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1 **Evaluation of Vis-NIR hyperspectral imaging as a process analytical tool to classify**
2 **brined pork samples and predict brining salt concentration**

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9

10 Abstract

11 Hyperspectral imaging in the visible and near infrared spectral range (450-1664 nm) coupled
12 with chemometrics was investigated for classification of brined and non-brined pork loins
13 and prediction of brining salt concentration employed. Hyperspectral images of control, water
14 immersed and brined (5, 10 or 15% salt (w/v)) raw and cooked pork loins from 16 animals
15 were acquired. Partial least squares (PLS) discriminative analysis models were developed to
16 classify brined pork samples and PLS regression models were developed for prediction of
17 brining salt concentration employed. The ensemble Monte Carlo variable selection method
18 (EMCVS) was used to improve the performance of the models developed. Partial least
19 squares (PLS) discriminative analysis models developed correctly classified brined and non-
20 brined samples, the best classification model for raw samples (Sen = 100%, Spec = 100%, G
21 = 1.00) used the 957–1664 nm spectral range, and the best classification model for cooked
22 samples (Sen = 100%, Spec = 100%, G = 1.00) used the 450-960 nm spectral range. The best
23 brining salt concentration prediction models developed for raw (RMSE_p 1.9%, R²_p 0.92) and
24 cooked (RMSE_p 2.6%, R²_p 0.83) samples used the 957-1664 nm spectral range. This study
25 demonstrates the high potential of hyperspectral imaging as a process analytical tool to
26 classify brined and non-brined pork loins and predict brining salt concentration employed.

27

28 Keywords

29 Hyperspectral imaging, chemometrics, brining, prediction, classification, pork meat, process
30 analytical technology.

31

32 1. Introduction

33 Process analytical technology (PAT) is defined as a system for designing, analysing and
34 controlling manufacturing through timely measurement of critical quality and performance
35 attributes of raw and in process materials and processes, with the goal of ensuring final
36 product quality (FDA, 2004). The adoption of PAT in the food industry is driven by the
37 requirements of regulators, consumers and companies, as well as environmental sustainability
38 (O'Donnell, 2014).

39 Brining enhances the flavour, texture and shelf life of meat and is widely employed in meat
40 processing. Salt acts as a water binding ingredient in meat products, and helps to solubilise
41 meat proteins and to enhance water holding capacity (WHC) by altering the myofibril
42 structure of proteins (Ruusunen and Puolanne, 2005). Salting also influences the juiciness of
43 meat and product cooking yield (Inguglia et al., 2017; Xiong, 2005). However excess salting
44 may dehydrate meat samples (Barat et al., 2009). Variability in salt uptake can lead to
45 textural defects and can influence the shelf life of the brined pork (Alvarado and McKee,
46 2007; Fulladosa et al., 2015). Furthermore, the ability to classify brined and non-brined pork,
47 and to predict the brining salt concentration employed during processing are also important
48 from an industry perspective.

49 Titration techniques are commonly used for salt content determination in meat products
50 (Sharedeh et al., 2015). However these techniques are time consuming, require sample
51 preparation, use of chemicals as well as trained operators (De Prados et al., 2015). Non-
52 destructive technologies have been investigated to monitor the salting process including x-ray
53 absorptiometry, microwave dielectric spectroscopy (Castro-Giráldez et al., 2010), computed
54 tomography (Vestergaard et al., 2004), magnetic induction (Schivazappa et al., 2017), laser
55 induced breakdown spectroscopy (Dixit et al., 2018) and NIR spectroscopy (Campos et al.,

56 2017; Collell et al., 2011; Collell et al., 2012; Gaitán-Jurado et al., 2008). Application of any
57 of these techniques has not been reported to date to monitor pork brining processes, to
58 classify brined and non-brined pork or to predict brining salt concentration employed.

59 Spectroscopic sensors provide mainly chemical information but not the spatial information
60 required for analysis of heterogeneous samples such as meat samples (Millar et al., 1996;
61 Prieto et al., 2006). Hyperspectral imaging (HSI) may be suitable for online assessment of
62 brining processes as it provides both spatial and spectral information of samples by
63 combining imaging and spectroscopic tools. HSI is also non-invasive and does not require
64 sample preparation (Gowen et al., 2007). Hyperspectral images or hypercubes are three-
65 dimensional blocks of data, comprising one spectral (wavelength (λ)) and two spatial
66 dimensions (pixels (X, Y)). Each pixel in a hyperspectral image contains the spectrum of that
67 specific position, representing the light-absorbing and/or scattering properties of the spatial
68 region represented, which can be used to characterise the composition of that particular pixel.
69 Hyperspectral imaging has been investigated as a process analytical tool for food applications
70 including on line process control. (Gowen et al., 2007). HSI was used to study salting kinetics
71 of raw pork samples at a fixed brine concentration of 30% salt (Liu et al., 2013). The
72 potential of Vis-NIR hyperspectral imaging to classify brined and non-brined meat samples
73 or predict the brining salt concentration has not been reported to date.

