A linear regression approach to compare precaecal amino acid digestibility in broilers, turkeys and ducks

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Abstract
It was the objective to compare the precaecal (pc) digestibility of amino acids from solvent extracted meals of soybean (SBM) and rapeseed (RSM) between broilers, turkeys and ducks. Diets with inclusion levels of 0, 150 and 300 g SBM or RSM per kg of feed were offered ad libitum from d 14 to 21 post hatch. Six pens of 12 birds per species were allocated to each diet. Digesta were sampled on a pen basis from a section of the intestine between Meckel’s diverticulum and 2 cm anterior to the ileo-caeco-colonic junction. Titanium dioxide was included as an indigestible marker. The amount of amino acids digested until the terminal ileum depended linearly on the intake of the respective amino acid. Partial pc digestibilities for the two protein sources under test were determined by linear regression analysis. Digestibilities ranged from 62% to 92% for valine (RSM, ducks) and methionine (RSM, broilers). There were significant differences in the digestibility within one protein source between broilers, ducks and turkeys.

Introduction
Poultry species are known for differences in the development of their digestive tract during growth (Jamroz et al., 2002), which may cause differences in nutrient digestion. While precaecal (pc) digestibility of amino acids becomes increasingly relevant in terms of feed protein evaluation, it is not known whether values determined in one species can be applied in feed compounding for another species. It was the objective of this study to compare the pc digestibility of amino acids from solvent extracted meals of soybean (SBM) and rapeseed (RSM) in broilers, turkeys, and ducks. The linear regression approach was used because values do not need correction for endogenous amino acid losses (Rodehutscord et al., 2004).

Materials and Methods
Identical diets were used for all three species. Five diets were prepared containing 0, 150, and 300 g of either SBM or RSM per kg of diet. The meals replaced corresponding amounts of maize starch in the basal diet. Consequently, the changes in amino acid concentration of the diets originated from the meals only. The concentration of crude protein varied between 165 and 286 g/kg of diet. TiO\textsubscript{2} was included as indigestible marker. All diets were pelleted without using steam. During the first 14 days post hatch, birds received a species-specific commercial starter feed. For each species, 6 pens of 12 birds were then allocated to each treatment. Feed was supplied \textit{ad libitum}. On day 21 all birds were asphyxiated with CO\textsubscript{2}, the gut section between Meckel’s diverticulum and the ileo-caeco-colonic junction was isolated, and the content of the terminal two thirds of this section gently flushed out with demineralised water (Kluth et al., 2005b). Digesta of birds within one pen were pooled and immediately frozen. After freeze drying, samples were ground to pass through a 0.5 mm sieve for chemical analysis. Amino acid analysis followed standard procedures using an AA analyser and ninhydrin after an oxidation step and hydrolysis as specified by Timmler and Rodehutscord (2003). TiO\textsubscript{2} in the diets and digesta was determined photometrically (Brandt and Allam, 1987). The digestibility of amino acids and crude protein were calculated for each pen. Values were then used to determine the partial pc digestibility of amino acids from SBM and RSM using the slopes of linear regressions (Rodehutscord et al., 2004). Multiple linear regressions

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548
were calculated to investigate differences between the two protein sources and/or the three species according to Kluth et al. (2005a).

**Results and Discussion**
The pc digestibility of the individual amino acids from the five diets ranged between 62 and 92%, with the lowest and highest values determined for valine (RSM, ducks) and methionine (RSM, broilers). These data are not shown because they were only needed for the further calculations of digestibilities for the test meals. The amounts of amino acids digested up to the terminal ileum depended linearly on the intakes of amino acids for all the amino acids studied. An example is shown in the figure. The linearity in the relationship between intake and pc flow confirms results from earlier studies on N excretion and amino acid flow (Mitchell and Bert, 1954; Krawielitzki and Bock, 1976; Short et al., 1999, Rodehutscord et al., 2004). When quantitative data are considered as shown in the figure, the slopes of these linear regressions can be interpreted in terms of partial pc digestibility of the supplemented protein source.

