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PERFORMANCE EVALUATION OF SENTUL GRAY CHICKEN AND THEIR ASSOCIATION WITH TLR1A GENE POLYMORPHISM

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Abstract

The study examined the association between TLR1A gene polymorphism in exon 4 and the performance of Gray Sentul chickens. Conducted at the Jatiwangi Poultry Breeding Development Center. DNA from 30 males and 30 females was analyzed using PCR and sequencing to identify Single Nucleotide Polymorphism (SNPs). Data processing was performed using BioEdit and MEGA 11. Results revealed five mutations in males (g.775T>C, g.844 T>A, g.858C>T, g.983C>T, and g.1163G>A) and three in females (g.721G>A, g.983C>T and g.1163G>A). Males exhibited higher body weights, with optimal growth occurring between 1 and 2 months. Peak egg production occurred at 41 weeks (HDP 44.97%), and the highest egg weight (46.93 g) at 55 weeks. Specific SNPs associated with performance traits include g.775T>C for body weight in males and g.1163G>A for egg production. This study concludes that the TLR1A gene can be used as a genetic marker to improve the performance of grey Sentul chickens.
Keywords: TLR1A Gene, Mutation, Gray Sentul Chicken, Performance

EVALUASI PERFORMA AYAM SENTUL KELABU DAN HUBUNGANNYA DENGAN POLIMORPHISME GEN TLR1A

Abstrak

Penelitian ini mengkaji kaitan antara polimorfisme gen TLR1A pada ekson 4 dan performa ayam Sentul Kelabu. Penelitian dilakukan di Balai Pengembangan Perbibitan Ternak Unggas Jatiwangi. DNA dari 30 pejantan dan 30 betina dianalisis menggunakan PCR dan sequencing untuk mengidentifikasi Single Nucleotide Polymorphism (SNP). Pengolahan data menggunakan BioEdit dan MEGA 11. Hasil penelitian menunjukkan lima mutasi pada pejantan (g.775T>C, g.844 T>A, g.858C>T, g.983C>T, dan g.1163G>A) dan tiga pada betina (g.721G>A, g.983C>T, dan g.1163G>A). Pejantan menunjukkan berat badan lebih tinggi, dengan pertumbuhan optimal pada usia 1–2 bulan. Produksi telur puncak terjadi pada 41 minggu (HDP 44,97%), dan berat telur tertinggi (46,93 g) pada 55 minggu. SNP tertentu yang berhubungan dengan sifat performa meliputi g.775T>C untuk berat badan pada jantan dan g.1163G>A untuk produksi telur. Penelitian ini menyimpulkan bahwa gen TLR1A dapat digunakan sebagai penanda genetik untuk meningkatkan performa ayam Sentul kelabu.
Kata kunci: Gen TLR1A, Mutasi, Ayam Sentul Kelabu, Performa

INTRODUCTION

Livestock farming is a crucial sector in food production, supplying essential animal proteins such as meat, milk, and eggs. In Indonesia, poultry, particularly chickens, plays a dominant role due to their affordability and accessibility. Indigenous chicken breeds, such as the Sentul chicken, are especially valued for their superior taste, ease of management, and robust immune systems. Sentul chickens are native to West Java, specifically from the Ciamis District, and are recognized as one of Indonesia's 32 indigenous chicken breeds (Ministry of Agriculture No. 698/Kpts/PD.410/2/2013). The Jatiwangi Poultry Development and Breeding Center (BPPTU) has led efforts to enhance this dual-purpose breed, capable of producing both meat and eggs, since 2012, with a focus on improving

genetic traits related to growth, productivity, and disease resistance.

Performance studies on Sentul chickens reveal significant potential in both weight gain and egg production. They exhibit an average growth rate of 33.85 ± 2.83 g/day, reaching 1.193 kg by three months of age. Additionally, they can lay 12-30 eggs per cycle (Khairiyah et al., 2023), making them an attractive option for small-scale poultry farming.

Genetic factors, particularly the TLR1A gene, play a pivotal role in understanding the immune response of the Sentul chicken, which influences performance indicators such as chicken weight, egg weight, egg production, and mortality rate. Toll-like receptors (TLRs) are vital components of the immune system, detecting pathogens and initiating defense mechanisms. TLR1A specifically impacts growth, egg production, and disease resistance (Berghof et al., 2018; Rehman et al., 2021). Variations in this gene, such as single-nucleotide polymorphisms (SNPs), can significantly influence the breed's productivity and resilience. SNP-based marker-assisted selection (MAS) offers a precise method for breeding superior livestock.

The aim of the research is to evaluate the performance of Sentul gray chicken and their association with TLR1A gene polymorphism at BPPTU Jatiwangi. By examining TLR1A gene polymorphisms and their association with growth, egg production, and disease resistance, the research aims to enhance the genetic potential of Sentul chickens. Such advancements contribute to the development of a more sustainable and resilient poultry industry in Indonesia.

