GENETIC PARAMETER ESTIMATES FOR PRODUCTION TRAITS, GLUTATHIONE PEROXIDASE AND HAEMATOLOGICAL PARAMETER IN JAPANESE QUAIL

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A DISSERTATION SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES, AHMADU BELLO UNIVERSITY, IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (ANIMAL SCIENCE)

DEPARTMENT OF ANIMAL SCIENCE,
FACULTY OF AGRICULTURE,
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ZARIA, NIGERIA

FEBUARY, 2017

DECLARATION

I hereby declare that this dissertation titled "Genetic parameter estimates for Glutathione peroxidase and haematological traits in relation to production in Japanese quail" has been written by me in the Department of Animal Science, Ahmadu Bello University, Zaria, under the supervision of Prof. B.I Nwagu and Dr. M. Kabir. The information derived from the literature has been duly acknowledged in the text and the list of references provided. No part of this dissertation was previously presented for another degree or diploma at any university.

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SHATU BULAMA Date

Name of Student

CERTIFICATION

This dissertation entitled GENETIC PARAMETER ESTIMATES FOR PRODUCTION TRAITS GLUTATHIONE PEROXIDASE AND HAEMATOLOGICAL PARAMETER IN JAPANESE QUAIL by Bulama Shatu meets the regulations governing the award of the degree of Master of Science in Animal Science of Ahmadu Bello University, Zaria, Nigeria and is approved for its contribution to knowledge and literary presentation.

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Prof. B.I. Nwagu. Date
Chairman, Supervisory Committee

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Member Supervisory Committee

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DEDICATION

This dissertation is dedicated to my caring parents, my beloved husband and my sons Ali and Abubakar.

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ABSTRACT

A study was designed to estimate genetic parameters of growth, haematological and glutathione peroxidase enzyme activity and egg production characteristics in the base, F_1 (first filial) and F_2 (second filial) generations of Japanese quail. A total of 100 day old chicks were raised on diet containing 26% CP and 2741 ME Kcal/Kg until 4 weeks of age, and then were introduced to breeder diets containing 24%CP and 2900 ME Kcal/kg; 45 females and 15 males were randomly selected using a mating ratio of 1male: 3 females. Bird shank length, body length and thigh length of the quails were measured in cm at four and six weeks of age. Birds were weighed in Grams at two, four and six weeks of age. Growth rate during the periods of two, four and six weeks were calculated. About 1.5ml of blood was collected at six and nine weeks of age and evaluated for glutathione peroxidase (GPx) in plasma and other haematological variables. Also, Egg production measures such as age at sexual maturity, egg number and egg weight at nine weeks, days in lay and rate of lay were recorded. Obtained data were subjected to one-way analysis of variance to test sex effect, generational effect of egg production, Phenotypic correlation between growth, haematological, enzyme activity and egg production variables and heritability estimate were also determined in the F_1 and F_2 generation. The result showed that GPx enzymes activity and blood plasma constituents are positively correlated with growth traits and egg production traits. Heritability of Glutathione peroxidase based on sire variance was high. (F_1 0.51: F_2 0.55). In conclusion glutathione peroxidase activity were high in females than in males (Females 12.75u/g, Males 12.18u/g) GPx enzymes activity and blood plasma constituents are positively correlated with growth traits and egg production traits. Therefore selection for either of the traits (GPx enzymes and Blood

constituents) may lead to improvement in the other traits (Growth and Egg traits). Correlation among blood parameters could be use as a good indicator to other traits. Heritability of Glutathione peroxidase based on sire variance was high. (F_1 0.51, F_2 0.55). This indicates that there are higher chances of passing the gene from the parent to the next generation. Also the higher the heritability the higher the gain in selection response.

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CHAPTER ONE

1.0 INTRODUCTION

Current trends indicate that 80% of the world's populations are living in the under-developed countries and a significant number of these have large food deficits. An increased production of animal protein would make an important contribution towards filling this deficit (FAO 1992). Poultry production is a fast means of meeting the ever-increasing demand for animal protein supply especially in Africa, where intake of anima protein is relatively low. This is because poultry production has a rapid turnover rate. In other words, several tons of meat and eggs can be produced in a relatively short interval of time. This prompted breeders to put more interest in the breeding of quails.

The production of Japanese quails (*Coturnix coturnix japonica*) has gained tremendous interest among Nigeria populace especially because they are the smallest avian species farmed for meat and egg production (Panda and Singh, 1990). Quail have short generation interval and early sexual maturity (5-6 weeks); fast growth rate, attaining market weight (150-180g) in six week. Quail can produce 250-280 eggs per year have lower feed and space requirements than domestic fowl (Anthony *et al*., 1993). They are also known for their low caloric value in addition to having quality protein of high biological value (Haruna *et al*., 1997). Studies using Japanese quails in breeding experiments have demonstrated that this species offer scientist several advantages in exploring breeding systems and certain problems of poultry breeding.

Estimation of genetic parameters is primordial to the establishment of strategies to be used in animal breeding programmes because with the study of parameters, such as heritability, repeatability and correlation between traits, the evaluation of response to selection for a trait and

genetic associations among traits become possible. Experimental research established that body weight of Japanese quail responded quickly to selection (Nestor and Bacon, 1982; Caron *et al*., 1990; Marks, 1993). At the same time Japanese quail farming for meat production has expanded in several countries (Baumgartner, 1994; Yalcin *et al*., 1995; Minvielle, 1998). Estimation of genetic parameters for Japanese quail mostly focused on the weekly live weight (Anthony *et al*., 1993; Marks, 1996; Saatci *et al*., 2003). In Japanese quail, heritability of body weight varies from 0.3 to 0.72 (Kocak *et al*., 1995; Abdel *et al*., 2006 and Saatci *et al*., 2006). If there is a genetic correlation between characters under selection, the overall response to selection will change according to the heritability of the traits examined, and the strength and sign of the genetic covariance among them (Jesen *et al*., 2003).

Genetic correlation is important to animal breeders because they represent the correlation between the breeding values of two traits. A genetic correlation between two traits will result in correlated response to selection (Falconer, 1989). A wide range of heritability estimates for body weight has been cited by many researchers (Caron *et al*., 1990, Abdel *et al*., 2006 and Saatci *et al*., 2006). Genetic studies on Japanese quail will enable breeders design suitable improvement programmes for the bird, therefore reliable estimate of genetics parameters are necessary to predict the direct and indirect selection responses.

Physiological and haematological parameters are good indicator to predict and estimate productive and reproductive performance (Emmerson, 2003). Several investigations were conducted to relate chicken performance with some parameters of blood (Attia, 2002 and Alm EL Dein *et al*., 2008). Genetic research is now directed toward the investigation of the relationship between physiological, biochemical and metabolic markers to the productive efficiency of farm animals. Biochemical traits include blood group, blood proteins and enzymes

which have been studied with a view to explain the physiological basis of performance traits and the zeffect of heterosis (Orunmuyi *et al*., 2007). A wide range of heritability has been reported in Japanese quail for some blood constituents (Avci *et al*., 2007 and Bahie EL Deen *et al*., 2009). In Japanese quail, heritability of blood constituents ranges from 0.45 to 0.51 Farahat *et al*. (2010a). It has been experimentally proved that all traits of production, reproduction and genetic diseases are controlled by the biochemical activities in the body of the individuals and these are accomplished by the several types of proteins such as serum protein, enzymes, and hormone (Das and Deb, 2008)

Glutathione peroxidase belongs to the family of selenoproteins and plays an important role in the defense mechanisms of mammals, birds and fish against oxidative damage by catalyzing the reduction of a variety of hydroperoxides, using glutathione as the reducing substrate (Mahan, 1999). It is the cell's most important antioxidant, neutralizing "free radicals" that would otherwise damage or destroy the cells. The body produces free radicals during metabolism. Under any form of stress, such as chemical toxicity or bacterial infections, the body generates many more free radicals. If glutathione is in short supply, these free radicals can overwhelm the cell (McCord, 2000).

Glutathione is also the main detoxifying agent in the body. It converts damaging chemical substances (toxins) into harmless products that the body eliminates. Such chemicals include cancer-producing substances, heavy metals, herbicides, pesticides, smoke and other pollutants (Fridovich, 1999). Thus, glutathione provides important protection against many environmental hazards (Arthur, 2000). Damages due to free radicals lead to cellular injury, cancer, aging, atherosclerosis, other pathological disorders and dysfunctions in some organs. Glutathione peroxidase activity is considered as markers for evaluation of oxidative stress and in maintaining

the health, productive and reproductive characteristics of the animals (Spurlock and Savage, 1993). Heritability estimate for glutathione peroxidise in quails ranges from 0.45 to 0.51 reported by Gehan *et al.*(2010). There are some observations about the correlation of antioxidant enzymes activities and body weight, weight gain, growth rate in quails (Gehan *et al*., 2010), chickens and rabbits (Mezes *et al*., 1994; Farahat *et al*., 2008 a and b and Ragab *et al*., 2010).

1.1 JUSTIFICATION

Commercial poultry breeding has amongst its objectives, the improvement of production potential and disease resistance. Over the years there has been much emphasis on growth improvement that is positively associated with some aspect of immunological performance of poultry as reported by Yunis *et al*. (2000) and Cheema *et al*. (2003).

Some experiments have shown that glutathione peroxidise activity was found to correlate with several production traits (Lingas *et al*.,1991, Mezes *et al*., 1994 and Mezes *et al*.,1996). It has also been reported that glutathione peroxidase activity and most of blood constituents are genetically and phenotypically correlated with each other with high significant values (Gehan *et al*., 2010).

Significant relationship between blood biochemical features related to health such as glutathione peroxidase activities and blood constituents with performance are needed for the design of breeding programmes aimed at improving the balance between production and health traits. The Information on the relationship of glutathione peroxidase and haematological traits to performance traits of Japanese quails raised in Nigeria are, scanty. The present work therefore was designed to evaluate the following hypotheses:

1.2 HYPOTHESES

H_0: Glutathione peroxidase has no association with physiological and productive performance of Japanese quails.

Haematological parameters have no association with physiological and performance of Japanese quails.

H_A: Glutathione peroxidase has association with physiological and productive performance of Japanese quails.

Haematological parameters have association physiological and productive performance of Japanese quails.

1.3 OBJECTIVES

1. To measure performance character (Body weight, growth rate and morphometrical body measurements) in F_1 and F_2 generations.
2. To estimate the genetic parameters for egg production, body weight and morphometric traits.
3. To estimate the genetic parameters for glutathione peroxidase and haematological parameters.
4. To estimate the level of glutathione peroxidase in males and females.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Japanese Quail

The Japanese quail belongs to the order Galiformes, family *Phasinidae,* genus *Coturnix* and species *japonica*. The scientific designation for Japanese quail is *Coturnix japonica*, different from the common quail *"Coturnix coturnix*" (Thear, 1998; Mizutani, 2003). The first record of wild Japanese quail appeared in the eight century in Japan and these species are found in Japan, Korea, Eastern China, Mongolia and Sakhalin as migrating birds. The plumage color of the wild type is predominately dark cinnamon brown. However, adult female have pale breast feathers that are speckled with dark colour spots. Adult males have uniform dark rusted feathers on the breast and cheek (Mizutani, 2003). This sex differences in plumage color appears at about 3 weeks of age. Domesticated Japanese quail retain wild type plumage, although they have a variety of other colourations, including white plumage (Mills *et al*., 1997). The Japanese quail, originally domesticated around the 11th century as a pet song bird (Howes, 1964; Crawford, 1990; Kayang *et al*., 2004), has since gained value as a food animal (Wakasugi, 1984; Kayang *et al*., 2004). Several features accounted for the utility of this bird. First, it has attained economic importance as an agricultural species producing eggs and meat that are enjoyed for their unique flavour (Kayang *et al*., 2004). Egg production is important in Japan and Southeast Asia, while meat is the main product in Europe (Baumgartner, 1994) and are often bred as dual-purpose birds in other Asian countries (Minvielle, 1998). Secondly, the low maintenance cost associated with its small body size (80-300 g) coupled with its rapid growth - enabled quail to be marketed for consumption at 5 - 6 weeks of age; its early sexual maturity - resulting in short generation

interval (3-4 generation per year), resistance to diseases and high egg production; rendered it as an excellent laboratory animal (Woodard *et al*., 1973; Baumgartner, 1994; Yalcin *et al*., 1995; Oguz and Minvielle, 2001). Thirdly, Japanese quail is also the smallest avian species farmed for meat and egg production (Baumgartner, 1994).

2.2 Blood Parameters in Japanese Quail

Over the years many researchers have focused their genetic studies on improving only economic traits. This improvement of physiological parameters is negatively associated with some aspects of immunological performance in poultry and has led to undesirable effects as reported by Yunis *et al*. (2000) and Cheema *et al*. (2003). A broader perspective of improved and efficient genetic study has emerged because, selection, breeding and genetic improvement have a marked effect on characteristics of the blood biochemistry; as researchers utilize the biochemical parameters of the blood as markers in livestock species to enhance productivity and reproductive performance (Nguyen and Tran, 2003 and Emmerson, 2003). Pagot (1992) noted that genetic resources such as serum enzymes, serum proteins and bilirubin have been established as genetic markers in farm animals. A wide range of the blood biochemistry and its relationship to poultry species performance has been reported in literature. In chickens, Abdel Latif (2001) looked at total protein in Dandarawi and Golden Montazah hens; glucose was studied in Dandarawi and Golden Montazah chickens (Attia, 2002) and local Iraqi fowl (Al-Hillali *et al*., 2007); Alkaline Phosphatase activity in Rhode Island (Orunmuyi *et al*., 2007) and Glutathione peroxidase enzyme activity in two broiler strains (Ragab *et al*. 2010) while Dutta (2010) studied the haemato-biochemical parameters in a number of chicken breeds. Bahie El-Deen *et al*. (2009) studied total protein.

Commercial poultry breeding has amongst its objectives, the improvement of production potential and disease resistance. The blood biochemical analysis is a valuable tool for evaluating traits in breeding for high productivity (Obeidah *et al*., 1978) and as indicator for the health of animal and helps both in diagnosis and clinical monitoring of disease (Karesh *et al*., 1997). Its evaluation indicates the extent of damage in various vital organs and status of the disease. Serum biochemical profiling has been used in several species of domestic livestock to monitor herd health and to detect subclinical disease. Existence of any significant relationship between blood biochemical features (such as glutathione) with animal performance is needed for the design of breeding programs aimed to improve the balance between production and health traits.

