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Handheld NIRS analysis for routine meat quality control: Database transfer from at-line instruments

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ABSTRACT

Innovative advances in Near Infrared Spectroscopy (NIRS) instrumentation have enabled the development of new miniaturized spectrometers that combine NIRS technology with micro-electro-mechanical platforms, thus opening up new horizons for industrial NIRS applications. Many agro-food industries, laboratories and research centres already have large databases/libraries, built up over many years using NIR spectrometers; it is clearly important to preserve these data sets in order to avoid having to research and develop NIRS applications from scratch every time a new instrument appears on the market. Three standardization algorithms—Direct Standardization (DS), Piecewise Direct Standardization (PDS) and Spectral Difference by Wavelengths (SDW)—and varying numbers of standardization samples were evaluated for transferring meat quality databases from a high-performance at-line NIRS monochromator to a handheld based on micro-electro-mechanical systems (MEMS) NIRS spectrometer. The SDW algorithm and the use of 8 standardization samples yielded the best Standard Error of Prediction (SEP) values for the three chemical parameters transferred (0.72% for fat, 0.73% for moisture and 0.66% for protein). The successful transfer of the database to the MEMS-NIRS device enables a new approach for fast, low-cost, on-line/in-situ analysis of meat products.

1. Introduction

Near Infrared Spectroscopy (NIRS) has been widely tested for the quantitative prediction of chemical composition in meat products. High-performance spectrometers working in controlled laboratory environments—i.e. at-line—have demonstrated potential for this purpose, though sample preparation remains laborious; several on-line approaches have been also tested [1–4]. However, for industrial purposes there is clearly a need for cost-effective, non-destructive, quality control systems that enable measurements to be made quickly, accurately and easily. Traditional NIR spectroscopy sensor designs are not suited to these challenges, and recent years have seen the development and marketing of new handheld devices offering a whole range of advantages: small size, robustness, low cost, ergonomic design, ease of analysis, simple user interface and portability. These new devices enable new applications to be implemented directly in an industrial setting [5].

The many databases constructed to date for at-line analysis using non-portable instruments have required considerable investments in terms of time (years), resources, labour and analytical costs. Moreover, they may contain specific samples which are critical for the construction of robust models, since they represent the variability encountered over a long period. It is clearly crucial to preserve these data sets in order to avoid having to research and develop NIRS applications from scratch every time a new instrument appears on the market. However, calibration models obtained using one instrument cannot yet be readily used on a different instrument, even when the optical and electronic design is the same since they do not produce exactly the same spectrum for the same sample analyzed [6], due to a number of constraints such as wavelength accuracy, dynamic range, distance of sample to optics, detector photometric response or functionality changes with temperature [7]. Fearn [8] and Feudale et al. [9] have reviewed various mathematical algorithms and methodologies, known as calibration transfer or standardization strategies, to transform models or data measured on a given device so that they can be used by a different device.

Miniature handheld near-infrared (NIR) spectrometers are powerful instruments that can be based on a combination of micro-electro-mechanical system (MEMS) technology and digital transform spectroscopy (DTS), although there are other technologies to design this kind of devices. They have several advantages over traditional instrumental designs, especially for non-destructive on-line or in-situ analysis. The MEMS silicon chip is a fixed, rapidly-tunable, high-contrast pixelate optical filter or diffraction grating for wavelength selection. Used in conjunction with DTS and a single detector, it enables equipment costs to be lowered, while ensuring the elimination

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of detector noise and providing a robust design with non-moving parts [10]. A number of recent papers have evaluated this technology in the agro-food area [11–15].

A large feed dataset has been successfully transferred from a NIRS scanning monochromator instrument to a MEMS-NIRS spectrometer using a simple correction based on the Spectral Differences at each Wavelength between the two instruments (SDW algorithm) [12]. However, no published studies have yet focused on transferring calibration models for predicting quantitative chemical composition in highly moisture-sensitive meat products. There are two critical factors in the database transfer process: the mathematical algorithm applied for standardization and the use of an optimal number of standardization samples [8,9,16].

