The state of the art about the development of mid-infrared based fatty acids predictions and their applications along the dairy food chain

M. Whittaker[1], S. Orlandini[2], C. Baumgartner[2], S. Holroyd[3], G. Scott[3], P. Jamieson[3], D. Santschi[4], M. Bahadi[4], B. Harris[5], K. Sanders[5] and H. Soyeurt[6]

[1]The Cattle Information Service, Stafford Park 1, Telford, Shropshire, England
[2]International Committee of Animal Recording, Arthur van Schendelstraat 650, 3511 MJ Utrecht, The Netherlands
[3]Fonterra Co-Operative Group Limited, 2226 State Highway 56, Longburn, New Zealand
[4]Lactanet, 555, Boul. Des Anciens-Combattants, Sainte-Anne-de-Bellevue, Quebec, Canada
[5]Livestock Improvement Corporation, 605 Ruakura Road, Newstead 3286, New Zealand
[6]TERRA Research and Teaching Centre, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

Abstract

Milk mid-Infrared (MIR) spectrometry has been used since the 1980's to analyse milk components. Today advanced analytical techniques and powerful data processing tools allow additional value to be derived from this spectral information. For instance, milk MIR spectra can be used to quantify the fatty acid (FA) composition in dairy milk. Research into milk FA prediction has the potential to significantly impact the dairy chain, from analysis of the nutritional value of milk and also in management benefits to the farmer. However, the application of this technology at the farm level is currently limited. The ExtraMIR project aims to reduce that gap and support the dairy chain in future market needs. This research investigates the variability and reliability of reference data sets for statistical FA modelling to predict the milk FA composition using MIR spectra. Various published FA models from 8 different countries (Belgium, USA, Netherlands, Italy, Australia, Canada, France and China) are analysed using the R square mean-centred cross validation ranking method (Grelet *et al.,* 2021), also taking into account the reference sample size. The variations in accuracy of the Fatty Acid prediction models, specifically for the individual FA C12:0, ranged from 0.92 in the best examples to 0.71 in the poorest examples. This suggests that models analysed are highly imprecise and only for use in detecting extreme values. This knowledge will be combined with the various practical applications of ExtraMIR analysis in the field, where FA data is fed back into the agricultural industry, to aid and benefit farmers in on-farm management and future proofing milk production. Typically, the main constraint between application of FA models across different countries arises from the variability within farming systems. This is due to differences in climate, nutrition and breed. With research visits to Belgium, New Zealand and Canada not only were these constraints clear to witness but also the demands within the agricultural markets were different. These differences in demand generated research focuses specific to the needs of the national agricultural industries which further deviated from the aspirations of the international agricultural focus areas. This differing of objectives can also give rise to innovation within research areas and dairy consultancy organisations. Given that the benefits of milk FA's can be used as an indicator of ration quality of cattle feed, animal health and welfare concerns, environmental footprint of milk production and the technological properties of milk. This will contribute to closing the gap between

the existing extensive research and the application in the field from advisory service providers.

Introduction

Milk MIR spectra can be used to quantify the fatty acid (FA) composition in dairy milk. The applications in the agricultural Research into milk FA prediction offers potential benefits to the dairy industry, including at the farm level, through analysis of the nutritional value of milk. However, the application of this technology at the farm level is currently limited.

The purpose of this study is to investigate the variability and reliability of reference data sets for statistical FA modelling to predict the milk FA composition from MIR spectra. The application potential is analysed using the R square mean-centred cross validation ranking method published by Grelet *et al.* (2021).

Material and methods

The reliability of data sets used in 6 different published research papers, in 6 different countries, focused on statistical FA modelling predictions, was analysed using a classification table developed for mean-centred cross-validation of RPD, relative RMSE and R^2. For the purpose of analysis the data sets were converted to R^2, allowing for comparison between the studies. The ranking method of Grelet *et al.* (2021) was used to analyse the models. Phenotypes including fine milk components, blood components, status of dairy cows and technological properties of milk were used in order to perform a non-supervised K-means Near Neighbour (KNN) clustering of models, with seven clusters, following 3 parameters: their mean-centred cross-validation RPD, relative RMSE and R^2.

