Genotypes giving resistance to CAE in goats

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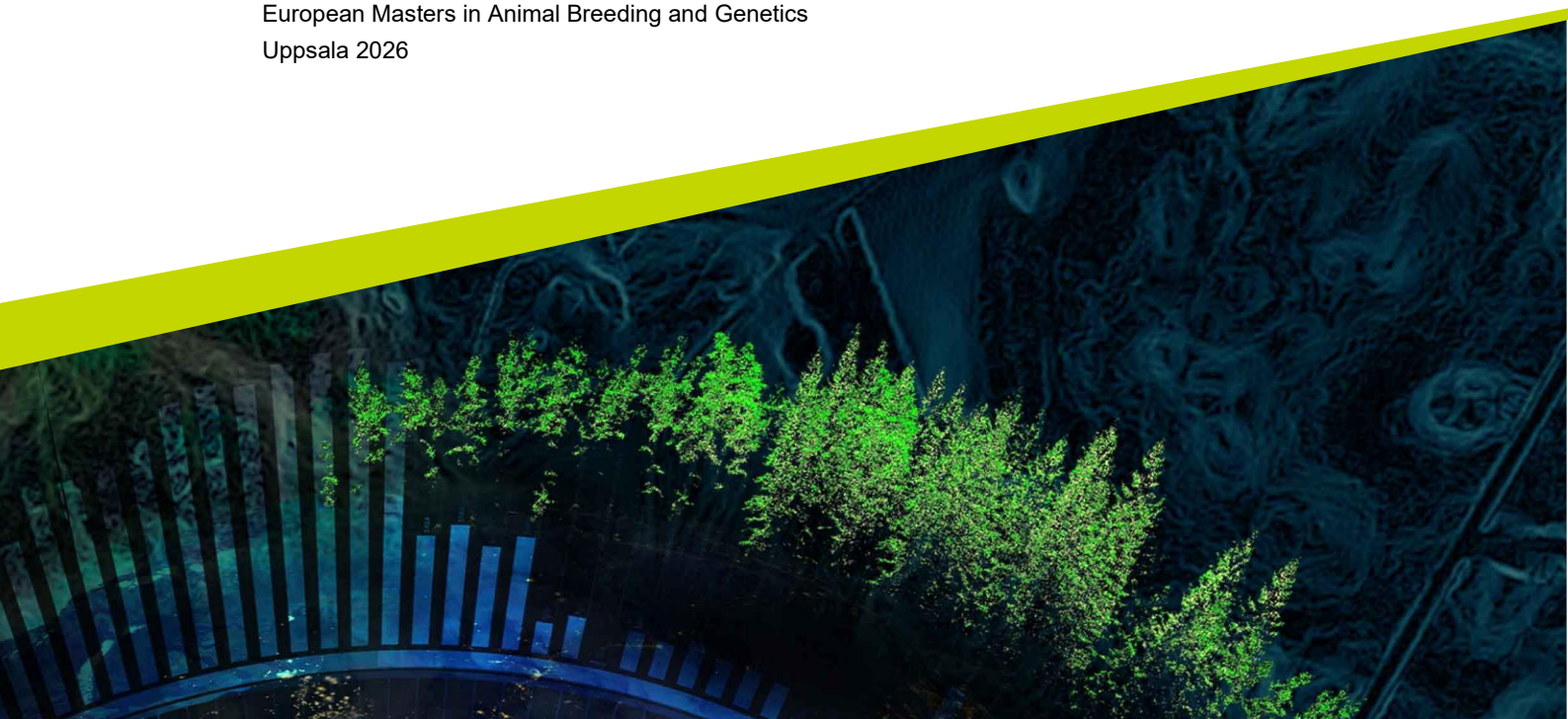

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Abstract

Caprine arthritis-encephalitis (CAE), caused by the caprine arthritis encephalitis virus (CAEV), is a chronic infectious disease that negatively affects animals over the world while it remains difficult to control due to long incubation periods and subclinical infections. Current eradication strategies rely on management and serological testing but challenges in their conduction highlight the need for alternative approaches.

Genetic resistance to small ruminant lentiviruses has emerged as a promising control strategy. The CCR5 gene, which encodes a chemokine receptor involved in viral entry into macrophages, has previously been associated with CAE susceptibility. A polymorphism in the promoter region of CCR5 (g.1059T) has been linked to increased proviral load.

This study investigated variation in the CCR5 gene in Swedish Landrace goats and aimed to evaluate its association with CAE using ELISA seropositivity, to validate previous findings and assess the potential of genetic markers for improved disease control.

However, significant association between CCR5 genotypes and CAE prevalence could not substantially be proven in this study. Genotypes of some breeds in the study and the absence of proviral load data restrict definitive conclusions. Further studies with larger populations and proviral load measurements are required before considering CCR5-based breeding strategies for CAE control.

Keywords: CCR5, CAE, Caprine arthritis encephalitis, Goat, SRLV, Small ruminant lentiviruses

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Abbreviations

Abbreviation	Description
SLU	Swedish University of Agricultural Sciences
CAE	Caprine Arthritis Encephalitis
FIV	Feline immunodeficiency virus
HIV	Human immunodeficiency virus
BIV	Bovine immunodeficiency virus
HW equilibrium	Hardy Weinberg equilibrium

1. Introduction

The Swedish countryside, while not overpopulated with the ovine and caprine domestic species, is native to four different goat breeds: the Göinge Goat, the Jämt Goat, the Lapp Goat and the Svensk Lantras Goat.

The Svensk Lantras (Swedish Landrace) is the most common goat breed in Sweden, primarily used for homestead milk production. The Swedish Landrace Goat population has fluctuated greatly over the past century. From over 50,000 goats in the 1920s, numbers fell sharply to around 6,000 by the 1970s–2000s and as low as 3,000 in 2002. Renewed interest in traditional farming during the 1970s and 80s helped save the Swedish Landrace Goat, whose milk production provided vital income for farmers. Conservation efforts and breeding programs have since helped the population recover to about 20,000 by 2018. The Swedish Landrace shares a lot of similarities with the Norwegian Landrace goat breed, since breeding animals have been moved across the border thousands of times over the years (Svenska Getavelsförbundet, 2025). To reduce inbreeding, a higher risk factor in isolated herds, breeders used Norwegian genetic material between the 1970s and 1990s, creating a broader genetic base built on eight key bloodlines imported by the Swedish Goat Breeding Association (Svenska Getavelsförbundet, 2025).

Often versatile, the Swedish landrace appearance varies across the breed. Phenotypically, all colors, horn shapes, and hair types are accepted to the breed standards. There are no strict rules regarding the characteristics of the breed. Most goats have horns, but polled individuals also occur within the breed. Colors can vary, ranging from completely white to completely black. Because no selection has been made for hair length, variation is also acceptable for this feature. The average live weight of the Swedish Landrace, when kept on a proper diet for optimal growth, is around 75 kg, while animals weighing 90-100 kg can be observed frequently. The Swedish landrace goat is considered by the breed's organization a highly productive goat breed. On high-yield farms with proper nutrition, productivity averages 1000-1400 liters per year, with individual animals reaching 2000 liters. The national average is between 500-700 liters (Svenska Getavelsförbundet, 2025).

The Swedish Goat Breeding Association, recognized for the Swedish Landrace Goat is called Svenska Getavelsförbundet. Breeders are required to register their animals to the organization according to the Swedish Board of Agriculture's regulations. Pedigree registration includes detailed ancestry information. Any breeder, whether a member of the Swedish Goat Breeding Association or not, can register their goats in the official herdbook by completing the breeds standards.

Today, the breed is mainly used for small-scale artisanal dairy production, with some larger farms supplying shops and restaurants. Although goat meat has had

limited significance in Sweden, demand has grown since the 2000s, partly due to immigration. Goat skins are also used by craftspeople, adding further economic value to goat farming (Svenska Getavelsförbundet, 2025).

A chronic viral disease known as caprine arthritis-encephalitis (CAE) affects goats all over the world and has a major negative impact on Swedish goat farms, and the overall industry's economics and welfare. The prevalence of caprine arthritis-encephalitis (CAE) in Swedish goats remains uncertain (Persson et al., 2022). Goat farms that are affected by Caprine Arthritis Encephalitis (CAE) face large economic losses due to the disease's association with decreased milk production, weight loss, and increased mortality in both adults and offsprings (Persson et al., 2022).

The infection can present clinically in a total of five forms: encephalomyelitis, interstitial pneumonia, interstitial mastitis, arthritis, cachexia and chronic implications (SVA, 2021; Patel et al., 2012). While encephalitis is more common in young goats, arthritis is the most prevalent symptom in adult goats, though the disease can vary in severity and impact on the herd's overall health and productivity. Since few infected goats show clinical symptoms and many stay asymptomatic, subclinical infections are thought to be the most common in Sweden. The slow, progressive nature of CAE and its incubation period, which can last anywhere from months to years, make it difficult to diagnose and manage within impacted herds (Persson et al., 2022).

