

Modification of the chicken caecal microbiome by *Campylobacter jejuni* colonization and by a feed additive

Alexandre Thibodeau, Philippe Fravalo, Étienne Yergeau, Julie Arsenault, Ludovic Lahaye, Ann Letellier

Campylobacter jejuni is a foodborne pathogen causing severe enteritis in humans with chickens being the most important identified source of C.jejuni. It colonizes the chicken caecum up to 10^9 CFU/g of caecal matter. Despite this, chickens were rarely proven affected by C.jejuni presence. The effect of such intense colonization on the chicken caecal microbiome is unknown. Efforts are made to control this pathogen at the farm and some in-feed control measures are showing encouraging results. Modifications of the chicken intestinal microbiome by these measures are often hypothesized as part of their mechanism of action. In this study, 4 groups of 15 chickens were used. Chickens received or not a feed additive, based on a protected mix of organic acids and essential oils, tested as a C.jejuni control option, from hatch to the end of the experiment. Fourteen days old chickens were then infected or not with C.jejuni. Birds were euthanized at 35 days of age. Caecal content from each chicken was recovered. C.jejuni caecal levels were determined by culture on mCCDA. DNA was also extracted to perform in-depth microbiome analysis. Levels of C.perfringens, E.coli, lactobacillis, enterobacteria and Bifidobacterium were evaluated by real time PCR. In each group, DNA from 8 chickens was subjected to 16S rDNA sequencing using the Ion Torrent technology. Sequences analysis was performed with Mothur and the Greengenes database. The feed additive lowered the C.jejuni presence in the chicken caecum by 0.6 log. C.jejuni colonization was associated with increased Bifidobacterium levels. Alpha-diversity was not much affected by C.jejuni presence but beta-diversity was. The relative abundance of the phylum composing the caecal microbiome of C.jejuni colonized chickens was different than the one composing the *C.jejuni* negative birds but this change was unexpectedly mild. The feed additive did not impact the chicken caecal microbiome diversity but lowered Streptococcus relative abundance. Overall, these results show that C.jejuni does not greatly disturb the chicken caecal microbiome and that the feed additive impacted C.jejuni counts with no effects on the caecum diversity.