Results and discussion

The seven groups of models are recorded below in Table 1, with the range of their performance indicators and their interpretation for potential applications.

Model Analysis 1

The interpretation and cluster groupings from Table 1 have been applied to a study conducted by Grelet at al (2021) in Belgium which looked into large scale phenotyping in the dairy sector using milk MIR spectra. Table 2 contains the fatty acid and the subsequent interpretation of the reference material.

When applying the interpretations from the classification groupings to the R^2 values given in Table 2, the quality of the reference data suggests that the grouped fatty acids have a strong correlation, falling within the any allocation and quality control classification and that the applications in the field would be well received and factually accurate. However, C18:2c9t11 has ranked poorly and should not be used as part of any research other than to detect extreme values.

Table 1. Characteristics of the 7 K-mean clusters resulting from the classification of 57 milk MIR models following their mean-centred cross-validation RPD, relative RMSE and R2 (adapted from Grelet et al., 2021).

Cluster	RPDcv	Relative RMSEcv	R^2cv	Interpretation for application
1	> 6	<5%	> 0.97	Any application
2	4.2 - 6	<10%	0.94 - 0.97	Quality control
3	3 - 4.2	<10%	0.89 - 0.94	Quantitative screening
4	2 - 3	<25%	0.74 - 0.89	Rough screening
5	1.5 - 2	<25%	0.55 - 0.74	Allows to compare groups, discriminate high or low values
6	1.5 -2	>25%	0.55 - 0.74	Highly imprecise, can be used to detect extreme values
7	< 1.5	-	< 0.55	Not recommended

Model Analysis 2

The interpretation and cluster groupings have Table 1 have also been applied to a study conducted by Rutten *et al.* (2009) in the Netherlands, which looked into prediction bovine milk fat composition using infrared spectroscopy based on milk samples collected in winter and summer. Table 3 contains the summer and winter milk analysis correlations alongside the cluster group ranking.

Table 3 shows that the reference data used in this study ranked very low again the cluster group ranking scores and averages around group 4 which would suggest that the data should only be used as a method of rough screening. There are some higher scores in the groupings of 2 and 3 which would then be useable as quality control and quantitative screenings.

Model Analysis 3

The interpretation and cluster groupings have Table 1 have also been applied to a study conducted by Ferrand-Calmels *et al.* (2014) in France which investigated the prediction of fatty acid profiles in cow milk by mid-infrared spectrometry. Table 4 contains the comparison of methods used to develop calibration equations on the MilkoScan FT6000 analyser data for FA cow milk (g/100 mL of milk) on the validation set.

Table 2. Details of the 7 K-mean clusters resulting from the classification of 57 milk MIR models following their normalised cross-validation RPD, relative RMSE and R2 (Grelet et al., 2021).

