

## A supplement of bovine colostrum and probiotics increased protein digestibility in dogs but did not influence microbiome

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**Introduction:** In the dog, dietary interventions -such as dietary fiber, prebiotics, and probiotics- aimed to improve the canine GI microbiome and associated health indices. The effect of feeding bovine colostrum (BC) to dogs is gaining increasing attention (1). Probiotics are thought to induce beneficial effects but the results of microbiota analysis in experimental conditions are scarce or inconsistent.

This study aimed to determine the impact of a supplement of probiotics and BC on the faeces quality, main nutrients digestibility coefficients, fecal microbiome and plasma IgA in healthy experimental dogs.

**Animals, material and methods:** Eight adult neutered female Beagle dogs (mean±SD, 8±0.0 y, 9.6±0.5 kg BW) were used in a crossover design (2 groups of dogs, n=4) after approval of the university ethical committee. A commercial diet (as if- 92% DM, 26% CP, 17% fat, 6% ash, 1.9 % CF) was offered once a day in a fixed amount to keep the BW stable over the study. The supplement (Test-T) contained 4 strains of probiotics (*Lactobacillus rhamnosus*, *Lactobacillus helveticus*, *Bifidobacter animalis*, *Bifidobacter longum*, total of  $2.9 \times 10^8$  CFU) + 1 g of micronized BC + microcrystalline cellulose up to 5 g; the placebo (P) supplement contained 5g of microcrystalline cellulose. The supplements were vacuum packed and the stability of T was tested. Supplements were directly added on the kibble before the meal. After a transition period of 1 week (wk), dogs received the diet with T or P during 3 wk. They were kept in metabolism cages during the 3<sup>rd</sup> wk for total faeces collection and scoring (scale 1-5, Waltham faeces score), blood samples and sampling for metagenomic analysis (5g taken directly in the rectum using a tube, direct transport to the lab and analysis by 454-pyrosequencing of the 16S rRNA gene). After 1 wk of washout, the dogs switched for the 2<sup>nd</sup> period. The results were analysed using Proc GLM (SAS) to study the effects of treatment (T or P), dog (+ sequence) and period. STAMP software (2) was used to highlight statistical differences of proportions in the bacterial population between samples with the two-sided Fisher's exact test (3) including the confidence intervals from the Newcombe-Wilson method (4). The differences were considered significant for a corrected p-value of less than 0.05.

**Results and discussion:** There were no differences between treatments for faecal characteristics: faeces consistency score (T:  $2.4 \pm 0.3$  versus P:  $2.4 \pm 0.2$ ) and the number of defecations (T:  $2.8 \pm 0.7$  versus P:  $2.8 \pm 0.5$ ). Apparent digestibility coefficients for main nutrients were not different between treatments with the exception of crude protein (T:  $85.2 \pm 1.8\%$  vs P:  $83.7 \pm 1.2\%$ ). No difference of bacterial populations was observed after 3wk of dietary intervention. Further, the strains of probiotics contained in the T supplement were not found in the faeces. By contrast, plasma IgA was significantly increased in T ( $247 \pm 80$  mg/dL) versus P ( $226 \pm 71$  mg/dL).

**Conclusion:** The T supplement containing BC, 4 strains of probiotics and microcrystalline cellulose had very limited effects on faecal characteristics and microbiome in healthy dogs. However, the increased digestibility coefficient of protein must be highlighted.

**References:** 1. Satyaraj & al., BJNutr. 2013, 2. Parks & Beiko 2010, 3. Rivals & al. 2007, 4. Newcombe 1998.