A retrovirus that is closely related to the human immunodeficiency virus (HIV), bovine immunodeficiency virus (BIV) in cattle, and feline immunodeficiency virus (FIV) in cats, the caprine arthritis-encephalitis virus (CAEV) is the cause of the disease (Patel et al., 2012). The Caprine arthritis-encephalitis virus (CAEV) and Maedi-Visna virus (MVV) in sheep together constitute the small ruminant lentiviruses (SRLVs), a group of the Retroviridae family that causes chronic and progressive diseases in small ruminants (Persson et al., 2022). Long-term infection is caused by CAEV's primary infection of monocytes and macrophages (Patel et al., 2012). CAEV does not suppress the immune system like many other lentiviruses do, therefore infected animals can continue to have an immunological response even after the infection has persisted (Leroux et al., 2010).

The understanding that caprine arthritis-encephalitis (CAE) in goats has a viral origin is relatively recent. The disease, which farmers had long referred to as “big knees” because of the characteristic swelling of the carpal joints, was first linked to a viral infection after the virus was isolated in the United States in 1980 from arthritic goats that had previously shown signs of encephalitis (Persson et al., 2022).

In contrast to the epizootic outbreak of maedi-visna (MV) in Iceland, CAE was initially thought to be a hereditary disorder in regions of central Europe with high

infection rates, largely because of its apparent vertical transmission pattern. Infected animals can remain asymptomatic carriers for long periods of time, even years, continuing to transmit the virus, which makes controlling and eradicating the disease particularly difficult. No effective vaccines are currently available, and some experimental vaccines have been reported to even worsen clinical symptoms (Patel et al., 2012).

A clear understanding of the routes of transmission is essential for the development of effective control programs. Colostrum and milk are considered the main routes of transmission of SRLVs from mother to offspring. This is supported by the success of eradication programs in which newborns are separated immediately after birth and reared on bovine colostrum and milk.

The significance of intrauterine transmission remains uncertain. Evidence indicates that up to 10% of fetuses born to infected dams may become infected *in-utero*. However, this route of vertical transmission is difficult to assess, as results depend greatly on the diagnostic techniques employed and the host immune response. When PCR is used, viral sequences amplified from caesarean-derived fetuses were compared with those of the dam to confirm infection. When serology is used, the long and variable period before seroconversion complicates confirmation of intrauterine infection, and any postnatal contact with infected animals is ruled out. Nevertheless, the success of eradication programs based on immediate separation at birth and rearing on bovine colostrum and milk suggests that intrauterine transmission is of limited epidemiological significance (Peterhans et al., 2004).

Another possible way of spreading the virus is through contaminated placental tissues (Blacklaws et al., 2004). The disease is also considered to be transmitted through aerosols, but the exact transmission route is not established (Peterhans et al., 2004). Even though SRLVs have been found in semen, it is still unknown how this pathway contributes to transmission (Peterhans et al., 2004). However, there are various ways that infected rams and bucks can spread the infection to females. Recent studies have detected CAEV-infected cells in the goat genital tract, suggesting a possible route for vertical transmission from doe to embryo or fetus (Peterhans et al., 2004). However, no data is available on the viral content of oocytes. The spread of the virus can be further aided by humans, especially when farmers are handling infected and uninfected flocks without changing their clothing, footwear, or equipment. An additional potential risk factor is transmission via contaminated milking equipment (Blacklaws et al., 2004). It is unlikely that other farm animals, like cats and dogs, can spread the disease (Persson et al., 2022). Furthermore, the movement and trade of live animals represent a major risk factor for the dissemination of SRLV infections between herds. Finally, dairy products are unlikely to be involved in the transmission of SRLVs (Peterhans et al., 2004).

SRLVs cause major economic losses, prompting coordinated control efforts across Europe. In 1998, a European Co-operation in the field of Scientific and Technical Research (COST) action united 16 European countries to harmonize SRLV research and define key knowledge gaps regarding SRLVs (Peterhans, 2004). In Norway, an eradication program proved highly successful. Before implementation, 86% of herds were CAEV-positive, but most are now free of CAE (Persson et al., 2022). In Sweden cases of CAE are compulsory to report to the Swedish Board of Agriculture (SVA, 2021). A voluntary control program that was started in 1999 in Sweden uses ELISA-based serological testing to identify and eradicate infection in approximately 12% of the goat population. Due to socioeconomic concerns, participation is still low, particularly among native goat breeders and small-scale farmers (Persson et al., 2022).

Recent advances in the research of SRLV's have shown that even if control measures that have been based on early diagnosis and accurate management have been in place, often limited success is achieved due to re-emergence of seropositivity and disease in controlled flocks. Nowadays, keeping infected and healthy herds strictly separated, providing uninfected goat or bovine colostrum and milk to newborns, isolating them from their dams as soon as possible after birth, and frequently testing and removing positive animals are the key tactics in battling the disease. Generation-based herd management, raising offspring separately to establish disease-free herds while gradually removing infected adults is also effective. Animal welfare, however, is still crucial to both the farmers and the research community since concerns persist regarding animal suffering and the negative impact of CAE on their quality of life.

A deletion in the *CCR5* gene in humans has been shown to result in a prominent level of protection against HIV infections (Kaslow et al., 2005). The *CCR5* gene, found on chromosome 22, is an essential co-receptor that enables the entry of viruses that infect macrophages into host cells. *CCR5* expression levels have been shown to affect the progress of the disease and worsen its clinical symptoms in affected animals.

Previous studies by Colussi et al. (2019) identified a mutation at the g.1059T locus in Italian goats, where the T'T' genotype was linked to an increase in viral load. They explored an area located in the promoter region of the gene where transcription initiates (Colussi et al., 2019). Likewise, it was shown that a common four-base deletion in the CCR5 promoter/ has been associated with the manifestation of noticeably lower provirus levels homozygous sheep (White et al., 2009). Moreover, past studies showed an association between the genetic variation in the ovine transmembrane 154 *(TMEM154)* protein coding gene and infection susceptibility to certain SRLV subtypes (Colitti et al., 2025).

There is a growing need to target the disease in a more efficient way. Genetic selection of resistant animals based on the *CCR5* and *TMEM154* gene presents an

intriguing option for infection control, given the great genetic and antigenic heterogeneity of these viruses and the lack of an effective therapy or vaccine. Selecting against susceptibility to certain viral subtypes can represent a control strategy to reduce infection prevalence in sheep and goats (Colitti et al., 2025). Genetic variances in unaffected animals that present resistance to the virus are considered promising. The development of herds and animals resistant to CAE seems a prominent solution to both the research community and farmers across Sweden.

Derived from our research, we aimed to gather more valuable data to validate previous results by examining blood samples from Swedish goats. Moreover, we aimed to examine the variation in the *CCR5* gene and its effect on CAE, to try and identify whether the variant in the promoter region of the gene could help with the battling of the disease through the correlation that the g.1059T mutation confers resistance.

2. Material and Methods

This thesis explored through genetic analysis and by gathering and comparing data regarding CAE, variation in the promoter region of the *CCR5* gene. Five different Swedish goat herd lines and their genomic information formed the base for this thesis.

2.1 Datasets and Blood Samples

Blood samples from 94 different individuals, which had previously undergone evaluation following screening and confirmatory ELISA testing, were provided to us through Jonas Johansson Wensman. All samplings were conducted prior to the start of the analysis. For this research, a total of 84 samples were examined. These samples consisted of the breeds Jämtget (9 samples), Lappget (8 samples), Göingeget (10 samples), crossbred individuals from Swedish Landrace and Jämtget breeds (10 samples), purebred Svensk Lantras goats (39 samples) and goats of the Nubian breed (8 samples).

Phenotypes (positive or negative) regarding CAE, for part of the samples were also available. More precisely, 44 out of the 84 animals tested negatively for caprine arthritis and encephalitis, 39 of them were positive while only 1 was unidentified.

Apart from the identity and nation identity tag numbers of the animals, our blood samples were given an additional laboratory name for the undertaking of the laboratory-based section of the research.

2.2 DNA Extraction

DNA extraction was conducted according to the QIAprep ® Spin Miniprep Kit, Quick start protocol and QIAsymphony® DNA Handbook. The DNA samples were then put through NanoDrop to measure the concentration, and later aliquots were done and a working solution diluted to 4ng/µl.

Upon completion of DNA extraction, an aliquot plate was prepared to facilitate the sequencing process.

2.3 Big Dye Cycle Sequencing Manual

Sanger sequencing was performed using the BigDye® Direct Cycle Sequencing Kit following the manufacturer's instructions. The kit integrates PCR amplification, post-PCR clean-up, and cycle sequencing into a streamlined workflow optimized for M13-tailed primers.

2.3.1 PCR Amplification

Genomic DNA of suitable quality was amplified using primers containing the mandatory M13 forward (5′-TGTAAAACGACGGCCAGT-3′) and M13 reverse (5′-CAGGAAACAGCTATGACC-3′) sequences at the 5′ ends of the gene-specific primers.
Reactions (10 µL) contained BigDye® Direct PCR Master Mix, M13-tailed primers, and 4 ng template DNA, and were cycled as recommended (initial denaturation, 35 cycles of denaturation/annealing/extension, followed by a final extension).

