



Development of NIRS models to predict protein and amylose content of brown rice and proximate compositions of rice bran



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ABSTRACT

With the escalating persuasion of economic and nutritional importance of rice grain protein and nutritional components of rice bran (RB), NIRS can be an effective tool for high throughput screening in rice breeding programme. Optimization of NIRS is prerequisite for accurate prediction of grain quality parameters. In the present study, 173 brown rice (BR) and 86 RB samples with a wide range of values were used to compare the calibration models generated by different chemometrics for grain protein (GPC) and amylose content (AC) of BR and proximate compositions (protein, crude oil, moisture, ash and fiber content) of RB. Various modified partial least square (mPLSs) models corresponding with the best mathematical treatments were identified for all components. Another set of 29 genotypes derived from the breeding programme were employed for the external validation of these calibration models. High accuracy of all these calibration and prediction models was ensured through pair *t*-test and correlation regression analysis between reference and predicted values.

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1. Introduction

Rice (*Oryza sativa* L.) is one of the main food crops of the world and is the major staple food of India and other Asian countries. Rice production in India has remarkably increased in the recent past and reached to approximately one-third of the total rice production of the world. But rice grain quality remains an important concern for rice breeders, producers and consumers. Protein digestibility corrected amino acid score (PDCAAS) which indicates the presence of essential amino acids and overall protein quality, was comparatively higher in rice (0.55) than the other important cereals such as wheat (0.40). Therefore, storage protein in rice grain is being considered as the potential substitute of powdered milk for its low hyper susceptibility for babies (Chrastil, 1992). Bio-fortification of rice with protein through conventional breeding is a significant approach toward value addition of rice. But it had negative correlation with yield and affected some of the eating and cooking quality parameters (Vasal, 2002). Grain protein and

amylose contents are two important quality parameters that greatly affect the physicochemical as well as cooking quality of rice (Champagne et al., 1997). Therefore, amylose content must be considered in selection of elite lines for improved GPC. Apparent amylose content (AC), possibly the most important chemical characteristic, has been predicted accurately by NIR spectroscopy using milled rice flour (Bao, Cai, & Corke, 2001; Bean et al., 1990; Delwiche, Bean, Miller, Webb, & Williams, 1995; Shu, Wu, Xia, Gao, & McClung, 1999a) milled whole grain (Delwiche et al., 1995; Windham et al., 1997) and brown rice flour samples (Shu, Wu, Xia, Gao, & McClung, 1999b). NIRS can also be used for estimation of grain protein content (Delwiche, McKenzie, & Webb, 1996; Shu et al., 1999b). But the accuracy of prediction with NIRS depends on grain physical status, chemical constituents, grain temperature, color, cleanliness, quantity used for measurement and above all, the statistical model (regression) developed in NIR software. Therefore, it is very crucial to develop a new approach on available methods to select the appropriate statistical model for prediction. Wu and Shi (2007) established that whole brown rice is best for calibration for AC as lower standard error of calibration (SEC) and higher coefficient of determination (RSQ) were observed. Hu et al. (2014) indicated that use of brown rice flour is better as compared to milled flour for estimation of GPC under 2,8,8,2/mPLS/Inverse MSC combination. In this experiment, we used brown rice samples for prediction of AC and GPC.

Abbreviations: NIRS, near-infrared spectroscopy; RB, rice bran; BR, brown rice; AC, amylose content; GPC, grain protein content; mPLS, modified partial least square.

