# Book of Abstracts of the 76th Annual Meeting of The European Federation of Animal Science

Innsbruck, Austria, 25st – 29th August , 2025

### Poster Session 28



## Session 29. Novel infrared approaches and phenotypes to enhance sustainability of livestock industry

Date: Tuesday 26 August 2025; 14:30 - 18:00
Chair: Manuelian / Machefert

### Theatre Session 29

## Enhancing and combining MIR models to provide individual cow environmental score

*T. Przybylski[1], C. Grelet[1], H. Atashi[2], Y. Ben Mohamed[3], J. Leblois[4], F. Dehareng[1]*
*[1] Walloon Agricultural Research Center, Chée de Namur 24, 5030 Gembloux, Belgium, [2] TERRA Teaching and Research Center, Gembloux Agro-Bio Tech, University of Liège, Pass. des Déportés 2, 5030 Gembloux, Belgium, [3] Eliance – Maison Nationale des Eleveurs, Rue de Bercy 149, 75595 Paris, France, [4] Walloon Breeders Association Group, Rue des Champs Elysées, 4, 5590 Ciney, Belgium*

Holicow is an Interreg NWE project focused on developing a holistic herd management tool for farmers, leveraging more than 60 million milk recordings and over 500 existing predictive MIR models. In the frame of this project, our work aimed to assess the performance of individual dairy cows according to environmental aspects, with the final objective to provide an environmental score for each cow. One of the primary challenges was the identification and the valorisation of existing data and models providing insights on environmental impact of dairy cows. A total of 20 relevant MIR indicators were identified, and corresponding models were run on the MIR database. Several new indicators were also created based on the existing models. Those 20 indicators were merged into five dimensions: methane emissions, nitrogen efficiency, energetic efficiency, longevity, and grazing. These indicators are combinations of carefully selected pre-existing models that have been trained on cleaned data. The days in milk at milk recording time was found to significantly influence the indicators, prompting the adoption of a longitudinal approach to account for the days in milk artefact. To deliver synthesized information to farmers, two methods were developed: a spider graph for visualizing the dimensions and an agglomerative hierarchical clustering approach for refining these inputs. Those tools will enable the comparison of cows within herds, of farms within regions. Together with methods for assessing milk production, milk processing, cow welfare, fertility, and heat stress, this method constitutes a comprehensive, collaborative tool accessible to farmers and advisors.



## Using MIR Data to Predict Individual Global Scores for Walloon Holstein cows

*H. Atashi[1], Y. Chen[1], C. Bertozzi[2], M. Tran[2], B. Christiaens[2], P. Lemal[1], J. Evrard[3], N. Gengler[1]*
*[1] TERRA Teaching and Research Center, Gembloux Agro-Bio Tech, University of Liège, Pass. des Déportés 2, 5030 Gembloux, Belgium, [2] Walloon Breeders Association Group, Rue des Champs Elysées, 4, 5590 Ciney, Belgium, [3] Regional Association for Animal Registration and Health (ARSIA), ASBL, 5590 Ciney, Belgium*

Mid-infrared (MIR) spectroscopy has been widely applied in the dairy industry for milk quality analysis. Extending its application to health and welfare monitoring could provide significant benefits. The aim of this study was to explore the potential of using MIR data to predict the health and welfare conditions of dairy cows. Two individual welfare scores (SGI-I and SGI-II) were defined based on the Welfare Quality© Protocol. SGI-I was based on feeding, housing, and health, while SGI-II included behavioral data in addition to feeding, housing, and health. The dataset consisted of 3,291 records on 2,381 animals for SGI-I, and 1,473 records on 1,229 animals for SGI-II. The mean (SD) SGI-I and SGI-II were 69.92 (10.28) and 65.90 (9.65), respectively. 75% of the records for each SGI were used for training, with the remaining 25% used for testing the models. Data from 212 MIR spectra, along with parity, milk yield (MY), fat/protein percentage (FP, PP), somatic cell score (SCS), and days in milk (DIM) were used to optimize the prediction models. The root mean square error (RMSE) and mean absolute error (MAE) for the developed models were 9.21 and 7.25 for SGI-I, and 8.51 and 6.78 for SGI-II, respectively. The developed models were used to predict SGIs for a large number of animals for DIM when MIR data were available: The number of predicted SGIs records (animals) for the 1st, 2nd, and 3rd lactations were 169,708 (30,202), 157,939 (23,107), and 115,671 (16,126), respectively. The mean heritability for direct SGI-I and SGI-II were 0.22 and 0.27, respectively, while for MIR-based predicted SGI-I and SGI-II were 0.22 and 0.24, respectively. The mean genetic correlation between direct SGI-I and SGI-II was 0.88, and between MIR-based predicted SGI-I and SGI-II was 0.78. Both direct and MIR-based predicted SGIs were negatively correlated with MY and SCS and positively corrlated with FP and PP, indicating that higher MY and SCS are associated with lower health/welfare conditions.