

EFP-006 Amino Acid Profiling of Feed Ingredients and Finished Feeds of Ruminants, Monogastrics and Fish by Near Infra-Red Reflectance Spectroscopy

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MINI ABSTRACT

Two hundred feed ingredients and finished feeds for ruminants, monogastrics and fish were analyzed by high performance liquid chromatography (HPLC) for all amino acids. The HPLC data were used for calibration and validation of near infrared reflectance spectroscopy (NIRS), a quick, non-destructive and economical tool for feed quality assessment. The coefficient of determination (R^2) for calibration and validation equations ranged between 0.96-0.99 and 0.93-0.98 except for cysteine ($R^2 = 0.83$ and 0.80), respectively with standard errors of 0.03-0.25 and 0.04-0.37, respectively, showing the suitability of NIRS for accurately profiling the amino acid contents of feed samples.

Key words: Amino acids, Feed ingredients, Finished feeds, Prediction, HPLC, NIRS

INTRODUCTION

Knowing the amino acid content in feed ingredients and finished feeds is important since amino acid content specifically of essential amino acids (lysine, methionine etc.) affect livestock and fish performance. Conventionally amino acids are analyzed by chromatographic techniques - mainly by HPLC- which is complex, labor intensive, consumes chemicals and is generally expensive. In contrast NIRS is safe, non-destructive, efficient, economic and environment friendly. It can be used for simultaneous determination of multiple traits from a single scan and is therefore ideal for rapid but comprehensive feed quality evaluation. However, to date the application of calibration curves developed for amino acids was limited as indicated by a ratio of performance deviation (RPD) value (<3) and non-publishing of RPD values for validation. Hence, objective of this work was to develop and validate calibration models of NIRS for amino acids in feed ingredients and finished feeds used for feeding poultry, swine, cattle and fish.

MATERIALS AND METHODS

A total of 200 feed samples including feed ingredients and finished feeds for cattle, pig, poultry and fish were ground through a 1 mm sieve and analyzed for the eighteen amino acids by HPLC. All amino acids except tryptophan were analyzed AOAC (2000). The tryptophan content of the feed samples was analyzed after alkaline hydrolysis. The NIRS instrument used was a FOSS XDS Rapid Content Analyzer with software package WinSIVER 4.6.8. The 200 feed samples were scanned in above particle size using small circular cups of 50 mm diameter.

RESULTS

The calibration model statistics calculated were standard error of calibration (SEC) and the coefficient of determination (R^2_{cal}). The model was tested by splitting 200 samples into a calibration and validation set each of 100 samples. The performance of the validation set was tested based on the standard error of validation (SEV) and the coefficient of determination (R^2_{val}). Ratio of performance deviation for both calibration (RPD_{cal}) and validation (RPD_{val}) were also calculated to evaluate the performance of the calibration and validation. The coefficient of determination (R^2) value of calibration and validation ranged between 0.96-0.99 and 0.93-0.98 for all amino acids except for cysteine with respective SE value between 0.03-0.25 and 0.04-0.37, showing the robustness of NIRS equation for predicting amino acid contents in animal feeds/feed ingredients. Only for cysteine were relatively low R^2 value of 0.83 for calibration and 0.80 for validation observed. Ratio of performance deviation (RPD) for calibration and validation equations was 4.71-9.77 and 3.83-7.88, respectively indicating the higher performance of equations ($RPD > 2.5$) except for cysteine calibration (2.40) whose RPD value was at boarder line.

Table 1. Calibration, validation statistics and good-of-fitness (R^2) of amino acids

Amino acid	Calibration				Validation			
	n	Mean (%)	SEC	R^2_{cal}	N	Mean (%)	SEV	R^2_{val}
Aspartic acid	91	2.10	0.19	0.98	100	2.01	0.26	0.96
Serine	90	1.01	0.08	0.98	100	0.99	0.09	0.97
Glutamic acid	93	3.57	0.25	0.98	100	3.45	0.37	0.97
Glycine	89	1.18	0.15	0.97	100	1.48	0.22	0.97
Histidine	93	0.60	0.07	0.96	100	0.57	0.09	0.93
Arginine	91	1.75	0.14	0.98	100	1.69	0.22	0.95
Threonine	90	0.87	0.05	0.99	100	0.83	0.07	0.98
Alanine	89	1.14	0.10	0.97	100	1.15	0.11	0.98
Proline	90	1.30	0.09	0.98	100	1.35	0.16	0.96
Cysteine	93	0.35	0.06	0.83	100	0.37	0.07	0.80
Tyrosine	92	0.65	0.07	0.97	100	0.69	0.09	0.93
Valine	90	1.14	0.07	0.99	100	1.10	0.11	0.96
Methionine	89	0.35	0.03	0.97	100	0.37	0.05	0.95
Lysine	91	1.04	0.13	0.97	100	1.04	0.18	0.94
Isoleucine	92	0.87	0.09	0.98	100	0.83	0.09	0.96
Leucine	91	1.60	0.13	0.97	100	1.54	0.16	0.95
Phenylalanine	90	1.00	0.07	0.99	100	0.97	0.09	0.98
Tryptophan	90	0.24	0.03	0.97	100	0.23	0.04	0.94

REFERENCE

AOAC, 2000. *Official Methods of Analysis*, 17th ed. Association of Official Analytical Chemists, Gaithersburg, VA. USA.

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