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RB is the pericarp and germ of *O. sativa* L. seeds and constitutes about 10% of rough rice grain (Juliano, 2003). It consists of three fused layers –pericarp, seed coat, nucellus and little aleurone layer. It is a byproduct in the milling process and has been used as a feed-stock and has the potential to be used as a food ingredient and oil source. As compared to other portion of a whole grain, RB contains highest amount of protein, crude fat, crude ash, crude fiber, total dietary fiber, phenolics, γ -oryzanol, vitamin-E, anthocyanin pigment and some essential minerals (Fe, Zn). Colored RB have high antioxidant properties (Yawadio, Tanimori, & Morita, 2007). In fact, very limited literature is available regarding estimation of proximate composition of RB with NIRS. As RB is the most nutritious part of grain, its stabilized form can be used for value added product development (Bagchi, Adak, & Chattopadhyay, 2014). The proximate compositions of RB also provide the valuable information regarding metabolism of some macronutrients in rice grain under “biofortification” breeding programme. Therefore, it is a holistic effort to evaluate the nutrient composition of RB as well as whole brown rice in nondestructive and high throughput way. Recently, NIRS have been extensively used for rapid and nondestructive estimation of grain quality, especially in case of cereals, pulses and oilseeds (Velasco, Mollers, & Becker, 1999). In any breeding programme related with value addition, it is an essential tool to determine the nutritional composition with high throughput and near accuracy. It requires minimum sample preparation; therefore, it is a cost effective as well as time and labor saving method. But, calibration with reference data, generated through laboratory method is the primary requirement to establish the calibration model of the samples. It is based on the absorption of molecular overtone and combination vibrations of hydrogenous groups X–H (X = C, N, O) in the near-infrared region of the electromagnetic spectrum (from 750 to 2500 nm). However, a lot of chemical constituents of grain in many crops were evaluated with NIRS but only few reports are available on the evaluation of proximate composition of RB. Therefore, the objectives of this experiment were (a) to obtain a near accurate prediction model for amylose and protein content of rice grain with minimum sample preparation and (b) to evaluate the proximate composition of RB under most suitable statistical model developed with NIRS.

2. Materials and methods

2.1. Materials

Around 173 rice germplasm, including popular cultivars and lines derived from the breeding programme for the improvement of grain protein content in rice with wide range of variation were taken for calibration of NIR spectrophotometer. Among these, seed samples of 129 lines were utilized for calibration of both GPC and AC and rest 44 samples were used for AC only. In addition, another set of 86 RB samples derived from various rice germplasm and breeding lines were used for calibration of crude fiber, protein, crude oil, ash and moisture content. Finally, 29 BC₃F₄ lines derived from rice breeding programme were utilized for validation of these parameters. The seed samples were derived from the cultivated Indica rice grown at dry and wet season at CRRRI experimental field over three years (2012–2014).

2.2. Sample preparation

Rice grains were harvested at maturity and sun-dried naturally for further processing to a grain moisture of 12–13%. The dried grains were stored at 20 °C and <60% RH in a closed chamber for analysis of amylose and protein. Brown rice samples (10–15 g) were prepared through rice huller (Satake Corporation, Japan)

and after cleaning it was immediately used for analysis with NIRS. The RB samples were also prepared through rice miller (Satake Corporation, Japan) as a byproduct after dehusking of the grain and subsequently laboratory and NIR analysis were accomplished for moisture, ash, crude fiber, crude oil and crude protein. In order to compare the performance of different calibration models, the samples in the reference and prediction sets were kept unchanged for all calibration models, developed for amylose and protein content of brown rice but in case of bran, it was different.

2.3. Chemical analysis of the sample

The total nitrogen content of RB and BR samples was determined by taking 10 dehusked grains (or 100 mg defatted bran) as per AOAC (1990) and used to calculate crude protein content (%N \times 5.95). The amylose content (AC) was measured according to Juliano (2003) using iodine reagent for generating blue colored complex, the intensity of which was measured spectrophotometrically (Thermo spectronic) at 620 nm. The moisture content was estimated by digital moisture meter (OSWA scientific, India). Crude fiber content of bran was also estimated according to Maynard (1970). Ash and crude oil content of bran were analyzed as per AOAC, 1990 using muffle furnace and soxhlet apparatus respectively. Hexane was used for crude oil extraction from RB samples.

3. Calibration of NIRS for BR and RB

Before NIR analysis, the samples were kept at room temperature (25 °C) for 6 h to balance the moisture and temperature as these factors can affect the reflectance and absorbance of NIR wave. The NIRS was calibrated with the help of three softwares related to NIR spectroscopy (model: FOSS- NIRSDS 2500, FOSS Analytical, Sweden). The software ISI Nova scan, Mosaic solo and WinISI III Project Manager v 1.50e (Windows Infra Soft International, USA) were used for scanning, configuration and calibration of samples respectively. A small cup (size: inner diameter 66 mm and height 25 mm) was used for scanning of the sample with full spectrum (400–2500 nm) taking about 15 g of each sample. The reflectance spectra ($\log 1/R$) from 400 to 2500 nm were recorded at 2 nm intervals. After incorporating the laboratory value in spectra file, the regression equation was developed and simultaneously, various trial and error methods of mathematics (e.g. – “1,4,4,1”, “1,2,3,1” etc.) under modified partial least square (mPLS) were also developed to find out a best regression equation for prediction of different parameters (Table 1). The first digit of these mathematics indicates the order of the derivative (0 represents no derivative, 1 is first derivative of $\log 1/R$ and so on), the second digit is the gap in data points over which the derivative was calculated, the third and fourth digit refers to the number of data points used in the first and second smoothing, respectively. Generally, the fourth digit of the mathematics remains unaltered i.e. Cross validation for calibration under SNV (standard normal variate) plus detrend scatter correction method was performed for avoiding overfit (Wu & Shi, 2004). After making different equations with different mathematics, another set of known samples (24) was scanned for prediction to get external validation and pair *t*-test was performed to obtain any significant variation between laboratory value and predicted value. The best equation was identified on the basis of lowest SEC (standard error of calibration) and SECV (standard error of cross validation) and highest 1 – VR (1 minus variance ratio) and RSQ (coefficient of determination) (Wu, Shi, & Zhang, 2002). All the spectra files were generated from WIN ISI software to justify reflectance and absorbance of the different samples with graphical representation. Only cross-validation

