Relationships between somatic cell count and milk yield in the Sarda dairy sheep breed

S. Salaris, S. Sechi, S. Casu and A. Carta

Research Unit: Genetics and Biotechnology, DIRPA-AGRIS Sardegna- Sassari, Italy

Introduction

In recent years there has been increasing emphasis on reducing milk somatic cell count (SCC) to improve milk quality in ruminants.

In dairy sheep:

- ***SCC in bulk milk*** has been used as an ***indicator*** of *hygiene*, *animal welfare* and *prevalence of mastitis*.

- ***SCC*** is often included in the ***parameters*** for determining ***milk price***

- ***SCC individual recording*** has been implemented for several European breeds:

Lacaune and Pyrenean breeds in France, Sarda in Italy and Manchega, Churra, and Latxa in Spain.

- ***SCC*** has been included as ***selection criterion*** only in few breeds

Introduction

In Sardinia, a specific part of the Rural Development Plans is aimed at improving animal welfare.

Bulk milk SCC is the main indicator for evaluating if the farmer may access to the economic subsidies.

Farmers involved in selection schemes are debating the inclusion of SCC as selection criterion.

Introduction

SCC is considered an indirect measure of subclinical mastitis

- relationships between **subclinical mastitis** and **milk yield** are well known
- relationships between **SCC** and **production traits** are controversial

It is crucial to assess the relationships between SCC and the production traits

- to show farmers the potential effects on production traits
- to assess the profitable economic weights of SCC in milk pricing.

In dairy sheep relationship between SCC and MY is often deduced **indirectly:**

infected ewes show a higher SCC and at the same time a lower milk yield

aim of this study

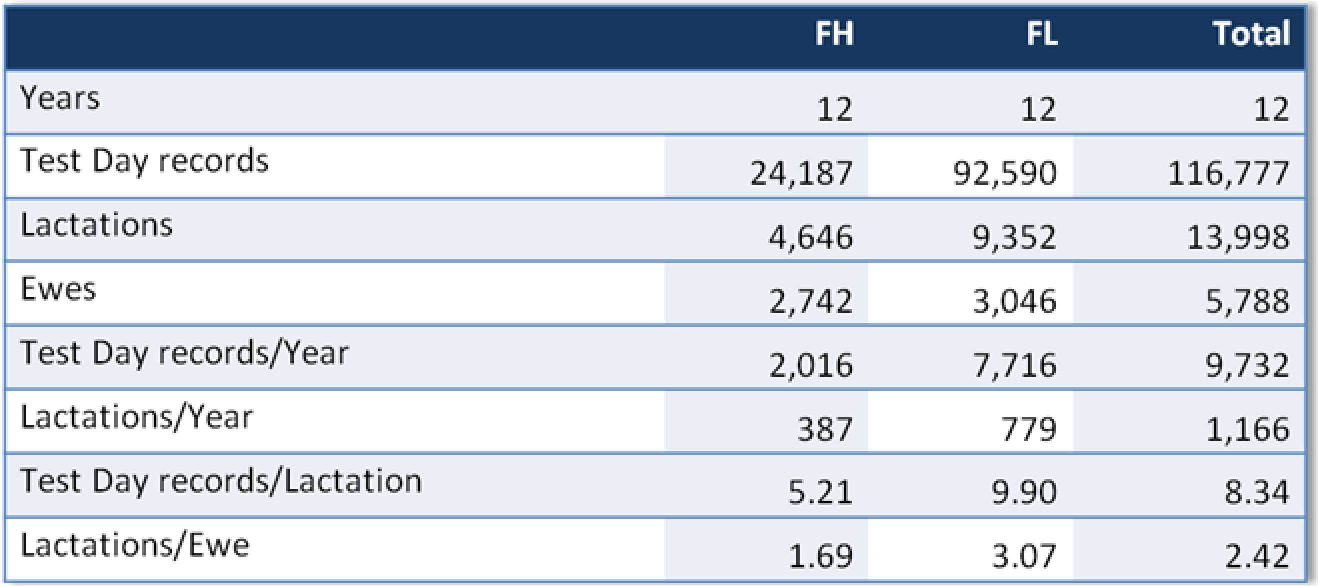
- to evaluate the **raw relationship between SCC and milk yield**
- to estimate the **genetic correlation** between SCC and milk yield in view of including SCC as selection criterion for mastitis resistance

Material and methods

From 2000 to 2011, test day (**TD**) records were collected from two flocks of AGRIS.