2.3 Free Radicals and Antioxidant Defence

2.3.1 Free radicals

Free radicals are defined as molecules having an unpaired electron in the outer orbital (Gilbert, 2000). They are generally unstable and very reactive. Examples of oxygen free radicals are superoxide, hydroxyl, peroxyl, alkoxyl and hydroperoxyl (HO_2) radicals. Nitric oxide and nitrogen dioxide (NO_2) are two nitrogen free radicals. Oxygen and nitrogen free radicals can be converted to other non-radical reactive species, such as hydrogen peroxide (H_2O_2), hypochlorous acid (HOCl), hypobromous acid (HOBr) and peroxynitrite ($ONOO^-$). Reactive oxygen, reactive nitrogen species and reactive chlorine species are produced in animals and humans under physiological and pathological conditions (Evans and Halliwell, 2001).

2.3.2 Functions of free radicals

Free radicals played important role in the origin of life and biological evolution, implicating their beneficial effects on the organisms (McCord, 2000). For example, oxygen radicals exert critical

actions such as signal transduction, gene transcription and regulation of soluble guanylate-cyclase activity in cells (Zheng and Storz, 2000). Also Nitrogen oxide (NO) is one of the widest spread signalling molecules and participates in virtually every cellular and organ function in the body (Ignarro *et al*., 1999). Physiological level of NO produced by endothelial cells are essential for regulating the relaxation and proliferation of vascular smooth muscle cells, leukocyte adhesion, platelet aggregation, angiogenesis, thrombosis, vascular tone, and haemo-dynamics (Ignarro *et al*., 1999). In addition, Nitrogen oxide (NO) produced by neurons serves as a neurotransmitter and NO generated by activated macrophages is an important mediator of the immune response (Fridovich,1999). However, as oxidants and inhibitors of enzymes containing an iron-sulphur centre, free radicals and other reactive species cause the oxidation of biomolecules (e. g., protein, amino acids, lipid and DNA), which leads to cell injury and death (Fridovich, 1999; McCord, 2000). For example, radiation-induced ROS markedly alter the physical, chemical and immunological properties of superoxide dismutase (SOD) (Fang, 2002), which further exacerbates oxidative damage in cells. The effect of free radicals is deleterious to mammalian cells and mediates the pathogenesis of many chronic diseases, but is responsible for killing pathogens by activated macrophages and other phagocytes in the immune system (McCord, 2000). Thus, there are two faces of free radicals in biology in that they serve as signalling and regulatory molecules at physiologic levels, but as highly deleterious and cytotoxic oxidants at pathologic levels (Fridovich, 1999).

2.3.3 Scavenging of free radicals

The removal of free radicals is achieved through enzymatic and non-enzymatic reactions. NO is rapidly oxidized by oxyhemoglobin to form NO (nitrate), the major stable oxidation end and product of NO in the body (Wu *et al*., 1999). NO also reacts with glutathione (reduced; GSH) to form nitrosothiol or with heme to yield heme-NO. Physiologically, nitrosothiol can serve as a vehicle to transport NO in plasma, thereby increasing the biological half-life of physiological concentrations of NO (Rassaf *et al*., 2002). In addition, tyrosine residues of proteins can be nitrosylated by NO or its derivative peroxynitrite. Moreover, GSH can scavenge and peroxynitrite ($ONOO^-$) with the formation of oxidized glutathione (GS-SG), which is converted back to GSH by the NADPH-dependent glutathione reductase (Sies, 1999).

The tocopheroxyl radical can be returned to the active form of tocopherol by recycling reactions with other antioxidants including ascorbic acid, glutathione, carotenoids and ubiquinol (Surai, 1999b). The second product of antioxidant action of vitamin E is a hydroperoxide. Hydroperoxides are toxic substances and if not removed impair membrane structure and function (Gutteridge and Halliwell, 1990). Therefore hydroperoxides must be removed from the cell in the same way as H_2O_2 but catalase cannot react with these compounds. Only Se-dependent GPx can convert these compounds into non-reactive products (Flohé, 1999).

Therefore it appears that as the major antioxidant in the biological system, vitamin E performs only half the job of removing free radicals and producing hydroperoxides. The second part of the process is dependent on the activity of GPx. As a reducing agent, vitamin C reacts with a vitamin E radical to yield a vitamin C radical, while regenerating vitamin E. Like a vitamin E radical, a vitamin C radical is not a reactive species; because its unpaired electron is energetically stable

(Fang, 2002). A vitamin C radical is converted back to vitamin C by GSH. Glutathione, the most abundant thiol-containing substance of low molecular weight in cells, is synthesized from glutamate, cysteine, and glycine. N-acetylcysteine is a stable, effective precursor of cysteine for intracellular GSH synthesis (Sies, 1999).

2.4 Glutathione Peroxidase in Biological System

In general, an integrated antioxidant system has been described in avian tissues (Surai, 1999a, 2002); and it has been suggested that the first line of cellular antioxidant defence is based on the activity of three enzymes: superoxide dismutases (SOD), glutathione peroxidise (GSHPx) and catalase. In this respect GSHPx has received only limited attention in relation to poultry production. However, during recent years the importance of this enzyme in the antioxidant protection of tissues has become increasingly appreciated. Since the major form of GSHPx is selenium-dependent, the role of selenium in animal nutrition has attracted considerable attention (Mahan, 1999). Selenium is recognized as having anti-carcinogenic and antiviral properties and is known to have important roles in reproductive function and development, immune competence and aging. These selenium functions have been described recently in a series of comprehensive reviews. The role and responses to dietary selenium in poultry nutrition appeared during the 1970s; and recent understanding of antioxidant system functions and new discoveries regarding the GPx enzyme family are the basis for further development in the selenium nutrition of poultry. The importance of selenium in animal nutrition lies in the fact that both first (detoxification of H_2O_2 formed by SOD action) and second (detoxification of hydroperoxides) levels of antioxidant defence in the cell rely on the activity of Se dependent GPx, which in turn depends on adequate Se status in the cell. Furthermore, even at very high levels of dietary vitamin E there is a need for selenium (Surai, 2000). This is in agreement with data showing that high levels of dietary

vitamin E do not replace cellular GPx in protecting mice from acute oxidative stress (Cheng *et al*., 1999). During selenium deficiency lipid peroxidation is accelerated and damage to biological molecules can be lethal for the cell (Halliwell and Gutteridge, 1999) .A delicate antioxidant/prooxidant balance in the body are an important determinant of chicken health, embryonic development, sperm quality and probably productive and reproductive characteristics of poultry. There are different ways in which the antioxidant system can be altered or regulated. The most important regulation is the animal response to stress condition by synthesizing antioxidant enzymes, (e. g. SOD and GPx). However, this response will be effective only if cofactors such as selenium for GPx and Cu, Zn and Mn for SOD are available. Therefore, dietary Se is a crucial factor regulating GPx activity and the efficiency of the antioxidant system (Surai, 1999a; 2000; 2002; Surai and Dvorska, 2001).

2.5 Genetics of GPx Enzyme Activity

Several factors are known to affect the GPx activity including dietary selenium, age and sex, oestrus cycle, and environmental factors including exposure to ozone or ingestion of peroxidised lipids. Also there are some publications suggesting significant role for genetics in regulation of its activity. Gehan. (2003) have shown that GSH concentration is controlled by a single pair of alleles has a positive relation between GSH concentration and GPx activity. Such an association might explain the origin of the genetic differences.

2.5.1 Phenotypic variation of GPx enzyme activity in different animal species

There are numerous data about the phenotypic variations of GPx enzyme activity in different animal species. The actual activity of the enzyme depends on the rate of gene expression (Condeell and Tappel, 1983, Takahashi *et al*., 1987) and also affected by the amount

of substrate, e. g. lipid peroxides (Sies, 1986 and Sagar *et al*., 1998), selenium supply (Rotruck *et al*., 1973) and amino acid (methionine and cysteine) supply (Wang *et al*., 1997). Among the above mentioned factors the genetic one has importance, but it is markedly modified by the environmental factors. The presence of the enzyme activity in so many animal groups implies the wide spread occurrence of genetic information for the specific assimilation of the selenium atom Considering the phylogenetic distribution of total GPx activity, the rodent limb of the phylogenetic tree has the highest activity. The regulation of GPx gene expression relevant to species difference was studied by Toyoda *et al*. (1989) and these results suggested that GPx activity in the cytosol of all guinea-pig tissues examined are extremely low as compared with those in mice and rats. The species difference of GPx activity observed in rodents might be due to incapability of gene transcription. It is well-known that various animal species and various strains of mice show different degrees of susceptibility to oxidant gases such as nitrogen dioxide and ozone. However, the biochemical causes of the differences in susceptibility to oxidant gases between various animals still remain in question. Antioxidant protective enzymes were examined in the lung of four animal species exposed to a mixture of nitrogen dioxide and ozone for two weeks. Male mice, hamsters, rats and guinea pigs were used. The most characteristic change is the significant increase in GPx activity in hamsters and rats followed by mice and guinea pigs are genetically deficient in this enzyme (Ichinose *et al*., 1988).

The activity of GPx in seminal plasma varied markedly among species. In boar and stallion the seminal plasma activity is absent, while the human and ram GPx activity are rather low. In contrast, bovine seminal plasma displays a high activity (Saaranen *et al*., 1989). To better define the species-specific antioxidant systems and to ascertain the influence of the intracellular redox status on the immune system of different animal species, Chiaradia *et*

al. (2002) determined lymphocyte GPx activity in horse, sheep and dog. Sheep presented the highest GPx activity, dogs have the lowest and horses display intermediate values. Species-specific expression of GPx has been found in fowl seminal plasma and spermatozoa (Surai *et al*., 1998a; 1998b, 1998c). Studied in five avian species, the total GPx activity in seminal plasma is significantly higher in turkeys than in ducks and geese. In contrast, waterfowl species; geese and ducks are characterised by the highest sperm GPx activity. Such high expression of GPx in duck semen is shown to be acompensatory mechanism to protect drake spermatozoa with high levels of PUFA and low vitamin E concentration against lipid peroxidation (Surai *et al*., 2000). It is important to note that the Se-dependent form of GPx comprised between 77.7% (chicken) and 87.4 %(guinea fowl) of total enzymatic activity. The enzyme is distributed between spermatozoa (40%) and seminal plasma (60%) (Surai *et al*., 1998a).

2.5.2 GPx activity in chicken

Hull and Scott (1976) reported that GPx activity was equivalent in both chick strains of muscular dystrophic and non-dystrophic in plasma and liver, but was significantly increased in dystrophic once. GPx activity was as sayed in the superficial pectoral muscles of genetically dystrophic chickens (line 413) and their control (line 412) by Mizuno (1984) and he found that in dystrophic chickens GPx activity was significantly elevated at all stages of development studied and their developmental time courses was quite different from those in the controls. Broiler chickens showed significantly lower blood GPx activity than Leghorn-type chickens (Shen *et al*., 1992). The involvement of lipid peroxidation in the development of liver haemorrhages in layer hen chickens was investigated in two White Leghorn strains of birds, a commercial layer strain and strain UCD-003, which is pre disposed to the development of liver haemorrhages. Liver GPx activity and egg production in UCD-003 birds was lower than in

the normal birds (Wu and Squires, 1997). Antioxidant enzyme activity in Pulmonary Hypertension Syndrome (PHS) inbroilers was reported by Iqbal *et al*. (2002) and they found that lung mitochondria and liver GPx activity was elevated in broiler with PHS compared to healthy bird, higher GPx activity in PHS could be due to up-regulation of the expression of this enzyme an important adaptive response to greater hydrogen peroxide production as a result of electron leakage from the respiratory chain (Iqbal *et al*., 2001a). Also lung mitochondria isolated from broilers selected for PHS resistance exhibited lower GPx activity compared to lung mitochondria from broilers that were not selected for PHS resistance and there were no differences in GPx activity in liver. Greater hydrogen peroxide production was observed in broilers that were not selected for PHS resistance than in selected lung mitochondria as a consequence of greater electron leakage from the respiratory chain (Iqbal *et al*., 2001b). These findings therefore indicate that broilers that were not selected for PHS resistance lung mitochondria experience an inherently greater degree of oxidative stress than broilers that selected for PHS resistance lung mitochondria that would potentiate hydrogen peroxide formation. Lung mitochondria from broilers that were selected for PHS resistance birds exhibited higher GPx that would help in catabolising the greater hydrogen peroxide. Genetic resistance to PHS is associated with lower oxidative stress and improved mitochondrial function (Iqbal *et al*., 2001 a, b). However, no differences were found in the GPx activity in the liver of birds of two strains of single comb white leghorn chickens (Squires and Wu, 1992).

Previous studies have indicated that growth responses of young chicks to severe uncomplicated nutritional deficiency of Se may involve a hereditary component. Bunk and Combs (1981) observed that Leghorn chicks fed an amino acid-based diet containing an exceedingly low amount of Se, but adequate with respect to all other known nutrients, showed considerable

variation in effects on growth and survival. They found that although one-third of the population showed severely depressed growth with associated pancreaticexocrine dysfunction, an equal proportion was able to grow apparently normally. This observation was also made by LaVronga and Combs (1982), who tested the hypothesis that variance in the growth response to severe Se deficiency is due to hereditary factor. Their results showed the feasibility of developing, through selective breeding, lines of Single Comb White Leghorn chickens that differed in sensitivity to dietary Se-deficiency as measured by impairment in the growth of young chicks. Further, they showed that such line-related differences in growth were associated with analogous differences inmethionine-methyl group oxidation rate, which suggests that a lesion in the metabolism of the sulphur-containing amino acids may be the site of hereditary involvement in the metabolic need for Se. Subsequent studies by Halpin and Baker (1984) found similar evidence of aberrant sulphur-amino acid metabolism in one meat-type strain of chicken but effects in a Leghorn strain or a crossbred strain. The extent to which the consequences of nutritional Se deficiency may differ among genotypes is of fundamental importance to understanding the role of Se in normal metabolism and of practical significance to poultry feeding particularly in parts of the world with endemic Se deficiency (Cunningham *et al*., 1987).

2.6 Factors Affecting Gpx Activities

2.6.1 Effect of breed on GPx activity

The activity of GPx in seminal plasma varied markedly among species. In boar and stallion the seminal plasma activity is absent, while the human and ram GPx activity are rather low. In conterast, bovine seminal plasma displays a high activity (Saaranen *et al*., 1989). To better define the species-specific antioxidant systems and to ascertain the influence of the intracellular redox

status on the immune system of different animal species, Chiaradia *et al*. (2002) determined lymphocyte GPx activity in horse, sheep and dog. Sheep presented the highest GPx activity, dog had the lowest and horses displayed intermediate values. Species-specific expression of GPx has been found in fowl seminal plasma and spermatozoa (Surai *et al*., 1998b). Studied in five avian species, the total GPx activity in seminal plasma is significantly higher in turkys than in ducks and geese. In contrast, waterfowl species; geese and ducks are characterized by the highest sperm GPx activity.

