuu, [n.d.](#)).

Indigenous SMC are currently under threat from both extinction and inbreeding due to the small numbers, particularly among purebred animals (Tapio et al., 2006).

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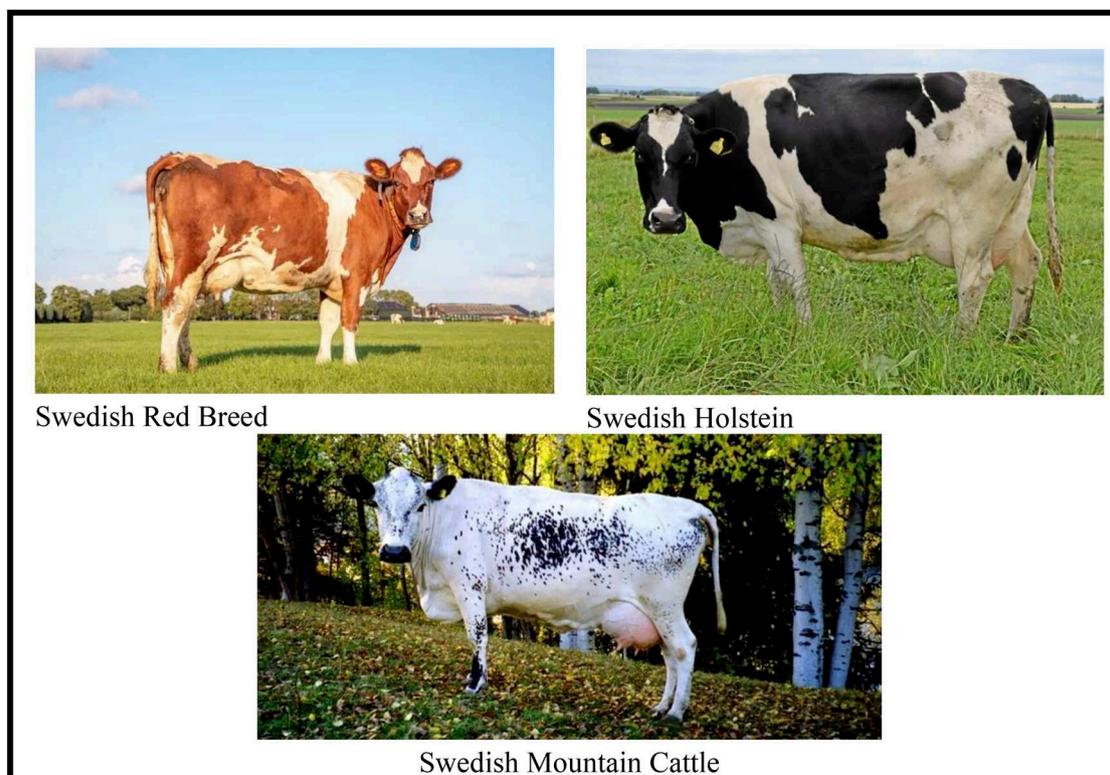
This article has been corrected with minor changes. These changes do not impact the academic content of the article.

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To address this, the 'Project Save the Swedish Mountain Cow' (*Projekt Rätta Fjällkon*) was launched in 1993 by concerned farmers and the World Wildlife Fund (WWF) which led to the establishment of the Swedish Mountain Cattle Breeding Association (*Svensk Fjällrasavel*) in 1995. This effort has helped improve genetic diversity (Upadhyay et al., 2019) through the preservation of important lines of sperm (Nilsson, 2007), though the population remains small. Data from 2021 shows that the SMC population consisted of only 7,802 breeding individuals: 2,032 males and 5,770 females (Hinken et al., 2025). Of these, it was estimated that around a mere 420 were actively used in industrial milk production, representing a small fraction of Sweden's total dairy herd of approximately 300,000 cows (LRF, 2025).

