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Genetic Correlation Between Growth Hormone SNPs and Selection Parameters in Japanese Quail: Multi-Generation Study

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Abstract

THIS STUDY was to evaluate selective breeding on body weight over three generations in Japanese quail and to understand the association between three GH gene SNPs and growth. The analysis included the average body weight at 2, 4, and 6 weeks of age which showed an increasing direction from the basic population to generation three (G3). The most significant growth observed was at 2-weeks where there was a 35.8% increase by G3 signifying good early growth selection. The results also evaluated selection response, selection differential as well as realized heritability for 4-week bodyweight thus demonstrating strong genetic response during first generation (G1 by 35.8% increase) but reduced responses in subsequent generations. Genotypic analysis was done using SNPs located within growth hormone gene showing frequency shifts among different alleles. Different SNP genotypes consistently correlated higher than usual weights thus giving pointers towards future breeding strategies; additionally additive effects varied across generations which implies need for specific approaches aimed at manipulating genes responsible for controlling weight gain within particular periods during ontogeny while taking care not to interfere with other important biological processes occurring simultaneously. The study therefore showed that (BV) breeding values for 4-week body weight increased significantly between G1 and G3 but subsequent increases became smaller indicating possible genetic limits being reached. In conclusion, this study was significant for Japanese quail industry because it will help farmers optimize their breeding plans towards attaining desired weights using selective breeding methods during early maturity periods too.

Keywords: Japanese quail, short-term selection, growth hormone, SNP, EBV.

Introduction

Selective breeding has been used in farming systems since time immemorial; its primary goal has always been selecting individuals displaying favorable attributes while providing them with higher chances of reproducing among themselves so that their offspring can inherit those desirable qualities too. *Coturnix coturnix japonica* commonly referred to as Japanese quail are widely known because they have got quick growth rates, good feed conversion ratios besides being highly prolific when compared against most other breeds kept under similar conditions. The selective breeding mainly concentrating on size which affects commercial viability thus production efficiency and profitability hence this trait serves as a key consideration during such exercises [1-4].

Artificial selection involves choosing particular animals having preferred characteristics then

allowing these ones alone to mate together thereby increasing chances that all future generations will equally possess such traits. It is employed in various sectors aimed at improving different aspects of performance including speed of development, disease resistance, fertility rate among others [5,6]. Growth attributes especially mass is very critical within poultry farming due to direct influence on meat output levels coupled with general returns from sales made after slaughtering birds ready for consumption [7] The small size plus fast growth rate exhibited by quails makes them excellent models for studying selective breeding given shorter generation interval and higher reproductive potentiality compared to other domesticated avian species [8-10]. Breeders select quails showing superior growth rates so as to enhance overall bodyweight, improve uniformity as well maximize productivity but achieving sustainable genetic gains in weight is not easy because there may be genetic plateaus which require fresh thinking about how best this can be overcome [11-13].

The complicated genetic setup for growth aspects in poultry consists of many genes that have additive as well as non additive effects. Additive effect is the incremental impact of one gene towards a phenotype while non-additive effect describes how alleles at different points interact [14-17]. Appreciating the genetic foundation of growth qualities is important because it helps in creating successful breeding approaches and finding out the main body-weight-related markers which are genetically based. Different studies on chicken genetics control over growth rates have shown some genes plus quantitative trait loci (QTLs) linked with body weight and growth rate. For example, changes in body mass may be caused by various SNPs connected with GH signalling pathways; these include receptors such as GHR and IGFs receptor genes among others [17-20]. Moreover, it has been found out that single nucleotide polymorphisms within these regions can affect an individual's speed at which they grow hence becoming useful tools for selective breeding programs aimed at improving productivity [21].

In Japanese quail, previous works showed that there were differences between individuals when it came to their weights due to variations found on certain types or groups of genes relating them with growth rates. A case point is where some particular SNP variants representatives were discovered within GH gene which had strong connections not only within themselves but also across different parts responsible for this kind performance change [22] . Knowledge concerning such factors enables farmers make appropriate choices about what variety should

be chosen so as achieve better results through increase rate at which birds gain mass. One problem associated with selective breeding might be described as follows by geneticists: sometimes things may go too far up until everything stops working altogether – this is known as "genetic plateaus". This term refers when no further gains can be made via traditional means because population gets close enough towards its gene ceiling for any given characteristic [23] . In many instances concerned with weight improvement programs in poultry farming there comes a time when farmers notice that their animals are no longer growing as fast as they used to do during initial periods of development hence indicating presence plateau [24].

There are a number of reasons why such plateaus occur, including limited gene pool sizes and complex interactions between genes or between them and environmental factors which could lead to diminishing returns from selection. Once this happens there will be no more room left for betterment thus requiring either introduction new materials or use advanced genomics tools so that these issues can be addressed accordingly [25,26]. The usage of whole genome sequencing together with marker assisted selection based on MAS may also provide some additional clues about what drives growth traits within populations leading towards faster rates of improvement [27-29].

Improvements in molecular genetics have allowed for the detection of growth trait related genetic markers which can be used in selective breeding programmes. SNPs are one type of such genetic marker that informs about changes in DNA sequences and their association with phenotypic traits [30]. In poultry, growth-related gene SNPs have been found to be linked with body weight variations and growth rates thereby providing valuable selection targets [31]. These have also helped to examine the genetic mechanisms responsible for body weight and growth rate disparity among Japanese quails. For instance, investigations have shown that SNPs within the growth hormone gene could contribute towards better growth performances thus indicating their potential usefulness in selective breeding programmes [32]. Different generations may reveal useful information on selection efficiency as well as identify genes affecting large size by considering frequencies of particular alleles or genotypes during analysis [33].

The main aim of this study is to assess how different generations' selective breeding impacts body weights in Japanese quail; however, it will mainly concentrate on the genetic basis behind these traits. This research therefore seeks to enlighten us

more about breeders' success rates when they use various strategies while also looking at what may cause improvement in live weights through understanding associations between SNP's and growth performances using data collected at different ages for birds reared under commercial conditions. Such findings would enable one make sense out them so that optimal programs can be designed not only for japonicus but other poultry breeds too leading increased productivity levels coupled with economic gains across the sector.

Material and Methods

The study protocol was approved by medical Research Ethics Committee (MREC) of national Research Centre, Egypt, under the ethical approval code (13050409). The relevant Egyptian laws and the Egyptian Drug Authority (EDA) and Ministry of Health and Population (MOHP) and Institutional Animal care and Use Committee (1ACUC) decrees, guidelines and recommendations shall be adopted and followed during the conduct of this research.

Birds and managements

The Japanese quail population was taken from the farm of the Animal Production Research Institute, Ministry of Agriculture, Egypt that contains up to 600 birds. No traits will be selected for in the population before the experiment begins. To make a selection (S) line and a control (C) line, birds were randomly chosen from the population then allocated equally into two lines for reproduction which they were individually leg-tagged. In one cage there were four females and one male meant for mating. Food and water were given ad libitum. Daily eggs were collected and each labelled with dam number to maintain pedigree records. When hatched, they were raised together in group housing at 60 birds/m2 floor space. Quails should have access to artificially lighted houses for 24 hours daily while being fed on a standard commercial feed containing 28% CP and 2,900 kcal ME/kg feed throughout the experimental period. Body weights at six weeks of age shall be analysed; superior birds will then be selected as parents for subsequent generations through random mating using a sire: dam ratio of one to four (1:4) which aims at producing three generations with different characteristics.

