Accuracy of genomic predictions for sheep milk fatty acid composition

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Introduction [1]

- Italy produces about 4.1% of the world's sheep milk (**FAOSTAT, 2016**))
- The Italian dairy sheep stock: 5,500,000 heads (**FAO, 2014**), 60% of which are of Sarda breed

Introduction [2]

- The average gross milk production of the Sarda dairy industry is about 500,000 tonnes per year

- Almost all milk is destined to cheese production Pecorino Romano (Reg. CE n.1107/96), Pecorino Sardo (Reg. CE n.1263/96) Fiore Sardo (Reg. CE n.1107/96)

- The breeding program of the Sarda breed involves 220,268 ewes (ICAR, 2014)

Introduction [3]

- Current breeding goals are lactation milk yield, udder morphology and scrapie resistance
- interest in milk quality, especially on novel phenotypes related to **nutritional characteristics**, as milk fatty acid (**FA**) composition
- Milk FA genetic variability has been estimated in cow and Sheep
- Problem of high cost of milk phenotyping in small ruminants
- Difficult routine measure of MILK FA composition

Introduction [4]

Difficult routine measure of MILK FA composition

❑ Possible options

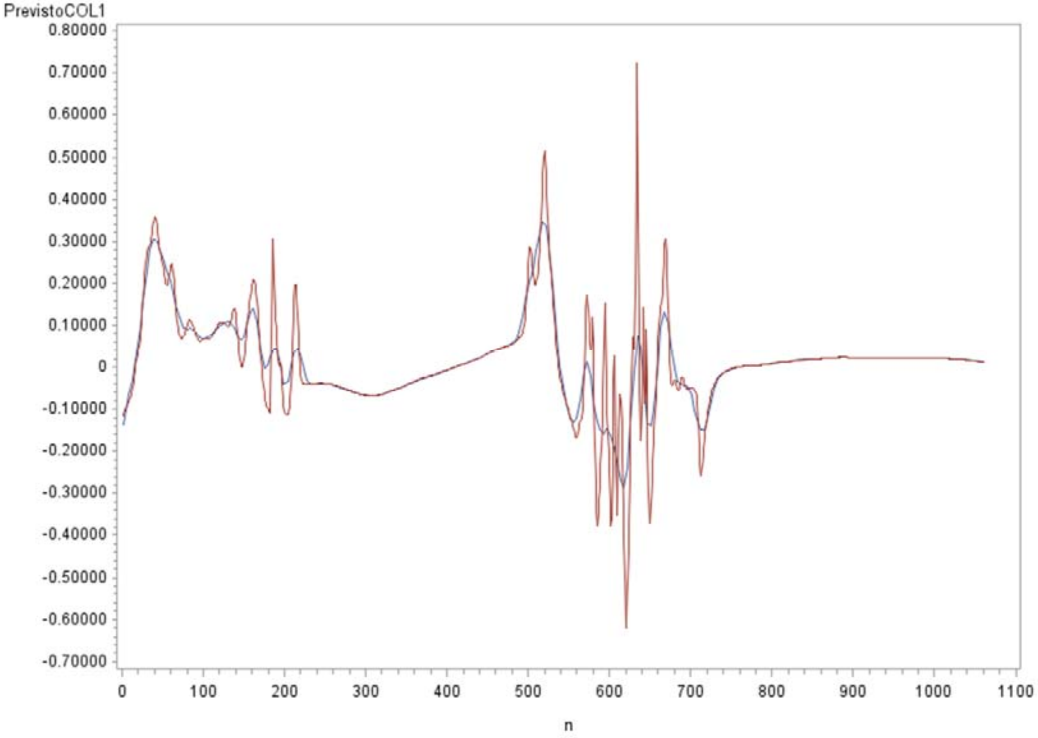
✓ Use of phenotypes easy to measure routinely

✓ Genomic selection

Introduction [4]

