

Genetic analysis of poultry for market weight

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Abstract. Poultry genomics studies have provided valuable insights into a variety of traits, with much of the attention focused on areas such as memory-related diseases and allergies. However, less attention has been paid to understanding the genetic basis of economically critical traits in poultry, particularly those that affect carcass yield and market weight. In this study, we explored the genetic determinants of these economically important traits, specifically focusing on the relationship between poultry chromosomes and outcomes such as carcass yield and market weight, which are key factors in poultry production efficiency. Our results revealed significant associations between specific bird chromosomes and these traits, with most chromosomes exceeding the significance threshold. This indicates that genetic factors have a strong influence on both carcass yield and market weight, suggesting that genetic factors play a more critical role in these traits than previously understood. Despite the strong associations observed, Principal Component Analysis (PCA) indicated that these chromosomes may be underrepresented, possibly due to limitations such as insufficient sample size, variable data quality, or complex data structure. These factors may contribute to the discrepancy between expected and observed results. Nonetheless, our study adds to the existing body of knowledge by highlighting the genetic basis of economically important traits in birds. These findings highlight the importance of improving experimental methods to increase the accuracy and reliability of poultry genetic research. The genetic insights gained from this study may help develop more targeted breeding strategies to increase carcass yield and market weight. Our study lays the foundation for future research that could lead to major advances in poultry breeding and production practices. By improving our understanding of the genetic factors that influence economically important traits, we can contribute to the development of more efficient and productive poultry farming methods, ultimately benefiting both the industry and consumers.

Keywords: poultry, genetic analysis, market weight.

1. Introduction

Among all domestic animals, poultry is the most special one. Poultry are particularly significant due to their economic and nutritional value in both meat and egg production. In the poultry genetic research, chicken are marked as milestone in domestic animals, because their genomes were completely sequenced in 2004[1]. This plays an important role in the subsequent genetic research on poultry. The complete genome enables scientists to identify genes that can be edited for desirable traits, such as fast growth and more meat production. The genome difference between strains can tell the variations between their phenotypes and abilities. In the current study, the Russian white, a layer breed, is the result

of hybridizing White Leghorn from different cold regions to enhance cold tolerance[2]. This crossbreeding not only increases egg production but also significantly reduces the costs associated with maintaining temperature in cold climates. The Russian White can survive temperatures below freezing as adults, making it more economical to raise them in the harsh Russian winter.

Genome study play a crucial role in controlling poultry pathogens and diseases through gene editing. By modifying host factors related to virus entry or replication, people can enhance poultry resistance to diseases and improve poultry production capacity. Specifically, gene editing knockout the avian leukosis virus (ALV) sub-receptor *tva*, *tvb*, and *tvc* genes using CRISPR-Cas9 can effectively increase poultry's resistance to ALV[3]. Although this is a complex method to apply, it is highly efficient for resisting viruses. By utilizing gene editing, poultry industry can achieve higher surviving rates per farm for well-studied pathogens and viruses. This area also holds significant potential for future development, as pathogens and viruses will continue to evolve at a rate that outpaces human research.

However, as people all know, the poultry market is separated into two industries, broiler industry and layer industry. These chickens have similar genomes, but people have different goals for these two industries. For example, the meat production of broilers and the egg production or egg allergy of layers have been greatly improved due to the in-depth genetic research. In a previous study, scientists have approved that gene editing target to the *MSTN* gene, one of the genetic markers, can increase meat production and will not have an effect on the quality[4]. This is one of the genetic markers which people have discovered associated with the meat production. This can be useful for the broilers to get more meat production without any quality issues in the same period of times by genomic studies. It can satisfy both the processor and consumers. The more meat yields means that processors can gain more profits from selling it. For consumers, the meat quality is the major consideration, and this improved meat can achieve their goals, meaning that they are willing to buy it.

For the layers, there are more problems need to be resolved. For example, the egg allergenicity. Ovalbumin and Ovomucoid are both allergenic proteins in egg. By using the CRISPR/Cas9 system, scientists successfully separate the egg from ovalbumin and ovomucoid and mutate both[5]. This study showed people that mutated ovalbumin can reduce allergenicity and it is possible to mutate ovomucoid, which means it is also capable to reduce allergenicity. By applying this new mutated product, the producers can have more customers. For the customers, they do not need to worry about food allergy from the egg. That is helpful for both the company and consumers.