Table 1
Calibration and external validation of brown rice (BR) samples using different mathematical treatments in NIRS.

Amylose Chemometrics	Calibration								External validation				
	N	Mean	Range	Est. max%	SEC	1 – VR	SECV	SD	N	SEP(C)	Bias limit	RSQ	Slope
1,5,5,1	168	21.66	15.6–25.16	28.00	1.341	0.501	1.491	2.115	29	1.668	0.895	0.487	1.003
1,6,6,1	169	21.63	15.6–25.16	28.05	1.318	0.494	1.520	2.140	29	1.599	0.912	0.529	1.011
1,4,4,1	168	21.65	15.6–25.16	28.00	1.346	0.497	1.497	2.115	29	1.669	0.898	0.486	1.005
2,4,4,1	173	21.53	15.6–26.17	28.34	1.458	0.326	1.862	2.272	29	1.680	1.117	0.540	0.975
1,2,3,1	169	21.62	15.6–25.16	28.09	1.435	0.457	1.584	2.156	29	1.724	0.950	0.452	0.953
Protein Chemometrics	N	Mean	Range	Est. max%	SEC	1 – VR	SECV	SD	29	SEP(C)	Bias limit	RSQ	Slope
1,3,4,1	128	10.75	6.81–13.37	15.92	0.656	0.807	0.756	1.722	29	0.982	0.453	0.749	0.943
1,4,4,1	128	10.76	6.81–13.37	15.92	0.656	0.807	0.756	1.722	29	0.872	0.454	0.749	0.943
1,4,3,1	128	10.75	6.81–13.38	15.92	0.656	0.807	0.755	1.722	29	0.872	0.453	0.749	0.943
2,3,3,1	129	10.83	6.93–13.37	15.75	0.707	0.685	0.919	1.638	29	0.951	0.552	0.698	0.988
2,4,4,1	129	10.837	6.93–13.38	15.75	0.712	0.688	0.914	1.638	29	0.972	0.548	0.683	0.981

N.B.: SEC = standard error of calibration; 1 – VR = 1 minus variance ratio; SECV = standard error of cross validation; SD = standard deviation; SEP(C) = standard error of prediction; RSQ = coefficient of determination.

Bold values indicate lowest.

to assess the calibration equations might not be sufficient. A subsequent external validation of the initial calibration model using samples independent from the calibration set led to further NIRS performance values for each constituent.

4. Statistical analysis

To obtain linear regression coefficient of reference vs. predicted values of different parameters, MS excel was used. Further, to compare calibrated values with predicted ones, *t*-test was performed using SAS version 9.3 (base command: PROC TTEST) (Kong et al., 2015; SAS Institute Inc., 2001). All the data and spectra generated for evaluating calibration and prediction under different mathematics was developed by WinISI III Project Manager software version 3.1.