2.3.2 Cycle Sequencing

An amount of 3 ul of the following mixture was deposited directly into the PCR product and was used per sequencing reaction. Sequencing was performed directly on unpurified PCR product using BigDye® Direct Sequencing Master Mix and either the supplied M13 forward or reverse sequencing primer. Reactions were cycled following the manufacturer's thermal protocol (enzyme activation, denaturation, 25 cycles of sequencing, final hold).

2.3.3 Purification of Sequencing Products

Unincorporated dye terminators were removed prior to capillary electrophoresis. Purification was carried out using the BigDye® XTerminator® Purification Kit, employing the SAM™/XTerminator® premix, plate sealing, vortexing, and centrifugation steps specified by the protocol.

2.3.4 Capillary Electrophoresis

Purified products were analyzed on an Applied Biosystems capillary electrophoresis instrument using POP-7™ polymer, Dye Set Z, and the BigDye® Direct mobility and calibration files supplied with the kit. Instrument-specific run modules recommended for BigDye® Direct chemistry were applied to ensure correct mobility compensation and base calling.

2.4 Sequencing region

The samples were sequenced for the variant of the *CCR5* gene located in the promoter region of the gene. The region of interest and part of the *CCR5* gene sequenced was at position 779-1107, in the promoter region of the Caprine reference sequence HQ650162.1. The variant of interest is variant g.1059 and in the targeted region tccacaaaca.

The variation analyzed is the previously published mutation g1059 C > T, with a frequency % (MAF) of 0.19, described by Colussi et al, 2019.

2.5 Software and programs

2.5.1 Chromas

Chromatogram files from Sanger sequencing were visualized and edited using Chromas software (version 2.6.6). Base calls were manually checked, corrected when necessary, and low-quality regions were trimmed. Edited sequences were exported in FASTA format for subsequent alignment and analysis in BioEdit.

Chromas is a software program designed for viewing and editing DNA sequencing chromatograms (Technelysium Pty. Ltd., 2019). It allows users to visualize base-calling peaks, manually correct sequencing errors, trim low-quality regions, and export sequences for further analysis in programs like BioEdit or other bioinformatics tools.

2.5.2 BioEdit Sequence Alignment Editor

DNA and protein sequences were edited, aligned, and analyzed using BioEdit software (version 7.2.5). Sequences were manually checked and corrected, aligned using the integrated tools, and exported in appropriate formats for downstream analyses. Basic sequence manipulations, such as translation, reverse complement, and motif searches, were also performed within BioEdit.

BioEdit is a sequence alignment editor, which allows researchers to edit, align, and analyze DNA, RNA, and protein sequences, providing tools for sequence visualization, translation, motif searches, and basic phylogenetic analysis. Its intuitive interface makes it widely used in molecular biology and bioinformatics research (Hall, 1999).

2.5.3 BLAST

Sequence similarity searches were performed using the BLAST tool (NCBI BLAST). Nucleotide sequences were queried against the NCBI database to identify homologous sequences, target the preferred region, and guide analyses.

BLAST (Basic Local Alignment Search Tool) is a widely used bioinformatics program for comparing nucleotide or protein sequences against databases to identify regions of similarity. It helps in annotating sequences, inferring function, and exploring evolutionary relationships by rapidly finding homologous sequences in public repositories (NCBI BLAST; Altschul et al., 1997).

2.6 Genomic Analysis

2.6.1 Genotype Frequencies

Genotype frequencies were systematically calculated for the entire dataset, as well as separately for each of the individual breeds, to allow for a comparison of

genetic variation both across and within breeds. Percentages of each genotype were also calculated respectively for both all animals as well as per breed.

$$Genotype\ Frequency = \frac{Amount\ of\ the\ genotype}{Total\ number\ of\ individuals}$$

2.6.2 Allele Frequencies

Allele frequencies were calculated for the full dataset and for each breed group individually to enable comprehensive comparisons of genetic variation both within and between groups.

$$Allele\ Frequency = \frac{Total\ amount\ of\ the\ allele}{Total\ number\ of\ individuals\ x\ 2}$$

2.7 Genotype distribution by phenotype association

Animals (82) with two ELISA phenotypes (pos, neg) and three genotype categories (C/C, C/T, and T/T) had genotypic and serological data available. A table (Genotype × Phenotype) was created, and Fisher's exact test was used to assess the link between genotype distribution and ELISA outcome. Furthermore, a dominant genetic model that separated individuals with the C allele (C/C and C/T) from T/T was assessed. The ELISA phenotype was coded as neg = 1 and pos = 0, and the association was studied using both Fisher's exact test and logistic regression. Total allele counts per individual were employed to calculate allele frequencies. RStudio (Posit team., 2025) was used for all statistical analyses, and the ggplot2 package was used to create graphical representations (Wickham H., 2016).

2.8 Genotype–Phenotype Association test in animals that seroconverted over time.

After analysis of the blood samples that were collected from the animals which belonged in herd H (Appendix 1), it was noticed that some animals seroconverted over time. Based on the two ELISA measurements, animals that were tested two times were assigned to two phenotype groups, pos for those that were positive in both tests and (pos) which obtained one negative and later, one positive result. To investigate if genotype differences are present between the two groups within the herd, a Chi-square test was run as well as a logistic regression analysis where Phenotype (pos=1, mixed=0) was modeled as a function of genotype coded additively (0,1,2). Odds ratios and 95% CI were calculated. An allelic association test where C vs T allele frequencies were compared using Fisher’s exact test was

also run through the same script, and the Hardy–Weinberg equilibrium was tested separately for each group using both chi-square and exact tests.

Genotype data were converted to allele counts (C=2 in C/C, C=1 in C/T, C=0 in T/T) to calculate allele frequencies for each phenotype group. All analyses were conducted in R version 4.4.1 (R Core Team, 2024).

3. RESULTS

3.1 Phenotype data

The distribution of positive and negative cases appeared generally evenly distributed, according to the phenotypic classification of the animals in the data set. Positive samples indicate animals that have antibodies against CAE, which have been infected or have been infected with the disease, while negative samples indicate animals that did not have antibodies.

A total of 39 animals were classified as positive, representing a significant portion of the dataset. A slightly larger group of 44 individuals showed a negative phenotype. In addition, one individual was recorded as having an unknown phenotype, either due to missing information or unclear classification. Although this represents only a very small portion of the total data, it highlights the existence of small gaps in the documentation of the phenotype.

3.2 Genomic information analysis

3.2.1 BioEdit run overview.

In figure 1 below, the mutation discussed in this research, in position 224 after the alignment of the sequences. The forward runs of the samples CHI10104 to CHI1127 contain all the described phenotypes, homozygous T/T and C/C, and heterozygous C/T and homozygous C/C. In total in this batch, 15 of the sequences contain the T allele (T/T genotype, 6 of them contain the Y allele (C/T genotype) and 3 the C allele (C/C genotype). The zoomed in region, position 224, can be seen also in figure 2.

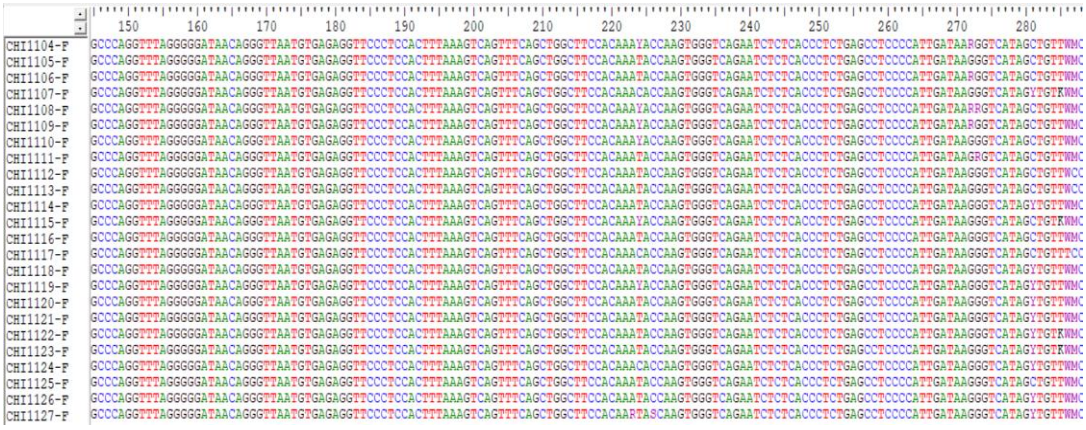

Figure 1. BioEdit run overview.