Body weights at 4-weeks of age were analysed by an animal model so as to predict breeding values. The animal model allows us predict breeding values by analysing body weight at 4-weeks. The animal model allows us predict breeding values by analysing body weight at 4-weeks. A constant ratio is used in generation replacement, and so selection intensity is a function of number of birds at each stage.

Selection parameters

The selection differential, selection response, selection intensity, realized heritability and estimated breeding value were estimated as follows [34] ;

Selection Differential: The difference between the mean body weight of selected individuals and the base population. $SD = Xp - X0$ Where, Xp : the selected parents` mean , and $X0$: the population mean.

Selection Response: The change in mean body weight from one generation to the next, attributable to selection.

Selection Intensity: The degree to which the best individuals are selected compared to the average of the population. $i = SD/ \delta p$ Where, SD : the selection differential, and δp: the phenotypic standard deviation of the trait.

Realized Heritability: The ratio of the selection response to the selection differential, indicating the proportion of the trait's variance that is due to genetic factors.

$h^2 r = R / SD$ where, R: actual response of selection, and SD: the selection differential of previous generation.

The breeding value (BV) is an estimate of an individual's genetic worth, particularly for a specific trait, such as body weight at a certain age. In a selection program, breeding values are often calculated using the formula:

BV = Heritability * (Observed Trait Value- Mean Trait Value).

Genomic DNA Extraction

Genomic DNA was extracted from blood with the use of an appropriate DNA blood Kit according to the protocol recommended by the manufacturer. The DNA quality will be estimated by a spectrophotometer.

PCR amplifications

The PCR reaction performed using two of primers to amplifying the growth hormone (GH) using primers as follows: F:5-TCCAGTAGGGGTTGAGATGC-3; R:5-CTGTCTGAGGTGCCGAAAAC-3, with size product 466 bp [35]. PCR amplification reactions were carried out in 50 µl of overall volume that comprised of 50 ng of template DNA, 10 pmol of every primer, 0.25 U of Taq DNA polymerase, 10 mM of Tris- HCl (pH.9.0), 250 mM of dNTPs mix, 30 mM of KCl, 1.5 mM of MgCl2 and sterile nuclease free water to obtain the ultimate volume of 50 ml. The following cycling conditions was used to

carry out the PCR reaction: pre-denaturing at 94^0C for 5 minutes, denaturing at 94^0C for 30 seconds, annealing at an appropriate (54.5^0C) for 30 seconds and extension at 70^0C for 1:30 minutes for 35 cycles and finally, an extension at 70^0C for 10 minutes. An analysis of the amplified fragments was carried out in 1.5% agarose stained with ethidium bromide. In addition, a 100 bp DNA ladder was added in agarose gel electrophoresis so as to examine the size of amplificon product. Gel documentation system was used to obtain the images, and the software available with the gel documentation system was used to determine the size of the amplicon.

Statistical Analysis

Bioneer Inc. (Daejeon, Republic of Korea) purified PCR products and sequenced them. CLUSTALW 2.0.12 was used to perform multiple sequence alignments so as to detect conserved regions and possible polymorphic sites among collected sequences. The sequences obtained were then subjected to similarity searches using BLAST programs from NCBI against Genbank database. SAS statistical package provided robust framework for analyzing the data statistically while evaluating them genetically within Hardy-Weinberg equilibrium context and other population genetics metrics. To find out whether identified SNPs were significantly associated with 4 weeks body weight a chi-square test was conducted based on allele frequency distribution among these groups.

Results

Selective breeding is key to improving body weight and other growth traits in Japanese quail. This study presents an extensive examination of how selective breeding affects body weight over multiple generations, shedding light on genetic factors that influence growth as well as the efficiency of breeding methods used. Genetic plateaus pose challenges for breeders but molecular genetics can help overcome them; thus, these two aspects will be addressed by our research with the aim of optimizing programs for artificial selection and enhancing poultry production.

Descriptive analysis of selected body weight

Table 1 provided data on body weights at three ages (2, 4 and 6 weeks) for four groups: base population; G1; G2 and G3. Descriptive statistics include mean, standard deviation (SD), standard error (SE), minimum (Min), maximum (Max), and mode. Results showed that average body weight increased with each generation from the base population to G3 at every age level considered here. At two weeks of age there was a clearly upwards direction across generations which means that early

growth rate has been improved through selective breeding most noticeably between BP and G3 (+35.8%).

For the second week average body weight continued to rise albeit less dramatically than during week number one; this indicates ongoing success of selection but perhaps slowing down some as birds grow older. At six weeks minimum change occurred between different groups' mean values representing possible levelling off or lack thereof in terms of further genetic progress at this age. Each generation has an upwardly displaced mode that represents the most frequent weight observed; this shows the overall increase in mass and efficacy of the means employed. The growth in average body mass registered between G1 and G3 at six weeks old is quite slight when compared with earlier ages. There could be a levelling off point for genetic improvements in terms of size at later stages as indicated by this study though those gains may not have been achieved because they were not tried out or due to external factors. These results provide evidence that selective breeding programs can enhance weights among Japanese quails.

Since there is a consistent rise in mean values throughout generations accompanied by decrease in diversity it is clear that these traits possess heritability and are effectively selected upon. However, if no additional materials are used during selection or more rigorous methods applied beyond 6 weeks then we might hit our limits with further gains since this age seems to be showing signs of plateauing after which new genes must be brought into play lest we create an opportunity for inbreeding depression coupled with genetic bottlenecking. With time, across several generations (which were characterized by successive increases) average weights steadily increased while their dispersion decreased thus indicating successfulness in terms of using selection process on Japanese quails' masses. Although these findings show that continued choosing might result into betterment but still there should also arise concerns about possibility having reached maximum improvements at later life stages This particular investigation was very important while trying to come up with ways on how best we can breed animals towards attaining specific target weights especially within poultry industry where rapid growth rates lead early marketability.

Selection response analysis

Table 2 results showed response to selection, selection differential, realized heritability and selection intensity based on four-week body weight (BW4) of Japanese quail for three generations. These measures were important in ascertaining the

efficiency of a breeding plan as well as predicting future genetic gains. The mean selected weight rose from 186.69 g (Base) to 206 g (G1), resulting in a 19.31g response to selection. This substantial increase implies that there was indeed strong genetic response during first generation through this process of choice. Nevertheless, although it went up again up to mean selected weights of G2 which is 218.07g but declines back down so far only by another 12.07g i.e., selecting means between two consecutive generations continue increasing while responses towards selections decrease hence indicating that though still efficient but yet again not too much responsive because all favorable alleles may have been used up already or else no more improvement can be achieved due some environmental situations As for such things like these which we are talking about now? A slight increase was observed in the selected means for G2 over G3 i.e., from 222.30 grams to 4.23 grams wherefore signifying that selection at this point had become less effective.

