

## Effect of Supplemental Selenium Source on Dairy Cow Performance, Antioxidant Status and Apparent Absorption and Retention

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The objective of this experiment was to determine how source of selenium (Se) affects animal performance, antioxidant status and apparent absorption and retention. Multiparous Holstein cows (n=24; 597 ± 49 kg BW) were blocked by days in milk (161 ± 18) and randomly assigned to receive 0.3 ppm of either: 1) organic Se (selenized yeast; **ORG**); or, 2) inorganic Se (sodium selenite; **INO**) premix, top dressed and mixed into a ration daily. Following an 11-week adaptation period (blood and milk sampled monthly) cows received an intraruminal isotope dose of Se<sup>77</sup> (same chemical form as premix) followed by a 4-day period of blood and rumen fluid sampling, and total collection of feces, urine, and milk. Data was analyzed with PROC GLIMMIX in SAS with fixed effects of treatment, time, and their interaction, and random effects of block and cow. Daily DMI (23 ± 0.6 kg), milk yield (35 ± 1.2 kg), plasma glutathione peroxidase (64 ± 4.2 U), and serum Se (0.11 ± 0.003 µg/g) were not different ( $P > 0.1$ ) between treatments during adaptation period. Serum Se<sup>77</sup> maximum concentration (Cmax) and area under the curve (AUC) were not different ( $P > 0.1$ ) between treatments for 72 hours following infusion, but rumen fluid Se<sup>77</sup> AUC was higher ( $P = 0.02$ ) for ORG cows. Apparent absorption (64 ± 1.3%) and retention (44 ± 1.5%) of the Se<sup>77</sup> dose were not different ( $P > 0.1$ ) between treatments. Fecal excretion of the Se<sup>77</sup> dose was not different ( $P > 0.1$ ) between treatments (36 ± 1.4%), but ORG cows had lower ( $P < 0.01$ ) urinary excretion (13 ± 0.6% vs 17 ± 0.6%) and higher ( $P < 0.01$ ) milk excretion (6 ± 0.3% vs 2 ± 0.3%) compared to INO cows. These results indicate that ORG Se improved Se content of milk and decreased Se excretion into the environment, but Se status of the cow was not affected by Se source at this supplementation level.

## Synchrotron-based Study to Determine the Inherent Molecular Structure Changes Induced by Steam Pressure Times in Faba Bean Seeds

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Synchrotron technology is currently a valuable instrument to examine detailed intrinsic molecular features in a variety of materials including feed ingredients. Heat processing methods commonly used in the feed industry alter the physicochemical structure of feeds, modifying their degradation behavior when fed to livestock animals. Traditional research tools are unable to detect processing induced molecular structure changes associated to nutrient supply. Hence, this study aimed to determine the extent of protein molecular structure modifications related to steam pressure processing times in faba bean seeds. Analyzed samples belong to CDC Snowbird variety heated at 121 °C for 0, 30, 60, 90, and 120 min. SAS software 9.4 (SAS Institute, Inc., Cary, NC, US) was used for statistical analysis with significance declared at  $P < 0.05$ . Results showed variations in the spectra protein related areas and heights with a lower amide I area ( $P < 0.01$ ) found at 0 min (47.53 AU, infrared absorbance units) compared to 30 min (54.16 AU) and 120 min (57.01 AU). Amide II area was higher ( $P = 0.01$ ) at 30 min (24.36 AU) compared to 60 and 90 min (22.06 and 22.16 AU, respectively). The  $\alpha$ -helix to  $\beta$ -sheet ratio was higher ( $P < 0.01$ ) at 0 min (1.09 AU) compared to all heating times (avg. 1.01 AU). Protein molecular structure changes associated with heat processing can be directly identified using synchrotron technology. The increased knowledge in the area of feed molecular structure will benefit the application of precise dairy feeding strategies as we get a better understanding of the close relationship between individual inherent structure characteristics of each feed nutrient and the overall degradation behaviors of feedstuffs when fed to cattle.