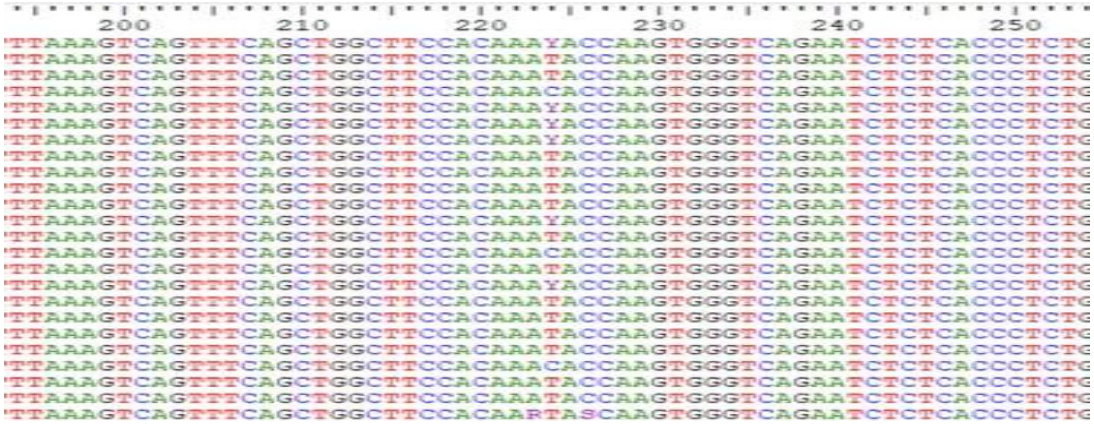

Figure 2. Zoomed in region of targeted position 224.

3.2.2 Genotype Visualization based on Forward and Reverse Sequencing Reads

To illustrate the C/C genotype, sample CHI10107 was used as a representative example. In the magnified region of the forward sequencing run (figure 3), the C genotype is clearly observed at position 290. This represents the C/C genotype and indicates that the sample is homozygous at that position for the C allele. The reverse sequencing run confirmed the C/C homozygous genotype. In this orientation, the alleles appear as the complementary bases to those observed in the forward run (figure 4). The presence of a single, unambiguous G peak is consistent with a homozygous G/G call in the reverse read, which corresponds to a C/C genotype in the forward orientation.

For the visualization of the T/T and C/T genotypes, samples used as a representative example can be found in Appendix 2.

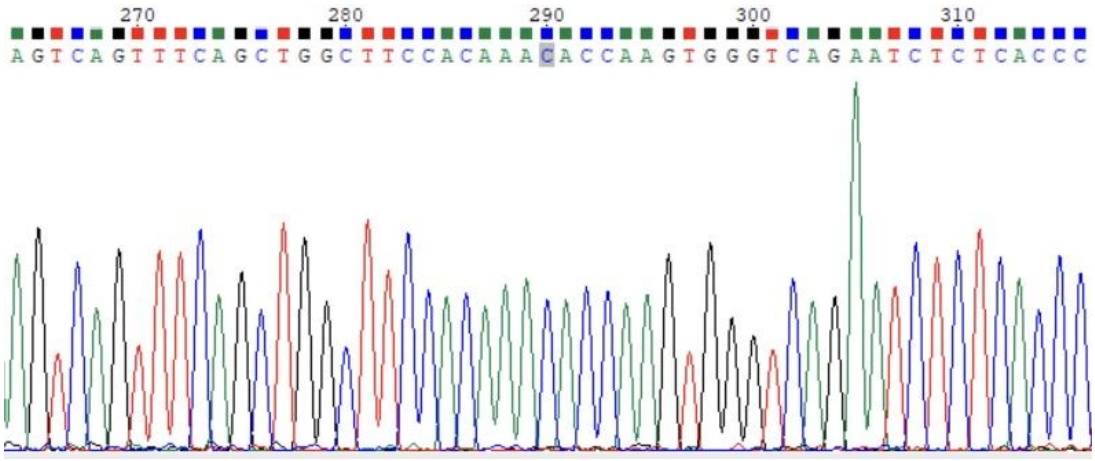

Figure 3. Sample CHI10107 with C/C genotype. Forward Run zoomed in region.

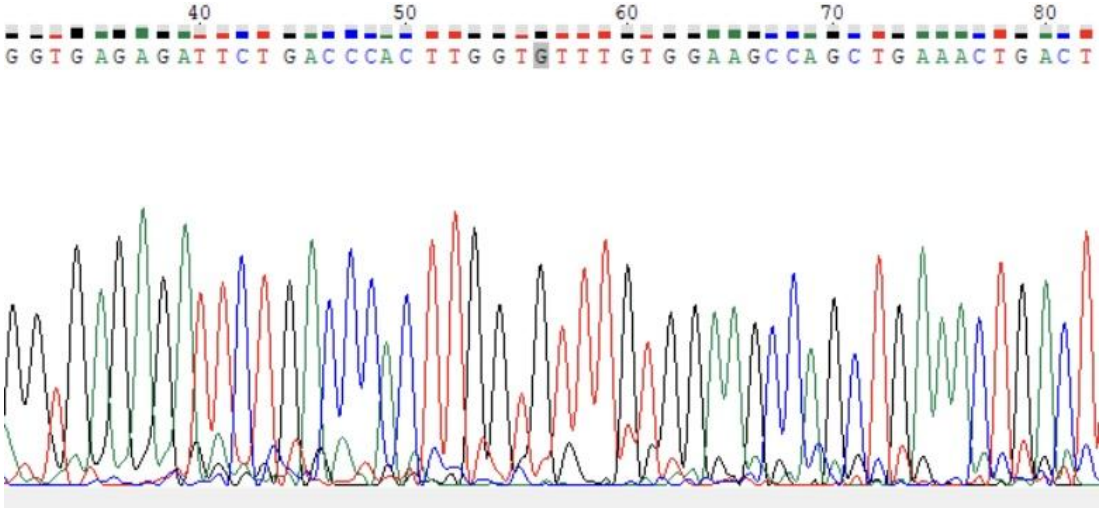

Figure 4. Sample CHI10107 with C/C genotype. Reverse Run zoomed in region.

3.3 Genotype Analysis

The genotype frequencies across all breeds combined presented a clear pattern. The T/T genotype was the most observed, with a frequency of 0.524. The genotype frequencies are followed by the heterozygous T/C genotype at 0.369, while the C/C genotype was the least frequent, with a frequency of 0.095, represented the homozygous genotype.

Table 1. Genotype Frequencies of all animals.

GENOTYPE	FREQUENCIES	COUNT
T/T	0.524	44
C/T	0.369	31
C/C	0.095	8

In the Jämtget population, only the T/T genotype was observed, with a frequency of 1.0, and 18 individuals, indicating complete absence of both the C/C and T/C genotypes. Consequently, no association analysis could be conducted in Jämtget breed and thus the samples were not considered in further association analysis.

In the Lappget population the T/T genotype presented a frequency of 0.375, with 3 individuals out of 8 individuals present in the breed. The T/C was noted as the predominant genotype with a frequency of 0.625, with 5 individuals out of the 8 animals. The C/C genotype was not detected in this breed.

In the crossbred breed group of the Swedish landrace × Jämtget population, the T/T and T/C genotypes were equally represented, each with a frequency of 0.5,

with 5 individuals out of the 10 in the group, while the C/C genotype was again absent.

A similar pattern was observed in the Göingeget population, where the T/C genotype was the most common at a frequency of 0.6 with 6 individuals out of the 10, followed by T/T at 0.4 with 4 individuals, while no individuals were carrying the C/C genotype.

The Svensk Lantras group exhibited a broader distribution of genotypes. The T/T genotype occurred at a frequency of 0.421, with 16 individuals out of 38, while the heterozygous C/T exhibited a frequency at 0.421 with 16 individuals. The homozygous C/C genotype was observed at 0.158, with 6 individuals.

In the breed group of the Nubian population, the T/T occurred at a frequency of 0.875, with 7 individuals out of the 8, and C/C genotypes were equally represented, each with a frequency of 0.125, with 1 individual out of the 8 in the group, while the C/T genotype was absent.

Table 2. Genotype Frequencies of all breeds

BREED	T/T FREQUENCY	C/T FREQUENCY	C/C FREQUENCY	T/T COUNT	C/T COUNT	C/C COUNT
JAMGET	1	0	0	18	0	0
LAPPGET	0.375	0.625	0	3	5	0
CROSSBRED	0.5	0.5	0	5	5	0
GOINGET	0.4	0.6	0	4	6	0
SVENSK LANTRAS	0.421	0.395	0.184	16	16	7
NUBIAN	0.875	0	0.125	7	1	0

3.4 Allele Frequencies

Across all breeds combined, the T allele was clearly the dominant variant in the population. It reached a frequency of 0.717, corresponding to 119 observed allele counts, while the C allele was much less common, with a frequency of 0.283 and 47 counts. This distribution indicates that, overall, the T allele represents more than two-thirds of all alleles identified in the dataset. The relatively lower count of the C allele reflects its more restricted presence across the populations and serves as a baseline for examining variability among breeds.

Table 3. Allele Frequencies of all animals.

ALLELE	FREQUENCIES	COUNT
T	0.717	119
C	0.283	47

In the Jämtget population, the allele distribution showed complete fixation for the T allele. This lack of variation suggests either a strong founder effect, intense selection, or a naturally homogeneous parental background. Regardless of the cause, the Jämtget breed group displayed no allelic diversity.

In contrast, the Lappget population exhibited a distribution of both the T and C allele in the breeds dataset. The T allele frequency was 0.688 while the C allele reached 0.313. Although the T allele remained the majority allele, the presence of the C allele at over 30% suggests appreciable genetic diversity at this locus in this breed.