5. Results and discussion

5.1. Selection of best NIR equation for determination of amylose content and total protein content of brown rice

Amylose is an essentially linear polymer of α -(1–4)-linked-D-glucopyranosyl units with up to 0.1% α -(1–6) linkages. In rice AC% varied from 0% to 30% depending on genotypes and agro-climatic variations. It is mainly associated with sensory properties of cooked rice whereas protein in rice varies between 5% and 20% and is associated with textural properties of cooked rice (Juliano, 2003). Rice protein is hypoallergenic in nature and mainly concentrated in RB layers. Therefore, considering the above facts, we selected both the BR and RB samples for analysis under NIRS. A total of 173 and 129 samples were used for calibration of amylose content (AC) and grain protein content (GPC) of brown rice respectively. But for prediction, 29 samples were used for both the parameters. To find out the best mathematical treatments with scatter correction (SNV + D), five regression equations were developed using five random mathematical treatments (“1,5,5,1”, “1,6,6,1”, “1,4,4,1”, “2,4,4,1” and “1,2,3,1” for AC and “1,3,4,1”, “1,4,4,1”, “1,4,3,1”, “2,3,3,1” and “2,4,4,1” for GPC) for brown rice (Table 1). The prediction equations for these parameters were developed by modified partial least squares (mPLS) regression and evaluated by the external validation.

The results in Table 1 showed the effects of different mathematical treatments with SNV + D for calibration equations with brown rice samples (about 15 g), scanned by using small cup. For AC, the pretreatment of “1,6,6,1” and “1,4,4,1” with each combined with

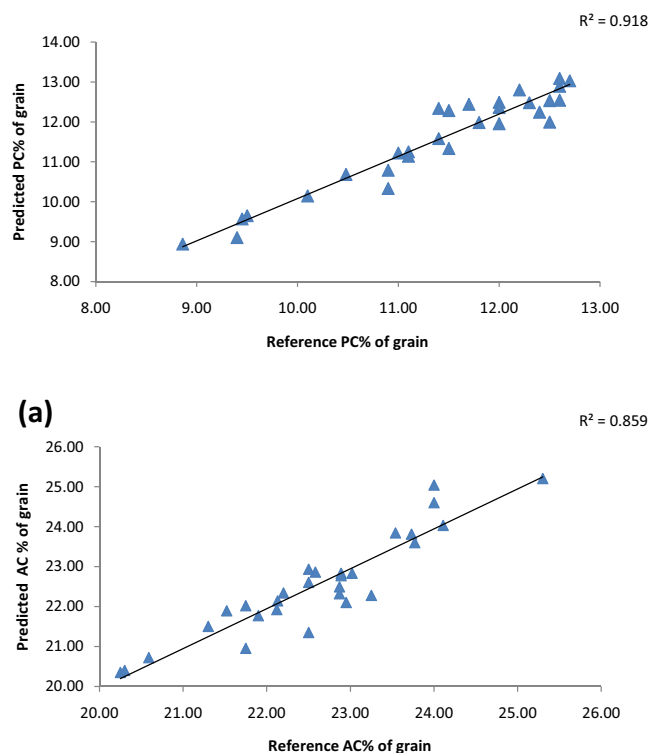


Fig. 1. Reference values versus NIR predicted values plots for (a) amylose and (b) protein content of brown rice. The R^2 indicates that there are very little difference between reference and predicted value in both AC and PC.

SNV + D were better than others. The other pretreatments were found to be less precise in external validation. For the equations of GPC, the pretreatment method of “1,4,4,1” and SNV + D had a better effect than others, whereas others were more or less similar based on external validation. In brief, both “1,6,6,1” and “1,4,4,1” mathematical treatments are best for AC showing high coefficient of determination (RSQ: 0.529–0.486; 1 – VR: 0.494–0.497) and low standard error (SEC: 1.318–1.346; SECV: 1.520–1.497 and SEP(C): 1.59–1.669). In case of GPC of brown rice, “1,4,4,1” and “1,4,3,1” treatments were best among others showing high coefficient of determination (RSQ: 0.749; 1 – VR: 0.807) and low standard error (SEC: 0.656; SECV: 0.756–0.755 and SEP(C): 0.872). But considering lowest SEC and SEP(C), “1,6,6,1” was best for AC and both “1,4,4,1” and “1,4,3,1” were best for GPC prediction of brown rice.

