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Enhancing the Accuracy of NIRS Prediction with Adaptive Machine Learning for Assessing Fermented Citronella Feed Quality

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ABSTRACT

The valorization of agricultural residues as alternative feed resources is increasingly critical for enhancing livestock sustainability. This study investigates the potential of sequential fermentation to improve the nutritional quality of citronella (*Cymbopogon nardus* L.) residues and evaluates the use of near-infrared spectroscopy (NIRS) combined with machine learning (ML) models for rapid feed quality assessment. Citronella residues were subjected to sequential fungal and lactic acid bacterial fermentation, and their feed quality attributes, including moisture, crude protein, crude fiber, ether extract, and ash content, were measured using standard laboratory methods. NIR spectra were acquired from 1000 to 2500 nm and analyzed using partial least squares regression (PLSR), ridge regression, adaptive boosting (AdaBoost), and support vector machine regression (SVMR). Principal component analysis (PCA) revealed a high degree of spectral homogeneity with sufficient underlying variability to enable robust modeling. Among the models evaluated, AdaBoost and SVMR consistently outperformed linear models, achieving high coefficients of determination ($R^2 \geq 0.99$) and low root mean square errors (RMSE). Particularly, SVMR and AdaBoost achieved high predictive accuracy for moisture, crude protein, and ether extract content, with residual predictive deviation (RPD) values far exceeding standard thresholds. The integration of sequential fermentation, NIRS, and advanced ML algorithms presents a rapid, non-destructive, and sustainable approach to upgrading and monitoring alternative fibrous feed sources, supporting broader initiatives in circular bioeconomy and sustainable animal production.

Keywords: near-infrared spectroscopy; machine learning; sequential fermentation; citronella residues; feed quality assessment

INTRODUCTION

In a global scenario that aims to reduce waste, environmental problems and promote supply chain sustainability, the utilization and processing of agricultural waste as animal feed is becoming an important strategy for the livestock industry (Gasparini *et al.*, 2024; Jalal *et al.*, 2025). Agricultural by-products are often rich in carbohydrates, namely in the form of cellulose and hemicellulose. Agricultural by-products, in this case waste biomass from citronella distillation, are one of the most abundant sources. According to Manurung *et al.* (2015), every 1000 kg of citronella leaves that are distilled will produce 8 kg of essential oil, while the remaining 992 kg of biomass from citronella leaves is discarded as waste. Citronella residues contain a number of nutrients that can be used as feed ingredients for ruminants including 5.82% crude protein, 2.79% crude fat, and 35.03% crude fiber (Sari *et al.*, 2017), which consists of cellulose (35%–40%), hemicellulose (25%–30%), and lignin (15%–20%) (Singh *et al.*, 2019). The presence of lignin in this biomass is a major obstacle to the effective utilization of cellulose and hemicellulose by rumen microbes. Lignin levels in feed are negatively correlated to dry matter digestibility, leading to low digestibility values that result in low VFA (volatile fatty acid) production (Susanti *et al.*, 2020).

Considering the potential, nutrient composition and limiting factors contained in citronella residues, processing is needed to improve the quality of citronella waste as a feed ingredient. This processing aims to increase nutrient content and digestibility, reduce antinutritional compounds and extend shelf life. Biological degradation of lignin by fungal lignolytic enzymes is a viable and environmentally friendly alternative method. Most of the data available in the literature indicate that white-rot fungi have been used to improve the nutritional quality of potential feedstuffs, such as wheat straw, rice straw, sugarcane bagasse, and oil palm fronds (Tuyen *et al.*, 2013). In addition to biological methods, chemical treatments such as urea-molasses treatment have also demonstrated significant improvements in nutrient digestibility and animal growth performance, as shown in Azikheli buffalo calves (Rashid *et al.*, 2025). These microorganisms are able to increase the nutritional value of straw by degrading lignin (Tuyen *et al.*, 2013), promoting the release of cellulose and hemicellulose from lignocellulose (Niu *et al.*, 2018). Although white weathering fungi have great potential in selectively removing lignin in biomass, this method requires further optimization to make the feed more palatable through the ensiling process. Sequential fermentation will produce feedstuffs with more digestible energy (fungal delignification), as well as better palatability and storability (lactic acid, low pH, and short-chain fatty acids/SCFA from the ensilage process (Sun *et al.*, 2024). Laboratory testing (wet chemical analysis/WCA) has been commonly used to evaluate the nutritional quality of feed, including fermented feed ingredients; however, this method is considered inefficient and environmentally unfriendly because it takes a long time and uses chemicals in the testing process. Therefore, the implementation of alternative analysis techniques that are practical, fast, real-time time and efficient is essential for monitoring feed quality parameters.