Easy to measure phenotype

MILK FTIR spectra



Aim of the work

- ✓ **Evaluation of accuracy of genetic merit prediction in traditional selection or GS for milk FA profile in sheep**

- ✓ **Comparison between GC-measured and FTIR predicted FA phenotypes**

Data

- ✓ 769 Sarda ewes, 48 flocks located in Sardinia
- ✓ Individual milk samples between April and July 2014
- ✓ FA composition by Gas Cromatography (**FA_GC**)
- ✓ Analysis of milk samples with MilkoScan-FT6000 and storage of FTIR spectra
- ✓ PLS prediction of milk FA composition from FTIR spectra (**FA_FTIR**)

Partial Least Squares prediction

- ✓ 889 ewes
- ✓ FTIR spectra derived for MiloScanFT6000
- ✓ 700 animals of training (**FA_GC and FTIR spectra**)
- ✓ 189 of prediction (**FA_FTIR**)
- ✓ 100 replicates

Genotyping & QC

- Genomic DNA extracted from nasal swab
- Animals genotyped with the Illumina Infinium Ovine SNP50 v1 BeadChip
- Animal call rate>95%
- SNP call rate 97.5%
- MAF 1%
- HW P<0.01
- 44,619

Genetic merit prediction

- ✓ 669 training animals (born<2012)
  - SNP & Phenotype

- ✓ 100 prediction animals (born >2011)
  - SNP

TRADITIONAL

- ✓ Prediction of EBV using BLUP methodology with **A** matrix (5089 animals)

GENOMIC SELECTION

- ✓ Prediction of GEBV with a single step approach with **H** matrix

Model

Data (**FA_GC** or **FA_FTIR**) were analysed with the following mixed linear model

$$\mathbf{y = \mu + FTD + PAR + DIM + LM + ALT + a + e}$$

Prediction accuracy was calculated from the inverse of the LHS according to Misztal et al. (2013)

Aireml90 Blupf90 (Legarra et al., 2010)

FA_GC composition

FA	Mean	SD	Min	Max	CV
C4:0	2.67	0.37	1.52	4.05	13.83
C6:0	1.75	0.37	0.46	2.65	21.02
C8:0	1.60	0.46	0.28	2.84	28.46
C10:0	5.52	1.76	0.87	10.18	31.86
C12:0	3.48	1.00	1.08	8.15	28.78
C14:0	10.81	1.54	5.28	18.42	14.23
c9-C14:1	0.20	0.08	0.04	0.68	42.43
C16:0	25.95	2.97	18.51	36.69	11.43
c9-C16:1	0.89	0.26	0.41	2.30	29.01
C18:0	10.29	2.51	1.37	21.00	24.38
t11-C18:1	2.06	1.03	0.46	5.77	50.21
c9-C18:1	17.23	3.64	5.37	34.75	21.11
C18:2n-6	2.09	0.51	0.92	4.32	24.33
C18:3n-3	0.89	0.50	0.20	3.35	55.76
c9,t11-C18:2	1.03	0.47	0.28	3.16	45.52

RESULTS: FA composition

FA group	Mean	SD	Min	Max	CV
SCFA	11.64	2.66	3.31	18.65	22.84
MCFA	47.19	4.09	33.54	70.35	8.67
LCFA	41.17	5.31	15.51	63.14	12.90
SFA	67.63	3.92	49.43	82.97	5.80
MUFA	25.90	3.64	11.95	45.26	14.04
PUFA	6.46	1.43	2.79	12.24	22.16
TFA	4.55	1.50	1.75	13.68	32.95
OBCFA	4.78	0.61	2.72	6.94	12.78
de novo	23.46	4.70	8.06	39.91	20.05