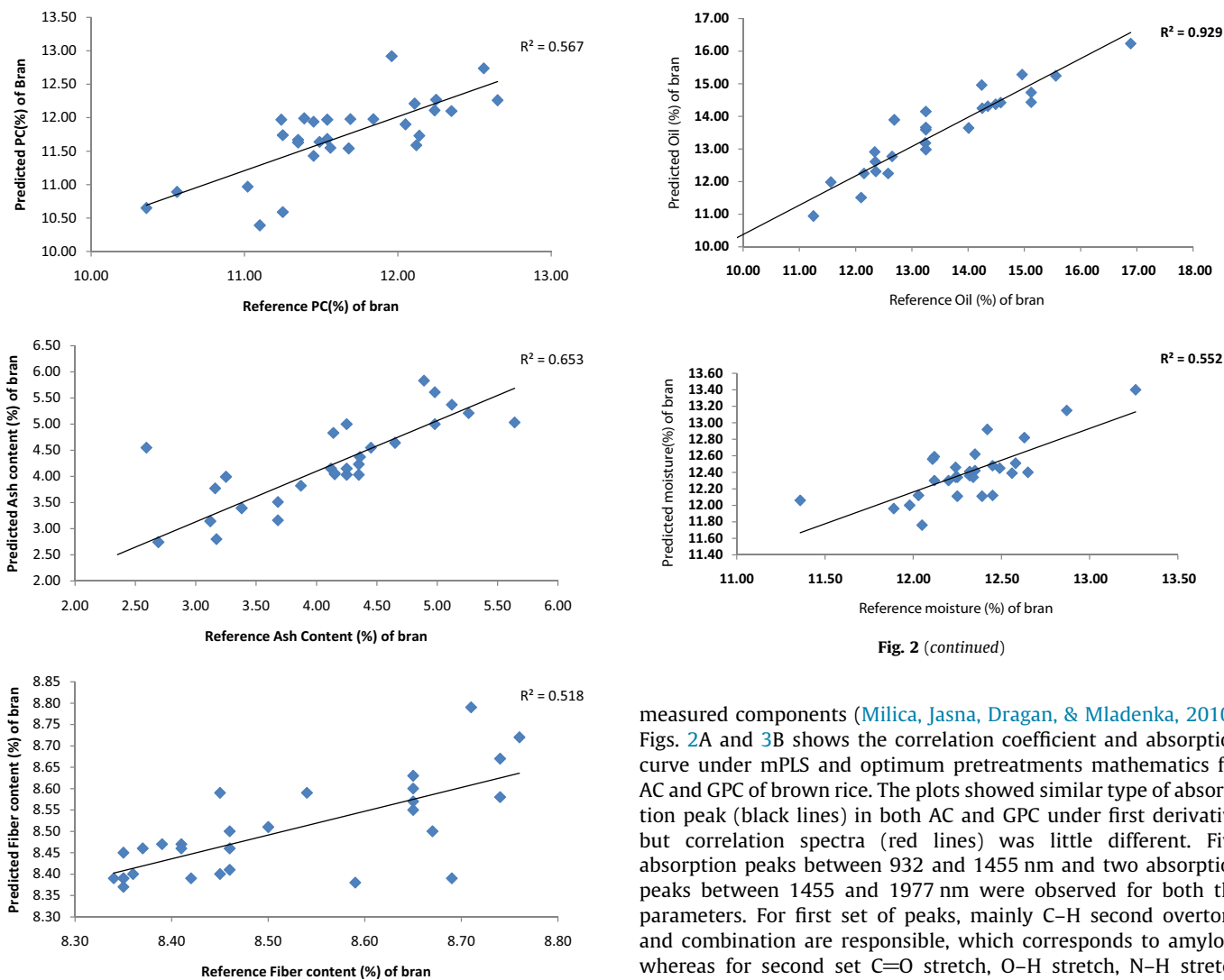


Fig. 2 (continued)

Fig. 2. Reference versus NIR predicted values plots for moisture, protein, ash, oil and dietary fiber content of rice bran. The R^2 indicates that there are very little difference between reference and predicted value for all the proximate compositions.

For calibration of AC the mean, range and estimated maximum (%) of data set under “1,6,6,1” were 21.63, 15.6–25.6 and 28.05 respectively, where as for GPC these were 10.76–10.75, 6.81–13.37 to 6.81–13.38 and 15.92 for both “1,4,4,1” and “1,4,3,1” pretreatments. Therefore, these calibration equations for AC and GPC of brown rice were incorporated in the NIRS for future analysis of the samples.

The reference values versus predicted values plots with optimal models in the predicted set of GPC and AC are shown in Fig. 1. The models for protein and amylose content of brown rice illustrate good accuracy. It was observed that the points are randomly distributed around the line for both the parameters and the R^2 was 0.859 and 0.918 for AC and GPC respectively. It indicates that these calibration models could quantify for predicting AC and GPC of brown rice and can be very useful in screening of large numbers of samples nondestructively with short period of time.