Near-Infrared Spectroscopy (NIRS) technology has become one of the nondestructive methods that can be used for analysis in various fields, including the evaluation of animal feed nutrition (Buonaiuto *et al.*, 2021; Giaretta *et al.*, 2019). NIRS, as an analytical method, works on the principle that every biological object has characteristic optical and electromagnetic properties in the form of spectra. The NIR spectrum of this object is then analyzed by chemometric methods to bring out information in the spectrum data set about the chemical content of the object. Previous research using NIRS as a non-destructive method has been able to determine the *in vitro* digestibility values of dry matter (DM), organic matter (OM), neutral detergent fiber (NDF), acid detergent fiber (ADF) (Samadi *et al.*, 2020), pH, NH_3, and volatile fatty acids (VFA) (Samadi *et al.*, 2023). In contrast to proximate analysis or other chemical methods, analysis with NIRS technology is carried out without damaging the product (non-destructive), can analyze quickly, requires simple preparations, and does not use chemicals. Furthermore, NIRS is able to determine several quality parameters simultaneously and can be used simultaneously (Samadi *et al.*, 2020, 2025; Wahyudi *et al.*, 2025).

Therefore, this study was conducted to develop a rapid, non-destructive testing model for evaluating the nutritional quality of citronella waste optimized through sequential fermentation, using NIRS technology. The research also aims to establish a comprehensive database for the NIRS instrument, facilitating the accurate prediction of the nutritional value of fermented citronella residues for potential use as an alternative feed resource. This study introduces a novel approach by combining sequential fermentation of citronella (*Cymbopogon nardus* L.) residues with advanced machine learning techniques for rapid feed quality assessment. While NIRS has been employed in feed analysis (Mendoza *et al.*, 2023), the integration of ensemble methods like Adaptive Boosting (AdaBoost) and Support Vector Machine Regression (SVMR) offers enhanced predictive accuracy over traditional linear models. Moreover, the application of sequential fermentation using both fungal and lactic acid bacterial strains to improve the nutritional profile of citronella residues is relatively unexplored.

MATERIALS AND METHODS

Preparation of Citronella Feedstuffs

Citronella residues were utilized as a substrate for sequential fermentation in this investigation. Citronella residues were obtained post-oil distillation from farmers in the Gayo Lues District of Aceh, Indonesia. The citronella residues were subsequently hand-chopped to achieve a homogeneous length of approximately 3 cm. The substrate was subsequently dried in an oven at 60 °C to make it ready for fermentation. The moisture level in citronella waste is 11.4%.

Fungal and LAB Strains

This study utilized various fungal strains, including *Phanerochaete chrysosporium* (PCH), *Pleurotus ostreatus* (POS), *Trichoderma viride* (TRV), and *Lentinula edodes* (LED), alongside the lactic acid bacteria *Lactobacillus buchneri* (LB), for sequential fermentation. The microbial strains were sourced from the Indonesian Culture Collection (InaCC) Laboratory of BRIN, Cibinong, Indonesia. Before fermenting citronella waste, the fungal strains were pre-cultivated following the protocol of Tuyen *et al.* (2013) with minor modifications. Specifically, the fungi were grown on PDA medium and incubated at 24 °C until their mycelia had extensively colonized the agar surface. Inoculum preparation involved transferring an agar fragment (1.5-2.0 cm) containing fungal culture onto sterilized cracked corn. The inoculated corn was then incubated at 24 °C until it was fully colonized by fungal mycelia. To preserve the inoculum and inhibit further growth, the colonized corn was stored at 6 °C in a controlled environment. Additionally, the bacterial inoculum was prepared by culturing LB in the nutrient broth medium, followed by incubation at 37 °C for 24 hours to ensure optimal bacterial proliferation.

Sequential Fermentation

A total of 30 samples were collected across all phases of fermentation. Sequential fermentation involves conducting a series of successive fermentations, utilizing the fermented material from one batch to inoculate the subsequent batch. In this study, Solid-State Fermentation (SSF) was initiated using 447 grams of dried citronella residues as the solid substrate. The substrate matrix was further enriched with nutrients, including 30 grams of molasses and 100 g of corn bran. Subsequently, the substrate was inoculated with 50 grams of spawn of each fungal strain (PCH, POS, TRV, and LED), and sterile water was added during mixing to maintain a total moisture content of 60%. Both the SSF substrates and the uninoculated controls were aerobically incubated at room temperature (approximately 37 °C) for 28 days in polyethylene bags. All treatments, including controls, were conducted in six replicates. In the subsequent batches, 50% of the total wet weight substrate was ensiled with a bacterial inoculant of LB at a concentration of 1×10^6 cfu/gram of substrate. The LB inoculum and 1% molasses were diluted in 25 mL of water and applied to the substrate via spraying. After thorough mixing, the substrate was packed into polyethylene bags, which were then vacuum-sealed to create anaerobic conditions. These bags were incubated at room temperature (28-29 ^{o}C) for 14 days to complete the fermentation process. This study did not involve human or animal subjects. All microbial strains used for fermentation were non-pathogenic and handled according to institutional biosafety guidelines. The citronella residues were collected from a local essential oil facility with consent, and their use complied with institutional and environmental regulations. No ethical approval was required for this work.

