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Impact of antibiotherapy on growing rabbits assessed by a whole-blood transcriptomic approach

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In previous studies, rabbits fed antibiotics have a decreased caecal activity and a modified caecal microbiota. Our aim was to study whether antibiotic supplementation could also influence blood parameters assessed by transcriptome analysis of gene expression profiles. We compared control animals (group C) to animals fed a diet supplemented with tiamulin and apramycin antibiotics (group AB) between 16 and 70 days of age (d). Growth performances were recorded at 29, 45, 60 and 70 d. The health status was monitored daily. These phenotypic data were analyzed with a general linear model. Transcriptomic studies of total blood were carried out by comparing the two groups at 29 and 45 d, using a 60K microarray enriched with well-annotated immunity-related genes. Statistical analyses were performed using Limma package in R. Daily gain (49.6g vs. 46.8g) and body weight (2662g vs. 2532g at 70 d) were higher ($P < 0.01$) in the AB group compared to the C group, respectively. Feed intake and gain-to-feed ratio did not differ between groups. The AB diet improved morbidity (3.4% for group AB vs. 16.0% for group C, $P = 0.01$) but no difference was observed during experimentation between groups for mortality (11% in average) and the health risk index (19% in average). The transcriptomic study showed a differential expression of 10 genes at weaning (29 d), but no difference between groups at 45 d. By comparing the two ages for each group, we detected 2539 differentially expressed (DE) genes in the group C, whereas no differential expression was found in the group AB. The DE genes classified by the IPA system were mainly related to cancer, gastrointestinal disease, and cell death and survival functions. Our results suggested a leveling of the gene expression in blood by antibiotics that needs to be further correlated with data on growth and health.