The spectra for regression coefficient (load plots) of AC and GPC of brown rice obtained from WinISI III software can be analyzed to evaluate optimum NIR calibration models as spectra variations at different wavelength (400–2500 nm) reflect the information regarding different functional groups (eg. O–H, N–H etc.) of

measured components (Milica, Jasna, Dragan, & Mladenka, 2010). Figs. 2A and 3B shows the correlation coefficient and absorption curve under mPLS and optimum pretreatments mathematics for AC and GPC of brown rice. The plots showed similar type of absorption peak (black lines) in both AC and GPC under first derivative but correlation spectra (red lines) was little different. Five absorption peaks between 932 and 1455 nm and two absorption peaks between 1455 and 1977 nm were observed for both the parameters. For first set of peaks, mainly C–H second overtone and combination are responsible, which corresponds to amylose whereas for second set C=O stretch, O–H stretch, N–H stretch and also C–H stretch first overtone were responsible which indicates protein of brown rice (Burns & Curczak, 1992). All these suggest that the models are authentic and this is why they yielded high predictive abilities. These calibration equations can only be used to analyze samples of advanced rice lines where enough samples are available for analysis because, for small size of sample (<5 g) standard error of prediction was higher (>1.00) (Delwiche et al., 1995; Wu & Shi, 2004).

For this study, the goal was to identify methodology applicable across a wide range of germplasms grown for high throughput screening for high protein rice, other grains and RB quality. Herein, the correlations had value as *t*-test showed *p*-values less than 0.01 and the estimates were within a range of variation. This indicated that NIR should be effective for pre-screening to establish relative (low, medium and high) concentrations of these compounds, which can then be followed by further analysis to confirm their exact values.

5.2. Selection of best NIR equation for determination of proximal components of RB

A total of 86 samples were used for calibration of proximate composition of RB. Due to large number of parameters, we applied two mathematical treatments (“1,2,3,1” and “1,4,4,1”) under SNV + detrend scatter correction. For the calibration set, reference values for ash, fiber, protein, oil and moisture ranged from 5.42 to 14.22%, 7.12–9.89%, 10.98–14.87%, 0.58–20.22% and 6.39–12.28%