Historically, this native breed that originates from northern Sweden was maintained within the country as part of Swedish livestock production systems. Today, however, dairy production almost exclusively relies on a few commercial breeds, primarily Swedish Holstein (SH) and Swedish Red Breed (SRB) (Eriksson & Petitt, 2020). SMC are only distantly related to modern dairy breeds and differ significantly from commercial breeds in terms of several genetic traits, including the frequency of milk casein alleles (Lien et al., 1999; Poulsen et al., 2017). The preservation of native breeds such as SMC is essential not only for cultural and historical reasons but also for maintaining traits that are valuable in low-input and resilient food systems. SMC are among the oldest cow breeds in Sweden (Eriksson, 1943), with the first formal breeding centres established in 1905. Although the breed was merged with the Swedish Red Polled, *Rödkulla*, in 1938 to form the Swedish Polled Breed (*Svensk Kullig Boskap*), efforts to maintain purebred Mountain Cattle persisted and genetic analyses based on microsatellites and SNP markers confirmed that SMC and Swedish Red Polled are distinct (Kantanen et al., 2000; Tapio et al., 2006; Upadhyay et al., 2019). In the past, cattle in northern Sweden exhibited a wide range of coat colours. At present, according to the breed standard, SMC should possess a predominantly white coat colour with red or black dots on their flanks, coloured ears, and polled (Swedish Mountain Cattle, 2022). However, selective breeding favouring white-coated animals has resulted in unintended genetic consequences. This phenotype is connected to the translocation of Cs29 allele from chromosome 6 to chromosome 29 (Hinken et al., 2025). In addition to its association with the white colour, the Cs29 translocation has been linked to gonadal hypoplasia, a condition characterised by underdevelopment of the reproductive organs in both sexes. Samples taken from SMC as recently as



**Figure 1.** Swedish dairy cow breeds.

2023–2024 revealed that the Cs29 allele was still present at a 40% frequency (Hinken et al., 2025). One contributing factor to this is the decline in the breeding population of SMC. Another possible factor is the use of artificial insemination bulls that carry the Cs29 translocation.

SMC are a smaller breed, typically weighing 400–450 kg (Figure 1), compared to the 700 kg SH or SRB (Alskog & Berg, 1995). SMC produce an average milk yield of approximately 5,000 kg, and although the fat- and protein contents are comparable to the milk from SRB, the total milk yield is roughly half (Växa Sverige, 2025).

Whilst SMC milk yield is lower, their milk is characterised as well suited for processing into dairy products (Poulsen et al., 2017). Despite the breed's historical and cultural significance, scientific research on SMC remains limited, with most studies to date focusing on genetic characterisation (Kantanen et al., 2000; Tapio et al., 2006; Upadhyay et al., 2019; Johansson et al., 2020). Although various initiatives have aimed to conserve and describe the breed's genetic diversity, there is a notable lack of published research on the composition and technological properties of SMC milk. Poulsen et al. (2017) reported about the superior milk coagulation properties and low frequency of non-coagulating milk compared to other breeds. They also observed a higher frequency of  $\kappa$ -casein B, which is positively associated with gel firmness and cheese yield.

This study aims to address the current knowledge gap by characterising the milk of Swedish Mountain Cattle in terms of its compositional properties. Specifically, the study focuses on gross composition, somatic cells and relative protein profile composition and compares these traits to those of the Swedish Red Breed and Swedish Holstein.

## Material and methods

### *Collection of milk samples from participating herds*

The milk samples from SRB ( $n = 89$ ) and SH ( $n = 20$ ) were collected from individual cows across 12 herds in the Swedish counties of Uppland, Södermanland, Västmanland, and Västerbotten in Sweden as described by Johansson et al., (2024). The milk samples from SMC ( $n = 75$ ) were collected from three herds located in the counties of Lappland, Norrbotten, and Gästrikland during February 2025. Both the modern and native cows were milked routinely using milking parlour. The milk samples were collected in association with evening milking. All cows were randomly selected during the indoor period without considering the diet, lactation number, milk yield or other on-farm management. A 100 mL sample was taken from each cow.