NIR Spectra Acquisition

The NIR spectra of the samples were collected using NIRFlex N-500 spectrometers (Büchi, Flawil, Switzerland). The spectra were measured in absorbance mode from 1000 to 2500 nm (corresponding to 10000 to 4000 cm^{-1} wavenumber units) with a resolution of 1 nm, yielding 1557 data points across the extended range. Each spectrum underwent 32 scans, and results were averaged. Spectra acquisition was performed at an ambient temperature of 29 to 31 °C.

Measurements of Feed Quality Attributes

Following the completion of spectral data acquisition, feed samples were analyzed using standard laboratory methods to evaluate their quality attributes. These laboratory measurements serve as valuable reference data for calibrating and validating the NIRS model. The quality attributes of fermented feed samples include metrics from major nutrients, such as moisture content, crude protein (CP), crude fiber (CF), ether extract (EE), and ash content. Moisture content was determined using thermogravimetric analysis, which calculates the weight difference before and after drying the sample at 110 °C until a constant weight is achieved. The CP content was measured using the Kjeldahl method, where nitrogen (N) content is multiplied by 6.25. CF concentration is assessed following sequential extraction with an acid, followed by alkali. Ether extract (EE) content was determined using n-hexane as the solvent, based on the Soxhlet extraction principle. Finally, ash content is determined through complete combustion in a furnace at 550 °C. All analyses were conducted according to the procedures established by the Association of Official Analytical Chemists (AOAC) International (Association of Official Analytical Chemists, 2006).

Cross-Validation and Exploratory PCA

In this study, no external data partitioning was applied due to the limited number of available samples. Instead, model evaluation was performed using internal cross-validation, ensuring that all samples contributed to both calibration and validation in a rotation-based approach. This method provides an efficient assessment of model generalization without reducing the training dataset size. Principal Component Analysis (PCA) was employed by The Unscrambler X 10.4 software (CAMO Software, Oslo Norway) for exploratory data analysis to investigate the spectral variation among the fermented citronella feed samples.

Machine Learning (ML) Models

To model and predict feed quality parameters, four machine learning algorithms were employed: Partial Least Squares Regression (PLSR), Ridge Regression, Adaptive Boosting (AdaBoost), and Support Vector Machine Regression (SVMR). PLSR is a linear regression technique that reduces the predictors to a smaller set of uncorrelated components and is particularly effective when the predictors are highly collinear. Ridge Regression is a regularized linear model that addresses multicollinearity by adding an L2 penalty term to the loss function, thereby improving the model's generalization performance. AdaBoost is an ensemble method that combines multiple weak learners in a sequential manner, where each learner attempts to correct the errors of its predecessor. SVMR is a robust nonlinear regression technique that maps input features into a high-dimensional space using kernel functions and constructs a hyperplane that best fits the data within a specified margin of tolerance (Hastie *et al.*, 2009).

Performance Evaluation of Prediction Models

The performance of the prediction models was evaluated using several statistical metrics: the correlation coefficient (r), the coefficient of determination (R^2), the root means square error (RMSE), the residual predictive deviation (RPD), and the Range Error Ratio (RER). The correlation coefficient (r) reflects the strength and direction of the linear relationship between predicted and observed values. The coefficient of determination (R^2) indicates the proportion of variance in the observed data that is explained by the model. RMSE measures the average magnitude of prediction errors, providing a direct measure of model accuracy in the same units as the predicted variable (Hastie *et al.*, 2009). An R^2 value > 0.8

indicates a model with strong predictive ability, while an RMSE lower than the actual standard deviation (SD) indicates superior predictive performance (Munawar *et al*., 2024; Samadi *et al*., 2023). RPD, calculated as the ratio of the standard deviation of reference data to RMSE, is used to assess the model's predictive capability, with higher values indicating better performance. RER, defined as the ratio of the range of reference data to RMSE, provides additional insight into the reliability of predictions across the full range of the dataset (Williams & Norris, 1987).