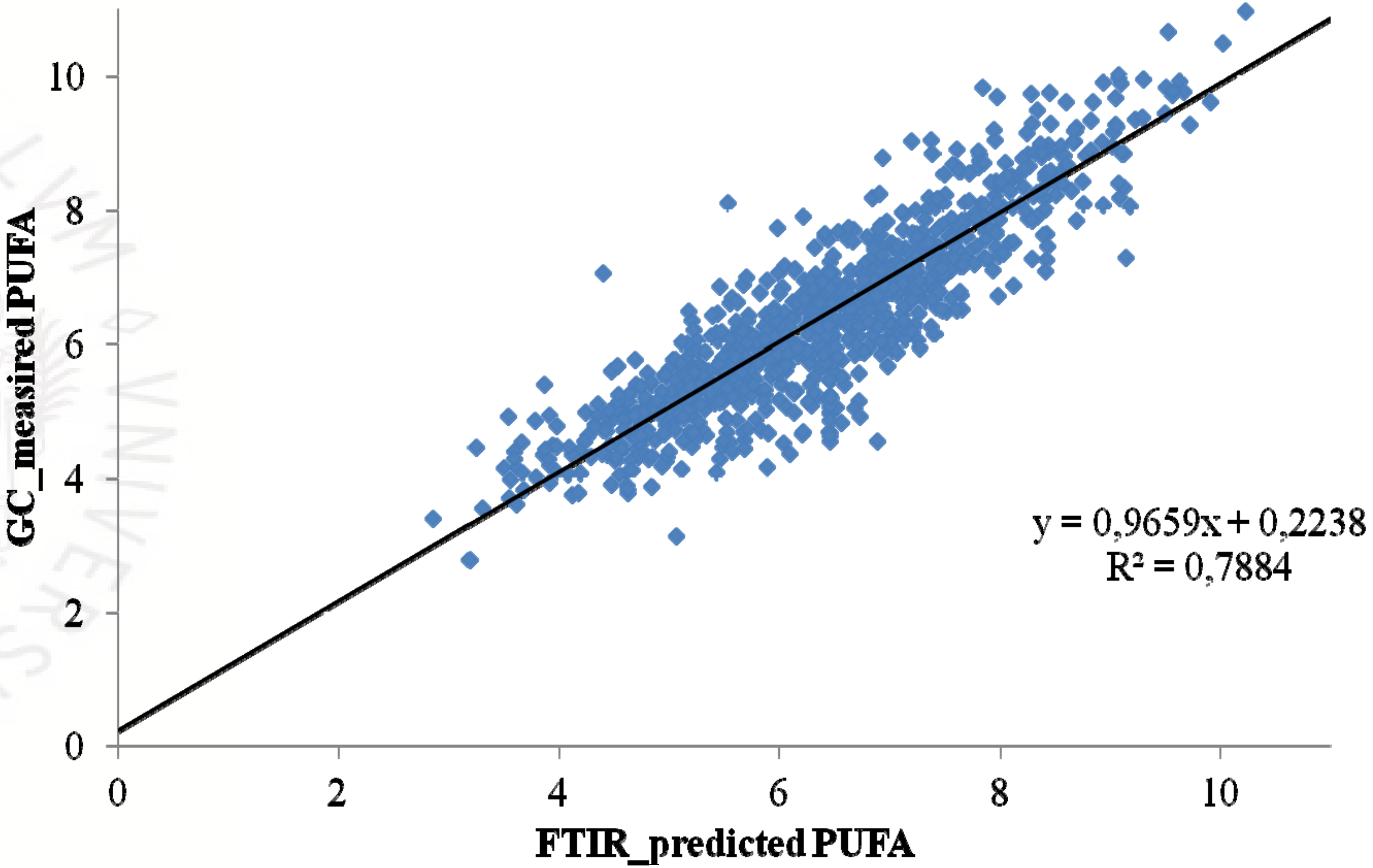
PLS goodness of prediction

	R^2		$b_{GC,FTIR}$	
Trait	Mean	Sd	mean	Sd
C4:0	0.78	0.03	0.96	0.04
C6:0	0.85	0.02	0.98	0.03
C8:0	0.87	0.02	0.98	0.02
C10:0	0.89	0.02	0.98	0.02
C12:0	0.86	0.02	0.98	0.04
C14:0	0.78	0.03	0.96	0.04
C18:0	0.72	0.02	0.94	0.04
t11-C18:1	0.74	0.02	0.96	0.05
c9-C18:1	0.83	0.02	0.97	0.03
C18:2n-6	0.52	0.04	0.88	0.07
C18:3n-3	0.71	0.03	0.94	0.06
c9,t11-C18:2	0.69	0.03	0.94	0.06

