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NON-INVASIVE MULTISPECTRAL IMAGE ANALYSIS FOR THE ASSESSMENT OF SPOILAGE IN POULTRY PRODUCTS

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INTRODUCTION

Multispectral image analysis is considered as a potential tool for rapid and no destructive evaluation of the quality of meat products. This alternative method has been applied on a variety of meat products resulting in the development of spoilage predictive models^{1,2}. The aim of this study was to correlate microbiological to multispectral data acquired from at-line measurements in a meat processing factory for two poultry products. Partial Least Squares- Regression (PLS-R) analysis was undertaken for the evaluation of the microbiological quality in these products.

MATERIALS AND METHODS

A) Microbiological analysis and Multispectral image analysis

B) Data processing

> Partial least squares (PLS) regression was implemented correlating spectral data to microbial

Fillets of chicken thigh (n=97) and chicken burger (n=131) were analyzed microbiologically for the determination of total viable counts (TVC) and Pseudomonas spp.



- MSI acquisitions were obtained at 18 different wavelengths (405-970 nm).
- For each monochromatic wavelength, a mean intensity of pixels and the corresponding standard deviation was CDA (Canonical estimated bv Discriminant Analysis) algorithm for the desirable ROI (Region of interest) of sample.

counts and time from slaughter.

For each product, three PLS- R models were developed for the assessment of: 1) TVC (log CFU/g), 2) *Pseudomonas* spp. (log CFU/g) and 3) time from slaughter (log(t)).

For chicken burger model assessing TVC, SNV transformation was applied at spectra data set in order to reduce noisy and collinear data areas.

MSI acquirement



Figure 2: Spectra of chicken thigh (A) and chicken burger (B) at 24 h (blue line) and 216 h (red line) at wavelengths: 405-970 nm.

RESULTS

Microbiological analysis



Fresh/CFCSpoiled/CFCFresh/PCASpoiled/PCAFresh/CFCSp	spoiled/CFC	Fresh/PCA	Spoiled/PCA
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Figure 1: Boxplots of Total Viable Counts (PCA media) and *Pseudomonas* spp. (CFC media) counts (log CFU/g) in fresh and spoiled samples of chicken thigh (A) and chicken burger (B).

- Initial microbial load of TVC and *Pseudomonas* spp. was at 4.3 log CFU/g and 4 log CFU/g \bullet respectively in chicken thigh while final number of counts at 216 h were estimated at 9 log CFU/g for TVC and *Pseudomonas* spp.
- For chicken burger, TVC and *Pseudomonas spp.* counts were initially 5.3 log CFU/g and \bullet 4.6 log CFU/g respectively. Samples were defined as spoiled at 6.1 log CFU/g (above 96 h) for TVC and at 5.8 log CFU/g for *Pseudomonas* spp.
- At Figure 3 is depicted the comparison between observed to predicted values (TVC, \bullet *Pseudomonas* spp. and time from slaughter) estimated by PLS- R application in data sets of chicken thigh and burger. In addition, for each model are provided values RMSE and R² of leave-one-out cross-validation which pointing good performance in all quantitative algorithm.

CONCLUSION

PLS-R models estimating TVC, *Pseudomonas* spp. and time from slaughter indicated good performance according to values RMSE and R² for Leave-one-out validation in both cases of poultry products. Hence, the application of these findings in the production and/or distribution line could assist for the proactive assessment of poultry products quality.

REFERENCES

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- Tsakanikas, P. et al., 2016, *Talanta*, 161, 606-614.



Figure 3: Correlation between observed to predicted values and indexes RMSE and R² for the estimation of TVC, Pseudomonas spp. and time from slaughter for chicken thigh (A: TVC, B: Pseudomonas spp., C: time from slaughter) and for chicken burger (D: TVC, E: Pseudomonas spp., F: time from slaughter), whereas solid line: the ideal y= x line; dashed lines: the 1 log unit area (A,B,D,E)







