P.37.-Near Infrared Reflectance Spectroscopy (NIRS) for identification of the specie in animal protein processed by-products

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From 3 October 2003 the EU has adopted Regulation (EC) nº 1774/2002 governing Animal By-Products (ABPs) and it adresses the possible risk inherent in recycling potential infectivity due to the absence of barrier within species and excludes the cannibalism, which may be induced by the intra-species recycling. The main aim of the present work was to develop and validate quantitative and qualitative NIRS models to identify the animal specie in ABPs.

A total of 280 samples of protein animal meals were collected from October 2002 to April 2004 from different providers in the framework of two projects[1,2]. The animal meals samples were identified by the providers as being from pure poultry (n=56), pure cattle (n=1), mixture cattle-poultry (n=1), mixture cattle-pork (n=3), mixture poultry-pork (n=3), blood (n=1), fish (n=8), hydrolised feather meal (n=1), feather meal (n=1) and mixture cattle-ewe-pork and poultry. The spectra of the meals samples were recorded in a FOSS NIRSystems 6500 instrument and thus, a NIRS spectral library of identified ABPs was build (training set). Modified PLS quantitative models were developed to predict the percentage of poultry, pork, cattle, ruminant and non-ruminant meat meals in protein ABPs and they explained 94%, 93%, 81%, 76% and 78% of the variance existing for the parameter "specie" in the complete spectral library. PLS2 discriminant models were also developed, using dummy variables (1=ruminant; 2=non-ruminant). The best model obtained explained the 82.7% of the variance and it had a SECV value of 0.19.

The NIRS chemometrics models were applied to the spectra of 29 samples provided by EFPRA as a blind set for external validation. All of these samples were far away (H > 3) of the center of the training set, measured by the Mahalanobis distance (H). The Mahalanobis distance of 13 of these samples was higher than 10; this means that the spectra of this population is far for the average spectrum of the training set. Despite of that, the predicted values obtained from the NIRS quantitative and qualitative models used together with the comparison of the spectra with other samples from the training sets provided the following information: 2 samples look as poultry greaves; 1 sample was identified as blood meal; 2 samples seem to be fish meals; 5 samples were rather similars to feather meal; 1 sample looks as mixture of poultry and cattle meals and 2 samples were mixture meals greaves. Another group of 16 unknown samples had lowest H values (between 3 and 7).These samples were identified as follow: 5 samples as mixture of poultry and pork meal, 8 samples as mixture of pork and cattle meals, 2 samples were identified as mixture of the three species (poultry, pork and cattle) and, finally, 1 sample was classified as hidrolysed feather meal.

This study shows the potential of NIRS technology to identify the animal specie in protein animal by-products. Collaboration with EFPRA is needed for a final evaluation of this out-house validation exercise. Further co-operation with renderers is important for enlarging the library file in order to build models which can be applied to all the rendered protein meals circulating at intra and inter-European Community level.

Keywords

Protein by-products, cannibalism, specie identification, discriminant analysis, partial least squares, NIRS technology