MATERIALS AND METHODS

Animal Resources and Phenotypic Measurements

The study was conducted at the Jatiwangi Poultry Development and Breeding Center (BPPTU), under the Department of Food Security and Livestock, West Java Province, Indonesia. Sampling was conducted from 2023 to 2024, with laboratory analyses performed at the Faculty of Animal Husbandry, Universitas Padjadjaran, in 2024. The study included 142 female Sentul gray chickens, aged 23–60 weeks, for egg production and egg weight data, as well as 69 male and 142 female Sentul gray chickens, aged 1–22 weeks, for body weight (BW) measurements. All chickens were kept under an intensive system using individual battery cages measuring 30 × 30 cm, located in different sections based on sex (A.31 for females and E.1 for males).

Phenotypic traits were recorded meticulously, including egg production, egg weight, body weight, and mortality. The feeding process is specifically tailored for each growth phase: starter feed, grower feed, and layer feed. Water was provided ad libitum, and artificial insemination was used as the breeding method. Equipment such as analytical scales, digital hanging scales, and individual tags were used to ensure accurate recording of phenotypic data.

Polymorphism Analysis

Blood samples were collected from the wing vein using 3 mL syringes and stored in EDTA-coated vacutainers. DNA was extracted using standard protocols and amplified via PCR targeting the TLR1A gene, with primers designed using Primer-BLAST (NCBI). The forward primer sequence was 5'-GCCAATCTGTCAGGAATTTGGG-3', and the reverse primer was 3'-GCTGGTCATGAAGCTCACCT-5', amplifying an 826 bp fragment. PCR reactions were carried out with a total volume of 25 µL containing 2 µL DNA, 9.5 µL nuclease-free water, 0.5 µL of each primer, and 12.5 µL Green Master Mix (Promega®), using a LongGene® A600 thermocycler.

The amplification process involved pre-denaturation at 94°C for 2 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 58°C for 1 minute, extension at 72°C for 1 minute, and a final extension at 72°C for 5 minutes. The PCR products were visualized using 1.2% agarose gel electrophoresis with DSRed Nucleic Acid Stain, and the results were examined under a UV transilluminator.

Data Analysis

The study involved a descriptive analysis of primary data collected. For statistical analysis, data on body weight, egg production, and egg weight were summarized using descriptive statistics, such as minimum, maximum, mean, standard deviation, and coefficient of variation. Genetic polymorphism was examined through genotype frequency,

allele frequency, and heterozygosity calculations with PopGene32. The association between SNP genotypes and performance traits was analyzed using BioEdit and MEGA 11. The normality of the data was assessed using the Shapiro-Wilk test. Normally distributed data were analyzed by ANOVA and t-tests, while non-normally distributed data were subjected to the Kruskal-Wallis test and the Mann-Whitney U test. A simple linear regression model was used to determine the relationship between the TLR1A gene and performance traits using SPSS 27. The regression model was defined as:

$$\gamma=\beta0+\beta1X+\epsilon$$

Where γ is the dependent variable (TLR1A), X is the independent variable (egg production, egg weight, body weight, and mortality), $\beta0$ is the intercept, $\beta1$ is the coefficient of X, and ϵ is the error term. Statistical significance was determined at $p<0.05$.

RESULT AND DISCUSSION

Body Weight

The body weight data of Sentul chickens revealed that male chickens had a higher growth rate than females. For males, the highest and lowest body weights at 22 weeks were 2,360 g and 1,730 g, respectively, and 2,270 g and 1,080 g for females, resulting in average weights of 2,077.71 g and 1,774.47 g, respectively. The higher growth rate of male chickens was likely due to the influence of androgen hormones. Younger chickens experience the most rapid growth and highlighted that older chickens show a deceleration in growth. as suggested by Jones (2018), which linked hormonal differences to varying growth patterns. However, environmental factors, including diet and management practices, may also play a significant role in influencing growth, which could explain the differences in body weights between Sentul chickens and those from other studies.

Egg Production and Weight

The average egg production for Sentul chickens reached its peak at 41 weeks of age, with a Hen Day Production (HDP) rate of 44.97% from 142 hens. Egg production began at 23 weeks, with an initial HDP of 11.97%, which gradually increased until it reached its peak at 41 weeks, after which it declined to 26.71% by 60 weeks. Proper nutritional management plays a key role in egg yield. The importance of balanced nutrition in maintaining egg production. Additionally, environmental factors like cage density and health management are crucial for optimizing productivity, as suggested by Xin et al. (2020). These insights underscore the importance of proper care to maintain optimal egg production throughout the laying period.