In the broiler industry, feed efficiency or feed conversion rate, rapid growth, and resistance to disease are three main objectives for growers. However, processors prioritize maximizing meat yield for increased profits. This paper investigates the genetic factors on chromosomes that influence market weight and carcass yield in broilers, game birds and layers. By comparing these genetic determinants, we aim to identify specific genes that could be targeted to improve overall market weight across various breeds. Also, we include feed conversion rate, daily weight gain, and end date for specific breeds. In this paper, we aim to find the genes on the chromosomes have the most significant impact on market weight and carcass yield in different poultry breeds.

2. Materials and methods

2.1. Collection of metadata

In this study, we collected metadata related to the weight information of different poultry strains by searching keywords such as "carcass weight," "market weight," and "poultry strain" across multiple academic and research platforms, including Google Scholar, Ovid, Web of Science, CNKI, and other reliable sources. Initially, thousands of papers and posts were retrieved, covering a broad range of strains. However, after screening, 51 papers and posts were retained because most of the others contained data that were inconsistent with the strains we needed or were too general. In particular, data on certain game bird strains were scarce, with only about 10 relevant articles available, and of these, only 2-4 articles provided weight-related data. To ensure reliability, we averaged the weight data for each strain from the available sources, providing a more consistent quantification of strain-specific weights.

2.2. *The Collection of genetic data*

This study utilized a previously published poultry genetic diversity dataset from Zhang et al. The dataset includes 15 different breeds of poultry, encompassing both game birds and broilers across various populations. The strains included in this dataset are as follows: 5 local Chinese strains (Beijing You, $n = 56$; Hongshan, $n = 96$; Shouguang, $n = 109$; Silkie, $n = 89$; Tibet, $n = 41$), 1 European local strain (Houdan, $n = 86$), 3 commercial strains (Rhode Island Red, $n = 478$; White Leghorn, $n = 230$; Cornish, $n = 10$), a wild ancestral population (Red Jungle Fowl, $n = 7$), and 5 game breeds (Luxi Game, $n = 10$; Henan Game, $n = 11$; Xishuangbanna Game, $n = 10$; Zhangzhou Game, $n = 11$; Turfan Game, $n = 10$). For each strain, the average market weight was determined based on available data, and random data assignment was performed within the observed range of market weights. This random assignment aimed to simulate the natural variability within each strain while adhering to realistic weight distributions (Table 1, see appendices).

2.3. *Analysis of the genetic data*

The experiment aimed to investigate the relationship between specific genetic markers or chromosomes in poultry and their associated market weights. To handle the large and complex dataset, we employed PLINK (version 1.9) for preliminary data processing, including quality control and identification of relevant genetic markers. Following this, we used R software for advanced data analysis. Specifically, we used R to generate visualizations such as Manhattan plots, QQ plots, and PCA (Principal Component Analysis) plots to explore the genetic architecture underlying weight traits in these poultry strains.

2.4. *Manhattan plot*

Given the large volume of genetic data, we utilized R to manage and plot the data efficiently. The Manhattan plot was generated using scatter plots, with the height of the data points representing the significance of each SNP (Single Nucleotide Polymorphism). The data points above the genome-wide significance threshold (5×10^{-8}) were highlighted to identify key genetic markers associated with market weight.

2.5. *PCA dimension reduction*

To reduce the dimensionality of the genetic data and highlight key patterns, we performed PCA using the results from the GWAS analysis. The PCA was plotted using R, with eigenvalues used to determine the contribution of each principal component. Variables were mapped onto the PCA space, and their $\cos^2$ values were calculated to assess the quality of representation in the reduced dimension space. This analysis helped us understand the relationships between different genetic variables and their influence on the weight traits. In our analysis of species variance, we focused on FCR, market weight, and daily weight gain, which are critical indicators of poultry production efficiency. As shown in Figure 1A, Xishuangbanna Game chickens had the highest average FCR (11.87), indicating they are the least feed-efficient species. In contrast, White Leghorn chickens had the lowest average FCR (1.39), suggesting they are the most feed-efficient and thus preferable for breeders aiming to optimize feed conversion.

3. Results

We collected and analyzed data from various existing experiments to compare daily weight gain, market day/end day, market weight/end weight, feed conversion rate (FCR), and average FCR across different poultry species. The data were incomplete due to variations in the original study designs and objectives. For example, Beijing You, Shouguang, Houdan, Rhode Island Red, White Leghorn, Cornish, Red Jungle Fowl, Luxi Game, and Zhangzhou Game lacked some daily weight gain and FCR data. Similarly, Hongshan and Tibetan chickens missed some FCR data, while Silky, Henan Game, Xishuangbanna Game, and Turpan Game lacked data on daily weight gain, market day/end day, and FCR. These compiled results are presented in Table 2 (see appendices).