2.6.2 Effect of sex on GPx activity

Several studies have suggested that many enzyme activities in animal tissues are affected by sex. Sex differences in GPx activity may be the result of differences in distribution of selenium in male and female, or they may be caused by metabolic differences (Finley and Kincaid, 1991). There are several hypotheses, which may provide a physiological basis for sex differences in Se concentration and GPx activity: Selenium distribution to tissues may be different for males and females because of the greater priority for Se by some tissues. For example, the testes of males have priority for Se during deficiency (Behne *et al*., 1982), where as the female has no comparable tissue Selenium deficiency appears to depress cytochrome P-450 activity in hepatocytes (Burk *et al*., 1978), but this effect of Se does not appear to be mediated by GPx (Burk, 1983). Because cytochrome P-450 activity is greater in male rat hepatocytes than in females (Schenkman *et al*., 1967; Montellano, 1986). A larger amount of hepatic Se may be associated with non-GPx functions, such as cytochrome P-450. This may result in less selenium available for GPx, and thus lower GPx activity.

Cytochrome P-450 has peroxidase activity (Montellano, 1986). Higher activity of this system in male rats may result in lower need for GPx. The higher metabolic activity of males in general, resulting in a greater need for oxygen radical protection. Males have greater plasma, kidney, cytosol and RBC GPx activity and Se centration than females in rats (Finley and Kincaid, 1991; Debski *et al*., 1992). Male rats have higher levels of glutathione peroxidase in myocardium than in females (Barp *et al*., 2002). Burk (1983) stated that GPx activity decreased more quickly in Se-deficient livers of male than female rats. GPx activity, however, is higher in female than in male rat's liver in both Se deficient and Se adequate diet (Burk, 1983; Capel and Smallwood 1983; Igarashi *et al*., 1984; Debski *et al*., 1992; Prohaska and Sunde, 1993; Sachdev and Sunde, 2001). GPx activity is more than double in hepatic mitochondria from rat's females than in those from males of the same age (Borras *et al*., 2003). However, Capel and Smallwood (1983) reported that no significant differences found in comparison of glutathione peroxidase activity of the blood and brain tissues of male and female rat.In mice liver GPx activity is higher in females compared to males (Prohaska and Sunde, 1993). GPx activity in red blood cells is higher in females than in males, but greater in plasma and aorta in males of Japanase quail (Godin *et al*., 1995). Blood glutathione peroxidase activities in normal dromedary camels were as sessed in the Canary Islands by Corbera *et al*. (2001) and they found that females have significantly higher blood glutathione peroxidase activity than males. However, sex had no apparent influence on GPx activity of the red blood cell (Jørgensen *et al*., 1977) and in whole blood (Lingaas *et al*., 1991) of pigs. No available data concerning the sex effect on GPx activity in chickens were found in the literature.

2.6.2. Effect of age on GPx activity

The life in an oxygen-rich environment has required the evolution of effective cellular strategies to detect and detoxify metabolites of molecular oxygen known as reactive oxygen species. The appropriate and in appropriate production of oxidants, together with the ability of organisms to respond to oxidative stress, is intricately connected to ageing and life span (Toren and Nikki, 2000). Nearly a century ago it was noted that animals with higher metabolic rates often have shorter life spans. These observations led to the formation of the rate-of-living hypothesis, which states that the metabolic rate of a species ultimately determines its life expectancy. Initially, the mechanistic link between metabolism and ageing was unknown. In the mid '50s, Denham Harman articulated a free-radical theory of ageing, speculating that endogenous oxygen radicals were generated in cells and resulted in a pattern of cumulative damage (Harman, 1956). According to its free radical theory, ageing can be viewed as a process of irreversible changes associated with an accumulation or integration of free radical induced damages in the cell (Harman, 1956). According to the free radical theory ageing proposes as consequence of the deleterious effects of oxygen free radicals produced during normal cellular metabolism (Harman, 1988). Virtually all cellular components, including DNA, proteins and lipids are susceptible to oxidative modifications (Stadman, 1981; Halliwell and Gutteridge 1984).

Oxidative damage to cellular structure and function was shown to be associated with age-related diseases, such as atherosclerosis, muscular dystrophy,arthritis, diabetes, pulmonary dysfunction, various neurological disorders and cancer (Yu,1994). Brown adipose tissue responds to physiological stimulation with high rates of mitochondrial O_2 consumption, and with high rates of lipid turnover, in rats. These are the most susceptible molecules to

peroxidation. Thus, it is important to elucidate the changes in antioxidant defence and lipid peroxidation that occur in this tissue during the life time of the organism. It was shown that during the development from young to mature adult age quantitatively increases of all the antioxidant enzymes, including GPx, take place in brown adipose tissue (Lopez-Torres *et al*., 1991).

In red blood cells of rats GPx activity increased with age was reported by Flohé and Zimmermann (1970), while the opposite tendency was found by Glass and Gershon (1984). In sheep, red blood cell glutathione peroxidase activity slightly decreased with age (Atroshi and Sankari, 1981), while increased as effect of ageing in porcine blood (Jørgensen *et al*., 1977). The GPx activity increased with age in liver of rats (Jang *et al*, 1998 and Palomero *et al*., 2001), but the opposite tendency was found in mice (Muradian *et al*., 2002). In the small intestine of rats the enzyme activity was not affected by age (Jang *et al*, 1998). In the rat brain, GPx activity after an initial fall increases steadily with age (Scarpa *et al*., 1987), however, no significant age-related changes were found in the activity in any of the brain areas (Vertechy *et al*., 1993). In the lung of rats the enzyme activity increased with age (Gumuslu *et al*., 2001).

In the kidney of Wistar rat's glutathione peroxidase activity showed an increase with age (Santa and Machado, 1986), but decreased with age in mice (Toshinai *et al*., 1997). Testicular glutathione peroxidase activity was twice as high in 4-months old animals as in weanling rats (Behne *et al*., 1986). Yidiz *et al*. (2002) reported that GPx activity in uteri was lower in young female sheep as compared to adult ones.In guinea pig, the activity of GPx decreased significantly with age in the mitochondrial fractions of cerebral cortex and hypothalamus (Vohra *et al*., 2001). Age-related changes in GPx activity in chickens have been considered closely. Red blood cell and blood plasma GPx activity decreased with age in Japanese quail

(Godin *et al*., 1995). Liver GPx activity increased reaching a maximum at age 20-30days of age (Kalytka and Donchenko, 1995). In contrast, GPx activity declined in the superficial pectoral muscles, blood and RBC during ageing from 1 week up to 4 months of age (Mizuno, 1984; Cestnik, 1985; Khan *et al*., 1995). In the semen of meat type cockerels from 25 to 60 weeks of age showed that GPx activity decreases with age (Kelso *et al*., 1996).

2.7 Phenotypic Correlation between GPx Activity and Production Traits

The erythrocyte GPx activity analysed in a flock of Finn sheep showed a negative correlation with body weight, weight gain and wool production (Atroshi and Sankari, 1981). It is proposed that the low glutathione peroxidase activity might represent an adaptation to low selenium intake. Similar results were obtained with chicken (LaVronga and Combs, 1982; Shen *et al*., 1992), pig (Lingaas *et al*., 1991) and rabbit (Mézes *et al*., 1999). Also there are some investigations directed to the GPx activity as a possible selection criteria for rabbit breeding as demonstrated a slight negative phenotypic correlation between carcass traits and enzyme activity of erythrocytes in NewZealand White and Pannon White rabbits (Virág *et al*., 1996). In chicken, liver GPx activity was positively correlated with egg production (Squires and Wu, 1992).

2.8 Growth Traits

Growth is an all-encompassing term which when studied in detail reveals an array of traits which could be selected for or against in any research work. Growth traits are either studied in absolute terms (absolute growth rate: GR) or relative terms as relative growth rate (RGR). Within these divisions several phenotype of growth traits could be studied such as whole body weight changes or changes in morphological parts of interest. (Aggre *et al*., 2003) stated that the simultaneous

consideration of both GR and RGR gives better information than examining only one of them to compare changes in growth.

2.8.1 Body weight

Aboul-Seoud, (2008) stated that estimates reported in the literature for body weight of Japanese quail at hatch i.e. body weight at 0 weeks (BW0) are limited because of the small magnitude of this weight and the sensitivity of the bird for handling at this age. However, body weight of Japanese quail at hatch was estimated by some investigators. Lepore and Marks (1971) reported an estimate of 6.0 g for body weight of both sexes at hatch. In random bred population (Marks, 1991) found that body weight at hatch ranged from 6.3 to 6.6 g. A higher estimates were reported for the two sexes by Marks (1980) as 8.8 g and by Aboul-Hassan (2000 & 2001a) as 8.6 and 8.3 g, respectively El-Fiky (2005) reported higher estimate for both sexes for this trait after four generations of selection for high body weight at 6 weeks of age as 8.11g. Abdel-Tawab (2006) estimated BW0 ranged between 8.48 and 9.38g among the selected line when selection was applied for increased egg weight produced within the first 10 weeks of lay.

For two weeks body weight (BW2), Sefton and Siegel (1974) showed the growth of Japanese quail during two successive generations to be an estimate ranging from 37.8 to 43.4g for males and from 38.7 to 45.1g for females. Within this range of estimates, Lepore and Marks (1971), Mousa (1993) and Aboul-Hassan (2000) reported an estimate of 43.6, 36.4 and 35.2g, respectively. Similarly, El-Fiky (1991) estimated BW2 as 41.0 and 45.1 g for males and females, respectively. Higher estimates were reported by Aboul-Hassan (2001a) as 46.4 g for the Brown strain of Japanese quail and 40.2 g for the White strain for body weight at two weeks of age for both sexes. Abdel-Fattah (2006) reported higher estimate for this trait as 54.06 and 54.80g for

males and females, respectively. Reports on four weeks body weight (BW4) showed estimates ranging from 82.0 – 84.2 for males and 85.5 – 88.0 for females according to Sefton and Siegel (1974). Aboul–Hassan (2000) reported higher estimates ranged between 99.5 and 101.6g for males and females of Brown strain of Japanese quail and between 82.2 and 84.3g for males and females of White strain. Furthermore, Aboul-Hassan (2001a) estimated BW4 of Brown and White strains of Japanese quail as 108.1 and 100.9g for the two sexes, respectively. Abdel-Fattah *et al*. (2006) reported higher estimates for this trait as 127.25 and 132.17g for males and females, respectively. Generally, the reported estimates of body weight of Japanese quail recorded at different ages indicate the high efficiency of this bird for growth (Darden and Marks, 1988a). However, the observed differences between the various estimates reported in the literature for body weight of Japanese quail recorded at a particular age may be possibly due to one or more of the different reasons such as: the differences in the climatic and managerial conditions under which different flocks were reared and to the possible differences in genetic makeup of the different flocks or to the differences in the statistical manipulation of the data used to obtain the estimates. The reported estimates for body weight of males and females Japanese quail at different ages indicate that females are consistently heavier than males (Wilson *et al.,* 1961; El–Ibiary *et al.,* 1966; Marks and Lepore, 1968 and Narayan, 1976).

2.8.2 Heritability estimates for body weight

Heritability estimates for body weight at hatch, 7, 14, 21 and 28 days old in Japanese quails were reported to be 0.38; 0.12; 0.31; 0.12 and 0.44 respectively, when Henderson methodology was used (Aggrey *et al.,* 2003). In Japanese quails, heritability values for body weight ranges between 0.47- 0.74 at 28 days old were reported by Minvielle (1998) in a review about animal improvement for production. Saatci *et al*. (2006) reported heritability estimates for body weight

of 0.32; 0.20; 0.21; 0.20 and 0.15 at hatch, 7, 14, 21 and 28 days old, respectively in one to one sire and dam pedigreed Japanese quail.

Resende *et al*. (2005) reported that the heritability estimates of their study was at variance with the estimates reported by Aggrey *et al.* (2003), probably because they employed the Henderson methodology, which analyzes the traits one by one. On the other hand, their study employed the multiple traits Gibbs sampler for animal models (MTGSAM) analysis, that evaluates the traits together, and therefore each trait contributes to the estimation of the others. The heritability estimate for BW28 is within the values presented by Minvielle (1998) heritability however increased with age. However, Saatci *et al*. (2003) reported that the heritability estimate reduced with age, probably because maternal environment and additive genetic effect were confused. There is great influence of the environment effect on body weight at hatch. This effect reduces when age increases. The genetic correlation between weights at different ages was high, except for the correlation between body weight at hatch and body weight at other ages. The fact that weight at hatch is limited by egg weight probably influenced this result. These results indicate that the growth in quails can be improved by selection.

2.8.3 Growth rate

Bakker (1974) reported that growth rate and weight for age are parameters that are often estimated in animal production research and used as selection trait in many breeding programs. Ricklefs (1985) showed that the major improvement due to selection for growth has occurred during the first two weeks post hatch expressed as relative or exponential growth rate. Growth may be viewed in different ways such as: absolute growth rate, relative growth rate and cumulative growth rate in time (Bakker, 1974).

The absolute growth rate may be defined as the weight increment per unit of time

$$(W2 – W1) / (T2 – T1)$$

In which (W2 – W1) is the weight increment in time interval (T2 – T1). This formula represents the average absolute growth rate or average daily gain.

The relative growth rate as defined by Brody (1945) is the absolute growth rate divided by the actual weight according to the following formula:

$$(W2 – W1) / 1/2 (W2 + W1)$$

Where: W1 = the weight at the beginning and W2 = the weight at the end of the period.

The cumulative growth could be represented by the curve of weight against time and is often ndescribed by mathematical growth functions (Parks, 1971).

For average daily gain from 0 to 2 weeks, varying reports exists as reported by several authors. Jones and Hughes (1978) stated that the average daily gain in Japanese quail was at a maximum 4.8 g/day during the first period from hatch to 3 weeks of age, while the gain was lower during the second period from 3 to 6 weeks of age. Lepore and Marks (1971); Sefton and Siegel (1974); Darden and Marks, (1989) and Aboul-Hassan (1997) reported an estimate of 2.64, 2.34, 2.43 and 1.66g/day for average daily gain from 0 – 2 weeks (ADG0-2) respectively. The corresponding estimates for the average daily gain from 2 – 6 weeks (ADG2-6) were reported by Lepore and Marks (1971); Sefton and Siegel (1974); Marks (1978); Darden and Marks (1989) and Aboul-Hassan (1997) as 3.21, 3.12, 3.17, 3.57 and 5.02g/day, respectively.

Furthermore, Aboul-Hassan (2000 and 2001a) estimated the ADG0-2 among Brown and White strains of Japanese quail as 2.62,1.91g/day for Brown strain and 2.06, 1.70g/day for White strain.

