A DYNAMIC MODEL FOR DIETARY AMINO ACIDS UTILISATION IN FISH LARVAE

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Improvement of growth performance in fish larviculture

Determination of dietary AA requirements

Understanding AA metabolism
Tracer studies:

=> Better understanding of amino acid metabolism

but interpretation limited to the comparison of a number of body compartments in a few time points, and relative (not absolute) numbers
Background

Modelling

• holistic approach to integrate knowledge on growth and metabolism
• identify most important processes and gaps in knowledge

Dynamic model => simulate metabolism and/or growth in time

Mechanistic model => processes are defined based on the underlying biochemistry & model parameters have (as much as possible) a biological meaning
Objectives

- Develop a dynamic mechanistic model that simulates AA metabolism of fish larvae.
- Assist in the interpretation of results obtained using tracer studies.
- Improve the understanding of larval digestion and absorption of dietary AA, and the postprandial AA metabolism and growth.
Data set to model

- Senegalese sole fed one meal of $^{14}$C-labelled Artemia

12 DAH

(20-30 min.)

1, 3, 6 or 24h incubation

Morais et al. (2004)
Data set to model

- Senegalese sole fed one meal of $^{14}$C-labelled Artemia

Morais et al. (2004)
Model Description

Gut Lumen
- Artemia → Digestion → AA → Evacuation

Gut Wall
- Protein Synthesis → Protein Degradation
- Protein → FAA
- AA Catabolism → Transport
- Faeces

Body
- Protein Synthesis → FAA
- AA Catabolism
- Protein Degradation
- CO₂
Model Description

Example of equations:
Gut wall protein synthesis = $K_{sGut} \times \text{Excess FAA in gut} + \text{Basal Ks}$
Gut wall AA catabolism = $K_{catGut} \times \text{Excess FAA in gut} + \text{Basal AA cat}$
Parameters from bibliography:

- Initial size of FAA and protein pools in sole (fasted) and *Artemia*
Model Calibration

Data from Morais et al (2004):

- % tracer intake
- Time after meal: 1 h, 3 h, 6 h, 24 h
- CO2, Body, Gut, Water
Model Calibration

Parameters to be calibrated with model:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basal AA Catabolism rate</td>
<td>ng/h</td>
</tr>
<tr>
<td>Delay onset of Digestion</td>
<td>min</td>
</tr>
<tr>
<td>Rate of Digestion &amp; absorption</td>
<td>min⁻¹</td>
</tr>
<tr>
<td>Gut AA catabolism rate</td>
<td>min⁻¹</td>
</tr>
<tr>
<td>Gut Protein Synthesis rate</td>
<td>min⁻¹</td>
</tr>
<tr>
<td>No of Artemia fed</td>
<td>n</td>
</tr>
<tr>
<td>Protein degradation rate</td>
<td>ng/h</td>
</tr>
</tbody>
</table>
Model Calibration

- Lines are simulated values
- Points (and shaded area) are mean values (and 95% confidence intervals) from Morais et al. (2004)

Body Protein

Time (h)

0 6 12 18 24

0 20 40 60 80

%
Model Calibration

- Lines are simulated values

- Points (and shaded area) are mean values (and 95% confidence intervals) from Morais et al. (2004)
Model Calibration Using Powersim Studio 7
Model Calibration

Parameters calibrated with model:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Mean</th>
<th>CV(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basal AA Catabolism rate</td>
<td>ng/h</td>
<td>502.6</td>
<td>18.6</td>
</tr>
<tr>
<td>Delay onset of Digestion</td>
<td>min</td>
<td>0.032</td>
<td>3.3</td>
</tr>
<tr>
<td>Rate of Digestion &amp; absorption</td>
<td>min⁻¹</td>
<td>0.539</td>
<td>3.9</td>
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<tr>
<td>Gut AA catabolism rate</td>
<td>min⁻¹</td>
<td>0.010</td>
<td>8.1</td>
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<tr>
<td>Gut Protein Synthesis rate</td>
<td>min⁻¹</td>
<td>0.161</td>
<td>2.0</td>
</tr>
<tr>
<td>No of Artemia fed</td>
<td>n</td>
<td>15.0</td>
<td>1.1</td>
</tr>
<tr>
<td>Protein degradation rate</td>
<td>ng/h</td>
<td>25.5</td>
<td>0.7</td>
</tr>
</tbody>
</table>

Using Powersim Studio 7

After about 9 million iterations
Model Output
Model Output

- Total
- AA catabolism
- Total Prot Synt
- Total Prot Degradation
Conclusions

- Food has a major contribution to the FAA pool composition - Rates of protein synthesis and AA Catabolism show a major increase after the meal.

- Peak for this postprandial metabolism occurs only 1 hour after the meal, and the rates returning to “basal” values 3 hours after the meal.

- This suggests a rapid handling of Artemia protein by larvae, and supports the need for feeding sole larvae at a high frequency (every 3-4 hours) in order to fully use its growth potential.

- Model Mechanistic nature => can be used with different AA tracers, and also for other fish species.
Future work

- Model several meals / days of feeding
- Model effects of few meals vs. continuous feeding
- Test (validate) with different experiments / ages / species
- Simulate metabolism of individual AA
  - => estimation of requirements
  - => better understanding of AA
- Integrate AA metabolism with energetics and growth
  - => better understanding of growth process
  - => defining feeding strategies
  - => growth predictions
Thank you!!
Model Output

Graphs showing the total protein and total FAA levels in the gut wall and body over time.
Model Output

The graph shows the model output with the following data points:

- **ng/hr** axis:
  - 0 to 5,000
  - 5,000 to 10,000

- Time scale from 00:00 to 18:00

- Three lines representing different processes:
  - Red line: Total AA catabolism
  - Green line: Total Prot Synt
  - Blue line: Total Prot Degradation