The difference between selections made during the first generation and base population is seen through a change in respective mean differences which represents their selective differentials; similarly with intensities such that both were just about same number. If one takes into account G1, then he will notice how close they were since each had an 18.39 g while second remained constant at 0.96 respectively. This would suggest evenness among them regarding selection pressures exerted upon organisms being reared under those conditions. This suggests consistent selection pressure, leading to the substantial response observed in G1. On other hand, the selection differential in G2 increased slightly to 18.93 g, but the selection intensity decreases to 0.91. This may indicate that while selection pressure remains, it is slightly less stringent, potentially contributing to the reduced response. The realized heritability revealed itself after calculations came out as 63% therefore it can be said on average around 63% of selection differentials used got transmitted.

Genotype Frequency and Hardy-Weinberg Equilibrium

Table 3 showed the frequencies for different genotypes and alleles at four SNP loci (110 bp, 150 bp, 310 bp, and 390 bp) in the GH gene over three generations (G1, G2 and G3) as depicted on (Figures, 1,2,3 and 4, respectively). The table presents observed genotype frequencies as well as those expected under Hardy-Weinberg equilibrium hypothesis and allele frequencies. At position 110bp of growth hormone gene segment where there was a G/A SNP variation, increasing frequency of G allele

accompanied by rising GG genotype frequency indicates some selective advantage acting upon this allele through generations. Decrease in heterozygous & recessive genotypes could be due to selection or non-random mating causing allelic shifts by drift

With respect to G/A SNP at 150 bp, the A allele's increasing frequency and rise of AA genotype shows it is positively selected whereas G allele's decline and GG genotype reveal an allelic shift probably due to selection on other grounds. For both C/T and G/T SNPs at 310 bps and 390 bps respectively; however, an increase in TT genotypes together with T allele frequency may indicate either positive selection for T alleles or drifts resulting from genetic factors especially among G3s. Genotype frequencies observed differ significantly from those expected under Hardy-Weinberg equilibrium suggesting possible effects such as non-random mating, selection or even drift which might have occurred during these studies. Based on various generations' alterations in frequencies of alleles detected through genotyping; it can be concluded that such changes were influenced by forces like evolutionary pressures arising out of natural or artificial environments that acted upon them over time. Also, non-random mating could have played a part here too given some deviations from HWE across populations throughout many years.

SNPs effectiveness on body weight

These results explore the connection between different SNP genotypes within growth hormone loci and body weight recorded at 4- weeks age in Japanese quail over generations. The dataset gives weights associated with each genotype for SNPs located at different positions along this gene region. Different associations between SNPs positioned elsewhere along different segments of the growth hormone but close to one another functionally (110-bp) were found when looking at their relation towards body weight. For example, G/A SNP located at position −150 bp showed that generally higher weights will be achieved if we take into account heterozygotes while lower ones are obtained when homozygote dominant individuals were considered; however homozygote recessive genotypes showed intermediate levels nevertheless they would vary depending upon generation studied more over AA genotype resulted into highest weights across all generations compared against GG type which caused lower weights besides higher than normal weight being recorded for G/A in G3.

In term of C/T SNP located at position −310 bp showed highest weights among TT genotype in G2 but lower in G3 whereas generally better weights were obtained with C/T across both generations.

With respect to G/T SNP located at position −390 bp; the highest body weight was associated with heterozygotes (G/T) especially so during third generation while lowest occurred among homozygote recessive individuals (TT) of second generation however there was intermediate weight recorded for TT subjects from third generation too. These findings suggested that some SNPs may be linked to variations in body weight and therefore certain genotypes will consistently showed higher body weight as time goes by Understanding such relationships could help selective breeding programs aimed at optimizing body weight in Japanese quail.

The additive and dominant effects of SNPs

The results of table 5 showed the additive and domination of SNPs in growth hormone gene for three generations selected Japanese quail. The additive effect measures the influence of each allele on the trait (body weight), while the dominance effect reflects the advantage or disadvantage of heterozygotes relative to homozygotes. In terms of additive effects, generally positive were shown and varied depending on SNP and generation. Over generations were frequently increasing additives, which meant that SNPs had bigger impact on body weight as time goes by. Variability in additional impacts demonstrated that different SNP may affect body weight differently at various times while dominant effects across SNPs and generation showed considerable variability positive effects in some cases suggest advantages for heterozygous individuals, while negative ones indicated less benefit or even potential disadvantage. This can be used to design breeding programs aimed at maximizing body weight among Japanese quails considering all these genetic inputs. What also draws a line under the needs for targeted genetic strategies is observable diversity in additive as well as dominance outcomes.

Estimated breeding value

The estimated breeding values summarized for 4-weeks of body weights of Japanese quail over three generations using observed trait values, mean trait value from base population and realized heritability as shown in Table 6. The breeding value (BV) is an estimate of how good individual genes are for a particular characteristic like height at certain ages BV18.53g during G1 implies that selected birds have potential to increase their 4-weeks weights by this figure above average base population (186.69g). High value at G1 indicated strong response to selection where bigger sizes were chosen hence more significant genes for such traits being present. The second-generation BV28 .56g indicated further genetic improvement concerning weigh up until 4-

weeks of age. This demonstrates increased selection pressure exerted during selection which indeed proved successful since heritability dropped slightly when compared with previous stages yet overall rise still took place showing us what was sought after had also been passed over onto subsequent levels thereby enhancing overall excellence.

During third-generation(G3) the BV was 32.4g suggesting continued but smaller gains made towards weight gain for 4-weeks after hatching has taken place. The slight dropped off between these two values might imply that we may already be near our best possible result when it comes to selecting animals based on their size or perhaps there isn't enough genetic variance left within population anymore since individuals are becoming increasingly homogeneous due either reduced heritability ceiling effect signalling new materials must be introduced maintain or take progress

Discussion

Productive performance of selected quail

Table 1 provided detailed body weight measurements for Japanese quail across four groups (base population, G1, G2, and G3) at three distinct ages (2, 4, and 6 weeks). The data, encompassing mean, standard deviation (SD), standard error (SE), minimum (Min), maximum (Max), and mode, illustrates the effects of selective breeding on body weight over successive generations. The data revealed a progressive increase in mean body weight from the base population to G3 across all age points. At 2 weeks of age, the mean body weight shows a clear upward trend, with the most substantial increase observed between the base population and G3 (+35.8%). This significant improvement in early growth rates underscores the effectiveness of the selective breeding strategies employed. Early growth is a critical trait in poultry breeding as it can lead to more efficient production cycles and better feed conversion rates [36].

At 4 weeks, the mean body weight continued to rise, although the percentage increase is less dramatic compared to 2 weeks. The findings indicated that while selection remains effective, the rate of improvement in body weight may be slowing as the quail age. The diminishing returns observed in later stages of growth were consistent with findings in other selective breeding programs where initial improvements are more pronounced and subsequent gains are smaller [7]. By 6 weeks, the mean body weight shows only a slight increase across generations. The analysis suggested a potential plateau in weight gain, implying that further genetic improvement at this age might be more challenging.