The purpose of this study is to transfer calibration models for predicting meat chemical composition (fat, moisture and protein) to a handheld MEMS-NIRS instrument, with no significant loss of performance, from a NIRS monochromator using a large database built up over a number of years using the latter high-performance at-line spectrometer. So, the present study sought to evaluate the performance of three standardization algorithms: Direct Standardization (DS) and Piecewise Direct Standardization (PDS) are fast, easy-to-use algorithms which have provided good results in similar studies; and the Spectral Differences at each Wavelength (SDW) algorithm has also performed well with the MEMS-NIRS instrument tested here. At the same time, the study aimed to optimize the number of standardization samples required when transferring databases and calibrations from a NIRS scanning monochromator (slave) to a MEMS-NIRS handheld instrument (master).

2. Materials and methods

2.1. Sample sets

A dataset of 342 Iberian pork-muscle samples (set *O*) captured using a high-performance NIRS monochomator was transferred to a handheld MEMS-NIRS spectrometer. The dataset comprised spectra for several ground Iberian pork muscles (*gluteus medius, masseter* and *longissimus dorsi*) collected in various years (1999, 2000, 2001, 2003, 2004 and 2009). The salient features of this database—sample characteristics, population structures, NIRS measurements, spectral repeatability, reference analysis and calibration development—have been described in detail by Zamora-Rojas et al. [17].

A separate set of 235 samples of ground Iberian pork muscle *(longissimus dorsi)* collected in 2010 was used for standardization and evaluation. When investigating highly moisture-sensitive products such as meat, most authors recommend the use of real samples rather than generic standards to perform the standardization, since the latter cannot represent the entire experimental domain or the range of spectrum patterns encountered for these products [8]. The SELECT algorithm developed by Shenk and Westerhaus [18]—a function available in the WinISI software package for choosing the most representative samples based on a Mahalanobis distance analysis—was used to split the dataset into a standardization set (30 samples, set *S*) and a validation-test set (205 samples, set V_{spec}) in order to enable spectral evaluation of the database transfer. In order to determine the optimal number of standardization samples required by each algorithm, the standardization set (set *S*) was subdivided into 12 sub-groups comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20 and 30 samples, respectively. In each case, the samples contained in the sub-group were identified by the SELECT algorithm as the most representative of the 30-sample standardization set. Sixty samples from the 205-sample validation set (set V_{spec}), also selected as the most representative using the SELECT procedure, were analyzed by wet chemistry for protein (ISO-R-1443), fat (ISO-R-937) and moisture (ISO-R-1442). These 60 samples, henceforth referred to as set V_{pre}, were used for validation of the calibration models transferred. These selections were based on MEMS-NIRS spectra since this instrument is the master.

2.2. Near Infrared Spectroscopy analysis

Two instruments were used for measuring the sample sets described above (sets *S* and V_{spec}); set *O* was measured only on the monochromator instrument:

1. A high-performance at-line NIRS monochromator (FNS) (Foss NIRSystems 6500 spectrometer, Foss-NIRSystems Inc., Sylver Spring, MD, USA), equipped with a spinning module. The instrument operates in the 400–2500 nm spectral range with a spectral wavelength interval of 2 nm. Ground and homogenized samples were analyzed in standard circular cups (diameter 3.75 cm). Two subsamples were analyzed for each sample and each spectrum was the average of 32 scans collected in reflectance mode.
2. A handheld MEMS (micro-electro-mechanical system)-based NIRS digital transform spectrometer (MEMS-NIRS) (Phazir1624, Polychromix Inc., Wilmington, MA, USA), working in reflectance mode in the spectral range 1600–2400 nm with a non-constant interval of around 8 nm (pixel resolution 8 nm, optical resolution 12 nm). Sensor integration time was 600 ms. The device was equipped with quartz protection to prevent dirt accumulation. Four spectra were taken for each sample—i.e. two spectra per sub-sample—and each spectrum was the mean of 10 scans with a lamp warm-up time of 45 seconds. These measurements were performed after monochromator analysis, removing the ground samples from the circular cup.

