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ASSOCIATION OF CYTOCHROME AND NADH GENES POLYMORPHISM WITH GROWTH TRAITS IN TURKEYS SELECTED FOR HIGHER BODY WEIGHT

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ABSTRACT: Increasing growth and meat yield is crucial to turkey breeding goals. Producers may produce birds that grow more effectively by discovering genetic markers linked to improved growth. This study aimed to improve the growth traits of the local Baladi turkeys through the selection for higher body weight (BW) at 6 months of age and to evaluate the relationships between Cytochrome and NADH gene polymorphism with the body weight (BW) of turkeys. Two lines of turkeys were compared: One line (S) was selected for higher body weight at 6 months. The second line is unselected random-bred control (C). Blood samples were collected from 200 turkey chicks one-month-old. Single nucleotide polymorphism between turkey genotypes was determined through DNA sequencing. Results: In Baladi turkeys, the selected line was significantly heavier than the control line in both males (5781.62 vs. 5501.75 g) and females (3376.44 vs. 3200.00 g) following one generation of selection for increased BW at 6 months of age. Realized response in BW increased significantly by 57.32 g per month during the period (0–6) months. Realized heritability estimates for BW at 6 months of age of turkeys were moderate in males (0.26) and females (0.29). A significant association of Cytochrome and NADH genes with body weight at different ages in turkeys was observed. Conclusion: Selection for increased body weight was effective in the genetic improvement of turkeys for growth traits. The Cytochrome and NADH genes can be used as genetic markers in marker-assisted selection programs to improve growth traits in turkeys.

Keywords: Selection, turkeys, body weight, Cytochrome, NADH, genes, polymorphism.

INTRODUCTION

Poultry production is a major economic contributor (Stadnicka *et al.,* 2023). Poultry farming generates numerous job opportunities, particularly in rural settings, where it is a primary income source for many families (Kusumandari and Damanuri, 2024).

Turkeys are mainly raised for meat. The global market for turkey meat has seen significant growth, with production figures reaching approximately 5.8 million tons in 2021 (FAO, 2023), accounting for about 4.2% of total poultry meat production (Kálmán and Szöllősi, 2023). The increased demand for meat worldwide has encouraged farmers and breeders to create turkeys that develop quickly. (Baldi and Gottardo, 2017 and Salter, 2017). Therefore, increasing growth and yield is crucial to the goals of turkey breeding which aim to increase production and reduce expenses. (Begli, *et al.,* 2019 and Abdalla, *et al.,* 2021). The local Baladi turkeys still lag the output of the common varieties. Therefore, additional research is required to genetically characterize this flock and evaluate its genetic diversity for use in crossing, selection, and breeding programs. Growth is a primary selection factor in poultry breeding (Xu *et al.,* 2013, Lyu *et al.,* 2023).

The most advanced molecular method, polymerase chain reaction (PCR), is used to identify different species in meat products. For authenticating meat and meat products, PCR amplification, PCR product sequencing (Amaral et al., 2015), and real-time PCR detection methods were created.

The avian Cytochrome P450 gene, specifically CYP1A5, plays a crucial role in energy production by metabolizing various compounds, including mycotoxins like aflatoxin B1 (AFB1) (Wang *et al.,* 2023 and Yuan, 2024). Furthermore, the presence of NADPH-cytochrome P450 oxidoreductase (POR) is vital for the functioning of Cytochrome P450 monooxygenases, which are responsible for synthesizing endogenous compounds and metabolizing exogenous ones, highlighting the interconnected role of different components in energy production (Zhou *et al.,* 2011). Overall, these findings underscore the significance of avian Cytochrome P450 genes in energy metabolism and maintaining cellular functions in birds. The NADH dehydrogenase gene, also known as ND genes or Complex I genes, encodes subunits of the mitochondrial enzyme complex called NADH dehydrogenase, which is part of the electron transport chain in aerobic respiration. (Jiménez-Gómez *et al.,* 2023). Variations in the avian NADH dehydrogenase gene can impact ATP generation through its effects on enzyme activity, reactive oxygen species production, and metabolic interactions with other enzymes. (Zhou *et al.,* 2011, Wang *et al.,* 2013). Due to the pivotal roles performed with the aid of using the proteins of the somatotropic axis that consist of an increased hormone, IGFs, their excessive affinity receptors, and binding proteins, the genes that code for them are taken into consideration as correct candidate genes to have a look at increase and improvement specifically throughout the early degrees of increase in poultry. These genes are also ideal targets for the development of molecular markers for Marker Assisted Selection (MAS) for faster growth (Xu *et al.,* 2013).

This study aimed to improve the growth of the local Baladi turkeys by applying the selection for higher body weight and assessing the sequences of candidate genes (Cytochrome and NADH) associated with growth in turkeys.

MATERIAL AND METHODS

Study period and location

During the breeding season of 2019, the experimental work for this study was conducted at the Poultry Research Centre, Poultry Production Department, Faculty of Agriculture, Alexandria University, Egypt. Molecular Genetics was performed at the Genetic Engineering and Biotechnology Laboratory, Plant Pathology Department,

Genetic branch, Faculty of Agriculture, Damanhour University, and molecular genetic laboratory, Desert Research Centre, Ministry of Agriculture.

Scheme for mating

A total of 193 birds were used in a random mating system to maintain the Egyptian Local Baladi turkeys' base population (G0) (48 Males and 145 Females). The selected parents (13 Males and 55 Females) were picked from the base population based on their highest 6-month body weight to reproduce the selected line in the first generation (F_1). The first generation (F1) of selection consists of the control (C) line, which was randomly selected from the base population, and the selected line (S), which was begun from the selected parents by mass selection for increased 6-month BW.

At seven months of age, eggs were pedigreed and collected daily for each pen. Four weekly hatches were used. At hatching, poults were pedigreed, and wing banded at one day old. Body weights (BW) of birds at 0, 1, 2, 3, 4, 5, and 6 months of age were recorded individually, and body weight gain (g) during the period (0-6) months of age (BWG). At 4 months of age, birds were sexed. All experimental birds were maintained under similar conditions and received the same managerial treatments. The different rations used were formulated to meet all nutrient requirements as established by NRC (1994).

