farms were located in Calabria Region (Southern Italy) and all milk samples were collected from October 2017 to February 2020. After collection, the samples were kept refrigerated at 4°C and immediately delivered to the laboratory of the University of Catanzaro for the analysis by MilkoScan FT+ (Foss, Hillerød, Denmark) instrument.

Standards Preparation for FT-MIR Analysis:

The milk mixtures were prepared by randomly pairing one of the 7 buffalo milk with one of the 7 cow milk and then blending them according to the following 17 proportions: 0, 1, 2.5, 5, 10, 20, 25, 30, 50, 70, 75, 80, 90, 95, 97.5, 99, and 100 % (vol/vol).

A total of 119 standards (17 mixtures x 7 different couples of buffalo-cow milk) were obtained. Before the analysis, standards (45 mL each) were warmed in a 40°C water bath for 20 minutes, slightly stirred for a few seconds and then analyzed by MilkoScan FT+ for the MIR spectra acquisition as the transmittance value at each of the 1060 points of wavelength from 5011 to 925 cm^{-1}. This instrument analyzes the chemical composition of milk according to the standards of the International Dairy Federation (FIL-IDF) by the Fourier Transform (FT) technology over the Mid-infrared spectral range. Spectra were stored as absorbances (A) using the transformation A= log(1/T), where T is the transmittance (Figure 1). Two spectral acquisitions were carried out for each sample, and the results were averaged before data analysis.

Chemometric analysis:

All spectral data were elaborated by Partial Least Square (PLS) regression using the TQ Analyst™ software ver. 8.0 (Thermo Fisher Scientific Inc., Madison, WI) in order to quantify the % (vol/vol) of bovine milk in buffalo milk. 85 spectra belonging from 5 out of 7 mixtures pairs (randomly chosen) were used as calibration standards. The remaining 34 spectra were used as independent validation standards. In this way, spectra were distributed in two sets (70% for training and 30% for validation) evaluated by PLS in order to develop a multivariate calibration model. The number of latent variables in the model was tested according to the method proposed by the software. After leave-one-out cross validation, the number of the principal components (factors) that minimized the RMSECV of the model was nine. After selecting

the number of latent variables (16), the PLS model was used to recognize the concentration of cow's milk in buffalo's milk.

The accuracy and precision of the calibration model are expressed as correlation coefficient (R^2) of the calculated vs. real values, as the root mean square error of calibration (RMSEC) and the root mean square error of prediction (RMSEP). The choice of the best model followed this rule: the higher R^2 and the lower RMSEC and RMSEP, the better the models were considered (17). Furthermore, a cross-validation using "leave-one-out" procedure was used to evaluate the overfitting of the calibration and the root mean square error of cross-validation (RMSECV) was calculated.

As suggested by Muik et al., (18), to improve the performance of the prevision, the following corrections were applied on original spectra: first derivative; smoothing by Norris derivative filter with 5 both as segment length and as gap between segments. Data were normalized by using the mean centering technique.

Results and Discussion

The qualitative composition of the bulk tank milk of the two different species was firstly observed in this study (Table 1). The buffalo milk average protein, fat, and lactose content were respectively 8.41 g/100, 4.64 g/100 and 4.83 g/100 g. The same parameters for cow milk were 3.83 g/ 100, 3.50 g/100 and 4.76 g/100 g. These data show the higher contents of protein and fat in buffalo milk than in cow's milk and are in agreement with those reported in previous studies (19, 20).

Two buffalo and cow milk representative MIR spectra, before and after spectral treatment, are reported in Figure 1. The absorbance regions that best correlated with the percentage of cow's milk in buffalo milk were suggested by the TQ analyst^{TM} and were those in the ranges 2989.12–2495.44 and 1481.06–987.38 cm^{-1} (Figure 1). As expected, the spectral regions corresponding to water interference (21) did not fall within the regions considered appropriate for a good calibration. More precisely, these spectral regions fall between 1680 to 1600 cm^{-1} and 3650 to 3000 cm^{-1} (O-H stretching) (21). Among spectral ranges

having no useful information there is also the area between 1765 to 1730 cm^{-1} associated with C=O stretching modes (triglyceride) and the area between 1700 to 1500 cm^{-1} containing the peak typical of amide I (C-O) and amide II (N–H) (22). Among other biomolecules populating the spectrum can be annotated lipids, whose absorption region is between 1477 to 1400 cm^{-1} (C-H stretching) and caseins (phosphate group) that are absorbing at 1100 cm^{-1} (23).

