



SP-P08

Development of a NIRS calibration equation for in situ analysis of green pasture

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Objectives: To develop a rapid method of analysing the quality of grass consumed by grazing beef cattle in order to optimise the administration of concentrate feed according to the characteristics of the grass at each time of the year, using NIRS equipment in the laboratory and in situ, using portable NIRS equipment.

Materials and methods: The experimental phase was developed between May 2018 and November 2021, in six suckler cow farms in and around Castilla y León, representing different ecosystems. In each farm, a pasture sample was taken every 45 days for chemical and NIRS analysis.

The constituents analyzed were moisture (%), crude protein (%), crude fiber (%), neutral detergent fiber (%), acid detergent fiber (%), lignin (%) and ash (%).

The grass sampling was carried out using two different techniques: random sampling following the classical methodology and targeted sampling using GPS collars, placed on animals from three of the herds, to obtain their most frequent locations, as sampling points.

All pasture samples, a total of 550, were analysed by the same instrument DS2500 (FOSS)-NIRS (near-infrared spectroscopy) in order to obtain their spectra in a range from 400nm to 2200nm at constant intervals of 0.5nm. Some of them (350) were also analysed by the Portable X-NIR-(Dinámica Générale).

The samples were not subjected to any kind of pre-treatment, following the same analysis protocol:

- 4 sub-samples were taken and scanned separately.
- Selection of spectra.
- Chemical analysis of the selected samples.
- Calibration and validation of the regression equations.

ISI Nova and Mosaic software (from FOSS) were used to collect the spectral data. For the development of the equations, different mathematical treatments and cross-validation were tested with the WINISI IV software (Infrasoft International), regression models were generated using MPLS (Modified Partial Least Squares), combining different mathematical treatments and light scattering correction using SNV (Standard Normal Variate) and Detrend mathematical techniques.

The statistics used for the selection of the best calibration equations were SEC, SEVC, R^2 , r^2 , SEP, RSQ, RPD and RER.

R^2 (RSQ): coefficient of determination; SEC(SEP): calibration/validation standard error; SECV: cross-validation standard error; (1-VR) r^2 : determination coefficient, RPD: Ratio between the standard deviation of the reference data for the validation group and the SEP. RER: Relationship between the range in the reference data for the validation group and the SEP.

Results and Discussion: The evaluation of the accuracy

and reliability of the obtained equations would need further discussion, but in general terms the results obtained indicate calibrations with r^2 values higher than 0.9 with are perfect for quantitative predictions. The lower r^2 values remain high (0.8-0.9), except for lignin (0.76) in the portable X-NIR.

These models also presented RPD greater than 3, a good indicator of the predictive capacity and robustness of the model, except for lignin and crude ash in the DS2500 NIR (2.43 and 2.42 respectively) and for lignin in the Portable X-NIR (2.12).

Therefore, the calibration models developed on both equipments give reliable and fast predictions in the laboratory and on the farm, so they can be used to evaluate the nutritional quality of a pasture area and adapt the complementary feeding in a short period of time (hours).

As a result of this work, a nutritional advice tool has been developed for extensive cattle farmers.

Keywords: Pasture, NIRS, extensive, cattle.

SP-P09

Association of antibiotic therapy expenditure in clinical mastitis and genomic prediction for mastitis in European Holstein cows

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Objective: The objective of this study was to determine the association of genomic predictions of wellness traits - in this case, mastitis - with the incidence of mastitis and, in particular, on antibiotic use, using a large European data set from Holstein cows in commercial herds.

Material & Methods: Data from 10 different farms in the United Kingdom (4 farms), the Netherlands (3 farms) and Italy (3 farms) were used for this preliminary analysis. In total, the dataset included 3987 lactations from 2482 cows from 2015-2021. Genomic data of young calves and heifers were compared with accurate records of the occurrence of clinical mastitis and treatments administered, which were obtained from the animals' farm documentation in herd management systems. The Clarifide Plus genomic evaluation (Zoetis, USA) was used to estimate the genetic risk of mastitis occurrence. The animals were divided into two groups (≤ 100 STA (Standardized Transmitting Abilities), > 100 STA) based on the genomic evaluation of the mastitis trait. Statistical analysis was performed with generalized linear mixed models using genetic evaluation group and lactation number and the interaction of these two variables as fixed effects; and country, herd and animals within the herd as random effects.

The target variables examined were incidence of mastitis, days under antibiotic treatment, and days under withdrawal time per lactation.