RESULTS

Reference Feed Quality Statistics

Table 1 presents the descriptive statistics of the feed quality attributes obtained from the fermented citronella residues, including moisture, crude protein, crude fiber, ether extract, and ash content. Each nutritional parameter was measured in 30 fermented citronella residue samples, ensuring consistent sample representation for model development. Moisture content showed a relatively narrow range (7.04%–8.82%) with a mean of 7.91% and an SD of 0.38, indicating low variability. Crude protein content ranged from 6.12% to 11.41%, with a mean value of 9.06% and a higher SD of 1.04, reflecting moderate variation across samples. Crude fiber was fairly consistent (mean 26.20%, SD 0.74), while ether extract and ash exhibited slightly wider variation, with SDs of 0.63 and 0.49, respectively. These results suggest that the dataset encompasses sufficient variability in key nutritional parameters, particularly in crude protein and ether extract, which is beneficial for the robustness of model training. Low variability in attributes like moisture and fiber, while indicative of good experimental control, may pose a challenge for calibration if not adequately represented in spectral variability.

Fermented Citronella Feed Spectra and PCA Analyses

The raw Near-Infrared (NIR) absorbance spectra of the fermented citronella feed samples are shown in Figure 1, covering the wavelength range from 1000 to 2500 nm. Each line represents the spectral profile of an individual sample. The spectra exhibit clear and consistent absorption features that correspond to the vibrational overtones and combinations of chemical bonds such as O–H, N–H, and C–H, which are commonly associated with moisture, protein, fiber, and lipid content in biological materials (Cen & He, 2007). Notably, absorption bands in the region around 1400-1450 nm and 1900-1950 nm are typically attributed to moisture-related O–H bond vibrations. Peaks near 2100-2200 nm often reflect the presence of proteins and fiber components due to N–H and C–H stretching. The variation in absorbance intensities among samples indicates chemical compositional differences, which are essential for establishing reliable calibration models.

Principal Component Analysis (PCA) was applied to the NIR spectral dataset to explore the natural

Table 1. Descriptive statistics of actual measurements of nutrient quality from fermented citronella residues in the dataset

Nutrient contents	N	Min	Max	Mean	SD	Variance
Moisture	30	7.04	8.82	7.91	0.38	0.14
Crude protein	30	6.12	11.41	9.06	1.04	1.08
Crude fiber	30	24.60	27.47	26.20	0.74	0.55
Extract ether	30	1.52	4.52	2.69	0.63	0.40
Ash	30	7.53	9.29	8.24	0.49	0.24

Note: N, number of sample datasets; Min, minimal; Max, maximal; and SD, standard deviation.

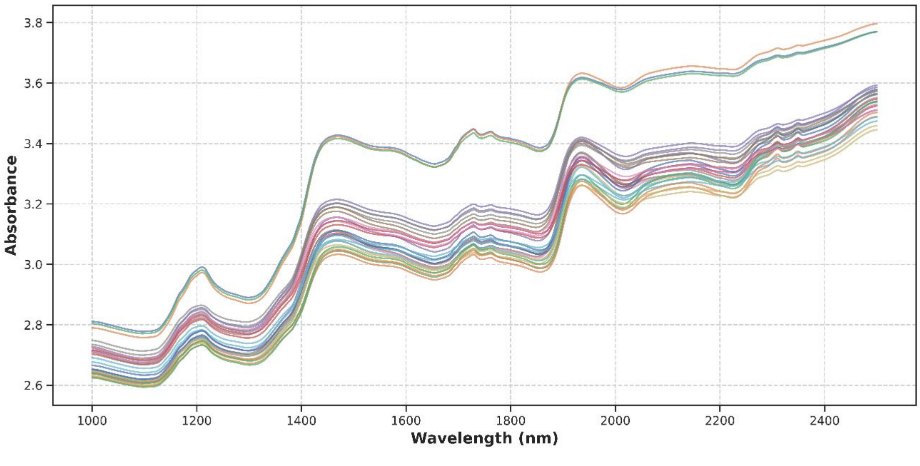


Figure 1. Feed sample raw near-infrared (NIR) absorbance spectra in the 1000-2500 nm wavelength range. Each colored line represents the absorbance spectrum of an individual sample. The spectral data exhibit distinct absorption features associated with organic functional groups, indicating variations in the chemical composition of the samples.

variability among the samples and to assess potential clustering prior to model development. As shown in Figure 2, the PCA score plot illustrates the distribution of samples along the first two principal components (PC-1 and PC-2), which together explain 99% of the total spectral variance (96% and 3%, respectively). This high cumulative variance indicates that the majority of spectral information is effectively captured within just two dimensions.

The distribution of samples within the PCA plot appears compact, with no extreme outliers, suggesting good homogeneity in the spectral data. The presence of a 95% confidence ellipse further confirms that all samples fall within the expected variability range, supporting the quality and consistency of the spectral measurements. This natural grouping of samples without distinct sub-clusters implies that while the samples originate from similar biological material, there is sufficient underlying variation to train predictive models across a spectrum of feed quality traits.