The crossbred population showed a similar pattern, though with a more pronounced dominance of the T allele. Here, the T allele was observed at a frequency of 0.75, compared to 0.25 for the C allele. Even though the C allele was present, its frequency was lower than in the Lappget breed group, suggesting a reduced level of allelic diversity relative to that breed.

Moreover, in the Göingeget population, the frequencies showed a distribution comparable to the crossbreed group. The T allele occurred at a frequency of 0.7, while the C allele was detected at 0.3. These values indicate that, although the T allele continues to predominate, the C allele is still observed at a moderately high level, contributing to within-breed variation.

The Svensk Lantras group displayed one of the more diverse allele distributions in the dataset. The T allele occurred at a frequency of 0.618, while the C allele reached 0.381. This represents the largest absolute number of C alleles detected in any group, reflecting either a larger sample size or a genuinely higher representation of this allele within this subset of individuals.

In the Nubian population, the T allele occurred at a frequency of 0.875, while the C allele was detected at 0.125.

Table 4. Allele Frequencies of all breeds.

BREED	T ALLELE FREQUENCY	C ALLELE FREQUENCY	T ALLELE COUNT	C ALLELE COUNT
JAMGET	1.0	0	18	0
LAPPGET	0.688	0.313	11	5
CROSSBRED	0.750	0.25	15	5
GOINGET	0.700	0.3	14	6
SVENSK LANTRAS	0.618	0.381	47	29
NUBIAN	0.875	0.125	14	2

3.5 Genotype distribution by Phenotype Association

3.5.1 Association test on all samples

A confirmation test was assessed to examine the possible association between the C/C or C/T genotype and the animals that have the negative phenotype in order to try and determine whether the C allele, in the mutation g.1059 T where C>T.

After quality control, one record with an unknown phenotype was removed. The distribution of genotypes according to ELISA status is shown in Table 1. In total 82 animals were analyzed and had available genotype and phenotype data.

The Fisher's exact test for all the samples revealed a p-value of 0.0298. Within-group genotype percentages where animals with the C/C genotype were more frequently observed in the positive (pos) phenotype group (15.8%) compared to the negative (neg) group (4.6%). Similarly, C/T animals are also more common in the pos group (44.7%) than in the neg group (27.9%). The T/T genotype is markedly more frequent in the neg group (67.4%) than in the pos group (39.5%). The overall allele frequencies in the sample were C = 27.8% and T = 72.2%.

Table 5. Genotypes by phenotype count in all samples.

GENOTYPE	NEGATIVE	POSITIVE
C/C	2	6
C/T	12	17
T/T	29	15

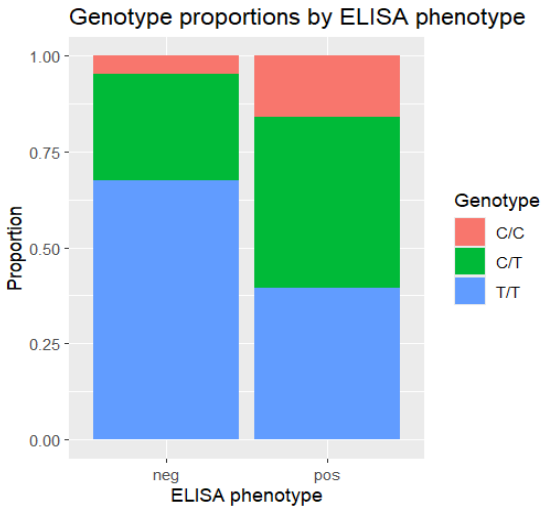

Figure 5. Genotype proportions by ELISA phenotype.

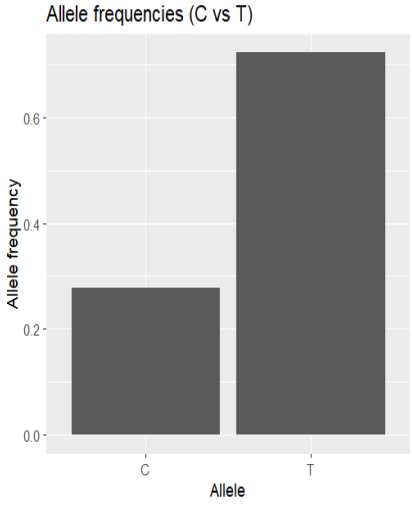

Figure 6. C vs T allele frequencies in all animals.

3.5.2 Association test on the Jämtget breed group

In the Jämtget animals, no phenotypic or genotypic variation was observed. All individuals were ELISA negative and carried the T/T genotype. Consequently, statistical association analyses, including Fisher's exact test or logistic regression, could not be performed.

3.5.3 Association test on Lappget breed

Most animals in the Lappget breed were ELISA negative (7/8), and only one animal was positive. No animals carried the C/C genotype, while the remaining genotypes (C/T and T/T) were observed at very low frequencies (Table 6). The Genotype × Phenotype contingency table contained empty cells (0 observations for T/T-positive), preventing the estimation of odds ratios and resulting in a Fisher's exact test p-value of 1. Overall, the sample size is insufficient to conduct a meaningful test.

Table 6. Genotype distribution by phenotype in the Lappget subset.

GENOTYPE	NEGATIVE	POSITIVE
C/T	4	1
T/T	3	0

3.5.4 Association test on the crossbred group (Svensk Lantras x Jämtget)

For the crossbred samples, the Genotype × Phenotype distribution is shown in Table x. All T/T animals were ELISA positive, while C/T animals were observed in both phenotypes, with only one negative individual. No C/C genotypes were present. The contingency table includes an empty cell (T/T–negative = 0), resulting in complete separation (perfect separation) and preventing reliable estimation of odds ratios. Fisher's exact test produced a p-value of 1 and an odds ratio of infinity.

Table 7. Genotype distribution by phenotype in the Crossbred subset.

GENOTYPE	NEGATIVE	POSITIVE
C/T	1	4
T/T	0	5

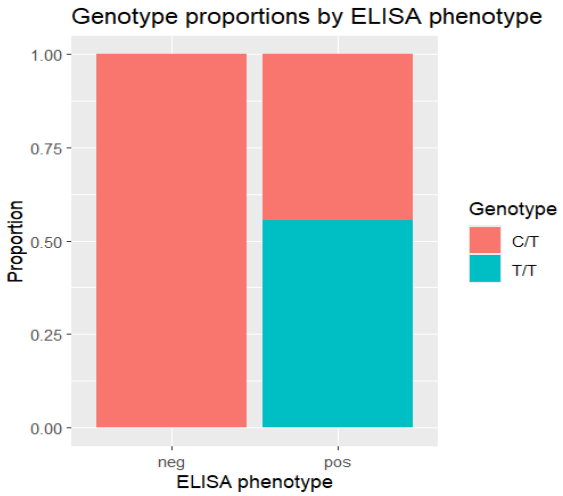

Figure 7. Genotype proportions by ELISA phenotype in the crossbred group.

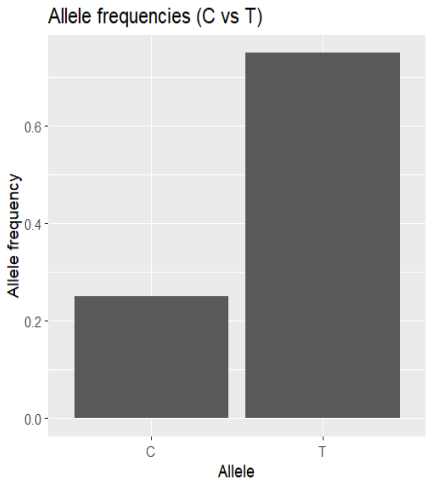

Figure 8. C vs T allele frequencies in the crossbred group.

3.5.5 Association test on the Göingeget breed

In the Göingeget, all animals displayed a negative (neg) phenotype. Due to the lack of phenotypic variation, it is not possible to conduct tests within the Göingeget breed.

Table 8. Genotype distribution by phenotype in the Goingeget subset.

GENOTYPE	NEGATIVE
C/T	5
T/T	4

3.5.6 Association test on the Svensk Lantras breed group

In the Svensk Lantras dataset, positive (pos) animals had higher frequencies of C/C and C/T genotypes compared to negative (neg) animals (Table 9). Fisher's exact test showed no statistically significant association with a p-value of p = 0.3674. Under a dominant model (C carriers vs. T/T), the OR was 0.29 (95% CI: 0.038–1.70, p = 0.136), and logistic regression gave similar results (OR = 0.28, 95% CI: 0.05–1.29, p = 0.114).

Table 9. Genotype distribution by phenotype in the Svensk Lantras subset.

