Feed-a-Gene

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

The development of models to predict the nutritional value of feedstuffs and feed mixture using NIRS

Samantha Joan NOEL (1), Henry Johs. Høgh JØRGENSEN (1), Knud Erik BACH KNUDSEN (1)

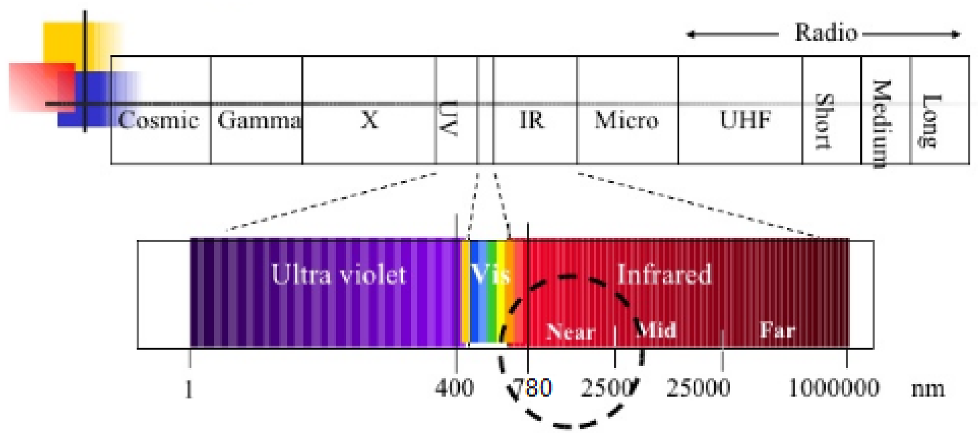
(1) Department of Animal Science, AU Foulum, Aarhus University, DK 8830 Tjele, Denmark

ABSTRACT

Fast and accurate methods of determining the nutritional value of feedstuffs are needed in order to be able to use this information in real time. This study used the near infrared spectrum (NIRS) of raw materials and swine feeds in combination with modelling to develop fast, inexpensive and accurate estimates of macronutrient and amino acid content as well as macronutrient digestibility and metabolizable energy (ME).

INTRODUCTION

Measurements in the near-infrared spectral (NIRS) range give information on the molecular bonds and thereby the complex chemical composition of a sample. By using a database of samples with known nutritional values, predictive equations can be modeled from NIR scans. Current methods to determine the nutritive value of pig feedstuffs are time consuming and very expensive (animal models), have low capacity (*in vitro* methods) or are not accurate enough to determine variation amongst feedstuffs of the same type (table values). NIRS estimates can provide fast or even real time predictions of nutritional values.



Electromagnetic spectrum


NIR scanner with a sample

MATERIALS AND METHODS

NIRS scans was carried out on 773 ground feed samples, where the nutritive value of the samples had been assessed in pig feeding trials, using a Foss NIRS DS2500 analyser. The samples included cereals (n=277), alternative ingredients (n=129) which comprised of cereal substitutes, protein concentrates, cereal by-products and grass meal and finally mixed diets (n=367).

Samples were randomly split (80:20) into a calibration set (n=619) to build the models with and an independent validation set (n=154) to test the models. Calibrations for macronutrients, amino acids, digestibility and ME were developed with WinISI software. The spectral range included wavelengths between 780 and 2500 nm, with data points every 0.5 nm, resulting 1,698 data points per scan. Spectra were mathematically pre-processed according to the SNV-D method (Barnes et al., 1989) with math treatment 2,8,4,1. Calibration models were built using the Modified Partial Least Squares method (mPLS) with all the sample types, also with subgroups (not shown) of samples divided into cereal, alternative ingredients and mixed diets groups and evaluated with the independent dataset. In addition cross-validation was also performed using the leave one out method on groups of 8 and used to determine the number of factors to include in the model.

RESULTS

Table 1. Prediction of amino acid content in pig feedstuffs (g/kg of CP)

	Calibration			Validation		
Constituent	N CAL	RSQ CAL	SECV	N Val	RSQ VAL	SEP(C)
CYS	395	**0.95**	0.44	94	**0.94**	0.44
LYS	395	**0.98**	1.3	94	**0.96**	1.05
MET	395	**0.97**	0.41	94	**0.94**	0.42
THR	395	**0.99**	0.71	94	**0.96**	0.68
TRP	163	**0.93**	0.45	37	**0.87**	0.45
Other AA	369-395	**0.91-0.99**		92-94	**0.92-0.97**	
CP	607	**0.98**	15.73	150	**0.95**	16.87