Phenotype (Fatty Acid)	R^2cv	Cluster Group Ranking	Interpretation
SAT FA (g/dL)	0.99	1	Any application
C18:1cis9 (g/dL)	0.95	2	Quality control
LCFA (g/dL)	0.95	2	Quality control
MCFA (g/dL)	0.97	2	Quality control
MONO FA (g/dL)	0.97	2	Quality control
Tot18:1cis (g/dL)	0.95	2	Quality control
Total _C18:1 (g/dL)	0.96	2	Quality control
UNSAT (g/dL)	0.97	2	Quality control
C10 (g/dL)	0.91	3	Quantitative screening
C12 (g/dL)	0.92	3	Quantitative screening
C14 (g/dL)	0.93	3	Quantitative screening
C16 (g/dL)	0.94	3	Quantitative screening
C4 (g/dL)	0.93	3	Quantitative screening
C6 (g/dL)	0.91	3	Quantitative screening
C8 (g/dL)	0.91	3	Quantitative screening
SCFA (g/dL)	0.93	3	Quantitative screening
C17 (g/dL)	0.80	4	Rough screening
C18 (g/dL)	0.84	4	Rough screening
Odd Fatty Acids (g/dL)	0.83	4	Rough screening
PUFA (g/dL)	0.77	4	Rough screening
Total Trans (g/dL)	0.80	4	Rough screening
18:1 trans (g/dL)	0.79	4	Rough screening
C14:1 (g/dL)	0.68	5	Allows to compare groups, discriminate high or low values
C16:1c (g/dL)	0.73	5	Allows to compare groups, discriminate high or low values
C18:2c9c12 (g/dL)	0.72	5	Allows to compare groups, discriminate high or low values
C18:3c9c12c15 (g/dL)	0.68	5	Allows to compare groups, discriminate high or low values
FA isoanteiso (g/dL)	0.75	5	Allows to compare groups, discriminate high or low values
Omega3 (g/dL)	0.66	5	Allows to compare groups, discriminate high or low values
Omega6 (g/dL)	0.72	5	Allows to compare groups, discriminate high or low values
Tot18:2 (g/dL)	0.69	5	Allows to compare groups, discriminate high or low values
C18:2c9t11 (g/dL)	0.74	6	Highly imprecise, can be used to detect extreme values

Table 3. Validation coefficients of determination (r2) for individual and groups of fatty acids expressed on the basis of milk and fat for all scenarios (Rutten et al., 2009).

	Fatty Acids - Milk (g/dL)									
Trait	AA	AA Cluster Group Ranking	WW	WW Cluster Group Ranking	WS	WS Cluster Group Ranking	SS	SS Cluster Group Ranking	SW	SW Cluster Group Ranking
C4:0	0.91	3	0.83	4	0.78	4	0.77	4	0.82	4
C6:0	0.96	2	0.89	3	0.89	4	0.89	3	0.90	3
C8:0	0.94	2	0.85	4	0.84	4	0.84	4	0.85	4
C10:0	0.92	3	0.75	4	0.81	4	0.81	4	0.76	4
C12:0	0.85	4	0.61	5	0.71	5	0.73	5	0.62	5
C14:0	0.94	3	0.81	4	0.84	4	0.85	4	0.82	4
C16:0	0.94	2	0.85	4	0.75	4	0.79	4	0.83	4
C18:0	0.82	4	0.58	5	0.64	5	0.70	5	0.59	6
C18:1 cis-9	0.92	3	0.69	5	0.79	4	0.81	4	0.68	6
C18:1 cis-11	0.27	7	0.18	7	0.15	7	0.23	7	0.12	7
C18:1 trans-4-8	0.48	7	0.23	7	0.13	7	0.20	7	0.15	7
C18:1 trans-9	0.53	7	0.32	7	0.27	7	0.29	7	0.27	7
C18:1 trans-11	0.63	6	0.26	7	0.09	7	0.17	7	0.18	7
C18:2 cis-9,12	0.36	7	0.19	7	0.14	7	0.17	7	0.15	7
C18:2 cis-9, trans-11	0.58	3	0.27	7	0.14	7	0.20	7	0.13	7
C18:3 cis-9,12,15	0.45	7	0.19	7	0.22	7	0.23	7	0.14	7
C6-C12	0.95	2	0.81	4	0.87	4	0.87	4	0.82	4
C14-C16	0.97	2	0.90	3	0.81	4	0.85	4	0.89	3
C18u	0.94	2	0.69	5	0.77	4	0.80	4	0.68	5
Ratio SFA:UFA	0.91	3	0.43	7	0.65	5	0.59	5	0.38	7

- AA - Calibration in half of all data and validation in the other half of all data.
- WW - Calibration in half on the winter data and calidation in the other half of the winter data.
- WS - Validation of the midel from scenario WW in all summer data.
- SS - Calibration in half of the summer data and validation in the other half of the summer data.
- SW - Validation of the model scenario SS in all winter data.