2.3. Data analysis

Spectral repeatability was evaluated using the Root Mean Square (RMS) statistic, calculated as the averaged root mean square of differences between replicates of the spectral values [19]. Zamora-Rojas et al. [17] have recommended a cut-off value of 11250 μlog(1/R) for ground pork analyzed in a NIRS scanning monochromator. Replicates with large RMS in both instruments were removed. Of the remaining spectra, the average spectrum of each sample was used for further calculations.

Since the FNS and MEMS-NIRS spectrometers differ both in wavelength range and in spectral wavelength interval step, a shape-preserving piecewise cubic interpolation aimed at preserving convexity to scattered convex data was used to trim the NIRS scanning monochromator range to the 100 wavelengths of the MEMS-NIRS device [12]. After trimming and interpolating, three standardization algorithms were evaluated for each standardization sub-group: the Direct Standardization (DS) algorithm [20], the Piecewise Direct Standardization (PDS) algorithm [21], and the Spectral Differences at each Wavelength (SDW) correction [12]. The first two procedures are based on the construction of a transformation matrix using standardization samples measured in both instruments. That matrix, calculated using a local Partial Least Squares (PLS) regression model for each wavelength of the master instrument and the corresponding wavelength on the slave instrument, was used to transform slave-measured spectra to the master instrument—i.e. to transfer the database from the FNS (slave) to the MEMS-NIRS device (master); MEMS-NIRS instrument has been selected as the master to simplify future NIR analysis—at user level—with this instrument, avoiding the use of a correction (standardization) for every single spectrum taken to look like spectra recorded in the FNS. In the case of the PDS algorithm, local multivariate models were computed for each spectral window around a given wavelength; this required optimization of the window size (ranging from 3 to 31) and of the number of latent variables used in each PLS model. The third procedure (SDW) involved adding to the slave instrument (FNS) the difference, at each wavelength, between

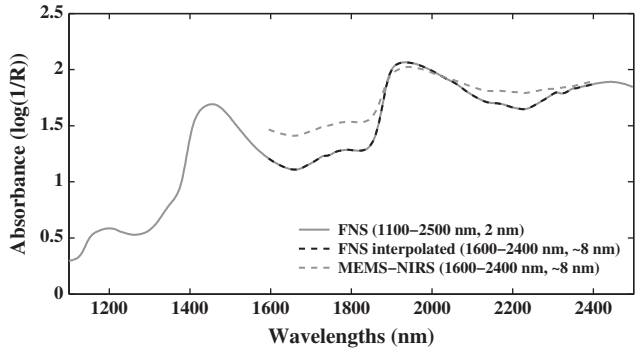

Fig. 1. Average spectra for ground pork samples measured with FNS and MEMS-NIRS devices.

the values of the average spectrum of the standardization set measured on MEMS-NIRS and the mean spectrum of the same samples measured on the FNS. The Root Mean Square Error (RMSE), calculated as the average of the absorbance differences for each wavelength before and after the application of the different standardization algorithms (DS, PDS and SDW) and procedures, was evaluated for each sample in the validation-test set (V_{spe}) to check standardization performance spectrally.

Once the best standardization procedures had been selected and the database had been transferred, multivariate quantitative models based on the Modified Partial Least Squares (M-PLS) algorithm for the prediction of fat, moisture and protein composition were constructed using the MEMS-NIRS spectrometer. Since the original database (set *O*, comprising 342 samples) came from a FNS instrument, the models constructed using that database, as published by Zamora-Rojas et al. [17], were taken as the starting-point for comparing the quantitative results of standardization. Thus, spectrum pre-processing, calibration development and statistical evaluation performed with the original database were evaluated against the transferred database. The following statistics were used to select the best models: Standard Error of Calibration (SEC), Standard Error of Cross-Validation (SECV), Determination Coefficient of Cross-Validation (R^2_{cv}) and Residual Predictive Deviation (RPD). The Standard Error of Prediction (SEP) derived from the validation of set V_{pre} (60 samples) was also used to compare calibration transfer performance, together with the statistics Global Mahalanobis distance (GH) (distance between a sample and the center of the calibration set) and Neighbor Mahalanobis distance (NH) (distance between any sample and the most similar sample in the calibration set).