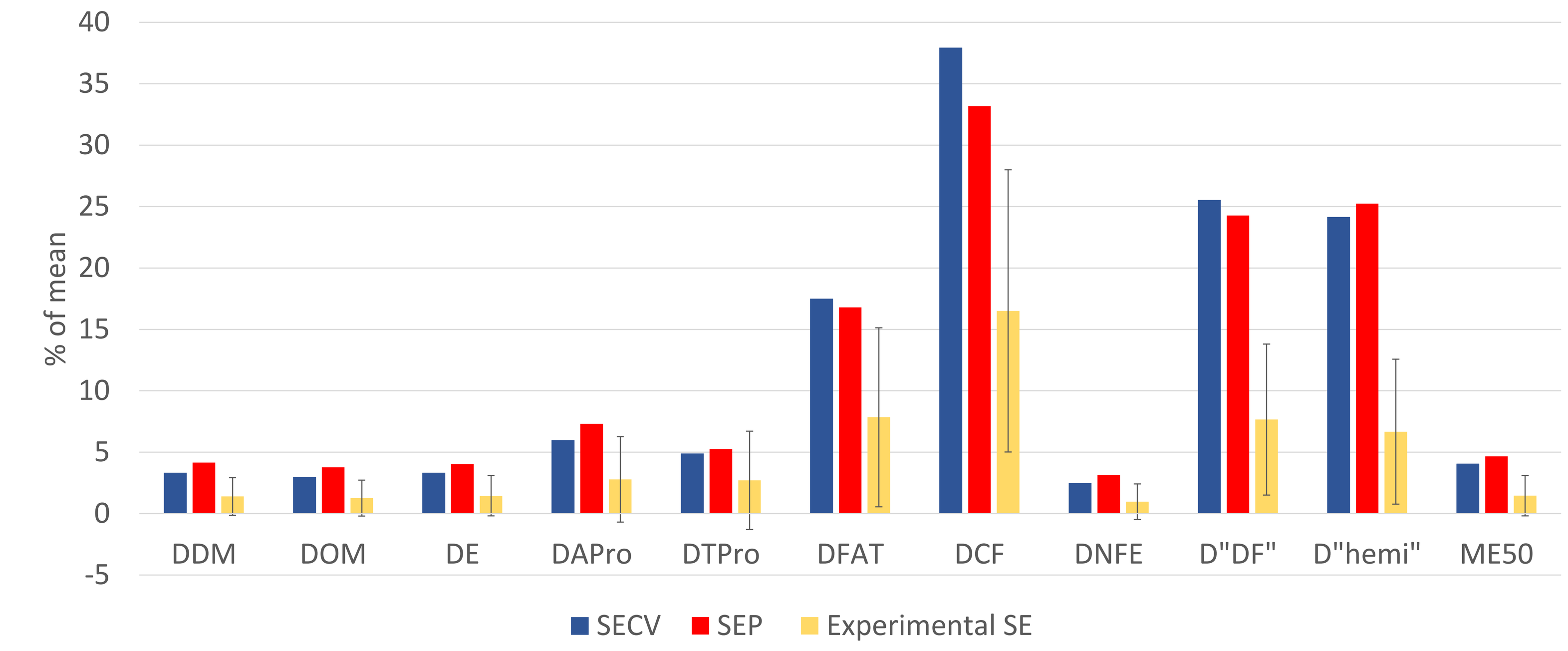
Table 2. Prediction of macronutrient content in pig feedstuffs

	Calibration			Validation		
Constituent	N CAL	RSQ CAL	SECV	N VAL	RSQ VAL	SEP(C)
Ash	593	**0.85**	10.53	149	**0.76**	10.31
Protein	607	**0.98**	15.73	150	**0.95**	16.87
Fat	573	**0.92**	9.47	140	**0.94**	8.65
Crude fiber	524	**0.97**	8.56	130	**0.95**	9.5
A-CHO	464	**0.98**	30.45	118	**0.97**	31.89
Starch	489	**0.95**	44.66	125	**0.93**	48.62
NDF	427	**0.95**	23.16	110	**0.9**	23.25
ADF	430	**0.97**	11.87	112	**0.95**	12.4
NFE	525	**0.98**	19.22	129	**0.98**	21.04
GE	584	**0.81**	87.46	146	**0.84**	78.94

Ash g/kg, Protein- crude protein g/kg, Fat g/kg, Crude fiber g/kg, Available carbohydrates (A-CHO: starch plus sugars) g/kg, Starch g/kg, NDF- Neutral detergent fibre g/kg, ADF – acid detergent fiber g/kg, NFE – Nitrogen free extract g/kg, GE- gross energy kcal.