The corresponding estimates for the ADG2-4 were 5.82, 5.4g/day for Brown strain and 5.02, 4.90g/day for White strain. For the ADG4-6, Lepore and Marks (1971); Sefton and Siegel

(1974); Marks (1978) and Aboul-Hassan (1997) reported an estimate of 1.36, 1.54, 2.02 and 3.30g/day. Also, Lepore and Marks (1971) and Sefton and Siegel (1974) reported an estimate of 2.40 and 2.34g/day for the ADG0-4. Aboul-Hassan (2000 and 2001a) estimated the ADG4-6 among two strains of Japanese quail (Brown and White) as 1.46, 2.30g/day for Brown strain and 1.12 , 2.0g/day for White strain . When these reported values are compared with the maximum body size, it can be adduced according to Wilson *et al.*, (1961) that it has a greater potential for growth than chickens and turkey. Sexual variations in average daily gain exist and the differences were in favor of the females as reported by (Sefton and Siegel, 1974; Marks, 1978; Aboul-Hassan, 2001a). However the growth rate of males and females Japanese quail should be considered distinct characteristic of population as reported by El-Ibiary *et al.*, (1966) and Sefton and Siegel (1974). This matter should be taken into account in any breeding program aimed at improving growth characteristics in Japanese quail.

2.9 Body Weight and Reproductive Traits

Body weight differences during the prebreeding period has been associated with changes in egg production, egg weight, egg number, egg mass and age at sexual maturity in chickens and quails (Aly, 1992; El-Bodgady *et al*., 1993; Ghanem, 1995; Camci *et al*., 2002 and Meky, 2007). In Japanese quails, Kocak *et al*. (1995) observed body weight at onset of sexual maturity at an age of 58.0 days to be 202.2 g. Sreenivasaiah and Joshi (1988) obtained body weight at sexual maturity of 122.9–128.2g. Sachdev and Ahuja (1986) found that for egg-line females with a body weight of 100-120, 121-140, and 161-180 g at sexual maturity, age at sexual maturity

averaged 9, 10 and 11 weeks respectively. Kiling *et al*. (1985) reported that early matured pullets laid their first egg before 136 days, while late pullets matured when they were 152 days of age. Japanese quails are heavier when they reach sexual maturity later, but early sexual maturity reduces the time for the onset of egg production thereby increasing "egg days" production (Nestor *et al*., 2000).

In domestic poultry species, negative correlations between reproductive performance and body weight have been widely reported (Jaap and Muir, 1968; Nestor, 1977; Dunnington and Siegel, 1984). Reproductive performance of broiler breeders decreases as broiler breeders become heavier and fatter (Appleby *et al*., 1994). In turkeys, selection for increased body weight resulted in decreased egg production, intensity of lay, and hatch of fertile eggs (Nestor et al., 2000). In Japanese quail, selection for increased body weight under differing nutritional environments resulted in decreased hatchability, egg production and increased abdominal and carcass fat (Marks, 1991). Joyner *et al*. (2004) reported a close positive relationship between age and egg size while a negative relationship exists between the hens age and egg production. Triyuwanta *et al*. (1992) reported that body weight of the progeny at hatching were enhanced by increasing maternal body weight and this positive maternal effect was still present at 40 days of age in dwarf broilers. Similarly, Yalçın *et al*. (1993) observed that females' body weight have an effect on body weight of broilers at hatch, 5, 6, and 7 weeks of age. Also, Yalçin *et al*. (1995) found that hatch weight of Japanese quail increased with increasing the maternal body weight.

2.9.1 Age at sexual maturity

In commercial poultry rearing, the index for sexual maturity is attained when 50% of the bird start to lay, however, in breeding research it is very important to estimate the individual birds'

age at first egg. There are numerous reports on the physiologic relationships associated with the onset of sexual maturity in avian females (Koçak *et al*., 1995; Eitan and Soller, 2001; Camci *et a*l., 2002; Deyab, 2008). Previous reports have shown that a number of factors contribute to the considerable variability observed in the onset of egg production in chickens, turkeys, and Japanese quail. The variability is thought to be a result of environmental, genetic, and physiologic factors including photoperiod, nutrition, body composition and age of the bird (Brody *et al*., 1980 and 1984; Krapu, 1981 and Asuquo and Okon, 1993). In a Japanese quail line selected for increased 4-wk body weight, differing photoperiods during rearing have been reported to delay the onset of sexual maturity (Nestor, 1985) or not influence it at all (Steigner *et al*., 1992; Anthony *et al*., 1993) compared with a random bred control line. Age at sexual maturity has been shown to have an effect on egg production traits such as egg number, egg weight, and egg mass and body weight at sexual maturity in chickens and quails (Shebl, 1991; Aly, 1992; El-Bodgady et al., 1993; Ghanem, 1995; Camci *et al*., 2002 and Meky, 2007). On this estimate, Kadry et al (1986); Steigner *et al*. (1989b); Aboul- Hassan and El-Fiky (1990) and Aboul-Hassan *et al*. (1999) estimated the age at first egg in Japanese quail as 49.5, 46.0, and 45.4 and 49.8 days, respectively. Marks (1980) studied the age at first egg in Japanese quail during 4 successive generations and found that it ranged between 54.4 and 60.4 days. The lowest estimate for this trait was obtained by Mizutani (2003) who reported an estimate of 38-42 days. Similarly, in a random bred line of Japanese quail, Steigner *et al*. (1989a) reported an estimate of 42.0 days for this trait. A wider range of values was reported by Inal *et al*. (1996) who observed that quails selected for body weight reached sexual maturity at 39.8–51.1 days of life. The actual mean of days to the first egg laid (age at first egg) was found to be 54.3 and 58.6 days for two strains of Japanese quail (Brown and White) as reported by El-Fiky *et al*. (2000). Within this

range of estimates, Sharaf and Mandour (1994) reported an estimate of 53.1 and 56.8 days for age at first egg in Brown and White strains of Japanese quail. Higher estimates for the same trait in Japanese quail were reported by El-Fiky *et al*. (1994), Shebl *et al*. (1996) and Tawefeuk (2001) which ranged between 55.7 and 64.7 days. Bahie El-Dean *et al*. (2008) reported age at sexual maturity in Japanese quail females (days) were 42.98, 50.05 and 61.89 for early age at sexual maturity group, medium and late groups; respectively. Oruwari and Brody (1988) concluded that the interaction between chronological age, body weight, and body composition for the onset of sexual maturity are inseparable. Others have suggested that there are multiple thresholds of minimum chronological age, body weight, and body composition influencing female sexual development (Dunnington and Siegel, 1984; *Soller et al*., 1984; Zelenka *et al*., 1984; Reddish *et al*., 2003).

2.9.2 Egg production

It is well known that egg mass increases as parental hen flock ages and incubated chick mass gets to its maximum at the end of the laying cycle in broiler (Danilov, 2000; Barnett *et al*., 2004; Maiorka *et al*., 2004 and Hamidu *et al*., 2007). Although egg size and production can be influenced by a number of factors such as improved breeding, increased body weight, composition of feed and nutrition plan, intensity and duration of light; a major factor determining egg size is the age of the bird (Asuquo and Okon, 1993). A close positive relationship exists between age and egg size while a negative relationship exists between the hens age and egg production (Joyner *et al*., 2004). They observed that as the birds advanced in age, the egg production decreased. The average egg weight of a laying flock increases as the birds get older mainly due to physical and physiological changes (Oluyemi and Roberts, 1979). Furthermore, hen's age have a constant and significant effect on proportion of egg weight, length and width

Of the eggs, yolk, egg white and egg shell in total egg mass; similarly Haugh unit, yolk, albumen weight and height increased significantly with age of the bird (Rossi and Pompei, 1995; Danilov, 2000; Luquetti *et al*., 2004; Akpa et al., 2006 and Egahi *et al*., 2011). Furthermore there is an increase in repeatability of egg quality traits with linear increase in age of laying Japanese quails (Akpa *et al*., 2008). For egg weight estimates, Kohler (1981) reported egg weight of 9.1 to 10.9 g in a selection experiment for improving this trait. Asasi and Jaafar (2000) reported that values for egg weight ranged between 9.76 and 11.63 g. Higher estimates for egg weight were reported by Sharaf (1992 and 1996); El-Sayed *et al*. (1993); Inal *et al*. (1996); Bahie El-Deen *et al*. (1998); Ali *et al*. (2002) Abdel-Azeem (2005) and Abdel-Tawab (2006) ranging from 10.00 to 11.86g. Furthermore, Inal *et al*. (1996) and Aboul-Seoud (2008) gave higher values for egg weight which ranged between 10.94 and 13.23 g among divergent selection experiment for body weight at 5 weeks of age in five generations. Environmental factors have been shown to have or not to have great effect on egg production. Faqi *et al*. (1997) reported that egg weight was reduced at higher ambient temperature. Gilbert (1980) observed that temperatures between 13^{o}C and 21^{o}C are recommended for optimal egg production. Egg production is highest when temperatures are within neutrality range (Smith, 1990). The maximum temperature associated with satisfactory laying performance of hens is approximately 30^{o}C at a high relative humidity of 75% (Daghir, 1995). Consequently, Munir and Mohammed (2010) reported that ambient temperatures above 30^{o}C are considered to have detrimental effect on the performance of laying Quail hens while Vo *et al*. (1980) found that the increase of ambient temperature from 21 to 35 °C decreased egg weight, egg number and egg production percent in single comb Leghorn. Prabakaran (1992) reported that egg weight was not affected by season, but henday egg production of Japanese quail at 13 to 24 weeks of age during summer was lower than in other

seasons. Generally, it is well accepted that the main consequences of heat stress is the reduction in feed intake which reduces metabolic heat production (May and Lot, 1992) leading to poor growth rate, low rate of egg production, reduced feed efficiency, immune-suppression and enhanced fat deposition due to hypothyroid activity (Geraert *et al*., 1996; Mashaly *et al*., 2004; Quinteiro et al., 2010). To reduce the deleterious effects of heat stress so as to enhance egg production, many practical approaches have been developed to facilitate thermo-tolerance of birds which minimizes the adverse effects heat stress has on productivity. These approaches include pre and / or post acclimation of birds (Abd El-Azim, 1991 and Arjona, 1998), use of some electrolytes and vitamins (Cftc *et al*., 2005) and dietary energy or lysine manipulation (Belnave and Brake, 2005; Gous and Morris, 2005).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental study location

The study was carried out at the poultry/quail unit of the Department of Animal Science Research Farm, Faculty of Agriculture, Ahmadu Bello University, Zaria. Zaria is geographically located in the Northern Guinea Savannah of Nigeria at latitude 11^0 09' 06'' and longitude 7^0 38' 35'' (Ovimaps, 2012), with an annual rainfall of about 1100mm. Rainfall starts late April or early May, reaching its peak in August and last until September. The harmattan temperature ranges between 17^0C to 30^0C while the hot season temperature ranges between 23^0C and 36^0C. The relative humidity ranges between 28% during harmattan, 37% in the hot season and 75% in the wet season (IAR, 2017).

3.2 Experimental Birds

A total of 100 Day old chicks were brought from College of Agriculture and Animal science Division of Agricultural College (DAC) Mando Road Kaduna. The birds were raised together in deep litter system until two weeks of age before sexing. 75 females and 25 males were randomly selected; the females were put in individual cage. Mating was carried out using a mating ratio of 1male: 3 females.

3.3 Management Practice

3.3.1 Brooding and Rearing

Before arrival of the birds, heat source (lanterns, kerosene stoves, electric bulb) were put in place. These birds were brooded with electric bulb and kerosene stoves in cartons which were

about 60 by 90 cm in length. The base of the cartons was laid with wood-shavings and then news-papers. The birds were brooded for about 2-4 weeks and thereafter they were transferred to cages. At about 6 weeks of age the sire were individually housed in cages with three dam so as to ensure mating. The birds were given water and feed *ad-libitum.* The diet containing 26% CP and 2741 ME Kcal/Kg was fed until 4 weeks of age, and then introduced to breeder diets containing 24%CP and 2900 ME Kcal/kg (Dafwang, 2006). Daily routine management practices were carried out.

3.3.2 Mating Procedure

Individuals from the base population were used as parents for the first generation. At the 6^{th} week of age, a mating procedure was done using a ratio of 1 male to 3 females to form a family which were housed in a pen to obtain fertile eggs for the next generation.

3.3.3 Egg collection and Hatching

Hatchable eggs were collected from the 6^{th} to the 9^{th} week of age from the base population and were marked according to sire number; batch hatching was used to ensure adequate number of chicks per sire. Eggs were daily collected in the morning and evening, those meant for hatching were marked based on sire number and were stored in egg trays under room temperatures for a maximum of 7 days before being placed in the incubator. Eggs were incubated for 18 days. They were maintained at a temperature of 37.8°C and humidity of between 78-80% for 15days in the setter and were then transferred for the last 3 days of incubation to the hatcher (90% humidity) which was divided into marked compartments according to sire number. Hatched chicks were colour marked according to sire number; this marking was repeated at two weeks of age until the birds were wing tagged at four weeks.

3.4 Recording of Data

3.4.1 Biometric measurements

Shank length, body length and thigh length were measured in centimetres using measuring tape at two, four and six weeks of age while individual birds were weighed in Grams using pocket mini digital scale (Diamond Series A04) with a sensitivity of 0.1g, at two, four and six weeks of age.

3.4.2 Blood collection

Blood samples were collected at 6 and 9 weeks of age from sample birds; about 1ml of blood were collected into two tube one containing Ethylene Diamine Tetra Acetic Acid (EDTA) as an anticoagulant and the other one without anticoagulant, the sample in the tube containing (EDTA) were analysed for concentration of total plasma (TP), Pack cell volume (PCV), Lymphocyte (Lymph), White blood cell (WBC), Haemoglobin (Hb). While the sample in the tube without (EDTA) were analysed for Glutathione peroxidase (GPx). Samples were collected and stored in ice box at 0°C, before taking it to the laboratory. Samples were analysed immediately it got to the laboratory.

3.4.3 Egg Production Traits

Ages at sexual maturity for females were recorded individually in days (ASM). Number of eggs laid (EN) and Average egg weights (AEW) were recorded from onset of lay till 9 weeks of production. Days in lay up to 9 weeks (DLAY) and Rate of lay (RLAY) were also recorded.

3.5 Data Collection

Data was collected from Base, F_1 and F_2 generation. The following measurements were made. Body length (BL): length between the tip of the rostrum maxillary (beak) and that of caudal (tail, without feathers) at 2, 4, 6, weeks of age in "mm". Shank length (SL): distance from the shank joint to the extremity of the digituspedis in "mm" at 2, 4, 6, weeks of age. Bodyweight (BW): live weight of individual birds was recorded in "g" at 2, 4, 6 weeks of age. Egg weight in "g" (EW) and number of egg laid (EN) up to 9 weeks were recorded. Days in Lay (DLAY) up to 9 weeks was measured in days, Age at sexual maturity in days (ASM), Rate of Lay (RLAY) and Glutathione peroxidase (GPx) activity in u/g at 6 and 9 weeks of age. TP in g/dl, PCV in ml, Lymph in %, WBC in ml, Hb in g/dl of individual blood at 6 and 9 weeks of age were also recorded.