Table 4. Comparison of the methods used to develop calibration equations on the MilkoScan FT6000 analyser data for FA in cow milk (g/100mL) on the validation set (Ferrand-Calmels et al., 2014).

Comparison of the methods used to develop calibration equations on the MilkoScna FT6000 Analyzer (Food Electric A/S Hillerod, Denmark) data for FA in cows milk																		
Fatty Acid	PLS R^2	Cluster Group Ranking	AG1PLS R^2	Cluster Group Ranking	AG2PLS R^2	Cluster Group Ranking	Elastic net R^2	Cluster Group Ranking	LASSO R^2	Cluster Group Ranking	Ridge Regression R^2	Cluster Group Ranking	First Derivative + PLS R^2	Cluster Group Ranking	Wavelet + PLS R^2	Cluster Group Ranking
C4:0	0.93	2	0.93	2	0.93	3	0.87	4	0.90	3	0.84	4	0.92	3	0.94	2
C6:0	0.96	2	0.96	2	0.97	1	0.93	3	0.93	3	0.84	4	0.96	2	0.96	2
C8:0	0.97	1	0.98	1	0.97	1	0.89	3	0.90	3	0.75	4	0.97	1	0.97	1
C10:0	0.95	2	0.95	2	0.96	2	0.84	4	0.85	4	0.62	5	0.96	2	0.96	2
C12:0	0.96	2	0.96	2	0.96	2	0.82	4	0.84	4	0.48	7	0.97	1	0.96	2
C14:0	0.95	2	0.95	2	0.95	2	0.84	4	0.86	4	0.74	5	0.96	2	0.95	2
C16:0	0.94	2	0.92	3	0.93	3	0.86	4	0.87	4	0.71	5	0.93	3	0.92	3
C18:0	0.85	4	0.89	3	0.85	4	0.76	4	0.77	4	0.46	7	0.85	4	0.87	4
Total trans 18:1	0.85	4	0.83	4	0.83	4	0.71	5	0.71	5	0.30	7	0.88	4	0.87	4
cis-9 C18:1	0.97	1	0.97	1	0.97	1	0.85	4	0.90	3	0.38	7	0.98	1	0.96	2
Total cis C18:1	0.97	1	0.97	1	0.96	2	0.84	4	0.90	3	0.37	7	0.98	1	0.95	2
Total C18:1	0.97	1	0.97	1	0.96	2	0.84	4	0.88	4	0.38	7	0.98	1	0.96	2
cis-9, cis-12 C18:2 (linoleic acid)	0.78	4	0.76	4	0.75	4	0.58	5	0.61	5	0.45	7	0.80	5	0.80	4
cis-9, trans-11 C18:2 (conjugated linoleic acid)	0.83	4	0.83	4	0.83	4	0.58	6	0.71	5	0.21	7	0.87	4	0.78	4
C18:3n-3 (linolenic acid)	0.86	4	0.69	5	0.25	7	0.54	7	0.58	6	0.30	7	0.82	5	0.85	4
SFA	1.00	1	1.00	1	0.99	1	0.96	2	0.96	2	0.91	3	1.00	1	0.99	1
MUFA	0.98	1	0.98	1	0.97	1	0.84	4	0.89	3	0.41	7	0.99	1	0.97	1
PUFA	0.78	4	0.81	4	0.81	4	0.71	5	0.73	5	0.53	7	0.87	4	0.82	4
trans FA	0.86	4	0.86	4	0.86	4	0.74	5	0.74	4	0.26	7	0.90	3	0.88	4
n-3	0.84	4	0.79	4	0.81	4	0.67	5	0.65	5	0.26	7	0.86	4	0.84	4