- **FH**: TD records were **monthly recorded**. In this flock **voluntary culling** based on milk yield and udder morphology was performed.
- **FL**: TD records were **fortnightly recorded** and each cohort was **simultaneously slaughtered** at the end of 4th lactation **without voluntary culling**.

Description of data



	FH	FL	Total
Years	12	12	12
Test Day records	24,187	92,590	116,777
Lactations	4,646	9,352	13,998
Ewes	2,742	3,046	5,788
Test Day records/Year	2,016	7,716	9,732
Lactations/Year	387	779	1,166
Test Day records/Lactation	5.21	9.90	8.34
Lactations/Ewe	1.69	3.07	2.42

Recorded traits

TD records (A4 method)	Lactation records (Fleishmann method)
milk yield (MYd),	milk yield (MY)
fat yield (FYd)	fat yield (FY)
protein yield (PYd)	protein yield (PY)
fat content (FCd) [1]	fat content (FC)[3]
protein content (PCd)[1]	protein content (PC)[3]
somatic cell count (SCCd)[1]	somatic cell count (LSCC)[3]
somatic cell score (SCSd)[2]	somatic cell score (LSCS)[2]

[1] FCd, PCd and SCCd were computed weighting for corresponding milk yields of the morning and afternoon milkings.

[2] SCSd and LSCS were log-transformed according to Ali and Shook (1980).

[3] FC, PC, and LSCC were computed as ratio of respective quantities with MY.

Material and methods

Lactations were considered performed by ewes with high probability to be *"infected"* when at least 2 SCCd were above 600 K or one SCCd was above 1,500 K.

(K= x 10^3 cells/ml)

TD data were split into two **classes of health status** (**HSC**):

- **"0"** if referred to lactations performed by ewes with a "*healthy*" udder
- **"1"** if referred to lactations performed by ewes with an "*infected*" udder

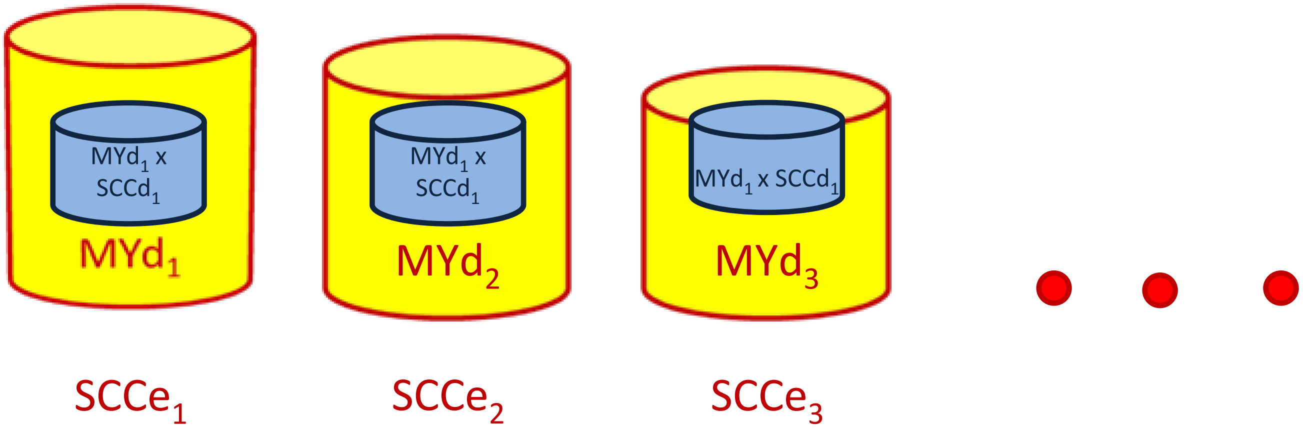
Descriptive statistics and correlations of somatic cells with production traits were calculated by flock and HSC

