Genetic correlations between measures of milk coagulation properties and their predictions by mid-infrared spectrometry

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Introduction

- Milk coagulation properties (MCP) play an important role in cheese production
- In Italy almost 73% of milk is used for cheese making (Ismea, 2002)
- Exploitable additive genetic variation exist for MCP (Ikonen et al., 1997, 1999; Cassandro et al., 2008)
- Genetic improvement of MCP could be an effective way to enhance the efficiency of cheese production

Introduction

- Assessment of MCP is difficult to be carried out routinely on large scale using standard method (e.g. computerized renneting meter, CRM)
- MIR (mid-infrared spectrometry) has been proposed as prediction tool of MCP at the population level but MCP prediction of phenotype is not very accurate (De Marchi et al., 2008)
- Might MIR be a useful indirect breeding goal for the improvement of MCP?

Aims

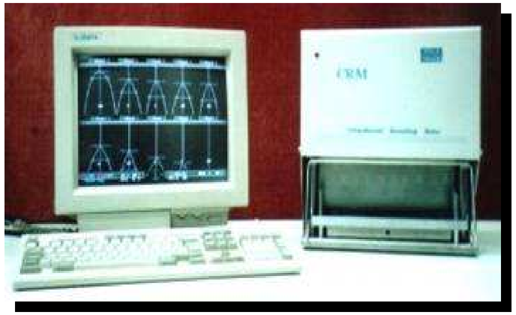
- Predict MCP of individual milk samples of Italian Brown Swiss breed using MIR
- Infer (co)variance components for MCP measured by CRM (mMCP) and predicted by MIR (pMCP)

Data

Data collection

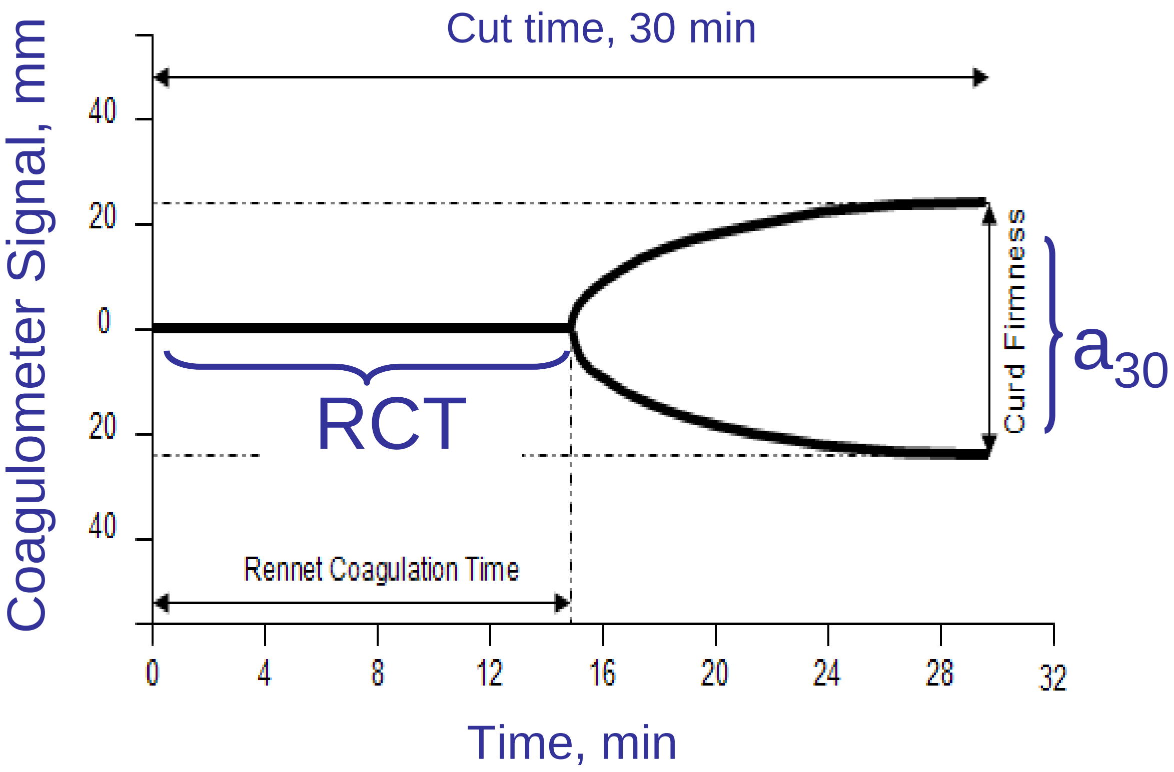
- From June 2006 to July 2007
- 30 herds located in Northern Italy
- 1,061 individual milk samples (Italian Brown Swiss cows) collected during morning milking
- Progeny of 50 sires (3 – 64 daughters)