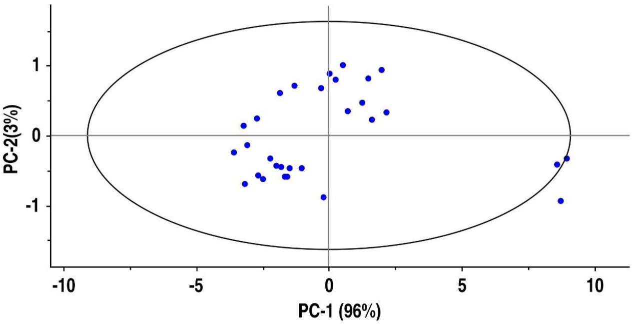


Figure 2. Principal component analysis (PCA) score plot based on the NIR spectral data of feed samples. The plot displays the distribution of samples along the first two principal components, PC-1 (96%) and PC-2 (3%), which together explain 99% of the total variance. Each blue dot corresponds to an individual sample, while the ellipse represents the 95% confidence region, indicating the natural grouping and variability among samples.

Performance of NIRS Predictive Model

The prediction performances of the four evaluated models-Partial Least Squares Regression (PLSR), Ridge Regression, Adaptive Boosting (AdaBoost), and Support Vector Machine Regression (SVMR)-are summarized in Table 2 and visualized in Figure 3. The results clearly show that both ensemble-based and kernel-based models (AdaBoost and SVMR) consistently outperformed the linear models (PLSR and Ridge) across all feed quality attributes. For moisture prediction, SVMR achieved the highest accuracy, with a coefficient of determination (R^2) of 0.99, a very low RMSE of 0.02, and high RPD (18.99) and RER (89.00) values, indicating excellent model reliability. Similarly, for crude protein, AdaBoost achieved optimal performance (R^2= 0.99, RMSE= 0.05, RPD= 20.80), followed closely by SVMR (R^2= 0.99, RMSE= 0.08). In the case of crude fiber, SVMR again demonstrated superior predictive power (R^2= 0.99, RMSE= 0.06), while AdaBoost performed best for ash content (R^2= 0.95, RMSE= 0.10, RPD= 4.91). For the ether extract, both SVMR and AdaBoost performed equally well, each achieving an R^2 of 0.99 and RMSE of 0.02, along with the highest RPD and RER values in the dataset (RPD= 31.61; RER= 150.00), highlighting their exceptional precision.

Table 2. Prediction performance of PSLR, Ridge, AdaBoost, and SVMR models in determining feed quality of fermented citronella residues

Nutrient contents	Method	r	R2	RMSE	RPD	RER
Moisture	PLSR	0.88	0.78	0.17	2.23	10.47
	Ridge	0.90	0.81	0.16	2.37	11.13
	AdaBoost	0.99	0.99	0.03	12.66	59.33
	SVMR	0.99	0.99	0.02	18.99	89.00
Crude protein	PLSR	0.86	0.75	0.51	2.04	10.37
	Ridge	0.97	0.94	0.24	4.33	22.04
	AdaBoost	0.99	0.99	0.05	20.80	105.80
	SVMR	0.99	0.99	0.08	13.00	66.13
Crude fiber	PLSR	0.91	0.83	0.29	2.56	9.90
	Ridge	0.94	0.88	0.25	2.97	11.48
	AdaBoost	0.97	0.95	0.15	4.95	19.13
	SVMR	0.99	0.99	0.06	12.37	47.83
Extract ether	PLSR	0.96	0.92	0.17	3.72	17.65
	Ridge	0.97	0.96	0.13	4.86	23.08
	AdaBoost	0.99	0.99	0.02	31.61	150.00
	SVMR	0.99	0.99	0.02	31.61	150.00
Ash	PLSR	0.93	0.88	0.17	2.89	10.35
	Ridge	0.96	0.92	0.13	3.77	13.54
	AdaBoost	0.97	0.95	0.10	4.91	17.60
	SVMR	0.96	0.93	0.12	4.09	14.67

Note: PLSR, partial least squares regression; AdaBoost, adaptive boosting; SVMR, support vector machine regression; r, coefficient of correlation; R^2, coefficient of determination; RMSE, root mean square error; RPD, residual predictive deviation; and RER, range error ratio.