Dilution effect

the **expected SCCd** (**SCCe**) was calculated on the basis of the amount of somatic cells at the first TD as:

$SCCe_n = (MYd_1 \times SCCd_1)/MYd_n$ where subscripts indicate TD order

$SCSe_n = \log_2 (SCCe_n/100) + 3$



$MYd_1 \times SCCd_1$ was assumed to be the individual base level of somatic cells

SCSe trend with lactation stage is only affected by milk yield and measures the dilution effect.

Material and methods

- Correlation between **SCSe** and **MYd**

  is expected to measure the relationships caused by the decreasing of milk yield.

- **DCS** was the difference between **SCSd** and **SCSe**

  - $DSC_n = SCSd_n - SCSe_n$

  Is expected to measure the deviation of SCSd from that due to the dilution effect on the SCSd base level.

- **DMY** was the single TD milk yield deviation from the first TD milk yield

  - $DMY_n = MYd_n - MYd_1$

- Correlation between **DSC** and **DMY** was calculated by flock and HSC

  to estimate the relationship between deviations from the base levels of SCSd and MYd

(lactations with a first SCCd greater than 600 x K were excluded in order to avoid bias of including animals with an infected udder at beginning of lactation)

Genetic parameters and correlations between lactation milk yield and somatic cell score

were calculated by flock with the following bi-trait repeatability animal model:

$$y = YALS + APM + ML + A + PE + e$$

where

y: MY and LSCS,

$YALS$: the fixed effect of Year x Age x Lambing Season combination (7 levels)

APM: the fixed effect of Age x Parity x Lambing month combination (5 levels)

ML: the fixed effect of Milking Length class (14 levels)

A: the random genetic effect

PE: the random permanent environmental effect

e: the random residual effect.

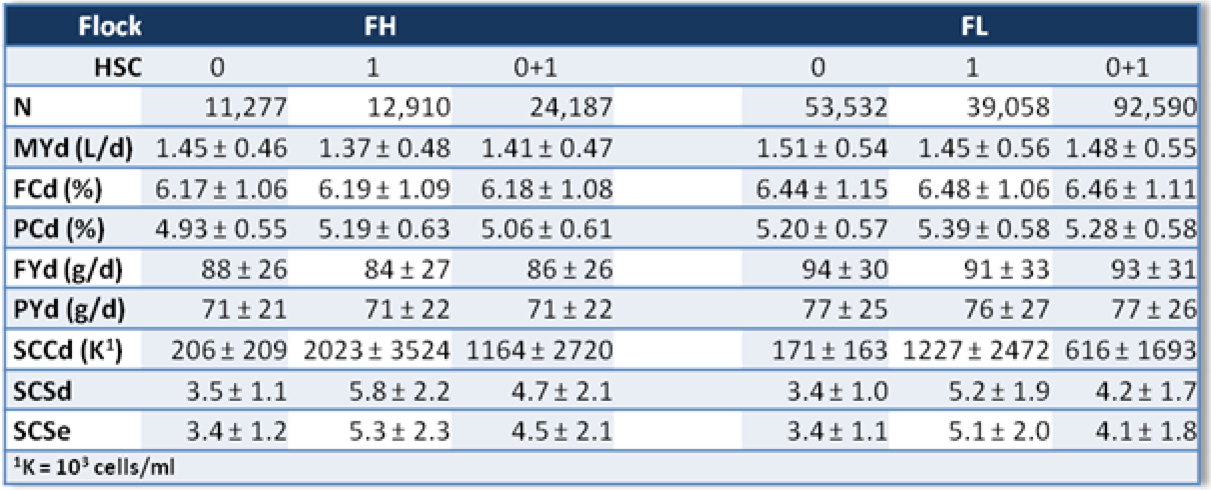
Known relationships until to grand-grandparents were considered in the pedigree file

(4835 and 4739 individuals for FH and FL).

