
Nitrogen and Amino Acid Digesta Flows in Broilers fed Heat Damaged Protein Ingredients

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Due to an increasing feed-food competition for quality protein, less digestible protein is expected to be fed to broilers in the future. However, pre-caecal indigestible protein in the diets of broilers may lead to hind-gut protein fermentation (PF) and the production of potentially health detrimental metabolites. To evaluate effects of PF on gut health, an experimental contrast in ileal N flow is required. Therefore, our objective was to develop a model that creates a contrast in protein fermentation by reducing protein digestibility within ingredients. To this end, we used severe toasting of protein sources and evaluated the effect on ileal nitrogen (N) and amino acid (AA) flows. Distal ileum content, excreta and caeca content were collected from 240 broilers fed one of six diets (8 replicate pens) for 30 days. Diets contained 20% soybean meal (SBM), high protein sunflower meal (SFM) or dehulled rapeseed meal (dRSM) as is, or heat damaged by secondary toasting at 136°C for 20 minutes (tSBM, tSFM or tdRSM). Toasting SBM increased the ileal flow of N (851 vs. 744 mg/d) and most of the AA (on average by 35 mg/d). The daily excreted N (excluding uric acid N) level did not differ between SBM and tSBM diets, some AA levels increased, such as Asp, Glu and Lys (mean increase: 34 mg/d). Toasting SFM had no effect on the flow of N and AA. Toasting dRSM increased the flow of N (862 vs. 665 mg/d) and all AA (mean increase 56 mg/day) through the distal ileum. Also, the excreted flow was increased: N (999 vs. 761 mg/d, excluding uric acid N) and AA (mean 71 mg/d). In conclusion, toasting dRSM, and to a lesser extent SBM, increased the flow of PF substrate into the hindgut of broilers, making these potential models to evaluate effects of PF on gut health. Whether these increased ileal flows of N and AA lead to increased PF will be further studied by caecal PF metabolite concentrations. The increase in N and AA from ileum to excreta might be the result of microbial growth. Microbe quantification will be needed to elucidate whether this is the case.