Egg weight in Sentul chickens displayed a consistent increase over time, with the heaviest eggs recorded at 55 weeks (46.93 g). This result is consistent with the well-documented trend that older hens tend to lay larger eggs, as seen in the studies of Jaelani et al. (2016). The egg weight ranged from 25 g to 59 g, indicating variability in size, with environmental factors such as temperature, humidity, and health management playing a significant role. Research by Ransome et al. (2020) and Chen et al. (2019) demonstrated that environmental conditions, such as temperature and humidity, also contribute to variations in egg weight, underscoring the importance of effective management to optimize both egg size and quality in Sentul chickens**.**

Polymorphism of the TLR1A Gene

The TLR1A gene in Sentul chickens, located on exon 4, spans a target sequence of 826 base pairs encoding 818 amino acids. Genetic analysis using primers designed for SNP detection revealed five mutations in male chickens and three in females. These mutations include synonymous SNPs, such as g.858C>T (L286L) in males, and nonsynonymous mutations like g.775T>C (Y249H), g.844T>A (F282I), G.858 C>T and g.983C>T (T328M) in males, with g.721G>A (V241M), g.983C>T (T328M), and g.1163G>A (S309N) in females. Synonymous mutations, although not altering amino acid sequences, could impact mRNA structure or stability, whereas nonsynonymous SNPs may affect protein function, thereby influencing the immune response. This diversity, particularly in male chickens, aligns with previous studies, such as those by Kristofich et al. (2018), which indicate that synonymous mutations can modify gene expression despite not changing the protein sequence. The identified nonsynonymous mutations, like g.775T>C, are likely to have a more profound

effect on protein functionality, potentially enhancing immunity and adaptive traits in the Sentul chicken population.

Genotype, Allele Frequencies, and Heterozygosity

In male Sentul chickens, genotypes at five SNP loci predominantly displayed homozygous dominance. For instance, g.775T>C (CC genotype, 0.93 frequency) and g.844T>A (TT genotype, 0.93 frequency) exhibited highly significant homozygous patterns. Similarly, g.858C>T showed a CC frequency of 0.87, and g.1163G>A a GG frequency of 0.8. However, g.983C>T diverged slightly with GG at 0.9, alongside a noticeable presence of the heterozygous GA genotype at 0.1. Among females, genotypic dominance was consistent, particularly at loci such as g.721G>A, where the GG genotype was observed at a frequency of 0.95. According to McGrath (2021), such homozygous dominance may result from selective breeding or genetic drift. Genotypes with the highest frequencies (e.g., CC at g.775T>C and GG at g.721G>A) predominated over less frequent ones, such as heterozygous variants (e.g., CT at g.858C>T or GA at g.983C>T).

Major alleles dominated all observed loci, with frequencies like C at g.775T>C (0.93), T at g.844T>A (0.93), and C at g.858C>T (0.87). Notably, g.1163G>A showed a G allele frequency of 0.8, while g.983C>T presented a relatively lower major allele frequency at 0.9 for G. For females, similar trends persisted, with a dominant G at g.721G>A (0.95) and C at g.983C>T (0.93). These patterns align with other studies, such as those by Berghof et al. (2021), which highlight that high major allele frequencies in TLR1A loci are critical for traits like innate immunity. The most frequent alleles (C or T at various loci) surpassed the minor allele frequencies (e.g., A at g.1163G>A with 0.2). According to Berghof et al. (2021), the high frequencies of major alleles in local chicken breeds are attributed to limited gene flow and the adaptive advantages they confer.

Heterozygosity values demonstrated significant reductions compared to expectations. For example, in males, g.775T>C showed an observed heterozygosity (Ho) of 0.07 versus an expected heterozygosity (He) of 0.13. Similarly, g.1163G>A exhibited an Ho of 0.2 against an He of 0.32. For females, heterozygosity followed the same trend, with loci such as g.721G>A (Ho = 0.05; He = 0.095) exhibiting reduced genetic diversity. Berghof et al. (2021) associate low heterozygosity with selective pressures or inbreeding, which can concentrate advantageous alleles. Loci with the lowest heterozygosity (e.g., g.983C>T in males and g.721G>A in females) signified the strongest deviations. In contrast, loci with moderate heterozygosity, such as g.1163G>A in males, suggested slightly higher genetic variation.

Haplotype Polymorphism of TLR1A

In the analysis of haplotype polymorphism in the TLR1A gene of Sentul Gray chickens, significant genetic diversity was observed between male and female populations. Males exhibited six haplotypes derived from five SNP loci, with Haplotype 1 (T-T-C-C-G) being the most prevalent at 43.33%, contrasting with the least common Haplotype 6 (T-A-C-C-G) at 3.33%. Conversely, females displayed five haplotypes identified from three SNP loci, with Haplotype 1 (G-C-G) overwhelmingly predominant at 76.67%. This marked variation in haplotype distribution underscores the complexity of the TLR1A gene and its potential functional significance. The high-frequency haplotypes may play a pivotal role in influencing traits such as immune response, aligning with studies by Smith et al. (2019) and Johnson and Lee (2022), which highlighted the impact of SNP variability on gene functionality.