74 The most common chemometric analysis tools used to evaluate and extract information from
75 hyperspectral imaging data are: (i) principal component analysis (PCA), (ii) partial least
76 squares (PLS) and (iii) variable selection. Spectral pre-treatments may be employed to correct
77 for the effects of natural variability in the shape and size of samples, light scattering and
78 differences in the effective path length on Vis-NIR spectra, which can cause difficulties in the
79 application of HSI for quality assessment (Esquerre et al., 2012b). PCA is one of the most
80 frequently employed techniques for reducing dimensionality of hyperspectral images and is

81 commonly used as an exploratory tool in analysis of hyperspectral imaging (Burger and
82 Gowen, 2011). PCA can be applied to any data matrix (properly transformed and scaled) to
83 extract the dominant patterns in the matrix in terms of complementary set of scores and
84 loadings plots; with the goal of finding relationships between objects, to delineate classes, to
85 detect outliers, or for data reduction (Geladi et al., 1989). Partial least squares discriminant
86 analysis (PLS-DA) is one of the most frequent classification methods employed in
87 hyperspectral imaging data for classification of objects belonging to one or more classes.
88 Calibration techniques such as partial least squares regression (PLS-R) are routinely
89 employed in hyperspectral imaging analysis for prediction of unknown concentrations and
90 generation of prediction maps to estimate spatial distribution of components in a sample
91 (Gowen et al., 2014). Variable selection methods have been demonstrated to improve the
92 performance of hyperspectral imaging models and to reduce the processing times required by
93 selecting the most informative wavelengths in reported studies including those for the early
94 detection of bruise damage in mushrooms (Esquerre et al., 2011), viability and vigour in
95 muskmelon seeds (Kandpal et al., 2016), fat and moisture content in ground beef (Zhao et al.,
96 2017), internal damage in cucumbers and whole pickles (Ariana and Lu, 2010) and mixing
97 quality of food powders (Achata et al., 2018).

98 The objective of this study was to investigate the potential of Vis-NIR hyperspectral imaging
99 combined with chemometrics as a process analytical tool to classify brined and non-brined
100 pork loins and predict the brining salt concentration employed for both raw and cooked
101 samples.

102

103 **2. Materials and methods**

104 **2.1. Pork samples**

105 Fresh pork loins (PLs) (*Longissimus dorsi*) from 16 animals were obtained from local
106 supermarkets and butchers' shops. PLs were trimmed of external fat and connective tissue
107 and divided into samples of 180 ± 20 g and 25 mm thickness ($N = 144$). Samples obtained
108 from each PL was randomly assigned to treatments.

109

110 **2.2. Sample preparation**

111 *2.2.1. Brined and non-brined pork samples*

112 Three types of PL samples were prepared:

113 i) 'Brined' - immersion in brining solutions at concentrations of 5%, 10% and 15% salt
114 (w/v), prepared using vacuum dried NaCl (food grade) and distilled water at a meat to
115 brine mass ratio of 1:8,

116 ii) 'Water immersed' - immersion in distilled water without salt (water immersed
117 samples (WI)) and

118 iii) 'Control' - samples without immersion in water or brine.

119 *2.2.2. Raw and cooked samples*

120 The control samples and half of the brine and water immersed samples were analysed
121 raw (5 (control + 4 treatments) \times 16 PLs = 80 raw samples) and the remaining samples
122 were cooked (4 treatments \times 16 PLs = 64 cooked samples) in a boiling water bath to a
123 final core temperature of 75 °C, measured by a VWR traceable total-range thermometer
124 (Visalia, CA, USA) placed in the geometric centre of the meat sample (Boccard et al.,
125 1981) and stored at 4 °C prior to analysis.

126

127 **2.3. Hyperspectral imaging systems**

128 Hyperspectral images of raw and cooked PLs were obtained using two line scanning
129 hyperspectral imaging systems (DV Optics, Padova, Italy), one in the visible-near infrared
130 (Vis-NIR) range of 400-1000 nm with a spectral resolution of 5 nm and the other in the near
131 infrared (NIR) range of 880-1720 nm with a spectral resolution of 7 nm. The Vis-NIR-HSI
132 system consisted of a CCD camera (580×580 pixels; Balsler, Ahrensburg, Germany), a
133 spectrograph (Spectral Imaging Ltd., Oulu, Finland), cylindrical light diffuser and moving
134 base. The NIR-HSI system consisted of an InGaAs camera (320×240 pixels; Sensors
135 Unlimited, Inc., Princeton, NJ, USA), a spectrograph (Spectral Imaging Ltd., Oulu, Finland),
136 five halogen lamps (3×50 W and 2×20 W), a cylindrical light diffuser, moving base and a
137 computer (Hernández-Hierro et al., 2014). The speed of the moving base was set at 3 mm/s
138 (spatial resolution 0.28×0.28 mm pixel size) and 20 mm/s (spatial resolution 0.3×0.3 mm
139 pixel size) for the Vis-NIR and NIR systems respectively. Calibration of both systems was
140 carried out as follows: 50 scan lines of black reference (I_b) were acquired and averaged by
141 taking a measurement after covering the spectrograph lens with a cap; a white tile with a
142 known reflectance (R_w) was placed on the moving base and used as a “white” reference (I_w)
143 by averaging 50 scan lines and finally the signal from the sample (I_s) was converted and
144 stored as reflectance (R) according to Equation 1 (Achata et al., 2015).

$$R = \frac{I_s - I_b}{I_w - I_b} R_w \quad (1)$$

146 Hyperspectral images of all samples were acquired at room temperature (~20 °C). Spectra
147 were acquired from both sides of all raw and cooked samples. Acquired 3-D data hypercubes
148 were saved in ENVI formatted files and imported into Matlab (The MathWorks Inc., Natick,
149 MA, USA) for further spectral data pre-processing and data analysis (Fig. 1), using in-house
150 developed functions and scripts.