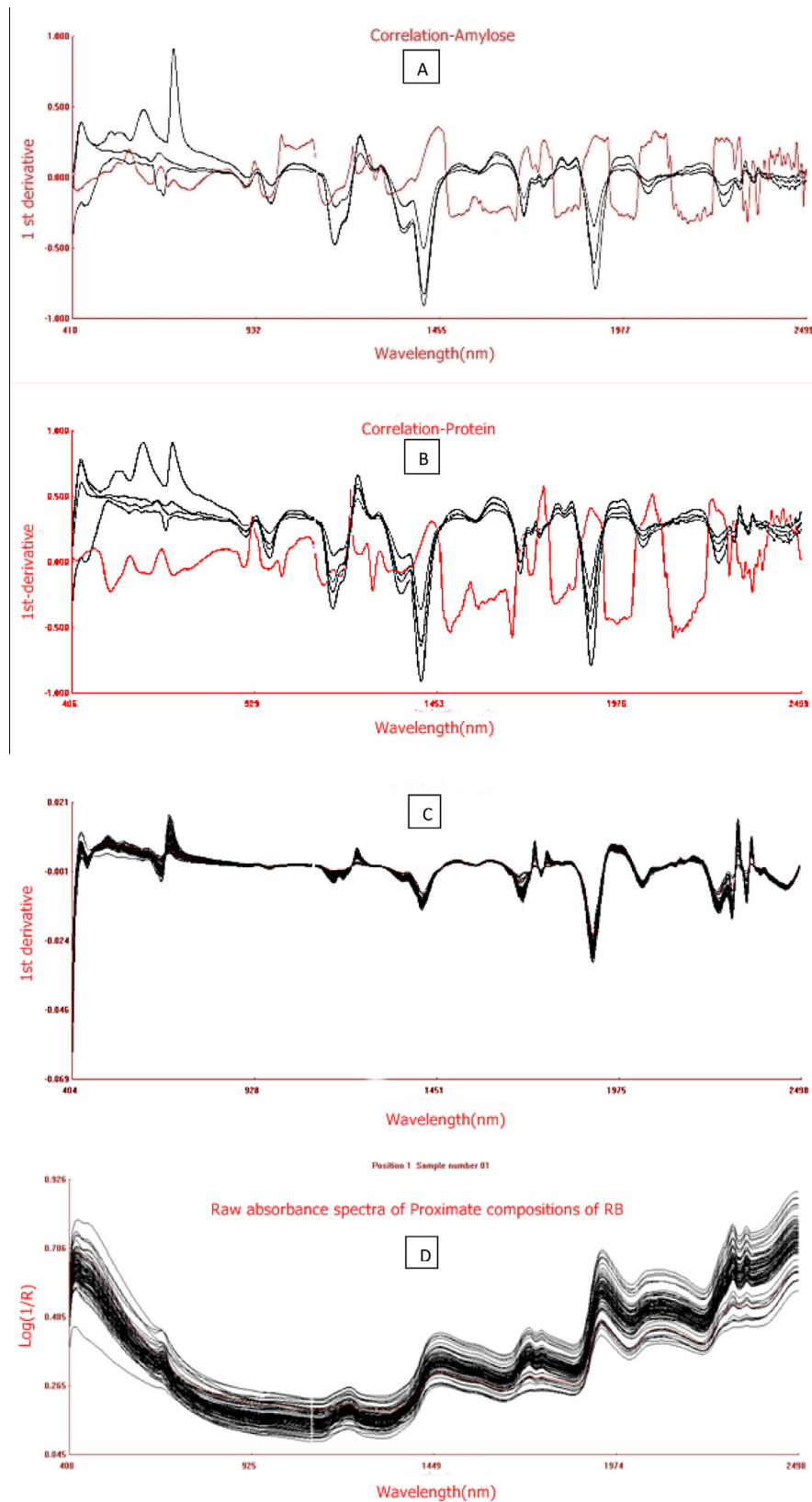


Fig. 3. Regression coefficient along with correlation plot of modified partial least squares model (mPLSs) calibration equations under first derivative for (A) amylose content of brown rice; (B) protein content of brown rice; (C) preprocessed first derivative absorbance spectra and (D) raw absorbance spectra of all proximate composition of rice bran samples.

respectively under optimum “1,2,3,1” mathematical pretreatment. The results in Table 2 showed the effects of different mathematical treatments with SNV + D for calibration equations with RB samples

(about 15 g), scanned by using small cup. For all the parameters, pretreatment of “1,4,4,1” with SNV + D under mPLS was better than “1,2,3,1” because it showed high or at par coefficient of

Table 2
Calibration and external validation for proximate compositions of rice bran (RB) samples using two mathematical pretreatments in NIRS.

1,2,3,1 chemometrics Parameters	Calibration								External validation				
	N	Mean	Range	Est. max%	SEC	1 – VR	SECV	SD	N	SEP(C)	Bias limit	RSQ	Slope
Ash	84	9.36	5.42–14.22	13.22	0.532	0.724	0.671	1.286	29	0.639	0.403	0.822	1.088
Fiber	78	8.37	7.12–9.89	9.92	0.398	0.293	0.432	0.546	29	0.813	0.260	0.334	1.458
Protein	84	13.29	10.98–14.87	16.03	0.415	0.659	0.531	0.915	29	0.435	0.319	0.833	0.955
Oil	82	14.12	0.58–20.22	26.56	0.487	0.977	0.621	4.147	29	0.865	0.373	0.956	0.986
Moisture	81	9.72	6.39–12.28	13.98	0.509	0.856	0.536	1.421	29	0.881	0.321	0.690	0.992
1,4,4,1 chemometrics Parameters	N	Mean	Range	Est. max%	SEC	1 – VR	SECV	SD	29	SEP(C)	Bias limit	RSQ	Slope
Ash	84	9.36	5.42–14.22	13.22	0.531	0.731	0.669	1.286	29	0.640	0.402	0.822	1.088
Fiber	78	8.37	7.12–9.86	9.92	0.398	0.304	0.423	0.518	29	0.814	0.260	0.333	1.457
Protein	84	13.29	10.98–14.87	16.03	0.413	0.660	0.532	0.915	29	0.432	0.319	0.835	0.958
Oil	82	14.12	0.58–20.22	26.56	0.487	0.978	0.620	4.147	29	0.866	0.372	0.955	0.986
Moisture	81	9.72	6.39–12.88	13.98	0.506	0.861	0.531	1.421	29	0.881	0.319	0.690	0.991

Table 3
t-Test for amylose and total protein content of brown rice and proximate compositions of rice bran (RB). It predicts that there was no statistical difference (at 1% level of significance) between calibrated and predicted values.