![Figure: Relationship between intake and digestion up to the terminal ileum for lysine from soybean meal (means and SD, n=6)](image)

Digestibility of amino acids for the two protein sources, determined by regression analysis, is shown in the table. No significant differences were detected in pc digestibility of amino acids between SBM and RSM in broilers and in turkeys, respectively. Ducks were characterized by a low level of digestibility. Some but not all amino acids from RSM were significantly lower digested than amino acids from SBM. With regard to RSM, significant differences were found between ducks and broilers for all amino acids. Basal endogenous amino acid loss may be different between species. However, if such differences exist, they did not cause the differences found between species. As digestibilities refer to the slopes of the regression only, they are not affected by basal endogenous loss.

**Conclusions**
Digestibility values determined in one poultry species cannot be applied to another. Differences between species in amino acid digestibility appear not to be similar for different protein sources.
Table: pc digestibility (%) of amino acids for the test proteins (±SE of estimate), determined by multiple linear regression analysis

<table>
<thead>
<tr>
<th></th>
<th>Broilers</th>
<th></th>
<th></th>
<th>Turkeys</th>
<th></th>
<th></th>
<th>Ducks</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SBM</td>
<td>RSM</td>
<td>SBM</td>
<td>RSM</td>
<td>SBM</td>
<td>RSM</td>
<td>SBM</td>
<td>RSM</td>
</tr>
<tr>
<td>Crude protein</td>
<td>81 ±3</td>
<td>82(^a) ±4</td>
<td>85 ±6</td>
<td>78 ±6</td>
<td>74(^A) ±2</td>
<td>69(^Bb) ±2</td>
<td></td>
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</tr>
<tr>
<td>Arginine</td>
<td>84 ±3</td>
<td>87(^a) ±5</td>
<td>85 ±6</td>
<td>79 ±7</td>
<td>76(^A) ±2</td>
<td>71(^Bb) ±3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cystine</td>
<td>73 ±4</td>
<td>76(^a) ±4</td>
<td>71 ±7</td>
<td>67 ±5</td>
<td>69 ±3</td>
<td>67(^b) ±2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Isoleucine</td>
<td>77 ±4</td>
<td>80(^a) ±5</td>
<td>82 ±6</td>
<td>75 ±7</td>
<td>69 ±2</td>
<td>65(^b) ±3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leucine</td>
<td>78 ±3</td>
<td>84(^a) ±4</td>
<td>83 ±6</td>
<td>79 ±6</td>
<td>74 ±2</td>
<td>73(^b) ±3</td>
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<td></td>
</tr>
<tr>
<td>Lysine</td>
<td>84(^a) ±4</td>
<td>83(^a) ±5</td>
<td>83 ±7</td>
<td>76 ±7</td>
<td>70(^b) ±3</td>
<td>66(^b) ±3</td>
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<tr>
<td>Methionine</td>
<td>87(^a) ±3</td>
<td>92(^a) ±3</td>
<td>87 ±6</td>
<td>86 ±5</td>
<td>76(^Ab) ±2</td>
<td>80(^Bb) ±2</td>
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<tr>
<td>Threonine</td>
<td>78(^a) ±4</td>
<td>77(^a) ±5</td>
<td>82 ±8</td>
<td>72 ±7</td>
<td>66(^b) ±3</td>
<td>64(^b) ±3</td>
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<tr>
<td>Valine</td>
<td>77(^b) ±4</td>
<td>77(^a) ±4</td>
<td>80 ±7</td>
<td>72 ±7</td>
<td>66(^b) ±3</td>
<td>62(^b) ±3</td>
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</tr>
</tbody>
</table>

\(^{A,B; a,b}\) amino acids not sharing a common superscript are significantly different between the two sources within species (upper case) and between species within protein source (lower case) (p<0.05)

References