Data



Computerized Renneting Meter
(CRM)

Milk-coagulation meter



Computerized Renneting Meter (CRM)

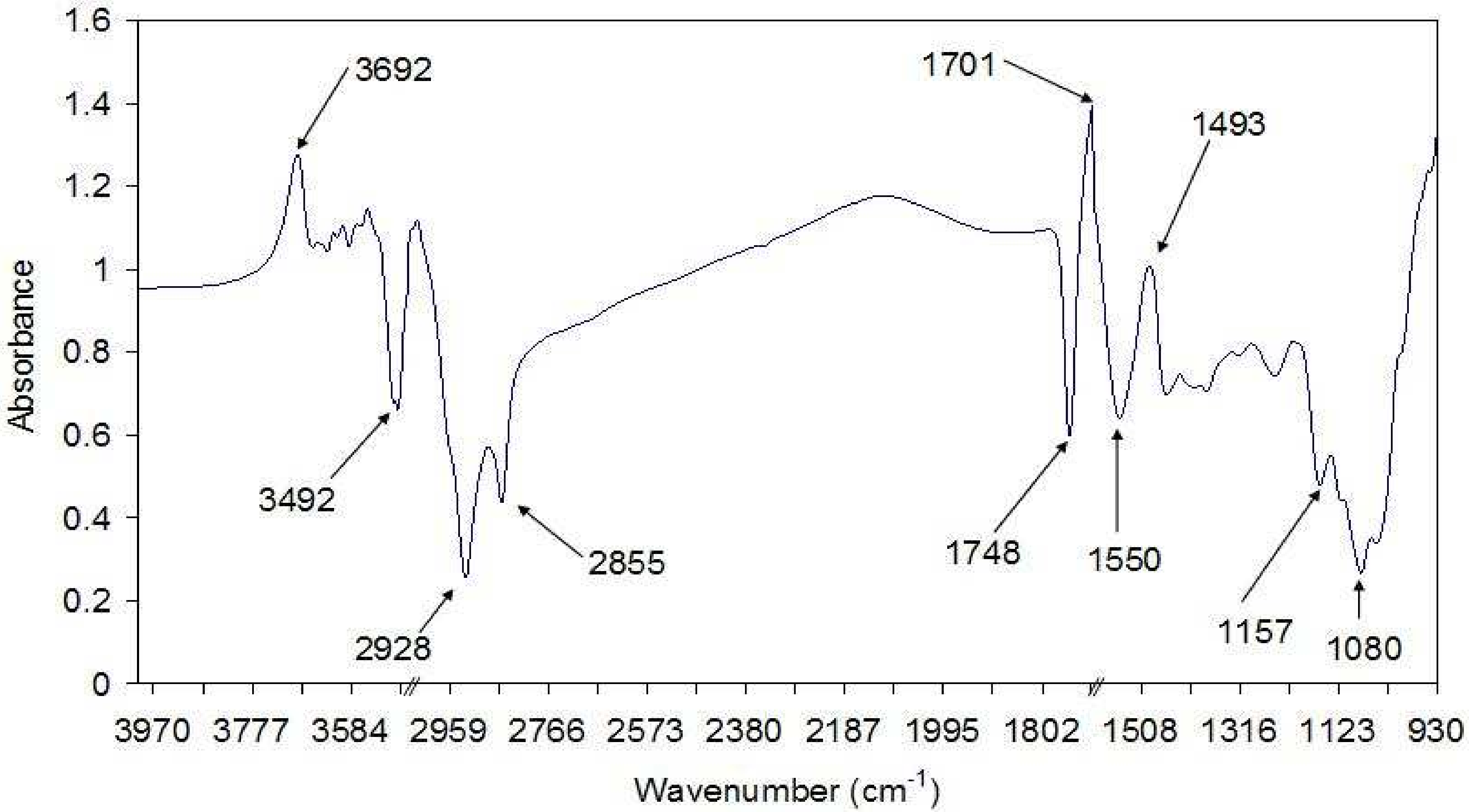
Rennet coagulation time (RCT, min) and curd firmness (a_{30}, mm) (Ikonen et al., 1999; Cassandro et al., 2008)