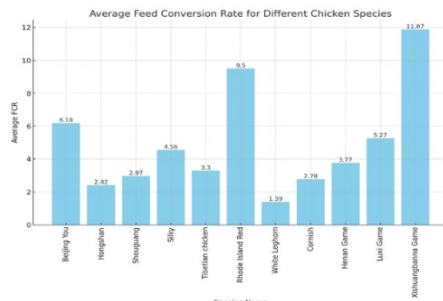
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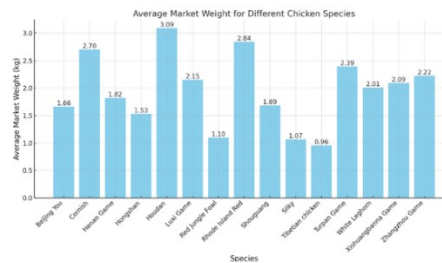
Figure 1B illustrates that Houdan chickens exhibited the highest average market weight at 3.08kg, while Tibetan chickens had the lowest at 0.96kg. This result suggests that Tibetan chickens might be less valuable in typical market conditions but could have been selected for other traits, such as survival in high-altitude environments, which are valuable in specific contexts.

Figures 1C and 1D present the daily weight gain and average daily weight gain across different chicken strains. The data showed that Shouguang chickens are the most efficient in terms of daily weight gain, while Tibetan chickens are the least efficient. Each dot in Figure 1C represents an individual experimental result, showing the variance within species, while Figure 1D averages these results to provide a clearer comparison across species.

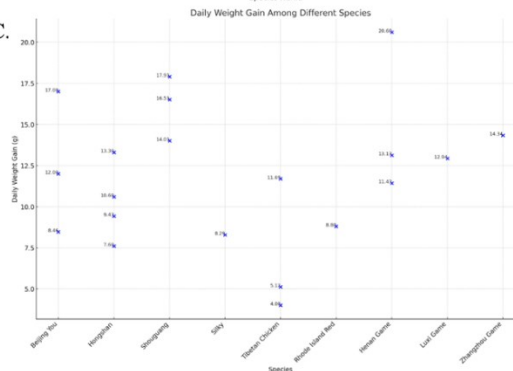
Figure 1: A.



B.



C.



D.

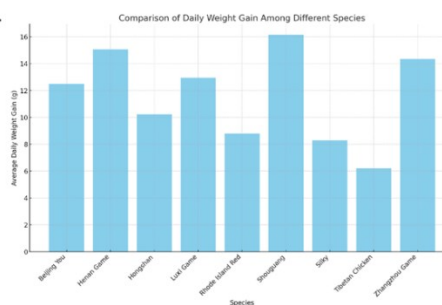


Figure 1. Performance Metrics for Different Chicken Species

- The bar graph represents the average market weight (in kilograms) of various chicken species, $n = 11$. Each bar indicates a specific species, and the height of the bar corresponds to its average market weight.
- This bar graph shows the average feed conversion rate (FCR) for different chicken species, $n = 15$. The FCR is a measure of the efficiency with which the chickens convert feed into body weight, with lower values indicating better efficiency.
- The scatter plot illustrates the daily weight gain (in grams) for various chicken species, $n = 9$. Each point represents a species, and the position along the y-axis shows the average daily weight gain for that species.
- This bar graph compares the average daily weight gain (in grams) among different chicken species, $n = 9$. The height of each bar indicates the average weight gain per day for the corresponding species.

To explore the genetic underpinnings of these traits, we conducted a Genome-Wide Association Study (GWAS). The Manhattan plot (Figure 2A) illustrates the p-values across the entire genome for each chromosome, with the x-axis representing the chromosomes in genomic order and the y-axis showing the $-\log_{10}$ transformation of the p-values. This plot allows for easier visualization of the

statistical significance of SNP associations with traits. A red line marks the genome-wide significance threshold set at 5×10^{-8} , with points above this line indicating significant SNPs. Our analysis revealed that all chromosomes contained SNPs above this threshold, with one particularly significant SNP (AX-76399137) on chromosome 3. Figure 2B provides a regional association plot for this SNP, which shows no significant association with nearby SNPs, suggesting that AX-76399137 may be an isolated marker of interest.

The QQ plot (Figure 2C) serves as a visual check for the distribution of observed p-values against what would be expected under the null hypothesis of no association. The significant deviation from the reference line, particularly at smaller p-values, indicates a strong association between the genome and market weight, suggesting the presence of genetic factors influencing this trait.