3.6 Statistical Analysis

Data were subjected to analysis of variance to test sex effect using the General Linear Model (GLM) procedure of SAS (2002).using to the following model:

$Y_{ijkl} = \mu + A_i + B_j + C_k + e_{ijkl}$

Where: μ: Over all mean

,A_i: Sire effect,

B_i: Sex effect,

C_k: Generation effect,

e_{ijkl}: Random error

3.7 Genetic Parameter Estimate

Heritability, phenotypic correlations were computed as follows

3.7.1 Estimation of heritability:

Heritability estimates were calculated as follows

$$h^2 = \frac{4\sigma_s^2}{\sigma_T^2}$$

Where:

h_s^2 = heritability estimate

σ^2_S= the sire component of variance.

σ^2_T: Total Variance**.**

3.7.2 Phenotypic correlations: Phenotypic correlations (r_p) between traits were estimated as follows:

$$r_p = \frac{\text{CovP}}{\sqrt{(\sigma^2_{px}\,\sigma^2_{py})}}$$

Where: r_p is the phenotypic correlation.

σ^2_{px} and σ^2_{py} are the parameters studied.

COVp is the appropriate covariance and is the standard deviation.

Growth rates (GR) during the periods (2, 4, 6 weeks) of age were calculated using the formular

$$GR = [W2- W1/ ½(W2+W1)] \times 100$$

Where:

W1: the weight at beginning of the period.

W2: the weight at end of the period.

CHAPTER FOUR

4.0 RESULTS

4.1 Growth Characteristics of the Base Generation

Table 4.1 showed the Least Square Means and coefficient of variation (CV %) of some biometric measurement and body weight for males, females and combined sexes of Japanese quail (Base generation) There were significant ($P<0.05$) differences in body weight, Shank length and body lenght at two, four and six weeks with the females consistently being heavier than the males. However, the males and females had non Significant difference ($P<0.01$) for Tight length (TL). Growth rate showed non significant differences between the sexes, but the female were out performing than the male at the fourth and sixth week. The males had a lowest value for coefficient of variation of 2.21% in BL_9 and a higest value of 17.14% in BW_4, while the females had a lowest value of 4.55% in BL_4 and a highest value of 17.87% in BW_4 and lowest and highest value of the coefficient variation for combined sex are 0.92% in SL_9 and 16.38% in SL_2 respectively.

4.2 Growth Characteristics of the F_1 Generation

Table 4.2 showed the Least Square Means and coefficient of variation (CV %) of some biometric measurement and body weight for males, females and combined sexes of Japanese quail in the first filial generation (F_1). Body weight (g), body length (mm) and shank length (mm) showed significant difference ($p<0.05$) across the groups studied with females out performing the male across all the experimental period. (2^{nd}, 4^{th}, 6^{th} and 9^{th} weeks) respectively. There was no significant ($p>0.05$) differences for thigh length (mm) for both sexes.

Table 4.1: Least Squares Means standard error for biometric measurement and Body weight for males and females sexes (base generation).

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
$BW_{2(}$g)	57.74^{a}±1.64	12.32	42.23^{b}±1.38	10.46
BW_4(g)	87.15^{a}±1.64	17.87	67.43^{b}±1.38	17.14
BW_6(g)	120.47^{a}±1.39	15.45	112.43^{b}±1.62	15.95
BW_9(g)	145.98^{a}±2.02	8.12	142.62^{b}±2.11	7.33
BL_2(mm)	20.00^{a}±0.21	7.82	19.88^{b}±0.25	6.18
BL_4(mm)	24.50^{a}±0.21	4.55	22.24^{b}±0.25	6.19
BL_6(mm)	27.91^{a}±0.21	5.53	25.83^{b}±0.25	2.90
BL_9(mm)	28.24^{a}±0.28	2.01	27.13^{b}±0.33	2.21
SL_2(mm)	4.78^{b}±0.08	15.34	2.58^{a}±0.09	17.03
SL_4(mm)	5.55^{a}±0.08	12.22	3.45^{b}±0.09	13.98
SL_6(mm)	6.41^{a}±0.08	10.55	4.47^{b}±0.09	10.47
SL_9(mm)	6.54±0.10	7.71	6.56±0.12	3.22
TL_2(mm)	4.49±0.10	9.89	4.40±0.12	11.58
TL_4(mm)	5.55±0.10	10.14	5.49±0.12	14.85
TL_6(mm)	7.52±0.10	10.05	7.75±0.12	11.69
TL_9(mm)	8.48±0.15	8.82	8.23±0.14	10.32
GR_2 (%)	50.00±0.00	12.32	50.00± 0.00	9.02
GR_4 (%)	25.17±0.17	12.78	22.23± 0.20	12.22
GR_6(%)	17.08± 0.17	9.78	16.19± 0.20	10.04

[ab]Means with different superscripts on the same row are significantly different ($p<0.05$)
BW_2: body weight at two weeks of age, BW_4: body weight at four weeks of age, BW_6: body weight at six weeks of age,BL_2: body length at two weeks of age, BL_4: body length at four weeks of age, BL_6: body length at six weeks of age, SL_2: shank length at two weeks of age, SL_4: shank length at four weeks of age, SL_6 :Shank length at six weeks of age, TL: Thigh length
GR_2: growth rate for two weeks, GR_4: growth rate for four weeks, GR_6: growth rate for six weeks of age.

Table 4.2. Least Means with standard error for biometric measuremen, body weight for males and females (F1generation).

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
BW_2(g)	46.80[a]±0.83	15.03	45.77[b]±1.43	18.23
BW_4(g)	79.01[a]±0.83	13.00	77.33[b]±1.43	6.00
BW_6(g)	123.48[a]±0.83	5.00	112.39[b]±1.43	14.00
BW_9(g)	155.82[a]±0.83	12.00	144.89[b]±1.43	12.00
BL_2(mm)	20.17[a]±0.21	12.00	19.89[b]±0.36	9.00
BL_4(mm)	23.00±0.21	10.00	22.90±0.36	6.00
BL_6(mm)	25.47[a]±0.21	9.00	24.66[b]±0.36	6.00
BL_9(mm)	25.68[a]±0.21	7.00	24.70[b]±0.36	10.00
SL_2(mm)	5.39[a]±0.11	13.00	5.31[b]±0.18	5.00
SL_4(mm)	6.60[a]±0.11	6.00	6.52[b]±0.18	14.00
SL_6(mm)	6.74[a]±0.11	9.00	5.79[b]±0.18	13.00
SL_9(mm)	6.81[a]±0.11	12.00	5.91[b]±0.18	4.00
TL_2(mm)	4.45±0.04	9.00	4.45±0.07	5.00
TL_4(mm)	5.67±0.04	13.00	5.62±0.07	14.00
TL_6(mm)	8.23±0.04	8.00	8.18±0.07	15.00
TL_9(mm)	8.28±0.04	5.00	8.30±0.07	12.00
GR_2 (%)	50.00±0.00	14.00	50.00± 0.00	6.00
GR_4 (%)	40.77[b]±0.15	15.00	40.81[a]±0.19	12.00
GR_6 (%)	36.01[a]±0.15	12.00	31.19[b]±0.19	5.00

[ab]Means with different superscripts on the same row are significantly different ($p<0.05$) BW_2: body weight at two weeks of age, BW_4: body weight at four weeks of age, BW_6: body weight at six weeks of age,BL_2: body length at two weeks of age, BL_4: body length at four weeks of age, BL_6: body length at six weeks of age, SL_2: shank length at two weeks of age, SL_4: shank length at fou r weeks of age, SL_6 :Shank length at six weeks of age, TL: Thigh length GR_{2-4}: growth rate from two to four weeks, GR_{4-6}: growth rate from four to six weeks, GR_{2-6}: growth rate from two to six weeks of age.

4.3 Growth Characteristics of the F_2 Generation

Table 4.3 showed the Least Square Means and coefficient of variation (CV %) of some biometric measurement and body weight for males, females and combined sexes of Japanese quail in the second filial generation (F_2). Only Body weight and growth rate indicated significant ($P<0.05$) sexual dimorphism in Japanese quail in this generation, all other traits were statistically similar. The trends for growth rate were similar to what was obtained in the F_1 generation. Body weight indicated superiority of the female over the male from the 2^{nd} week through to the 9^{th} week.The females had highest value for Coefficient of variation of 17.00% in BW_4 and lowest value of 3.00% in $SL_{4,}$ while the males had highest value for coeffience of variation of 18.80% in BW_4 and lowest value of 2.01% in $BL_{6.}$

4.4 Haematological Profiles of the Base Generation

The means, standard errors and coefficient of variation (CV %) for glutathione peroxidase and haematological profiles of males, females and combined sexes of Japanese quail are as shown in table 4.4. Sex significantly ($p<0.05$) influenced GPx_6 and GPx_9 (g), TP_6 and TP_9 (g/dl), $Lymp_6$ (%) with the females having higher values than the males. All other traits only showed nominal differences between sexes.

4.5 Haematological Profiles of the F_1 Generation

The means, standard errors and coefficient of variation (CV %) for glutathione peroxidase and haematological profiles of males and females of Japanese quail in the F_1 are as shown in table 4.5. Significant ($p < 0.05$) differences between sexes were observed in GPx_6, PCV_9, TP_6, WBC_6 and $Lymp_6$ with higher values in the females compared to the males and PCV_6 where the males were superior to the females. The males had a lowest value for coefficient of variation of 11.95%

in GPx_6 and a highest value of 47.77% in TP_9 while the females had a lowest value of 13.96% and a highest value of 51.15% in GPx_6 and TP_9 respectively.

4.6 Haematological Profiles of the F_2 Generation

Table 4.6 showed the mean,s standard errors and coefficient of variation (CV %) for glutathione peroxidase and haematological profiles of males and female of Japanese quail in the F_2 generation. Significant ($p<0.05$) differences were observed between the sexes for GPx_6, GPx_9, TP_6 and TP_9, with higher values in the female. The males had a lowest value for coefficient of variation of 15.21% in $LYMP_9$ and a highest value of 39.95% in WBC_6 while the females had a lowest value of 15.80% and a highest value of 38.01% in GPx_9 and WBC_6 respectively.

Table 4.3.Least Squares means standard error for biometric measurement and body weight for males and females (F_2 generation).

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
BW_2(g)	54.78^{a}±0.58	16.73	48.12^{b}±0.67	17.63
BW_4(g)	90.12^{a}±0.58	17.00	88.93^{b}±0.67	18.80
BW_6(g)	130.58^{a}±0.57	15.00	124.27^{b}±0.67	14.00
BW_9(g)	158.37^{a}±0.58	12.40	155.97^{b}±0.67	12.00
BL_2(mm)	21.73±0.11	12.08	20.55±0.13	4.55
BL_4(mm)	23.48±0.11	17.00	23.28±0.13	5.53
BL_6(mm)	25.57±0.11	9.00	24.96±0.13	2.01
BL_9(mm)	25.87±0.11	7.87	25.08±0.13	15.34
SL_2(mm)	6.34^{a}±0.09	19.10	5.65^{b}±0.10	12.22
SL_4(mm)	6.98^{a}±0.09	3.00	6.55^{b}±0.10	4.55
SL_6(mm)	7.77^{a}±0.08	9.23	6.60^{b}±0.10	13.00
SL_9(mm)	7.73^{a}±0.08	12.45	7.22^{b}±0.10	11.58
TL_2(mm)	5.19±0.23	7.67	4.44±0.26	14.85
TL_4(mm)	5.74±0.23	15.00	5.68±0.26	11.69
TL_6(mm)	8.09±0.22	8.67	8.06±0.27	10.32
TL_9(mm)	8.25±0.22	15.00	8.24±0.27	9.02
GR_2 (%)	50.00±0.00	16.34	50.00±0.00	12.22
GR_4 (%)	39.21^{b}±0.23	15.08	45.89^{a}±0.25	10.04
GR_6 (%)	30.98^{a}±0.23	13.40	28.44^{b}±0.25	5.00

[ab]Means with different superscripts on the same row are significantly different ($p<0.01$)
BW_2: body weight at two weeks of age, BW_4: body weight at four weeks of age, BW_6: body weight at six weeks of age,BL_2: body length at two weeks of age, BL_4: body length at four weeks of age, BL_6: body length at six weeks of age, SL_2: shank length at two weeks of age, SL_4: shank length at four weeks of age, SL_6 :Shank length at six weeks of age, TL: Thigh length GR_2: growth rate for two weeks, GR_4: growth rate for four weeks, GR_6: growth rate for six weeks of age.

Table 4.4.Least Squares Means standard error for glutathione peroxidase activity and haematological parameters for males and females (base generation)

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
GPx_6 (g)	12.33^{a}±0.29	15.33	10.98^{b}±0.34	15.33
GPx_9 (g)	11.97^{a}±0.29	13.39	10.90^{b}±0.34	13.39
PCV6ml (%)	27.58±1.56	33.22	25.78±1.81	33.22
PCV9ml (%)	36.35±1.56	24.76	36.52±1.81	24.76
TP_6 (g/dl)	9.26^{a}±0.28	21.92	8.68^{b}±0.33	21.92
TP_9 (g/dl)	10.68^{a}±0.28	10.75	9.96^{b}±0.33	10.75
Hb_6 (g/dl)	9.14±0.52	33.60	8.52±0.61	33.60
Hb_9 (g/dl)	11.81±0.52	26.73	11.30±0.61	26.73
WBC_6 (/ml)	9.08±0.52	24.98	8.39±0.60	24.98
WBC_9 (1/ml)	10.61±0.52	32.61	10.35±0.60	32.61
$LYMP_6$ (%)	52.34^{a}±1.66	22.48	50.71^{b}±1.93	22.48
$LYMP_9$ (%)	46.32^{a}±1.66	13.55	46.09^{b}±1.93	13.55

abMeans with different superscripts on the same row are significantly different ($p<0.05$)
GPX6: glutathione peroxidase at six weeks, GPX9: glutathione peroxidase at nine weeks, PCV6: pack cell volume at six weeks, PCV9: pack cell volume at nine weeks, TP6; total protein at six weeks, TP9: total protein at nine weeks, LYMP6: lymphocyte at six weeks, LYMP9: lymphocyte at nine weeks, WBC6 and WBC9: white blood cell count Hb6 and Hb9: haemoglobin at six and nine weeks

Table 4.5. Least Squares Means standard error for glutathione peroxidase and haematological parameters for males and females in the F_1generation

