

Novel formulas to calculate methane production from concentrations while using sniffersC.I.V. Manzanilla-Pech¹, M.H. Kjeldsen², T. Villumsen¹ and J. Lassen^{1,3}¹Center for Quantitative Genetics and Genomics, Faculty of Science and Technology, Aarhus University, C. F. Møllers allé 3, 8000 Aarhus C, Denmark, ²Department of Animal Science and Veterinary Science at Aarhus University, Blichers Allé 20, 8830 Tjele, Denmark, ³Viking Genetics, Ebeltoftvej 16, Assenstoft, 8960 Randers, Denmark, Denmark; coralia.manzanilla@qgg.au.dk

Sniffers are widely used to measure methane emissions in dairy cattle. However, sniffers measure concentrations of methane (MeC) and carbon dioxide. To be able to compare animals across countries and other methane recording methods, it is needed to transform MeC to methane production in g/d (MeP) that is the gold standard trait. Madsen *et al.* formula has been widely used to calculate MeP in dairy cattle from MeC and carbon dioxide concentration. Though, this formula was developed based on a limited number of animals, not similar to modern dairy cows. Recently, Kjeldsen *et al.* have developed couple of formulas based on a data set with larger number of animals (n=1,502) in different countries (n=12) and production systems. The first formula uses ECM and BW as the Madsen *et al.* formula, however the coefficients have been re-estimated based on the new data set. The second formula has DMI and BW as main drivers of methane emissions, this formula could be convenient when DMI is available. However, these new formulas have never been tested for genetic purposes, only for nutritional purposes, where their correlations with respiration chamber and GreenFeed data is from 0.68 to 0.76. Thus, the general aim of this paper is to test these formulas in a large database, 24k methane records from 650 cows measured during 7 years in Danish Cattle Research Center, Aarhus University, Denmark. The specific objectives are: (1) to calculate MeP with these updated formulas; and (2) estimate genetic parameters including genetic correlations with the previous formula; (3) to calculate EBV correlation between the formulas. Preliminary results showed similar heritabilities (0.19-0.23) to the previous formula (0.21) and high genetic correlation (0.79-0.82) between the new formulas and the previous formula. The genetic correlation between these two new formulas was close to unity (0.99).

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Predicting methane production and intensity from milk mid-infrared spectraS. Fresco^{1,2}, A. Vanlierde³, R. Lefebvre¹, M. Gaborit⁴, D. Boichard¹, R. Bore⁵, S. Fritz^{1,2}, N. Gengler⁶ and P. Martin¹¹Université Paris-Saclay, INRAE, AgroParisTech, GABI, Domaine de Vilvert, 78350 Jouy-en-Josas, France, ²Eliance, 149 Rue de Bercy, 75012 Paris, France, ³Walloon Agricultural Research Centre, Valorization of Agricultural Products, 9 Rue de Liroux, 5030 Gembloux, Belgium, ⁴INRAE, UE326 Domaine Expérimental du Pin, l'Ermite, 61310 Exmes, France, ⁵Institut de l'Élevage, 149 Rue de Bercy, 75012 Paris, France, ⁶ULiège – GxABT, 2 Passage des déportés, 5030 Gembloux, Belgium; solene.fresco@eliance.fr

Selecting dairy cows against methane (CH₄) emissions is one of the solutions to reduce greenhouse gas emissions. However, as large-scale phenotyping is challenging, proxies have been developed to supply the amount of data necessary to genetic analyses. One of them is predicting CH₄ emissions from milk mid-infrared spectra. This study aimed at comparing prediction equations developed from two reference CH₄ for two CH₄ traits: MeP (g/d) and MeI (g/kg of fat- and protein-corrected milk [FCPM]). Methane emissions were recorded using GreenFeed devices, for 278 cows from nine different experiments. These reference CH₄ emissions were averaged over 1 or 2 weeks and were associated to 1,035 and 680, respectively. Equations were derived using Partial Least Square regression. A second dataset including 104 spectra and 1-week or 2-week CH₄ averages from 46 cows was used as an external validation to assess the performance of each equation based on R² and % of RMSE/observations mean (E). Performance was similar for both reference CH₄ time periods. Equations calibrated on 2-week CH₄ averages tended to have lower R² and E than the one on 1-week CH₄ averages. The average R² (E) were 0.28 (17.7) and 0.43 (17.3) for MeP and MeI, respectively. Indirectly predicting MeP by multiplying predicted MeI by FPCM was found to be as accurate as MeI and more accurate than predicting directly MeP. As selection of MeI presents two disadvantages – lower efficiency when selecting a ratio than the two traits separately and a potential increase of milk production at a given MeP, which would be detrimental to high producing cows' fertility and health – using CH₄ predicted from MeI multiplied by FPCM can be of great interest in genetic selection.