Table 4 highlights the variability of different coefficient models when applied to the same reference data set. The Ridge Regression method generally ranks very low across all fatty acid types with the average cluster group being 7, suggesting this would not be a good method to use for application in the field and further research studies. The first derivative + PLS R^2 shows great variability in ranking scores, with multiple fatty acids groupings in the any application interpretation but also some scores are within group 5 which are less reliable and suitable for comparing groups and discriminating

Table 5. Fitting statistics of each prediction equation estimating fatty acid concentrations using the model development data sets expressed as g/100g of milk (Fleming et al., 2017)

Individual Fatty Acid	R^2	Cluster Group Ranking	Interpretation
C4:0	0.66	5	Allows to compare groups, discriminate high or low values
C6:0	0.38	7	Not recommended
C8:0	0.37	7	Not recommended
C10:0	0.66	5	Allows to compare groups, discriminate high or low values
C11:0	0.21	7	Not recommended
C12:0	0.71	5	Allows to compare groups, discriminate high or low values
C13:0	0.19	7	Not recommended
C14:0	0.80	4	Rough screening
C14:1	0.61	5	Allows to compare groups, discriminate high or low values
C15:0	0.61	5	Allows to compare groups, discriminate high or low values
C16:0	0.86	4	Rough screening
C16:1	0.62	6	Highly imprecise, can be used to detect extreme values
C17:0	0.53	7	Not recommended
C17:1	0.31	7	Not recommended
C18:0	0.73	6	Highly imprecise, can be used to detect extreme values
C18:1 in-9 trans	0.60	5	Allows to compare groups, discriminate high or low values
C18:1 in-9 cis	0.79	4	Rough screening
C18:2n-6 trans	0.17	7	Not recommended
C18:2n-6 cis	0.62	5	Allows to compare groups, discriminate high or low values
C18:3n-3	0.58	6	Highly imprecise, can be used to detect extreme values
C18:2 cis-9,cis-12	0.65	5	Allows to compare groups, discriminate high or low values
C22:6n-3	0.22	7	Not recommended
SFA	0.94	2	Quality control
MUFA	0.84	3	Quantitative screening
PUFA	0.66	5	Allows to compare groups, discriminate high or low values
UFA	0.84	4	Rough screening
Short-Chain	0.72	5	Allows to compare groups, discriminate high or low values
Medium-Chain	0.90	3	Quantitative screening
Long-Chain	0.83	4	Rough screening

high or low values. The most successful method of regression in this study was AG1 PLS R^2, scoring very well throughout on most of the individual fatty acids.

Model Analysis 4

The interpretation and cluster groupings have Table 1 have also been applied to a study conducted by Fleming *et al.* (2017) in Canada, which investigated predicting milk fatty acid content with mid-infrared spectroscopy in Canadian dairy cattle, using differently distributed model development sets. Table 5 contains the statistics of each prediction equation estimating fatty acid concentrations using the model development data sets expressed as g/100g of milk.

The data in Table 5 shows high variability in the classification grouping, with no fatty acids falling into the number 1 grouping. There are also several fatty acids that fall into the category of not recommended, which would suggest that the reference data set used in this study does not have a good fit in to the regression model used.

Model Analysis 5

The interpretation and cluster groupings in Table 1 have also been applied to a study conducted by Wang *et al.* (2017) in Australia, which investigated the use of mid-infrared spectrometry to predict milk fatty acid, energy balance and methane emissions. Table 6 contains the Pearson correlations between milk fatty acids and energy balance derived using individual cow data and the prediction accuracy using MIR data on the fatty acids compared with the cluster group rankings.

Table 6 contains no classification groups 1, 2 or 3 which means that the categories of any application for quality control and quantitative screening have been removed from the analysis. The fatty acids groupings are largely focused around 4 and 5 which would fall into the rough screening and group comparison and discrimination high or low value categories. This study therefore would not be accurate enough to use in the field but would be of use as a general screening method based on the reference data set that was used.