Results and discussion

Descriptive statistics by flock (FH and FL) and health status class (HSC=0 “healthy”; HSC=1 “infected”)

TD records



Flock	FH			FL		
HSC	0	1	0+1	0	1	0+1
N	11,277	12,910	24,187	53,532	39,058	92,590
MYd (L/d)	1.45 ± 0.46	1.37 ± 0.48	1.41 ± 0.47	1.51 ± 0.54	1.45 ± 0.56	1.48 ± 0.55
FCd (%)	6.17 ± 1.06	6.19 ± 1.09	6.18 ± 1.08	6.44 ± 1.15	6.48 ± 1.06	6.46 ± 1.11
PCd (%)	4.93 ± 0.55	5.19 ± 0.63	5.06 ± 0.61	5.20 ± 0.57	5.39 ± 0.58	5.28 ± 0.58
FYd (g/d)	88 ± 26	84 ± 27	86 ± 26	94 ± 30	91 ± 33	93 ± 31
PYd (g/d)	71 ± 21	71 ± 22	71 ± 22	77 ± 25	76 ± 27	77 ± 26
SCCd (K[1])	206 ± 209	2023 ± 3524	1164 ± 2720	171 ± 163	1227 ± 2472	616 ± 1693
SCSd	3.5 ± 1.1	5.8 ± 2.2	4.7 ± 2.1	3.4 ± 1.0	5.2 ± 1.9	4.2 ± 1.7
SCSe	3.4 ± 1.2	5.3 ± 2.3	4.5 ± 2.1	3.4 ± 1.1	5.1 ± 2.0	4.1 ± 1.8

[1]K = 10^3 cells/ml

Lactation records

	FH			FL		
HSC	0	1	0+1	0	1	0+1
N	2203	2443	4646	5545	3807	9352
MY (L)	221 ± 56	220 ± 60	221 ± 58	255 ± 70	259 ± 69	257 ± 69
FC (%)	6.04 ± 0.62	6.09 ± 0.68	6.07 ± 0.65	6.25 ± 0.73	6.32 ± 0.71	6.27 ± 0.72
PC (%)	4.9 ± 0.41	5.16 ± 0.48	5.04 ± 0.47	5.09 ± 0.36	5.28 ± 0.36	5.16 ± 0.37
FY (Kg)	13.4 ± 3.8	13.4 ± 3.9	13.4 ± 3.8	16.0 ± 4.8	16.3 ± 4.7	16.1 ± 4.7
PY (Kg)	10.8 ± 3.0	11.3 ± 3.2	11.1 ± 3.1	13.0 ± 3.8	13.7 ± 3.7	13.3 ± 3.8
LSCC (K)	206 ± 117	2096 ± 2295	1200 ± 1915	165 ± 83	1177 ± 1308	577 ± 974
LSCS	3.8 ± 0.8	6.8 ± 1.3	5.4 ± 1.8	3.6 ± 0.7	6.0 ± 1.2	4.6 ± 1.5
ML (day)	153 ± 30	160 ± 32	157 ± 31	173 ± 31	183 ± 30	177 ± 31

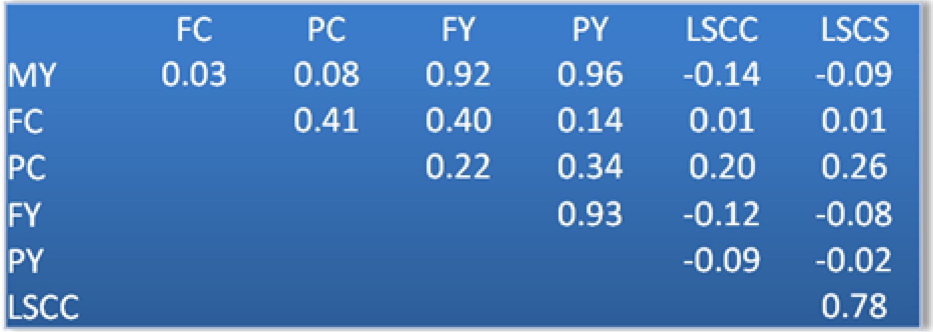
[1]K = 10^3 cells/ml

- Production traits were similar but slightly higher in FL than in FH
- SCCd and LSCC in FH were approximately twice than in FL
- The percentage of lactations included in HSC 0 were 47.4% in FH and 59.3% in FL

The different percentage of infected animals does not seem sufficient to explain the difference in SCC suggesting that other management factors are involved.