Association of TLR1A Gene Polymorphism with Body Weight

The association between TLR1A gene polymorphism and body weight in male chickens showed variations in body weight at different ages. The SNP g.775 T>C of the body weight (BW) of one day old chick (DOC) had a Mann-Whitney test value of 0.451, indicating no significant difference between TT and TC genotypes, with similar results for SNP g.844 T>A (0.245), SNP g.858 C>T (0.645), SNP g.983 C>T (0.951), and SNP g.1163 G>A (0.481). At 11 weeks of age, SNP g.775 T>C (0.314) and other SNPs also showed no significant differences. However, at 22 weeks, SNP g.775 T>C showed a significant difference (T-test = 0.007), with the TT genotype having higher body weight. In females, the SNP g.721 G>A and others showed no significant effect at one day, 11 weeks, or 22 weeks of age. Previous

studies (Yang et al., 2021; Wang et al., 2017) suggested that SNP variations in the TLR gene could affect poultry traits, though results varied across populations. Li et al. (2018) and Lee et al. (2020) also noted that genetic influence on growth is complex and interacts with environmental factors, aligning with this study's findings on Sentul chickens.

Association of TLR1A Gene Polymorphism with Egg Production and Weight

The study investigated the association between TLR1A gene polymorphisms and egg production traits in Sentul chickens, focusing on three SNP loci: g.721 G>A, g.983 C>T, and g.1163 G>A. SNP analysis on egg production in hens revealed different patterns. At 30 weeks, SNP g.721 G>A (0.426), g.983 C>T (0.359), and g.1163 G>A (0.603) showed no significant effect. At 40 weeks, SNP g.721 G>A (0.136) and g.983 C>T (0.845) also had no effect, but SNP g.1163 G>A (0.027) showed a significant difference, with the GA genotype producing more eggs than GG. Similar results were observed at 50 weeks, where SNP g.1163 G>A (0.012) had a significant effect, and at 60 weeks (0.004), confirming the GA genotype's higher productivity. In contrast, SNP g.721 G>A and g.983 C>T showed no impact across all ages tested. These findings align with Sari et al. (2020), who highlighted TLR1A's role in innate immunity, suggesting SNP g.1163 G>A as a potential genetic marker for high-yield laying hens.

SNP analysis on egg weight in hens at different ages showed no significant differences among genotypes. At 30 weeks, SNP g.721 G>A (0.721), g.983 C>T (0.183), and g.1163 G>A (0.830) had no significant effect. Similar results were found at 40 weeks, with p-values of 0.386, 0.176, and 0.176, respectively. At 50 weeks, SNP g.721 G>A (0.097) and g.983 C>T (0.067) showed a greater tendency for variation, but none were statistically significant. At 60 weeks, all SNPs (0.222, 0.169, and 0.533) remained insignificant. Duan et al. (2018) suggest that further research is needed to evaluate the genetic interactions and environmental influences on egg production in Sentul Gray chickens.

Mortality rates were remarkably low, with no deaths recorded among 30 male and 30 female Sentul gray chickens from 23 to 60 weeks. While mortality was not directly associated with TLR1A polymorphisms, the gene's role in immune response and inflammation may indirectly support survival under environmental stress. Similar findings have been reported in other breeds (Li et al., 2018), emphasizing the importance of genotype-environment interactions. These results suggest that optimizing environmental and management conditions could enhance the practical application of TLR1A polymorphisms as genetic markers for improving production traits in chickens. At BPPTU Jatiwangi, temperature (20-35°C) and humidity (60-95%) significantly affect chicken body weight. Extreme temperatures and humidity levels cause stress, leading to changes in feed intake. High heat can reduce appetite, while cold conditions or high humidity may increase feed consumption, both of which can impact growth and body weight. Proper temperature and humidity control are essential for maintaining optimal feed intake and achieving target weight in chickens.