Model Analysis 6

The interpretation and cluster groupings in Table 1 have also been applied to a study conducted by Zhao *et al.* (2022) in China based on the prediction of milk fatty acid content by mid-infrared spectroscopy in Chinese Holstein cows. Table 7 contains the best prediction accuracy of prediction models for each fatty acid expressed as g/100g of milk.

Table 6. Pearson correlations between milk fatty acids and energy balance derived using individual cow data and the prediction accuracy using MIR data on the fatty acids.

Individual Fatty Acid	R^2	Cluster Group Ranking	Interpretation
Un-identified	0.54	7	Not recommended
C4:0	0.73	5	Allows to compare groups, discriminate high or low values
C6:0	0.78	4	Rough screening
C8:0	0.76	4	Rough screening
C10:0	0.72	5	Allows to compare groups, discriminate high or low values
C10:1	0.61	5	Allows to compare groups, discriminate high or low values
C12:0	0.72	5	Allows to compare groups, discriminate high or low values
C14 iso	0.68	6	Highly imprecise, can be used to detect extreme values
C14:0	0.73	5	Allows to compare groups, discriminate high or low values
C14:1	0.56	6	Highly imprecise, can be used to detect extreme values
C15 iso	0.68	5	Allows to compare groups, discriminate high or low values
C15 anteiso	0.55	6	Highly imprecise, can be used to detect extreme values
C15:0	0.72	5	Allows to compare groups, discriminate high or low values
C16 iso	0.69	5	Allows to compare groups, discriminate high or low values
C16:0	0.74	4	Rough screening
C16:1	0.62	5	Allows to compare groups, discriminate high or low values
C17 iso	0.53	7	Not recommended
C17 anteiso	0.49	7	Not recommended
C17:0	0.61	6	Highly imprecise, can be used to detect extreme values
C17:1	0.52	7	Not recommended
C18:0	0.80	4	Rough screening
C18:1 t9	0.65	5	Allows to compare groups, discriminate high or low values
C18:1 t10	0.59	6	Highly imprecise, can be used to detect extreme values
C18:1 t11	0.58	6	Highly imprecise, can be used to detect extreme values
C18:1 cis	0.63	5	Allows to compare groups, discriminate high or low values
C18:1 c9	0.51	7	Not recommended
C18:1 c11	0.65	5	Allows to compare groups, discriminate high or low values
C18:2 n6	0.56	6	Highly imprecise, can be used to detect extreme values
C18:3 n3	0.57	6	Highly imprecise, can be used to detect extreme values
C20:0	0.79	4	Rough screening
C20:1 c11	0.68	5	Allows to compare groups, discriminate high or low values
CLA	0.65	6	Highly imprecise, can be used to detect extreme values

Table 7. Best prediction accuracy of different prediction models for each fatty acid expressed as g/100g of milk (Zhao et al., 2022).

Fatty Acid	R^2	Cluster Group Ranking	Interpretation
C8:0	0.75	4	Rough screening
C10:0	0.61	5	Allows to compare groups, discriminate high or low values
C11:0	0.57	6	Highly imprecise, can be used to detect extreme values
C12:0	0.79	4	Rough screening
C13:0	0.24	7	Not recommended
C14:0	0.66	5	Allows to compare groups, discriminate high or low values
C15:0	0.45	7	Not recommended
C16:0	0.64	6	Highly imprecise, can be used to detect extreme values
C17:0	0.65	5	Allows to compare groups, discriminate high or low values
C18:0	0.66	5	Allows to compare groups, discriminate high or low values
C20:0	0.52	5	Allows to compare groups, discriminate high or low values
C22:0	0.70	5	Allows to compare groups, discriminate high or low values
C24:0	0.64	5	Allows to compare groups, discriminate high or low values
C14:1	0.63	5	Allows to compare groups, discriminate high or low values
C16:1	0.54	7	Not recommended
C18:1n9c	0.60	6	Highly imprecise, can be used to detect extreme values
C20:1	0.54	7	Not recommended
C22:1n9	0.51	7	Not recommended
C18:2n6c	0.59	6	Highly imprecise, can be used to detect extreme values
C18:3n3	0.60	6	Highly imprecise, can be used to detect extreme values
C18:3n6	0.18	7	Not recommended
C20:3n6	0.50	7	Not recommended
C20:4n6	0.44	7	Not recommended
C20:5n3	0.33	7	Not recommended
LCFA	0.68	5	Allows to compare groups, discriminate high or low values
MCFA	0.64	5	Allows to compare groups, discriminate high or low values
MUFA	0.61	6	Highly imprecise, can be used to detect extreme values
PUFA	0.71	5	Allows to compare groups, discriminate high or low values
SCFA	0.66	5	Allows to compare groups, discriminate high or low values
SFA	0.66	5	Allows to compare groups, discriminate high or low values
UFA	0.62	6	Highly imprecise, can be used to detect extreme values