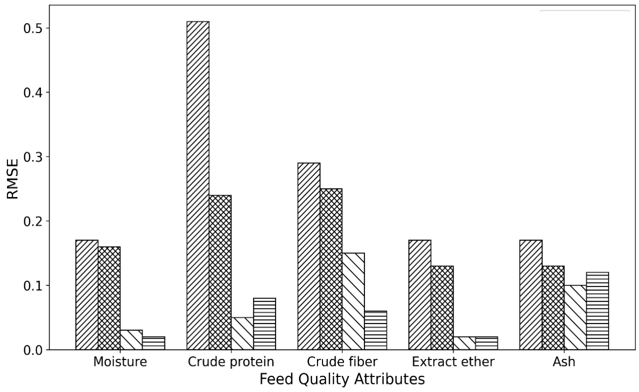
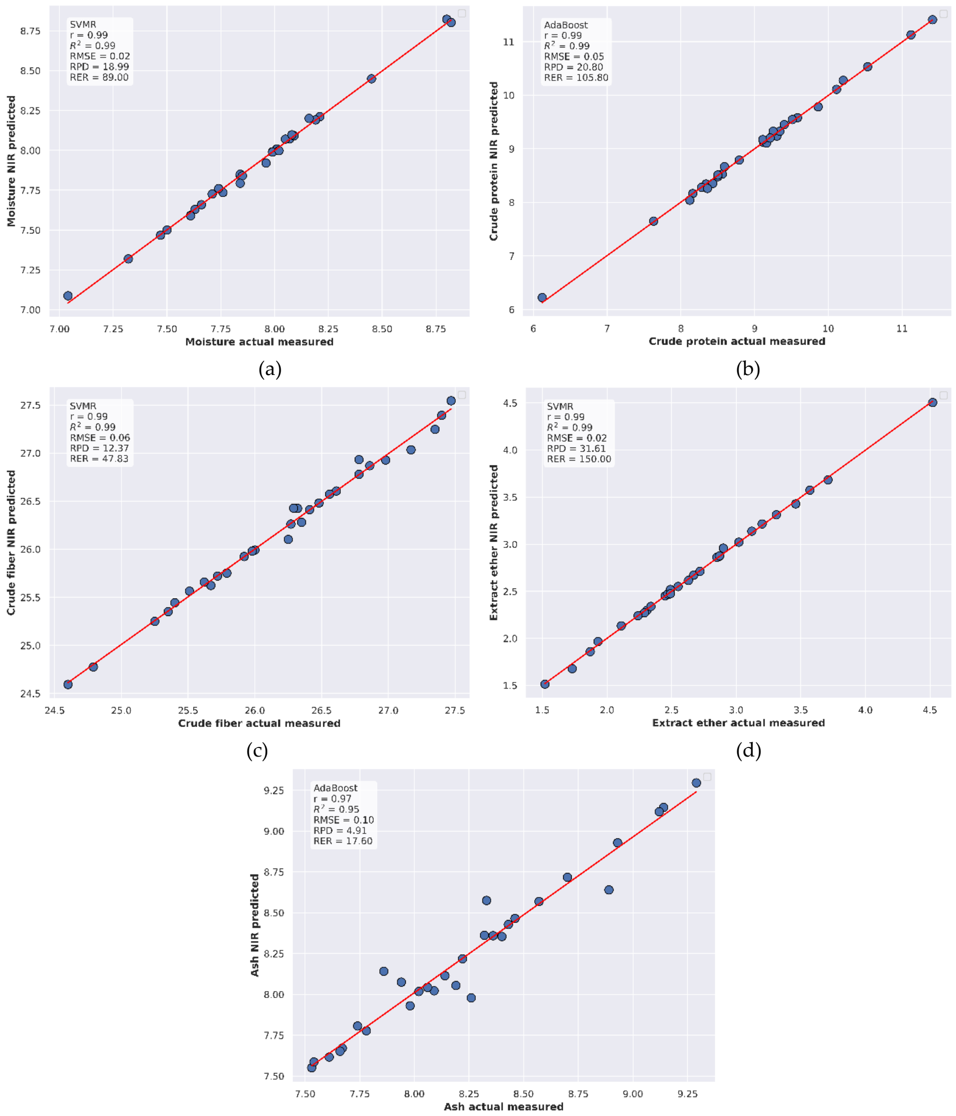


Figure 3. Comparison of root mean square error (RMSE) values for predicting feed quality attributes using different machine learning algorithms: ▨ partial least squares regression (PLSR), ▩ ridge regression, ⧅ adaptive boosting (AdaBoost), and ▤ support vector machine regression (SV MR).