Mid-infrared spectra acquisition

- MIR spectra were collected over the spectral range of 4,000 to 900 cm^{-1} using a Milko-Scan FT120

- 4 calibration subsets (training set) were defined to estimate prediction equations which were used for the prediction of MCP on the 4 validation sets (test set)

Mid-infrared spectra acquisition



Example of algorithm unprocessed MIR spectra for milk

Statistical analysis/ 1

The reliability of the predictive models were determined using:

- Root Mean Square Error of Calibration (**RMSE**)
- Correlation coefficient (**r**)
- Range Error Ratio (**RER**)
  - RER < 3 little practical utility
  - 3 < RER < 10 limited to good practical utility
  - RER > 10 high utility value

(Williams, 1987; Hubert et al., 2003; Downey et al., 2005)

Statistical analysis/ 2

Bayesian bivariate mixed model

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{c} + \mathbf{Z}_2\mathbf{a} + \mathbf{e}$$

where:

- $\mathbf{y}$ vector of **predicted** and **measured milk coagulation properties**
- $\boldsymbol{\beta}$ vector of non genetic effects (DIM: 10 classes, parity: 3 classes)
- $\mathbf{c}$ vector of herd effects (30 classes) $\mathbf{c} \sim N(\mathbf{0}, \mathbf{P} \otimes \mathbf{I})$
- $\mathbf{a}$ vector of animal additive genetic effects $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G}_0 \otimes \mathbf{A})$
- $\mathbf{e}$ vector of residual effects $\mathbf{e} \sim N(\mathbf{0}, \mathbf{R}_0 \otimes \mathbf{I})$

Convergence assessed by inspection of trace plot

After burn-in (100,000) the number of the samples were 2,000,000

Results

Descriptive statistics

Trait	Mean	CV (%)	Min	Max
RCT, min	15.0	27	2.0	29.3
a_{30}, mm	41.7	21	6	64.0
Milk Yield, kg/d	28.6	28	7.4	68.0
Days in milk, d	202	62	6	597
Milk fat, %	3.98	19	0.9	6.9
Milk protein, %	3.72	10	2.7	5.4
Casein, %	2.88	10	1.9	4.2
SCS	2.4	90	-4.5	8.7
pH	6.7	2	3.6	7.2
Acidity, SH°/50 ml	3.2	13	0.8	4.8

RCT=rennet coagulation time (min); $\mathbf{a_{30}}$ = curd firmness (mm);

Prediction models

	Training set					
Parameter	N	Mean	CV	r	RMSE	RER
Subset 1	171					
- RCT		15.1	27	0.78	2.27	7.65
- a_{30}		41.9	21	0.70	6.24	5.60
Subset 2	170					
- RCT					2.63	5.37
- a_{30}					5.72	6.75
Subset 3						
- RCT		14.8	26	0.83	2.15	9.81
- a_{30}		41.8	20	0.68	6.06	7.00
Subset 4	171					
- RCT		15.3	28	0.80	2.53	7.81
- a_{30}		41.5	22	0.70	6.58	6.96

3 < RER < 10 : limited to good practical utility

(Williams, 1987)

Prediction models

	Trainin			Test set		
Parameter	N	Mean	CV	N	Mean	CV
Subset 1	171			862		
- RCT		15.1	27		14.9	26
- a_{30}		41.9	21		41.7	20
Subset 2	170			863		
- RCT		15.2	27		14.9	26
- a_{30}		40.8	20		41.9	21
Subset 3	175			858		
- RCT		14.8	26		14.8	25
- a_{30}		41.8	20		41.7	21
Subset 4	171			862		
- RCT		15.3	28		14.9	25
- a_{30}		41.5	22		41.7	20