GENOTYPE	NEGATIVE	POSITIVE
C/C	1	6
C/T	2	12
T/T	6	10

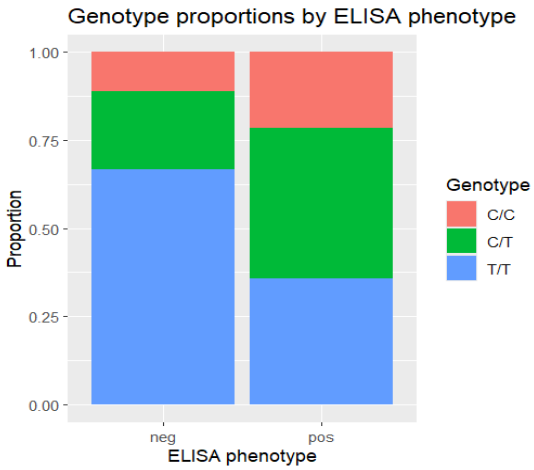

Figure 10. Genotype proportions by ELISA phenotype in Svensk Lantras group.

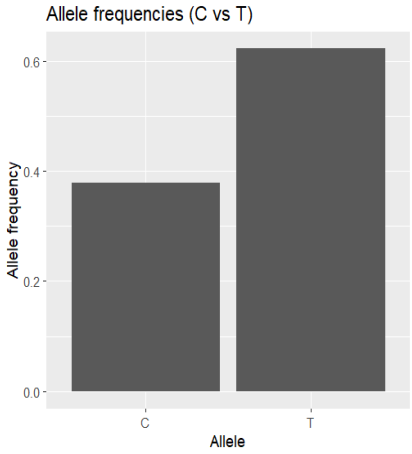

Figure 9. C vs T allele frequencies in the Svensk Lantras group.

3.5.7 Association test on the Nubian breed group

In the Nubian breed, all animals displayed a negative (neg) phenotype, with only one C/C individual and seven T/T individuals. Consequently, no analysis was possible within the group.

3.6 Genotype–Phenotype Association test in animals that seroconverted over time

During the ELISA analysis of the blood samples, some of the animals (as seen in Appendix 1, indicated by the brackets (pos)) were tested two times. The first time the analysis was conducted the results indicated no antibodies for the CAE and the samples were at first characterized as negative. However, after a second run, antibodies were detected and the samples were indicated positive. Statistical tests were run to evaluate if there are genotype differences between the samples with phenotypes pos and (pos). Samples originate from herd H (Appendix 1).

The observed genotype counts for the SNP under investigation are presented in Table 11. A chi-square test was performed to assess potential differences in genotype distribution between the *(pos)* and *pos* groups. The analysis did not reveal any statistically significant association with $\chi^2 = 0.342$, df = 2 and a p-value = 0.843, indicating that the proportion of C/C, C/T and T/T genotypes does not differ between the two groups.

Table 10. Observed genotype counts per group in the second association test.

GROUP	C/C	C/T	T/T
(pos)	2	5	3
pos	4	7	7

3.6.1 Allele frequencies

Allele frequencies were calculated by converting genotype data to allele counts. As shown in Table 12, allele C appeared with a frequency of 45% in the mixed group and 41.7% in the pos group, whereas allele T appeared with frequencies of 55% and 58.3%, respectively. Fisher's exact test showed no significant difference between the two groups with a p-value of p = 1, suggesting that allele distribution is comparable across groups.

Table 11. Allele frequencies per group in the second association test.

GROUP	ALLELE C (n, %)	ALLELE T (n, %)
(pos)	9 (45%)	11 (55%)
pos	15 (41.7%)	21 (58.3%)

3.6.2 Logistic regression

A logistic regression model was applied to evaluate whether genotype could predict group assignment. Genotypes were coded additively (C/C = 0, C/T = 1, T/T = 2). The model indicated no significant effect of genotype on the likelihood of an animal belonging to the pos group OR = 1.13, 95% CI: 0.39–3.28, p = 0.820. These results suggest that genotypes do not influence group status.

3.6.3 Hardy–Weinberg equilibrium

Hardy–Weinberg equilibrium (HWE) was assessed separately for each group. For the pos group, both the exact test (p = 0.379) and chi-square test (p = 0.620) indicated no deviation from HWE. Similarly, the (pos) group was in equilibrium (exact test p = 1, chi-square p = 0.634).

4. Discussion

In this study, genomic information extracted from blood samples of Swedish goats from six different bloodlines and breeds, were utilized to assess both genotypes and allele frequencies. We were interested in exploring possible genotypes associated with CAE expression by researching the targeted region.

4.1 CCR5 and CAE

The Caprine *CCR5* gene structure and variability was first described by Collusi et al. in 2019. The variant g.1059 T, located in the promoter region, revealed an interesting association with high proviral loads. An explanation for this is alteration of the transcriptional level, specifically, overexpression of the *CCR5* receptor on the cell surface. Therefore, this could increase virus internalization and proviral load. (Colussi et al., 2019). A further explanation would be that the variant g.1059 T might not be directly associated with the high proviral load, but rather that it is linked with another unknown functional variant outside the present dataset. The caprine *CCR5* sequence contains two exons, and exon II includes the entire open reading frame (ORF), which is in line with the structure previously reported for the ovine *CCR5* gene. A 352-amino acid protein that is 98% identical to its ovine counterpart is encoded by the coding sequence. The caprine *CCR5* gene's entire coding sequence (CDS) and promoter region have both been added to GenBank by Collusi et al.

Collusi et al. suggested that herd susceptibility to CAEV could be reduced by selectively excluding goats that carry the g.1059 T mutation. Removing animals that are genetically predisposed to higher proviral loads may help limit both the development of clinical disease and viral transmission. In this context, the use of marker-assisted selection could represent a valuable and innovative complementary approach for controlling CAEV infection, particularly in herds with high levels of seroprevalence.

A variant in the chemokine (C-C motif) receptor 5 (*CCR5*) gene has been associated with resistance to HIV infection in humans (Kaslow et al., 2005) and to small ruminant lentivirus (SRLV) in sheep (Colussi et al., 2019). In sheep, a frequent four-base deletion in the *CCR5* promoter has been linked to a markedly reduced proviral load, with an approximately a 3.9-fold difference between genotypes (White et al., 2009).

In goats, the same alleles have been discussed to provide resistance to the disease. The C-C motif in the genotypes of our samples was indeed present in our dataset even though it was the least prevalent genotype. Specifically, in the full dataset (n = 82), a significant association between genotype and ELISA phenotype was detected (Fisher’s exact test p = 0.0298), with the T/T genotype

being more common among ELISA-negative animals and C-allele carriers (C/C and C/T) overrepresented among ELISA-positive animals. Overall allele frequencies (C = 27.8%, T = 72.2%) indicate that the T allele predominates in the sampled populations as a whole dataset.

At the breed level, this association disappeared due to strong breed effects. Several breeds (Jämtget, Göingeget, Nubian) lacked phenotypic variation because all animals were ELISA-negative, while others had exceedingly small sample sizes preventing meaningful statistical testing. The Swedish Landrace was the only breed with sufficient variation for analysis and showed a similar trend to the full animal dataset, but the association was not statistically significant.

Across most breeds, the C allele was rare or absent, substantially reducing the power of the tests and indicating that allele frequency differences mainly reflect other structures rather than disease association. Consequently, the lack of consistent within-breed replication means the biological significance remains uncertain. Larger, better-balanced datasets and analyses that account for population structure will be necessary to clarify whether this SNP plays a meaningful role in CAEV susceptibility.

The previously published study of Collussi et al., showed that the g.1059 T mutation was significantly associated with high proviral load, also after correction for multiple testing, with a higher proviral load in the individuals carrying the g.1059 T mutation. Various alternatives of setting the cut-off led to similar results, pointing to an association between *SNP 1059* and high proviral load values. In their study, twenty-two cases (5 wild type, 17 mutated) and 68 non-cases (39 wild type, 29 mutated) were analyzed, and the chi-square test demonstrated the presence of eight SNPs statistically associated with high proviral load.

In this study, the same region was analysed using a different phenotype (ELISA seropositivity). Our results indicate that the C allele is not associated with protection. Data analysis (after removal of null values) showed that among ELISA-positive individuals (n = 38) there were 6 C/C, 17 C/T, and 15 T/T genotypes, whereas among ELISA-negative individuals (n = 43) there were 2 C/C, 12 C/T, and 29 T/T genotypes. When grouping C-carriers (C/C + C/T) versus T/T, C-carriers accounted for 60.5% of positives compared with 32.6% of negatives, while T/T individuals accounted for 39.5% of positives versus 67.4% of negatives, indicating that the C allele is clearly more frequent among ELISA-positive samples. Consequently, the data does not support the hypothesis that the C allele confers immunity. It is emphasized that statistical association does not imply causality, and further biological or experimental data are required to support a mechanistic interpretation.

Differences between studies likely arise from the use of distinct phenotypic measures, as ELISA measures antibody response rather than proviral load, and from variation in population structure or infection stage. ELISA measures

antibody response rather than proviral load. Consequently, the apparent differences between our findings and those of Colussi et al. are likely attributable to the assessment of different phenotypic endpoints (serology vs proviral load), as well as possible differences in population structure, breed composition, or infection stage. Overall, our findings cannot support that the C allele confers immunity and thus be consistent with the literature identifying the T allele as a risk allele, while ELISA data alone are insufficient to infer protection, highlighting the need for proviral load (PCR) and longitudinal analyses.