The milk samples were stored at  $-20^{\circ}\text{C}$  and transported frozen to the Department of Molecular Sciences, the Swedish University of Agricultural Sciences (SLU), Uppsala for analysis of gross composition, somatic cells and milk protein profile. Upon arrival, the milk was thawed overnight at  $4^{\circ}\text{C}$  and aliquoted. The pH was measured using a pH meter (Seven Compact S210, Mettler-Toledo, Stockholm, Sweden) after equilibration of the thawed milk samples for 60 min at room temperature.

### *Milk sample preparation*

Whole milk was used for analysis of gross composition, somatic cell count (SCC) and pH. Milk defatted by centrifugation at  $1\ 864 \times g$  and  $+4^{\circ}\text{C}$  for 10 min (Sorvall Super T21, Sorvall Products L.P., Newton, CT, USA) was used for the remaining analyses of milk protein profile. The defatted milk samples were stored at  $-20^{\circ}\text{C}$  until use.

### *Analysis of gross composition*

Milk gross composition was analysed at the Department of Applied Animal Science and Welfare, SLU, Uppsala. Total fat, protein and lactose, total solids, saturated fatty acids (SFA), unsaturated FA (UFA), mono-unsaturated FA (MUFA), poly-unsaturated FA (PUFA), myristic acid (C14:0), palmitic acid (C16:0), stearic acid (C18:0), and oleic acid (C18:1c9) were analysed by mid-infrared spectroscopy. SCC was determined by flow cytometry (Delta Instruments CombiScope™ FTIR 600HP, PerkinElmer, Springfield IL, USA).

## Milk protein profiles

Protein separation was performed with a 7 100 capillary electrophoresis (CE) system (Agilent Technologies Co., Santa Clara, CA, USA) using an unfused silica standard capillary, as described by Johansson et al., (2013). In short, separations were performed after adding 0.017 M D, L- dithiothreitol (DTT) to the sample buffer on the day of sample preparation to disrupt disulphide bridges in the milk proteins. Milk (300 µL) was mixed with sample buffer (700 µL), incubated at room temperature for 1 h, and defatted by centrifugation for 10 min at 10 000 × *g* (Hitachi-Himac CT 15R, Tokyo, Japan). UV-vis absorbance at a wavelength of 214 nm was used for detection. Calculation of the relative concentration of individual proteins was based on peak area and expressed as the percentage of total integrated area in the electropherogram using Agilent 7 100 CE, version Rev.C01.08(210) software.

## Statistical analyses

Minitab 18.1 software (Minitab Inc., State College, PA, USA) and Simca 17.0 software (Sartorius Stedim Data Analytics AB, Umeå, Sweden) were used for univariate and multivariate analysis, respectively. The variation in gross composition SCC and protein profile of the milk samples was explored using ANOVA with Tukey post hoc test in Minitab. In these analyses, the three breeds (SMC, SRB, and SH) were used as fixed factors. Milk quality attributes were normally distributed and used as response variables. The model took the following form:

$$Y_{ij} = \mu + \alpha_i + e_{ij}$$

Where  $Y_{ij}$  is the response (dependent variable, milk quality attributes) for observation  $j$  in breed (SMC, SRB, SH)  $i$ ;  $\mu$  is the general mean;  $\alpha_i$  is the effect of breed  $i$  and  $e_{ij}$  is the random residual.

For the multivariate statistics, principal component analysis (PCA) (Wold et al., 1987) was conducted using unit variance-scaled, auto-transformed settings to explore the total variation in milk quality traits as influenced by the breed of the individual cows. The corresponding loading plot was examined to identify variables that seemed to be associated, using the largest discriminatory power associated with the investigated responses (breed). A confidence interval of 95% was used in all statistical analyses.

## Results and discussion

### Gross composition of Swedish Mountain Cattle compared to modern dairy breeds

In this study, a wide range of variables were analysed to gain deeper insights into the milk composition of Swedish Mountain Cattle (SMC) compared to modern dairy breeds: Swedish Red (SRB) and Swedish Holstein (SH).