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
GPx_6 (g)	13.75^{a}±0.19	13.96	12.18^{b}±0.33	11.95
GPx_9 (g)	11.95^{a}±0.20	16.05	10.80^{b}±0.34	14.22
PCV_6ml (%)	20.94^{b}±0.86	33.46	25.83^{a}±1.50	32.63
PCV_9ml (%)	21.58^{a}±0.90	18.62	25.70^{b}±1.56	19.53
TP_6 (g/dl)	8.48^{a}±0.34	28.62	7.91b±0.59	24.17
TP_9 (g/dl)	6.20±0.36	51.15	6.10±0.62	47.77
Hb_6 (g/dl)	11.51±0.24	19.04	11.98±0.41	17.68
Hb_9 (g/dl)	8.97±0.25	17.87	8.50±0.43	20.10
WBC_6 (ml)	7.84^{a}±0.40	33.78	7.23^{b}±0.68	36.22
WBC_9 (1ml)	9.83±0.41	36.71	9.20±0.72	45.85
$LYMP_6$ (%)	53.82^{a}±0.93	15.79	48.48^{b}±1.61	19.76
$LYMP_9$ (%)	45.90^{a}±0.97	14.46	44.50^{b}±1.68	14.19

^{ab}Means with different superscripts on the same row are significantly different ($p<0.05$)
GPX_6: glutathione peroxidase at 6 weeks, GPX_9: glutathione peroxidase at 9 weeks , PCV_6: pack cell volume at 6 weeks, PCV_9: pack cell volume at 9 weeks, TP_6; total protein at 6 weeks, TP_9: total protein at 9 weeks, $LYMP_6$: lymphocyte at 6 weeks, $LYMP_9$: lymphocyte at 9 weeks, WBC_6 and WBC_9: Hb_6 and Hb_9: haemoglobin at 6 and 9 weeks

Table 4.6. Least Squares Means standard error for glutathione peroxidase and haematological parameters for males and females in the F_2 generation

Traits	Females		Males	
	LSM±SE	CV%	LSM±SE	CV%
GPx_6 (g)	14.95[a]±0.27	17.26	14.61[b]±0.32	15.33
GPx_9 (g)	15.61[a]±0.27	15.80	14.57[b]±0.32	15.92
PCV_6ml (%)	26.55±0.63	18.89	26.29±0.76	18.14
PCV_9ml (%)	26.58±0.63	19.57	27.67±0.76	17.80
TP_6 (g/dl)	11.62[a]±0.38	31.93	11.20[b]±0.46	27.87
TP_9 (g/dl)	11.85[a]±0.38	26.54	10.35[b]±0.46	28.57
Hb_6 (g/dl)	13.13±0.52	31.32	12.86±0.63	32.08
Hb_9 (g/dl)	13.04±0.52	30.16	13.94±0.63	35.52
WBC_6 (ml)	9.41±0.44	38.01	9.47±0.53	39.95
WBC_9 (ml)	10.41±0.44	37.28	9.61±0.53	31.04
$LYMP_6$ (%)	55.86[a]±1.16	18.17	52.78[b]±1.39	15.67
$LYMP_9$	53.92[a]±1.16	19.08	50.89[b]±1.39	15.21

[ab]Means with different superscripts on the same row are significantly different ($p<0.05$)
GPX_6: glutathione peroxidase at 6 weeks, GPX_9: glutathione peroxidase at 9 weeks , PCV_6: pack cell volume at 6 weeks, PCV_9: pack cell volume at 9 weeks, TP_6; total protein at 6 weeks, TP_9: total protein at 9 weeks, $LYMP_6$: lymphocyte at 6 weeks, $LYMP_9$: lymphocyte at 9 weeks, WBC_6 and WBC_9: Hb_6 and Hb_9: haemoglobin at 6 and 9 weeks

4.7 Egg Production Traits between the Generations

Table 4.7 showed the egg production characteristics of the Japanese quails across generations. Age at Sexual Maturity (days) had the lowest (4.72%) coefficient of variation in the F_2 generation while egg number at the ninth week in the base generation (42.46%) had the highest value. Significant ($p < 0.05$) generational differences existed for all measured variables. ASM was better in the F_2 generation with the value (47.08 in days) compared to the value of base and F_1 generation (49.23 and 49.87 in days) respectively. Egg weight at the ninth week (EWT_9 in g) were higher in the F_2 (8.83) and was close to the value obtained for F_1 (8.55) but differed from the base population which had the least weight (8.06). Egg number at the ninth week (EN_9) and rate of lay (RLAY in eggs/day) followed similar trend as EWT_9. The number of days in lay (DLAY) was highest in the F_2 (15.93) and differed from the base population (13.77) which ranked next and the F_1 (13.13) which ranked least for this variable across the generations.

4.8 Phenotypic Correlation between Growth Traits and Egg Production Traits in F_1 Generation

Table 4.8 showed the phenotypic correlation coefficient between growth and egg production traits in the F_1 generation, BW_2 showed positive correlation coefficient with all the growth traits except with BW_6, BL_6 and TL_6. BW_2 showed no significant ($p>0.05$) differences with growth and egg production traits at 6 and 9 week. SL_2, TL_2, BL_2 and BW_4 also showed similar ($P>0.05$) trend of non-significant correlation but had significant positive correlation with growth traits at second and fourth week. BW_6 was significantly and positively correlated with SL_6, TL_6 and BL_6. SL_6 showed positive correlation with all the egg traits. Positive coefficient was observed between ASM, EW_6 and EW_9 but negatively correlated with EN, DLAY and RLAY.

Table 4.7.Least Squares means (± standard error) and coefficient of variation for egg production traits across the generations.

Traits	Bas		F_1		F_2	
	LSM±SE	CV%	LSM±SE	CV%	LSM±SE	CV%
ASM (days)	49.23^{b}±0.70	9.87	49.87^{b}±0.70	10.54	47.08^{a}±0.70	4.72
EWT_9 (g)	8.06^{b}±0.09	7.20	8.55^{a}±0.08	5.41	8.83^{a}±0.08	5.63
EN_9	31.85^{b}±1.80	42.46	33.44^{a}±1.80	34.21	33.46^{a}±1.80	24.47
DLAY(days)	13.77^{b}±0.70	35.28	13.13^{c}±0.70	40.13	15.93^{a}±0.70	13.91
RLAY (eggs/day)	2.38^{b}±0.10	38.25	2.67^{a}±0.10	17.81	2.70^{a}±0.10	19.93

^{abc}Means with different superscripts on the same row are significantly different ($P<0.05$)
ASM: age at sexual maturity, EWT_9: egg weight at nine weeks, EN_9: egg number at nine week, DLAY: days in lay, RLAY: rate of lay.

Table 4.8: Phenotypic Correlation between Growth traits and Egg production traits in Generation F_1

Traits	BW_2	SL_2	TL_2	BL_2	BW_4	SL_4	TL_4	BL_4	BW_6	SL_6	TL_6	BL_6	ASM
BW_2													
SL_2	0.73***												
TL_2	0.24*	0.31**											
BL_2	0.43***	0.38**	0.18^{ns}										
BW_4	0.85***	0.64***	0.31**	0.51***									
SL_4	0.81***	0.71***	0.24*	0.43***	0.82***								
TL_4	0.48***	0.52***	0.14^{ns}	0.34**	0.57***	0.59***							
BL_4	0.31**	0.09^{ns}	0.13^{ns}	0.23*	0.32**	0.24*	0.20^{ns}						
BW_6	0.20^{ns}	0.09^{ns}	0.06^{ns}	-0.03^{ns}	0.14^{ns}	0.14^{ns}	0.06^{ns}	0.04^{ns}					
SL_6	0.33**	0.20^{ns}	0.10^{ns}	-0.03^{ns}	0.27*	0.19^{ns}	0.04^{ns}	0.08^{ns}	0.84***				
TL_6	0.07^{ns}	-0.03^{ns}	0.10^{ns}	-0.03^{ns}	0.01^{ns}	0.00^{ns}	0.02^{ns}	0.11^{ns}	0.21*	0.25*			
BL_6	0.12^{ns}	0.12ns	0.13^{ns}	-0.15^{ns}	0.03^{ns}	0.02^{ns}	0.04^{ns}	0.11^{ns}	0.63***	0.63***	0.05^{ns}		
ASM	-0.06^{ns}	-0.09^{ns}	0.08^{ns}	-0.04^{ns}	-0.05^{ns}	-0.10^{ns}	0.14^{ns}	0.12^{ns}	0.32**	0.24*	0.05^{ns}	-0.22*	
EW_9	-0.06^{ns}	-0.11^{ns}	0.15^{ns}	-0.05^{ns}	-0.11^{ns}	-0.05^{ns}	0.12^{ns}	0.05^{ns}	0.31**	0.27*	-0.23*	0.17^{ns}	0.28*
EN_9	-0.03^{ns}	-0.15^{ns}	0.11^{ns}	-0.05^{ns}	-0.05^{ns}	-0.11^{ns}	0.13^{ns}	0.15^{ns}	0.43**	0.24*	0.09^{ns}	0.16^{ns}	0.93***
DLAY	0.06^{ns}	0.09^{ns}	0.08	-0.04	0.05	-0.1	-0.14	0.12	0.2^{ns}	0.24*	0.05^{ns}	0.22*	1.00***
RLAY	0.08^{ns}	0.08^{ns}	0.03^{ns}	-0.09^{ns}	-0.07^{ns}	0.00^{ns}	0.09^{ns}	0.04^{ns}	0.23*	-0.12^{ns}	0.09^{ns}	-0.22*	0.64***

ASM: age at sexual maturity, EWT9: egg weight at nine weeks, EN9: egg number at nine week, DLAY: days in lay, RLAY: rate of lay: body weight at two weeks of age, BW_4: body weight at four weeks of age, BW_6: body weight at six weeks of age,BL_2: body length at two weeks of age, BL_4: body length at four weeks of age, BL_6: body length at six weeks of age, SL_2: shank length at two weeks of age, SL_4: shank length at four weeks of age, SL_6 :Shank length at six weeks of age, TL2:tight length at two weeks of age,TL4:tight length at four weeks of age,TL6:tight length at six weeks of age. ns: non significant, ***(P,0.001), **(P<0.01), *(P<0.05).

4.9 Phenotypic Correlation between Growth Traits and Egg production Traits in F_2 Generation

Table 4.9 showed the phenotypic correlation coefficient between growth and egg production traits in the F_2 generation. All the growth traits were significantly and positively correlated with one another except TL_4 and TL_6 but negative correlation was observed between growth traits and egg production traits except TL_4, BL_4 and BW_6 which were positively correlated with DLAY. ASM was positvely correlated with EN and DLAY and negatively correlated with RLAY.

4.10 Phenotypic Correlation between Glutathione Peroxidase, Haematological Variables and Growth Traits in F_1 Generation.

Table 4.10 illustrated the phenotypic correlation between glutathione peroxidase activities, haematological variables and growth traits at different periods in F_1 generation. PCV_6, PCV_9 and TP_9 indicated non significant ($p>0.05$) correlation with all measured variables of growth traits. Hb_6 was significantly ($p<0.05$) and positively correlated with BW_2, SL_2, TL_2, BW_6 and BW_4 while Hb_9 showed significant ($p<0.05$) and negative correlation with BW_2, SL_2, BW_4, SL_4. WBC_6 was positively and significantly correlation with SL_4, BW_6 and BL_6 while WBC_9 was significantly ($p>0.05$) and positively correlated with BW_2, BW_4, SL_4 and TL_4. GPx_6 showed positive and significant ($p<0.01$) correlation with all growth traits measures except TL_4, BL_4, TL_6 and BL_6 while GPx_9 showed similar trend with the exception of TL_2,TL_4 and TL_6 respectively. $LYMP_6$ indicated significant and positive correlation with all the growth traits except TL_2, TL_4, TL_6 and BL_{2-6}, $LYMP_9$ which was positively correlated with all the BW (2-6) measured but insignificantly correlated with all other traits.

Table 4.9: Phenotypic Correlation between Growth traits and Egg production traits for Generation F_2

Traits	BW_2	SL_2	TL_2	BL_2	BW_4	SL_4	TL_4	BL_4	BW_6	SL_6	TL_6	BL_6	ASM
BW_2													
SL_2	0.81												
TL_2	0.07^{ns}	0.01^{ns}											
BL_2	0.77***	0.82***	0.07^{ns}										
BW_4	0.52***	0.48***	-0.06^{ns}	0.36**									
SL_4	0.47***	0.39**	-0.02^{ns}	0.33**	0.82***								
TL_4	0.39**	0.38**	-0.05^{ns}	0.31**	0.79***	0.67***							
BL_4	0.38**	0.33**	-0.08^{ns}	0.30**	0.68***	0.61***	0.67***						
BW_6	0.74***	0.74***	0.04^{ns}	0.69***	0.43***	0.38**	0.26*	0.24*					
SL_6	0.66***	0.72	0.09^{ns}	0.70***	0.43***	0.36**	0.27*	0.31**	0.82***				
TL_6	0.02^{ns}	0.15	0.09^{ns}	0.14^{ns}	0.00^{ns}	-0.03^{ns}	-0.03^{ns}	0.08^{ns}	0.05^{ns}	0.14^{ns}			
BL6	0.42***	0.42	0.02^{ns}	0.44***	0.35**	0.28*	0.29*	0.27*	0.49***	0.53***	0.14^{ns}		
ASM	-0.05^{ns}	-0.04^{ns}	-0.13^{ns}	-0.06^{ns}	-0.16^{ns}	-0.19^{ns}	0.23*	0.20*	-0.10^{ns}	-0.11^{ns}	-0.09^{ns}	0.20*	
EW_9	-0.03^{ns}	-0.04^{ns}	0.01^{ns}	-0.11^{ns}	0.12^{ns}	0.05^{ns}	0.11^{ns}	0.03^{ns}	-0.11^{ns}	-0.02^{ns}	-0.14^{ns}	0.00^{ns}	-0.00^{ns}
EN	-0.05^{ns}	-0.05^{ns}	0.13^{ns}	0.01^{ns}	0.00^{ns}	0.07^{ns}	0.00^{ns}	0.01^{ns}	0.09^{ns}	0.11^{ns}	-0.05^{ns}	0.12^{ns}	0.55***
DLAY	-0.05^{ns}	0.04^{ns}	0.13^{ns}	0.06^{ns}	0.16^{ns}	0.19^{ns}	0.23*	0.20*	0.10^{ns}	0.11^{ns}	0.09^{ns}	0.20*	1.00***
RLAY	-0.09^{ns}	-0.08^{ns}	0.05^{ns}	-0.03^{ns}	-0.08^{ns}	-0.02^{ns}	-0.14^{ns}	0.10^{ns}	0.05^{ns}	0.07^{ns}	-0.11^{ns}	0.02^{ns}	-0.02^{ns}

ASM: age at sexual maturity, EWT9: egg weight at nine weeks, EN9: egg number at nine week, DLAY: days in lay, RLAY: rate of lay: body weight at two weeks, BW_4: body weight at four weeks , BW_6: body weight at six weeks of age,BL_2: body length at two weeks, BL_4: body length at four weeks , BL_6: body length at six weeks , SL_2: shank length at two weeks , SL_4: shank length at four weeks , SL_6 :Shank length at six weeks, TL2:tight length at two weeks of age,TL4:tight length at four weeks of age,TL6:tight length at six weeks. ns: non significant, ***(P,0.001), **(P<0.01), *(P<0.05).