Figure 2.

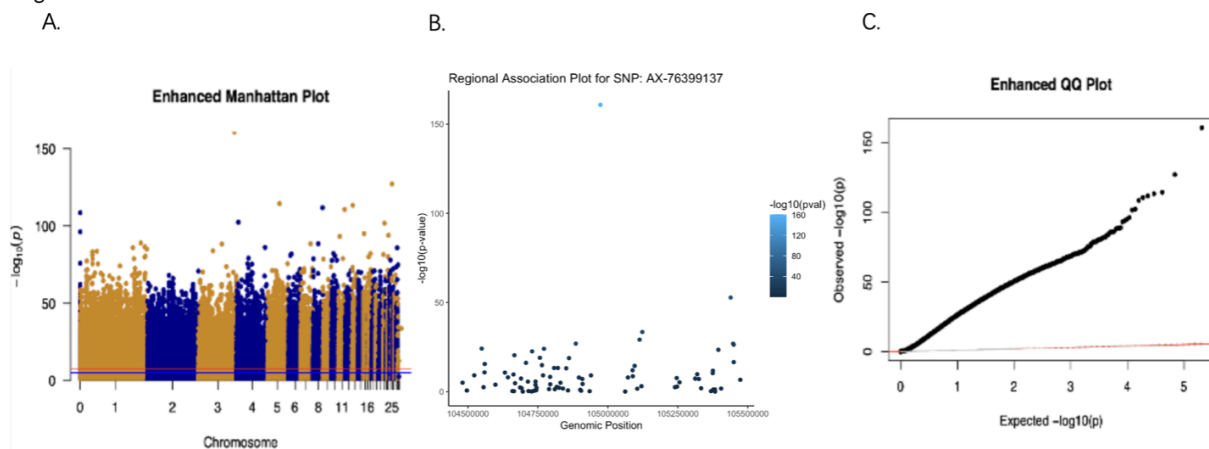


Figure 2. Genome-Wide Association Study (GWAS) in Chicken Species

- A. Results of a genome-wide association study (GWAS), showing the significance of associations between genetic variants and a trait of interest. The x-axis represents the chromosomes, and the y-axis represents the negative logarithm of the p-value, indicating the strength of the association. The threshold line indicates the significance level for identifying important genetic loci.
- B. Regional association plot for the SNP AX-76399137, indicating the significance of the genetic association in the specified genomic region. The x-axis represents the genomic position, and the y-axis represents the $-\log_{10}(\text{p-value})$, with a higher value indicating stronger evidence of association. The color gradient visualizes the level of significance, with darker colors representing higher $-\log_{10}(\text{p-value})$ values.
- C. This quantile-quantile (QQ) plot compares the observed distribution of p-values from a GWAS to the expected distribution under the null hypothesis of no association. Deviations from the red line suggest the presence of genetic associations. The x-axis represents the expected $-\log_{10}(\text{p})$ values, while the y-axis represents the observed $-\log_{10}(\text{p})$ values.

We also performed a Principal Component Analysis (PCA) to visualize data structure and variance. The scree plot (Figure 3A) shows that the first two dimensions captured very little variance (0.3% in Dim 1 and 0.2% in Dim 2), indicating that the data are high-dimensional with no single dimension capturing much of the variance. The PCA cos2 plot (Figure 3B) identifies variables best represented by the first two dimensions, with higher cos2 values indicating better representation. Most variables had low cos2 values, suggesting poor representation in these dimensions. Figure 3C further illustrates this by showing that only a few variables significantly contribute to Dim 1 and Dim 2, indicated by longer vectors and green coloring, while most SNPs cluster near the origin, reflecting their poor representation.