151

152 2.4. Spectral data pre-processing

153 Obtained hypercubes were treated as follows:

- 154 – The spectra obtained from both HSI systems were trimmed to spectral ranges of 450-
155 960 nm and 957-1664 nm to remove the noise present at both ends of the spectra.
- 156 – Hypercubes were unfolded by rearranging the three-dimensional hypercubes (X, Y, λ)
157 into a two-dimensional matrix ($X * Y, \lambda$) to facilitate algorithm development.
- 158 – The background was removed using a mask which was created by comparing the
159 mean value of each pixel's spectrum and removing pixels with mean spectrum value
160 < 0.7 .
- 161 – Dead pixels and spikes were removed by replacing the affected values with the mean
162 values of adjacent bands in the same spectrum. Regions of interest (ROI) were
163 carefully selected from each sample to avoid edge effects detected following analysis
164 of PCA scores maps.
- 165 – The mean spectra of both sides of each sample was calculated and used for model
166 development.

167

168 **2.5. Data analysis**

169 Principal component analysis (PCA), partial least squares discriminative analysis (PLS-DA),
170 and partial least squares regression (PLS-R) chemometric methods were carried out in
171 combination with spectral pre-treatments on both reflectance and logarithm transformed
172 ($\log(1/R)$) Vis-NIR and NIR-HSI spectral data. EMCVS was applied to improve the
173 performance of the developed models.

174 For both PLS-DA and PLS-R model development, raw and cooked spectral data sets were
175 randomly split into calibration sets ($n = 53$ raw; $n = 43$ cooked) to construct the models and
176 validation sets ($n = 27$ raw; $n = 21$ cooked) to test the models. The following spectral pre-

177 treatments were employed to remove scattering effects or baseline shifts and to improve the
 178 models' performance: standard normal variate (SNV), median scaled (MS), Savitzky-Golay 7
 179 points, second order polynomial first derivative (FD), Savitzky-Golay 7 points, second order
 180 polynomial second derivative (SD), linear detrending, second-order polynomial (LD) and
 181 asymmetric least squares (AsLs), and all combinations of any two selected pre-treatments.

182 PLS-DA models were developed to discriminate between brined (5, 10 or 15% (w/v), class =
 183 0) and non-brined (control & WI, class = 1) samples using a threshold of 0.5. PLS-R models
 184 were developed to predict brining salt concentration (BSC). The number of latent variables
 185 (LVs) was selected by analysis of the root mean square error of cross validation (RMSE_{CV})
 186 and roughness of the regression vector (Gowen et al., 2011).

187 A variable selection approach was also investigated to improve the performance of the
 188 models developed. The ensemble Monte Carlo variable selection method (EMCVS) selects
 189 wavelengths with the largest mean normalised regression coefficients, which are estimated
 190 from an ensemble of Monte Carlo procedures (Esquerre et al., 2011). The EMCVS method
 191 was selected as it outperformed other variable selection methods in most cases in previous
 192 studies (Esquerre et al., 2011; Esquerre et al., 2017). This method compares the mean of the
 193 standardised regression coefficients (\bar{C}_j) for each variable in an ensemble of K ($K = 200$ in
 194 this study) Monte Carlo procedures with a threshold in order to select the most informative
 195 wavelengths. Only wavelengths with \bar{C}_j value greater than the threshold were retained. For
 196 each Monte Carlo procedure regression coefficients (β) were calculated N times using M
 197 randomly selected samples to calculate the normalised regression coefficient (C_{jk}) as in Eq.2.

$$198 \quad C_{jk} = \frac{\bar{\beta}_{jk}}{S(\beta_{jk})} \quad (2)$$

$$199 \quad \bar{\beta}_{jk} = \left(\sum_{i=1}^N \frac{\beta_{ijk}}{N} \right) \quad (3)$$

$$S(\beta_{jk}) = \left(\sum_{i=1}^N \frac{\beta_{ijk} - \bar{\beta}_{jk}}{N-1} \right) \quad (4)$$

201 Where $\bar{\beta}_{jk}$ and $S(\beta_{jk})$ are the mean and standard deviation of the regression coefficient of
 202 the j th variable ($j = 1, 2, 3, \dots, p$) over N times ($N = 200$ for this study) of all PLS runs and β_{ijk}
 203 is the regression coefficient for the j th variable in the i th PLS model ($i = 1 \dots N$) for the k th
 204 Monte Carlo procedure ($k = 1 \dots K$). EMCVS was applied iteratively until no more variables
 205 were removed from the data set (Esquerre et al., 2012a; Esquerre et al., 2017).