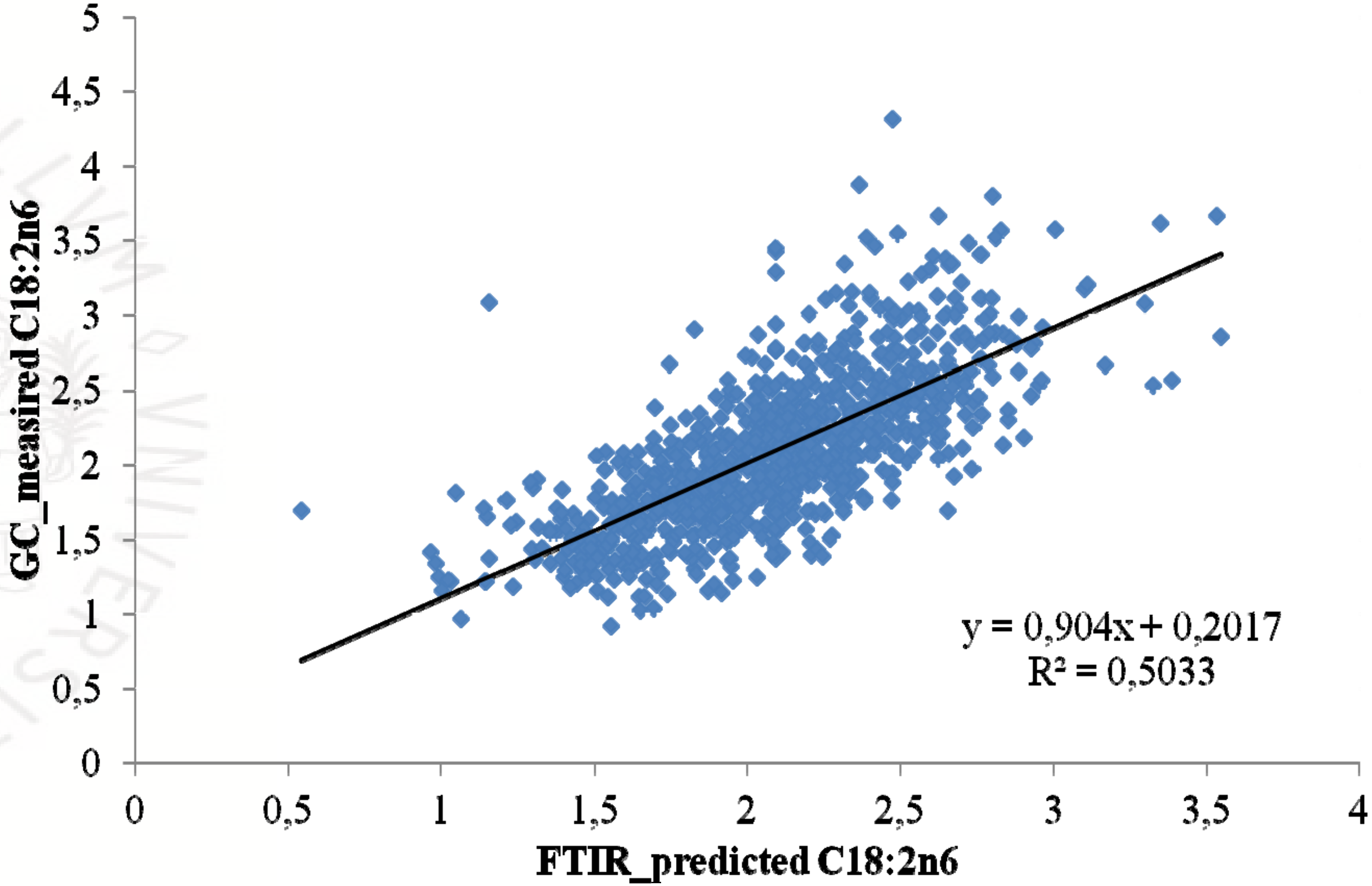
PLS goodness of prediction

	R^2		$b_{GC,FTIR}$	
Trait	Mean	Sd	mean	Sd
MUFA	0.79	0.03	0.97	0.04
PUFA	0.81	0.02	0.96	0.04
TFA	0.78	0.03	0.98	0.06
de novo	0.89	0.02	0.99	0.02
n3/n6	0.89	0.02	0.99	0.02

Prediction accuracy for PUFA



Prediction accuracy for C18:2n6



PLS predictions

✓Moderate to high goodness of prediction

✓Partially in agreement with previous reports in sheep

✓Studies differ in sample size, sampling frequency, statistical model, precorrection

✓Moderate to low r^2 for FA related to human health

Genetic and genomic prediction accuracy

	TR (n=669)[1]			
	BLUP		ssGBLUP	
Trait	GC	FTIR	GC	FTIR
C4:0	0.59	0.66	0.66	0.78
C6:0	0.33	0.43	0.60	0.68
C8:0	0.52	0.42	0.61	0.66
C10:0	0.56	0.49	0.60	0.62
C12:0	0.57	0.55	0.56	0.55
C18:0	0.65	0.57	0.53	0.54
C18:1t11	0.70	0.60	0.42	0.41
C18:1c9	0.58	0.26	0.62	0.50
C18:2ω6	0.11	n.a.	0.26	0.11
C18:3ω3	0.11	0.24	0.22	0.39
CLAc9t11	0.60	0.58	0.40	0.41
MUFA	0.35	n.a.	0.57	0.48
PUFA	0.36	0.56	0.37	0.50
ω6:ω3	0.73	0.46	0.54	0.50
TFAnoVA	0.49	0.48	0.47	0.58
Denovo	0.46	0.43	0.55	0.56

