Alpine goats divergent for functional longevity differ in metabolic profile during transition period

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Perinatal rumen microbiota in relation to feed utilization and biochemical parameters in sheep

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This study aimed to investigate the relationship between rumen microflora and nutrient digestion, rumen fermentation and biochemical parameters in sheep. Blood, rumen fluid and faeces samples (n=10) were collected on days -21, -14, -7, 3, 7 and 14 (Q21, Q14, Q7, H3, H7 and H14) relative to expected parturition. Dynamic changes of average daily feed intake (ADFI), nutrient digestibility, rumen fluid and serum parameters were detected. The 16S rRNA sequencing was performed for rumen microflora and the Random Forest method was used to predict Perinatal time-related changes. All data were evaluated by one-way ANOVA. The results showed that the digestibility of dry matter (DMD), crude protein (CPD) and neutral detergent fibre (NDFD) in Q7 d was higher than that in H3 d ($P<0.05$); Compared with Q21 d, ADFI and total volatile fatty acids (T-VFA) increased after lambing, while acetate to propionate ratio (A/P) decreased ($P<0.05$); Serum concentrations of glucose, β-hydroxybutyric acid (BHBA), 25-hydroxy vitamin D3 (25HVD3) and neuropeptide Y (NPY) were increased in H14 d compared to Q21 d; Total cholesterol (TC), high density lipoprotein cholesterol (HDL-C), glucagon and leptin were the highest at Q21 d and decreased after lambing ($P<0.05$). The 16S rRNA gene sequencing revealed that rumen microflora composition also differed in rumens before and after lambing ($P<0.05$). Nineteen perinatal time-related bacterial genera were predicted, in which the relative abundance of *Anaeroplasma* and *Lachnospiraceae_ND3007_group* was the highest at Q21 d, and was positively correlated with rumen pH, acetate and TC, negatively correlated with propionate ($P<0.05$), *Endomicrobium*, *Suttonella*, *M2PT2-76_termite_group* decreased after parturition and were positively correlated with HDL-C and TC, negatively correlated with T-VFA, 25HVD3 and NPY ($P<0.05$); *Ruminococcus* and *UCG-005* is increasing in H3 d, and *Ruminococcus* is positively correlated with T-VFA, 25HVD3 and NPY ($P<0.05$), while *UCG-005* is negatively correlated with NDFD, CaD, PD, CPD and DMD ($P<0.05$). These results suggest that rumen bacterial community in the perinatal period of ewes affect feed utilization and rumen fermentation patterns, and play an important role in shaping biochemical parameters.

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The objective was to study associations among functional longevity and plasma indicators of metabolic adaption in Alpine goats during periparturient period. Two Alpine goat strains divergent for longevity (LGV+ and LGV-) were produced by AI selecting for extreme functional longevity but nondifferent milk yield. A total of 174 primiparous goats were studied in 2018, 2019, 2020 and 2021. Jugular plasma collected on wk -4, -3, -2, -1 relative to expected parturition, and wk 1, 2, 4, 13, 24, 33 of lactation was analysed for NEFA, BHB, glucose, urea and bilirubin. Data were analysed using SAS mixed models with repeated measures, including strain, litter size (LS), wk, and interactions as fixed effects, and year and goat (year) as random effects. Significant wk effects were observed for all metabolites. LGV- goats had greater plasma NEFA on wk-3 (181 vs 123 μM; strain × wk prepartum: P=0.05), and greater BHB prepartum (0.45 vs 0.41 mM; strain effect: P=0.04) than LGV+, which denotes greater fat mobilization and partial oxidation in late gestation LGV- goats. 35% of goats carried multiple foetus (LS2+) and LS not differ with LGV. Prepartum plasma NEFA, BHB and bilirubin were greater for LS2+ compared to single (LS1; $P<0.001$; 260 vs 174 μM; 0.51 vs 0.39 mM; 0.069 vs 0.056 mg/dl, respectively), whereas glucose was lower for LS2+ ($P<0.001$; 49.8 vs 54.7 mg/dl). Conversely, plasma NEFA was greater for LS1 during wk 1 and wk 2 postpartum ($P<0.05$; 558 vs 442 on wk 1, and 421 vs 330 μM on wk 2, respectively), reflecting greater availability of body reserves to support lactation in LS1. Prepartum incidence of BHB>0.80 mM was significantly greater for LS2+ than LS1 (30 vs 3.7%), and for LGV- carrying LS2+ than LGV+ carrying LS2+ (42 vs 28%). Marked LS effects were observed in plasma metabolite profiles in primiparous goats. LGV strains differ in their metabolic adaptations peripartum. This study has received funding from the EU H2020 research and innovation program under grant agreement No 772787 (SMARTER) and from APISGENE (ACTIVEGOAT).