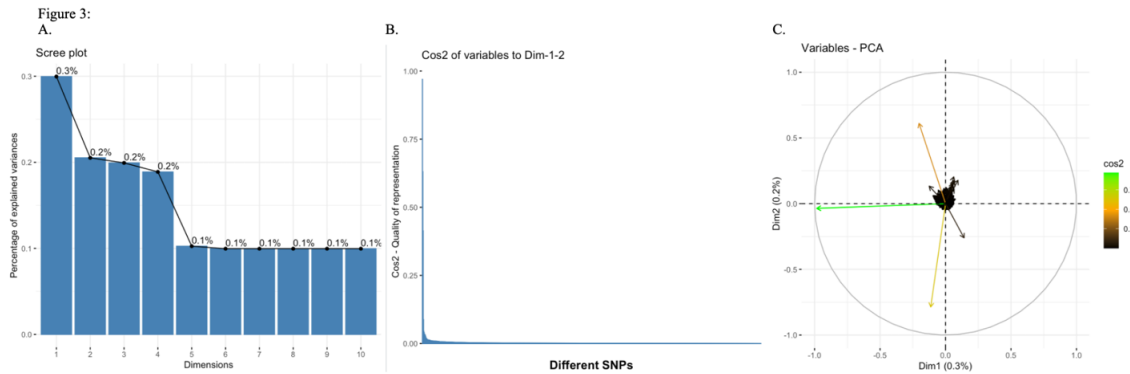


Figure 3. Comprehensive Analysis of Principal Component Analysis (PCA) Results

- The scree plot depicts the percentage of total variance explained by each principal component. The x-axis represents the principal components, and the y-axis shows the percentage of explained variance. The plot helps in identifying the components that capture the most variance in the data.
- The cos2 plot illustrates the quality of representation of each variable on the first two principal components. The x-axis lists the variables, and the y-axis shows their cos2 values. Higher values suggest that the variable is well represented by these two components.
- The PCA biplot represents the variables in the dataset projected onto the first two principal components. The arrows indicate the direction and magnitude of each variable's contribution to the principal components, while the color gradient (from brown to green) shows the quality of representation (cos2 values), with green indicating better representation.

4. Discussion

4.1. Feed Conversion Rate (FCR)

FCR is a key measure of livestock production efficiency, as it reflects how well a species converts feed into body mass. It is calculated by dividing the amount of feed consumed by the body weight gained for average in different poultry experiments. Our results (Figure 1A) show that White Leghorn chickens have the lowest FCR (average 1.39), indicating the highest feed efficiency, while Xishuangbanna Game chickens have the highest FCR (11.87), indicating the least efficiency. A lower FCR is more desirable because it indicates that the chicken is more efficient in converting feed into body mass and increasing the market weight. These findings are critical for breeding programs focused on improving feed efficiency, as selecting for lower FCR could lead to significant cost savings in poultry production within the same amount of feed but increasing meat production. Figure 1B illustrates that Houdan chickens exhibited the highest average market weight at 3.08kg, while Tibetan chickens had the lowest at 0.96kg. This result suggests that Tibetan chickens might be less valuable in typical market conditions but could have been selected for other traits, such as survival in high-altitude environments, which are valuable in specific contexts.

4.2. Market weight

Market weight is a crucial factor for poultry processors. More weights or larger for a bird is probably more meat yield for this animal, aiming for higher weights is to maximize profits. However, this can lead more feeds for farms to raise larger birds, so this is the reason we also need to consider about FCR. From Figure 1B, the Houdan chicken's high market weight (average 3.08kg) suggests it is a desirable breed for commercial production. In contrast, Tibetan chickens have the lowest average market weight (0.96kg), which could make them less desirable for conventional markets. However, their selection for survival in high-altitude environments indicates they have been bred for different purposes, highlighting the importance of context when selecting breeds.

4.3. Daily Weight Gain

Daily weight gain offers a detailed measure of growth efficiency over time, which is crucial for long-term productivity. A higher daily weight gain can reduce the overall time for birds to reach market weight, which also meaning that it can decrease cost for feeding and housing. From Figure 1D, Shouguang chickens, with the highest average daily weight gain (approximately 16 grams per day), are the most efficient species, while Tibetan chickens, with only 6 grams per day, are the least efficient. These findings suggest that selecting for higher daily weight gain could improve overall production efficiency.

4.4. Manhattan Plot Analysis

A Manhattan plot is a scatter plot used in genome-wide association studies (GWAS) to display the results of multiple genetic markers across the genome. The significance threshold line on the Manhattan plot represents a critical value that distinguishes statistically significant genetic associations from associations that may arise due to random factors. The Manhattan plot (Figure 2A) reveals significant genetic markers across all chromosomes (mostly above the significance threshold line), with one SNP (AX-76399137) on chromosome 3 being particularly notable. However, the lack of association with nearby SNPs in the regional plot (Figure 2B) suggests that this SNP may be an isolated genetic marker of interest. This could inform future studies aimed at understanding the genetic architecture of market weight and other traits.

4.5. QQ plot Analysis

The QQ plot (Figure 2C) shows a strong positive relationship between expected and observed results, with significant deviations indicating strong associations. This suggests that the observed genetic markers are likely influencing market weight, emphasizing the importance of these findings in the broader context of poultry genetics.

