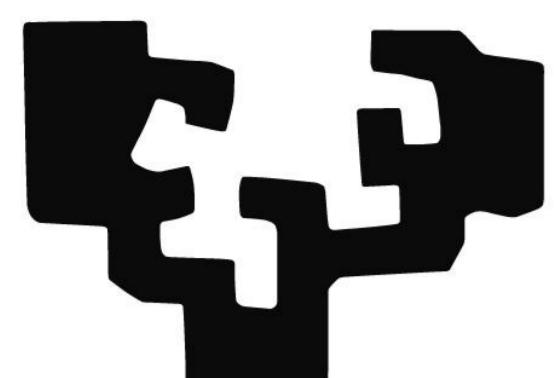


# RELATIONSHIP BETWEEN GENE EXPRESSION OF STEAROYL-COA DESATURASES (SCD1 & SCD5) AND THE FATTY ACID PROFILE IN ADIPOSE TISSUE OF CATTLE BREEDS IN THE BASQUE REGION

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## INTRODUCTION

➤ The concern of consumers regarding the amount and type of fat in the diet has been increased in relation with the negative implications of saturated FAs (SFA) while some monounsaturated FAs (MUFA) and polyunsaturated FAs have been recognized as beneficial for health.

➤ The stearoyl-CoA 9-desaturase (SCD) is a lipogenic enzyme that catalyzes the conversion of some SFA to MUFA. The SCD1 genotype has been associated with the FA composition in beef and dairy cattle but also transcription factors like SREBP1 that control SCD and FA biosynthesis.

➤ Therefore, differences in the expression level of previously associated SCD1, SREBP1 and a novel SCD5 could affect expression and differences in FA composition of adipose tissues in beef cattle.



## OBJECTIVE

➤ Correlate SREBP1 and SCD isoforms, (SCD1 & SCD5).

➤ Correlate gene expression of SCD1, novel SCD5 and FA profile in backfat tissue from cattle breeds in the Basque Country.



## MATERIAL & METHODS

### Survey

Three commercial groups:

Pirenaica breed < 30 mo, n=62  
Salers breed < 30 mo, n=12  
Friesian breed > 30 mo, n=15

### FATTY ACID PROFILE

SP2560, 100m

• GC 175°C. Total FAMES  
• GC 150°C. Trans-18:1

Base (NaOCH<sub>3</sub>)

Direct Methylation  
+ I.S. (23:0Me)

### GC/FID

	Least square means of age at slaughter and carcass traits of cattle sampled.		
	Pirenaica (n=62)	Salers (n=12)	Friesian (n=15)
Age at slaughter (month)	17.1 (10.3-90.2)	12.6 (10.3-14)	63.2 (31.9-93)
Cold carcass weight (kg)	297 (187-530)	324 (286-357)	274 <sup>b</sup> (196-346)
Conformation	10.6 (8-15)	8.4 (8-10)	2.8 <sup>a</sup> (1-5)
Fat cover	5.4 (2-9)	5.7 (5-7)	3.1 (1-7)
SEM	3.6	7.3	0.33
			0.21

SEM: standard error of the mean;

## GENE EXPRESSION

### RNA extraction

Reverse Transcription  
• ReverTra Ace®  
• cDNA

Real-Time PCR  
• Taqman probes

SPEARMAN  
DATA ANALYSIS  
ANOVA



Bovine backfat samples were collected from animals slaughtered in a commercial abattoir located in Basque country, northern Spain over 5 weeks in June-July.

## RESULTS

➤ When expression of SCD1, SCD5 and SREBP1 were given in relative amount (-ΔCt), significant differences ( $P \leq 0.01$ ) were observed among genes (Fig. 1). This expression pattern was previously observed by Lengi and Corl (2007) in several tissues.