The plateau effect was often observed in breeding programs when the trait approaches its genetic ceiling, indicating that further gains may require more intensive selection or the introduction of new genetic material [37]. This plateau could be due to genetic limits or environmental constraints that affect growth rates [23,25].

The reduction in standard deviation and standard error from the base population to later generations, particularly at 2 and 4 weeks, indicated not only an increase in average body weight but also a more uniform population in terms of body weight. This uniformity suggests that the selection process is successfully narrowing the range of body weights, which can be advantageous for standardizing production outcomes and improving overall flock performance [38] (Flisar et al., 2014). At 6 weeks, however, the standard deviation in G2 (34.24 g) is higher than in G1 (21.09 g) and G3 (21.90 g). This increase in variability may result from environmental factors or genetic variation introduced through the selection process. Environmental conditions, such as diet and housing, can impact growth and contribute to variability in body weight [38,39]. Additionally, genetic variation introduced through selection could lead to a broader range of phenotypes, contributing to increased variability.

Each generation revealed an upward shift of the mode's position which corresponds with overall gains in weight throughout generations and effectiveness of the method used. This indicated that steps are being taken to ensure development among birds is uniform by selecting for heavier weights during each stage of breeding so as to make them most common within a population. The relative lack of progress seen between 6 weeks at G3 when compared against those same aged groups earlier on (G1) might suggest some level off point was reached at this age,; perhaps because it takes longer before any further improvement can be made genetically while quails come close maximum possible size genetically [38]. It may require breakthroughs beyond current capabilities or new approaches altogether if additional genetic enhancements were to take place during such periods where no much change is recorded.

These results confirm that selective breeding can increase the weight of Japanese quail effectively. Continuous growth in average values over generations coupled with reduced variations points out heritability success achieved through applied selections; nevertheless, stagnation observed after six weeks implies need for more intensive methods aimed at preventing potential inbreeding depression caused by limited gene pools which could occur should no extra material be added into breeding [13,40]. Also, this study gives insights on how best to optimize programs targeting specific weights among birds bred for meat production purposes mainly used within poultry industry so far known fastest growing rates giving earliest maturity times leading higher profits realized too soonest periods but still needs further work because there might always be a plateau somewhere along the line if one continues choosing only those animals showing very rapid gains.

Selection parameters for 4-weeks body weight

Table 2 represents the data collected during the selection process for 4-week body weight in Japanese quail across three generations. The table shows various metrics used to evaluate the effectiveness of a selection program and predict future genetic gains such as: selection response, differential, intensity and realized heritability. Selection response is an important measure of how well selective breeding works; it is defined as the difference between mean weight of selected individuals from one generation to another. For instance, there was a positive selection response of 19.31 g following initial generation where birds were chosen based on their high heritability traits [34]. On the other hand, from G1 to G2 the response to selection decreased with selected mean increasing to 218.07 g and corresponding response of 12.07 g. This decline in response to selection represents a slowdown in the rate of genetic progress. There could be several reasons for this, such as depletion of favorable alleles, decrease in genetic diversity or environmental limitations [41]. As the population nears its genetic limit for any given trait further improvement becomes difficult due to decreasing returns in terms of selection responses [42,43].

Direction is maintained from G2 into G3 by a slight increase in mean body weight at 222.30 g but there is an even lesser response to selection which is only 4.23 g. This substantial fall indicated that there might be reached either some kind of ceiling whereafter no more response can be obtained through additional selective pressure or ceiling was never achieved because it lacked enough strength within this particular program design feature(s) for driving greater gains during subsequent phases; plateaus have frequently been observed when traits are bred close up against their genetic limits and/or when selection pressure fails to reach necessary levels [40,41,44]. This plateau should therefore serve as an indication that we need other strategies if our aim still remains improving body weight; these may involve infusion fresh bloodlines into current ones

already being used or refining methods adopted during candidate evaluation process.

Selection differential refers to the difference between average weights among those individuals selected as parents compared with base population means; while base population had undergone no such criterion whatsoever during this experiment hence its value stood at zero per bird on average across all birds measured before any selections were made so far whereas post-selection population recorded 19.31g difference between them indicating high potentiality for improvements through genetics alone. The higher number means greater chances for selecting better performers leading to larger responses in subsequent generations as demonstrated by increased sizes between parents' average weights and base population mean values selected for reproduction purposes [45]. In G1, selection differential was slightly lower i.e., 18.39g were recorded but selection intensity remained same with value 0.96 showing high levels of selection pressures on individuals used during breeding process which resulted into significant changes occurring within the first generation only; However, those for G2 where there was a slight rise up to stand at 18.93g while at same time reducing down its intensity level down to 0.91.The implications behind diminished returns could have been caused by reduction in number meeting stringent requirements thus leading to reduction in response [46].

The realized heritability was estimated at 0.63 across generations which means that approximately sixty three percent (63%) of what parents had differentially contributed towards their offspring's phenotypic characteristics actually got transmitted from one set to another during each round since it represents an average achievement over all pairs involved throughout entire phase so far covered by experiment. A realized heritability value of this magnitude was considered moderate given the fact that heritability for body weight usually range from 0.3 to 0.7 depending on specific populations studied under varying selection pressures within diverse environments constituting them according [47].It can also be seen as relevant because the higher such figures are the more likely it becomes for them being associated with genetic superiority while lower ones may imply otherwise due other sources like chance factors acting jointly with environmental influences besides those attributable solely unto genetic configuration per se without any interference coming from outside forces [47,48].

The patterns of selection response and heritability observed mean that although there were signs of reduced productivity the selection process worked in increasing mass. There was a plateau effect at some point which implies that more gains would need different methods like bringing new genetic materials into breeding populations or bettering environmental management strategies. Also, further advancements could be realised by using genomic tools alongside advanced breeding techniques [49].

Changes of allele and genotype frequencies

Results showed the different changes in growth hormones across three generations of Japanese quail, particularly at positions 110 bp, 150 bp, 310 bp and 390bp. In regards to this, genotype frequency and allele frequency were also analysed basing on Hardy-Weinberg Equilibrium (HWE) expectations which brought out some important findings about these SNPs in relation to selective pressures, genetic drifts as well as other evolutionary factors. The G allele frequency of SNP at position 110 bp of the growth hormone gene was observed to have increased significantly along with GG genotype over time. This could mean that there might be some advantage for G alleles over others because they tend to improve on certain growth characteristics. In fact, when people breed animals or plants under artificial conditions such as those used in agricultural programs; it becomes very common finding positive selections towards particular variants hence this view does not come as a surprise [34].

Furthermore; non-random pairing among individuals during mating seasons can lead into shifting of allelic frequencies especially within smaller sized populations where by chance alone would cause more variation [50]. Another way through which selection acts is change in dominance levels; this has been supported by decrease shown from heterozygous(G/A) to homozygous recessive (AA) genotypes which indicates increasing supremacy exhibited by one type [51-53]. Also, there could be random fluctuation due to less number so far affected by sampling error thus leading into an increase or decline of certain alleles [54,55]; For example if we look at SNP located at position 150-bp away its A-allele gets selected against.