Parameters (%)	Data set	Number	<i>t</i> -Value	<i>P</i> -value	Significance
Amylose content (BR)	Calibration	173	0.93	0.36	NS
	Prediction	29			
Protein Content (BR)	Calibration	129	–2.5	0.02	NS
	Prediction	29			
Moisture content (RB)	Calibration	86	–1.92	0.06	NS
	Prediction	29			
Protein content (RB)	Calibration	86	–1.15	0.26	NS
	Prediction	29			
Oil content (RB)	Calibration	86	–0.69	0.49	NS
	Prediction	29			
Crude fiber content (RB)	Calibration	86	0.81	0.42	NS
	Prediction	29			
Crude ash content (RB)	Calibration	86	–0.89	0.38	NS
	Prediction	29			

determination (RSQ and 1 – VR) and low or at par standard error (SEC: 0.398–0.531; SECV: 0.423–0.669 and SEP(C): 0.432–0.881) (Table 2). Actually, “1,4,4,1” was slightly better regression equation than “1,2,3,1”. Further, Table 3 showed the non-significant difference between calibrated and predicted value ($p > 0.01$) under this regression equation.

RB is an excellent source of fat (10.25–16.62%), protein (14–18%), moisture (9–12%), ash (7–9%) and total dietary fiber (20–30%) (Azizah & Luan, 2000). The reference values, obtained from our laboratory versus predicted values in NIRS, plots with optimal models in the predicted set of RB parameters are shown in Fig. 2. A total of 29 samples were selected for prediction of these RB parameters against the optimal calibration equation and observed that *R* square varied from 0.518 to 0.929 and correlation coefficient (*R*) was 0.720–0.964 (not shown in figures). The range of different parameters of RB was also nearly same as previous reports. It suggests that this calibration model could quantify for predicting these RB compositions with near accuracy and can be very useful in screening of large numbers of samples with short period of time.

The whole as well as average NIR spectra under first derivative and absorbance spectra of five constituents of RB were shown in Fig. 3C and D respectively. There were total six (two peaks between 932 and 1455 nm, two peaks between 1455 and 1977 nm and two peaks between 1977 and 2499 nm) major peaks were observed. The first two peaks may be the overtone from the C–H stretching

of a CH₂ group (generally found at 1215 nm) or corresponding to the second overtone of C–H stretching of CH₃ group (generally found at 1195 nm) (Osborne & Fearn, 1986). This functional group is present in the oil or fiber molecule, an important nutritional compound of RB. The peaks at 1450–1974 nm corresponds to the absorption band of moisture (typically 1490 and 1540 nm) and protein (typically at 1471–1530 nm), due to corresponding to the first overtone of O–H and N–H stretching. The last observed peaks were found at 1974–2490 nm, which could correspond to the absorbance band of ash, fiber or protein molecules. The first overtone of the OH stretching/bending combination mode is at 1960 nm and N–H/C–H bending in plane is at 2050–2070 nm (Burns & Curczak, 1992). All these results suggest that this model will be very useful for prediction of RB proximate compositions.

6. Conclusion

This study demonstrated the potential of NIRS for rapid prediction of AC and GPC of BR samples. The major outcome of this study largely depends on the variations and precision in the reference values and suitable regression equations used. The models for the AC obtained in this work were more precise than the models reported by Hu et al. (2014), Barton et al. (2000) where SECV were higher (1.927 and 1.830) as compared to this study (1.520). For the GPC of BR, the current results were slightly less precise to those

obtained by Hu et al. (2014) (generated through “2,8,8,2”/mPLS/ MSC regression model) because SEC and SECV was slightly higher in our study. However, they used rice flour and milled rice which was destructive in nature but we used brown rice, which can be used for further analysis; even for growing seedlings. Therefore, for AC, “1,6,6,1”/mPLS/SNV + D and for GPC, “1,4,4,1”/mPLS/SN V + D are the best calibration model developed under NIRS if non-destruction of the grain and minimal sample preparation will be considered. But, the novelty of this study lies on development of NIRS models for proximate compositions of RB. The prediction model developed through “1,4,4,1” with SNV + D under mPLS was better because it showed high coefficient of determination and low standard error (SEC: 0.398–0.531; SECV: 0.423–0.669 and SEP(C): 0.432–0.881) for all these bran constituents. In fact, very limited literature is available till now in this aspect. However, our study will be helpful for the effective utilization of NIRS in high throughput screening of rice bran samples for their proximate composition as well as AC and GPC of any rice samples in nondestructive way.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.foodchem.2015.05.038>.

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