Abstract: Feeding Saccharomyces cerevisiae fermentation product (SCFP) has previously altered fecal microbiota, fecal metabolites, and immune cell function of adult dogs. The objective of this study was to further measure circulating immune cell numbers and activity, antioxidant status, and oxidative stress marker concentrations of adult dogs fed SCFP in an extruded diet. Sixteen adult pointer dogs (8M, 8F; mean age = 8.35 y; mean BW = 27.13 kg) were used in a randomized crossover design study. All dogs were fed a control diet for 4 wk, then randomly assigned to the control or SCFP-supplemented diet and fed to maintain BW for 10 wk. A 6-wk washout preceded the second 10-wk experimental period with dogs receiving opposite treatments. After baseline/washout and treatment phases, pre- and post-prandial blood samples were collected. Oxidative stress and immune cell function were measured using commercial ELISA kits, circulating immune cell numbers were analyzed using flow cytometry, and mRNA expression of oxidative stress genes were analyzed using RT-PCR. Change from baseline data were analyzed using the Mixed Models procedure of SAS 9.4, with P < 0.05 being significant and P < 0.10 being trends. Changes in unstimulated lymphocytes and stimulated IFN-g secreting T-cells were lower (P < 0.05) in SCFP-fed dogs, while change in stimulated T cells were lower (P < 0.05) in control-fed dogs. The stimulated cytotoxic T cells delta trended lower (P < 0.10) in SCFP-fed dogs. Change in serum superoxide dismutase (SOD) concentrations were higher (P < 0.05) and change in catalase mRNA expression was lower (P < 0.05) in SCFP-fed dogs. All other immune cells, oxidative stress markers, and gene expression were unaffected by treatment. In conclusion, SCFP-fed dogs have increased SOD, which supports lower acute-inflammatory responses and aligns with some immune stimulation data.

Keywords: canine, oxidative stress, Saccharomyces cerevisiae fermentation product

PSXI-4 Use of Foodomics Analysis to Biochemically Compare Different Pet Food Ingredient

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Abstract: With an increased focus on pet health and longevity, ingredient nutritional quality and functionality is of great interest to the pet food industry. Characterizing the natural bioactive molecules present in different ingredient categories may identify those most likely to support health and/or manage disease. Over the past couple decades, high-throughput ‘omics’ technologies have been used to characterize the DNA, RNA, proteins, and metabolite profiles of dogs and cats. Similar technologies may now be applied to foods, a process referred to as ‘foodomics’. The objective of this study was to use foodomics analysis to characterize and compare various fruit-, vegetable-, tuber-, legume-, and grain-based ingredients. A total of 35 ingredients were subsampled, ground with liquid nitrogen, and sent to Metabolon, Inc. (Durham, NC) for untargeted high-throughput metabolomics analysis using gas chromatography-mass spectrometry and liquid chromatography-mass spectrometry. Over 640 named bioactive molecules were identified in the samples. Principal component analysis showed that ingredient classes tended to cluster together and separately from others, with distinct fruit-, vegetable-, and grain-based clusters identified. Legumes clustered most closely to tubers and vegetables. Random forest analysis had a nearly perfect predictive accuracy and was used to identify molecules most influential in separating ingredient classes. This dataset has provided a foundation from which the pet foodomics field may grow and has identified molecule signatures specific to ingredient type. Consequent studies may identify bioactive molecules possessing beneficial properties (e.g., antioxidant, antibacterial) that may be used to target obesity or support digestive health, skin and coat health, and joint health. Such analysis may also identify ingredient-specific biomarkers that may increase food consumption accuracy.

Keywords: companion animal, foodomics, ingredient functionality