Results and discussion

Raw correlation between lactation production and somatic cells traits

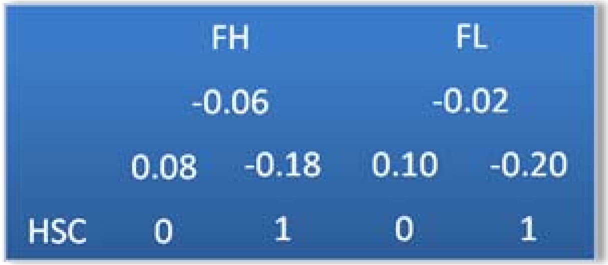


	FC	PC	FY	PY	LSCC	LSCS
MY	0.03	0.08	0.92	0.96	-0.14	-0.09
FC		0.41	0.40	0.14	0.01	0.01
PC			0.22	0.34	0.20	0.26
FY				0.93	-0.12	-0.08
PY					-0.09	-0.02
LSCC						0.78

The overall correlation between LSCS and MY were close to zero

Correlation between MY and LSCS by flock (FH; FL) and health status class

(HSC=0 “healthy”; HSC=1 “infected”)

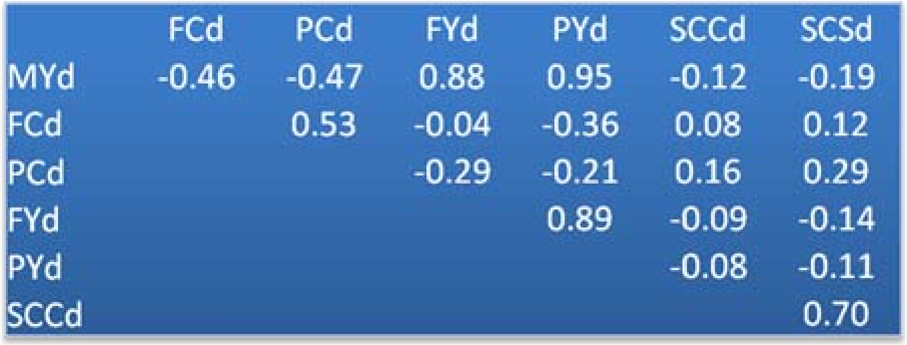


	FH		FL	
	-0.06		-0.02	
	0.08	-0.18	0.10	-0.20
HSC	0	1	0	1

These results indicate that a moderate negative relationship between lactation MY and LSCS is detected only in ewes with a higher probability of having an “infected” udder.

Results and discussion

Raw correlation between TD production and somatic cells traits

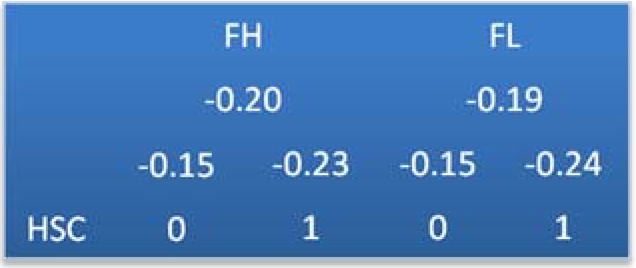


	FCd	PCd	FYd	PYd	SCCd	SCSd
MYd	-0.46	-0.47	0.88	0.95	-0.12	-0.19
FCd		0.53	-0.04	-0.36	0.08	0.12
PCd			-0.29	-0.21	0.16	0.29
FYd				0.89	-0.09	-0.14
PYd					-0.08	-0.11
SCCd						0.70

The overall correlation between SCSd and MYd was moderately negative

Correlation between MYd and SCSd by flock (FH; FL) and health status class

(HSC=0 “healthy”; HSC=1 “infected”)



	FH		FL	
	-0.20		-0.19	
	-0.15	-0.23	-0.15	-0.24
HSC	0	1	0	1

The relationships were generally higher in the TD analysis than lactation one, suggesting a potential impact of the dilution effect.