Allele frequencies shifts seen here are therefore resultants of selective pressures inherent within animal breeding schemes that aim for rapid changes through increasing frequency advantageous alleles [47-49]. Such changes can also be inferred from departure genotype frequencies from those expected under random mating conditions as proposed in Hardy Weinberg formula; which might imply either selection acting upon them or simply non-random distribution across generations due to some factors selecting against certain traits.

The T alleles at positions 310 bp (C/T) and 390 bp (G/T) are considered to be under positive selection or have shifted due to genetic drift as indicated by the increase in the frequency of the TT genotype among individuals of G3. In further generations, it could be assumed that this type of deviation provides some kind of preference because such may enhance growth abilities or cause other advantageous characteristics [56]. Also, there may have been non-random mating followed by selection or genetic drift considering that these SNPs do not conform to Hardy-Weinberg equilibrium expectations. Indeed, small populations exposed to strong selective pressures are prone to experiencing great changes in allele frequencies caused by random factors like genetic drifts [54,55]. The deviations observed show that there has been an influence on distribution across generations through evolution where forces such as this shape genetic structures thus affecting allelic diversity among different population samples.

The changes in genotype and allele frequencies that appear between one generation and the next described in Table 3 illustrate how selection pressures, genetic drifts, and other evolutionary forces work on a growth hormone gene. These findings showed that genetic change was dynamic when responding to selective breeding methods and underscores the need for tracking hereditary differences so as to comprehend and optimize breeding results [57]. In order to gain more knowledge about what causes these changes, future investigations could apply sophisticated genomic tools alongside statistical techniques so as to better understand the underlying genetic structures as well environmental impacts on them. Additionally, such studies should also consider integrating genomic selection strategies while at the same time increasing genetic diversity within populations meant for breeding purposes this is because it will help counteract any undesirable effects brought about by random mating also ensure continuous improvement towards enhancing growth traits [49].

Relationship between SNPs in growth hormone and body weight

Table 4 offered some useful data regarding how different (SNPs) within GH relate with body weight at 4-weeks among various generations of Japanese quail; these results can be useful for understanding which parts of DNA segments influence particular characteristics during development stages. It is important to know this relationship because it helps us know what factors are responsible for controlling growth rates hence, we shall be able come up with suitable programs for selecting those desirable

qualities only. There was complex association between G/A SNP located at position 110bp where genotypes interacted significantly with each other showing heterozygosity advantage over successive years through enhanced production. The non-uniform distribution pattern shown by G/A genotypes across generations reflects over-dominance hypothesis which means that both alleles were equally favored resulting into highest possible heterozygous individuals being produced frequently than homozygotes thus promoting growth.

However, GG genotype generally indicated lower body weights meaning either there was no positive effect caused by AA homozygote state or any other combination involving G allele failed to show benefits for growth. It was also discovered that AA genotype had higher body weight especially in generation three which implies A-allele could be important factor towards promoting heavier mass thus may become target during selection programs aimed at improving this trait among quails. The reason behind such an increment observed within g3 corresponding to heterozygotes selected over many years is because they tend to possess more favorable alleles leading better performances [38,43,47]. Heterozygosity at the G/A SNP position 150 bp recorded highest average body weight values during both G2 and G3. The finding supports the idea that A-allele enhances growth characters when present at these two locations consistently selected across subsequent generations. In addition, it was interestingly noted that GG genotype showed lowest body weight particularly in G2 where no other type had ever weighed much less than itself suggesting some negative effects could result from frequenting too often here; if indeed so then one may conclude against selecting for any more individuals having such an attitude. Increasing body weights of G/A heterozygotes in generation three implies there might still exist advantages associated with having one copy each from different parents [58].

When designing breeding plans, it is necessary to know the effect of each specific gene. The AA and GG genotypes have different impacts on body weight and this showed that some traits are allele-dependent. The use of selection for AA could greatly improve growth rate especially if other desirable characteristics were linked with A-allele. At 310 bp site a C/T SNP had an interesting pattern where G2 had the heaviest birds under TT genotype but these weighed less than those in G3. This shift between generations might be indicative of changes in selection pressures or genotype by environment interaction affecting growth expression [56] . Considering both generations performed best overall at C/T locus may imply that having heterozygosity at

this point also promotes better growth. TT being associated with high weight in G2 but lower weights for G3 may indicate environmental effects on or genetic background modifications to expression potential of TT-genotype for growth according to [56].

The complexity of genetic control over growth can be demonstrated through variability associated with CC as well as TT genotypes which affect body mass differently. Different interpretations were made from observations thus showing that many factors such as [59] Lush (1945) stated play significant roles including genes involved, surrounding them environmentally and how they interact among themselves at various positions within chromosomes influencing development rates too much. In case 390-bp position SNPs were tested G/T genotype showed close linkages while having highest body weights when evaluated against any other marker especially during G3. Through heterozygous genotypes exhibiting positive effects towards growth suggested by these findings might have been brought about due to action favorably contributed by all alleles [34]. On the contrary, lowest weight was recorded within G2 for individuals carrying homozygous T allele hence performing moderately in terms of gaining weight during next cycle after birth until maturity is reached. The fact that there is an increase in weight for G/T genotypes at G3 indicates its potential role under positive selection which can then lead to higher rates of [55] mentioned growth over several generations.

The connection between SNPs' genotypes in the growth hormone and weight at 4-weeks demonstrated that certain genetic modifications can affect Japanese quail's growth traits. The changing consequences of different genes over generations show how intricate an organism's genetics are, as well as what kind of breeding strategies should be used for them [49]. Also, observed interactions between genotype and environment together with possible alteration in selection pressure among generations gives a hint that programs should be flexible enough to respond to these changes by including genomic selection or marker assisted techniques which will enhance improvement on size.

Genetic Effects of SNPs on body weight

In Table 5, the findings revealed some additive and dominance effects of SNPs within the growth hormone that make things grow over three selected generations. Essentiality of these genetic parameters lies with their ability to tell us more about specific alleles as they work individually or jointly towards influencing body weight; this being one important characteristic required in order to achieve maximum

efficiency through artificial selection for better meat production. It was found out that generally, there was an increase in additive effect sizes with each passing generation because many more such mutations become important during selection process while aiming at larger sizes [60].

For example: The G/A SNP at position 110 bp displayed a progressive rise in additive effect from 0.34 (G1) up until it reached its peak value of 0.62 during G3; on average across all three different measurements taken into account hereof being equal to around about 48%. This suggested therefore that if we keep picking birds whose parents have "G" type instead of other types then eventually this species will become bigger than ever before thanks to those alleles' positive contribution towards mass gain which so far remains latent within quails themselves only waiting for chance like this one [61].

