The Effect of Crude Protein Level in Diets on Serum Biochemical 
Indexes and Intestinal Microflora of Yellow Quails

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Abstract: A study was carried out to determine the effect of crude protein level in diets on Serum Biochemical 
Indexes and Gastrointestinal Microflora of yellow quails. Four diets with different crude protein levels 17.75%, 
19.95%, 21.85%, 24.08% were used to feed 192 yellow quails during 50-day-old to 95-day-old in this 
experiment. The quails were randomly assigned to 4 groups by similar body weight, each of which was 
subdivided into 4 replicates of 12 quails each. At 95-day-old, two quails per replicates were selected 
randomly and slaughtered to collect the blood the caecal contents. The blood sample was used to analysis 
serum biochemical. The caecal contents was detected the *coli bacillus*, *lactobacillus* and *bifidobacterium*. 
The results showed that ALT of diet 1 was significant low (p<0.05); there was no significant of AST in all 
treatment (p>0.05). Serum TP of treatment 3 is high than treatment 1 (p<0.05). And serum BUN and P was 
no significant in all treatment (p>0.05). The *coli bacillus* and *bifidobacterium* were decreased and 
*lactobacillus* increased with the increased in dietary protein though there were no significant different 
(p>0.05). These results indicated that the different level of dietary protein could not effect on gastrointestinal 
microflora significantly but significantly effect on serum biochemical indexes of yellow quails.

Key words: Yellow quail, serum biochemical, gastrointestinal microflora

INTRODUCTION
Producing performance is an important indicator of 
general health, but it is not always right. Because it will 
damage the liver of birds and usually have a high 
production to intake excessive amounts of CP in shirt 
time. Blood biochemical characteristics could be very 
important as indicator traits in breeding for the highest 
productive performance birds (Peterson et al., 1982; 
Hassan et al., 2006; Hassaan et al., 2008). Yellow 
quails were wide used in quail breeding in China. But it 
is not clear which CP level of diets is the optimum level 
for them. On the other hand, different diets CP level will 
effect on the nutritional digestion. Then the mounts of 
nutrition reached the hindgut will be changed. This could 
impact on intestinal microflora. The present study was 
conducted to the effect of crude protein level in diets on 
Serum Biochemical Indexes and hindgut Microflora of 
yellow quails.

MATERIALS AND METHODS
Animals and dietary treatments: In this study, one 
hundred and ninety two eleven-week-old Chinese 
yellow quails were randomly assigned to four 
groups by similar body weight, each of which was 
subdivided into four replicates of 12 quails each. The 
quails were housed in wire cages, on a schedule with 
16 h light and 8 h darkness. The quails received diets 
with different crude protein levels 17.75%, 19.95%, 
21.85%, 24.08% as four diets. The composition and the 
calculated nutrient content of the experimental 
Treatments are presented in Table 1. Feed and water 
were available freely. The experimental diets were 
designed as:

Sample collection and analyses: Feed samples were 
dried in an oven of 105°C for 6 h for Dry Matter (DM) 
determination. The CP was determined by the Kjeldahl 
method, crude fiber and crude fat according to the AOAC 
(1984). At 95-day-old, two quails per replicates were 
selected randomly and slaughtered to collect the blood 
and the caecal contents. Serum were collected after 
centrifugation (3000r/min for 15 min), decanted and 
stored at -20°C until biochemical analyses were done. 
Commercial kits were used for the determination of the 
following serum constituents according to the procedure 
outlined by the manufacturer, Total Proteins (TP), Blood 
Urea Nitrogen (BUN), Phosphorus (P), Aspartate 
Aminotransferase (AST) and Alanine Aminotransferase 
(ALT) (Shanghai Jiancheng Bio-Product Co., Ltd., 
China). The fecal sample (1 g) in cecum was placed in 
an anaerobic glove box within 1 h of collection and 
homogenized in prepared asepsis physiological saline 
diluted from 1⁰¹ to 1⁰⁹ fold. Portions (100 µL) of 
each dilution were spread onto the surfaces of plates 
which contained the following agar media and were 
incubated anaerobically at 37°C.

