

Unraveling the effects of restricted and ad libitum diets on intestinal microbiota in rabbits

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Aiming to assess the effect of restricted and ad-libitum diets on intestinal microbiota diversity (eubacteria and archaea) in rabbits, a 16S rDNA-based metabarcoding assessment through MiSeq platform was performed. Caecum and faeces samples from 11 adult animals (66-days-old) fed ad-libitum and 13 fed under restricted (75%) standard diet were assessed. Growth rate was individually recorded and the association between this trait and microbiome compositions was studied as well. Globally, a total of 1823 OTUs without singletons were clustered from 2.195.158 contigs. Taxonomic assignment (Greengenes database gg_13_5_otus) revealed that intestinal microbiota was dominated by Firmicutes (76.3%), followed by Bacteroidetes (7.5%) and Tenericutes (7.5%). No overall differences between diets and faeces-caecum were detected based on Unifrac distances and PCoA analysis. However 7 OTUs were differentially represented between samples of caecum and faeces. It is noteworthy that 19 OTUs were overrepresented in samples from animals feed ad libitum, and 2 (order YS2 (Cyanobacteria)) were overrepresented in animals fed under restriction. OTU richness was positively (pFDR=0.012) associated to daily growth rate. The present study provides evidences of bacterial taxa and microbiome diversity associated to different diets and growth rate in rabbits.

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