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Prediction of protein and amylose content and gelatinization temperature of rice at different stages of processing

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Introduction

This study focused on developing near infrared (NIR) spectroscopy calibrations to predict protein content, amylose content and gelatinization temperature from rice samples at the brown rice, milled rice and ground milled rice stages of processing. The information would assist rice plant breeders in providing a useful and reliable tool for screening early generation lines.

Materials and methods

Samples

A total of 713 samples were obtained from breeder's collections at five European research centres, commercial varieties and experimental lines. The samples were analysed by NIR spectroscopy at different processing stages. Two hundred and fifty five samples were analysed as brown rice, 506 samples were analysed as milled rice and all 713 were analysed as ground milled rice.

Reference analysis

Whole milled grains were ground in a Perten 3100 hammer mill using a 0.8 mm screen. Protein content, amylose content and gelatinization temperature were measured on ground milled grains.

Protein content was expressed as % on a dry matter basis following total nitrogen determination using the Kjeldahl method. Amylose content and gelatinization temperature were measured using differential scanning calorimetry [1]. Amylose content was calculated from the energy of amylose/lyso-phospholipid complex formation while gelatinization temperature was evaluated from the onset temperature of the enthalpy variation observed from starch gelatinization.

Near infrared spectroscopy

About 3 g of grains of brown rice, grains of milled rice or homogenized powder were scanned in diffuse reflectance on a Foss NIRSystems 6500 spectrometer using small ring cups. Analysis of the grain samples was undertaken in duplicate and an average spectra saved (RMS limit within 2 spectra was set at 300 μ Abs). The ISI NIRS 2 version 4.11 (InfraSoft International) software package was used.

Results

Mathematical models using the partial least squares regression method (PLS) were developed to predict the different criteria in the NIR region between 908 nm and 2,500 nm. The statistical parameters of standard error of calibration (SEC), coefficient of determination (R²), standard error of prediction (SEP) and the ratio of standard deviation divided by SEP (ratio of performance to deviation (RPD)) were calculated and used to evaluate the quality of the fit of the relationships and to compare the different equations (Table 1).

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Table 1. Population and calibration statistics for the three processing stages for protein content (%), amylose content (%) and temperature of gelatinization (TGEL) (°C).

Processsing stage	Constituent	Population			Calibration						
		n	Mean	SD	SEC	R ²	SEC	SEL	SEP	RPD	T
Ground milled rice											
	Protein	554	7.7	1.4	0.09	1	0.11	0.08	0.15	9.5	12
	Amylose	630	19.9	2.8	0.75	0.93	0.89	0.75	0.99	2.9	15
	TGEL	597	60.5	5.4	1.2	0.95	1.41	0.72	1.55	3.5	13
Milled rice											
	Protein	411	7.6	1.5	0.15	0.99	0.19	0.08	0.27	5.5	12
	Amylose	428	19.9	2.8	0.95	0.89	1.26	0.75	1.44	1.9	15
	TGEL	406	61.5	4.6	1.16	0.94	1.47	0.72	1.36	3.4	13
Brown rice											
	Protein	214	6.9	0.95	0.15	0.98	0.22	0.08	0.25	3.8	11
	Amylose	219	20.5	3.1	1.42	0.79	1.88	0.75	1.55	2	8
	TGEL	213	62.6	4.8	1.06	0.95	1.61	0.72	1.95	2.5	13

n: number of samples chosen by the model (Student t test at 5%)

SD: standard deviation of the calibration population

SEC: standard error of calibration R²: coefficient of determination.

SECV: standard error of cross-validation SEL: standard error of the laboratory SEP: standard error of prediction

RPD: ratio of performance to deviation (SD.SEP⁻¹)

T: number of PLS terms

The performance of the model for each processing stage was tested by estimating the SEP on a set of 30 independent samples. These validation sets were randomly selected and predicted with equations developed on the remaining samples. This is illustrated for brown rice in Figures 1.

Protein content could be predicted by NIR spectroscopy with the following estimates of accuracy using;

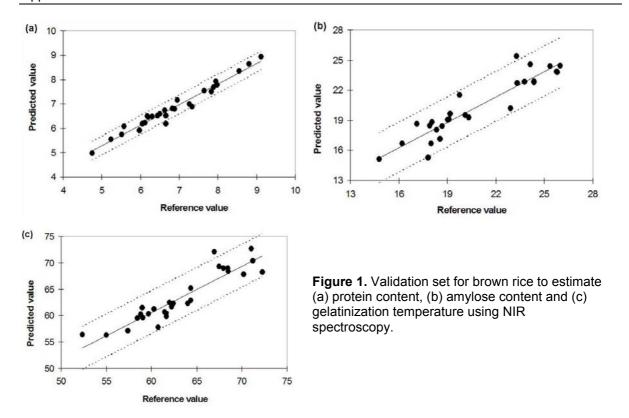
- Ground milled rice (SEP = 0.15%, RPD = 9.5)
- Milled rice (SEP = 0.27%, RPD = 5.5)
- Brown rice (SEP = 0.25%, RPD = 3.8)

These results were consistent with those obtained by Barton [2], whose SECV values for protein were 0.25% on brown rice and 0.18% on flour.

Not surprisingly, the SEP value for amylose content decreased with each successive processing step: being 1.55% for brown rice, 1.445% for milled rice) and 0.99% for ground milled rice.

Gelatinization temperature could be predicted directly from brown rice (SEP = 1.95° C, RPD = 2.5). This degree of accuracy will enable sample screening with a fine-tuning of the estimates using the values predicted for milled grains (SEP = 1.36° C, RPD = 3.4) or ground milled grains (SEP = 1.55° C, RPD = 3.5).

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Conclusion

The measurement repeatability tests conducted on sub-samples showed that the average spectrum of two sub-samples was sufficient to represent a grain sample.

This study confirmed that NIR spectroscopy analysis of whole brown rice is sufficiently accurate for routine screening of early generation lines based on protein content, amylose content and gelatinization temperature. The accuracy can be fine-tuned using whole milled grains or ground milled grains.

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