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Table 1: Composition (air dry basis, %) and nutrient levels (DM basis, %) of trial diets

<table>
<thead>
<tr>
<th>Items</th>
<th>Treatments 1 (CP 17.75%)</th>
<th>Treatments 2 (CP 19.95%)</th>
<th>Treatments 3 (CP 21.85%)</th>
<th>Treatments 4 (CP 24.08%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ingredients</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corn</td>
<td>64.00</td>
<td>60.00</td>
<td>56.00</td>
<td>51.00</td>
</tr>
<tr>
<td>Soybean meal</td>
<td>27.00</td>
<td>30.00</td>
<td>30.00</td>
<td>31.00</td>
</tr>
<tr>
<td>Corn gluten meal</td>
<td>1.00</td>
<td>4.00</td>
<td>8.00</td>
<td>11.00</td>
</tr>
<tr>
<td>Wheat bran</td>
<td>2.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Fish meal</td>
<td>1.00</td>
<td>1.00</td>
<td>1.00</td>
<td>2.00</td>
</tr>
<tr>
<td>Soybean oil</td>
<td>1.00</td>
<td>1.00</td>
<td>1.00</td>
<td>1.00</td>
</tr>
<tr>
<td>Premix 2</td>
<td>4.00</td>
<td>4.00</td>
<td>4.00</td>
<td>4.00</td>
</tr>
<tr>
<td>Total</td>
<td>100.00</td>
<td>100.00</td>
<td>100.00</td>
<td>100.00</td>
</tr>
</tbody>
</table>

Nutrient levels are calculated on the measured values of ingredients. Per kilogram mixed additives: Provides: VA 1200000 IU; VE 40000 IU; VE 500 mg; VB2 70 mg; VB6 60 mg; VB5 400 mg; Folic acid 20 mg; Pantothenic acid 300 mg; Fe 1800 mg; Cu 200 mg; Mn 1400 mg; Zn 1200 mg; Se 5 mg; Ca 20%; P 4%; NaCl 8%; Met 2.5%; Lys 1.5%

Table 2: Measuring method of gastrointestinal microflora of quails

<table>
<thead>
<tr>
<th>Medium</th>
<th>Method</th>
<th>Time/h</th>
<th>Temperature°C</th>
</tr>
</thead>
<tbody>
<tr>
<td>MacConkey medium</td>
<td>E. coli</td>
<td>24</td>
<td>37</td>
</tr>
<tr>
<td>MRS agar medium</td>
<td>Lactic acid bacterium</td>
<td>Anaerobic</td>
<td>48</td>
</tr>
<tr>
<td>BL medium</td>
<td>Bifidobacterium</td>
<td>Anaerobic</td>
<td>48</td>
</tr>
</tbody>
</table>

Table 3: Serum biochemical indexes of quails in different dietary protein level

<table>
<thead>
<tr>
<th>Item</th>
<th>Treatments 1 (CP 17.75%)</th>
<th>Treatments 2 (CP 19.95%)</th>
<th>Treatments 3 (CP 21.85%)</th>
<th>Treatments 4 (CP 24.08%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serum AST (KU)</td>
<td>9.45±0.96</td>
<td>7.83±1.75</td>
<td>11.43±2.49</td>
<td>6.25±0.92</td>
</tr>
<tr>
<td>Serum ALT (KU)</td>
<td>14.77±3.31</td>
<td>17.86±2.45</td>
<td>30.07±7.86</td>
<td>20.92±4.90</td>
</tr>
<tr>
<td>Serum TP (mg/ml)</td>
<td>55.18±4.39</td>
<td>81.88±7.90</td>
<td>95.62±12.83</td>
<td>75.63±10.00</td>
</tr>
<tr>
<td>Serum BUN (mmol/L)</td>
<td>0.03±0.00</td>
<td>0.06±0.02</td>
<td>0.03±0.01</td>
<td>0.03±0.00</td>
</tr>
<tr>
<td>Serum P (mmol/L)</td>
<td>3.30±0.44</td>
<td>2.46±0.52</td>
<td>2.38±0.56</td>
<td>3.23±0.80</td>
</tr>
</tbody>
</table>