WinISI software (Infrasoft International, Port Matilda, PA, USA) was used for spectral repeatability evaluation and for calibration development. MATLAB ver 7.6 (The MathWorks, Natick, USA) was used for calibration transfer calculations (trimming, interpolating and SDW). PLS Toolbox (Eigenvector Research, Manson, USA) was used for DS and PDS algorithms.

3. Results and discussion

The first point to highlight is the difference in spectral range and wavelength interval between instruments (Fig. 1). In order to evaluate the influence of instrumental design differences, M-PLS models were constructed using the FNS and the database (set *O)* over the wavelength range common both to the FNS and the MEMS-NIRS instrument (1600–2400 nm) and also using the same wavelength interval (a non-constant step of around 8 nm). The results are shown in Table 1. Results on the FNS for accuracy and performance when the wavelength range was trimmed to 1600–2400 nm were similar, for all three chemical parameters, to those reported by Zamora-Rojas et al. [17] using the 1100–2500 nm range. When the 400 wavelengths of the FNS in the 1600–2400 nm range were interpolated to the 100 wavelengths of the MEMS-NIRS device, the models constructed using the NIRS scanning monochromator displayed a larger number of PLS factors, except in the case of protein, and a drop in accuracy. SEP values were 0.5% for fat, 0.63% for moisture and 0.55% for protein using measurements performed on the FNS instrument with the trimmed and interpolated M-PLS models (Table 1). This represents an increase of 0.06% and 0.25% in the SEP values of set V_{pre} compared to the reference models (range 1100–2500 nm, wavelength interval 2 nm) for fat and moisture, respectively. However, in the case of protein the SEP was lower in the trimmed and interpolated FNS model compared to the one selected as reference. These results indicate that the spectral range and wavelength interval can influence the model's predictive ability. The unstandardized trimmed and interpolated models constructed using the FNS spectrometer were not suitable for spectra measured on the MEMS-NIRS instrument. The SEP values obtained were 4.34% for fat, 0.63% for moisture and 2.57% for protein, indicating that the moisture parameter—unlike the other two—may not require standardization. Nevertheless, the Global Mahalanobis distance (GH) and Neighbor Mahalanobis distance (NH) indicated major differences between FNS database spectra and MEMS-NIRS spectra (GH = 30.91 and NH = 23.00, respectively) probably due to the lack of wavelength accuracy and absorbance scale changes, confirming the need for standardization.

Table 1
Statistics for M-PLS models to predict fat, moisture and protein using FNS instrument.

Parameter	Range (nm)/wavelength interval (nm)	Mean (%)	SD (%)	No. PLS factors	SEC (%)	SECV (%)	R^2_{CV}	RPD_{CV}	SEP (%)	GH	NH
Fat	*1100–2500/2	7.03	3.51	6	0.34	0.35	0.99	10.02	0.44^+	0.80^+	0.46^+
	1600–2400/2	6.82	3.30	6	0.32	0.33	0.99	10	0.38^+	1.07^+	0.31^+
	1600–2400/~8	6.71	3.21	12	0.37	0.38	0.99	8.44	0.50^+	1.14^+	0.27^+
									$4.34^\wedge$	$30.91^\wedge$	$23.00^\wedge$
Moisture	*1100–2500/2	70.07	3.35	7	0.44	0.46	0.97	7.28	0.38^+	0.80^+	0.46^+
	1600–2400/2	70.51	2.71	5	0.44	0.45	0.97	6.02	0.48^+	1.07^+	0.31^+
	1600–2400/~8	70.51	2.72	12	0.43	0.45	0.97	6.04	0.63^+	1.14^+	0.27^+
									$0.63^\wedge$	$30.91^\wedge$	$23.00^\wedge$
Protein	*1100–2500/2	21.52	1.68	7	0.49	0.52	0.90	3.23	0.76^+	0.80^+	0.46^+
	1600–2400/2	21.49	1.67	7	0.49	0.52	0.90	3.21	0.68^+	1.07^+	0.31^+
	1600–2400/~8	21.51	1.67	5	0.61	0.62	0.86	2.69	0.55^+	1.14^+	0.27^+
									$2.57^\wedge$	$30.91^\wedge$	$23.00^\wedge$