Previous findings by Glantz et al., (2009) indicated that farms that contain a higher proportion of SRB cows tend to produce milk with increased fat and protein contents compared to farms that predominantly house SH cows. This suggests possible breed-specific differences in milk composition. However, to date, a comprehensive comparison including SMC has been lacking.

In the present study, differences in milk gross composition among SMC, SRB, and SH were evaluated using one-way ANOVA (Table 1). Our results confirmed earlier observations, showing a significantly higher total fat content in SRB milk compared to both SH and SMC ( $p = 0.001$ ). Similarly, total protein levels were highest in SRB, followed by SMC and SH. Although these differences were not statistically significant, the protein values corresponded well with previously published Swedish data (Gustavsson et al., 2014; Poulsen et al., 2017; Priyashantha & Lundh, 2021).

The fatty acid composition varied between breeds. SRB milk exhibited higher levels of saturated fatty acids (SFA) ( $p < 0.001$ ), notably palmitic acid (C16:0) ( $p = 0.002$ ), compared to SMC. Stearic acid (C18:0) concentrations were also significantly higher in SRB than in both SMC and SH ( $p < 0.001$ ). No differences were found between SMC and SRB regarding the levels of unsaturated fatty acids (UFA), monounsaturated fatty acids (MUFA), or oleic acid (C18:1c9), although SH milk displayed significantly lower concentrations of these components. Additionally, polyunsaturated fatty acids (PUFA) and myristic acid (C14:0) were lowest in SH milk ( $p = 0.001$  and  $p = 0.003$ , respectively), as was the total solids content ( $p = 0.001$ ).

**Table 1.** Comparison of the gross composition of milk samples from Swedish Mountain Cattle (SMC), Swedish Red Breed (SRB), and Swedish Holstein (SH). Mean value and standard deviation for the different parameters are indicated,  $n$  = number of individual cows.

Parameter	SMC			SRB			SH			$p$ -value
	SMC Min	SMC Max	Mean ( $n = 75$ )	SRB Min	SRB Max	Mean ( $n = 89$ )	SH Min	SH Max	Mean ( $n = 20$ )	
Total protein (g/100 g)	2.56	4.72	3.63±0.41	2.56	5.14	3.72±0.41	2.58	4.24	3.57±0.40	0.196
Total fat (g/100 g)	3.04	6.97	4.68±0.90 <sup>B</sup>	2.72	10.90	5.23±1.73 <sup>A</sup>	2.98	5.62	4.22±0.91 <sup>B</sup>	<b>0.001</b>
SFA (g/100 g) <sup>a</sup>	2.01	4.81	3.15±0.68 <sup>B</sup>	1.96	8.33	3.79±1.34 <sup>A</sup>	2.02	3.90	2.93±0.68 <sup>B</sup>	<b>&lt;0.001</b>
UFA (g/100 g) <sup>a</sup>	0.85	1.73	1.20±0.94 <sup>A</sup>	0.61	2.19	1.26±0.23 <sup>A</sup>	0.58	1.45	0.94±0.25 <sup>B</sup>	<b>&lt;0.001</b>
MUFA (g/100 g) <sup>a</sup>	0.61	1.34	0.92±0.15 <sup>A</sup>	0.40	1.77	0.96±0.31 <sup>A</sup>	0.41	1.16	0.71±0.20 <sup>B</sup>	<b>&lt;0.001</b>
PUFA (g/100 g) <sup>b</sup>	0.05	0.20	0.08±0.05 <sup>AB</sup>	0.01	0.24	0.10±0.02 <sup>A</sup>	0.01	0.13	0.07±0.03 <sup>B</sup>	<b>0.011</b>
C14:0 (g/100 g) <sup>a</sup>	0.39	0.97	0.62±0.15 <sup>AB</sup>	0.34	1.52	0.68±0.25 <sup>A</sup>	0.38	0.71	0.52±0.12 <sup>B</sup>	<b>0.003</b>
C16:0 (g/100 g) <sup>a</sup>	0.75	2.33	1.43±0.37 <sup>B</sup>	0.77	3.88	1.72±0.63 <sup>A</sup>	0.79	2.04	1.40±0.42 <sup>B</sup>	<b>0.002</b>
C18:0 (g/100 g) <sup>a</sup>	0.19	0.67	0.38±0.08 <sup>C</sup>	0.35	1.26	0.69±0.22 <sup>A</sup>	0.33	0.85	0.52±0.13 <sup>B</sup>	<b>&lt;0.001</b>
C18:1c9 (g/100 g) <sup>a</sup>	0.51	1.13	0.74±0.13 <sup>A</sup>	0.35	1.42	0.76±0.23 <sup>A</sup>	0.27	0.92	0.55±0.17 <sup>B</sup>	<b>&lt;0.001</b>
Lactose (g/100 g) <sup>a</sup>	3.94	5.09	4.78±0.17 <sup>A</sup>	4.55	5.05	4.66±0.18 <sup>B</sup>	5.56	5.05	4.83±0.12 <sup>A</sup>	<b>&lt;0.001</b>
Total solids (g/100 g) <sup>a</sup>	11.0	16.77	13.76±1.05 <sup>AB</sup>	11.39	19.85	14.30±1.83 <sup>A</sup>	11.86	15.03	13.05±0.95 <sup>B</sup>	<b>0.001</b>
SCC (x10 <sup>3</sup> cells/mL)	9	2470	184±333	12	1543	180±252	30	377	111±96	0.561
pH	6.44	6.91	6.73±0.09 <sup>A</sup>	6.33	6.64	6.45±0.10 <sup>B</sup>	6.13	6.64	6.39±0.14 <sup>C</sup>	<b>&lt;0.001</b>

