

Improvement and validation of milk fatty acid predictions using mid-infrared spectrometry

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Fatty Acids

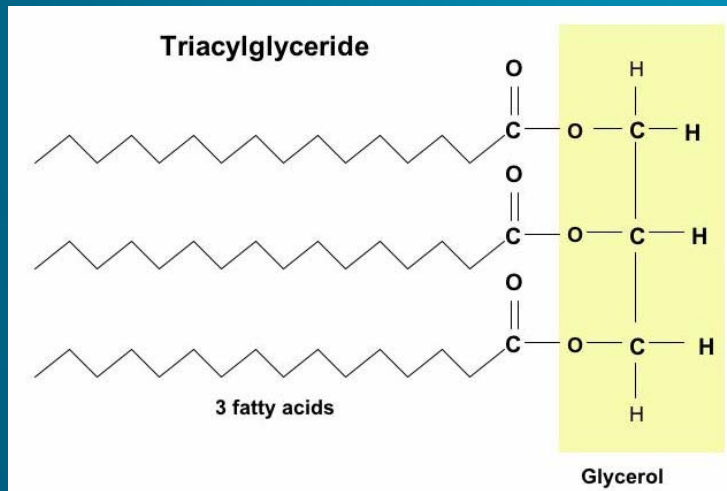
- Generally, 2.5 to 7.0% of fat in bovine milk
- 96% of fat is composed by triglycerides
 - Groups of fatty acids (FA):

– **Saturated** (SAT): 70%

– Unsaturated (UNSAT): 30%

- **Monounsaturated** (MONO): 25%

- **Polyunsaturated** (POLY): 5%



- Gas chromatography:
 - Major advantage: accuracy
 - Major disadvantages:
 - Expensive reagents
 - Time consuming
 - Skilled staff



- Gas chromatography:
 - Major advantage: reliability
 - Major disadvantages:
 - Expensive reagents
 - Time consuming
 - Skilled staff

→ Find an alternative method



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 - Major disadvantages:
 - Expensive reagents
 - Time consuming
 - Skilled staff



- Mid-InfraRed (MIR) spectrometry:
 - Fast analysis (up to 500 samples/hour)
 - Cheap analysis
 - Used in routine milk recording

Collection of samples in Belgium



High variability:

→ *For milk recording scheme:*

- March 2005 to December 2007
- 475 cows in 8 herds
- 6 dairy breeds

→ *From milk payment scheme*



Collection of samples in Belgium

Analysed by Mid-Infrared
(MilkoScan FT6000)

Spectra were exported



Collection of samples in Belgium

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Spectra were exported

Selection of interesting samples by Principal Component Approach

Chromatographic analysis

Mid-Infrared spectrum

CALIBRATION SET (N=239)



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(MilkoScan FT6000)

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CALIBRATION SET (N=239)

PLS approach was used to estimate the calibration equations

Methodology

- 4 methods were tested:
 - (1) Partial Least Squares regressions (PLS)



- 4 methods were tested:
 - (1) Partial Least Squares regressions (PLS)
 - (2) PLS + repeatability file:
 - Spectra provided by different spectrometers for the same milk samples



- 4 methods were tested:
 - (1) Partial Least Squares regressions (PLS)
 - (2) PLS + repeatability file (REP)
 - (3) PLS + first derivative applied to the spectra:
 - Correction of baseline drift



- 4 methods were tested:
 - (1) Partial Least Squares regressions (PLS)
 - (2) PLS + repeatability file (REP)
 - (3) PLS + first derivative (DER)
 - (4) PLS + DER + REP



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Selection of interesting samples by Principal Component Approach

Chromatographic analysis

Mid-Infrared spectrum

CALIBRATION SET (N=239)

PLS approach was used to estimate the calibration equations

Internal validation
by cross-validation

External validation
by adding new samples

Collection of samples in Belgium

Analysed by Mid-Infrared
(MilkoScan FT6000)

Spectra were exported

Selection of interesting samples by Principal Component Approach

Chromatographic analysis

Mid-Infrared spectrum

CALIBRATION SET (N=239)

PLS approach was used to estimate the calibration equations

Internal validation
by cross-validation

Cross-validation :

- 20 groups

Collection of samples in Belgium

Analysed by Mid-Infrared
(MilkoScan FT6000)

Spectra were exported

Selection of interesting samples by Principal Component Approach

Chromatographic analysis

Mid-Infrared spectrum

CALIBRATION SET (N=239)

PLS approach was used to estimate the calibration equations

362 new samples :

- Collected in Belgium, Ireland and Scotland
- Between April 2008 and August 2009
- from several breeds and cows

