Modeling beef quality using NIRS

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Introduction

A commercial on-line measurement system that can objectively and accurately measure or predict key meat quality indicators and/or attributes does not currently exist. This study investigated the viability of such a system through NIRS. Quality indicators pH and glycogen concentration are considered, along with the attributes of tenderness and water holding capacity (WHC). This paper discusses the data analysis techniques in some detail, the subsequent potential NIRS test accuracies and compares these with the accuracies of reference test methods.

The commercial benefits of measuring meat quality indicators and attributes on-line early post slaughter include the opportunity to optimise downstream processing parameters, allow process control, feedback to farmers and enable improved returns through better allocation and categorisation of product to key customers and consumers. The use of NIRS in the measurement of meat quality has shown promise in prior studies.[1]

This study was lab based in that samples were removed from freshly slaughtered animals and measured in the lab as they aged, without freezing at any stage. Various treatments were applied to samples to generate a suitable variation of reference data in the absence of sample numbers large enough to randomly capture the desired variation.

Materials and methods

Meat quality indicators and attributes were measured in eighty beef *M. longissimus lumborum* (LL) from early *pre rigor* through to completion of *post rigor* ageing. A range in the attributes was created by subjecting the LLs to various *pre rigor* treatments including electrical stimulation, restraint wrapping and temperature. Throughout the *pre* and *post rigor* period the LLs were measured using NIR, between 6 and 13 time points spanning approximately 94 hours resulting in a total of 786 samples. Samples were reference tested as described previously.[2]

Spectra were collected through a robust fibre optic probe manufactured by Makura[3] (approx 16mm diameter viewed region) coupled with a KES spectrophotometer[4] (spectral range 400 nm to 1700 nm, with selected 5 nm wavelength intervals). 20 different positions were scanned, on

Figure 1. Data acquisition using KES spectrophotometer and fibre-optic reflectance probe.

each freshly cut loin surface in order to cover the entire area (Figure 1), resulting in a dataset of approximately 16,000 spectra each an average of 30 sub-spectra.

The data analysis was performed using PLS_Toolbox[5] within Matlab R2006b.[6] Spectra from unique samples were split into calibration and validation datasets in the ratio 2:1. For each sample in the calibration set, spectra were pre-selected from the acquired 20 spectra down to the 8 most similar based on PCA first vector distance from the mean. The calibration set for modeling glycogen was an exception in that a single spectrum was used per sample taken at the same site as the reference measurement was taken, for those time points up until *rigor* was reached.

A variety of preprocessing methods were tested on the calibration set of the 8 most similar spectra per sample, a dataset of 4200 spectra. The preprocessing methods were evaluated by cross-validated predictive performance of PLS models on both reflectance (REFL) and absorbance (ABS) datasets. The optimal component number for the PLS models for each method was determined, followed by selection of the best model for each attribute as determined by least *RMSEC*. Typically the most successful preprocessing method was a combination of Standard Normal Variate scaling (SNV) and General Least Squares weighting (GLS). Models were then applied to the 20 spectra in the validation set resulting in twenty predictions per sample. Non-conforming predictions were removed by selecting Mahalanobis distance[7] less than 2, and then averaged to provide a single result for every validation sample.

Table 1. Meat quality measurement and validation metrics.

		Attribute			
		pH	Tenderness (N)	Glycogen (mg g^{-1})	WHC (cm^2g^{-1})
	Total Samples	785	381	102	451
	Parameter Range	5.15–7.17	19–265	0.0–18.7	0.4–25.6
	Parameter SD	0.49	47	4.6	2.4
	Pre-processing	REFL, SNV+GLS	ABS, GLS	REFL, SNV+GLS	ABS, GLS
	PLS Factors	4	3	4	2
Validation	Spectra	4398	2135	617	2567
	Samples	253	124	35	149
	R^2_{VAL}	0.83	0.58	0.72	0.67
	$RMSEP_{VAL}$	0.20	28.29	2.69	1.42
	SD_{VAL}	0.41	32.83	4.15	1.81
	RPD_{VAL}	2.1	1.2	1.5	1.3
Precision	Lab test	0.17	19	3.3	1.03
	Sampling	0	13	0	0.73

Results and discussion

Pre-selecting spectra to a reduced calibration dataset tends to select only those most consistent spectra across the face of the muscle and seeks to represent the muscle against the reference measurement. Scans containing lumps of fat or connective tissue whose attributes are less related to meat quality are hence less represented, scans of voids and poorly prepared surfaces will also be omitted. Similarly the validation set is filtered at the final prediction step where predictions from the 20 scans were mostly consistent across the muscle, except for few significantly different predictions expected to be due to scans of non-lean tissue. Averaging consistent predictions as opposed to all predictions was found to deliver better performance suggesting variation in the muscle is present, and that in application several scans per muscle will be required to get a representative prediction.