All models were pre-treated with SNV + DT (1, 10, 5, 1). SD: Standard Deviation; SEC: Standard Error of Calibration; SECV: Standard Error of Cross-Validation; R^2_{CV}: Determination Coefficient of Cross-Validation; RPD: Residual Predictive Deviation; SEP: Standard Error of Prediction; GH: Global Mahalanobis distance; NH: Neighbor Mahalanobis distance (SEP, GH and NH values were calculated with validation set V_{pre} comprising 60 samples).
*Published by Zamora-Rojas et al. [17].
+Spectra measured on FNS instrument.
^Spectra measured on MEMS-NIRS device.

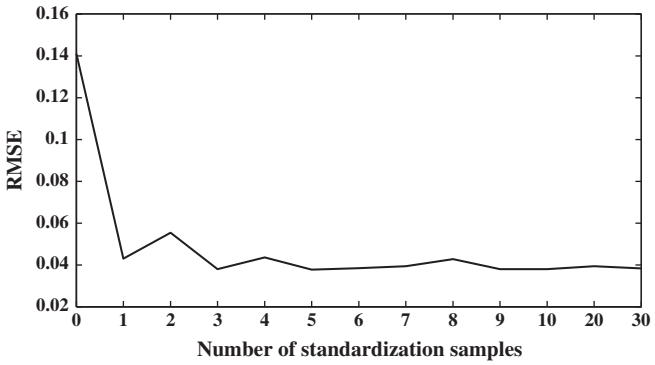

Fig. 2. Average Root Mean Square Error (RMSE) values for spectral differences before and after SDW standardization for the validation set V_{spe} (205 samples) based on the number of standardization samples used.

After trimming and interpolation, the various standardization strategies were evaluated using the sub-groups formed for that purpose. The SDW algorithm calculated the difference between the mean spectrum of the standardization sub-group measured in the handheld MEMS-NIRS instrument and the mean spectrum of the same samples measured in FNS. This was done for each standardization sub-group, and the differences were added to each spectrum measured on the FNS to obtain the standardization validation-test set V_{spec} (205 samples) as on the MEMS-NIRS spectrometer. Fig. 2 shows the average RMSE values calculated as the mean of all the RMSE tests performed, by wavelengths, for the SDW algorithm, depending on the number of standardization samples used. The use of 5 standardization samples yielded the minimum RMSE value (0.0377), indicating that 5 samples measured in both instruments may be enough to ensure a successful calibration transfer. DS and PDS were also evaluated. DS recorded a minimum average RMSE value using 4 standardization samples, while PDS required 10 standardization samples with a window size of 7 wavelengths (influence of different number of standardization samples in the DS and PDS algorithms not shown).