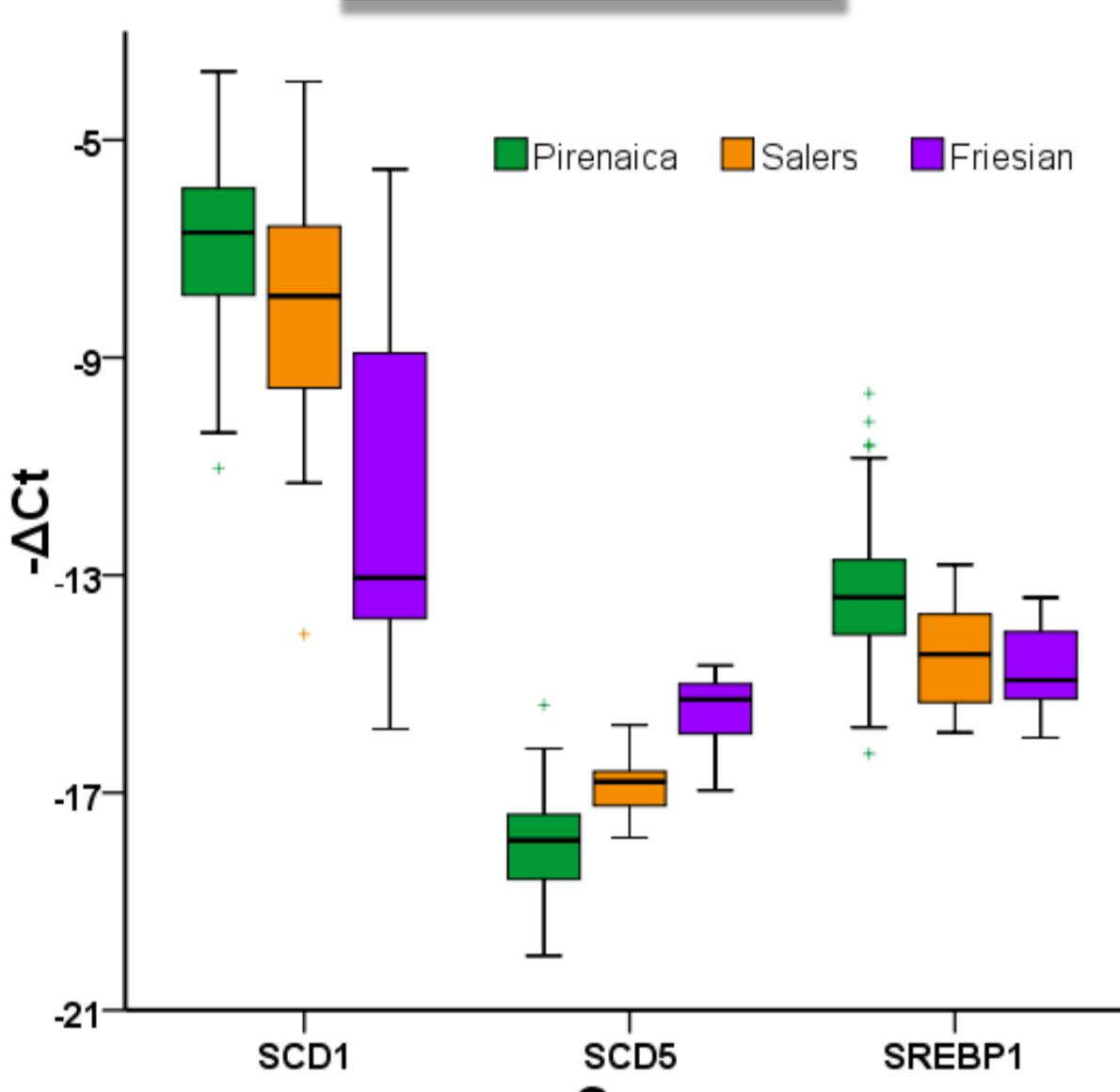
