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Ruminal microbiota of sheep is being studied to evaluate its impact on animals' energy balances in early lactation stage. The establishment of ruminotypes could be a useful tool to summarize the large dataset of ruminal microbiota abundances. The feasibility of directional selection of gut microbiota enterotypes has been demonstrated in pigs, proving the existence of genetic determinism of the host on enterotypes. Sixty-five Lacaune dairy sheep were studied and their ruminal contents and blood were sampled at 2 weeks (D1), 3 weeks (D2), 4 weeks (D3) and 6 weeks (D4) after lambing. Ewes were weighed on each date and were fed the same diet with hay, grass silage and concentrates. During the first month, lambs remained with the ewes: milk recording (milk quantity, fat and protein contents, somatic cell count) were performed at D4. Ruminal microbiota was analysed by sequencing the 16s rRNA gene for bacteria and sequences were computed with the FROGS pipeline to obtain relative abundances of ASVs which were then labelled according to genus level. Clustering of microbiota genera abundances using Jensen-Shannon divergence and partition around medoids clustering algorithm has led to 2 groups. Spls-da of these two clusters revealed a first ruminotype caracterised by *Mogibacterium*, *Lachnospiraceae NK3A20 group* and *Acetitomaculum* genera (RuM) and a second one by *Prevotella*, *Prevotella_9* and *Lachnospiraceae NK4A136 group* genera (RuP). Over time, a significant shift towards RuP is noted (D1: 22%, D2: 34%, D3: 58%) which becomes a minority again after weaning (D4: 14%). At D1, RuM is associated with higher non esterified fatty acids (p=0,04), beta-hydroxybutyrate (p<0,01), isobutyrate (p=0,01) and lower total volatile fatty acids (p<0,01) compared with RuP. At D2, RuM is associated with lower weekly weight loss (p=0,03) compared to RuP. At D3, ruminotypes were not associated with zootechnical traits. At D4, RuM was associated with lower milk protein and fat contents (p<0,02). Characterization of the specific metabolic pathways of these 2 clusters is underway via a functional inference approach, in order to make links with the zootechnical traits.