Posterior medians for RCT

Trait	Variance components and heritabilities				
	σ^2_A	σ^2_H	σ^2_E	h^2	*P* (h^2>0.10)
Subset 1					
- RCT	5.5	1.6	9.7	0.33 (0.08)	100
- pRCT	4.1	1.5	4.5	0.40 (0.10)	100
Subset 2					
- RCT	5.0	1.9	8.0	0.33 (0.08)	100
- pRCT	3.2	1.6	3.6	0.37 (0.09)	100
Subset 3					
- RCT	4.4	1.7	8.6	0.30 (0.08)	100
- pRCT	3.4	1.4	4.2	0.37 (0.09)	100
Subset 4					
- RCT	4.9	1.4	7.7	0.34 (0.08)	100
- pRCT	3.9	1.4	6.0	0.35 (0.09)	100

RCT= rennet coagulation time measured by CRM; **pRCT**=rennet coagulation time predicted by MIR

σ^2_A = genetic variance; σ^2_H = herd variance; σ^2_E = residual variance;

Posterior medians for a_{30}

	Variance components and heritabilities				
Trait	σ^2_A	σ^2_H	σ^2_E	h^2	*P* (h^2>0.10)
Subset 1					
- a_{30}	18.1	9.7	52.1	0.22 (0.07)	0.97
- pa_{30}	17.1	4.7	19.8	0.41 (0.10)	100
Subset 2					
- a_{30}	18.2	9.7	52.1	0.22 (0.07)	0.98
- pa_{30}	17.1	4.8	19.8	0.41 (0.11)	100
Subset 3					
- a_{30}	22.0	9.9	50.2	0.27 (0.07)	0.99
- pa_{30}	22.0	4.6	15.8	0.49 (0.09)	100
Subset 4					
- a_{30}	19.0	8.3	48.2	0.24 (0.08)	0.98
- pa_{30}	12.2	7.3	24.5	0.27 (0.09)	0.99

a_{30}= curd firmness measured by CRM; **pa_{30}**= curd firmness predicted by MIR

σ^2_A = genetic variance; **σ^2_H** = herd variance; **σ^2_E** = residual variance;

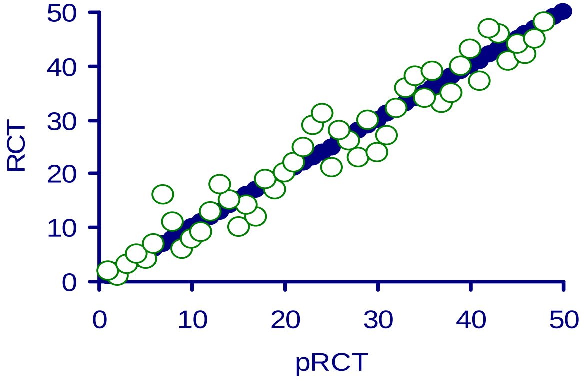
Genetic (r_A) and phenotypic (r_P) correlation

	r_A		r_P	
Trait	Median	SD	Median	SD
Subset 1				
- RCT – pRCT	0.91	0.07	0.67	0.02
- a_{30} – pa_{30}	0.71	0.15	0.51	0.03
Subset 2				
- RCT – pRCT	0.93	0.06	0.61	0.03
- a_{30} – pa_{30}	0.74	0.15	0.51	0.03
Subset 3				
- RCT – pRCT	0.91	0.06	0.72	0.02
- a_{30} – pa_{30}	0.87	0.11	0.54	0.03
Subset 4				
- RCT – pRCT	0.96	0.03	0.69	0.02
- a_{30} – pa_{30}	0.77	0.16	0.48	0.04

