



Session 96 Poster

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Heritability of novel metabolite-based resilience biomarkers in dairy goatM. Ithurbide¹, T. Fossier², M. Tournet³, J. Pires³, T. Larsen⁴, N.C. Friggens⁵ and R. Rupp¹¹INRAE, Genphyse, Castanet Tolosane, France, ²INRAE, P3R, Small Ruminants Phenotyping Facility, Osmoy, France, ³INRAE, Université Clermont Auvergne, Vetagro Sup, 3UMR Herbivores, Saint-Genès-Champanelle, France, ⁴Aarhus University, Faculty of Agricultural Sciences, Research Centre Foulum, 8830 Tjele, Denmark, ⁵INRAE, AgroParisTech, Université Paris-Saclay, UMR 0791 Modélisation Systémique Appliquée aux Ruminants, Paris, France; marie.ithurbide@inrae.fr

The aim of this study was to estimate the heritability (h^2) of metabolite-based resilience biomarkers in dairy goat. Metabolites were measured repeatedly during two periods of stress: around parturition and during a feeding challenge (48 h with straw only) in early first lactation in two INRAE facilities (P3R Bourges and Paris). The 4 blood metabolites were: glucose (Glu), beta-hydroxy-butyrate (BOHB), urea and non-esterified fatty acids. The 14 milk metabolites were: BOHB, Glu, urea, glucose-6-phosphate (Glu6P), galactose, isocitrate, glutamate, NH_2 -groups, lactate dehydrogenase (LDH), choline, malate, urate, triacylglycerol, and cholesterol. The metabolite trajectories were described both by simple mean concentration per challenge period and by a functional PCA method. Variance components were estimated using an animal model (wombat®) for blood metabolites around kidding, and for trajectories of blood and milk metabolites upon the feeding challenge on 201, 228 and 138 goats respectively. The model included the fixed effects of facility and year. The total pedigree included 1,148 animals. We found 25 blood and milk metabolites parameters (out of 159) that were significantly heritable ($h^2\text{-}2\text{SE} > 0$) with h^2 estimates ranging from 0.30 (± 0.03) to 1.00 (± 0.25) with SE from 0.03 to 0.33. Among them: milk urate, BOHB, LDH, and Glu6P during feeding challenge and blood Glu around kidding. The heritability estimation of 250-d milk yield, fat and protein content were respectively 0.26 (± 0.16), 0.53 (± 0.19) and 0.68 (± 0.19), showing the consistency of our dataset despite the small number of individuals. These results show the potential of metabolite-based biomarkers for genetic selection of resilience. This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER).

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Poster 17

Rumen size of sheep: difference between a modern and a native Norwegian sheep breedB.A. Åby¹, M.A. Bhatti² and G. Steinheim¹¹NMBU, Department of Animal and Aquacultural Sciences, Box 5003, 1432 Ås, Norway, ²NMBU, Department of International Environment and Development Studies, Box 5003, 1432 Ås, Norway; bente.aby@nmbu.no

Globally, sheep account for approx. 4% of the GHG emissions from the livestock sector, mainly through enteric methane (CH_4) emissions. Rumen size is shown to be relevant for enteric CH_4 emissions, with larger rumen volumes being associated with higher emissions. Breed variation in rumen size, relative to body size, may thus be one factor contributing to between-breed differences in CH_4 emissions. Two of the most contrasting sheep breeds in terms of selection history in Norway are the Norwegian white sheep (NWS; large, long tailed composite breed) and the Old Norwegian Spæl (ONS; small Nordic Short-tailed landrace). These breeds were previously compared in two experiments at NMBU, where adult ONS ewes had lower enteric CH_4 , corrected for dry matter intake, when fed harvested grass silage and fresh cut grass. In this pilot study, we therefore hypothesized that there would be significant differences in rumen size between the breeds. The test animals (23 adult ewes, 40 lambs) came from two farms in Viken county rearing both breeds. On October 18, 2022, the animals were slaughtered at a commercial abattoir (Nortura Gol) shortly after the summer grazing period. Rumens were collected and ruminal contents were removed before the organs were cleaned and visceral fat removed. The rumens were then weighed after being squeezed dry. The data for lambs and adult ewes were analysed separately using two general linear models. Both models included the effects of carcass weight, breed, and farm. Additionally, the effect of birth year was included for adult ewes, while age at slaughter was included for lambs. For adult ewes, rumen weight corrected for carcass weight, was lower ($P < 0.05$) for ONS compared to NWS (LSMEANS 1,589 vs 1,832 grams), while there were no breed differences for lambs. Our results suggest that previously observed breed differences between ONS and NWS in enteric CH_4 emissions (i.e. lower enteric methane emissions, corrected for dry matter intake, for ONS) may be linked to differentiation in rumen size. However, this needs to be confirmed in a controlled study also including enteric CH_4 measurements on the test animals.