Statistical analysis

Variation between lines:

Data were analyzed for variation between the lines (S and C) using the general linear model of IBM SPSS Statistic 28 software (IBM, SPSS, 2021). Differences were tested for significance using the Duncan test (Duncan, 1955).

$$Y_{ijklm} = \mu + G_i + s_{ij} + H_k + X_l + e_{ijklm}$$

Where: Y_{ijklm} = observation for each dependent variable, μ = overall mean, G_i = fixed effect of i^{th} line, s_{ij}= random effect of j^{th} sire within i^{th} line, H_k = fixed effect of k^{th} hatch, X_l = fixed effect of l^{th} sex, and e_{ijklm} = random error.

The interaction between the fixed effects was excluded from the model because it was not significant, and the sex effect was excluded from the model for early ages.

Selection measurements:

Selection differential in actual units of measurement was calculated for males and females as the difference between the average body weight at 6 months of age of the parents and the mean of their generation (Falconer and Mackay, 1996). Intensity of selection (i) is the standardized selection differential or selection differential in units of phenotypic standard deviation (σp).

$$i = S/\sigma p$$

The realized response to selection (R) was estimated by the following equation:

$$R_t = (S_t - S_{t-1}) - (C_t - C_{t-1})$$

Where R_t = Realized gain due to selection in t^{th} generation, and S and C = Average performance of the selected and control populations (Guill and Washburn, 1974).

Realized heritability (h^2) of the selected trait (body weight at 6 months of age) was obtained as the ratio of realized response (R) to selection differential (S) (Falconer and Mackay, 1996).

$$h^2 = R/S$$

Molecular Genetic analysis:

Blood sampling

Blood samples were collected from 200 turkey chicks one month old from the offspring in the selected and control lines. About 1 ml of blood was collected from the wing veins of the birds using vacationer tubes containing EDTA for DNA extraction. Blood samples were stored at -20ºC till further analysis.

DNA extraction, primer design, and PCR amplification

Turkey genomic DNA was extracted from the blood samples using Thermo Scientific Mini Kit #K0781, #K0782 (Thermo Fisher Scientific, USA, https://www.thermofisher.com/ie/en/home.html) and then quantified using a spectrophotometer (pg T80). The final concentration was adjusted to 50 ng/ul. PCR primers were designed with NCBI

(https://www.ncbi.nlm.nih.gov/) and primer3 (https://primer3.ut.ee/). PCR amplification was carried out in 25ul reaction volumes containing 1µl DNA, 1µl forward primer, 1µl reverse primer, 12.5 µl master mix, and 9.5 µl nuclease-free water. The amplified PCR products were separated by electrophoresis on 1.5 % agarose in 1X TBE buffer, ethidium bromide, and visualized with UV light of transilluminator (Genetics Nippon, https://www.nippongenetics.eu/en/). Primer sequences and PCR protocols for the studied genes are shown in Table (1).

PCR purification

PCR products were purified using *Geneaid* kits to get a highly purified PCR amplicon of the target regions for each gene from female turkeys that were chosen at random in the selected and control lines.

PCR products sequencing

Forward Sanger sequencing of the purified amplicons was performed to explore the genetic polymorphism among the studied individuals. Sequencing was carried out through the Macrogen sequencing service (Macrogen, South Korea, https://www.macrogen.com/en/main). The sequencing results were aligned using the Bioedit program (V. 7.7.1) to detect the different single nucleotide polymorphisms (SNPs).

RESULTS AND DISCUSSION

Mean of body weight (BW) at different ages:

Means of BW at different ages (0, 1, 2, 3, 4, 5, 6 months) of Baladi turkey by line are presented in Tables (1-3). For the selected line, the means of BW were 48.88, 258.68, 824.21, 1775.31, 2721.46, 3529.45, and 4404.61 g at 0, 1, 2, 3, 4, 5, 6 months, respectively. The corresponding means for the control line were 47.37, 250.40, 814.50, 1726.94, 2665.69, 3394.28, and 3967.25 g. The same trend was observed for body weight gain (0-6 months). At all ages studied, the means of BW in the selected line were significantly higher than those in the control line.

Regression analysis cleared that BW increased significantly by 768.03 and 710.67 g per month within the ages (0-6 months) for the selected and control lines, respectively. The monthly increase of BW of the selected line was significantly higher than that of the control line (Figure 1). This could be explained by using the individual selection to increase BW in the selected line at 6 months**.**

Males had significantly higher BW at 4 and 5 months of age than females (Table 2). Mean BW at 6 months of age was significantly higher in males (5599.07 g) than in females (3419.71g) (Table 3). The same trend was observed for body weight gain (0-6 months) (Table 3).

Selection for 6-month body weight (BW):

Table (4) presents the means of body weight at 6 months of age (g) for Baladi turkey by generation, line, and sex. Body weight means in the base population at 6 months of age were 6441.66 and 3085.51 g for males and females, respectively, with an average of 3920.20 g. Body weight means of the selected parents at 6 months of age were 7500.00 and 3700.00 g for males and females, respectively, with an average of 4426.47 g.

After one generation of individual phenotypic selection for higher BW at 6 months of age (F_1) in Baladi turkey, the selected line (S) was significantly heavier at 6 months of age than the control line (C) in males (5781.62 vs. 5501.75 g), females (3376.44 vs. 3200.00 g), and both sexes (4404.61 vs. 3967.25 g).

A significant increase in the body weight of the selected lines of turkeys was reported in the literature (Clark *et al.,* 2019). The live body weight of turkeys is one of the most important selection traits, determining their meat production quality. The reported levels of the heritability coefficient of live body weight between 0.44 and 0.61 allow a rapid improvement of this trait through extensive selection (Oblakova, 2006).

Selection parameters:

Selection differential & Selection intensity:

Table (5) presents selection differential values and intensity of selection (i) for body weight (BW) at 6 months of age in Baladi turkeys by sex. Selection differential values for body weight at 6 months of age were 1058.34 g in males and 614.49 g in females, with a cumulative value of 1672.83 g for both sexes.

The magnitude of the selection differential depends on two factors: the proportion of the population included among the selected group and the phenotypic standard deviation of the character. The selection differential increases with the decrease of the proportion of the selected group (the increase of selection intensity, i) and the increase of the phenotypic standard deviation of the character. The selection intensity indicates the average of the selected proportion in phenotypic standard deviations (Falconer and Mackay, 1996).