4.2 Allele frequencies

The observed differences in allele frequencies illustrate how variation for a given candidate mutation can vary markedly between breeds, even when they coexist within the same broader population. Breeds with more balanced allele distributions may benefit from increased variability at this locus, whereas those showing fixation or near-fixation may be at greater risk of reduced genetic flexibility. In a previous master thesis that investigated CCR5 in four Swedish goat breeds, Tiilikainen (2021) suggested that in their study, Jämtget demonstrated full fixation of the T′T′ genotype. The C′C′ genotype was most common in Göingeget, along with a significant percentage of heterozygous individuals. The T′T′ genotype was particularly common in the Swedish Landrace. The initial mutation in Lappget had genotype frequencies of 71% T′T′ and 29% T′C, which corresponded to allele frequencies of 86% for T′ and 14% for C′. Lappget frequencies changed to 61% T′T′ and 39% T′C when combined with data from the previous research of Gunnarsson et al. (2020), with allele frequencies of roughly 81% T′ and 19% C′ (Tiilikainen, 2021). With a T′ allele frequency of 100%, the results of Tiilikainen were compelling with our results in the same breed group where the C allele was completely absent in the Jämtget. In the Lappget breed group, our results demonstrated a higher frequency of the C allele (0.313) compared to the Tiilikainen samples (0.14). Meanwhile, in the Göingeget, our research demonstrated a higher frequency of the T allele than in the Tiilikainen samples. Lastly in the Svensk Lantras breed group, in our study the C allele was more common (0.25) than in the Tiilikainen samples (0.1). However, small sample size in a population could influence the results when calculating allele frequencies. Therefore, in breeds with small sample sizes such as the Jämtget, the Göingeget, the Lappget and the Nubian, the estimates of their allele frequencies might not be representative for those specific breeds. These findings underscore the importance of breed-specific monitoring and the potential need for management strategies aimed at preserving genetic diversity, particularly for populations that appear genetically uniform.

4.3 Milk production

Although the relationship between milk production and CAE in Swedish goats was not investigated in this study, we considered it relevant to mention the impact of the disease on milk production. The results of earlier research on milk production losses in infected animals have been inconsistent since individual-level losses cannot be precisely measured. Total herd productivity has ultimately decreased since infected animals are removed from production and culled. Furthermore, diseased animals are typically less productive than unaffected ones, especially if they show symptoms of cachexia.

4.4 Treatment

There is currently no effective treatment for SRLV infection, and the virus's high mutation rate has so far prevented the development of a vaccine. SRLV affects the production and welfare of sheep and goats worldwide; the estimated seroprevalence is 80–90% in dairy goats and 60–82% in Italy. (Colussi et al., 2019)

Control strategies therefore rely largely on herd management practices, primarily the identification and culling of infected animals based on serological testing. However, variability in serological responses, both within individual animals and across flocks, complicates accurate diagnosis. In herds with high seroprevalence, an alternative strategy involves selecting seronegative offspring raised on artificial feeding systems. Separating young and healthy animals from infected individuals also requires substantial additional management effort, particularly when phased culling strategies are applied, as multiple distinct groups must be maintained simultaneously. Increased biosecurity measures are necessary to prevent transmission via handlers or equipment under these conditions.

As CAE does not affect the T-cells and is not immunosuppressive, affected animals are still able to produce antibodies (Leroux et al., 2010). Along with current control efforts, breeding could be a useful tool if it proves to be an effective strategy for disease control. Production losses associated with the disease would be reduced if it could be further restricted. Furthermore, animal welfare would also be improved, as CAE is a disease with severe symptoms that cause suffering and ultimately result in the animal's death. Containing CAE would also decrease the risk of losing breeds/genetic materials from being forced to cull sick animals. All this would also improve the economic aspect of production, with healthier and more productive animals. Consequently, breeding for CAE-resistant animals represents a potentially promising and sustainable control strategy.

5. Conclusion

Through this study, significant correlations could not be proven between genotype and prevalence of disease in the samples we studied. Details about the data, proviral loads of the animals, as well as more information about the progress of the disease and the symptoms should be accounted in the research.

More studies need to be conducted, with more animals tested for CAE, to increase the sample size of the homozygous animals. Most importantly a proviral load test could be conducted on the homozygous animals and the C allele carriers to investigate if the pro viral load increases or decreases in those sero-positive animals.

For the mutation, there were variations in allele frequencies and genotypes both within and across some of the breeds. Certain breeds would consequently be easier to breed since they show more genetic diversity. In any case bigger sample sizes from some breeds are needed.

The frequency of genotypes and alleles in Swedish goat breeds is presented in this study, which could be used for additional research on the association between the genotypes of Swedish goats and the occurrence of CAE. Before breeding is taken into consideration to control the disease, more research is required. Assuming breeding proves to be an effective approach in the future, it could potentially be applied to enhance production and animal welfare by increasing the possibility of controlling the disease.

Overall, there is currently not enough data to establish a connection between the prevalence of CAE in Swedish goats and the mutation in the *CCR5* gene. The occurrence of the disease could possibly be influenced also by other undiscovered genes.

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Popular science summary

Caprine arthritis-encephalitis (CAE) is a chronic viral disease that affects goats all over the world. The disease can cause neurological issues, joint pain, and decreased movement, sparking concerns about animal welfare while harming farmers financially. One of the primary challenges in managing CAE is that diseased goats may not exhibit symptoms for an extended period, making it challenging to identify and eradicate the disease. Current control methods rely mainly on management practices and blood tests, which can be costly and challenging to apply consistently.

The idea for an alternative approach to control the disease, suggests breeding for animals that are less vulnerable to infection. According to previous research, a goat's vulnerability to CAE may be influenced by a gene called CCR5, which is involved in the way pathogens enter immune cells. A small genetic variation in a region of this gene has been linked to higher levels of the virus in infected animals

The aim of this study was to examine genetic variation in the CCR5 gene in Swedish Landrace goats and to investigate whether these variations were associated with CAE infection. Blood samples of the animals in this study were used to identify the genotype of each animal. This way, our study aimed to validate previous results and explore if disease control could be improved through specific breeding.

The results did not clearly demonstrate a connection between the occurrence of CAE infection in the goats and CCR5 gene variations. However, the absence of information on the viral load and the very small number of animals from specific breeds limit the conclusions. Before CCR5-based breeding techniques can be suggested as an effective approach of controlling CAE, further studies involving larger goat populations and additional infection measurements are required.

Appendix 1

Breed	Sample Number	Phenotype	Herd
jämtget	CHI1041	neg	A
jämtget	CHI1042	neg	A
jämtget	CHI1043	neg	B
jämtget	CHI1044	neg	B
jämtget	CHI1045	neg	B
jämtget	CHI1046	neg	B
Jämtget	CHI1069	neg	F
Jämtget	CHI1070	neg	F
Jämtget	CHI1071	neg	F

Breed	Sample Number	Phenotype	Herd
lappget	CHI1047	neg	C
lappget	CHI1048	neg	C
lappget	CHI1074	neg	G
lappget	CHI1075	neg	G
lappget	CHI1077	neg	G
lappget	CHI1078	pos	G
lappget	CHI1079	neg	G
lappget	CHI1080	neg	G

Breed	Sample Number	Phenotype	Herd
sv lantras x jämtget	CHI1049	neg	D
sv lantras x jämtget	CHI1050	pos	D
sv lantras x jämtget	CHI1051	pos	D
sv lantras x jämtget	CHI1052	pos	D
sv lantras x jämtget	CHI1053	pos	D
sv lantras x jämtget	CHI1054	pos	D
sv lantras x jämtget	CHI1055	(pos)	D
sv lantras x jämtget	CHI1056	pos	D
sv lantras x jämtget	CHI1057	pos	D
sv lantras x jämtget	CHI1058	pos	D

Breed	Sample Number	Phenotype	Herd
Göingeget	CHI1059	neg	E
Göingeget	CHI1060	neg	E
Göingeget	CHI1061	neg	E
Göingeget	CHI1062	neg	E
Göingeget	CHI1063	neg	E
Göingeget	CHI1064	neg	E

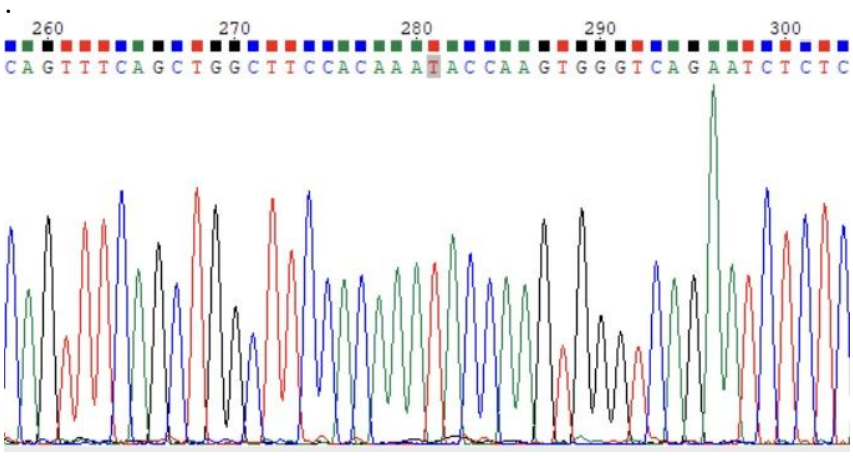
Göingeget	CHI1066	neg	E
Göingeget	CHI1067	neg	E
Göingeget	CHI1068	neg	E