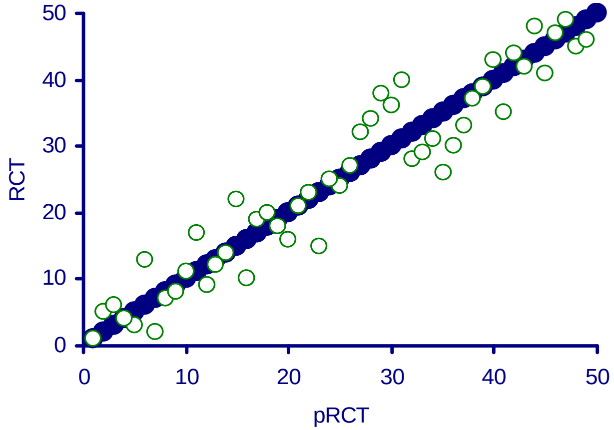
RCT=rennet coagulation time measured; **pRCT** = rennet coagulation time predicted by MIR; **a_{30}** = curd firmness measured; **pa_{30}** = curd firmness predicted by MIR

Relationships between sire rankings for RCT observed and predicted

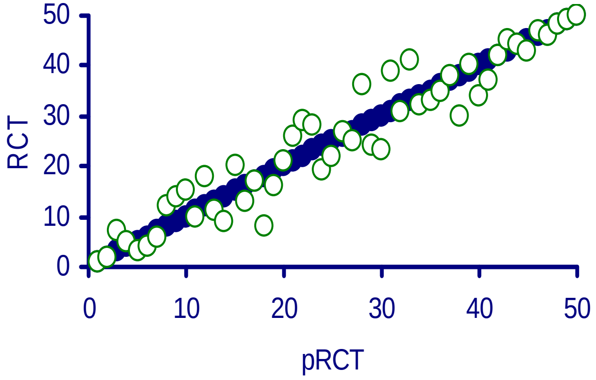
RCT, r = 0.97



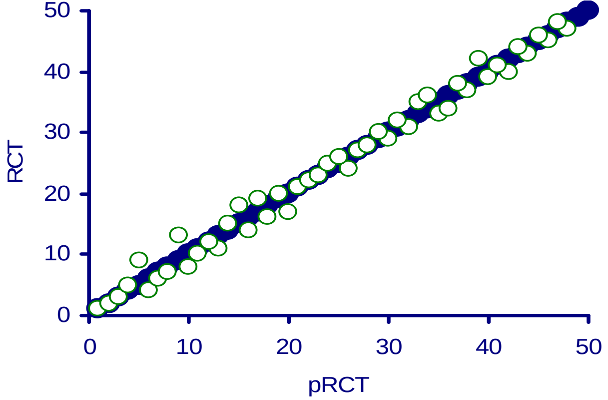
RCT, r = 0.96



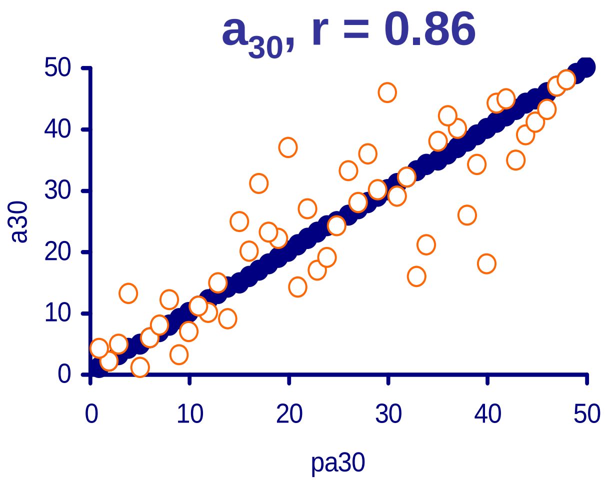
RCT, r = 0.96

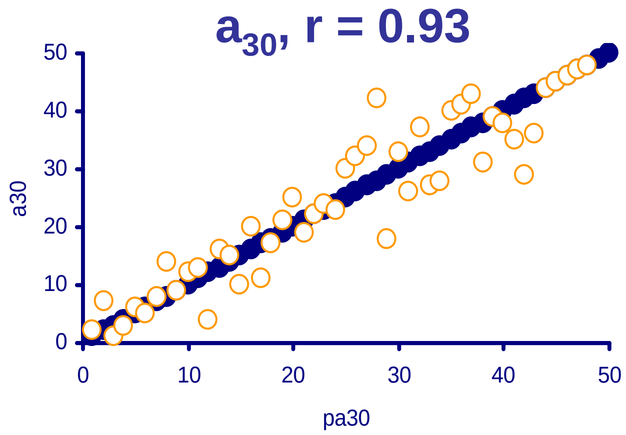


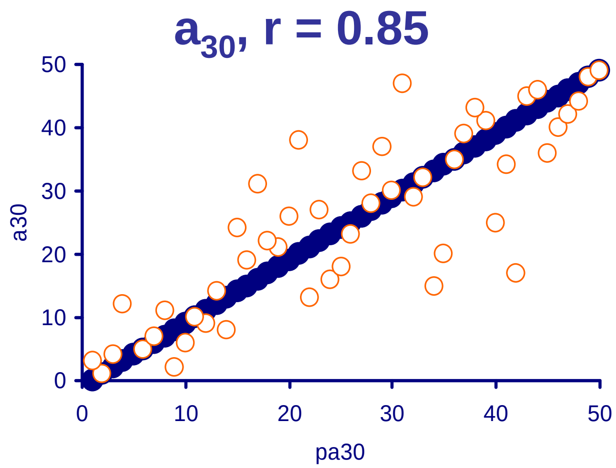
RCT, r = 0.99

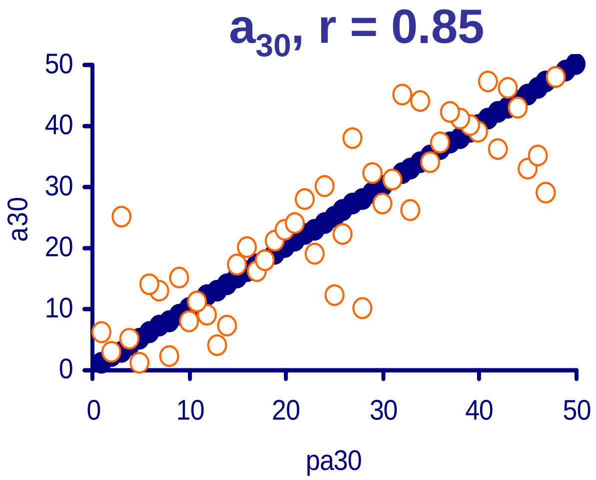


Relationships between sire rankings for a_{30} observed and predicted


a_{30}, r = 0.86