The selection intensity value (i) of BW at 6 months of age for Baladi turkey was greater in males (1.22) than in females (1.00), with a value of (1.06) for both sexes (Table, 5). However, the values of selection differential depend mainly on the available number of parents needed to renew the flock (Falconer and Mackay, 1996).

Realized selection response:

After one generation of selection for higher BW at 6 months of age in Baladi turkey, the realized response of BW was greater in males (279.87 g) than females (176.44 g), with a cumulative value of (437.36 g) for both sexes (Table 5). The realized responses of applying selection for higher BW at 6 months of age were 1.51, 8.28, 9.71, 48.37, 55.77, 135.17, and 437.36 g for the ages (0, 1, 2, 3, 4, 5, 6 months), respectively (Tables 1-3). The realized response in BWG (0-6 months) was 435.85 g due to selection for higher BW at 6 months (Table 3). Regression analysis cleared that realized response in BW because selection for higher BW at 6 months of age, increased significantly by 57.32 g per month during the age (0-6 months) (Figure 2). These findings demonstrate that BW of both sexes increased because of selection for higher BW in Baladi turkeys.

The high responses to selection for BW at 6 months of age of turkeys (Table 5) may be due to the increase in selection intensity, phenotypic standard deviation, and heritability estimate of this trait. This finding was supported by Falconer and Mackay (1996). Additionally, in this study, additive gene action in body weight at the start of selection. Selection is a basic tool to exploit and improve the productive potential of birds (Ahmad *et al.,* 2018). On the other hand, the Short-term selection response might be attributed to alleles segregating in the great response obtained in the present study supporting the hypothesis that there was a considerable population (Fuller *et al.,* 2005).

In research involving selection for body weight (BW) in turkeys, individual selection is crucial. Selection is an important tool for changing gene frequencies to better-fit individuals for one or more breeding purposes. Falconer and Mackay (1996) stated that artificial selection produces changes in gene frequency by separating the adult individuals of the parent generation into two groups, the selected and the discarded that differ in gene frequencies. Taskin *et al.* (2016) concluded that body weight is a very important factor in selection studies, and it also increases the efficiency of the selection program with other selection features. In the turkey sector, breeding goals are primarily focused on enhancing growth characteristics. Selection in the pure lines achieves genetic advances in the turkey sector. Because of its significant influence on carcass value, the expense of producing meat, and the ease of selection brought about by its high heritability and breeding programs, body weight continues to be the most important feature for selection (Case, 2011). Strong favorable genetic associations between the body weight of turkeys at various ages were reported. However, between the ages of 17 and 24 weeks, turkey

body weight has a higher heritability (Abdalla *et al.,* 2022, Nestor, *et al.,* 2008). Working on two lines of commercial turkeys, the F line was selected for a higher 16-week body weight, and the random-bred Control Line 2 (RBC2) was maintained without purposeful selection for any feature. The F-line turkeys are now 2.5 times heavier than the RBC2 turkeys due to 50 generations of selection favoring greater body weight (Clark *et al.,* 2019).

Realized Heritability (h^2):

Realized heritability estimates for BW at 6 months of age in turkeys were moderate in males (0.26) and females (0.29) with an average of (0.26) for both sexes (Table 5).

Working on two lines of commercial turkeys, the line selected for higher 16-week BW, and the random-bred Control Line, Nestor, *et al*. (2000 and 2008) reported that the actual selection differentials after 10 generations of selection were 0.62 kg in males and 0.53 kg in females. In addition, Genetic increases in 16-week BW were 0.19 kg in males and 0.16 kg in females. Genetic increases in 16-wk BW in the F line were positively associated with BW at other ages (8, 20, and 24 weeks). Also, the realized heritability estimates for 16-week BW in the selected line were 0.33 in males, 0.28 in females, and 0.30 in both sexes.

Association analysis of Genes:

Polymerase chain reaction amplification for Cytochrome gene:

As an important candidate gene affecting growth, polymerase chain reaction amplification (PCR) for Cytochrome gene Fragments was amplified using PCR. The amplified product was 660 bp, indicating that the amplicon was Cytochrome for the selected group as shown in Figure (3).

Polymerase chain reaction amplification for NADH gene:

As an important candidate gene affecting growth, polymerase chain reaction amplification (PCR) for NADH gene Fragments was amplified using PCR. The amplified product was 611 bp, indicating that the amplicon was Cytochrome for the selected group as shown in Figure (3).

Association analysis of Cytochrome gene polymorphism and studied traits:

According to sequencing alignment results of the Cytochrome gene, the region between 325-335bp is considered a polymorphic region containing 3 polymorphic SNPs (Figure 4). The individuals carrying the (C) Allele are the selected line, while individuals carrying the (G) Allele are the control line. Results of statistical analysis to detect the association between these SNPs and the phenotypes of the studied traits revealed a significant association between the first SNP and BW at hatch with a mean of 46.79 g for individuals carrying (C) Allele and 42.04 g for those carrying (G) Allele, 1-month BW with a mean of 264.33 g, for individuals carrying (C) Allele and 175.00g for those carrying (G) Allele, 2-month BW with a mean of 754.67 g for individuals carrying (C) Allele and 578.50 g for those carrying (G) Allele, 3-month BW with a mean of 1552.67 g for individuals carrying (C) Allele and 1343.00 g for those carrying (G) Allele, 4-month BW with a mean of 2353.67 g for individuals carrying (C) Allele and 1974.00 g for those carrying (G) Allele, 5-month BW with a mean of 2786.00 g for individuals carrying (C) Allele and 2599.50 g for those carrying (G) Allele, and 6-month BW with a mean of 3160.33 g for individuals carrying (C) Allele and 3094.33 g for those carrying (G) Allele. These results in the present study cleared that the means of BW in the selected line were significantly higher than those in the control line at all ages studied (Table 7).

The second and third SNPs didn`t show any significant association with studied traits. According to the previous results, the first SNP can be used as a genetic marker in marker-assisted selection programs of body weight traits at different ages in turkeys.

