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Application of Infrared Spectroscopy with Multivariate Analysis and Soft Independent Modelling of Class Analogies (Simca) for the Detection of Meat Species

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ABSTRACT

Meat speciation is currently monitored using various chemical and biological methods that rely on proteins, DNA, and RNA. However, these approaches are slow, costly, and difficult for automation. Infrared spectroscopy presents itself as a convenient analytical tool for monitoring food quality. This study aimed to evaluate the potential of FTIR spectroscopy and multivariate analyses in identifying meat species. Dried powders were prepared from defatted goat meat, chicken and pork. Initially, powders from single meat species were subjected to spectral scanning in the range of 400-400 cm^{-1}. Subsequently, mixtures of chicken and goat, pork and goat, and chicken and pork in a 50:50 ratio were prepared and analysed using FTIR spectroscopy. Chemometric analyses, employing multivariate analysis, were conducted for each sample. Spectral signatures of 16-18 samples for each type of mixed powder were acquired. Results of Principal component analysis showed clear clustering of samples with sum of PC1 and PC2 described 98% variance. Further, SIMCA correctly classified the chicken, goat and pig powder into their respective classes with an accuracy of 93.75%, 88.88% and 93.75% respectively. In conclusion, NIR spectral analysis proves to be a novel, rapid, and cost-effective technique for identifying meat species in various meat and meat products. Experiments were carried out in ICAR-CIPHET, Ludhiana.

Keywords: FTIR spectroscopy, chemometric analysis, Principal Component Analysis, SIMCA, meat adulteration

INTRODUCTION

Meat is the main source of vitamins, proteins, fatty acids and essential amino acids. As the population increased, the demand for meat and its quality also increased globally. Among all food categories, meat and meat-derived products are especially vulnerable to fraudulent practices due to their high economic value, complex supply chains, and strong consumer demand. Common forms of meat fraud include species substitution, mislabeling, and adulteration of processed products with cheaper meats or non-meat ingredients. Meat adulterating and its derived products involves adding external substances to increase weight, thereby lowering production costs while altering the product's inherent quality. Over the last few years, adulteration has become widespread and now regularly includes the substitution or mixing of different animal species. A frequent example is the addition of cheaper meats to more expensive varieties. The primary motivation for this adulteration is economic gain, achieved through the substitution of high-value meats with cheaper alternatives, such as beef or lard in other foodstuffs. Therefore, effective oversight depends on advanced techniques capable of verifying species origin in both raw and highly processed meat products, ensuring compliance with legal, safety, and religious standards.

In response to this critical need, extensive research has

been dedicated to developing robust analytical techniques. Although several methods like spectrometric, biochemical tests etc., are available to detect meat adulteration (Naveena et al. 2017), genomic methods with DNA/RNA prevails to be the best owing to its high specificity and trace detection sensitivity (Vishnuraj et al. 2023). Chromatographic and isotopic methods also provide valuable data for detection and traceability (Montowska and Pospiech 2010). These techniques face limitations related to cost, throughput, or susceptibility to interference in processed samples. Among spectroscopic techniques, Fourier Transform Infrared (FTIR) spectroscopy, particularly in Attenuated Total Reflectance (ATR) mode, has gained significant prominence (Meza-Márquez et al. 2010). It enables rapid, non-destructive analysis by generating a unique chemical "fingerprint" of a sample. The true power of this approach is realized through integration with advanced chemometric, statistical tools that extract meaningful patterns from complex spectral data for classification and quantification. Several studies have successfully employed Fourier-transform infrared (FTIR) spectroscopy combined with chemometric techniques to identify meat adulteration (Meza-Márquez et al. 2010). Building on this approach, the present study investigates the potential of FTIR paired with chemometric analysis, to identify adulterants specifically in goat meat.

MATERIALS AND METHODS

Sample preparation and fat extraction

Meat samples from pig, chicken and lamb were collected from a local meat shop. Firstly, the samples were washed by distilled water to remove any contamination that might be stuck on the surface of the meat samples. Then, the meat samples were cut into small elements (1 cm x 1 cm) and kept at -20ºC until they are used for the fat extraction process. Meat fat was extracted by Soxhlet method and remaining meat samples were dried at 100 ±1 °C for 12 hours. The powders were then processed using a kitchen grinder and sieved through mesh size no. 4. Initially, powders from single meat species were subjected to spectral scanning in the range of 400-400 cm^{-1}. Subsequently, mixtures of chicken and goat, pork and goat, and chicken and pork in a 50:50 ratio were prepared and analyzed using FTIR spectroscopy in the same wavelength range. A total of 16-18 samples were subjected to FTIR spectral analysis.

ATR-FTIR Analysis

ATR-FTIR analysis was performed on the fresh ground meat samples as described by Dashti et al. (2022). FTIR spectrometer (Agilent Technologies, USA) was equipped with a ZnSe ATR interface, triglycine sulfate (DTGS) detector and KBR as the beam splitter. Meat samples were placed in good contact with a horizontal positioned attenuated total reflectance element at room temperature. The surface of the ATR interface was cleaned with ethanol and dried before measuring the next sample. Before each sample scan, a new reference air background spectrum (an average of 32 scans) was acquired. The spectra were recorded in the range between 650 and 4000 cm (2500 to 15384 nm) at a resolution of 16 cm 1 with 200 scans. All ATR-FTIR spectra were recorded as transmittance values at each data point but they were converted to absorbance (log1/transmittance). The Cary 630 MicroLab PC software was used for data collection and chemometric analysis.