Results and discussion

Some authors (Green et al., 2006; de los Campos et al., 2009; Koop et al., 2010) studied the effect of dilution effect, i.e. *low milk yield corresponds to higher percentages either for fat and protein or somatic cells, in cattle and goat milk.*

This is a crucial point for the farmer which may be induced to incorrectly conclude that there is a negative effect of SCC on milk yield and vice versa a positive one on contents.

Correlation between MYd and SCSe by flock (FH; FL) and health status class (HSC=0 "healthy"; HSC=1 "infected")

	FH		FL	
	-0.25		-0.33	
	-0.29	-0.23	-0.38	-0.33
HSC	0	1	0	1

This result shows that the actual relationship between milk yield and somatic cells is lower than that due to mere effect of dilution. The explanation is that at the end of lactation the amount of somatic cells is lower than the initial one. This difference is more evident in "healthy" ewes.

Results and discussion

DSC ($DSC_n = SCSd_n - SCSe_n$) was on average 0.79±1.73 in FH and 0.27±1.43 in FL

DMY ($DMY_n = MYd_n - MYd_1$) was on avergae -0.22±0.47 in FH and -0.45±0.55 in FL .

Correlation between **DMY** and **DSC** by flock (FH; FL) and health status class

(HSC=0 “healthy”; HSC=1 “infected”)

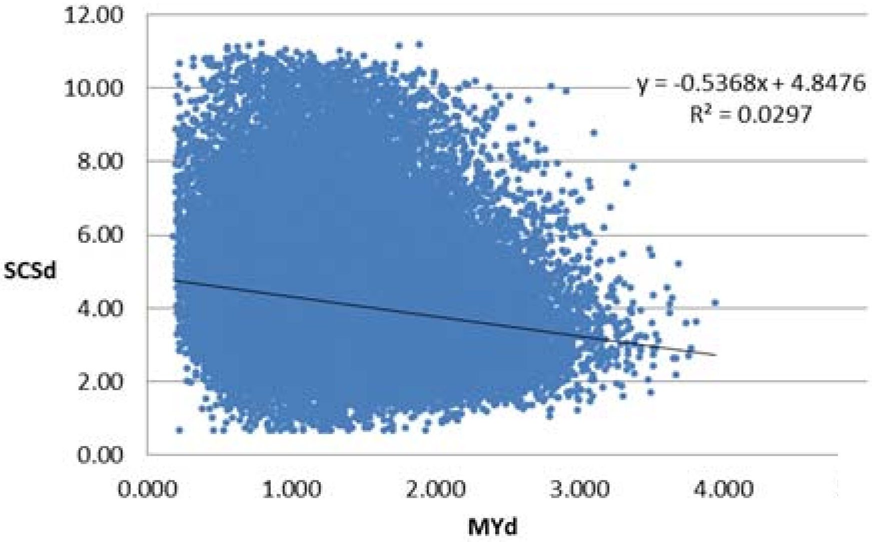
	FH		FL	
	-0.04		0.11	
	0.13	-0.09	0.26	0.03
HSC	0	1	0	1

The overall correlation between DSC and DMY was close to zero in both flocks and this result showed that the negative correlation found between SCSd and MYd is likely to be affected by dilution effect.