Means within a row with different superscripts differ ( $p < 0.05$ ).

Mean values ± SD. Min = minimum; Max = maximum. Differences between the groups were evaluated by 1-way ANOVA and were considered significant at  $p < 0.05$ .

SFA = saturated fatty acids; UFA = unsaturated fatty acids; MUFA = monounsaturated fatty acids; PUFA = polyunsaturated fatty acids; SCC = somatic cell count.

<sup>a</sup>Number of observations SRB = 75.

<sup>b</sup>Number of observations SRB = 75; SH = 13.

Lactose content was the highest in SMC and SH, and the lowest in SRB ( $p < 0.001$ ), which is consistent with the findings by Glantz et al., (2009).

It is important to note that milk gross composition is highly influenced by feeding practices, which were not standardised or included as variables in this study. As a result, certain differences observed between the breeds may reflect dietary effects as well as genetic factors.

Somatic cell count (SCC), a common indicator of udder health, also varied between breeds. Whilst Persson Waller et al., (2009) reported a lower SCC in SRB cows compared to SH, our results demonstrated the opposite pattern: SH cows had lower SCC values than both SRB and SMC. However, the differences were not statistically significant and were likely influenced by the relatively low number of samples from SH cows. This limitation may have also possibly affected the detection of other potential breed-related differences.

According to EU Regulation 853/2004, the legal bulk milk SCC limit is  $400 \times 10^3$  cells/mL. In this study, mean SCC levels across all breeds ranged from 111 to  $184 \times 10^3$  cells/mL, and thus remained well below the regulatory threshold. These values indicate good udder health across the studied herds and may explain the absence of significant SCC differences among the breeds.

### Milk protein profile in Swedish Mountain Cattle and modern dairy breeds

Milk composition varies between cattle breeds, consequently affecting key technological properties such as coagulation. Whilst breed-specific differences influence milk characteristics, previous studies have shown that individual cow genetics may have a more decisive impact on coagulation behaviour than breed alone (Wedholm et al., 2006). In particular, the protein composition, especially the relative proportion of casein fractions, plays a critical role in curd formation, cheese yield, and final cheese quality (Salamończyk et al., 2019).

In this study, the overall milk protein profiles were broadly similar across breeds (Table 2), yet significant differences were found. SMC exhibited higher relative concentrations of  $\alpha$ s1-casein ( $p = 0.001$ ), total  $\beta$ -casein ( $p < 0.001$ ), and  $\beta$ -casein A1 ( $p = 0.006$ ), all of which are associated with improved cheese-making potential (Wedholm et al., 2006).