Palócz *et al.,* (2019) Studies show that hepatic cytochrome P450 gene expression can be affected by feed additives, which may indirectly influence weight management in chickens. The expression of specific cytochrome genes, such as CYP1A4, has been linked to metabolic

processes that could affect weight gain or loss in avian species. Research on the apoVLDL-II gene indicates that polymorphism at specific loci (VLDL9 and VLDL17) is significantly associated with chickens' body and fat weight. (Musa and Chen, 2007). This suggests that genetic variations in cytochrome-related genes may also play a role in weight regulation among different avian breeds. The cytochrome b gene has been utilized for phylogenetic analysis, revealing relationships among avian species that may correlate with their weight and ecological adaptations. (Sheldon *et al.,* 1999; Awad *et al.,* 2015).

Understanding these relationships can provide insights into how weight and genetic factors interact in avian evolution. While the focus has been on specific gene sequences and their associations with weight, it is essential to consider that environmental factors and overall genetics also play significant roles in avian weight dynamics.

Association analysis of NADH gene polymorphism and studied traits:

According to sequencing alignment results, the regions of NADH gene polymorphism (119bp and 258bp) are considered polymorphic regions containing 2 polymorphic SNPs (Figure 5). The individuals carrying the (A) Allele are the selected line, while individuals carrying the (T) Allele are the control line. Results of statistical analysis to detect the association between these SNPs and the phenotypes of the studied traits revealed a significant association between the second SNP and BW for the individuals carrying A and T Alleles at all ages studied. For the individuals carrying the (A) Allele (selected line), the means of BW were 47.63, 272.00, 771.00, 1539.00, 2322.00, 2748.50, and 3160.00 g at the ages (0, 1, 2, 3, 4, 5, 6 months), respectively. The corresponding means for those individuals carrying the (T) Allele (control line) were 42.04, 175.67, 578.50, 1343.00, 1974.00, 2599.50, and 3094.33 g (Table 8). However, BW was significantly higher for the individuals carrying the (A) Allele (selected line), than those individuals carrying the (T) Allele (control line).

On the other hand, the first SNPs didn`t show any significant association with studied traits. According to the previous results, the second SNP can be used as a genetic marker in marker-assisted selection programs of body weight in turkeys.

The relationship between BW and NADH gene sequences in avian species is complex, involving various mitochondrial genes that influence growth and metabolic traits. Lu *et al*. (2016) indicated that specific variants in the NADH dehydrogenase subunit 2 (ND2) gene are associated with certain growth traits, although no significant correlation with body weight was found in one study.

Additionally, the metabolic implications of NADH-related genes, such as malate dehydrogenase, suggest a role in energy metabolism that could indirectly affect body weight through muscle development and fat composition. (Hong-Ying *et al*., 2006). Polymorphism in this gene correlates with growth traits, indicating its potential influence on body composition. Variants like mt.A5703T and mt.T5727G showed significant associations with muscle fat content but not body weight. (Lu *et al.,* 2016).

CONCLUSION

The findings demonstrated that when Baladi turkeys were selected for higher 6-month BW, their growth performance considerably improved. Furthermore, the relationship between specific SNPs of the cytochrome and NADH genes and body weight can be utilized as a genetic marker in a marker-assisted selection scheme to enhance turkey growth performance.

Table (1): Primers for genes used in this study.

Gene Name	Forward/Reverse Primers sequence 5` 3`	Product size (bp)	Location	Pre-denaturation	Denaturation	Annealing	Extension	Final extension
Cytochrome	F CCACAAAGCACAGTTACGGG R ATATCGTTGCGTGCCAGCTA	660	NC_015022.2	95ºC /5 m	95ºC /45 s	54ºC/30 s	72ºC/45 s	72 ºC/5 m
NADH	F CGCCCAGCTAAACCCTAA R GTTCCTGACCGAGGAACCAG	611	NC_010195.2			55ºC/30 s		

Table (2): Means and standard error (SE) of turkeys' body weight (g) at different ages by line.

Age (month)	Line						Sig
	Selected			Control			
	N	Mean	SE	N	Mean	SE	
0	413	48.88^{a}	0.36	123	47.37^{b}	0.42	*
1	338	258.68^{a}	3.91	105	250.40^{b}	5.03	*
2	297	824.21^{a}	13.32	84	814.50^{b}	11.09	*
3	243	1775.31^{a}	29.83	71	1726.94^{b}	36.84	****

* $P \leq 0.05$ **** $P \leq 0.0001$

Different letters in the same row indicate significant differences ($P \leq 0.05$)

Table (3): Means and standard error (SE) of turkeys' body weight (g) at different ages by line and sex.

Line & Sex	Body weight (g) at different ages (Month)					
	4			5		
	N	Mean	SE	N	Mean	SE
Selected	213	2721.46^{a}	53.60	161	3529.45^{a}	99.05
Control	62	2665.69^{b}	70.81	50	3394.28^{b}	111.52
Sig		***			***	
Males	134	3021.05$^{\alpha}$	36.99	97	4078.44$^{\alpha}$	55.40
Females	141	2412.21$^{\beta}$	22.56	114	3003.04$^{\beta}$	28.34
Sig		****			****	

*** $P \leq 0.001$ **** $P \leq 0.0001$

Different letters (small and Latin) in the same column indicate significant differences ($P \leq 0.05$)

Table (4): Means and standard error (SE) of body weight (g) and body weight gain (g) of turkeys at 6 months of age by line and sex.

Line & Sex	N	Body weight (6 months)		Body weight gain (0-6 months)	
		Mean	SE	Mean	SE
Selected	131	4404.61^{a}	67.80	4355.73^{a}	68.84
Control	39	3967.25^{b}	126.06	3919.88^{b}	127.98
Sig		****		****	
Males	69	5599.07$^{\alpha}$	133.62	5550.19$^{\alpha}$	134.00
Females	101	3419.71$^{\beta}$	63.39	3371.42$^{\beta}$	64.12
Sig		****		****	

**** $P \leq 0.0001$

Different letters (small and Latin) in the same column indicate significant differences ($P \leq 0.05$)

Table (5): Means and standard errors (SE) of body weight at 6 months of age (g) in Baladi turkey by generation, lines, and sex.