Figure 4 illustrates the scatter plots comparing predicted versus actual values for each feed quality attribute using the optimal machine learning model identified in Table 2. These plots provide a visual representation of the predictive accuracy and model agreement with reference measurements. For moisture content (Figure 4a), the SVMR model shows excellent agreement between predicted and measured values, with data points tightly clustered along the identity line (y= x), reflecting minimal prediction error and high consistency. Similarly, the crude protein prediction using AdaBoost (Figure 4b) demonstrates a strong linear relationship, with limited dispersion and a high correlation coefficient, confirming the model's capacity to generalize across varying protein levels. In the case of crude fiber (Figure 4c), the SVMR model maintained high predictive power, capturing subtle variations in fiber content with precision. Ether extract



(a) (b)

(c) (d)

Figure 4. Scatter plots illustrating the predictive performance of the optimal machine learning models for various feed quality attributes: (a) moisture content predicted by SVMR, (b) crude protein predicted by AdaBoost, (c) crude fiber predicted by SVMR, (d) ether extract predicted by SVMR, and (e) ash content predicted by AdaBoost. Each plot displays data points representing the agreement between model-predicted values and corresponding reference measurements used for calibration. The red line represents the identity line (y = x), indicating perfect agreement between predicted and actual values.

(Figure 4d), which exhibited the highest RPD and RER values, was also predicted with near-perfect accuracy by both SVMR and AdaBoost, as evidenced by the almost complete overlap of predicted and actual values. For ash content (Figure 4e), AdaBoost achieved solid predictive agreement, though a slightly wider spread in data points suggests minor variation in model precision compared to other parameters.

DISCUSSION

Overall, the models with non-linear learning capacity (AdaBoost and SVMR) demonstrated strong generalization, particularly in predicting attributes with high variability such as crude protein and ether extract. PLSR and Ridge, while simpler and computationally efficient, demonstrated moderate performance, suggesting that linear models may not be sufficient to fully capture the complexity of NIR spectral relationships in sequentially fermented citronella residues. These results highlight the capacity of nonlinear models to capture subtle spectral features related to the chemical composition of the feed samples.

The high predictive accuracy observed for crude protein, particularly in the AdaBoost and SVMR models ($R^2 > 0.99$), is consistent with the presence of N–H and C–H combination bands in the Near-Infrared (NIR) range, especially between 2050 and 2250 nm. These bands are associated with amide groups and amino acids, which contribute significantly to protein signals in fermented plant materials (Pucetti *et al.*, 2024). Similarly, the reliable prediction of crude fiber content can be attributed to the absorption features of cellulose and hemicellulose, which exhibit strong combination and overtone bands of O–H and C–H bonds in the 2100–2200 nm region. These vibrational characteristics have been successfully used to differentiate and quantify fibrous components in silage and plant-based feedstuffs (Zhang *et al.*, 2021). For ether extract (fat) content, the extremely high RPD values (e.g., 31.61) can be explained by distinct C–H stretching vibrations of CH_2 and CH_3 groups, which absorb strongly in the 1700–1800 nm and 2300–2400 nm regions. These spectral features are well-documented markers for fat quantification using NIR spectroscopy, especially in oils and lipid-rich samples (Tsegay *et al.*, 2023).

The findings of this study are consistent with a growing body of research demonstrating the high predictive capability of NIRS for feed quality assessment. For example, Hossain *et al.* (2024), in a systematic review of 54 studies, reported that NIRS can accurately predict key nutritional attributes such as crude protein, fiber, and moisture across various feed types when properly calibrated with chemometric models. Similarly, Balehegn *et al.* (2022) emphasized that NIRS, when combined with robust reference data and calibration protocols, is particularly valuable in contexts requiring rapid and low-cost analysis—especially for fibrous, plant-based feeds such as those evaluated in this study. Additionally, Cozzolino (2021) noted that the strong predictive power of NIRS is due to its ability to capture broad overlapping absorption bands from key functional groups (O–H, N–H, C–H), which are central to the quantification of nutritional parameters in both foods and feedstuffs. Compared to these previous studies, the extremely high R^2 and RPD values reported here, particularly for ether extract and crude protein, reinforce the robustness of the selected machine learning models and demonstrate the viability of applying NIRS-ML integration to novel substrates such as fermented citronella residues.