In contrast, SMC milk demonstrated significantly lower relative concentrations of  $\alpha$ s2-casein,  $\beta$ -casein B, and  $\kappa$ -casein compared to the modern breeds ( $p < 0.001$ , Table 2). Given that SMC is traditionally associated with superior coagulation properties, largely attributed to a high frequency of the  $\kappa$ -casein B variant (Poulsen et al., 2017), it would be of considerable interest to determine the actual proportion of this variant in the

**Table 2.** Comparison of the protein fraction of milk samples from Swedish Mountain Cattle (SMC), Swedish Red Breed (SRB), and Swedish Holstein (SH). Mean value and standard deviation for the different parameters are indicated,  $n$  = number of individual cows.

Protein fractions <sup>a</sup> (%)	SMC			SRB			SH			$p$ -value
	SMC Min	SMC Max	Mean ( $n = 75$ )	SRB Min	SRB Max	Mean ( $n = 89$ )	SH Min	SH Max	Mean ( $n = 20$ )	
Total casein	75.87	90.56	86.35±2.74 <sup>B</sup>	64.63	92.76	85.86±4.17 <sup>B</sup>	80.08	93.09	88.60±3.71 <sup>A</sup>	<b>0.010</b>
Total whey protein	6.50	12.90	9.45±1.26	2.79	21.07	10.31±3.50	3.56	15.35	8.90±3.77	0.051
$\alpha_{s1}$ -casein	24.77	34.53	30.51±1.90 <sup>A</sup>	24.52	33.67	29.46±1.78 <sup>B</sup>	26.20	33.13	30.40±1.77 <sup>AB</sup>	<b>0.001</b>
$\alpha_{s2}$ -casein	1.35	5.73	3.50±1.0 <sup>B</sup>	3.62	8.91	6.83±1.02 <sup>A</sup>	4.96	8.91	6.84±0.94 <sup>A</sup>	<b>&lt;0.001</b>
Total $\beta$ -casein	40.56	52.48	47.53±2.56 <sup>A</sup>	21.89	50.08	42.69±3.96 <sup>B</sup>	35.63	31.53	44.31±3.39 <sup>B</sup>	<b>&lt;0.001</b>
$\beta$ -casein B	0.00	1.22	0.25±0.32 <sup>B</sup>	0.00	2.22	0.56±0.53 <sup>A</sup>	0.00	1.40	0.48±0.46 <sup>AB</sup>	<b>&lt;0.001</b>
$\beta$ -casein A1	0.00	47.77	18.24±12.29 <sup>A</sup>	0.00	45.38	15.73±14.53 <sup>A</sup>	0.00	21.53	7.42±10.42 <sup>B</sup>	<b>0.006</b>
$\beta$ -casein A2	0.00	47.77	29.04±12.51 <sup>AB</sup>	0.00	47.57	26.41±15.44 <sup>B</sup>	21.78	50.42	36.41±10.45 <sup>A</sup>	<b>0.014</b>
$\kappa$ -casein	2.14	8.83	4.81±1.14 <sup>B</sup>	3.18	9.98	6.88±1.38 <sup>A</sup>	4.37	9.95	7.06±1.65 <sup>A</sup>	<b>&lt;0.001</b>
$\alpha$ -lactalbumin	0.99	2.84	2.01±0.36 <sup>AB</sup>	0.20	5.70	2.11±1.02 <sup>A</sup>	0.34	2.69	1.59±0.92 <sup>B</sup>	<b>0.033</b>
$\beta$ -lactoglobulin	4.77	10.45	7.53±1.26	0.29	15.85	8.20±2.87	3.16	12.86	7.31±2.95	0.077

Means within a row with different superscripts differ ( $p < 0.05$ ).

Mean values  $\pm$  SD. Min = minimum; Max = maximum. Differences between the groups were evaluated by 1-way ANOVA and were considered significant at  $p < 0.05$ .