Sex	Statistic	Generation (0)		Generation (F_1)		Sig S vs C
		Population		Lines		
		Base	Selected Parents	Selected (S)	Control (C)	
Male	N	48	13	56	13	
	Mean	6441.66	7500.00	5781.62[a]	5501.75[b]	****
	SE	125.22	89.44	121.12	187.48	
Female	N	145	55	75	26	
	Mean	3085.51	3700.00	3376.44[a]	3200.00[b]	****
	SE	50.93	22.22	52.32	95.35	
Both	N	193	68	131	39	
	Mean	3920.20	4426.47	4404.61[a]	3967.25[b]	****
	SE	34.39	35.07	67.80	126.06	

**** $P \leq 0.0001$

Different letters in the same row indicate significant differences ($P \leq 0.05$)

Table (6): Selection differential (g), intensity of selection (i), realized response (g), and realized heritability (h^2) for body weight at 6 months of age by sex and generation for turkey.

Sex	Generation	Selection differential (g)	Selection intensity (i)	Realized response (g)	Realized h^2
Male	0	1058.34	1.22	--	--
	1	--	--	279.87	0.26
Female	0	614.49	1.00	--	--
	1	--		176.44	0.29
Cumulative	0	1672.83	1.06	--	--
	1	--	--	437.36	0.26

Table (7): Means and standard error (SE) of body weight (g) at different ages for the selected (Allele C) and control (Allele G) lines of the first SNP in Cytochrome gene polymorphism.

Age (Month)	Lines & Alleles				Sig
	Selected (Allele C)		Control (Allele G)		
	Mean	SE	Mean	SE	
Hatch	46.79[a]	0.62	42.04[b]	1.29	**
1	264.33[a]	10.34	175.00[b]	16.74	***
2	754.67[a]	13.55	578.50[b]	21.47	****
3	1552.67[a]	23.21	1343.00[b]	33.32	*
4	2353.67[a]	51.52	1974.00[b]	69.86	**
5	2786.00[a]	17.39	2599.50[b]	11.26	***
6	3160.33[a]	10.04	3094.33[b]	14.22	*

* $P \leq 0.05$ ** $P \leq 0.01$ *** $P \leq 0.001$ **** $P \leq 0.0001$

Different letters in the same row indicate significant differences ($P \leq 0.05$)

Table (8): Means and standard error (SE) of body weight (g) at different ages for the selected (Allele C) and control (Allele G) lines of the second SNP in NADH gene polymorphism.

Age (Month)	Lines & Alleles				Sig
	Selected (Allele A)		Control (Allele T)		
	Mean	SE	Mean	SE	
Hatch	47.63[a]	0.51	42.04[b]	1.29	**
1	272.00[a]	14.43	175.67[b]	16.74	**
2	771.00[a]	13.86	578.50[b]	21.47	***
3	1539.00[a]	34.06	1343.00[b]	33.32	*
4	2322.00[a]	75.06	1974.00[b]	69.86	*
5	2748.50[a]	21.56	2599.50[b]	11.26	***
6	3160.00[a]	10.04	3094.33[b]	14.22	*

* P ≤ 0.05 ** P ≤ 0.01 *** P ≤ 0.001

Different letters in the same row indicate significant differences (P ≤ 0.05)

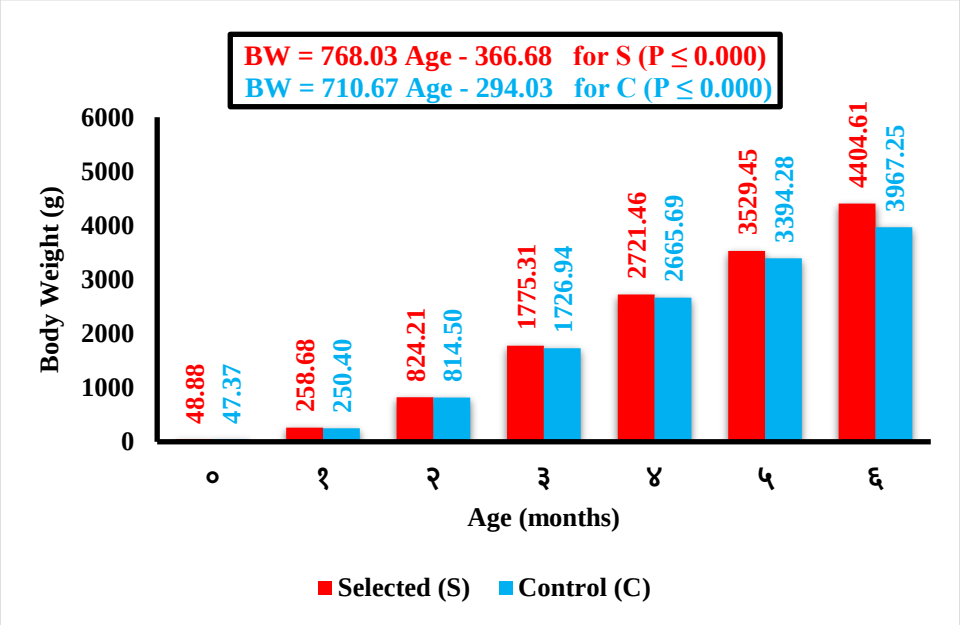


Figure (1): Means of BW (g) at different ages (month) for S and C lines along with regression analysis.