The integration of Near-Infrared Spectroscopy (NIRS) with advanced machine learning algorithms in this study highlights a robust, rapid, and sustainable approach to assessing feed quality in sequentially fermented citronella residues. The high predictive accuracy achieved, particularly by non-linear models such as AdaBoost and SVMR, confirms their suitability for modeling complex biological matrices. These findings are consistent with previous studies where machine learning models, particularly ensemble and kernel-based techniques, outperformed traditional linear methods in predicting chemical and nutritional components in agricultural residues (Cen & He, 2007; Samadi *et al.*, 2023). The successful prediction of key quality indicators such as crude protein and ether extract content, both critical to ruminant nutrition, demonstrates the practical relevance of this approach. Comparable results have been showed in other contexts, such as rice straw and wheat straw fermentation, where models like SVMR and random forest exhibited superior accuracy in nutrient prediction (Niu *et al.*, 2018; Sun *et al.*, 2024). Moreover, the exceptionally high RPD and RER values observed in the present study (e.g., RPD = 31.61 for ether extract) substantially exceed the commonly accepted threshold (> 3.0) for quantitative prediction (Williams & Norris, 1987), reinforcing the analytical strength of the NIRS–ML framework. In addition to improving analytical efficiency, the use of NIRS reduces the environmental footprint of feed evaluation by eliminating the need for chemicals and reducing laboratory waste, aligning with sustainable feed production practices (Pasquini, 2018). This is particularly relevant for smallholder or decentralized feed systems where access to conventional laboratories may be limited. From a broader agri-industrial perspective, valorizing citronella residues as an alternative fibrous feed supports waste minimization and circular economy goals. As demonstrated by Manurung *et al.* (2015), citronella biomass, typically discarded after oil extraction, has untapped nutritional value. Our findings support the view that appropriate processing, such as sequential fermentation and biological delignification, can transform this biomass into a viable feed source, similar to efforts reported for other lignocellulosic materials like sugarcane bagasse and oil palm fronds (Tuyen *et al.*, 2013).

This study has particular relevance for tropical livestock production systems, especially in regions like Indonesia where citronella is widely cultivated for essential oil extraction (Widiaswanti *et al.*, 2024). The large volume of residual biomass generated postdistillation represents a locally available, underutilized resource. Integrating fermented citronella residues into ruminant diets could reduce reliance on conventional forages and help mitigate seasonal feed shortages common in tropical livestock systems. Moreover, valorizing such agro-industrial byproducts supports more sustainable and circular feed systems, which are essential for improving feed security and resilience in smallholder-based tropical livestock sectors.

Beyond its environmental and nutritional relevance, the approach also offers practical value in day-to-day feed management and decision-making. Portable and handheld NIRS devices have been shown to deliver rapid, on-site assessment of feed composition, allowing for real-time decision-making without the need for laboratory infrastructure. For instance, Walelegne *et al.* (2023) demonstrated that handheld NIRS devices could reliably estimate key nutritional parameters such as crude protein, fiber fractions, and digestibility in oilseed meals, even under field conditions. Similarly, Rego *et al.* (2020) developed a portable IoT-based NIRS system for dairy forage analysis, highlighting its applicability in remote and resource-limited environments, especially when integrated with cloud-based processing for real-time feedback. Moreover, Modroño *et al.* (2017) evaluated two commercial handheld NIRS instruments and confirmed their utility in farm-level feed monitoring, reporting high predictive performance ($R^2 > 0.88$ for crude protein and fiber), thereby reducing the need for sample transport and laboratory turnaround time. These findings underscore the potential of portable NIRS solutions to transform feed quality control into a proactive, data-driven process - enhancing nutritional precision, reducing overfeeding, and improving economic outcomes across livestock systems. Beyond the technical contributions of this study, it is important to consider how such findings can be communicated to broader audiences. In an era where misinformation about animal production and sustainability is widespread, effectively sharing evidence-based practices - such as the use of NIRS for feed quality assessment and the valorization of citronella residues - is essential. Social media and other digital platforms offer opportunities to extend the reach of scientific knowledge, foster public engagement, and counter misconceptions. As demonstrated by Lamanna *et al*. (2025), targeted communication strategies can improve public understanding of complex topics in animal agriculture, ultimately supporting informed dialogue around sustainable livestock systems.

CONCLUSION

This study demonstrates the successful integration of sequential fermentation and machine learning-assisted near-infrared spectroscopy (NIRS) for the rapid and non-destructive assessment of feed quality in citronella (*Cymbopogon nardus* L.) residues. The sequential application of fungal and lactic acid bacterial fermentation improved the nutritional profile of the fibrous feed material, and the use of NIRS combined with advanced machine learning (ML) models enabled accurate prediction of key quality attributes including moisture, crude protein, crude fiber, ether extract, and ash. Among the models evaluated, adaptive boosting (AdaBoost) and support vector machine regression (SVMR) consistently achieved superior performance, with coefficients of determination (R^2) exceeding 0.99 and exceptionally high residual predictive deviation (RPD) values, confirming their robustness and predictive power. The results validate the applicability of non-linear, ensemble-based models for modeling complex biological matrices such as fermented plant residues. The proposed approach offers a fast, environmentally friendly alternative to conventional chemical analyses and supports the development of sustainable livestock feeding systems. Moreover, it provides a foundation for the practical valorization of citronella waste as an alternative fibrous feed in ruminant nutrition. Future research should aim to expand the spectral database, explore fermentation process optimization, and evaluate model deployment in field-ready NIRS devices for real-time feed quality monitoring.

CONFLICT OF INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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