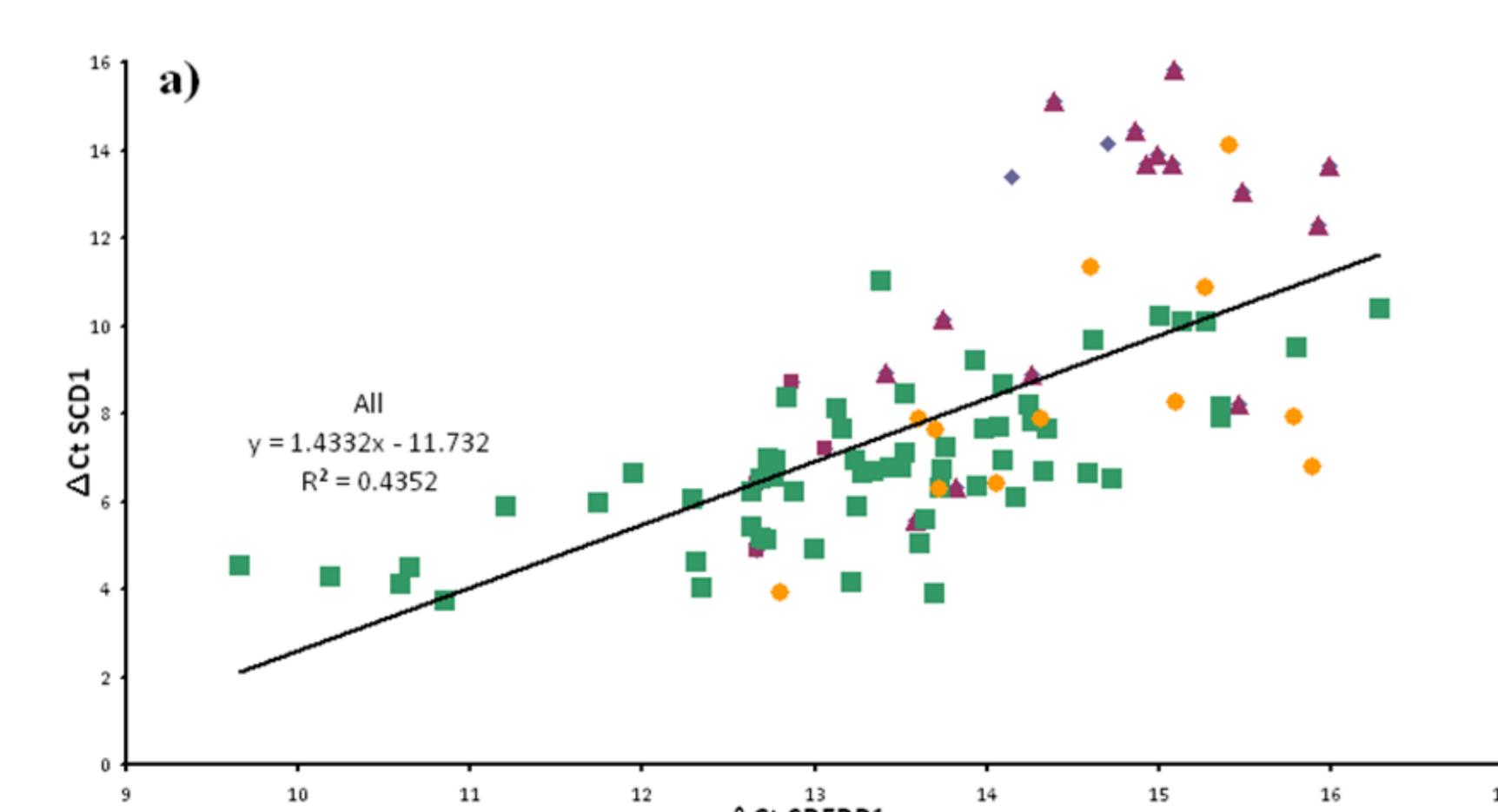