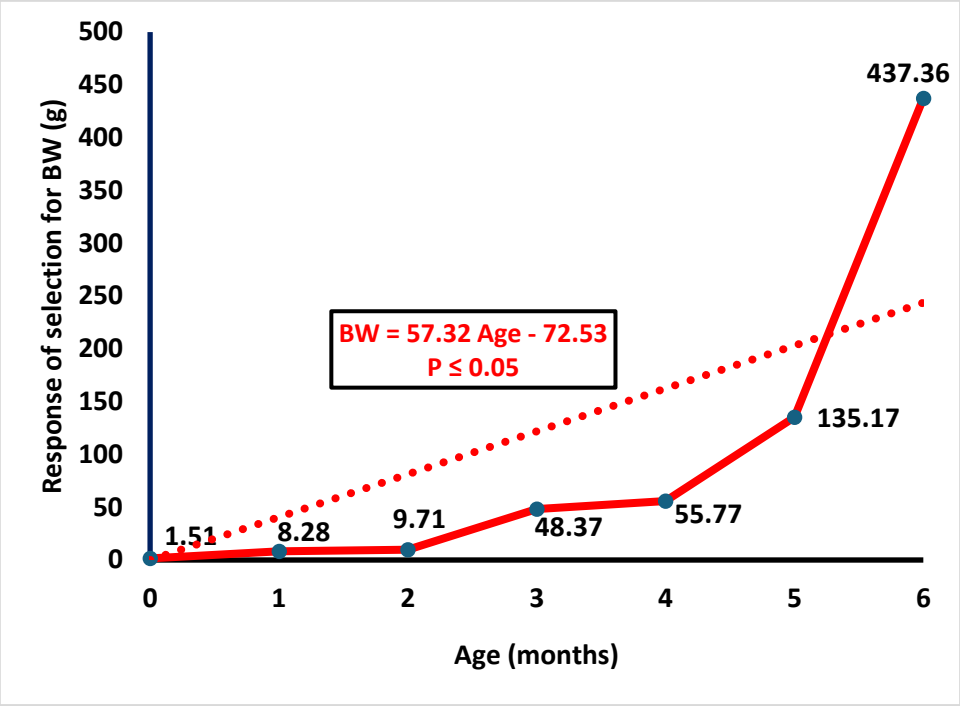


Figure (2): Regression of realized responses in BW (g) on Ages (months)

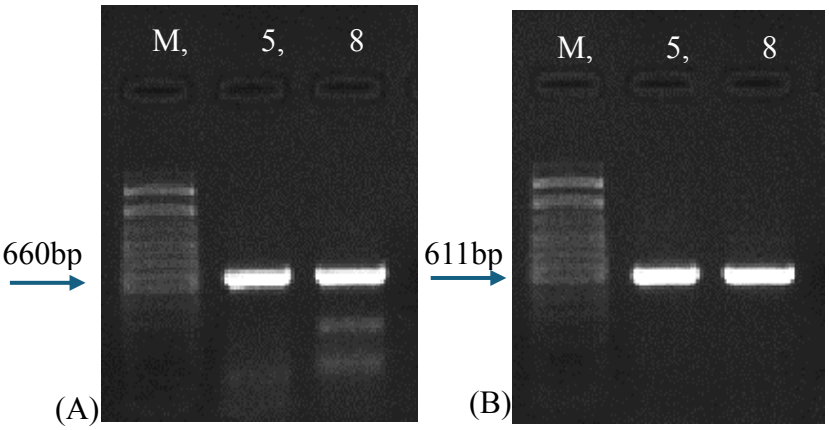


Figure (3): PCR amplification for the select studied genes where (A) Cytochrome (B) NADH