Breed	Sample Number	Phenotype	Herd
svensk lantrasget	CHI1081	pos	H
svensk lantrasget	CHI1082	pos	H
svensk lantrasget	CHI1083	pos	H
svensk lantrasget	CHI1084	(pos)	H
svensk lantrasget	CHI1085	(pos)	H
svensk lantrasget	CHI1086	pos	H
svensk lantrasget	CHI1087	(pos)	H
svensk lantrasget	CHI1088	pos	H
svensk lantrasget	CHI1089	pos	H
svensk lantrasget	CHI1090	(pos)	H
svensk lantrasget	CHI1091	pos	H
svensk lantrasget	CHI1092	pos	H
svensk lantrasget	CHI1093	(pos)	H
svensk lantrasget	CHI1094	pos	H
svensk lantrasget	CHI1095	(pos)	H
svensk lantrasget	CHI1096	pos	H
svensk lantrasget	CHI1097	(pos)	H
svensk lantrasget	CHI1098	(pos)	H
svensk lantrasget	CHI1099	pos	H
svensk lantrasget	CHI1100	pos	H
svensk lantrasget	CHI1101	pos	H
svensk lantrasget	CHI1102	pos	H
svensk lantrasget	CHI1103	(pos)	H
svensk lantrasget	CHI1104	pos	H
svensk lantrasget	CHI1105	pos	H
svensk lantrasget	CHI1106	pos	H
svensk lantrasget	CHI1107	(pos)	H
svensk lantrasget	CHI1108	pos	H
svensk lantrasget	CHI1109	(pos)	H
Swedish Landrace	CHI1110	neg	I
Swedish Landrace	CHI1111	neg	I
Swedish Landrace	CHI1112	neg	I
Swedish Landrace	CHI1113	neg	I
Swedish Landrace	CHI1114	neg	I
Swedish Landrace	CHI1115	neg	I
Swedish Landrace	CHI1116	neg	I

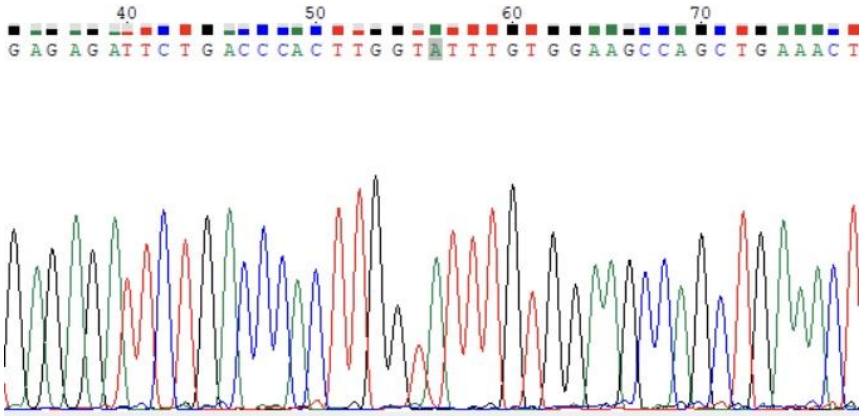
Swedish Landrace	CHI1117	neg	I
Swedish Landrace	CHI1118	neg	I
Swedish Landrace	CHI1119	-	I

Breed	Sample Number	Phenotype	Herd
Nubian	CHI1120	neg	J
Nubian	CHI1121	neg	J
Nubian	CHI1122	neg	J
Nubian	CHI1123	neg	J
Nubian	CHI1124	neg	J
Nubian	CHI1125	neg	J
Nubian	CHI1126	neg	J
Nubian	CHI1127	neg	J

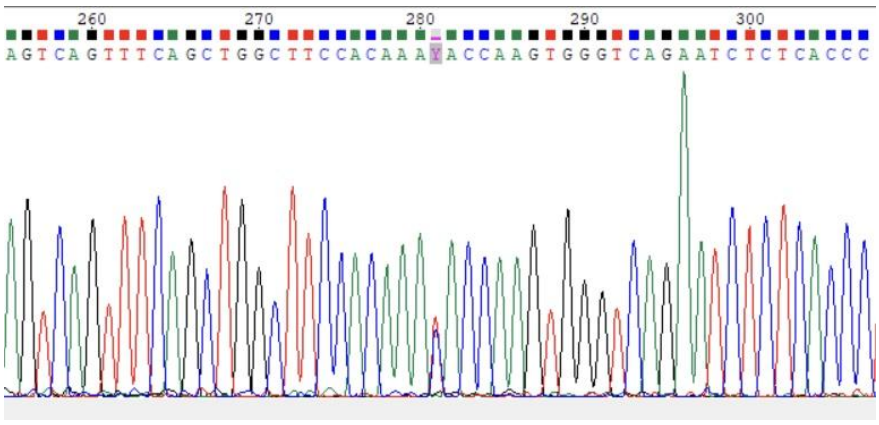
Appendix 2



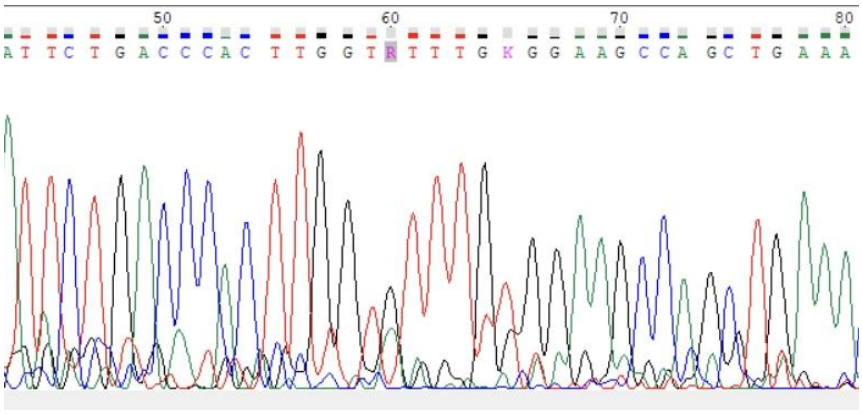
Sample CHI1041 with T/T genotype. Forward Run zoomed in region.



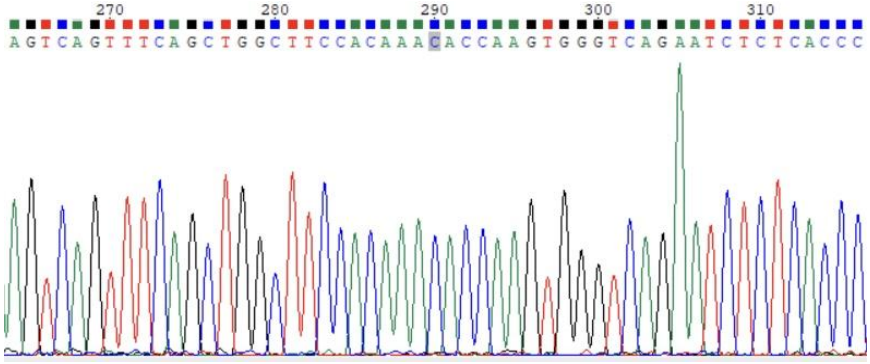
Sample CHI1041 with T/T genotype. Reverse Run zoomed in region.



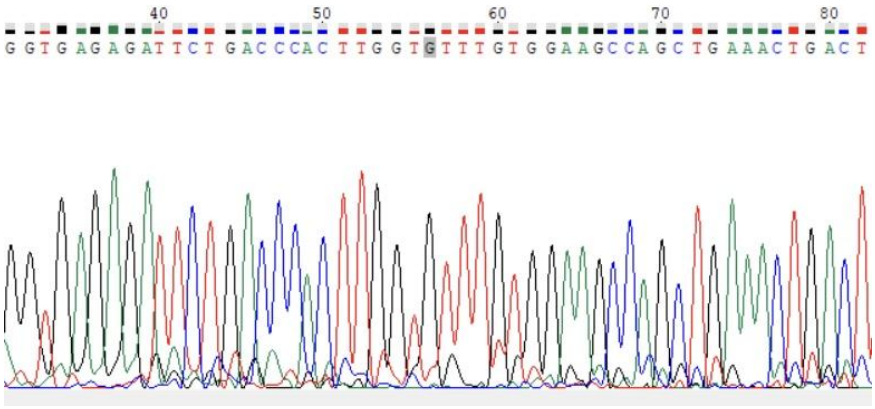
Sample CHI10108 with C/T genotype. Forward run zoomed in region.



Sample CHI10108 with C/T genotype. Reverse Run zoomed in region zoomed in region.



CHI10107 with C/C genotype. Forward Run zoomed in region.



Sample CHI10107 with C/C genotype. Reverse Run zoomed in region.

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