The peaks at 1200–900 and 1045 cm^{-1} are associated with lactose, and those at 3000–2800 cm^{-1} and 1400–800 cm^{-1} are related to carbohydrates, monosaccharides and polysaccharide groups (C-O-C) (15). All the spectra were pre-processed for the outliers detection (24) through the Chauvenet test and no outliers were found among the 119 spectra (24).

The performance of PLS calibration models for both original and pre-treated spectra is shown in Table 2. Both calibrations showed good results, but the spectral pre-processing allowed to significantly improve the quality of the prediction as indicated by the lower RMSEP values. Generally, a good model should have lower RMSECV, RMSEP and higher R^2 but small differences between RMSEP and RMSECV (8).

Both the high value of the correlation coefficient and the low RMSEP value indicated the success of the PLS regression on the pre-processed spectra and, for these reasons this calibration model may be preferred to the one elaborated on the raw spectra. Figure 2 shows calibration results for the detection of bovine milk percentage in buffalo milk using the calibration model on the pre-treated spectra. It can be observed that data points in the plot of the calculated vs. actual values (Figure 2A) drew a line with a 45 degrees angle with respect to both axes. No bias, intended as a systematic difference between expected and true values, was detected. For this reason, the data points in the % difference plot (Figure 2B) were distributed randomly above and below the zero line within a concentration ranging from -7% to +7% of the actual value. The differences between calculated and actual values of the validation standards were similar to those observed for the calibration standards, this feature indicates that there was no overfitting for the considered calibration.

In a similar work detecting the adulteration of cow, sheep and goat milk by FTIR spectroscopy in combination with multivariate statistical methods, Nicolaou et al. (25) obtained calibration models characterized by prediction error higher than those observed in the present study and ranging from 3.95%

141 to 8.03%. However, recent research that used FTIR method with multivariate statistical analysis was
142 successful in the differentiation between buffalo milk and buffalo milk added with cow milk (15).

143 In our research, the applied PLS regression models were able to detect as little as 3% cow in buffalo
144 milk, reaching a good accuracy (Table 2). Although the adulteration of buffalo milk with cow's milk is
145 unlikely to occurs at concentrations below 3% due to limited economic convenience, from a scientific and
146 technical points of view is relevant to have such a sensitive and cheap method for the detection of this
147 type of fraud.

148 This is of major importance, especially considering that the presence of small quantities of cow's milk
149 in buffalo milk may be life threatening in the case of consumers with allergies to cow milk proteins.
150 Cow's milk has about 30 potentially allergenic proteins and, the foods that contain it must necessarily
151 declare it on the label (26). Other recent studies applied spectroscopy associated with multivariate
152 statistics to verify the authenticity of buffalo milk. Silva et al. (27), analysed lyophilized milk samples
153 with attenuated reflectance Fourier transform infrared spectroscopy (ATR-FTIR) in association with PCA
154 and artificial neural network. The authors could detect differences between different milk species only
155 accounting for 40% of adulteration and could not assess the content of cow's milk added to buffalo milk,
156 but only its presence. Also, Gonçalves et al. (16) developed a similar method for the quantification of
157 buffalo's milk adulterants (e.g. cow's milk) using MIR spectroscopy coupled to PLS and MLR. The
158 obtained results were similar to the ones here presented, with R^2 of 0.9938 and RMSEP of 3.484% for the
159 adulteration. Durakli Velioglu et al. (28), similarly to Gonçalves et al. (16), when researching the
160 authenticity of buffalo's milk by fluorescence spectroscopy associated with PCA and PLS, found models
161 with an R^2 of 0.98. Instead, RMSEC, RMSECV, and RMSEP values were determined as 2, 7 and 4%,
162 respectively, indicating slightly higher prediction errors than the values in our findings.

163 In the study of Lapcharoensuk et al. (29), a near-infrared (NIR) spectroscopy model was used to
164 quantitatively detect buffalo milk adulteration with cow milk, but on pasteurized milk samples. The
165 authors yielded a R^2 of 0.998 and RMSEP of 2.121.

166 Although the RMSEP obtained in all these works are very similar to that obtained in our study, most of
167 the above-mentioned authorsonly used adulterations ranging from 10-90% (v/v) while we used

adulterations ranging from 1-99% (v/v). Moreover, we enrolled cow milk samples coming from 7 different breeds while the other studies used only 2 different breeds.