206

207 3. Results and discussion

208 3.1. Spectral data

209 Mean log (1/R) spectra of the ROIs for the 450-960 nm and 957-1664 nm spectral ranges are
 210 presented in Fig 2a and 2b. It can be observed that baseline shifts and wavelength-dependent
 211 variations obscure trends in the spectra associated with the experimental treatments applied.
 212 To reduce scattering effects and baseline shifts, Savitzky-Golay spectral pre-treatment (7
 213 points, second order polynomial SD) was applied as shown in Fig. 2a and 2b.

214 The main features observed in the 450-960 nm spectra of raw samples in the spectral region
 215 of 545-585 nm can be attributed to myoglobin and oxymyoglobin absorptions (Millar et al.,
 216 1996; Rannou and Downey, 1997). Brined samples have higher absorption at 580 nm than
 217 non-brined samples, which may be related to the oxidation of myoglobin pigments to
 218 oxymyoglobin in the presence of salt (Eskin et al., 2013). This is in accordance with
 219 previously reported meat studies where the oxidation of myoglobin caused an increase in
 220 absorbance at 545 and 575 nm (Kerry et al., 2003; Rannou and Downey, 1997). Spectra of
 221 cooked PLs in this region (450-960 nm) exhibit large peaks at 545, 580 and 650 nm which
 222 correspond to myoglobin, oxymyoglobin and metmyoglobin respectively (Millar et al., 1996).

223 The main features that differentiate brined and non-brined samples observed in the 957-1664
224 nm spectral range of raw samples are at 1153 and 1398 nm, which correspond to the second
225 overtone of C–H bond stretching and C–H combination bands respectively (Osborne et al.,
226 1993). At these wavelengths brined samples have larger peaks than non-brined samples.

227 In cooked samples, large differences in second derivative spectra of brined and non-brined
228 samples are observed at 1405 nm which correspond to O-H bonds in free water. When salt is
229 added to water, rearrangement of intermolecular hydrogen bonds occurs, resulting in changes
230 to the shape and position of the water peaks in NIR spectra (Gowen et al., 2015).

231

232 **3.2. Principal component analysis**

233 PCA was carried out as an exploratory analysis to detect clustering and outliers using the
234 mean spectra of the hyperspectral images acquired from all raw and cooked samples. Score
235 maps of all samples in the 450-960 nm and 957-1664 nm spectral ranges were visually
236 assessed. The first principal component of both raw and cooked samples explained > 89% of
237 the variance in the spectra, which may be related to experimental treatments applied (Fig. 3).
238 PC1 score maps show a general trend with respect to experimental treatments applied to raw
239 samples. WI and control samples have similar scores and a clear trend was observed with
240 respect to the brining salt concentration. PC1 score maps of cooked samples also show a
241 trend with respect to experimental treatments applied. No clear trends were observed for PC2
242 score maps of either raw or cooked samples.

243 Scores and loadings plots for PCA models developed using mean spectra of raw and cooked
244 samples are presented in Fig. 4. Plots of PC1, PC2 and PC3 scores show a general trend with
245 respect to experimental treatments applied to both raw and cooked samples. PC1 and PC2
246 explained > 97% of the variance in the mean spectra. The PC1 loadings plot for raw samples

247 in the 450-960 nm spectral range show peaks at around 475, 540, 580, 640 and 725 nm which
248 may be related to oxidised/denatured derivatives of myoglobin, myoglobin, oxymyoglobin,
249 metmyoglobin and the 3rd overtone of O-H bond stretching in H₂O respectively (Liu et al.,
250 2000; Millar et al., 1996). The corresponding PC2 loadings plot shows peaks at 555, 585, 640
251 and 725 nm.

252 PC1 loadings plot in the 957-1664 nm spectral range for raw samples shows peaks at around
253 978 nm which correspond to 2nd overtone of O-H bond stretching and may also have
254 contribution from the pigment heme groups in deoxymyoglobin and oxymyoglobin (Liu et
255 al., 2000), at 1181 and 1230 nm due to 2nd overtone of C-H bond stretching in -CH-, -CH₂-
256 and -CH₃ groups (Shenk et al., 2001; Siesler et al., 2002), and at 1314 nm by combinations of
257 C-H bond stretching in -CH₃ groups (Shenk et al., 2001).

258 PC1 and PC2 loadings plots in the 450-960 nm spectral range for cooked samples show peaks
259 at around 540 and 640 nm, related to the effect of salt on the myoglobin and metmyoglobin
260 pigments of the brined samples (Eskin et al., 2013). PC1 loadings plot in the 957-1664 nm
261 spectral range for cooked samples show peaks at around 985, 1188 and 1391 nm
262 (combinations of C-H bonds) related to water protein interaction (Prieto et al., 2006). PC2
263 loadings plot shows peaks at 992, 1146, 1279 and 1461nm (first overtone symmetric N-H
264 bond stretching (Shenk et al., 2001).

265 PCA scores show trends with respect to the BSC employed, which are influenced mainly by
266 heme pigments and water absorption. These results are in general agreement with those
267 reported by Perisic et al. (2013) with a Vis-NIR system in the spectral region of 400-2500
268 nm. These authors found differences in the PCA scores of bovine meat samples due to
269 different salt concentrations.

