The gut microbiome profile varies between two maternal rabbit lines with different longevity

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Resilience and longevity are important objectives of selection in rabbits' production but are difficult as criteria of selection. Line LP of this experiment was founded using longevity, which is a criterion for better resilience. On the other hand, selection for residual litter size variance has been used as an indirect criterion of resilience selection. However, both longevity and the residual variance have a low heritability. Another indirect criterion to increase longevity and resilience in rabbit production can be based on knowledge of the rabbit's gut microbiome. The gut microbiome is important in regulating traits related to health and welfare and it plays a key role in immune system development. Therefore, the aim of this research was to compare the gut microbiome profile between two maternal rabbit lines, LP and a standard maternal line A, and two groups of animals from line LP with different longevity (LLP and HLP, females up to two parities and with more than fifteen parities, respectively). Rabbit excretes two types of faeces: hard faeces which contain poorly digestible large particles and soft faeces which consist of fermented soft fine particles from caecum fermentation; in this study a total of 134 soft does faeces samples (31 A and 103 LP), two weeks after the first parity were collected and sequenced using the bacterial 16S rRNA gene. After filtering and quality control, the sequences were analysed using QIIME2. Sequences were clustered into ASVs using DADA2. The final table had 59072 ASVs. For taxonomic annotation we used a Naive Bayes classifier. This classifier was pre-trained on the SILVA database ("silva-138-99-nb-classifier"). Differences between A and LP lines in both alpha (Shannon and Pielou Evenness) and beta (Bray-Curtis and Jaccard) diversities indexes were observed. Differences between LLP and HLP groups for Shannon and Pielou evenness α-diversities indexes were also observed but not for Bray-Curtis and Jaccard ß-diversities indexes. The PLS-DA analysis allowed us to discriminate between the two lines and LP groups. The classification performance was higher than 80 % and the permutation test (~50%) indicated the ASVs identified in the PLS-DA did not randomly discriminate between groups. These preliminary results support that gut microbiome profile could be related to longevity and might be used to improve resilience in rabbit commercial lines.