Conclusions

In this study, we demonstrated that Mid-Infrared (MIR) Spectroscopy in combination with PLS regression analysis provides an accurate, simple and rapid method for quantitative assessment of the adulteration of buffalo milk with cow's milk. For this reason, we believe that the proposed calibration can be a useful tool for expanding the possibilities of combating fraud in laboratories equipped for routine milk analysis using dedicated FTIR instruments at no additional cost.

Acknowledgments

We are grateful to Vincenzo Mollace for the research instruments. We want to acknowledge the Interdepartmental Services Centre of Veterinary for Human and Animal Health and the Department of Health Sciences University "Magna Græcia" of Catanzaro for their support to the realization of the present research.

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Tables and Figures

Table 1. Mean ± standard deviation of the fat, protein, and lactose content of the milk samples

Milk components	**Buffalo milk (N=7)**	**Cow milk (N=7)**
Fat (g/100 g)	8.41 ± 0.29	3.83 ± 0.31
Protein (g/100 g)	4.64 ± 0.11	3.50 ± 0.29
Lactose (g/100 g)	4.83 ± 0.16	4.76 ± 0.13

Table 2. Calibration statistics for analysis of bovine milk content (% vol/vol) in bufalin milk using partial least square (PLS) regression at frequencies 2989.12 - 2495.44 and 1481.06 - 987.38 cm-1

Spectral treatment	**R^2 cal**	**RMSEC**	**R^2 val**	**RMSEP**	**RMSECV**	**N° of Factors**
Normal	0.99857	2.08	0.99770	6.06	2.63	10
First der., Norris filter	0.99861	2.04	0.99803	2.84	2.44	9

R^2 cal: coefficient of determination for calibration.

RMSEC: root mean square error of calibration.

R^2 val: coefficient of determination for external validation; RMSEP: root mean square error of prediction.

RMSECV: root mean square of cross-validation.