<sup>a</sup>Individual proteins are expressed as % of total integrated area in the chromatograms.

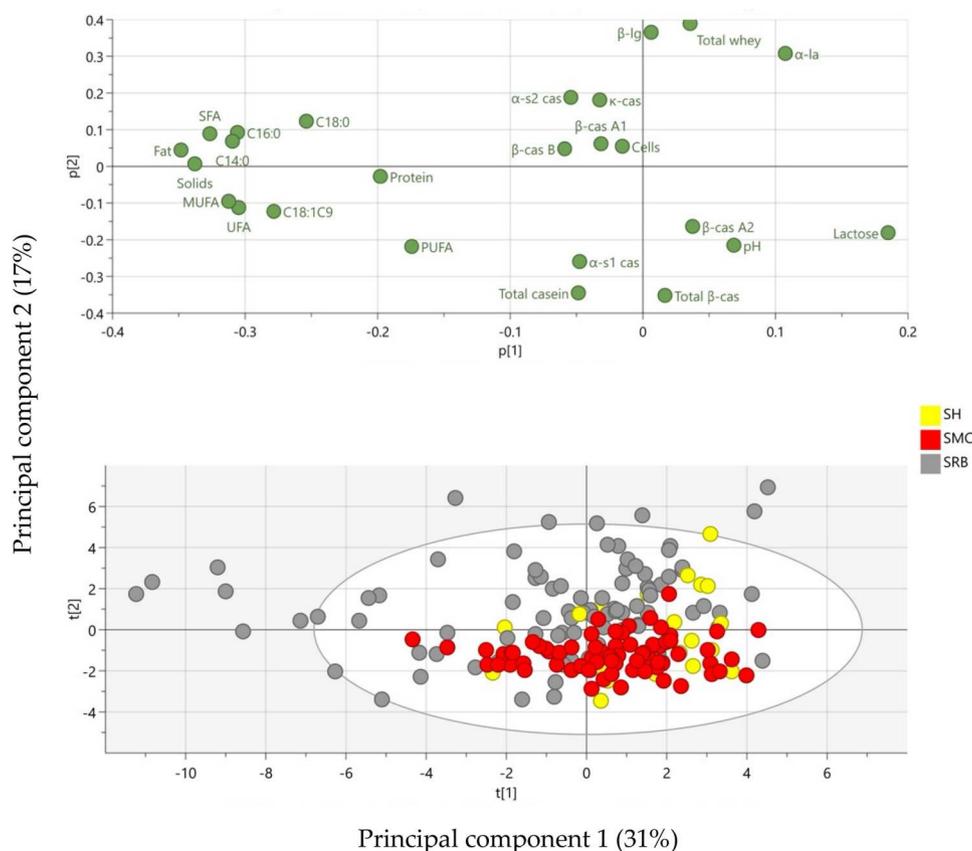
analysed samples. However, the specific  $\kappa$ -casein variants were not characterized in this study, which limits direct interpretation of the observed compositional differences.

Notably, the pH of milk from SMC was significantly higher than that of SRB and SH. The elevated pH in SMC milk may be linked to its compositional characteristics, particularly the lower  $\kappa$ -casein content. Caseins, together with colloidal calcium phosphate, play a central role in buffering milk. Lower concentrations of casein-bound phosphate and calcium reduce the release of hydrogen ions upon micellar dissolution, thereby increasing the equilibrium pH (Yang et al., 2018). Moreover, differences in  $\beta$ -casein variants can affect micellar hydration and mineral equilibrium. The  $\beta$ -casein B variant, which was less abundant in SMC milk, is associated with a higher degree of micellar mineralization and slightly lower pH compared to other variants (Marziali & Ng-Kwai-Hang, 1986; Dalgleish, 2011). Consequently, the lower proportion of  $\beta$ -casein B and  $\kappa$ -casein in SMC milk likely contributes to reduced micellar mineral association and a corresponding increase in milk pH.