RMSE values for each wavelength before and after application of the best transfer parameters for each standardization algorithm evaluating the V_{spe} set measured in both instruments are shown in Fig. 3. The results indicated considerable differences in spectra between FNS and MEMS-NIRS; however, those differences were reduced using either of the standardization algorithms with the optimized number of samples (SDW with 5 standardization samples, DS with 4 standardization samples or PDS with 10 standardization samples). Although these results confirmed that standardization successfully reduced spectral differences between instruments for the validation-test set V_{spe} (Fig. 4a), when the three algorithms were applied to the large database (set *O*) constructed over several

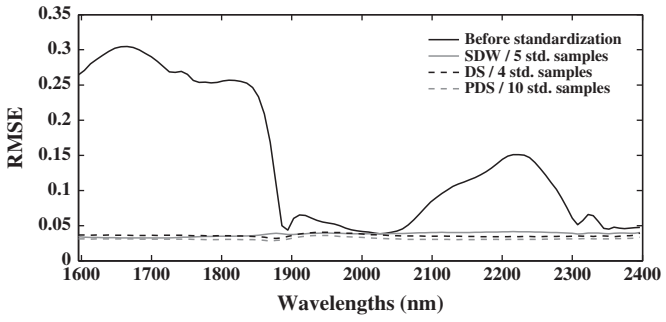

Fig. 3. Root Mean Square Error (RMSE) values for each wavelength before and after the application of the different standardization algorithms evaluated for the validation set V_{spe} (205 samples). std. samples = number of standardization samples.

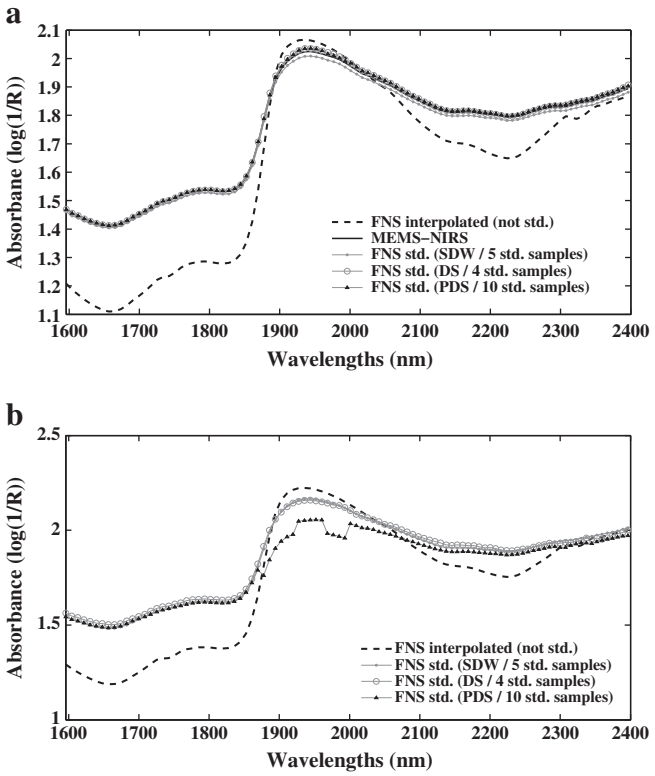

Fig. 4. Mean spectra of the standardization validation set V_{spe} (205 samples) (a) and the original calibration database *O* (342 samples) (b) before and after the application of the different standardization algorithms. not std. = unstandardized; std. = standardized; std. samples = number of standardization samples.

years using the FNS instrument, each strategy performed differently. Fig. 4b shows average spectra for the database *O* before (trimmed and interpolated FNS) and after application of the three standardization strategies. It is observed that SDW and DS strategies performed well, while the PDS algorithm displayed jumps at certain wavelengths, which modified spectral shape, thus indicating poor calibration transfer. These are observations based on the average spectra for all the samples of the database *O*, but a detailed analysis showed that the DS method proved unacceptably noisy, particularly at longer wavelengths, for individual samples especially for those collected at much earlier stages.