270

271 3.3. Discrimination of brined and non-brined samples

272 To discriminate brined (5, 10 and 15% (w/v)) and non-brined (control, WI) samples, a
273 classification approach using PLS-DA was evaluated by assigning arbitrary values to each
274 class (0 for brined and 1 for non-brined samples). The performance of the best PLS-DA
275 models developed to discriminate between brined and non-brined samples are presented in
276 Table 1. Sensitivity (Sen) is the proportion of true positives (class 1 samples) that are
277 correctly identified, while specificity (Spec) is the proportion of true negatives (class 0
278 samples) that are correctly identified by the model. The geometric mean of sensitivity and
279 specificity ($G = (\text{Sen}^2 \times \text{Spec}^2)^{0.5} / 100$) provides information of the performance of the model
280 in all classes while not being affected by the prevalence of each class in the dataset (Esquerre
281 et al., 2012b; Kubat et al., 1998).

282 All the developed models for raw samples presented in Table 1 have high discriminant ability
283 as evidenced by G values ≥ 0.91 in calibration, $G \geq 0.89$ in cross validation and $G \geq 0.95$ in
284 prediction. The best overall model developed for classification of raw samples demonstrated
285 high classification performance (Sen = 100%, Spec = 90%, $G = 0.95$) for cross-validation and
286 perfect classification for prediction (Sen = 100%, Spec = 100%, $G = 1.00$) datasets, and was
287 developed using the EMCVS method which selected 18 wavelengths (5 LVs) using SD pre-
288 treated reflectance data in the 957-1664 nm spectral range (Fig. 5). The 18 selected
289 wavelengths used to develop the discriminant model for raw samples are distributed over the
290 957-1664 nm spectral range and are shown in Fig. 5.

291 All developed models selected for classification of cooked samples in the 450-960 nm
292 spectral range achieved perfect classification (Sen = 100%, Spec = 100%, $G = 1.00$). G
293 values ≥ 0.97 for calibration, cross-validation and prediction datasets were achieved for
294 cooked samples using the 957-1664 nm spectral range. The best overall model (lowest
295 number of variables and LVs) was developed using the EMCVS method which selected 5

296 wavelengths (3 LVs) on the mean log (1/R) data without pre-treatments. The application of
297 the EMCVS method reduced the number of wavelengths employed and the number of latent
298 variables (LVs) in the models developed. Fig. 5 presents the classification of brined and non-
299 brined samples achieved using the best PLS-DA models for cooked samples and the selected
300 bands in the pre-treated mean spectra which achieved the best classification model
301 performance.

302 PLS-DA results for raw samples using the full 450-960 nm spectral range, show better
303 discrimination between brined and not brined samples when no spectral pre-treatments are
304 applied. Previous studies also found better classification results with raw spectra compared to
305 pre-treated spectra in this wavelength range (Folch-Fortuny et al., 2016). Engel et al. (2013)
306 reported a classification case study where less than 5.5 % of pre-processing strategies
307 produced a more accurate and less complex model compared to a model based on raw
308 spectral data. In the full 957-1664 nm spectral range, better discrimination results were
309 obtained when SNV+SD spectral pre-treatments were applied to reflectance and logarithmic
310 transformed spectra. This indicates that the spectra in this range may be affected by
311 multiplicative effects and curved baselines. Previous studies reported that classification
312 models in this region performed better using pre-treated spectra (Kandpal et al., 2016).
313 Discrimination results for cooked samples at both spectral ranges 450-960 nm and 957-1664
314 nm show good discriminant ability when no spectral pre-treatments were applied.

315 PCA and PLS-DA results obtained in this study indicate that discrimination between brined
316 and non-brined of both raw and cooked PLs, is due to the effect of salt on the absorption of
317 Vis NIR electromagnetic energy by myoglobin, O-H and C-H bonds. These results are in
318 accordance with the results reported by Prieto et al. (2015) who obtained the largest
319 regression coefficients in the discrimination of moisture enhanced from non-moisture
320 enhanced pork at the same absorption bands in a spectral range of 350–2500 nm.

321

322 **3.4. Prediction of brine salt concentration**

323 The performance of the PLS-R models was assessed using the root mean square error
324 (RMSE), the coefficient of determination (R^2) and the ratio of standard error of prediction to
325 standard deviation (RPD) for calibration, full cross validation, and prediction sets. The
326 performance of the best PLS-R models developed to predict BSC employed using different
327 spectral pre-treatments is presented in Table 2. The models developed for raw samples had
328 $RMSE_p \leq 3.5\%$; RPD_p values ranging from 1.7 to 3.2 and R^2_p values between 0.75 and 0.92
329 in all cases; while models developed for cooked samples had $RMSE_p$ values $\leq 3.1\%$; RPD_p
330 values ranging from 1.8 to 2.4 and R^2_p values between 0.75 and 0.83 in all cases. The best
331 PLS-R model for raw samples was developed using 34 selected wavelengths of SNV+LD
332 pre-treated $\log(1/R)$ spectra (LV 7, $RMSE_p$ 1.9%, RPD_p 3.2, R^2_p 0.92) in the 957-1664 nm
333 spectral range. Most of the selected wavelengths are in the spectral range from 1293 to 1391
334 nm, where the 2nd overtone of C-H stretching and the 1st overtone of combination of C-H
335 vibration modes are located (Fig. 6). The best PLS-R model for cooked samples was
336 developed using 9 selected wavelengths of SD+SNV pre-treated R spectra (LV 4, $RMSE_p$
337 2.6%, RPD_p 2.4, R^2_p 0.83) in the 957-1664 nm spectral range. The selected wavelengths (Fig.
338 6) are related to the 2nd overtone of C-H stretching (1160, 1202, 1286 nm), the 1st overtone
339 of combination of C-H (1328, 1370 nm), the O-H 2nd overtone (957 nm) and the O-H 1st
340 overtone (1461 and 1559 nm). There is potential to develop a process analytical technology
341 tool using these selected wavelengths for continuous monitoring of meat brining processes.

