

acids, 4.1%, dry matter basis [DMB]) could improve mobility in arthritic dogs. This study protocol was first approved by the facility's (Fergus, Ontario) Institutional Animal Care and Use Committee and followed throughout. Eighteen female and thirteen male dogs (12.13 ± 1.93 years old, 14.21 ± 2.64 kg) exhibiting lameness were radiographed to confirm arthritis in forelimb, hind limb, or both and were randomly assigned the diets. Dogs were offered control food (Crude Protein 23.9%, Fat 14.1%, Fiber 3.3%, DMB, without added omega 3 fatty acids) or test food once daily to maintain body weight for 56 days and evaluated by an veterinary orthopedic surgeon for arthritis (ACVS Canine Orthopedic Index© (0–4 scale from no to extreme arthritis)), as well as urine and serum ELISA analyses for cartilage synthesis/degradation (CTX-II, C1, 2C, C2C, and CP-II) and inflammation marker C-reactive protein at days 0, 28, and 56. Dietary effects were analyzed in Minitab v18 using ANOVA. Dogs fed test food had improved delta arthritis scores (day 56 minus day 0) compared to control (-0.81 vs 0.33 , $P < 0.04$). Urine and serum markers were minimally changed; however, serum C-reactive protein was lower ($P < 0.05$) in test- versus control-fed animals at day 28, but not day 56. These findings support a role of antioxidants and omega-3 fatty acids in the clinical management of arthritic dogs.

Effects of dietary macronutrient profile on fecal microbiota of female dogs after spay surgery

Thunyaporn Phungviwatnikul¹; Celeste Alexander²; Kelly S. Swanson^{1,2,3}

¹Department of Animal Sciences; ²Division of Nutritional Sciences;

³Department of Veterinary Medicine, University of Illinois at Urbana-Champaign

Obesity and/or estrogen reduction are known to impact the gut microbiota, but limited information is available in dogs. The aim of this study was to determine the effects of specially formulated diets on the fecal microbiota of female dogs after spay surgery. All procedures were approved by the University of Illinois Institutional Animal Care and Use Committee prior to experimentation. Twenty-four dogs were spayed and randomly allotted to one of three experimental diets: 1) moderate-protein, moderate-fiber diet (control), 2) high-protein, high-fiber diet (HPHF), or 3) high-protein, high-fiber diet plus omega-3 fats (HPHFO). All dogs were fed to maintain BW for 12 weeks after spay, then allowed to consume twice that amount for another 12 weeks. Fresh fecal samples were collected at weeks 0, 12, and 24. Total DNA was extracted and the V4 region of the bacterial 16S rRNA gene was determined by Illumina MiSeq sequencing. Data were analyzed using QIIME 2 and SAS 9.4. Change from baseline data was analyzed for relative abundance of microbiota. Principal coordinates analysis (PCoA) of weighted UniFrac distances revealed that HPHF and HPHFO clustered together and separately from controls at weeks 12 and 24 ($P < 0.05$). The relative abundance of Actinobacteria was greater and Fusobacteria lower in controls than those HPHF or HPHFO ($P < 0.05$). Relative abundance

of *Faecalibacterium* and *Megamonas* was lower ($P < 0.05$) in controls than HPHF or HPHFO. Our results suggest that high-protein, high-fiber diets may beneficially affect gut microbiota of spayed female dogs and alter the gut microbiome characteristics of obese subjects.

Serum metabolomics in obese dogs before and after weight loss

Vivian Pedrinelli¹; Thiago Henrique Annibale Vendramini²; Henrique Tobar Macedo²; Rafael Vessechi Amorim Zafalon²; Matheus Vinicius Macegoza²; Larissa Wünsche Risolia¹; Fernanda Maria Marins Ocampos³; Juliana Toloi Jeremias⁴; Cristina Ferreira Fonseca Pontieri⁴; Luiz Alberto Colnago³; Marcio Antonio Brunetto^{1,2}

¹Veterinary Nutrology Service, Veterinary Teaching Hospital, School of Veterinary Medicine and Animal Science - University of São Paulo, São Paulo, Brazil; ²Pet Nutrology Research Center, Nutrition and

Production Department, School of Veterinary Medicine and Animal Science, University of São Paulo (USP), Pirassununga, Brazil; ³Brazilian Agricultural Research Corporation (Embrapa-CNPDIA), São Carlos,

Brazil; ⁴Nutritional Development Center, Grandfood Industry and Commerce LTD, Dourado, Brazil

In recent decades the incidence of obesity in companion animals has increased significantly and has become a serious concern in veterinary medicine. To date, there are few published studies that evaluated and compared the metabolome of obese dogs with that of dogs in ideal body condition score, and not one that evaluated the effect the weight loss effect on the metabolic profile. Therefore, in the present study, the metabolic profiles of blood serum of obese dogs, control dogs, and dogs that were subjected to a weight loss program were analyzed. All procedures were previously approved by the Animal Use Ethics Committee (AUEC) of the School of Veterinary Medicine and Animal Science of the University of São Paulo (protocol number 4668091214). Approximately 20 metabolites were identified on the high-resolution ¹H Nuclear Magnetic Resonance (NMR) spectra of the animals' blood serum. The metabolomic assessment differed between obese dogs and animals in optimal body condition. Moreover, weight loss results in metabolomic profiles similar to those observed in lean animals. The metabolites that contributed to the differentiation of the groups were: glucose, lactate, glutamine, acetone, arginine, alanine, and citrate for the healthy animals (control and after weight loss); and lipids, cholesterol, and branched-chain amino acids for the obese animals. The present study is a pioneer in this type of evaluation in dogs and these results highlight the importance of maintaining or achieving an ideal body condition score for reducing deleterious effects of overweight in pets.