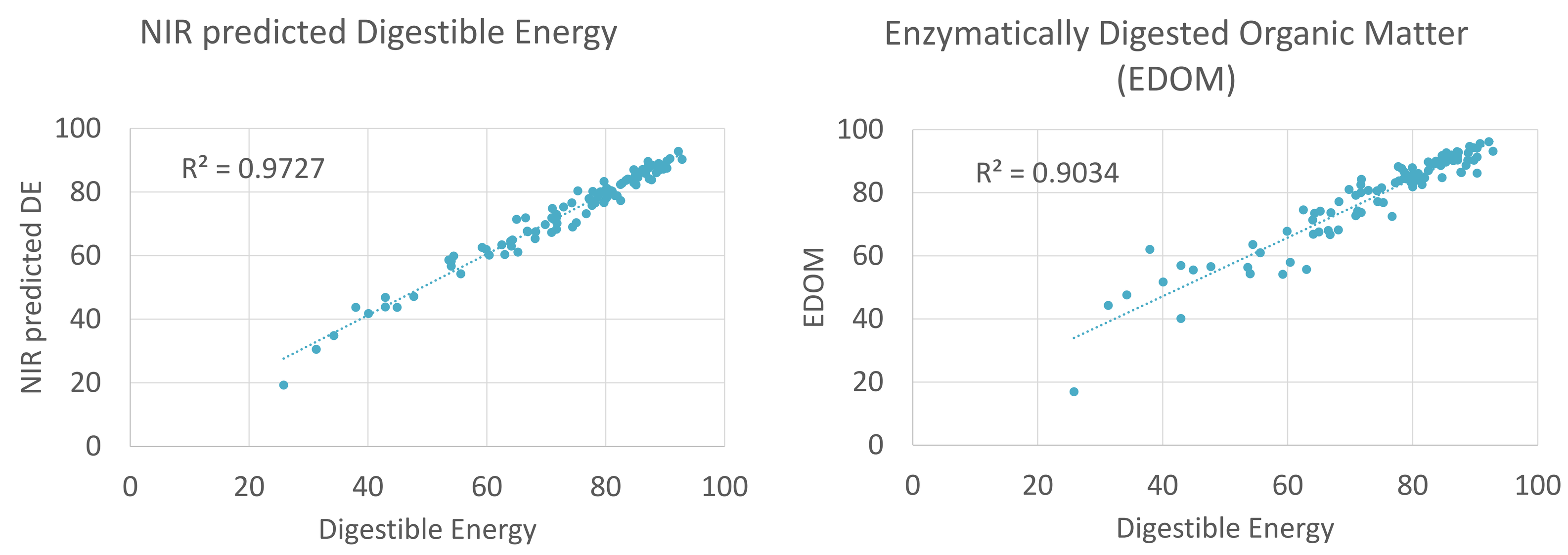
RESULTS

Relative standard error of the digestibility of nutrient fractions, NIRS error vs. experimental error