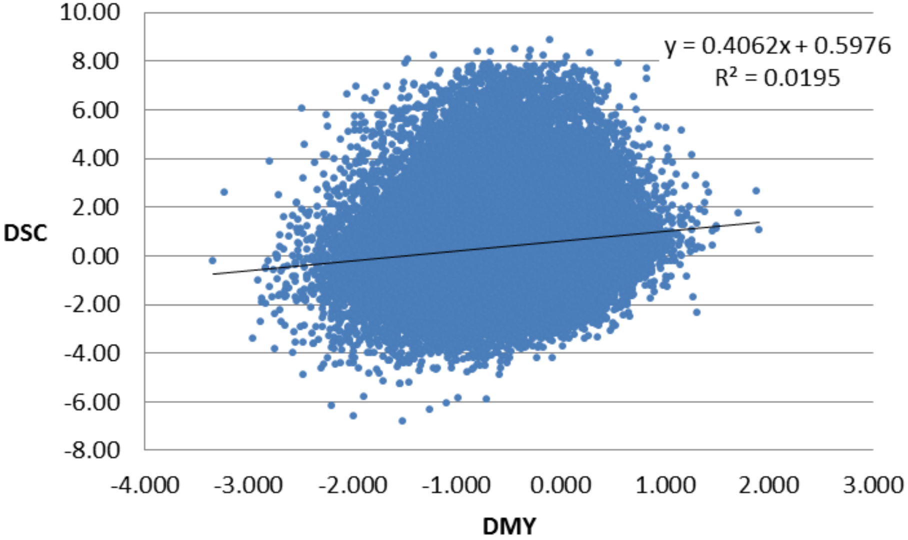
These results indicate that the detrimental effect of SCSd on milk yield is negligible and it exists only in ewes with a high probability to be “infected”. Moreover this result is not repeatable between flocks. On the contrary in “healthy” animals the relationships is moderately positive.

Results and discussion

Relationship between SCSd and MYd



Relationship between DSC and DMY



Results and discussion

Heritability (diagonal), genetic (above diagonal) and phenotypic correlation (below diagonal) of milk yield (MY) and somatic cell score (LSCS) by flock (FH and FL).

Flock	FH		FL	
	MY	LSCS	MY	LSCS
MY	0.37±0.04	0.18±0.14	0.47±0.03	-0.06±0.08
LSCS	-0.15±0.02	0.12±0.03	-0.18±0.02	0.22±0.03

The parameter estimates are followed by their approximate standard errors.

- Both MY and LSCS heritabilities are in agreement with estimates in other breeds.
- Higher heritabilities estimated in FL are probably due to the better accuracy of measures and consistency of data.
- The genetic correlations were low, discordant between two flocks and with high standard errors.
- These findings support the hypothesis that the true genetic correlations between LSCS and MY are around zero.

Results and discussion

Heritability (diagonal), genetic (above diagonal) and phenotypic correlation (below diagonal) of milk yield (MY) and somatic cell score (LSCS) by flock (FH and FL).

Flock	FH		FL	
	MY	LSCS	MY	LSCS
MY	0.37±0.04	0.18±0.14	0.47±0.03	-0.06±0.08
LSCS	-0.15±0.02	0.12±0.03	-0.18±0.02	0.22±0.03

The parameter estimates are followed by their approximate standard errors.

Different sign in the two flocks may be interpreted in the same way of differences found in literature between breeds.

In **FH** the **genetic correlation** was **unfavorable** and in agreement with values founded in dairy cow and in Lacaune breed

In **FL** the **genetic correlation** was **favorable** and in agreement with values estimated in Spanish breeds

The **different behavior** of the two flocks **suggests that genetic parameters estimate** for SCS at population level **should be checked by flock** or at least **flock class** accounting different average SCS levels.

Conclusion

- The raw relationships between somatic cell count and milk yield, even if negligible, are **negative only in animals with higher probability to have an "*infected*" udder**.

- In any case the dilution effect should be considered when TD yields are analyzed.

- The level of heritabilities of LSCS are in the range of literature and genetic correlations between LSCS and milk yield are low and different in sign in the two analyzed flocks.

Conclusion

The overall results combined with the **asymptomatic nature of subclinical mastitis** makes particularly difficult to convince farmers to select against SCC mainly in absence of an adequate payment system.

In this situation the implementation of **selection for udder morphology**, that was shown to be favorably related to machine milkability and udder health (Casu et al., 2010), may be an efficient and already available way for **genetically improving udder health**