No significant differences in  $\beta$ -casein A2 or  $\alpha$ -lactalbumin were found between SMC and the modern breeds. Nevertheless, SH milk contained 28% more  $\beta$ -casein A2 than SRB ( $p < 0.001$ ), whilst SRB milk had 25% higher  $\alpha$ -lactalbumin than SH ( $p = 0.033$ , Table 2). These findings provide a nuanced view of how breed-specific protein composition relates to milk functionality, highlighting that even moderate shifts in individual protein fractions may influence micellar stability, mineral interactions, and, consequently, processing behaviour.

### Variation in the composition of milk as influenced by cow breed

**Principal Component Analysis (PCA)** was conducted to investigate variations in milk composition among the three cattle breeds. The first two principal components explained 48% of the total variance in the dataset (PC1 = 31%, PC2 = 17%,  $R^2X(\text{cum}) = 0.446$ ). (Figure 2). SRB samples appeared slightly more spread along PC1 toward the negative side, whilst SH samples were more dispersed with an overlap with both SRB and SMC, and SMC formed a tight, centralised cluster within the 95% Hotelling's  $T^2$  ellipse, indicating low intra-breed variability and compositional homogeneity. Loadings analysis linked SMC milk with stable levels of  $\alpha_{s2}$ -casein,  $\beta$ -casein A1,  $\beta$ -casein B,  $\kappa$ -casein and total protein, which is consistent with favourable coagulation properties and thereby supports the potential of SMC milk for cheese production. SH milk was associated with whey proteins ( $\alpha$ -lactalbumin,  $\beta$ -lactoglobulin) and total whey, whereas SRB milk was linked to higher saturated fatty acids (C16:0, C18:0) and total fat. The clear separation of SMC from modern breeds, combined with its tight clustering, highlights the compositional stability of SMC milk, which is advantageous for standardised dairy processing. However, the partial overlap between breed clusters suggests that feeding regime and management may influence milk composition to a similar or greater extent than breed alone.



**Figure 2.** Principal component analysis plots illustrating the total variation in milk quality traits associated with Swedish Mountain Cattle (SMC) ( $n = 75$ ), Swedish Red Breed (SRB) ( $n = 89$ ), and Swedish Holstein (SH) ( $n = 20$ ). The loading plot (A) illustrates associations between the investigated traits, with variables grouped together being related. The greater the distance to the origin, the greater the contribution of the variable to the total variation. In the score plot (B) different colours indicate milk from the three breeds. Abbreviations: cas = casein;  $\alpha$ -La =  $\alpha$ -lactalbumin;  $\beta$ -Lg =  $\beta$ -lactoglobulin; SFA = saturated fatty acids; UFA = unsaturated fatty acids; MUFA = mono-unsaturated fatty acids; PUFA = polyunsaturated fatty acids.

## Conclusion

This study provides a comprehensive comparison of milk composition between Swedish Mountain Cattle and two modern dairy breeds, Swedish Red and Swedish Holstein. Our findings align with previous studies, confirming breed-specific differences regarding milk gross composition, with SRB exhibiting a significantly higher fat content and greater levels of saturated fatty acids. In contrast, SMC milk displayed a more balanced fat profile and higher lactose concentration among the three breeds.

Protein profiling revealed that SMC milk is characterised by elevated levels of  $\alpha$ s1-casein, total  $\beta$ -casein, and  $\beta$ -casein A1 – components positively associated with cheese-making potential. However, despite this favourable casein profile, SMC milk exhibited lower levels of  $\kappa$ -casein and  $\beta$ -casein B, as well as the higher milk pH. These factors are known to affect rennet coagulation and curd firmness.

The PCA results further underscored the compositional stability of SMC milk, suggesting less intra-breed variation and a unique biochemical signature centred around milk quality variables. Whilst SMC milk may not outperform modern breeds across all technological traits, its consistent composition and elevated levels of certain casein fractions may hold potential for specialised dairy applications, particularly in traditional and artisanal cheese production. Further studies incorporating genetic markers and standardised feeding regimes should seek to clarify the interplay between genotype, diet, and milk functionality in this native breed.

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