342 Prediction results based on full wavelength and with EMCVS selected bands achieved better
343 results with raw samples compared to cooked samples. Better prediction results were
344 achieved using the 957-1664 nm spectral range for both raw and cooked samples on the

345 logarithmic transformed spectra. De Prados et al. (2015) developed a prediction model for
346 salt content ($R^2 > 0.771$) in pork meat using ultrasound velocity, however no previous studies
347 have been reported on the use of HSI to predict brining salt concentration in meat.

348

349 **4. Conclusions**

350 The results presented in this study demonstrated the potential of Vis-NIR and NIR
351 hyperspectral imaging combined with chemometrics to (i) discriminate between brined and
352 non-brined pork loins using PCA (unsupervised) and PLS-DA (supervised) and (ii) to predict
353 BSC employed using PLS regression for both raw and cooked samples.

354 PLS-DA models developed perfectly classified raw and cooked pork samples as brined (5, 10
355 and 15% BSC) or non-brined (control and WI), while PLS-R models with good prediction
356 performance were developed to predict BSC employed ($RPD > 2.4$). The EMCVS variable
357 selection method applied further improved the performance of the PLS-DA and PLS-R
358 models developed.

359 This study demonstrates the potentiality of employing Vis-NIR hyperspectral imaging
360 coupled with chemometrics as a rapid and non-destructive process analytical technology to
361 monitor and control pork loins brining processes. Adoption of this PAT tool by meat
362 processors would enhance quality assurance, process control and validation in meat brining
363 processes.

364

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368

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508 **Table 1:** Performance of the PLS-DA models developed for discrimination of brined and non-brined samples

	Pre-treatment	EMCVS	# Bands	# LVs	Calibration			Cross validation			Prediction		
					Sen _C (%)	Spec _C (%)	G _C	Sen _{CV} (%)	Spec _{CV} (%)	G _{CV}	Sen _P (%)	Spec _P (%)	G _P
Raw 450-960 nm													
R	None	No	103	6	96	97	0.96	92	93	0.92	100	95	0.97
	AsLs+LD	Yes	19	5	100	97	0.98	100	97	0.98	100	89	0.95
log(1/R)	None	No	103	9	96	97	0.96	96	93	0.94	100	89	0.95
	LD	Yes	10	6	100	97	0.98	100	97	0.98	100	89	0.95
Raw 957-1664 nm													
R	SNV+SD	No	96	4	100	83	0.91	100	79	0.89	100	95	0.97
	SD	Yes	18	5	100	93	0.96	100	90	0.95	100	100	1.00
log(1/R)	SNV+SD	No	96	5	100	97	0.98	96	90	0.93	100	95	0.97
	AsLs+MS	Yes	13	6	88	97	0.92	88	97	0.92	100	100	1.00
Cooked 450-960 nm													
R	None	No	103	4	100	100	1.00	100	100	1.00	100	100	1.00
	None	Yes	8	4	100	100	1.00	100	100	1.00	100	100	1.00
log(1/R)	None	No	103	3	100	100	1.00	100	100	1.00	100	100	1.00
	None	Yes	5	3	100	100	1.00	100	100	1.00	100	100	1.00
Cooked 957-1664 nm													
R	None	No	102	2	100	100	1.00	100	100	1.00	100	93	0.97
	None	Yes	4	1	100	100	1.00	100	100	1.00	100	93	0.97
log(1/R)	None	No	102	1	100	100	1.00	100	100	1.00	100	93	0.97
	None	Yes	1	1	100	100	1.00	100	100	1.00	100	93	0.97

509 EMCVS, ensemble Monte Carlo variable selection; LD, linear detrending; FD, first derivative; MS, median scaled; SD, second derivative; SNV,
510 standard normal variate; AsLs, asymmetric least squares; Bands, wavelengths used for model development; LVs, latent variables; Sen_{CV},
511 sensitivity for cross-validation; Spec_{CV} specificity for cross-validation; Sen_P, sensitivity for prediction; Spec_P specificity for prediction.
512 The overall best models for raw and cooked samples are highlighted in bold.

514 **Table 2:** Performance of the PLS-R models developed for the prediction of brine salt concentration (BSC) in brined pork.