Dominance effects recorded variously across different SNPs as well as generations, with some showing negative values while others positive. A good example would be a G/A SNP located at position 110 bp where there was observed positive dominance effect values for G1 (0.49) and G2 (0.25), this implies that birds having both alleles display greater growth ability in comparison to those missing one or both of them due to being homozygotes. Nevertheless, by third generation negative value (-0.31) had emerged which suggests changing environment conditions may have affected allele frequencies thereby altering relative fitnesses between heterozygotes themselves also relative to other individuals [60,61]. The same pattern can be observed for second case study which is represented by C/T SNP found at position 310 bp; here we seen consistently positive dominance effects across three generations but especially noticeable during first two generations where such animals were registering higher growth rates in comparison with those belonging under any other categories covering either locus or allelic forms thereof

The G/A SNP at position 150 bp showed consistently negative dominance effects across generations, with a mean of -0.24. This pattern suggests that heterozygotes at this locus may be at a disadvantage compared to homozygotes, highlighting the complex interplay between genetic variants that can influence breeding outcomes. In contrast, the C/T SNP at position 310 bp generally showed positive dominance effects, particularly in G1 (0.15) and G2 (0.25), indicating that heterozygosity at this locus is beneficial for growth.

The shifts in dominance effects observed from one generation to another underscore the fact that genetic influences on traits such as body weight are

dynamic. Such changes could be caused by selection-driven alterations in allele frequencies, genetic drift or epistasis among different loci, which may then change the relative fitnesses of various genotypes with time [62,63,64]. It is therefore important to know the additive and dominant effects of SNPs for optimizing breeding strategies in Japanese quail. The rise of additive contributions over generations indicates that selection has been successful at increasing the abundance of alleles with positive impacts on weight; nevertheless, wide-ranging expressions exhibited by dominance effects point towards a need to account for heterozygosity and its influence on growth traits [65].

Using SNPs that have strong positive additive effects can help breeding programs make sustainable gains in body weight through continuous genetic improvement. However, these programs should also manage matings so as not to overly concentrate too many genes within individuals which might decrease general adaptability due to reduced heterozygosity besides causing potential declines in overall fitness [66-68]. Additionally, they ought to remain responsive enough during different periods by incorporating ongoing evaluations based on new molecular findings into selecting appropriate animals for future breeding seasons given changing environmental conditions alongside gene frequency alterations across generations. Thus selected traits include increased bodyweight and general growth performance among others as demonstrated by [64,69] during their study on this subject matter particularly using Japanese quails.

Estimation of breeding value for 4-weeks body weight

The results summarized in Table 6 illustrate the estimated breeding values (BV) for the 4-week body weight of Japanese quail across three generations. Breeding value is a crucial metric in quantitative genetics, representing the genetic merit of an individual for a particular trait. It is a predictive measure of an individual's genetic potential to pass on desirable traits to its offspring [34]. In this context, the BV values across generations reflect the genetic improvement in body weight achieved through selective breeding.

The 1st generation (G1) breeding value of 18.53 g indicated that the selected quail had a large genetic potential to increase their weight by 4-weeks above the base population mean of 186.69 g by this amount. The strong BV in G1 means that lots of birds with good genes for weight gain during infancy were found and bred through the selection process which is what happened here where this result was consistent with findings from other studies when

traits were targeted after intense selective pressures have been applied [70].

In G2, there was a further increase in BV up to 28.56g signifying better chances of gaining weight at four weeks genetically than before. This substantial rise between two generations shows that selection program was still successful as qualities selected for continued being supplied into subsequent generations. The slight drop in realizable heritability (from 0.96 recorded during G1 down to 0.91 observed in G2) implies that though selection is ongoing but maybe genetic variability related with body weight could be declining because individuals were more alike genetically now compared to what they were before [71,72]. In G3, it moves higher still at around 32.41 g per individual suggesting more genes contributing towards increased size while growing within the first month Nevertheless less change can be seen between these last two steps thus rate may slow down due either reduced variety or nearness to peak level concerning given feature improvement through selection.

Accordingly, the given directions in BV over three generations emphasize that genetic diversity is important for sustainable long-term improvement through genetics. While initial response seemed strong as indicated by BV generated upon selection, later generations showed nothing else except decreasing returns leading into doubts about sustaining them if any more new breeds will be tried out Keeping back some of these recently produced types might increase variety so that differentials necessary for setting levels are provided where they do not exist due only to limited number bases beyond which additional improvements cannot be responded by any population given their present status [43,47,72]. In addition to focusing on 4-week body weight, incorporating other traits such as feed efficiency, disease resistance, or reproductive performance might help maintain overall genetic progress and avoid the pitfalls of overly narrow selection objectives [43,69,72].

The BVs (breeding values) for Japanese quails' week body weight across generations depicted success achieved through effective selection but looking at third generation there are no more changes which can be seen thus indicating a need for caution when managing these gains Such strategic adjustments must therefore not be made carelessly in order not to lose what has already been gained up till now All these points should thus be considered together with predicted breeding methods if desirable characters like body weight among others are to continue improving.

Conclusion

Through time the selective breeding of Japanese quails has managed to increase their body weight especially during early ages which saw an improvement of about 35.8% at two weeks. However, later on this growth rate tends to slow down and it could mean that they are nearing the limit of their genes for weight gain. There was an improvement in weight uniformity which is important for standardization although there still existed some level of diversity at 4-weeks. According to genetic analysis conducted there were SNPs found out as having been selected positively due to them being linked with higher weights but there were also other factors like gene-environment interaction and drifts that affected results obtained. These findings suggest alternative methods should be used during breeding such as incorporating fresh genes or utilizing genomic tools so as to surpass this stagnation and improve further on growth traits.

Declaration of Conflict of Interest

The authors declare that there is no conflict of interest.

Ethical of approval

The study protocol was approved by medical Research Ethics Committee (MREC) of national Research Centre, Egypt, under the ethical approval code (13050409). The relevant Egyptian laws and the Egyptian Drug Authority (EDA) and Ministry of Health and Population (MOHP) and Institutional Animal care and Use Committee (1ACUC) decrees, guidelines and recommendations shall be adopted and followed during the conduct of this research.

TABLE 1. Descriptive data for body weight at different age of selected Japanese quail

	Mean	SD	SE	Min	Max	Mode
Base population						
2-weeks	83.19	10.63	0.43	51	115	89
4-weeks	186.69	22.82	0.93	88	246	189
6-weeks	238.64	31.56	1.33	151	262	214
G1						
2-weeks	95.95	10.78	0.88	62	122	95
4-weeks	206	18.97	1.59	149	249	202
6-weeks	264.58	21.09	2.12	205	315	273
G2						
2-weeks	106.33	12.67	0.57	80	149	114
4-weeks	218.07	20.59	1.17	144	275	220
6-weeks	265.81	34.24	2.04	185	369	281
G3						
2-weeks	113	13.39	1.28	80	142	118
4-weeks	222.3	25.25	2.67	153	292	208
6-weeks	267.16	21.90	1.80	234	345	250

TABLE 2. Selection response for 4 weeks of body weight, selection differential, selection intensity and realized heritability in selected Japanese quail

Generation	Selected mean	Selected parents	Selection differential	Response to selection	Selection intensity	Realized heritability
Base	186.69	206	19.31	-	0.97	
G1	206	224.39	18.39	19.31	0.96	
G2	218.07	237	18.93	12.07	0.91	
G3	222.30	-	-	4.23	-	
Sum			**56.63**	**35.68**		**0.63**