External validation
on independent new samples

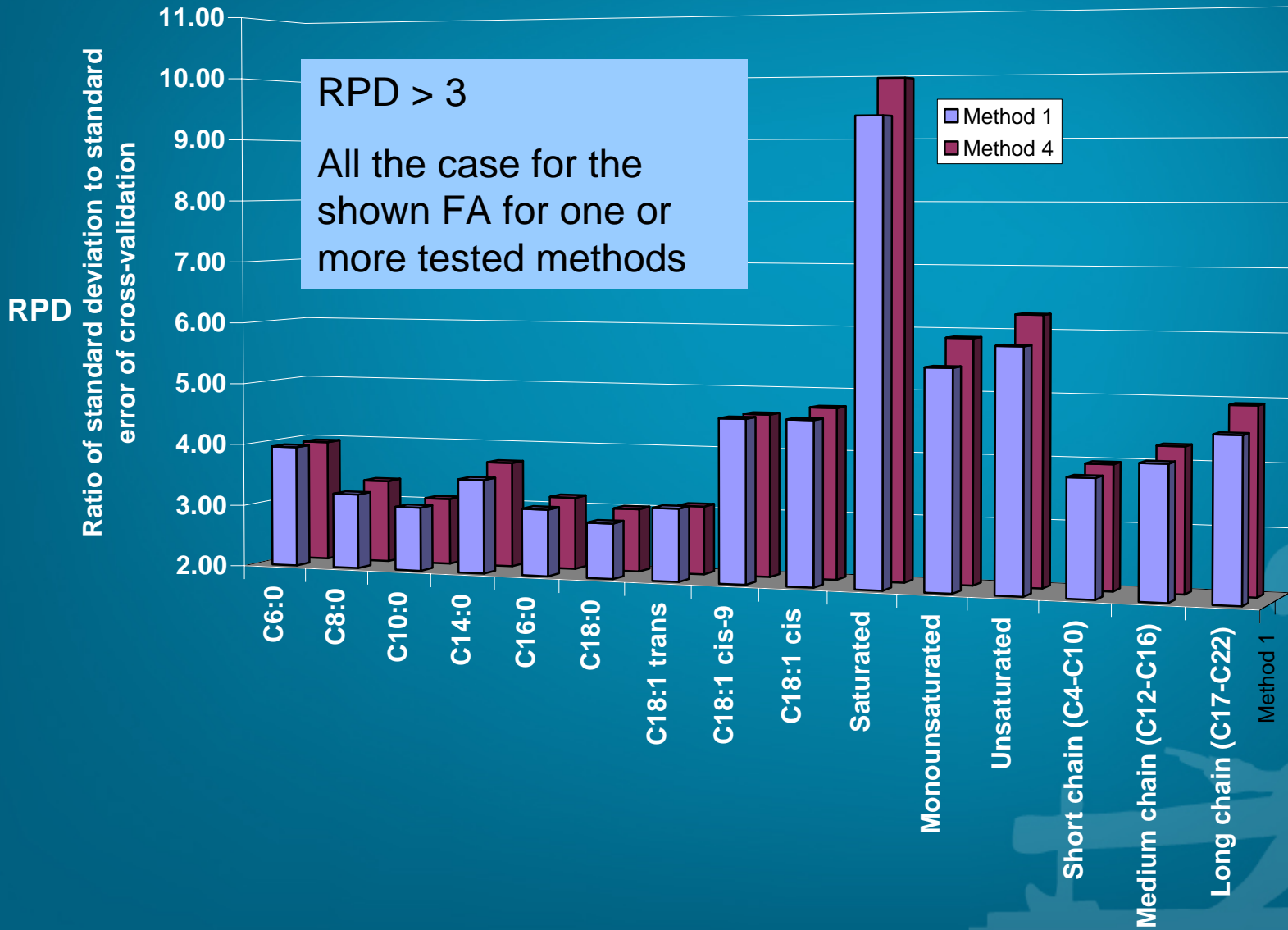
Most Interesting Results

Constituent	N=239	
	Mean	SD
C6:0	0.08	0.02
C8:0	0.05	0.02
C10:0	0.12	0.04
C14:0	0.48	0.14
C16:0	1.29	0.42
C18:0	0.49	0.23
C18:1 trans	0.15	0.09
C18:1 cis-9	0.89	0.36
C18:1 cis	0.96	0.37
Saturated	2.98	0.85
Monounsaturated	1.26	0.43
Unsaturated	1.46	0.48
Short chain (C4-C10)	0.39	0.11
Medium chain (C12-C16)	2.19	0.64
Long chain (C17-C22)	1.86	0.69

