HIGHLIGHT

Identification of potential markers of methane production in dairy cows using a multiplatform metabolomic approach
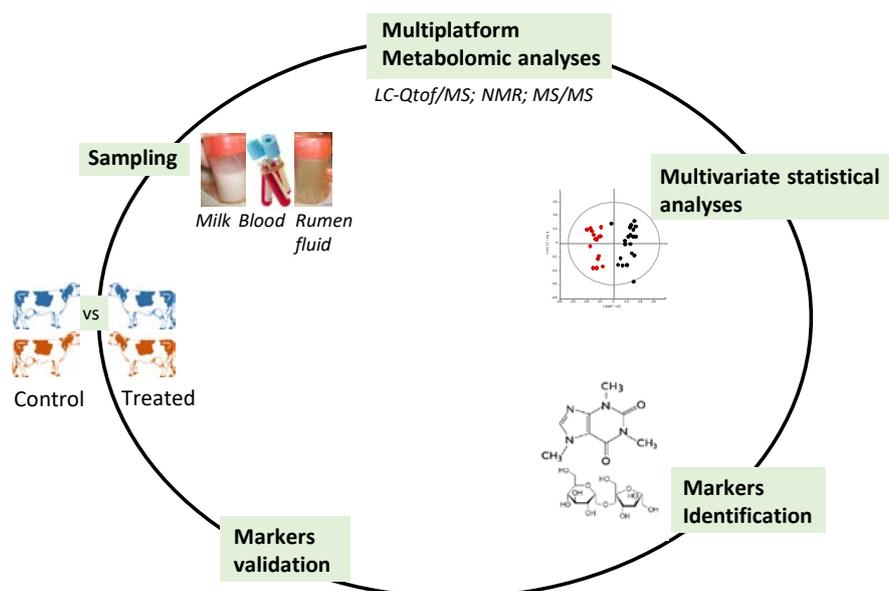
The reduction of methane emissions is a major challenge for the sustainability of ruminant production systems. The identification of low-emitting animals, either for genetic selection or for the verification of practices to limit emissions in the field, is a deadlock because methane measurement is not applicable on large number of animals. We have used metabolomic approaches to search for metabolites indicative of methane emissions in plasma, milk and ruminal fluid. Metabolomics allowed us to identify potential markers in these 3 matrices in relation to the reduction of methane emissions. For plasma (Yanibada et al, 2020), for example, 48 metabolites were identified, some of which are involved in methane metabolism. These results open interesting perspectives for the application of the measurements in the field.

Reducing enteric methane emissions from ruminants is important for improving the sustainability of the ruminant sector. The measurement of methane emissions is currently carried out using heavy techniques that are difficult to apply in commercial farms. An alternative method is the identification of indirect biological markers in matrices that are accessible in a minimally invasive manner.

Our approach, which aims at establishing a proof of concept, compared plasma, milk and rumen fluid metabolomes in dairy cows receiving or not a specific methane inhibitor.

The 3 biological matrices were analysed using complementary analytical techniques (multiplatform metabolomic approach).

This work was carried out as part of the Methane Consortium between INRA and 11 private partners (Adisseo France SAS, Apis-Gene, Deltavit, DSM Nutritional Products AG, In vivo-NSA, Lallemand, McKey Food Service, Techna France Nutrition, Valorex, Institut de l'élevage).

Legend: The different steps for the identification of markers and their validation for use in the field

Methane emissions were reduced by 23% in treated animals with no change in milk production, intake, body weight or biochemical health indicators. Multivariate analysis identified 48 plasma metabolites discriminating methane production and 10 impacted metabolic pathways. Certain metabolites, mainly of microbial origin, are linked to the metabolic pathway of rumen methane synthesis. Other impacted metabolic pathways concern energy and amino acid metabolism, suggesting a benefit of methane emission reduction for the host animal.

Similar work on milk, preceded by a methodological development (Yanibada et al, 2018) revealed, among the discriminating metabolites, 9 common to the 2 matrices. There is a strong correlation ($r^2 = 0.96$) between them for 2 metabolites (formic acid and stachydrin), which are associated with rumen microbes and methanogenesis.

Before their use in the field, the universality of candidate markers need to be validated on samples from different experimental and production conditions.

Learn more :

1- Yanibada, Boudra, Debrauwer, Martin, Morgavi, and Canlet, Evaluation of sample preparation methods for NMR-based metabolomics of cow milk. Heliyon, 2018. 4(10): p. 1-22.
https://doi.org/10.1016/j.heliyon.2018.e00856
2- Yanibada, Hohenester, Petera, Canlet, Durand, Jourdan, Boccard, Martin, Eugene, Morgavi, and Boudra, Inhibition of enteric methanogenesis in dairy cows induces changes in plasma metabolome highlighting metabolic shifts and potential markers of emission. Scientific Reports, 2020. 10(1): p. 15591.
https://doi.org/10.1038/s41598-020-72145-w

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