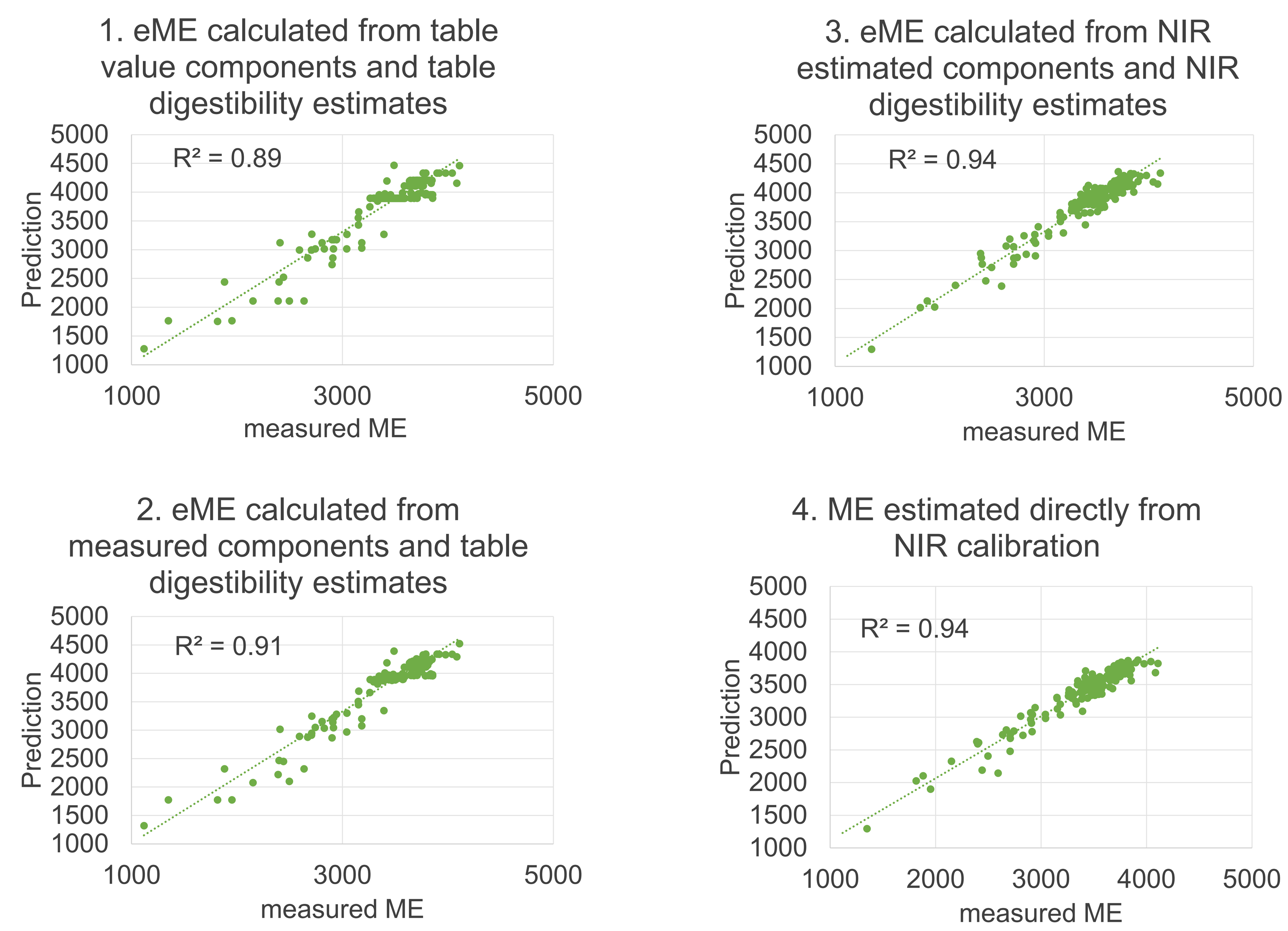


SECV – standard error of cross validation of the NIR calibration as a percentage of the mean value.
SEP – standard error of prediction of the NIR calibration as a percentage of the mean value.
Experimental SE – average standard error from measured values of digestibility as a percentage of the mean value. Error bars represent ± one SD.

Digestible energy predictions, EDOM vs. NIRS



Metabolizable energy predictions (eME), table values vs. NIRS

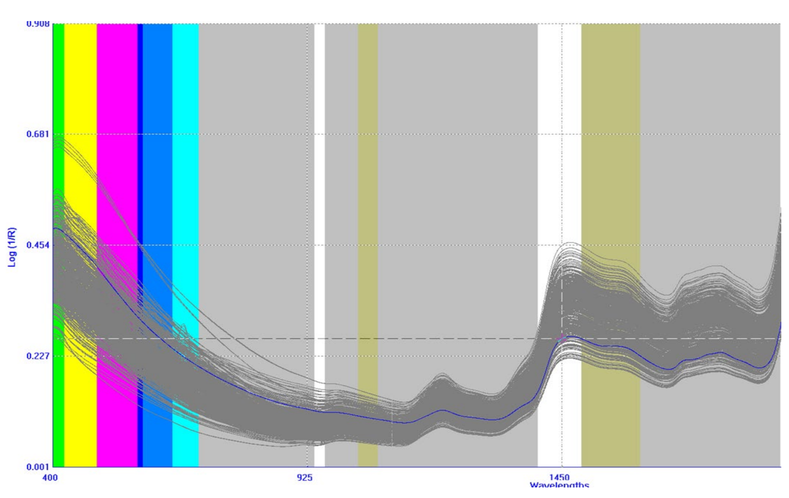


CONCLUSIONS

- NIRS can be used to estimate both chemical and biological values for pig feed.
- Models are working well for most constituents examined in this study.
- NIR predictions of digestible energy were better than those using the *in vitro* digestion of OM assay (EDOM) (R^2 0.97 vs. 0.9).
- NIR predictions of metabolizable energy are better than using table values (R^2 0.94 vs. 0.89).
- Thereby NIR offers a more accurate estimation of the digestibility of feedstuffs than the current estimation methods.

CONTACT

E-mail: samantha.noel@anis.au.dk



Feed-a-Gene

Feed-a-Gene is a European H2020 project involving 23 partners which aims to adapt feeds, animals and feeding techniques to improve the efficiency and sustainability of pig, poultry and rabbit production systems. It is coordinated by INRAE (France), started in March 2015 and will last 5 years. The project aims to reduce the environmental impact of monogastric livestock production by improving and diversifying animal diets and feed technologies and by integrating new selection criteria for these animals. The Feed-a-gene project further aims to develop new management systems for precision feeding and precision farming and to evaluate the overall sustainability of the different management solutions proposed in the project.

The Feed-a-Gene Project has received funding from the European Union's H2020 Programme under grant agreement no 633531.