Figure 1. Relative expression levels of SCD1, SCD5 and SREBP1 mRNA of Pirenaica, Salers and Friesian cattle.

➤ Total sample correlation analysis showed that SREBP1 and SCD1 are positively correlated ( $P \leq 0.001$ ) (Fig. 2.a). Within each breed, however, correlation between SREBP1 and SCD1 was positive and highest for Pirenaica ( $P \leq 0.001$ ), a trend was observed for Salers ( $P \leq 0.1$ ) and it was not significant for Friesian cattle. This indicates that some other factors may act as regulators.



➤ The correlation between SREBP1 and SCD5 was not clear due to differences between breeds (Fig. 2.b).

➤ The general correlation between SCD1 and SCD5 are negatively correlated ( $P \leq 0.001$ ) (Fig. 2.c).

➤ In general, when SCD1 expression was positively correlated with an individual FA, SCD5 expression was negatively correlated and vice versa (Fig. 3).

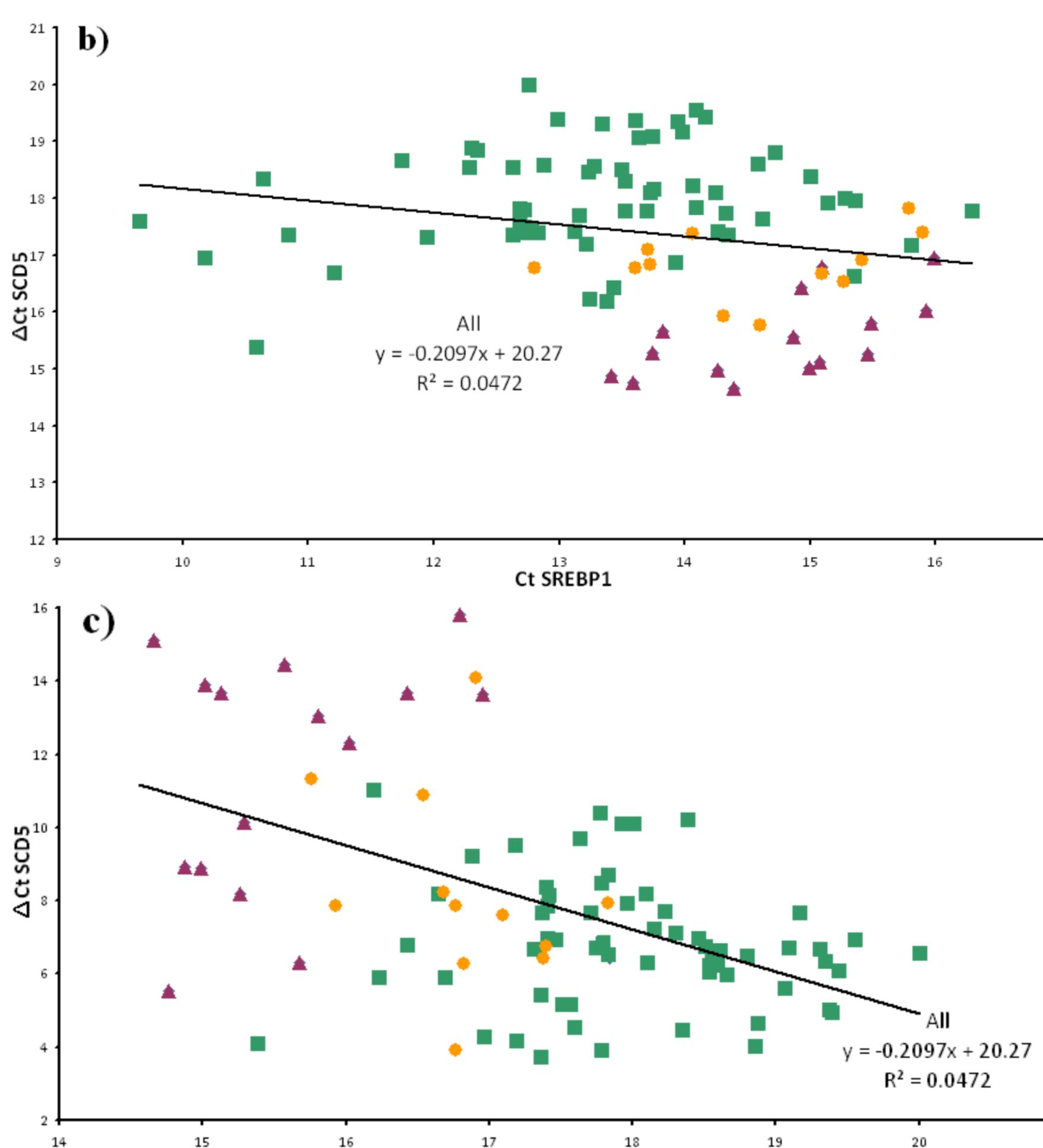


Figure 2. Correlation between gene expression in cattle breeds. a) Correlation between SREBP1 and SCD1 gene expression. b) Correlation between SREBP1 and SCD5 gene expression. c) Correlation between SCD1 and SCD5 gene expression.

## CONCLUSIONS

The gene expression of SREBP1 and SCD1 in Pirenaica were the highest ( $p < 0.05$ ) and also the correlation between SREBP1 and SCD1 expression. Moreover, cis-MUFA content in Pirenaica was significantly higher than in Friesian breed. Interestingly, the effect of SCD5 on FA profile of backfat tissue was in contrast to that of SCD1.