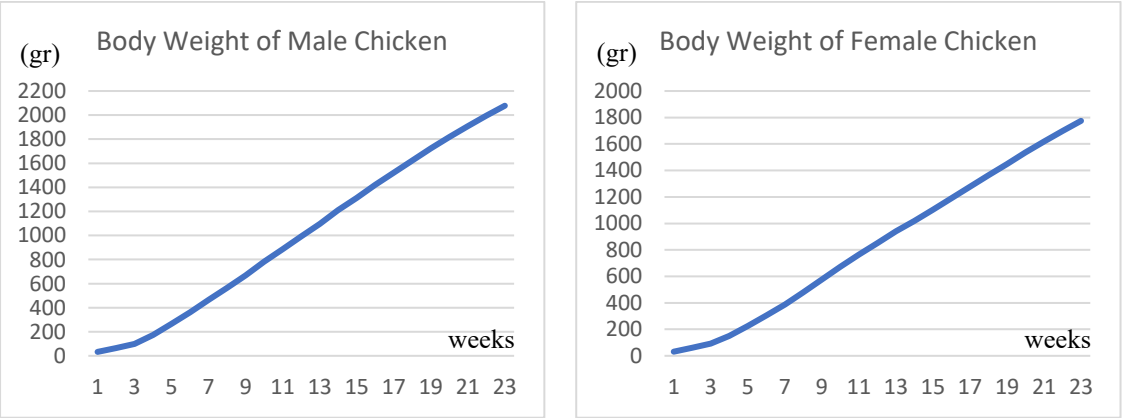

Figure 1. The Body Weight Data of Sentul Chickens

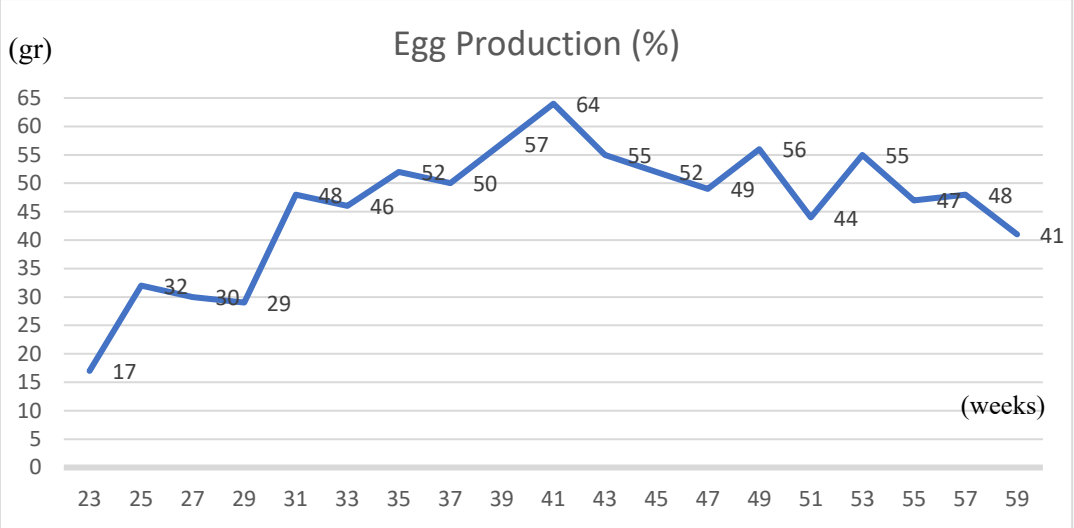

Figure 2. The Average Egg Production for Sentul Chickens

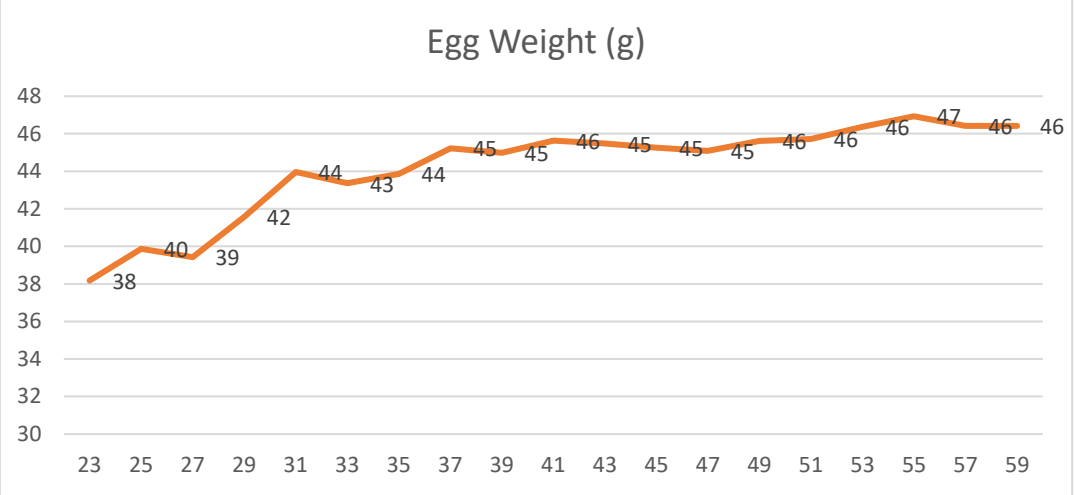

Figure 3. The Average Weight Production for Sentul Chickens

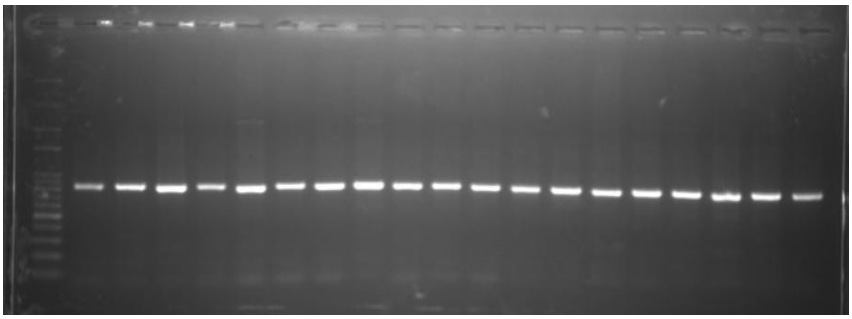

Figure 4. The Amplification Product of TLR1A Gene Fragment 826 bp

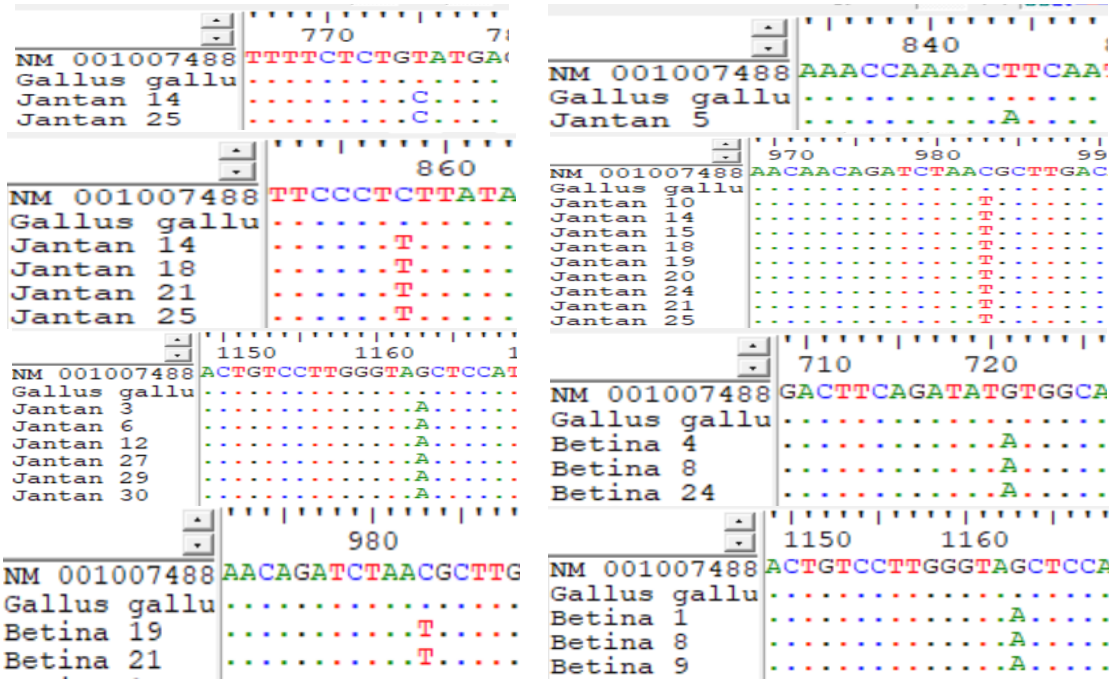

Figure 5. Identification of TLR1A Gene Polymorphism, Indicates Each Mutation

Table 1. Genotype Frequency, Allele Frequency, and Heterozygosity (male)

Mutation	SNP	Genotype Frequency			Allele Frequency		Ho	He
g.775 T>C	Non-synonimous	CC	CT	TT	C	T		
Y249H	Tyrosine to Histidine	0.93	0.07	0.0	0.93	0.07	0.07	0.13
g.844 T>A	Non-synonimous	TT	TA	AA	T	A		
F282I	Phenylalanine to Isoleucine	0.93	0.07	0.00	0.93	0.07	0.07	0.13
g.858 C>T	Synonimous	CC	CT	TT	C	T		
L286L	Leucine	0.87	0.13	0.0	0.87	0.13	0.13	0.23
g.983 C>T	Non-synonimous	GG	GA	AA	G	A		
T328M	Threonine to Methionine	0.9	0	0.1	0.9	0.1	0.00	0.18
g.1163 G>A	Non-synonimous	GG	GA	AA	G	A		
S388N	Serine to Asparagine	0.8	0.2	0.00	0.8	0.2	0.20	0.32

Note: Ho= observed heterozygosity; He= expected heterozygosity; s= significant ($p<0.05$).