	Pre-treatment	EMCVS	# Bands	# LVs	Calibration			Cross validation			Prediction		
					RMSE _C	RPD _C	R _c ²	RMSE _{CV}	RPD _{CV}	R _{cv} ²	RMSE _p	RPD _p	R _p ²
Raw 450-960 nm													
R	FD+SNV	No	97	7	2.7	2.2	0.79	3.7	1.6	0.60	2.6	2.2	0.84
	SD	Yes	18	8	2.2	2.6	0.86	2.3	2.5	0.84	3.5	1.7	0.76
log(1/R)	LD+FD	No	97	6	2.7	2.2	0.79	3.6	1.6	0.61	2.6	2.1	0.82
	FD	Yes	7	4	2.5	2.3	0.82	3.0	1.9	0.72	2.6	2.3	0.82
Raw 957-1664 nm													
R	AsLs+SNV	No	102	7	1.7	3.3	0.91	2.3	2.5	0.84	2.1	2.7	0.90
	SNV+FD	Yes	9	3	2.4	2.4	0.83	2.3	2.5	0.84	2.2	2.8	0.88
log(1/R)	MS+SNV	No	102	8	1.5	3.7	0.93	2.5	2.3	0.81	1.9	3.0	0.94
	SNV+LD	Yes	34	7	1.5	3.7	0.93	2.1	2.8	0.87	1.9	3.2	0.92
Cooked 450-960 nm													
R	SNV+LD	No	103	9	2.2	2.5	0.84	2.1	2.6	0.85	2.9	1.8	0.75
	LD	Yes	14	6	2.2	2.5	0.84	1.9	2.9	0.88	3.0	2.0	0.75
log(1/R)	AsLs+SNV	No	103	10	2.3	2.4	0.83	2.3	2.4	0.83	3.1	1.8	0.75
	SNV+SD	Yes	21	6	2.3	2.4	0.83	2.0	2.8	0.87	3.0	2.0	0.74
Cooked 957-1664 nm													
R	SD+AsLs	No	96	6	1.9	2.9	0.88	2.5	2.2	0.79	2.8	2.1	0.79
	SD+SNV	Yes	9	4	2.0	2.8	0.87	2.0	2.7	0.86	2.6	2.4	0.83
log(1/R)	MS+FD	No	96	7	1.8	3.0	0.89	1.9	2.9	0.88	2.7	2.0	0.79
	MS+FD	Yes	17	6	1.8	3.1	0.89	1.6	3.4	0.91	2.6	2.3	0.81

515 EMCVS, ensemble Monte Carlo variable selection; FD, first derivative; LD, linear detrending; SD, second derivative; SNV, Standard normal
516 variate; AsLs, asymmetric least squares; MS, median scaled; Bands, wavelengths used for model development; LVs, latent variables.
517 The overall best models for raw and cooked samples are highlighted in bold.

Figure captions

Fig. 1. Hyperspectral imaging and data analysis.

Fig. 2. Mean $\log(1/R)$ and second derivative of mean $\log(1/R)$ spectra of (a) raw and (b) cooked samples.

Fig. 3. PCA score maps of $\log(1/R)$ spectra of (a) raw and (b) cooked samples.

Fig. 4. PCA score plots and loadings of mean $\log(1/R)$ spectra of (a) raw and (b) cooked samples.

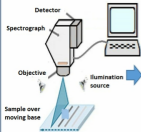
Fig. 5. Classification of brined and non-brined samples using the best PLS-DA models developed for (a) raw (SD on the reflectance spectra 957–1664 nm), and (b) cooked samples ($\log(1/R)$ spectra without spectral pre-treatment 450–960 nm).

Fig. 6. Brining salt concentration predicted using the best PLS-R models developed for (a) raw (SNV+LD spectral pre-treatments on the $\log(1/R)$ spectra 957–1664 nm), and (b) cooked samples (SD+SNV spectral pre-treatments on the reflectance spectra 957–1664 nm).

Highlights

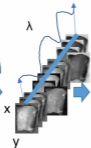
- Vis-NIR hyperspectral imaging is suitable for the assessment of brining of raw and cooked pork loins.
- Chemometric models were developed to classify brined and non-brined pork samples and to predict brining salt concentration employed.
- Spectral pre-treatments and variable selection improved performance of models developed.

HSI systems Vis - NIR

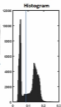


- Line scanning from 400 to 1720 nm.
- Raw and cooked samples scanned
- Data recorded as reflectance in ENVI format.