4.6. PCA Analysis

PCA reduces the dimensionality of the data, making it easier to identify patterns, but in this case, the low variance explained by each component suggests a complex underlying genetic architecture. The PCA results indicate that the data are highly complex, with no single dimension capturing much variance (Figure 3A). This suggests that multiple factors contribute to the traits under study, making it challenging to identify clear genetic predictors. However, the few variables that are well represented in Dim 1 and Dim 2 (as shown in Figure 3B and 3C) could provide a starting point for further investigation.

5. Conclusions

The weight gain of different chicken strains can be determined by different factors, such as the genes and experiment end time/ market day. From comparing between the game bird, broiler bird and layers, we get the Rhode Island red, Houdan, and Cornish to be the largest market weight species. From the genomic data, we can find the relationship between market weight and genetic information, which has a strong association.

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Appendices

Table 1. Real data collected from other experiments and reliable websites, related to the existing genomic data

Name	Weight Range (kg)	Count
Cornish	1.81 - 2.72	10
Turpan Game	2.58 - 4.22	10

Table 1. (continued).

Zhangzhou Game	1.56 - 2.76	11
Xishuangbanna Game	1.42 - 2.05	10
Luxi Game	2.10 - 2.55	10
Henan Game	2.25 - 3.50	11
Houdan	2.49 - 3.40	86
Rhode Island Red	2.90 - 3.90	478
White Leghorn	2.00 - 2.70	230
Silkies	1.36 - 1.81	89
Shouguang	2.00 - 2.55	109
Tibetan	0.70 - 1.52	41
Hongshan	1.80 - 2.10	96
Beijing You	1.40 - 1.60	56
Red Jungle Fowl	0.50 - 1.10	7

Table 2. Real data collected from other experiments and reliable websites

Species	Daily Weight Gain (g)	Market day/ End Day (days)	Market Weight/ end weight (kg)	Average FCR	FCR	References
Beijing You	12	110	1.5	6.185	5.28	[6-10]
Beijing You	17	140	2.2			
Beijing You		98	1.398			
Beijing You	8.465	175	1.54		7.09	
Hongshan	7.6	245	1.73			[11-13]
Hongshan	10.6	120	1.31	2.425	2.41	
Hongshan	9.43	120	1.13		2.44	
Hongshan	13.3	150	1.95			
Shouguang		140	2.55			[14-16]
Shouguang	14.01	70	1.02	2.967	3.22	
Shouguang	16.51	90	1.52		3.02	
Shouguang	17.91	90	1.65		2.66	
Silky			1.585	4.56	3.9	[17-20]
Silky	8.29	59	0.517		5.22	
Silky		183	1.1			
Tibetan Chicken	11.69	86	1			[21-24]
Tibetan Chicken	4	300	1.2			
Tibetan Chicken	5.12	103	0.525			
Tibetan Chicken	4	277.5	1.11	3.3	3.3	
Houdan		119	3.15			[25-29]
Houdan		119	3.29			
Houdan		119	2.835			
Rhode Island Red		98	3.4			[29-32]
Rhode Island Red		98	3.405			
Rhode Island Red		98	3.175			

Table 2. (continued).

Rhode Island Red	8.8	154	1.394	9.5	9.5
White Leghorn		112	2.35		[29,33-36]
White Leghorn		112	2.38		
White Leghorn		112	2.95		
White Leghorn		84	0.36	1.39	1.39
Cornish		49	2.265		[29,37-39]
Cornish		49	4.195	2.775	3.5
Cornish		35	1.65		2.05
Red Jungle Fowl		200	0.943		[40-42]
Red Jungle Fowl		84	1.25		
Henan Game			2.875		[43-46]
Henan Game	20.6	91	1.92	3.77	3.77
Henan Game	13.13	84	1.27		
Henan Game	11.43	84	1.22		
Luxi Game	12.935	180	2.325		[10,44,47-50]
Luxi Game		168	2.15		
Luxi Game		183	2.67	5.27	5.27
Xishuangbanna Game			1.735		[44,51,52]
Xishuangbanna Game		300	2.61	0.049	13.22
Xishuangbanna Game		300	1.93		10.52
Zhangzhou Game		240	2.76		[10,44,53-56]
Zhangzhou Game	14.34	154	1.41		
Zhangzhou Game	14.34	230	2.5		
Turpan Game			2.4		[10,44,57,58]
Turpan Game		240	2.52		
Turpan Game		180	2.25		