The data in Table 7 again shows no data falling into groupings 1, 2 or 3, which again limits the application for this of this study based on the reference data set. The common grouping for this data set is around 5, which places a lot of the individual fatty acid values in the comparison group and for use in discriminating high and low values. There are also 9 instances where the grouping falls into the not recommended category. This would suggest that the reference data set used has very limited applications in the field.

Conclusions

This study has highlighted that there is in some cases a lack in application value of the reference material. This has long been an issue in the industry where there is a disconnect between the amount of research that is being done and the actual application in the dairy industry. The general low scores using the cluster grouping method would suggest that there are some strengths in the research and that some studies are very positive for individual fatty acids or grouped fatty acids although few are good for both.

The variability between research studies in each country also reinforces the industry opinion that it is difficult to replicate the work of others between countries. Reference data sets are often unique to each country with nutrition, climate and milk system all leading to discrepancies between the milk quality observed in each country.

References

H. Soyeurt, J.A. Fernandez, A. Vanlierde, F. Stevens, N. Gengler, F. Dehareng (2020). Large scale phenotyping in dairy sector using milk MIR spectra: Key factors affecting the quality of predictions. Methods. 186(2), pp.97 - 111.

M.J. Rutten, H. Bovenhuis, K.A. Hettinga, H.J.F van Valenberg and J.A.M. van Arendonk. (2009). Predicting bovine milk fat composition using infrared spectroscopy based on milk samples collected in winter and summer. American Dairy Science Association. 92(12), pp.6202-6029.

M. Ferrand-Calmels, I. Palhiere, M. Brochard, O. Leray, J.M. Astruc, M.R. Aurel, S. Berbey, F, Bouvier, P. Brunschwig, H. Callat, M. Douget, F. Faucon-Lahalle, M. Gele, G. Thomas, J.M. Trommelscholager, H. Larroquet. (2013). Prediction of fatty acid profiles in cow, ewe and goat milk by mid-infrared spectrometry. Journal of Dairy Science. 97(1), pp.17-35.

A. Fleming, F.S. Schenkel, J. Chen, F. Malchiodi, V. Bonfatti, R.A. Ali, B. Mallard, M. Corredig, F. Miglior. (2017). Prediction of milk fatty acid content with mid-infrared spectroscopy in Canadian dairy cattle using differently distribu. Journal of Dairy Science. 100(6), pp.5073-5081.

T. Wang, H.N. Phuong, E. Wall, S. Smith and J.E. Pryce. (2014). The use of mid-infrared Spectrometry to predict milk fatty acid, energy balance and methane emissions for Australian dairy cows. Journal of Dairy Science. 97(9), pp.5863-5871. Author(s), year. Title. Edition if any. Publisher, address. Number of pages.

Ziuxin Zhao, Yuetong Song, Yuanpei Zhang, Gaozhan Cai, Guanghui Xue, Yan Liu, Ke. (2023). Predictions of milk fatty acid contents by mid-infrared spectroscopy in Chinese Holstein cows. Molecules. 28(666), pp.1-11.