110 Evaluation of High-Protein Diets Differing in Protein Source in Healthy Adult Dogs.
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Abstract: Given the dynamic market for protein-based ingredients in the pet food industry, demand continues to increase for both plant- and animal-based options. Animal and plant protein sources contain different amino acid profiles and vary in digestibility, which can affect the protein quality provided to the animal. Our objective was to evaluate the apparent total tract digestibility (ATTD) and compare protein quality of canine diets differing in protein source using healthy adult dogs. Four isocaloric and isonitrogenous, extruded diets were formulated to meet all AAFCO nutrient recommendations for adult dogs, with the primary difference being protein source: 1) chicken by-product meal (CBPM), 2) deboned chicken, dried chicken, and spray dried chicken (DC), 3) corn gluten meal (CGM), or 4) wheat gluten meal (WGM). Adult female beagles (n = 20; BW = 9.9 kg; age = 6.3 yr) were used in a replicated 4×4 Latin square design (n=12/treatment). Each period consisted of a 22-d adaptation phase, 5 d for total and fresh fecal collection, and 1 d for blood collection. All data were analyzed using the Mixed Models procedure of SAS 9.4. Diets contained similar crude protein (CP) concentrations (39.8%-41.7%), but DC had the most balanced AA profile (indispensable AA:dispensable AA ratio). Fecal scores were greater (P< 0.01) in dogs fed DC or CBPM than those fed WGM or CGM, but all remained within an appropriate range. Apparent dry matter digestibility was less (P< 0.0001) in dogs fed CBPM or CGM than those fed DC or WGM. Dogs fed CBPM had decreased (P< 0.0001) apparent organic matter, CP, and energy digestibilities than those fed the other 3 diets. Apparent CP digestibility was also reduced (P< 0.0001) in dogs fed DC or CGM than those fed WGM. Considering AA profiles and digestibility data together, the DC diet clearly provided the most and greatest quality protein of all diets tested.

Keywords: canine, digestibility, protein

107 Restricted Feeding and Weight Loss Positively Change Fecal Microbiota Populations of Obese Dogs. Patricia M. Oba1, Darcia Kostiuk2, Janelle Kelly2, Kelly S. Swanson1, 1University of Illinois at Urbana-Champaign, 2Champion Petfoods

Abstract: Canine obesity negatively influences health and well-being and appears to negatively modify gastrointestinal microbiota populations. Restricted feeding of a specially formulated diet and consequent weight loss may be used to improve health and modify gastrointestinal microbiota. In this study, we aimed to determine the effects of restricted feeding and weight loss on fecal microbiota populations of obese dogs. All procedures were approved by the University of Illinois IACUC prior to experimentation. Twenty-four obese spayed female dogs (BW = 15.2±1.7 kg; BCS = 8.7±0.4; age = 7.2±1.6 y) were used in a 24-wk weight loss study. A control (OR) food was fed during a 4-wk baseline to identify intake needed to maintain BW. After baseline (wk 0), dogs were allotted to one of two diets: OR or a test (FT) diet and then fed to lose 1.5% BW/wk. Fecal samples were collected at wk 0, 4, 8, 12, 16, 20, and 24 for microbiota and metabolite analyses. Fecal microbiota data were evaluated using QIIME2 and Mixed Models procedure of SAS, with P< 0.05 considered significant. Alpha-diversity was affected by diet and weight loss, with dogs fed OR having a greater alpha-diversity than those fed FT. Weight loss increased alpha-diversity (wk 16, 20, and 24 > wk 0 and 4). Beta-diversity, as assessed by weighted and unweighted PCoA plots, showed separation between dietary groups and between wk 0 and all the other time points after wk 8. Weight loss increased fecal Allobaculum and Ruminococcus torques. Weight loss also increased fecal Bifidobacterium, Faecalibaculum, Parasutterella in dogs fed both diets, but greater in dogs fed OR. Weight loss decreased fecal Collinsella, Turicibacter, Blautia, Ruminococcus gnavus, Faecalibacterium, Peptoclostridium in dogs fed both diets, but greater in dogs fed OR. Our data demonstrate that restricted feeding and weight loss alter fecal microbiota of obese dogs.

Keywords: canine microbiota1, weight loss, 6S rRNA sequencing