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Following *Campylobacter jejuni* colonization with the use of the high resolution melt analysis of the *flaA* gene

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Campylobacter jejuni is a major cause of foodborne infections. It is the zoonotic agent responsible for campylobacteriosis, a gastro enteric disease that may evolve to severe autoimmune disorders. Consuming or mishandling contaminated poultry meat products is an important source of human campylobacteriosis. Lowering *C.jejuni* presence at the farm level would reduce the risk for humans to acquire the pathogen through the food chain. In a recent trial, a microencapsulated blend of organic acids and essential oils was used in order to reduce the birds *Campylobacter* caecal load at slaughter. The blend was tested on 2 strains competing for intestinal colonization. Unexpectedly, the *C.jejuni* caecal level of the treated birds was 1.4 log higher than the control birds. To quickly identify what strains was present in the bird's caecum, the high resolution melt analysis (HRM) of *C.jejuni flaA* gene was realized, using as template the total DNA extracted from the chicken caecal content. The HRM analysis was done using an Illumina Eco QPCR with previously published *C.jejuni flaA* primers designed for HRM. DNA from 14 control birds and 12 treated birds was analyzed. Birds were 35 days old and had been simultaneously inoculated at 14 days of age with 2 well characterized *C.jejuni* strains. HRM showed that 3 *C. jejuni* HRM-*flaA* profiles were present in the bird's feces. Similar HRM-*flaA* profiles could be obtained by using DNA extracted from the inoculated strains. These results are suggesting that the feed additive positively selected for a *C.jejuni* strain. This is the first study to report the use of *C. jejuni* HRM-*flaA* analysis directly in chicken feces.