Growth Hormone Gene Polymorphism and its Relation to Quail Growth and Carcass

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In this study, it was aimed to determine the polymorphism of GH (growth hormone) gene in Japanese quails and the relationships between these genes and body weight and carcass traits. 3 genotypes (AA, AB and BB), 2 (A and B) alleles were detected by cutting the GH intron 1 region with restriction enzyme MspI. As a result of variance analysis, it was determined that the hatching weights of the animals with B allele and liver weights were higher. Thus, it is seen that GH gene and PCR-RFLP technique can be used in breeding studies.

Keywords:
Growth hormone
Quail
PCR-RFLP
MspI
Gene

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Introduction

Due to the fact that quail products are a quality food source are easy to grow and are a suitable source to meet the increasing protein need, interest in this branch of production is increasing day by day. For this reason, breeding of quail becomes important and in this context, the importance of genetic studies is increasing. Considering the yield of meat and eggs in quails, Growth hormone (GH) gene should be emphasized. While these genes have been studied quite a lot in chickens, there is not enough study in quail. To reveal the polymorphism of these genes and their relations with yield is important for the production of quail.

Growth hormone is a polypeptide produced and secreted from the anterior lobe of the pituitary gland. This hormone is a hormone that affects properties such as growth, body condition, egg production, and immunity. Therefore, this hormone is a candidate gene in yield studies in poultry (Nie et al., 2005).

GH performs its function by stimulating processes such as growth and fat metabolism with appropriate receptors on the wall of the target cells (Garrett et al., 2008).

Material and Methods

Research, it was carried out with 1 day old 84 quail purchased from a commercial firm. The birds with suitable body weights were attached to the quail growth cages by placing the wing number without sex determination. A standard diet was provided ad libitum during the 0-6 week age.

The body weights of the animals were weighed individually at the time of hatching and for a period of 6 weeks. Body weight gains calculated for each week. Following the last weighing, animals were slaughtered and cleaned to determine if genotypes have any effect on carcass, liver and abdominal fat weights. The blood was taken from jugular vein into 2 ml vacutainer tube containing EDTA as anticoagulant. Blood brought to the laboratory and kept until DNA isolation at -4 °C. Genomic DNA was isolated from blood samples according to the method describe in Miller et al. (1988). The concentration and purification of genomic DNA was quantified with a NanoDrop ND-1000 spectrophotometer, and 20 ng of genomic DNA was used for the PCR. Using the primers reported by Johari et al. (2013) for PCR processing of the GH gene, the PCR conditions were adapted to the
laboratory where the investigation will be conducted. The GH primer sequences were
F:5'-ATCCCCAGGCAAACATCCTC-3';
R:5'-CCTCGACATCCAGTCCACAT-3'
with size product 776 bp. PCR was performed using the
PCR Master Mix (Thermo Scientific, ferments). The kit
of master mix consisted of 2.5 µL of 10x PCR buffer, 2
mM of MgCl2 and 2 mM dNTPs (each). The PCR
reactions were carried out in a total volume of 25 µl
containing the following reaction mixture: 20 ng of
purified quail DNA, 15 µl of the master mix and 0.5 µl of
each primer. The following amplification profile was used:
initial denaturation at 94°C for 5 min, 35 cycles at 94°C for
30 s, annealing at 60°C for 30 s and extension at 72°C for
1 min, followed by a final extension step at 72°C for 10
min. PCR products were digested with restriction enzyme
MspI at 37°C for overnight. The digestion mixtures were
tested by electrophoresis on 2.5% ethidium bromide
stained agarose gels in 0.5x TE buffer. The gels were
photographed under UV light and the DNA bands were

PopGene 3.1 (Yeh et al., 1997) was used for allele and
genotype frequencies. The data used to compare the effect
of polymorphism of GH gene on body weight and carcass
traits of quails were tested with the use of anova at SPSS
(Kinnear and Gray, 1994). The genetic effect were
analysed using the following model:

\[ Y_{ij} = \mu + G_i + e_{ij} \]

\[ Y_{ij} \] is the observed value of dependent variable, \( \mu \) is
mean, \( G_i \) is the effect owing to genotype GH and \( e_{ij} \) is the
random residual error.

Results

In the study, a 776 bp fragment was amplified in the
GH locus. We were determinate three genotypes result of
restriction by MspI enzyme; AA (539, 237 bp), BB (776
bp) and AB (776, 539, 237 bp) (Figure 1 and 2). Alleles
found in this study were similar to those previously
identified and reported by Johari et al. (2013).

The intron-I of the GH (Forward and Reverse) were
amplified using PCR-RFLP method.

Allele A obtained from the digestion of GH with MspI
was more frequent in the quails. Genotype ab was more
frequent. The HW test showed that the studied fit the
theoretical proportions (\( P > 0.05 \)) (Table 1).

When we look at the weekly live weight results, it was
observed that there was no difference between the
genotypes other than the hatching weight. The hatching
weight was higher in animals with B allele (\( P < 0.05 \)).

When the carcass results were examined, it was found
that the liver weight was higher in animals with B allele
(\( P < 0.05 \)).