Table 4.10: Phenotypic Correlation between Glutathione peroxidase, haematological variables and growth traits in F_1 Generation

Traits	PCV_6	HB_6	WBC_6	TP_6	GPx_6	$LYMP_6$	PCV_9	Hb_9	WBC_9	TP_9	GPx_9	$LYMP_9$
BW_2	0.15^{ns}	0.43**	0.18^{ns}	-0.11^{ns}	0.33**	0.23*	-0.05^{ns}	-0.28*	0.25*	0.05^{ns}	0.28*	0.20*
SL_2	0.10^{ns}	0.33**	0.17^{ns}	-0.25*	0.24*	0.21*	0.01^{ns}	-0.26*	0.20^{ns}	-0.06^{ns}	0.22*	0.04^{ns}
TL_2	0.12^{ns}	0.40**	-0.01^{ns}	-0.11^{ns}	0.10^{ns}	0.03^{ns}	-0.01^{ns}	0.31**	0.05^{ns}	-0.02^{ns}	0.09^{ns}	-0.23*
BL_2	0.06^{ns}	0.10^{ns}	0.01^{ns}	0.02^{ns}	0.43**	-0.08^{ns}	-0.17^{ns}	-0.12^{ns}	0.20^{ns}	0.10^{ns}	0.33**	-0.10^{ns}
BW_4	0.17^{ns}	0.21*	0.14^{ns}	-0.09^{ns}	0.22*	0.23*	-0.13^{ns}	-0.22*	0.21*	0.08^{ns}	0.43**	0.28*
SL_4	0.02^{ns}	0.02^{ns}	0.21*	-0.11^{ns}	0.26*	0.20*	0.00^{ns}	-0.28*	0.27*	0.06^{ns}	0.24*	0.10^{ns}
TL_4	0.06^{ns}	-0.08^{ns}	0.03^{ns}	-0.09^{ns}	-0.04^{ns}	0.03^{ns}	-0.07^{ns}	-0.09^{ns}	0.24*	-0.10^{ns}	0.16^{ns}	0.11^{ns}
BL_4	-0.08^{ns}	-0.13^{ns}	-0.08^{ns}	0.10^{ns}	0.45**	-0.02^{ns}	-0.11^{ns}	0.07^{ns}	0.09^{ns}	0.00^{ns}	0.26**	-0.09^{ns}
BW_6	-0.05^{ns}	0.31**	0.26*	-0.10^{ns}	0.56***	0.26*	-0.13^{ns}	0.35**	-0.16^{ns}	0.07^{ns}	0.36**	0.29*
SL_6	0.02^{ns}	-0.15^{ns}	0.20^{ns}	-0.16^{ns}	0.36**	0.27*	-0.19^{ns}	-0.16^{ns}	-0.13^{ns}	0.13^{ns}	0.29*	0.06^{ns}
TL_6	0.03^{ns}	-0.02^{ns}	-0.19^{ns}	-0.05^{ns}	0.11^{ns}	0.00^{ns}	-0.14^{ns}	-0.09^{ns}	0.05^{ns}	0.08^{ns}	-0.04^{ns}	-0.01^{ns}
BL_6	-0.01^{ns}	-0.10^{ns}	0.22*	-0.16^{ns}	-0.12^{ns}	-0.12^{ns}	0.04^{ns}	0.00^{ns}	-0.05^{ns}	-0.07^{ns}	0.24*	0.05^{ns}

BW_2:bodyweight at two weeks of age.BW_4:body weight at four weeks of age.BW_6:body weight at six weeks of age.SL_2: shank length at two weeks,SL_4: shank length at four weeks ,SL_6:shank length at six weeks ,TL_2: tight length at two weeks ,SL_4:shank length at four weeks ,SL_6:shank length at six weeks ,BL_2:body length at two weeks ,BL_4:body length at four weeks,BL_6:body length at six weeks,PCV_6:pack cell volume at six weeks ,PVC9:pack cell volume at nine weeks,Hb_6:haemoglobin at six weeks,Hb_9:haemoglobin at nine weeks ,WBC_6:white blood cell at six weeks ,WBC_9:white blood cell at nine,TP_6:total protein at six weeks of age,TP_9:total protein at nine weeks of age,GPX_6 and GPX $_9$:glutathione peroxidase at six and nine weeks ,$LYMP_6$ and $LYMP_9$: lymphocyte at six and nine. *** ($p<0.0001$); ** ($p<0.01$); * ($p<0.05$) and ns = not significant ($p>0.05$)

4.11 Phenotypic Correlation between Glutathione Peroxidase, Haematological Variables and Growth Traits in F_2 Generation.

The phenotypic correlation between glutathione peroxidase activities, haematological variables and growth traits at different periods are as presented in Table 4.11.

PCV_6 had no significant ($p>0.05$) correlation with all measured growth traits while PCV_9 had Significant ($p<0.05$) and negative correlations with TL_4 across all growth traits. Hb_6 had positive and significant ($p<0.01$) association with BW_2 but was negative with BW_4 while Hb_9 indicated negative and significant relationship with BW_2, BW_4 and BW_6. WBC_6 and WBC_9 had similar trend with Hb_9 in relations to body weight measures. TP_6 was negatively and significantly correlated with BW_2 and BW_9 while TP_9 was positively correlated with BW_4 BW_2 and SL_2. GPx_6 was significantly and positively correlated with BW_2, SL_2, BW_4, SL_4, BW_6 and SL_6 respectively. GPx_9 showed similar trend as GPx_6 $LYMP_6$ had significant ($p<0.05$) and positive correlation with BW_2, BW_4 and BW_6 only while $LYMP_9$ had similar trend with $LYMP_6$ in relation to body weight.

Table 4.11: Phenotypic Correlation between Glutathione peroxidase, haematological variables and growth traits in F_2 Generation

Traits	PCV_6	Hb_6	WBC_6	TP_6	GPX_6	$LYMP_6$	PCV_9	Hb_9	WBC_9	TP_9	GPX_9	$LYMP_9$
BW_2	-0.07^{ns}	0.41**	0.31**	0.39**	0.50***	0.55***	0.12^{ns}	0.31**	0.35**	0.32**	0.41**	-0.44**
SL_2	-0.02^{ns}	0.06^{ns}	-0.26*	-0.06^{ns}	0.34**	-0.14^{ns}	-0.03^{ns}	-0.09^{ns}	0.05^{ns}	0.25*	0.21*	-0.08^{ns}
TL_2	0.03^{ns}	0.05^{ns}	-0.02^{ns}	0.13^{ns}	0.06^{ns}	0.08^{ns}	0.16^{ns}	-0.05^{ns}	0.10^{ns}	-0.09^{ns}	-0.01^{ns}	0.00^{ns}
BL_2	0.02^{ns}	0.10^{ns}	0.00^{ns}	0.00^{ns}	0.02^{ns}	-0.09^{ns}	-0.04^{ns}	-0.04^{ns}	-0.03^{ns}	-0.01^{ns}	-0.04^{ns}	-0.04^{ns}
BW_4	-0.04^{ns}	-0.25*	0.36**	-0.07^{ns}	0.33**	0.02^{ns}	-0.16^{ns}	-0.22*	0.42**	0.30**	0.26*	-0.14^{ns}
SL_4	-0.07^{ns}	0.04^{ns}	-0.09^{ns}	-0.08^{ns}	0.23*	0.04^{ns}	-0.17^{ns}	-0.06^{ns}	0.04^{ns}	0.00^{ns}	0.36**	-0.08^{ns}
TL_4	0.07^{ns}	-0.05^{ns}	-0.04^{ns}	-0.06^{ns}	0.02^{ns}	-0.01^{ns}	-0.21*	-0.06^{ns}	0.00^{ns}	-0.06^{ns}	0.06^{ns}	-0.21*
BL_4	0.05^{ns}	-0.08^{ns}	0.03^{ns}	-0.06^{ns}	0.03^{ns}	-0.02^{ns}	-0.20^{ns}	-0.05^{ns}	0.08^{ns}	-0.08^{ns}	0.06^{ns}	-0.11^{ns}
BW_6	0.01^{ns}	0.09^{ns}	0.46**	0.33**	0.41**	-0.36**	-0.13^{ns}	0.39**	-0.24*	0.05^{ns}	0.38**	-0.04^{ns}
SL_6	-0.03^{ns}	0.01^{ns}	0.11^{ns}	0.00^{ns}	0.44**	-0.10^{ns}	0.00^{ns}	-0.04^{ns}	-0.02^{ns}	0.00^{ns}	0.27*	0.02^{ns}
TL_6	0.01^{ns}	-0.04^{ns}	0.05^{ns}	0.09^{ns}	-0.06^{ns}	-0.05^{ns}	0.13^{ns}	0.06^{ns}	0.05^{ns}	-0.01^{ns}	0.30**	0.08^{ns}
BL_6	-0.05^{ns}	0.07^{ns}	-0.02^{ns}	0.09^{ns}	0.08^{ns}	-0.15^{ns}	0.02^{ns}	-0.14^{ns}	0.13^{ns}	-0.03^{ns}	0.16^{ns}	0.00^{ns}

BW_2:body weight at two weeks of age,BW_4:body weight at four weeks of age,BW_6:body weight at six weeks of age,SL_2:shank length at two weeks of age,SL_4:shank length at four of weeks age,SL_6:shank length at six weeks of age,TL_2:tight length at two weeks of age,TL_4:tight length at four weeks of age,TL_6:tight length at six weeks of age,BL_2:body length at two weeks of age,BL_4:body length at four weeks of age,BL_6:body length at six weeks of age,PCV_6:pack cell volume at six weeks of age,PCV_9:pack cell volume at nine weeks of age,Hb_6:haemoglobin at six weeks of age,Hb_9:haemoglobin at nine weeks of age,WBC_6:white blood cell at six weeks of age,WBC_9:white blood cell at nine weeks of age,TP_6:total protein at six weeks of age,TP_9:total protein at nine weeks of age,GPX_6 and nine:glutathione peroxidase at six and nine weeks of age,$LYMP_6$ and $LYMP_9$: lymphocyte at six and nine weeks of age.

*** ($p<0.0001$); ** ($p<0.01$); * ($p<0.05$) and ns = not significant ($p>0.05$)

4.12 Phenotypic Correlation between Egg Production, Glutathione Peroxidase and Haematological Parameters in F_1 Generation

Table 4.12 showed the correlation coefficient between Glutathione peroxidase, haematological measures and egg production traits in F_1 generation. PCV_6 showed significant ($p<0.05$) and positive relationship with all the haematological traits and GPx while being not significantly correlated with egg production triats. Hb and WBC had significant and positive correlation with all the haematological traits except TP while WBC_6 showed positive and significant relation with GPx, EN, RLAY and DLAY respectively. Non significant correlation coefficient was observed between TP, haematological and egg production traits. Positive and high correlation coefficient was observed between GPx and most egg production traits except RLAY similarly GPx had positive correlation with LYMP and WBC. ASM showed positive correlation with all the egg production traits.

Table 4.12: .Phenotypic Correlation between Egg Production, Glutathione peroxidase and Haematological Parameters in the F_1

Traits	PCV_6	Hb_6	WBC_6	TP_6	GPX_6	$LYMP_6$	PCV_9	Hb_9	WBC_9	TP_9	GPX_9	$LYMP_9$	ASM	EWT	EN	DLAY
PCV_6																
Hb_6	0.23**															
WBC_6	-0.16*	0.14*														
TP_6	0.15*	0.11*	0.02^{ns}													
GPX_6	0.16*	0.01^{ns}	0.36^{**}	0.06^{ns}												
$LYMP_6$	0.16*	-0.06^{ns}	0.26**	0.08^{ns}	0.12*											
PCV_9	0.16*	0.18*	0.13**	0.06^{ns}	-0.04^{ns}	0.08^{ns}										
Hb_9	0.20*	0.22**	0.18**	0.04^{ns}	-0.06^{ns}	0.20**	0.32**									
WBC_9	0.21*	-0.04^{ns}	0.12*	0.01^{ns}	0.12*	0.22**	0.26**	0.01^{ns}								
TP_9	0.25*	0.02^{ns}	0.09^{ns}	0.17*	0.06^{ns}	-0.10^{ns}	-0.17*	-0.11*	-0.19*							
GPX_9	0.15*	0.11*	0.25^{**}	0.05^{ns}	0.21**	0.14*	0.04^{ns}	0.15*	0.02^{ns}	-0.01^{ns}						
$LYMP_9$	0.15*	0.11*	0.11*	-0.14*	-0.05^{ns}	-0.03^{ns}	0.09^{ns}	0.02^{ns}	-0.15*	0.01^{ns}	0.18*					
ASM	0.05ns	0.01^{ns}	0.29**	0.09^{ns}	0.16*	-0.05^{ns}	0.00^{ns}	0.12*	0.06^{ns}	-0.06^{ns}	0.19*	-0.16*				
EWT_9	0.01ns	-0.08^{ns}	0.05^{ns}	0.01^{ns}	0.16*	0.07^{ns}	0.17*	0.04^{ns}	0.07^{ns}	-0.05^{ns}	0.17*	0.07^{ns}	0.18*			
EN	0.06ns	0.03^{ns}	0.24**	0.10^{ns}	0.19*	0.08^{ns}	0.05^{ns}	0.16*	0.04^{ns}	0.07^{ns}	0.15*	0.21**	0.93**	0.02^{ns}		
DLAY	0.05ns	-0.01^{ns}	0.29**	0.09^{ns}	0.16*	0.05^{ns}	0.00^{ns}	0.12*	0.06^{ns}	0.06^{ns}	0.19*	0.16*	1.00**	0.03^{ns}	0.18*	
RLAY	0.01ns	0.04^{ns}	0.19**	0.00^{ns}	-0.09^{ns}	0.08ns	0.11*	0.06^{ns}	0.14*	-0.04	-0.16*	-0.07^{ns}	0.64***	0.01^{ns}	0.17*	0.02ns

PCV_6:pack cell volume at six weeks of age,PCV_9:pack cell volume at nine weeks of age,Hb_6:haemoglobin at six weeks of age,Hb_9:haemoglobin at nine weeks of age,WBC_6:white blood cell at six weeks of age,WBC_9:white blood cell at nine weeks of age,TP_6:total protein at six weeks of age,TP_9:total protein at nine weeks of age.GPX_6:glutathione peroxidise level at six weeks of age,GPX_9:glutathione peroxidise level at nine weeks of age,$LYMP_6$:lymphocyte at six weeks of age,$LYMP_9$:lymphocyte at nine weeks of age.ASM:age at sexual maturity,EW9:egg weight at nine weeks of age,EN:egg number,DLAY:daily egg number,RLAY:rate *** ($p<0.001$); ** ($p<0.01$); * ($p<0.05$) and ns = not significant ($p>0.05$)

4.13 Phenotypic Correlation between Egg Production, Glutathione peroxidase and Haematological Parameters in F_2 Generation

Table 4.13 showed significant ($p<0.05$) and positive correlation for WBC_6 with GPx_6, GPx_9 $LYMP_6$, $LYMP_9$, TP_6 and TP_9 with the exception of Hb_9 that is negatively correlated. TP_6 was only positively correlated with $LYMP_6$, WBC_9 and Hb_9. Hb_6 only showed significant positive correlation with ASM while it was significantly and negatively associated with Hb_9 and all other egg production measures. GPx_6 showed significant and positive association with $LYMP_6$, and all the Egg production traits. $LYMP_6$ showed significant positive relationship with ASM and negative association with EN and DLAY. There was significant association between TP_9 and EWT_9. Association amongst egg production traits followed similar trend as with F_1 generation with variations only in magnitude of coefficients and level of significance.