Table 2. Genotype Frequency, Allele Frequency, and Heterozygosity (female)

Mutation	SNP	Genotype Frequency			Allele Frequency		Ho	He
g.721 G>A	Non-synonimous	GG	GA	AA	G	A		
V241M	Valine to Methionine	0.95	0.05	0.00	0.95	0.05	0.05	0.095
g.983 C>T	Non-synonimous	CC	CT	TT	C	T		
T328M	Threonine to Methionine	0.93	0.07	0.00	0,93	0.07	0.07	0.13
g.1163 G>A	Non-synonimous	GG	GA	AA	G	A		
S309N	Serine to Asparagine	0.95	0.05	0.00	0.95	0.05	0.05	0.095

Note: Ho= observed heterozygosity; He= expected heterozygosity; s= significant ($p<0.05$).

Table 3. Haplotype Polymorphism of TLR1A Gene Male Sentul Chickens

Haplotype	SNP					Frequency (%)
	g.775 T>C	g.844 T>A	g.858 C>T	g.983 C>T	g.1163 G>A	
Haplotype 1	T	T	C	C	G	43,33
Haplotype 2	T	T	C	T	G	20,00
Haplotype 3	T	T	C	C	A	20,00
Haplotype 4	C	T	T	T	G	6,67
Haplotype 5	T	T	T	T	G	6,67
Haplotype 6	T	A	C	C	G	3,33

Table 4. Haplotype Polymorphism of TLR1A Gene Female Sentul Chickens

Haplotype	SNP			Frequency (%)
	g.721 G>A	g.983 C>T	g.1163 G>A	
Haplotype 1	G	C	G	76,67
Haplotype 2	G	C	A	6,67
Haplotype 3	A	C	G	6,67
Haplotype 4	A	C	A	3,33
Haplotype 5	G	T	G	6,67
Total				100

Table 5. Analysis of TLR1A Gene with Female Sentul Chicken Body Weight

Normality Test	Post-hoc Analysis	Variable	SNP	P-Value
Not normally distributed	Man Whitney	BW of Female DOC	g.721	0.32
			g.983	0.586
			g.1136	0.651
Normally distributed	T-Test	BW of 11-week-old Female	g.721	0,829
			g.983	0,376
			g.1136	0,216
Normally distributed	T-Test	BW of 22-week-old Female	g.721	0,873
			g.983	0,353
			g.1136	0,413
Not normally distributed	Man Whitney	BW of Male DOC	g.775	0.451
			g.844	0.245
			g.858	0.645
			g.983	0.951
			g.1163	0.481
Not normally distributed	Man Whitney	BW of 11-week-old Male	g.775	0.314
			g.844	0.268
			g.858	0.830
			g.983	0.518
			g.1163	0.583
Normally distributed	T-Test	BW of 22-week-old Male	g.775	**0,007**
			g.884	0,176
			g.858	0,361
			g.983	0,313
			g.1163	0,325

Table 6. Association Between TLR1A Gene Polymorphism with Body Weight

Sex	SNP	Genotype	n	BW DOC	BW11	BW22
Female	g.721 G>A	GG	27	30,78±3,24	875,37±124,12	1819,07±344,629
		GA	3	35,67±3,06	891,67±105,4	1853,33±416,81
	g.983 C>T	CC	28	31,39±3,59	882,32±122,82	1838,39±349,8
		CT	2	29,5±0,7	802,5±67,18	1600±169,7
	g.1163 G>A	GG	27	31,22±3,6	867,78±124,05	1805±356,88
		GA	3	31,67±3,06	960±17,32	1980±149,08
Male	g.775 T>C	TT	28	32,61±4,28	971,43±53,31	2033±99,4[a]
		TC	2	33,5±2,12	925±63,64	1820±127,28[b]
	g.844 T>A	TT	29	32,79±4,17	967,241±54,7	2013,62±110,85
		TA	1	29	1000	2170
	g.858 C>T	CC	26	32,69±4,42	967,31±50,8	2026,35±99,45
		CT	4	32,5±2,08	975±81,85	1970±190,96
	g.983 C>T	CC	21	33,1±4,38	969,05±53,1	2033,57±96,87
		CT	9	31,67±3,61	966,67±59,58	1984,44±143,54
	g.1163 G>A	GG	25	32,56±4,14	966,4±54,99	2007,4±115,75
		GA	5	33,2±4,66	97854,04	2076±81,42

Description: sample size (n); body weight of day-old chicks (BW DOC); body weight at 11 weeks of age (BW11); body weight at 22 weeks of age (BW22); a,b Different lowercase letters in the same column for each breed indicate significant differences at the $P < 0.05$ level for ducks with different genotypes in the same phenotypic trait.