Hypercubes



Thresholding



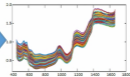
Background removal



Unfolding



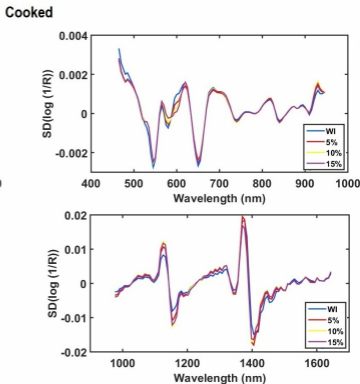
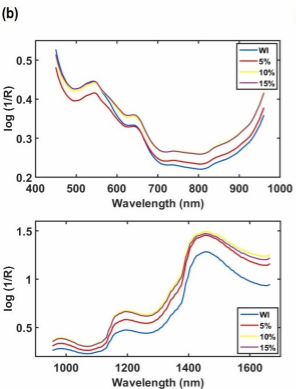
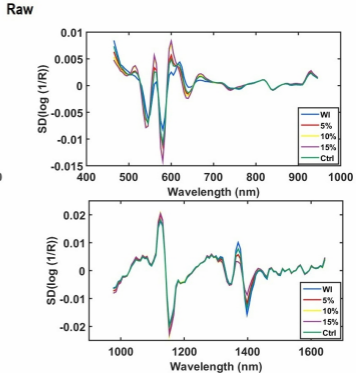
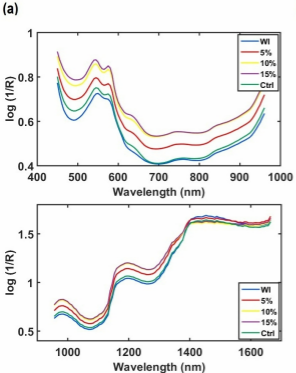
Spectral data pre-processing



- Remove noisy bands by trimming spectra
- Eliminate dead pixels

Data analysis

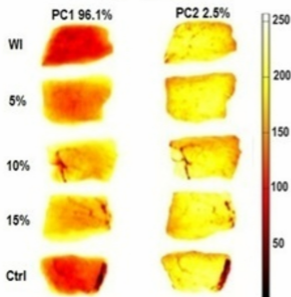
- Logarithmic transformation ($\log(1/R)$)
- PCA
- PLS-R
- PLS-DA
- EMCVS
- Spectral pretreatments (SNV, LD, MS, AsLs, SG-1st and 2nd derivative and combinations of any two of them)



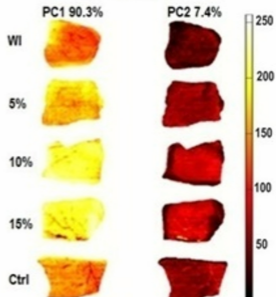
(a)

Raw

450 - 960 nm



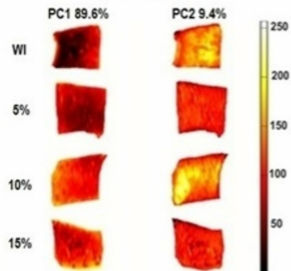
957 - 1664 nm



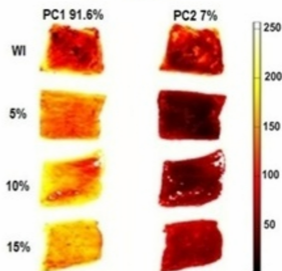
(b)

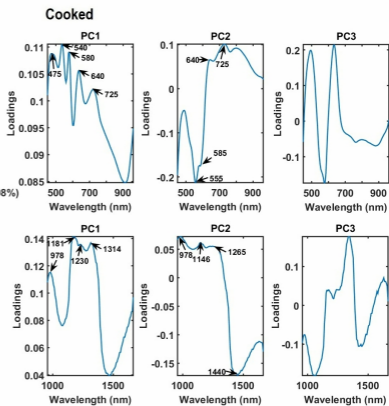
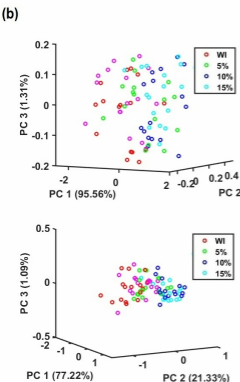
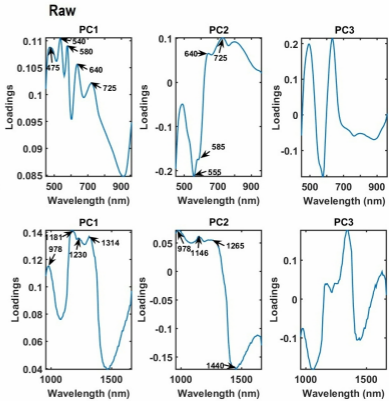
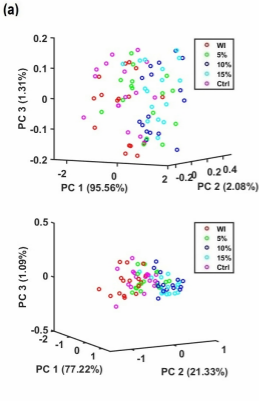
Cooked

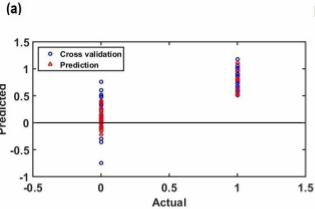
450 - 960 nm



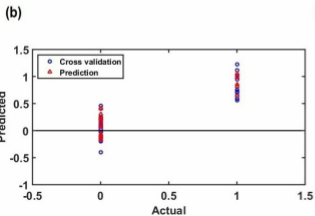
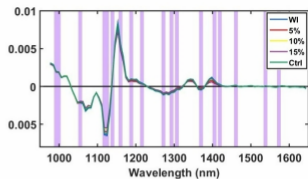
957 - 1664 nm







Raw



Cooked