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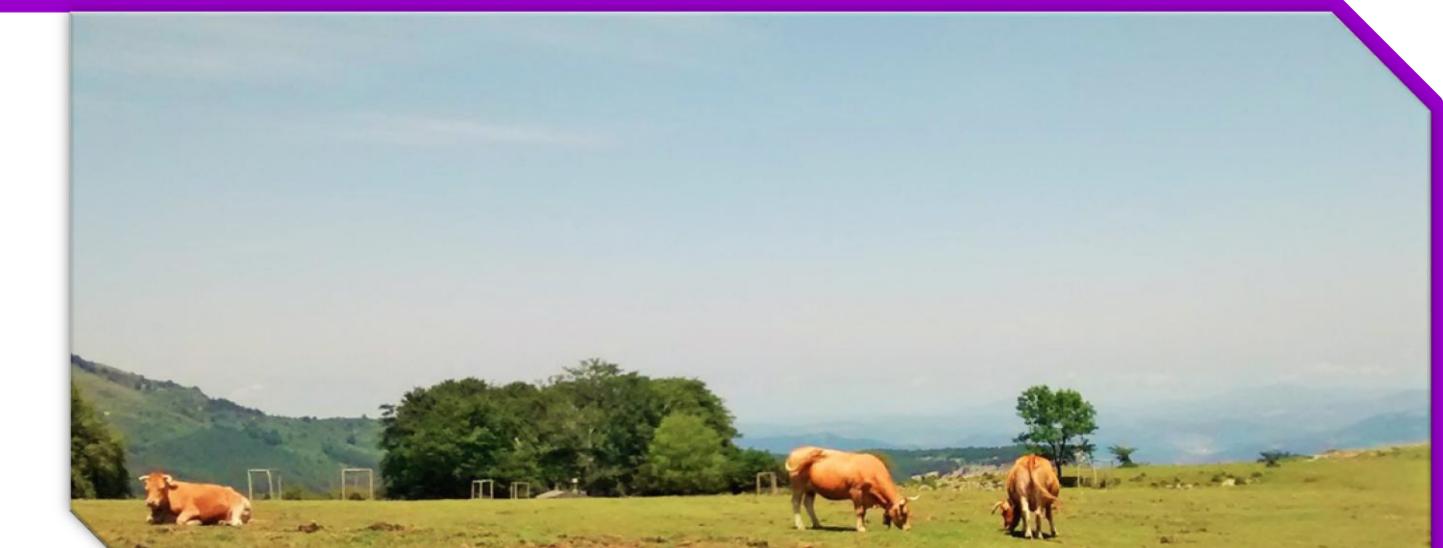
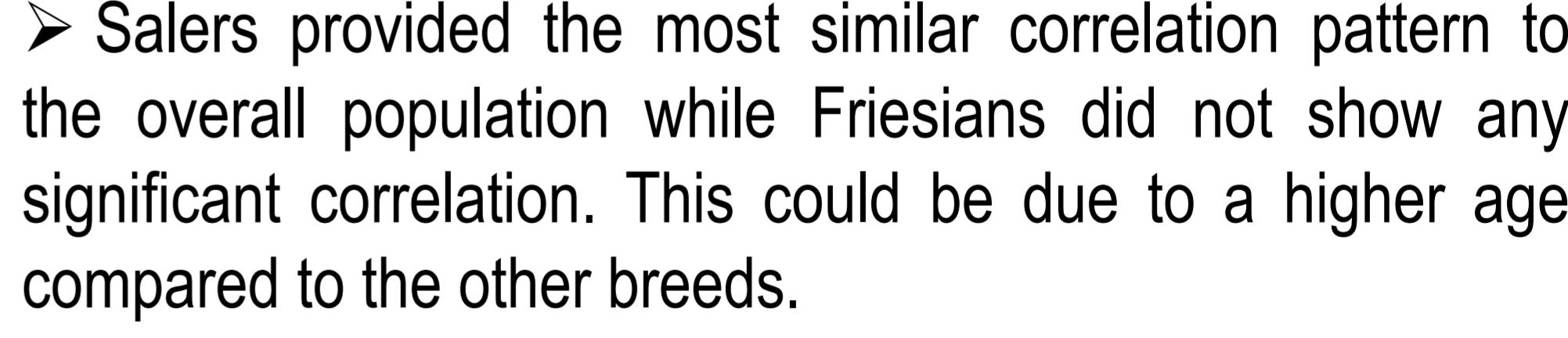


Figure 3. Correlations between expression level of SCD1 and SCD5 with 28 potentially related FAs fatty acids for overall population.



➤ Salers provided the most similar correlation pattern to the overall population while Friesians did not show any significant correlation. This could be due to a higher age compared to the other breeds.

➤ SCD1 expression was significantly higher in Pirenaica but similar cis-MUFA contents were found in Pirenaica and Salers ( $p > 0.05$ ) that could be associated to uncontrolled factors like feeding or potential higher expression of SCD5 in Salers breed as it was observed in Fig. 1.