TABLE 3. Observed vs. Hardy-Weinberg Predicted Genotype Frequencies for Growth Hormone Gene SNPs at Positions 110, 150, 310, and 390 bp

Genotype	G1		G2		G3	
G/A SNP at position 110 bp						
GG (Homozygous dominant)		X^2		X^2		X^2
	0.34	0.25	0.5	0.068	0.75	0.059
G/A (Heterozygous)	0.66	0.11	0.5	0.068	0.125	0.167
AA (homozygous recessive)	0.0	0.11	0.0	0.00	0.125	0.256
p^2	0.44		0.58		0.65	
$2pq$	0.45		0.38		0.30	
q^2	0.11		0.04		0.03	
Allele G frequency	0.66		0.75		0.81	
Allele A frequency	0.33		0.25		0.19	
G/A mutation at position 150 bp						
AA (Homozygous dominant)		X^2		X^2		X^2
	0.75	0.21	0.5	0.138	0.87	0.093
G/A (Heterozygous)	0.125	0.106	0.25	0.065	0.13	0.028
GG (Homozygous recessive)	0.125	0.025	0.25	0.094	0.0	0.00
p^2	0.44		0.58		0.65	
$2pq$	0.45		0.38		0.30	
q^2	0.11		0.04		0.03	
Allele A frequency	0.81		0.62		0.93	
Allele G frequency	0.19		0.38		0.07	
C/T mutation at position 310 bp						
CC (Homozygous dominant)		X^2		X^2		X^2
	0.28	0.075	0.5	0.27	0.44	0.055
C/T (Heterozygous)	0.57	0.172	0.5	0.028	0.28	0.016
TT (Homozygous recessive)	0.14	0.042	0.0	0.368	0.28	0.067
p^2	0.33		0.56		0.34	
$2pq$	0.48		0.38		0.48	
q^2	0.17		0.06		0.18	
Allele C frequency	0.58		0.75		0.58	
Allele T frequency	0.42		0.25		0.42	
G/T mutation at position 390 bp						
GG (Homozygous dominant)		X^2		X^2		X^2
	0.5	0.043	0.5	0.00	0.57	0.099
G/T (Heterozygous)	0.5	0.016	0.5	0.00	0.14	0.068
TT (Homozygous recessive)	0.0	0.00	0.0	0.00	0.29	0.134
p^2	0.56		0.56		0.41	
$2pq$	0.38		0.37		0.46	
q^2	0.06		0.06		0.13	
Allele G frequency	0.75		0.75		0.64	
Allele T frequency	0.25		0.25		0.36	

TABLE 4. Association between SNPs in growth hormone and body weight at 4 weeks of age of selected Japanese quail

Generation	Genotype		
	G/A SNP at position 110 bp		
	GG	**G/A**	**AA**
G2	186.71 ±8.89	205.95 ±10.78	0.0
G3	200.19 ±13.07	230.06 ±5.59	210.2 ±13.47
	G/A mutation at position 150 bp		
	AA	**G/A**	**GG**
G2	204 ±12.03	201.25 ±8.66	177.90 ±1.85
G3	207.16 ±17.26	216.37 ±19.88	0.0
	C/T mutation at position 310 bp		
	CC	**C/T**	**TT**
G2	192.2 ±18.66	199.5 ±8.78	222 ±5.47
G3	208 ±8.89 9.90	214.58 ±22.64	194.6 ±22.06
	G/T mutation at position 390 bp		
	GG	**G/T**	**TT**
G2	197.42 ±15.05	198.51 ±4.89	0.0
G3	205.96 ±9.47	227.36 ±17.36	194 ±22.06

TABLE 5. Additive and dominance effects of SNPs in growth hormone in selected Japanese quail

Generation	Additive effect	Dominance effect
	G/A SNP at position 110 bp	
G1	0.34	0.49
G2	0.5	0.25
G3	0.62	- 0.31
Mean	0.48 ±0.08	0.14 ±0.23
	G/A SNP at position 150 bp	
G1	0.62	- 0.30
G2	0.25	- 0.12
G3	0.87	- 0.3
Mean	0.58 ±0.18	- 0.24 ±0.06
	C/T SNP at position 310 bp	
G1	0.14	0.15
G2	0.5	0.25
G3	0.16	- 0.08
Mean	0.26 ±0.11	0.10 ±0.09
	G/T SNP at position 390 bp	
G1	0.5	0.25
G2	0.5	0.25
F3	0.28	- 0.29
Mean	0.42 ±0.07	0.07 ±0.18

TABLE 6. Estimated Breeding Values (BV) for 4-Week Body Weight Across Generations in Selected Japanese Quail

Generation	Observed trait value	Mean Trait Value (g)	Realized Heritability (h²)	Estimated Breeding Value (BV)
Base	186.69	186.69	-	-
G1	206	186.69	0.96	18.53
G2	218.07	186.69	0.91	28.56
G3	222.30	186.69	0.91	32.41

(A) GG

110   120
T G C G C A G T G A G G A G G C A G C

(B) AA

110   120
T G C A C A G T G A G G A G G C

(C)   G/A

110   120
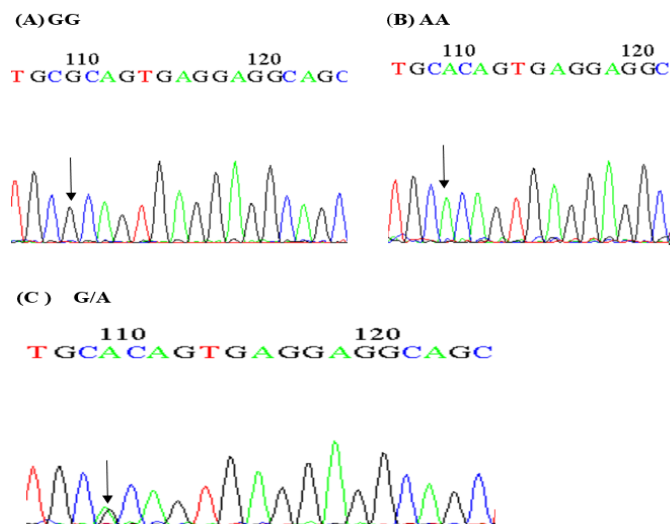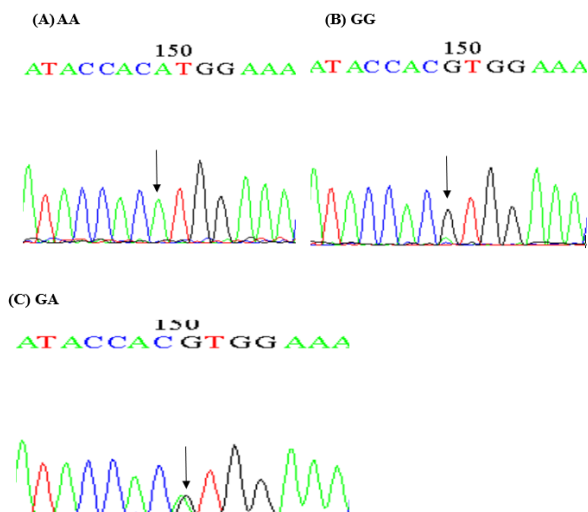T G C A C A G T G A G G A G G C A G C

Fig.1. Genotyping of Japanese quail using DNA sequence of G/A SNP at position of 110 bp of segment of growth hormone gene.   The three patterns were detected as (a) GG   genotype, (b) AA genotype   and (c) GA heterozygous.