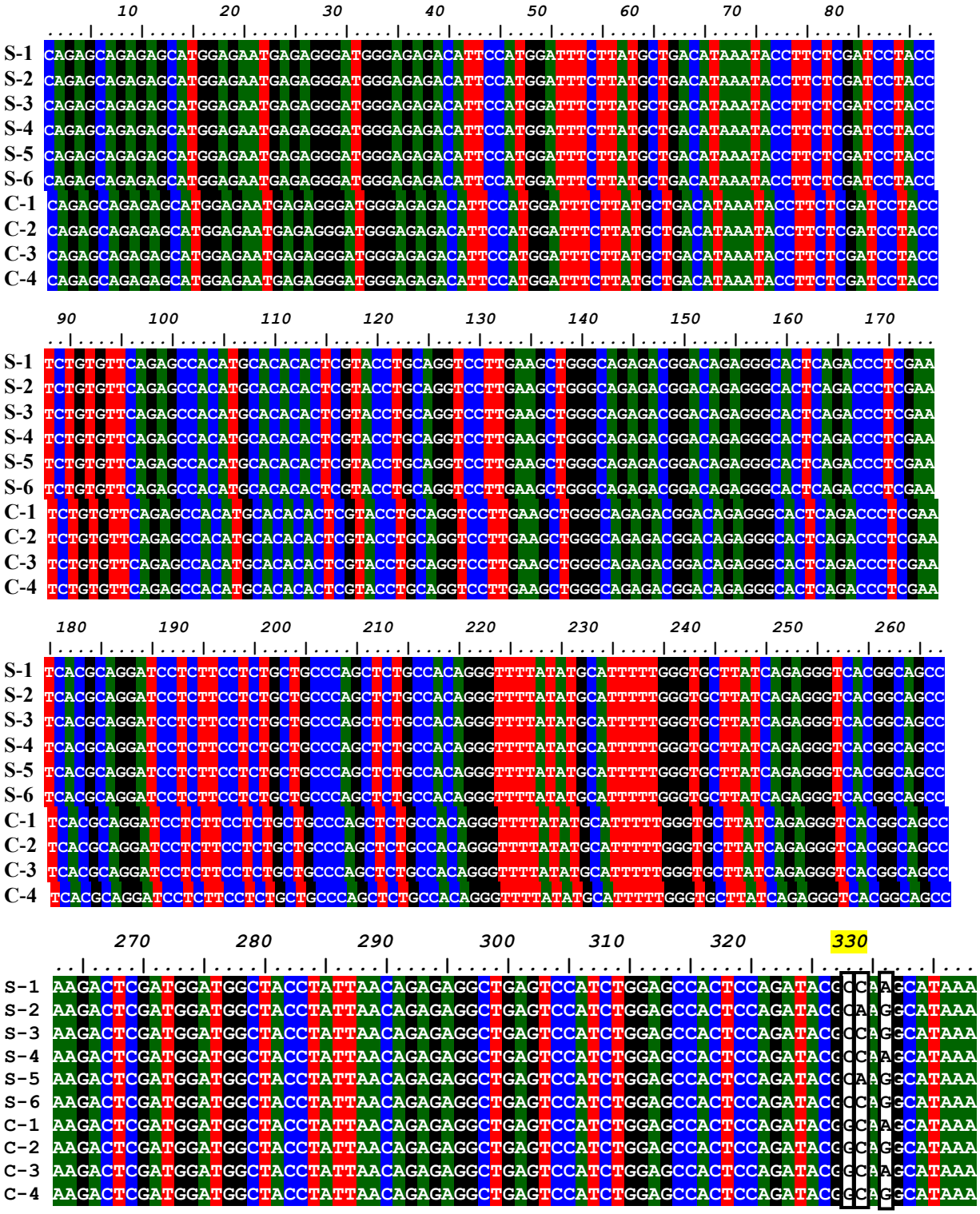
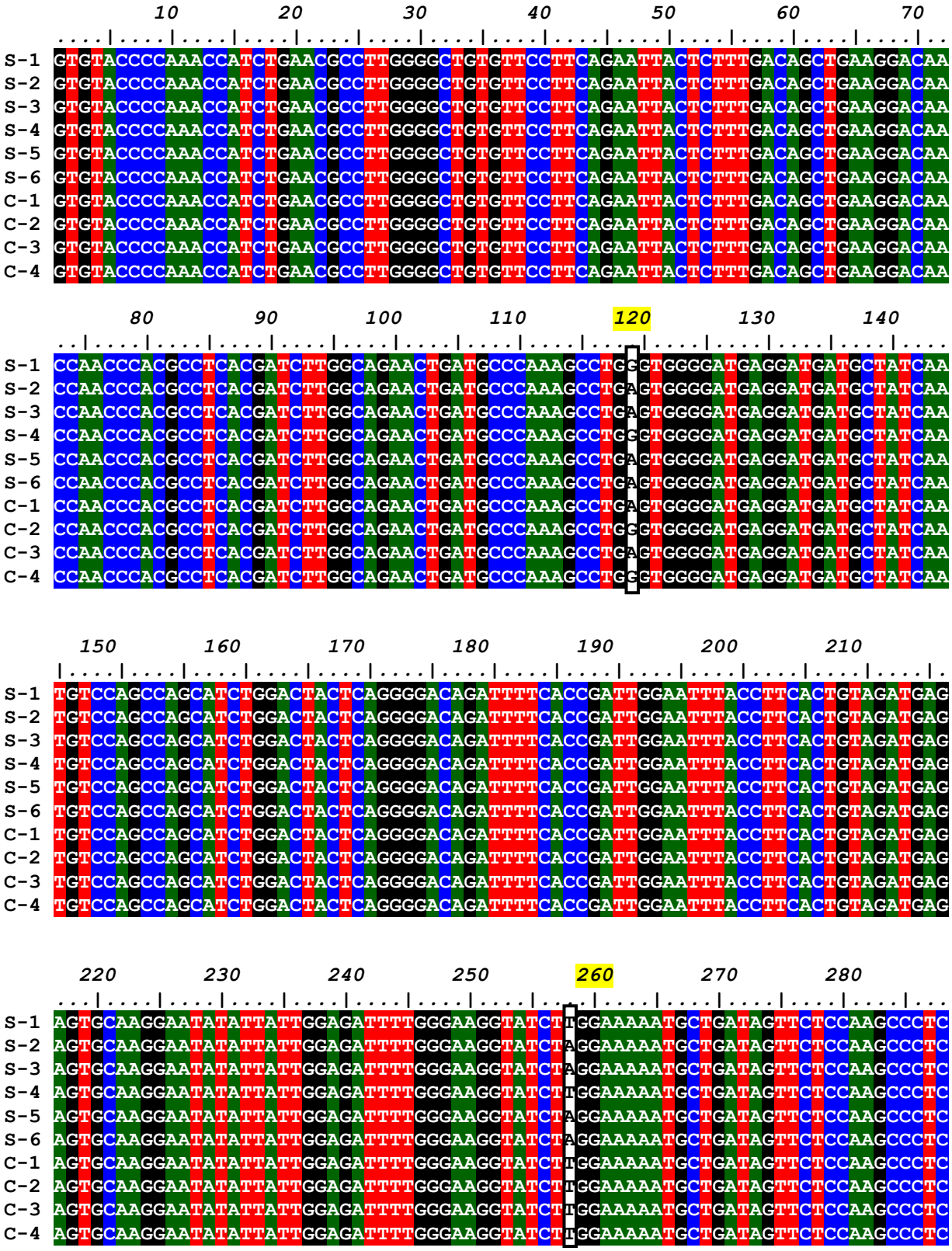


Figure (4): Cytochrome gene alignment sequence for the selected (S) and control (C) lines.


10 20 30 40 50 60 70
S-1 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
S-2 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
S-3 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
S-4 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
S-5 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
S-6 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
C-1 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
C-2 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
C-3 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
C-4 GTGTACCCCAAACCATCTGAACGCCTTGGGGCTGTGTTCCTTCAGAATTACTCTTTGACAGCTGAAGGACAA
80 90 100 110 120 130 140
S-1 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGGGTGGGGATGAGGATGATGCTATCAA
S-2 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
S-3 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
S-4 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGGGTGGGGATGAGGATGATGCTATCAA
S-5 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
S-6 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
C-1 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
C-2 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGGGTGGGGATGAGGATGATGCTATCAA
C-3 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGAGTGGGGATGAGGATGATGCTATCAA
C-4 CCAACCCACGCCTCACGATCTTGGCAGAACTGATGCCCAAAGCCTGGGTGGGGATGAGGATGATGCTATCAA
150 160 170 180 190 200 210
S-1 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
S-2 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
S-3 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
S-4 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
S-5 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
S-6 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
C-1 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
C-2 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
C-3 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
C-4 TGTCCAGCCAGCATCTGGACTACTCAGGGGACAGATTTTCACCGATTGGAATTTACCTTCACTGTAGATGAG
220 230 240 250 260 270 280
S-1 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTTGGAAAAATGCTGATAGTTCTCCAAGCCCTC
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S-6 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTAGGAAAAATGCTGATAGTTCTCCAAGCCCTC
C-1 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTTGGAAAAATGCTGATAGTTCTCCAAGCCCTC
C-2 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTTGGAAAAATGCTGATAGTTCTCCAAGCCCTC
C-3 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTTGGAAAAATGCTGATAGTTCTCCAAGCCCTC
C-4 AGTGCAAGGAATATATTATTGGAGATTTTGGGAAGGTATCTTGGAAAAATGCTGATAGTTCTCCAAGCCCTC