a_{30}, r = 0.93


a_{30}, r = 0.85

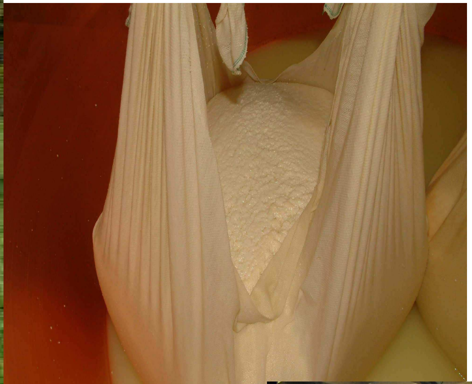

a_{30}, r = 0.85

Conclusions

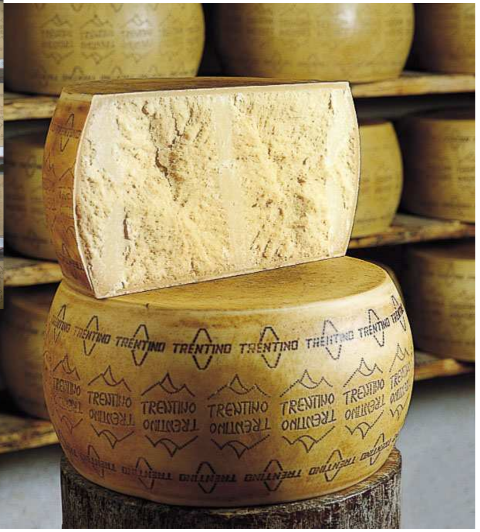
- MIR models showed fairly good predictions for MCP (RCT and a_{30})
- Genetic correlations between MCP measured and MCP predicted were very high for RCT and high for a_{30}
- Heritability for MCP predicted by MIR were higher than those measured by CRM
- No substantial differences in sire rankings when measured and predicted data were used

Implications

MIR prediction can be proposed as indicator trait for an indirect improvement of milk coagulation properties



Thanks for your attention!



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