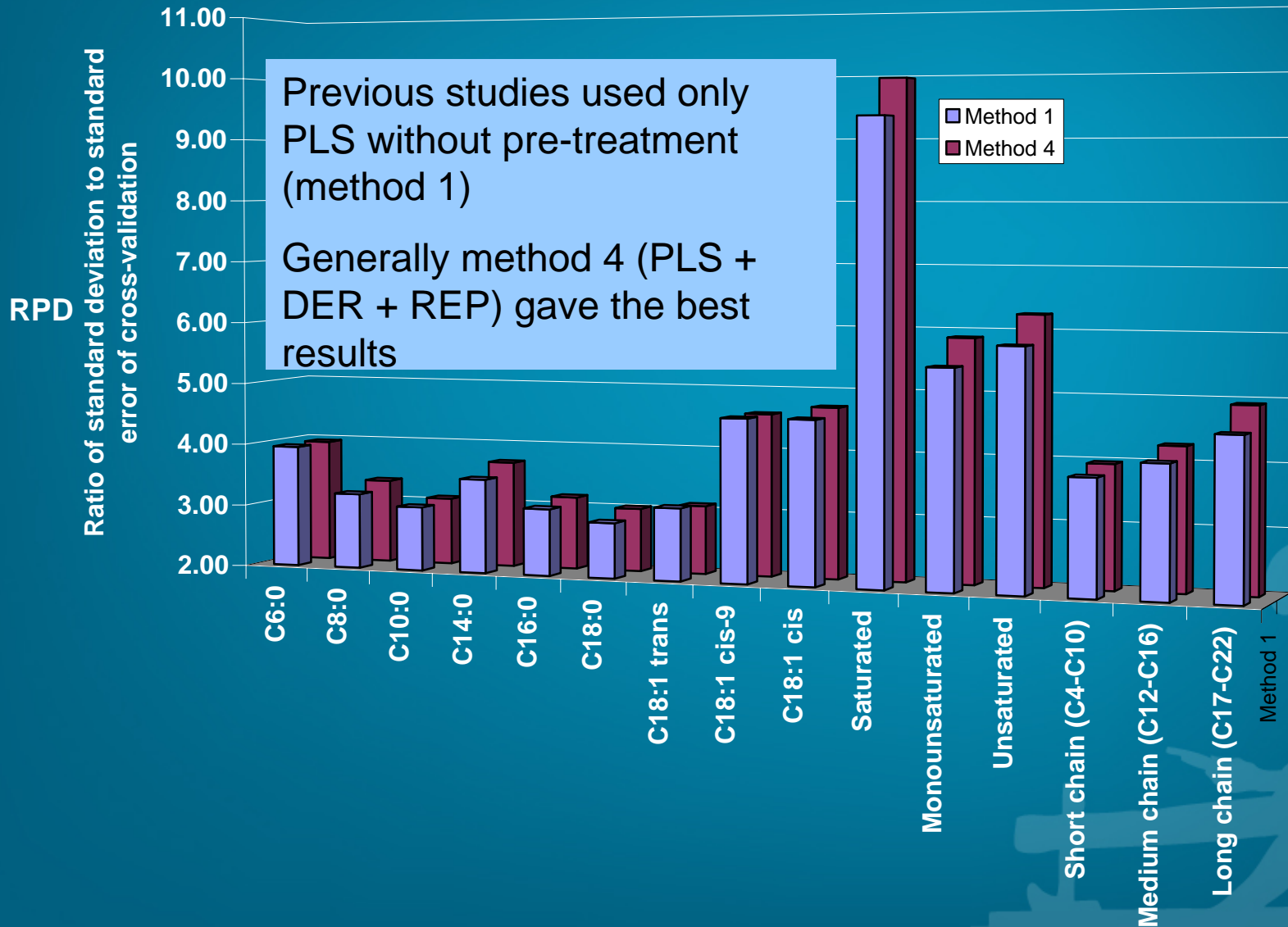
High variability of FA :

Coefficient of variation
(100/mean * SD) ranged
from 25% to 60%.

Most Interesting Results



Most Interesting Results



Most Interesting Results

	Method 4	
	R ² _{cv} (N=239)	R ² _v (N=362)
C6:0	0.94	0.90
C8:0	0.91	0.81
C10:0	0.89	0.73
C14:0	0.93	0.90
C16:0	0.90	0.90
C18:0	0.89	0.72
C18:1 trans	0.90	0.49
C18:1 cis-9	0.95	0.91
C18:1 cis	0.96	0.93
Saturated	0.99	0.98
Monounsaturated	0.97	0.95
Unsaturated	0.97	0.96
Short chain	0.94	0.93
Medium chain	0.95	0.94
Long chain	0.96	0.95

R²_{cv} and R²_v confirms the ability of MIR to predict some FA directly in milk

g/dl of milk	RPD (N=239)			
	1 (*)	2 (*)	3 (*)	4 (*)
C6:0	3.95	4.02	3.89	3.95
Total C18:1 trans	3.16	3.09	3.05	3.09
C18:1 cis-9	4.61	4.68	4.35	4.6
Saturated	9.34	10.01	9.55	9.95

RPD = ratio of SD to the standard error of cross-validation; 1 = PLS; 2 = PLS+REP; 3 = PLS+DER; 4 = PLS+DER+REP

Some FA could be better predicted using another method

Conclusion

- MIR can be used to quantify some FA directly on milk
- Prediction of fat and prediction of FA are decorrelated → interest to use specific equations to quantify FA (data not shown)
- Improvement of accuracy by:
 - Using a first derivative and a repeatability file to develop calibration equations
 - OR choosing the most appropriated method based on the studied FA

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