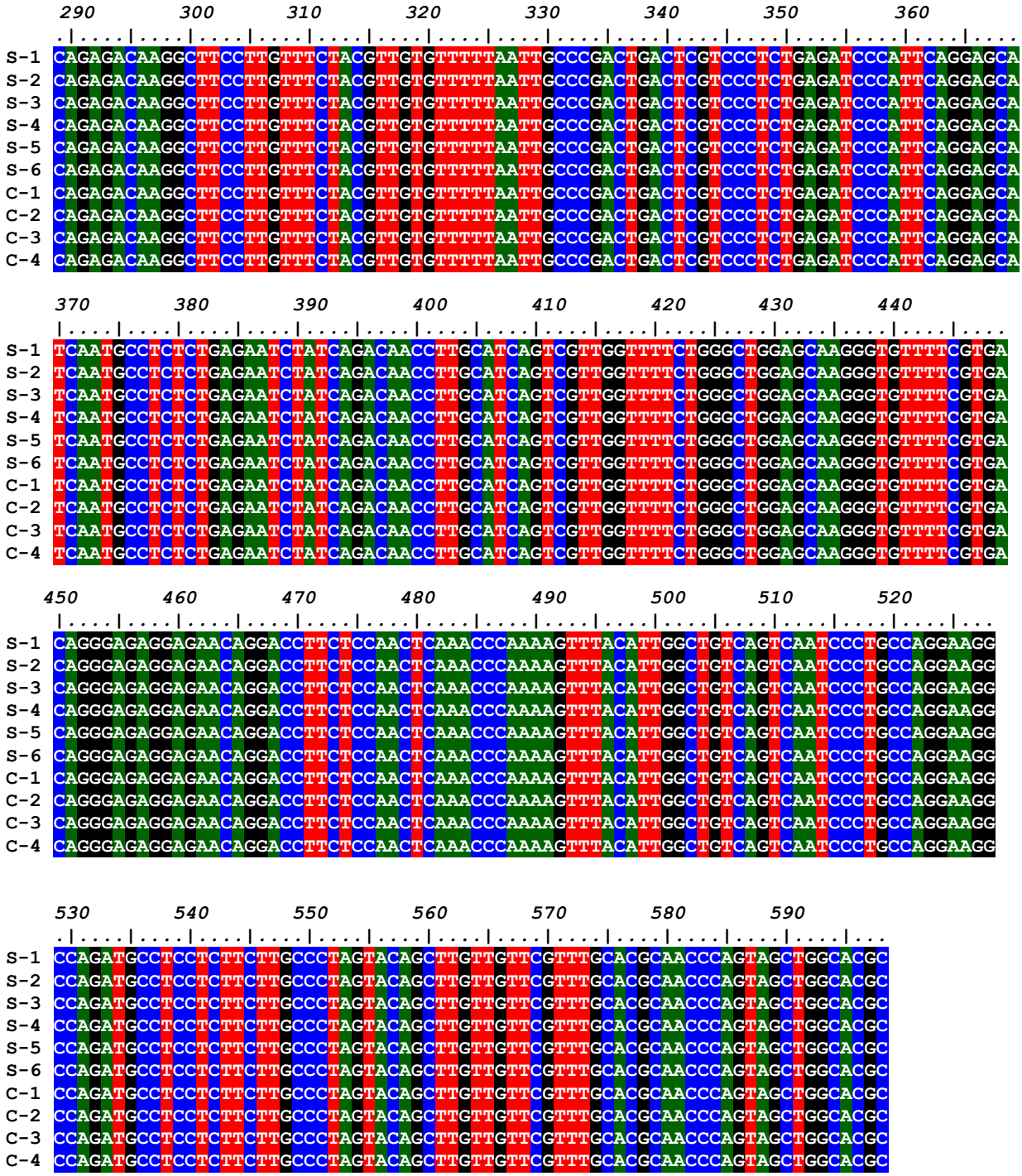

Figure (5): NADH gene alignment sequence for the selected (S) and control (C) lines.

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الملخص العربي

ارتباط تعدد أشكال جينات السيتوكروم، NADH بصفات النمو في الرومي المنتخب لزيادة وزن الجسم

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يعتبر زيادة النمو وانتاج اللحم في الرومي أمر بالغ الأهمية، ومن خلال اكتشاف المحددات الجينية المرتبطة بتحسين النمو، قد يمكن المنتجين من إنتاج طيور تنمو بشكل أكثر فعالية. وقد هدفت الدراسة إلى تحسين صفات النمو في الرومي البلدي المحلي من خلال الانتخاب لوزن الجسم العالي عند عمر 6 أشهر، وتقييم العلاقة بين جينات السيتوكروم وNADH مع وزن الجسم في الرومي. تمت مقارنة خطين من الرومي: خط منتخب لوزن الجسم العالي عند عمر ستة أشهر. والخط الثاني هو الكنترول بدون انتخاب. تم جمع عينات الدم من مائتان طائر عند عمر شهر واحد. كما تم تحديد تعدد أشكال النوكليوتيدات بين الأنماط الجينية في الرومي من خلال تسلسل الحمض النووي. أشارت النتائج الى أن الخط المنتخب كان أعلى معنويا في وزن الجسم مقارنة بخط الكنترول في كل من الذكور (5781.62 مقابل 5501.75 جم) والإناث (3376.44 مقابل 3200.00 جم) في الرومي البلدي وذلك بعد جيل واحد من الانتخاب لزيادة وزن الجسم عند عمر 6 أشهر. وقد زادت الاستجابة المحققة في وزن الجسم معنويا بمقدار 57.32 جم شهريًا خلال الفترة (6-0) أشهر. كما كانت تقديرات المكافئ الوراثي المحقق لوزن الجسم عند عمر 6 أشهر متوسطة في الذكور (0.26) والإناث (0.29). ولوحظ وجود ارتباط معنوي بين جينات السيتوكروم وNADH مع وزن الجسم في الرومي عند أعمار مختلفة. وقد خلصت الدراسة الى أن الانتخاب لزيادة وزن الجسم كان فعالا في التحسين الوراثي لصفات النمو في الرومي، ويمكن استخدام جينات السيتوكروم وNADH كمحددات وراثية في برامج الانتخاب بمساعدة الواسمات الوراثية لتحسين صفات النمو في الرومي.