(A) AA

150
A T A C C A C A T G G AAA

(B) GG

150
AT A C C A C G T G G AAA
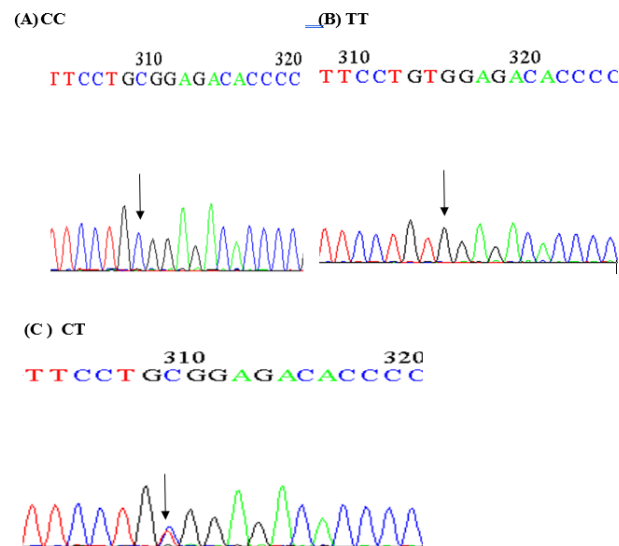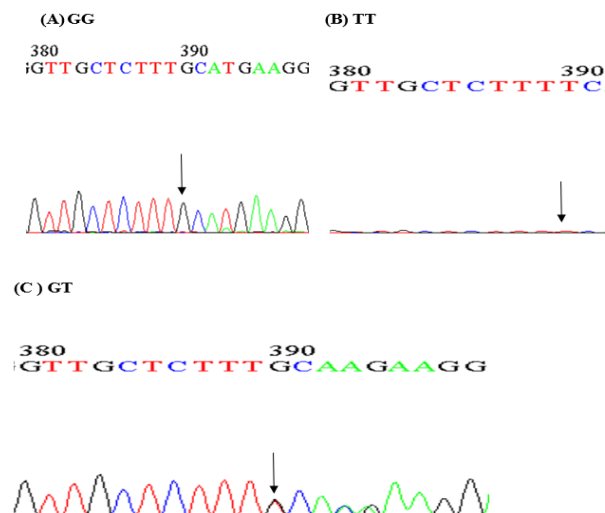
(C) GA

150
AT A C C A C G T G G AAA

Fig.2. Genotyping of Japanese quail using DNA sequence of G/A SNP at position of 150 bp of segment of growth hormone gene.   The three patterns were detected as (a) AA   genotype, (b) GG genotype   and (c) GA heterozygous.

(A) CC   **(B) TT**

310   320   310   320
TTCCTGCGGAGACACCCC   TTCCTGTGGAGACACCCC

(C) CT

310   320
TTCCTGCGGAGACACCCC

Fig.3. Genotyping of Japanese quail using DNA sequence of G/A SNP at position of 310 bp of segment of growth hormone gene. The three patterns were detected as (a) CC genotype, (b) TT genotype and (c) CT heterozygous.

(A) GG   **(B) TT**

380   390
iGTTGCTCTTTGCATGAAGG   380   390
GTTGCTCTTTTC.

(C) GT

380   390
iGTTGCTCTTTGCAAGAAGG

Fig.4. Genotyping of Japanese quail using DNA sequence of G/A SNP at position of 390 bp of segment of growth hormone gene. The three patterns were detected as (a) CC genotype, (b) TT genotype and (c) CT heterozygous.

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الارتباط الوراثي بين تعدد المظاهر الوراثية للنيوكلوتيدة الواحدة (SNPs) بهرمون النمو والمقاييس الانتخابية في السمان الياباني: دراسة متعددة الأجيال

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الملخص

تمثلت هذه الدراسة في تقييم الانتخاب الانتقائي للوزن على مدى ثلاثة أجيال في السمان الياباني وفهم العلاقة بين ثلاثة من انماط تعدد المظاهر الوراثية للنيوكليوتيدة الواحدة (SNPs) في جين هرمون النمو. شمل التحليل متوسط الوزن عند عمر 2 و4 و6 أسابيع، حيث أظهرت النتائج اتجاهًا تصاعديًا من المجموعة الأساسية إلى الجيل الثالث. وقد لوحظت أكبر زيادة في النمو عند عمر الأسبوعين، حيث كانت الزيادة بنسبة (35.8%) بحلول الجيل الثالث، مما يشير إلى نجاح الانتخاب المبكر للنمو. كما تم تقييم استجابة الانتخاب والفارق الانتخابي وكذلك العمق الوراثي لوزن الجسم في الأسبوع الرابع، مما أظهر استجابة وراثية قوية في الجيل الأول بزيادة قدرها (35.8%) ، ولكن مع تراجع الاستجابات في الأجيال اللاحقة. تم إجراء التحليل الجيني باستخدام تعدد المظاهر الوراثية للنيوكليوتيدة الواحدة الموجودة ضمن جين هرمون النمو، حيث أظهرت تغيرات في تكرارات الأليلات المختلفة. وقد كانت الأنماط الجينية المختلفة لتعددات SNP مرتبطة بشكل مستمر بزيادة في الأوزان أكثر من المعتاد، مما يوفر مؤشرات لاستراتيجيات تحسين الوراثي مستقبليا. بالإضافة إلى ذلك، تفاوتت التأثيرات الإضافية عبر الأجيال، مما يعني الحاجة إلى استراتيجيات محددة تهدف إلى التلاعب بالجينات المسؤولة عن التحكم في زيادة الوزن خلال فترات معينة أثناء مراحل النمو، مع الحرص على عدم التدخل في العمليات البيولوجية الهامة الأخرى التي تحدث في الوقت ذاته. وأظهرت الدراسة أيضًا أن قيم التربوية المقدرة (EBV) لوزن الجسم في الأسبوع الرابع زادت بشكل ملحوظ بين الجيل الأول والجيل الثالث، ولكن الزيادات اللاحقة أصبحت أقل. و بالنهاية تعتبر هذه الدراسة مهمة لصناعة السمان الياباني تجاريا لأنها ستساعد المزارعين على تحسين خططهم التربوية للوصول إلى الأوزان المطلوبة باستخدام طرق الانتخاب الوراثي خلال فترات النمو المبكرة.

الكلمات الدالة: : السمان الياباني، الانتخاب قصير الأمد، هرمون النمو، تعدد المظهر الوراثية للنيوكليوتيدة الواحدة، القيمة التربوية المقدرة.

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