These visual results were borne out by the fact that calibration models constructed using the PDS transfer matrices wholly lacked statistical significance and accuracy. Although the strategy worked well for the transfer of the 205 samples of the V_{spe} set measured at the same time in both instruments (Fig. 4a), it failed to work when samples measured in the NIRS monochromator in earlier years were transferred (Fig. 4b). This may be because samples measured in FNS at earlier periods underwent spectral changes due to instrumentation-related issues, moisture-sensitive sample conditions and other factors [17] known to affect the performance of meat-database standardization. Gemperline et al. [22] also indicated that these discontinuities in the PDS transferred spectra can be due to swap of eigenvalues that are similar in magnitude between adjacent windows what produce different models in neighboring windows. The discontinuities were particularly apparent with large time-lapse: samples from database *O* collected in 2009—i.e. a date close to the standardization-set collection date—were transferred correctly, while samples collected in 1999, 2000 or 2001 were not (not shown). It should be also mentioned that using a standardization set built with only samples from 2010 can have a risk of lack of robustness of the calibration transfer for samples of earlier periods as it is observed in the results.

Table 2
Statistics for M-PLS models to predict fat, moisture and protein transferred to the MEMS-NIRS device (1600–2400 nm with a non-constant step of around 8 nm).

Parameter	Standardization	Mean (%)	SD (%)	No. PLS factors	SEC (%)	SECV (%)	R^2_{CV}	RPD_{CV}	SEP (%)	GH	NH
Fat	DS method / 4 std. samples	6.53	2.88	3	0.61	0.61	0.96	4.72	0.59^	2.43^	0.09^
	SDW method / 8 std. samples	6.66	3.15	13	0.37	0.39	**0.98**	8.08	**0.72^**	**0.96^**	**0.28^**
Moisture	DS method / 4 std. samples	70.40	2.75	4	1.62	1.64	0.64	1.67	9.33^	2.43^	0.09^
	SDW method / 8 std. samples	70.48	2.73	12	0.44	0.47	**0.97**	5.81	**0.73^**	**0.96^**	**0.28^**
Protein	DS method / 4 std. samples	21.56	1.62	3	1.38	1.38	0.28	1.17	1.16^	2.43^	0.09^
	SDW method / 8 std. samples	21.50	1.66	5	0.62	0.66	**0.85**	2.51	**0.66^**	**0.96^**	**0.28^**

All models were pre-treated with SNV + DT (1,10,5,1). SD: Standard Deviation; SEC: Standard Error of Calibration; SECV: Standard Error of Cross-Validation; R^2_{CV}: Determination Coefficient of Cross-Validation; RPD: Residual Predictive Deviation; SEP: Standard Error of Prediction; GH: Global Mahalanobis distance; NH: Neighbor Mahalanobis distance (SEP, GH and NH values were calculated with validation set V_{pre} comprising 60 samples). ^Spectra measured on MEMS-NIRS device.
Bold values indicate the best transferred models.

The DS algorithm showed a noisy tendency at longer wavelengths when applied to the calibration set *O* (342 samples from different years). This tendency was most marked for samples collected at a much earlier stage, presumably for the reasons suggested above for PDS. The models obtained using the DS method and 4 standardization samples (this being the number yielding the lowest RMSE values for spectral differences between instruments) are shown in Table 2. The results suggest that the models obtained were not suitable for screening purposes in meat analysis, and especially for moisture or protein prediction, given that SEP values (9.33% and 1.16%, respectively) were larger than those shown in Table 1 and showed low R^2_{cv} (0.64 and 0.28, respectively). However, the models displayed acceptable predictive ability for the fat parameter (SEP = 0.59%).

The Spectral Differences by Wavelength (SDW) algorithm yielded a different pattern. Spectra transferred both from the validation set and from the calibration database retained their shape for all samples; as the mean spectrum for the calibration set *O* shows (Fig. 4a–b), but also a detailed individual analysis of the samples. This suggests that the SDW strategy is more robust than the other methods when is applied to samples measured at an earlier stage than the standardization set used.