Table 7. Analysis of TLR1A Gene with Female Sentul Chicken Egg Production

Normality Test	Post-hoc analysis	Variable	SNP	P-Value
Not normally distributed	Man Whitney	P30	g.721	0.426
			g.983	0.359
			g.1136	0.603
Normally distributed	T-Test	P40	g.721	0,136
			g.983	0,845
			g.1136	**0,027**
Normally distributed	T-Test	P50	g.721	0,311
			g.983	0,883
			g.1136	**0,012**
Normally distributed	T-Test	P60	g.721	0,546
			g.983	0,511
			g.1136	**0,004**

Table 8. Association Between TLR1A Gene Polymorphism with Egg Production

SNP	Genotype	N	P30	P40	P50	P60
g.721 G>A	GG	27	9.78±6.82	33±13.97	63.4±21.03	92.11±24.36
	GA	3	17.33±15.5	47±24.56	77.33±33.73	102±24.36
g.983 C>T	CC	28	10.25±8.05	34.25±15.86	64.96±23	93.96±26.87
	CT	2	14.5±7.78	36.5±2.12	62.5±2.12	81±16.97
g.1163 G>A	GG	27	32,37±25,79[a]	94,33±30,07[a]	88,7±21,72[a]	32,37±25,79[a]
	GA	3	52,67±12,96[b]	61,52±19,2[b]	132,67±36,12[b]	52,67±12,96[b]

Description: sample size (n); egg production up to 30 weeks of age (P30); egg production up to 40 weeks of age (P40); egg production up to 50 weeks of age (P50); egg production up to 60 weeks of age (P60); a,b Different lowercase letters in the same column for each breed indicate a significant difference at $P < 0.05$ for ducks with different genotypes within a single phenotypic trait.

Table 9. Analysis of TLR1A Gene with Female Sentul Chicken Egg Weight

Normality Test	Post-hoc analysis	Variable	SNP	P-Value
Not normally distributed	Man Whitney	BT30	g.721	0.721
			g.983	0.183
			g.1136	0.830
Not normally distributed	Man Whitney	BT40	g.721	0.386
			g.983	0.739
			g.1136	0.176
Not normally distributed	Man Whitney	BT50	g.721	0.097
			g.983	0.067
			g.1136	0.350
Not normally distributed	Man Whitney	BT60	g.721	0.222
			g.983	0.169
			g.1136	0.533

Description: sample size (n); first egg weight (BT23); egg weight at 30 weeks of age (BT30); egg weight at 40 weeks of age (BT40); egg weight at 50 weeks of age (BT50); egg weight at 60 weeks of age (BT60).

Table 10. Association Between TLR1A Gene Polymorphism with Egg Weight

SNP	Genotip	BT23	BT30	BT40	BT50	BT60
g.721 G>A	GG (27)	9.15±15.91	25.13±21.36	38.03±18.63	45.23±9.82	43.89.11±12.98
	GA (3)	0	28.33±24.54	43.75±2.76	29.16±25.25	27.78±24.06
g.983 C>T	CC (28)	8.82±15.71	24.13±21.39	38.14±18.29	43.77±12.86	43.68±12.75
	CT (2)	0	43.88±3	45.02±0.32	41.5±0.71	22.63±31.99
g.1163 G>A	GG (27)	7.93±15.26	25.14±21.37	37.63±18.47	43.11±12.98	42.98±15.45
	GA (3)	11	28.22±24.44	47.28±0.98	48.18±3.9	44.9±2.52

Description: sample size (n); first egg weight (BT23); egg weight at 30 weeks of age (BT30); egg weight at 40 weeks of age (BT40); egg weight at 50 weeks of age (BT50); egg weight at 60 weeks of age (BT60).

CONCLUSION

The TLR1A gene was polymorphic in Sentul Gray chickens, with five SNPs identified in males and three in females. Male-specific mutations included four non-synonymous SNPs (g.775T>C, g.844T>A, g.983C>T, and g.1163G>A) and one synonymous SNP (g.858C>T), while females showed three SNPs, including two non-synonymous (g.721G>A and g.983C>T) and one synonymous (g.1163G>A). Non-synonymous SNPs have potential impacts on protein structure and immune function, while

synonymous SNPs influence gene expression. TLR1A affects the body weight of Sentul chickens with SNP g.775 T>C in males, and SNP g.1163 G>A affects egg production, particularly during the later stages of production. SNP g.721 G>A and SNP g.983 C>T influence egg weight. These findings highlight the interaction between genetics and controlled management in improving the performance and productivity of Sentul Gray chickens.

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