Table 1 contains the performance statistics for all attributes.

The overall precision of the prediction $RMSEP_{VAL}$ is a combination of the variances in the NIR prediction itself, the reference laboratory tests and variance introduced in sampling. Where these latter two are known or may be estimated, their effect upon the overall variance may be removed. Results in Table 1 show that with this correction the precision of the NIR prediction is comparable to or better than the reference methods. Glycogen has the best prediction precision while reference methods for WHC and tenderness had low reference test precision. The attribute best measured by NIR was pH with a ratio of prediction to deviation[8] (*RPD*) of 2.1 and whose scatter plot is shown in Figure 2.

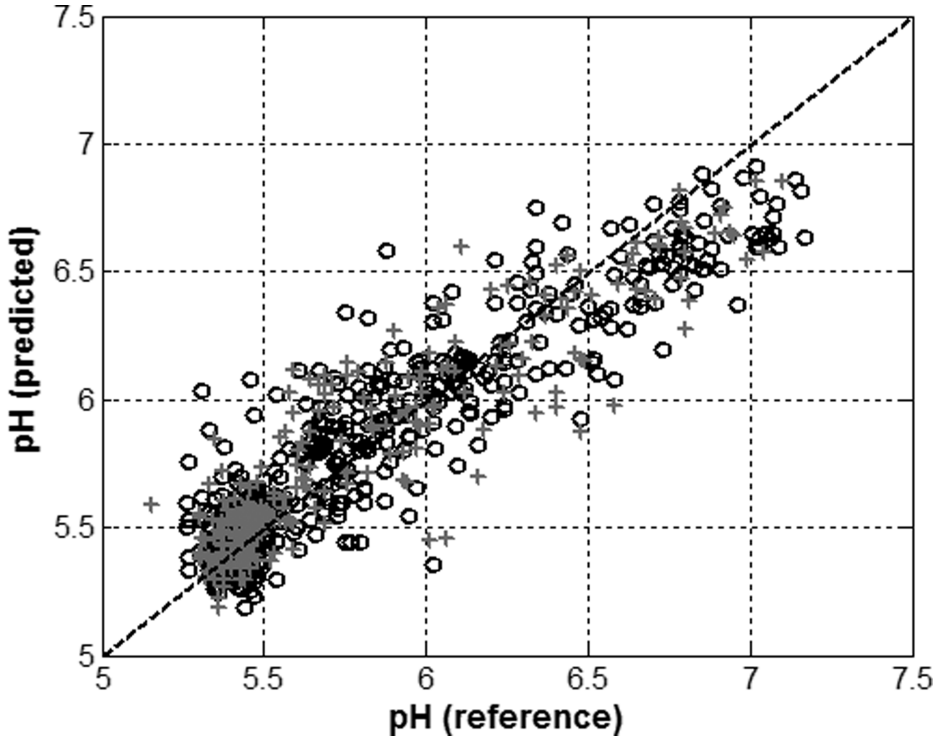

Figure 2. Best case PLS prediction for pH. REFL spectra pre-processed by SNV+GLS, four PLS factors. Calibration samples (black circles) and validation samples (grey plus symbols).

The dataset combines samples scanned at different time-points from slaughter through to completion of *post rigor* ageing, therefore confounding factors in the chemical process of aging are likely to be manifest in the attribute predictions at the various time-points. Analysis of the performance at particular time-points has not been covered within this study, nor has the prediction of future attribute values although both can be extracted from this dataset and will be the subject of further study.

Conclusion

Limitations of NIR prediction are generally linked to the variability of the meat itself and in the base or laboratory testing. The former has been addressed through multiple scan measurement and suitable consideration of appropriate scans to include, whereas the latter has been addressed through explicitly considering the laboratory and sampling variance.

We have shown very reasonable performance for all attributes investigated. When variability can be fully accounted for, coupled with the ability to predict in advance the eating quality of a piece of meat, using NIR measurements of meat can be regarded as a robust procedure with comparable accuracy to laboratory test results, and a viable solution for on-line measurement of meat quality attributes.

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