This method was applied to each standardization sub-group, evaluating the original database *O* in each case. A transferred database was thus constructed individually with the added differences calculated for each standardization sub-group. To evaluate the performance of the transferred models, the validation set V_{pre} (60 samples) measured on the MEMS-NIRS device was predicted using each model and SEP values for each analytical parameter were calculated. SEP values calculated for each transferred model, depending on the number of standardization samples used for the SDW algorithm, are shown in Fig. 5. Prior to standardization, SEPs were 4.34% for fat, 0.63% for moisture and 2.57% for protein; GH and NH were also very high (Table 1). However, SEP, GH and NH values were all reduced using the SDW method with 8 standardization samples (Table 2). Although 5 standardization samples yielded the best RMSE values for mean spectra measured in the two instruments using SDW, the best SEP values were obtained using a standardization sub-group of 8 samples (0.72%, 0.763% and 0.66% for fat, moisture and protein, respectively), which also provided a suitable spectral fitting as demonstrated by GH and NH values (0.96 and 0.28, respectively; Table 2). A similar study performed to transfer a large feed (heterogeneous product) database from a FNS instrument to a MEMS-NIRS device used 14 standardization samples, although no attempt was made to optimize that number [12].

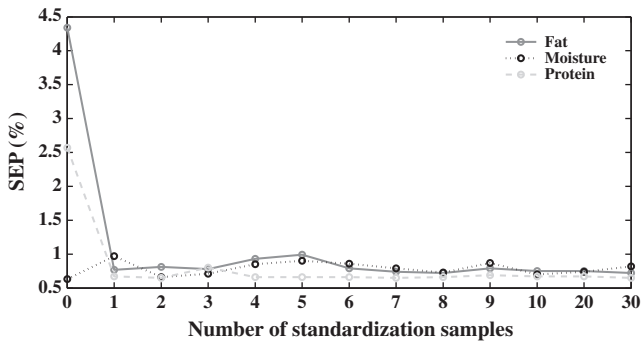

Fig. 5. Standard Error of Prediction (SEP) of the validation set V_{pre} (60 samples) measured on the MEMS-NIRS device for predicting chemical composition using the SDW-transferred models.

The SEP results obtained (Fig. 5) indicated that the prediction of moisture was not greatly improved using transferred rather than untransferred models; however, calibration transfer successfully reduced errors, especially GH and NH statistics, for fat and protein prediction. The statistics for the best transferred model (SDW/8 standardization samples) indicated greater accuracy than that obtained using the FNS models over the same wavelength range and interval as the MEMS-NIRS instrument without being transferred for predicting samples measured on the handheld device (Table 1). Moreover, the GH and NH statistics indicated good spectral matching with the library when standardization was performed by SDW, dropping from 30.91 (GH) and 23.00 (NH) to 0.78 (GH) and 0.26 (NH) for the MEMS-NIRS spectra of the validation set V_{pre}.

Although the performance of the transferred models (Table 2) proved slightly less accurate than the at-line models developed for the NIRS scanning monochromator (Table 1), they are still suitable for meat analysis. Moreover, the slight loss in accuracy is more than offset by the practical and technical advantages afforded by the handheld MEMS-NIRS spectrometer, which enables in-situ analysis with readily-available results for each individual sample. Moreover, sample presentation is easier—there is no need to fill the cup, as required by the monochromator—and analysis is faster; the FNS requires over 1 minute per subsample, while the MEMS-NIRS device requires only 2 seconds. Additionally, the MEMS-NIRS instrument is cheaper, and minimal staff training is required for routine analysis. The MEMS-NIRS instrument is thus highly suitable for meat industrial applications. Finally, model accuracy is likely to be improved when new samples analyzed directly in the MEMS-NIRS instrument are included in the database.

4. Conclusions

The Spectral Differences by Wavelength method (SDW) performed better than the other strategies tested for transferring quantitative models for the prediction of fat, moisture and protein composition in ground pork samples from a NIRS scanning monochromator to a handheld MEMS-NIRS instrument. Eight standardization samples were sufficient for standardization purposes. This study showed that large databases containing important sample spectra collected over several years can successfully be transferred to new devices that are more suitable for in-situ analysis at industrial level.

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