Genetic merit prediction accuracy

	VA (n=100)			
	BLUP		ssGBLUP	
Trait	GC	FTIR	GC	FTIR
C4:0	0.21	0.23	0.31	0.36
C6:0	0.12	0.15	0.27	0.31
C8:0	0.18	0.15	0.27	0.30
C10:0	0.19	0.17	0.27	0.28
C12:0	0.20	0.19	0.25	0.25
C18:0	0.22	0.20	0.24	0.24
C18:1t11	0.23	0.20	0.19	0.19
C18:1c9	0.20	0.09	0.27	0.22
C18:2ω6	0.04	n.a.	0.14	0.14
C18:3ω3	0.04	0.09	0.12	0.18
CLAc9t11	0.20	0.20	0.19	0.19
MUFA	0.12	n.a.	0.26	0.22
PUFA	0.13	0.19	0.18	0.22
ω6:ω3	0.23	0.16	0.24	0.22
TFAnoVA	0.17	0.17	0.21	0.26
Denovo	0.16	0.15	0.25	0.25

Some considerations

- ✓Low prediction accuracies for validation animals
- ✓Sample size, n. of records, genetic background of the trait
- ✓Comparable with results retrieved in the literature for FA composition in beef cattle

Some considerations

✓Similar values using either FA_GC or FA_FTIR

✓GS single step provided better results in comparison to traditional selection

✓The combined use of easy to measure phenotypes and GS may open interesting perspectives for the genetic improvement of FA composition in sheep

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