RESULTS AND DISCUSSION

Chemometric Discrimination of different meat Samples

The principal component analysis (PCA) results demonstrate the strong capability of the applied analytical approach to differentiate pork, chicken, and goat powder samples based on their compositional profiles. The clear species-specific clustering observed in the scores plot confirms that the selected variables capture intrinsic biochemical differences among meat types, which is essential for reliable authentication and quality control applications (Bro and Smilde 2014).

The resulting PCA scores plot revealed well-defined and repeatable clusters for each meat type. The first principal component (PC-1) described 96% of the total variance, serving as the major axis distinguishing the samples. High variance contribution by PC-1 suggests the presence of strong discriminatory markers related to muscle composition, protein profiles, lipid content, or other species-dependent constituents (Varmuza and Filzmoser 2009). The second component (PC-2) explained a smaller portion (2–3%) of the variance, reflecting subtle variability within groups.

Pork samples were clearly separated along the negative axis of PC-1 (Figure 1) and appeared tightly grouped, reflects high analytical repeatability and compositional uniformity, reinforcing the robustness of the current method for pork identification. Chicken and goat samples both occupied the positive region of PC-1 but formed distinct, adjacent clusters. Goat samples displayed broader scattering along PC-2, suggesting greater internal heterogeneity. This increased variability may be attributed to processing-related factors such as drying, particle size variation, or formulation differences commonly associated with powdered meat products (Varmuza and Filzmoser 2009). The ability of PCA to distinguish processed goat powder from fresh chicken samples highlights the sensitivity of the approach to both species-specific and matrix-dependent variations.

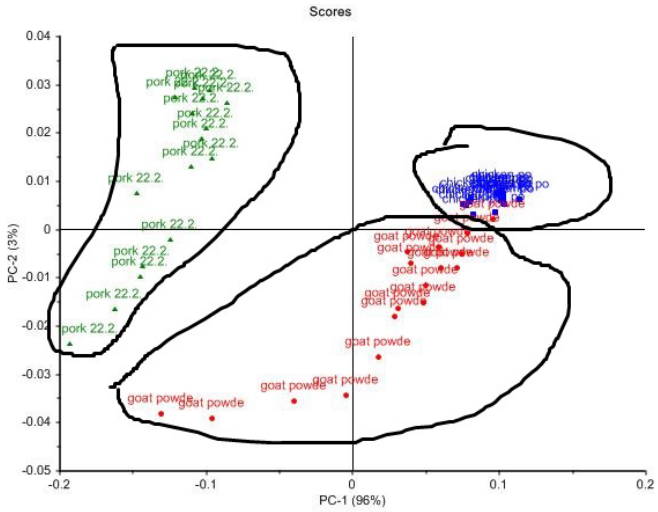

Fig. 1: Principal Component Analysis (PCA) scores of meat samples: The score plot illustrates the distribution of samples along the first two principal components (PC-1 and PC-2), explaining 96% and ~2–3% of the total variance, respectively. Distinct clustering of pork (green), chicken (blue), and goat powder (red) samples demonstrate species-specific discrimination with minimal overlap, indicating the effectiveness of the analytical method for meat authentication and adulteration assessment.

From an adulteration perspective, the pronounced separation between pork and non-pork samples is particularly relevant. In cases of intentional or accidental adulteration, mixed samples would be expected to deviate from authentic clusters and occupy intermediate positions within the PCA space, as shown in previous meat authentication studies (Luykx and van Ruth 2008). Therefore, the observed clustering pattern supports the application of PCA as a rapid, non-targeted screening tool for detecting meat adulteration, especially in regulatory and halal authentication contexts where pork contamination is of critical concern.

SIMCA classification results for chicken, goat and pig defatted powder were presented in Table 1. Spectral data in the wavelength range of 230–320 nm were analyzed using seven principal components. The SIMCA model has a high ability to correctly discriminate between the different meat powders, suggesting clear spectral differences among chicken, goat, and pig samples after defatting.

For chicken powder, out of 16 test samples, 15 samples were correctly classified, resulting in 93.75% accuracy. Similarly, 15 out of 16 samples being correctly identified in pig powder with an accuracy of 93.75%. Of the 18 goat samples tested, 16 were correctly classified with an accuracy of 88.88%.

Table 1. SIMCA classification results for defatted powder (chicken, goat and pig).

Wave number Range	Defatted powder	No of PC	No. of test samples	Number of samples classified			Mis-classification	Correct classification (%)
				Chicken powder	Goat powder	Pig powder		
230-320nm	Chicken powder	7	16	15	14	0	14	93.75
	Goat powder		18	04	16	0	04	88.88
	Pig powder		16	15	0	0	0	93.75

Chemometrically, the minimal overlap among clusters and tight grouping of replicates indicate good data quality, low instrumental noise, and high reproducibility. These characteristics validate the suitability of PCA as an exploratory tool prior to the development of supervised classification models such as Partial Least Squares–Discriminant Analysis (PLS-DA), Soft Independent Modeling of Class Analogy (SIMCA), or Linear Discriminant Analysis (LDA), which have been applied successfully in food authentication research (Manley 2014). Incorporating such supervised approaches could further enhance classification accuracy and provide quantitative evaluation through sensitivity, specificity, and cross-validation metrics.

Overall, the PCA-based discrimination observed in this study confirms the effectiveness of the analytical method for meat species differentiation. The findings support its potential application in routine microbiological quality control, authenticity verification, and surveillance of meat and meat-based products, particularly for detecting species substitution and adulteration in processed foods.

CONCLUSION

Overall, the PCA-based discrimination observed in this study confirms the effectiveness of the analytical method for meat species differentiation. The findings support its potential application of FTIR and chemometric in routine quality control, authenticity verification, and surveillance of meat and meat-based products, particularly for detecting species substitution and adulteration in processed foods.

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