Discussion

GH has been found to be associated with many yield
parameters and diseases. GH alleles identified were linked
to egg production, resistance to Marek’s disease (MD) and
avian leukosis (ALV) in the chicken (Kuhnlein et al., 1997;
Makhsoos et al., 2013). In other PCR-RFLP studies on this
gene, it was determined that some alleles may be linked to
laying performance (Mou et al., 1995).

In this study, it is aimed to investigate whether there is
a relationship between polymorphism in the quail GH gene
region and live weight and carcass results. As a result of
cutting the GH gene region with MspI enzyme, it was
determined that the A allele was at a higher frequency and
the ab genotype was at a higher frequency than other
genotypes and the population was in balance. According to
the weekly live weight results, only a significant
correlation was found between the hatching weight and
genotypes (\( P < 0.05 \)).

It was observed that the hatching weights of animals
with B allele were high. Studies have also found a
relationship between live weight and genotypes (Nasirifar
et al., 2018). It was determined from the carcass results that
there was a relationship between liver weight and
genotypes, and animals with B allele were high in liver
weight (\( P < 0.05 \)).

\[ 5' \ldots C \downarrow C \quad G \quad G \ldots 3' \]
\[ 3' \ldots G \quad G \quad C \uparrow C \ldots 5' \]

Figure 1. GH gene region MspI enzyme restriction model

Figure 2. DNA electrophoretic pattern obtained after
digestion of PCR amplified GH gene products with MspI,
M: 100 bp ladder marker.

Conclusion

As a result, quail has recently gained importance as an
alternative protein source. For this reason, quail farming is
increasing day by day. The use of productive animals in
breeding always increases the profit of the enterprise.
Therefore, since the growth hormone (GH) gene is a gene
directly related to yield, it is a gene that should be
emphasized in breeding studies. As obtained in this study,
breeding studies can be carried out by considering the
relationship between hatching weight and genotypes. With
PCR-RFLP studies with more animals, it is likely that there
will be relationships between this gene and other yield
characteristics. For this reason, PCR-RFLP method
appears to be a feasible method for determining GH gene
polymorphism and its relationship with live weight in
quail.
Table 1. The allele and genotype frequencies for GH gene as restriction by MspI.

<table>
<thead>
<tr>
<th>Genotype frequencies</th>
<th>Allele frequencies</th>
<th>Chi-Square χ²</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA(%)</td>
<td>AB(%)</td>
<td>BB(%)</td>
</tr>
<tr>
<td>39.69</td>
<td>46.62</td>
<td>13.69</td>
</tr>
<tr>
<td></td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td></td>
<td>0.63</td>
<td>0.37</td>
</tr>
</tbody>
</table>

Table 2. Weekly body weights of quails as affected by polymorphism for GH gene as restriction by MspI.

<table>
<thead>
<tr>
<th>Weeks</th>
<th>AA</th>
<th>AB</th>
<th>BB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hatching</td>
<td>7.76±0.17b</td>
<td>8.53±0.19ab</td>
<td>8.55±0.21a</td>
</tr>
<tr>
<td>1</td>
<td>16.53±0.83</td>
<td>18.26±0.91</td>
<td>15.5±2.10</td>
</tr>
<tr>
<td>2</td>
<td>31.27±2.81</td>
<td>33.09±1.56</td>
<td>34.25±3.45</td>
</tr>
<tr>
<td>3</td>
<td>55.67±3.42</td>
<td>58.91±2.44</td>
<td>58.00±6.75</td>
</tr>
<tr>
<td>4</td>
<td>86.53±5.13</td>
<td>92.13±3.44</td>
<td>91.25±11.03</td>
</tr>
<tr>
<td>5</td>
<td>122.13±13.00</td>
<td>123.35±3.55</td>
<td>114.75±4.67</td>
</tr>
<tr>
<td>6</td>
<td>159.00±4.67</td>
<td>165.00±3.06</td>
<td>160.12±8.13</td>
</tr>
</tbody>
</table>

*P<0.05 Different small letters within each line refer to a significant difference at values are Mean±SE.

Table 3. Carcass traits of quails as affected by polymorphism for GH gene as restriction by MspI.

<table>
<thead>
<tr>
<th>Carcass traits</th>
<th>AA</th>
<th>AB</th>
<th>BB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass weight</td>
<td>95.30±3.99</td>
<td>100.73±2.36</td>
<td>95.74±6.08</td>
</tr>
<tr>
<td>Liver weight</td>
<td>3.89±0.18b</td>
<td>4.65±0.17a</td>
<td>4.22±0.32ab</td>
</tr>
<tr>
<td>Abdominal fat weight</td>
<td>0.43±0.15</td>
<td>0.56±0.09</td>
<td>0.35±0.15</td>
</tr>
</tbody>
</table>

*P<0.05 Different small letters within each line refer to a significant difference at values are Mean±SE.

Acknowledgements

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References


Kinnear PR, Gray CD. 1994. SPSS for Windows. Department of Psychology University of Aberdeen, UK.