11Mean values within a row with no common superscript differ significantly (p<0.05)

Table 4: Intestinal microflora of quails in different dietary protein level (lgcfu/g)

<table>
<thead>
<tr>
<th>Item</th>
<th>Treatments 1 (CP 17.75%)</th>
<th>Treatments 2 (CP 19.95%)</th>
<th>Treatments 3 (CP 21.85%)</th>
<th>Treatments 4 (CP 24.08%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>6.42±0.11</td>
<td>8.53±0.40</td>
<td>8.28±0.46</td>
<td>8.34±0.430</td>
</tr>
<tr>
<td>Lactic acid bacterium</td>
<td>8.48±0.27</td>
<td>8.59±0.30</td>
<td>8.65±0.35</td>
<td>7.91±0.041</td>
</tr>
<tr>
<td>Bifidobacterium</td>
<td>8.45±0.11</td>
<td>8.58±0.55</td>
<td>8.60±0.35</td>
<td>8.70±0.400</td>
</tr>
<tr>
<td>Bifidobacterium/E. coli</td>
<td>1.00±0.02</td>
<td>1.03±0.043</td>
<td>1.06±0.03</td>
<td>1.04±0.030</td>
</tr>
</tbody>
</table>

Statistical analysis: Data were analyzed by SPSS 10.00 version for Windows. The differences between groups were determined by Variance Analysis (ANOVA). Duncan's multiple range test was performed when differences were significant. Data were expressed as Mean±SEM.

RESULTS

Serum biochemical indexes of quails in different treatments: The results (as in Table 3) showed that GPT of serum in Treatments 1 was significant low (p<0.05) than in Treatments 3. There was no significant of GOT of serum in all Treatments (p>0.05) but it was highest in Treatments 3 and it was very interesting that GPT of serum was highest in Treatments 3. Serum TP of Treatments 3 is high than Treatments 1 (p<0.05). And serum BUN and P was no significant in all Treatments (p>0.05).

Intestinal microflora of quails in different dietary protein level: The results (as in Table 4) showed that The colibacillus and bifidobacterium were decreased and lactobacillus increased with the increased in dietary protein though there were no significant difference (p>0.05).

DISCUSSION

The feeding of different-protein diet results in biologically significant abnormalities in quails (Okumura and Tasaki, 1969). Alterations in measurements such as
BUN and TP are not unexpected. BUN levels are dependent on dietary protein intake (Ozek and Bahtiyarca, 2004); thus, low-protein diets result in reduced BUN concentrations. Thus the BUN in treatment 3 and treatment 4 was lower than that in treatment 2. This maybe, because that feeds intake of quails was lower in treatment 3 and treatment 4. And BUN of all treatments was high unusually (Shen et al., 2008) indicated that the amino acids were not balance in all treatments. Serum AST and ALT activities (liver enzymes) were used to evaluate liver functions, the increase in their activities were related to the degenerations of hepatocytes or liver damage irrespective of its origin (Chen et al., 1999).

Intestinal microflora is a complex microbial system. The relationship between different microorganisms included coordination and competition. Intestinal microflora acts as an important role in host immune system (Backhed et al., 2005). Undigested nutrients can be accumulated in intestine, then the intestinal microorganisms can be caused growing fast, especially some microorganisms caused disease. Thus intestinal microbial flora can be changed. This can affect host health. Bifidobacteria are typical intestinal beneficial microorganisms and E. coli was considered as an alert actor which indicate a change of the intestinal microflora structure to unhealthy. So bifidobacteria/E. coli values (B/E value) (Wu et al., 2000) can evaluate the status of intestinal microflora. The results showed that with levels of diets protein was elevated B/E values was increasing and then decreasing, though it was not significant.

Conclusion: It is concluded that the different diets protein has affect on the Serum biochemical indexes and hindgut microflora of quails. And excess diets protein damaged animal health.

REFERENCES