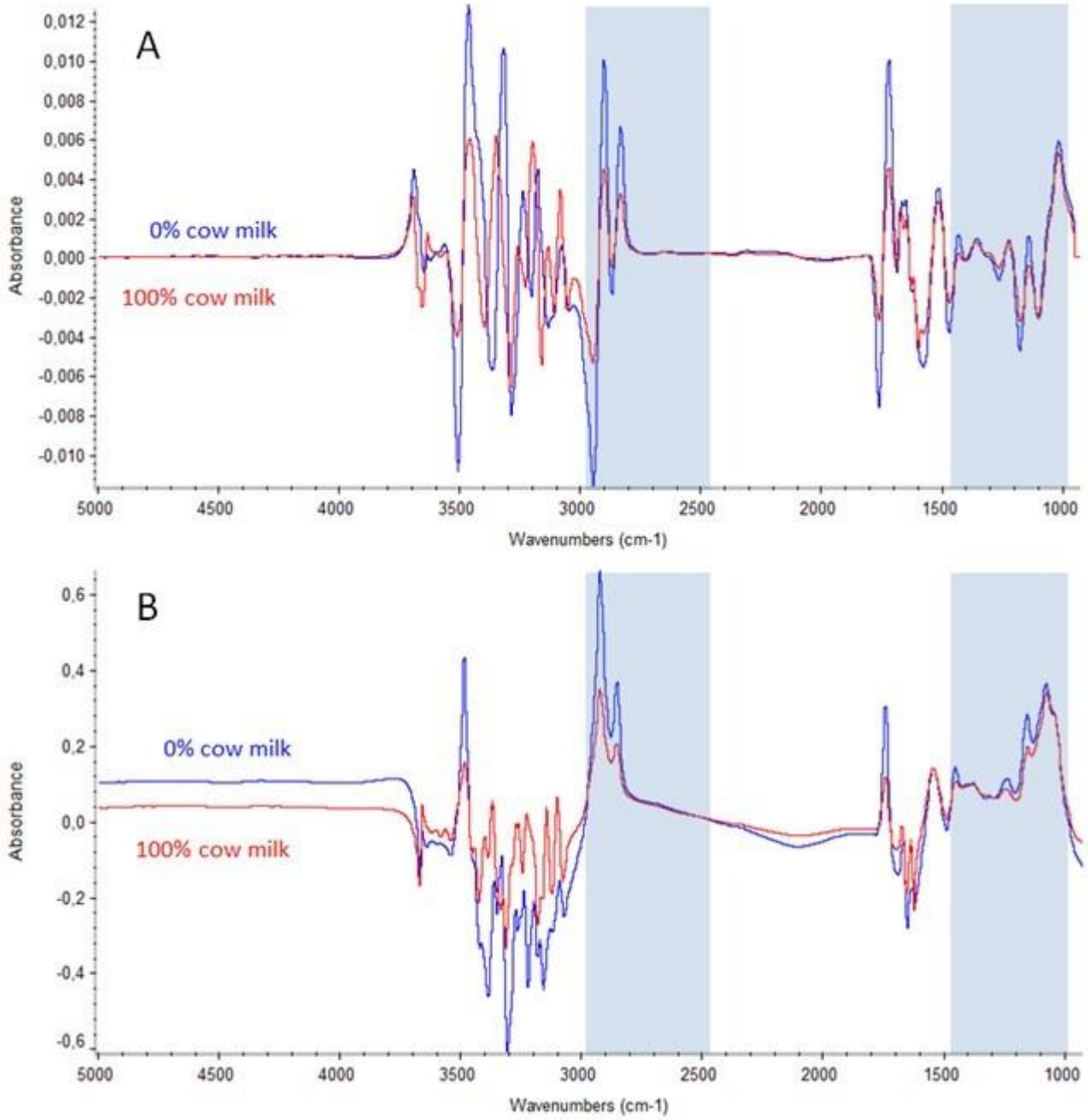

Figure 1. Treaded (A) and Original (B) MIR spectra. The spectral pre-treatment was performed by First derivative and Norris derivative filter smoothing. One of the 0% cow milk (=100% buffalo milk) standards and one of the 100% cow milk standards are shown in blue and in red, respectively. Spectral regions considered for the PLS calibration are indicated in blue shadow.

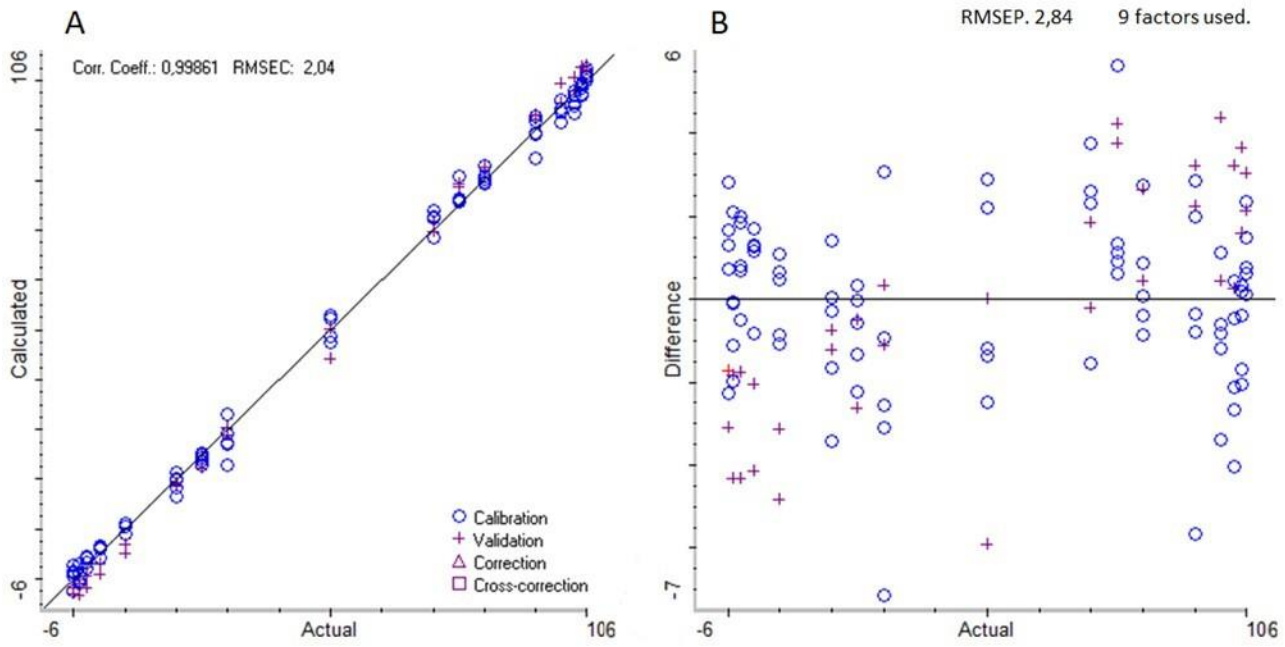

Figure 2. Calibration results for the prediction (% vol/vol) of cow's milk in buffalo milk using the PLS calibration after spectral pre-treatment. A-panel: calculated vs. actual plot of the 119 standards used as calibration (n=85) and validation (n=34) spectra; B-panel: difference plot showing the differences between calculated and actual values vs. the actual values.