Table 4.13: Phenotypic Correlation between Egg Production, Glutathione peroxidase and Haematological Parameters in the F_2 Generation

PCV_6:pack cell volume at six weeks of age,PCV_9:pack cell volume at nine weeks of age,Hb_6:haemoglobin at six weeks of age,Hb_9:haemoglobin at nine weeks of age,WBC_6:white blood cell at six weeks of age,WBC_9:white blood cell at nine weeks of age,TP_6:total protein at six weeks of age,TP_9:total protein at nine weeks of age.GPX_6:glutathione peroxidise level at six weeks of age,GPX_9:glutathione peroxidise level at nine weeks of age,$LYMP_6$:lymphocyte at six weeks of age,$LYMP_9$:lymphocyte at nine weeks of age.ASM:age at sexual maturity,EW9:egg weight at nine weeks of age,EN:egg number,DLAY:daily egg number,RLAY:rate, *** (p<0.0001); ** (p<0.01); * (p<0.05) and ns = not significant (p>0.05)

Traits	PCV_6	Hb_6	WBC_6	TP_6	GPx_6	$LYMP_6$	PCV_9	Hb_9	WBC_9	TP_9	GPx_9	$LYMP_9$	ASM	EWT	EN	DLAY
PCV_6																
Hb_6	-0.0^{9ns}															
WBC_6	0.04^{ns}	-0.06^{ns}														
TP_6	-0.04^{ns}	-0.0^{9ns}	0.20*													
GPx_6	0.14*	-0.10^{ns}	0.19*	0.03^{ns}												
$LYMP_6$	0.16*	0.01^{ns}	0.14*	0.16*	0.19*											
PCV_9	0.02^{ns}	0.00^{ns}	0.05^{ns}	0.07^{ns}	-0.10^{ns}	0.13*										
Hb_9	0.07^{ns}	0.14*	0.13*	0.12*	-0.10^{ns}	0.00^{ns}	0.03^{ns}									
WBC_9	0.01^{ns}	0.00^{ns}	0.02^{ns}	0.13*	0.09^{ns}	0.11*	0.00^{ns}	0.18*								
TP_9	0.09^{ns}	-0.06^{ns}	0.11*	-0.07^{ns}	0.08^{ns}	0.20*	-0.04^{ns}	0.17*	0.12*							
GPx_9	0.05^{ns}	-0.05^{ns}	0.18*	0.00^{ns}	-0.08^{ns}	0.06^{ns}	-0.06^{ns}	0.02^{ns}	0.18*	0.08^{ns}						
$LYMP_9$	-0.06^{ns}	0.05^{ns}	0.17*	-0.04^{ns}	-0.07^{ns}	0.16*	0.01^{ns}	0.20*	0.15*	-0.07^{ns}	0.17*					
ASM	-0.08^{ns}	0.14*	0.02^{ns}	0.02^{ns}	0.18*	0.15*	0.01^{ns}	0.18*	0.08^{ns}	-0.08^{ns}	-0.08^{ns}	-0.01^{ns}				
EWT_9	0.14*	0.19*	0.04^{ns}	0.06^{ns}	0.18*	0.08^{ns}	0.02^{ns}	0.01^{ns}	0.08^{ns}	0.19*	-0.06^{ns}	-0.07^{ns}	0.17*			
EN9	-0.03^{ns}	0.17*	-0.04^{ns}	-0.05^{ns}	0.19*	0.18*	0.01^{ns}	0.12*	0.11*	0.02^{ns}	0.10^{ns}	0.07^{ns}	0.55**	0.02^{ns}		
DLAY	0.08^{ns}	0.14*	-0.02^{ns}	-0.02^{ns}	0.16*	0.15*	-0.01^{ns}	0.18*	-0.08^{ns}	0.08^{ns}	0.08^{ns}	0.01^{ns}	1.00**	0.03^{ns}	0.18*	
RLAY	-0.08^{ns}	0.12*	-0.0^{5ns}	-0.04^{ns}	0.12*	0.10^{ns}	0.02^{ns}	0.02^{ns}	-0.06^{ns}	-0.04^{ns}	0.08^{ns}	0.07^{ns}	0.66**	0.01^{ns}	0.17*	0.02^{ns}

4.14 Heritability estimates (±standard error) of body weight and morphometric traits in the F_1 and F_2 Generations.

Heritability estimates and standard error of estimate are shown in Table 4.14. Estimates for BW_2 and BW_6 were (0.49 for BW_4 to 0.50 for $BW_{6\ in}$ F_1 and 0.51 for BW_2 to 0.55 for BW_6 in F_2). Estimates for SL were generally high ranging from 0.30 for SL_4 in F_1 to 0.51 for SL_6 in the F_1 generation. This estimate ranged from very low (0.02 in TL_6 of F_1) to high (0.48 in TL_2 for F_2 Generation). BL showed low (0.09 in BL_2 of F_1 Generation) to high (0.45 for BL_4 in F_2 Generation). Estimates for growth traits were generally higher in F_2 Generation than F_1 Generation.

Table 4.14: Heritability estimates (±standard error) of body weight and morphometric traits in the $F_1$and F_2 Generations.

Traits	F_1 Generation h^2 ±SE	F_2 Generation h^2 ±SE
BW_2	0.49±0.10	0.51±0.09
SL_2	0.50±0.07	0.40±0.07
TL_2	0.07±0.03	0.48±0.01
BL_2	0.09±0.03	0.23±0.06
BW_4	0.40±0.12	0.55±0.10
SL_4	0.30±0.06	0.47±0.05
TL_4	0.36±0.08	0.23±0.08
BL_4	0.08±0.01	0.45±0.04
BW_6	0.50±0.03	0.55±0.06
SL_6	0.51±0.14	0.43±0.11
TL_6	0.02±0.01	0.22±0.09
BL_6	0.19±0.07	0.11±0.06

BW_2: body weight at two weeks of age,BW_4:body weight at four weeks of age,BW_6:body weight at six weeks of age,SL_2:shank length at two weeks of age,SL_4:shank length at four weeks of age,SL_6:shank length at six weeks of age,BL_2:body length at two weeks of age,BL_4:body length at four weeks of age,BL_6:body length at six weeks of age.h^2:heritability.

4.15 Heritability estimate (±standard error) of Glutathione Peroxidase Activity, Hematological Parameters and Egg Production Traits.

Heritability estimates for GPx activity at six and nine weeks along with haematological parameters and egg production traits are represented in table 4.15. Estimates for GPx_6 and GPx_9 were high in both generations (0.41 and 0.51) and (0.50 and 0.52) respectively. The heritability estimates for PCV_6 and PCV_9 were 0.14 and 0.16 for F_1 while 0.09 and 0.12 for F_2 Generations respectively. Hb_6 and Hb_9 showed estimates of 0.33 and 0.42; 0.45 and 0.48 in each generation. Higher estimates of (0.70 and 0.58) and (0.70 and 0.60) respectively were obtained for TP_6 and TP_9 while medium estimates were obtained for WBC_6 and WBC_9 as (0.26 and 0.22) and (0.32 and 0.28) respectively. $LYMP_6$ and $LYMP_9$ showed moderate to high heritability estimates of (0.28 and 0.32) and (0.20 and 0.40) across the generations. Estimates for egg production measures were 0.29 and 0.30, 0.17 and 0.16; 0.26 and 0.29; 0.29 and 0.21; 0.32 and 0.24 for ASM, EWT_9, EN_9, DLAY and RLAY across the generations.

Table 4.15: Heritability estimate (±standard error) of glutathione peroxidase activity, Hematological parameters and Egg production traits.

Traits	F_1 Generation h^2 ±SE	F_2 Generation h^2 ±SE
GPx_6	0.41±0.13	0.50±0.15
GPx_9	0.51±0.21	0.52±0.19
PCV_6	0.14±0.05	0.09±0.07
PCV_9	0.16±0.09	0.12±0.09
Hb_6	0.33±0.10	0.45±0.19
Hb_9	0.42±0.11	0.48±0.15
TP_6	0.70±0.23	0.70±0.13
TP_9	0.58±0.18	0.60±0.21
WBC_6	0.26±0.11	0.32±0.08
WBC_9	0.22±0.15	0.28±0.16
$LYMP_6$	0.28±0.10	0.20±0.07
$LYMP_9$	0.32±0.13	0.40±0.14
ASM	0.29±0.11	0.30±0.07
EWT_9	0.17±0.05	0.16±0.02
EN_9	0.26±0.19	0.29±0.15
DLAY	0.29±0.12	0.21±0.08
RLAY	0.32±0.10	0.24±0.14

PCV_6:pack cell volume at six weeks of age,PCV_9:pack cell volume at nine weeks of age,Hb_6:haemoglobin at six weeks of age,Hb_9:haemoglobin at nine weeks of age,WBC_6:white blood cell at six weeks of age,WBC_9:white blood cell at nine weeks of age,TP_6:total protein at six weeks of age,TP_9:total protein at nine weeks of age.GPX_6:glutathnumber,RLAY:rate of lay

CHAPTER FIVE

5.0 DISCUSSIONS

5.1 Growth Characteristics of the Base, F_1 and F_2 Generation

Observed body weight of 42.49g and 87.29g at BW_2 and BW_4 in the base generation were lower than 46.61 and 108.02 obtained by Gehan *et al*. (2010) but agreed with the reported range of 35.2 – 46.4g and 87.3 -93.5g (Aboul-Hassan, 2001a). Differences in BW_6 and BW_9 between males and females with higher weight in females observed in this study was consistent with the reports of (Sefton and Siegel, 1974; El-Fiky, 1991; Aboul-Hassan, 2000 and Abdel-Fattah, 2006) that females are consistently heavier than males at all ages This was however, contradicted by the non significant ($p>0.05$) differences obtained at the 2^{nd} and 4^{th} week which may be unconnected to the randomness of the population in this generation. Caron *et al*. (1990) indicated that females grow faster and yielded larger muscles and more abdominal fat than males at the same age. Generally, the reported estimates for body weight of Japanese quail recorded at different ages indicate the high efficiency of this bird for growth**.** However, the observed differences between the various estimates reported in literature for body weight of Japanese quail recorded at a particular age may be possibly due to the differences in the climatic and managerial conditions under which different flocks were reared and to the possible differences in genetic make-up of the different flocks. The skeletal, growth and development indicators in this study were in agreement with the observation of Yannakopoulos *et al.* (1995) and Farahat (1998). Observed BL, SL and TL between sexes and for data at different ages were higher than the values reported by Ojo *et al*. (2014), however, the differences due to sexes in SL were in agreement with the findings of these authors.The fastest GR was shown during the period 2-6 weeks of age whereas, the slowest rate was obtained during the period 4-6 weeks of age for the

combined sexes, these results agreed with those obtained by Badawy (2008). While, Shalan (1998) and Abdel Fattah *et al*. (2006) found lower growth rates during 2-4 and higher growth rate at 4-6 weeks of age. It seems, however, that growth rate in males and females of Japanese quail should be considered distinct characteristic of population and should be taken into account in any breeding program aiming at improving growth characteristics in Japanese quail. (Gehan *et al*., 2010).

In the F_1 generation, the indication of highly significant ($p<0.01$) superiority of the females over the males in BW, BL and SL at different periods produced evidence of stabilization as the population moves from randomness to ordered association, so that, higher body weight, body length and shank length compared to the previous generation were obtained. The differences between the sexes agreed with the findings of Yannakopoulos *et al.,* (1995) and Farahat (1998) while the GR differences favouring the males at the 4^{th} week in the F_1 and F_2 generation agreed with the statement of Badawy (2008) and Gehan *et al*. (2010) that males had the highest value at four weeks of age, while this was reversed in the 6^{th} week. BW in F_1 and F_2 generation obtained and subsequent differences observed between the sexes were consistent with the work of Vali *et al*., 2005; Shokoohmand *et al*., 2007 and Alkan *et al*., 2010.

5.2 Haematological Profiles of the Base, F_1 and F_2 Generation

The significant ($p<0.05$) variation in GPx_6, GPx_9, TP_6 and TP_9 with higher values in the females obtained in this study for the base generation agreed with the findings of Godin *et al*. (1995); Abdel Kader (2003) and Gehan *et al*. (2010) while this same trend as observed with $LYMP_6$ was at variance with the report of Gehan *et al*. (2010). The lack of significant ($p>0.05$) sexual effect on all other haematological variables agrees with the observations of Gehan *et al*. (2010). All

observed blood profile values were within reported physiological range for quails (El Ghalid, 2005 and Bahie El Deen *et al*., 2009).

In the F_1 generation, the significant differences between sexes with higher values in the females for GPx_6 agreed with the findings of Gehan *et al*. (2010) that, GPx activity in red blood cells is higher in females than in males of Japanese quail. Similar results were obtained with GPx activity in rat liver, where females had higher activity than males (Capel and Smallwood 1983; Burk, 1983; Igarashi et al., 1984; Debski et al., 1992; Prohaska and Sunde, 1993; Sachdev and Sunde, 2001). Also, in mice liver GPx activity was higher in females compared to males (Prohaska and Sunde, 1993).

Sex differences in GPx activity may be the result of differences in distribution of selenium in male and female, or they may be caused by metabolic differences (Finley and Kincaid, 1991). Also, it has been reported that GPx activity is higher in female rats and dromedary camels (Corbera *et al*., 2001) than in the males though male rats have greater plasma, kidney, cytosol and RBC GPx activity and Se concentration than females in rats (Finley and Kincaid, 1991). The higher significant PCV_6 value obtained in males in F_1 generation compared to the females agreed with the report of (Mihailov *et al.*, 1999 and Abdel Azeem *et al.*, 2001) of higher haematocrit and PCV in male Japanese quail compared to the female.

The F_2 generation was noted to follow similar trend as the base generation with the exception of lack of differences in $LYMP_6$ which confirms the observation of Gehan *et al*. (2010) in this respect.

5.3 Egg Production Traits between the Generations

Observed significant ($p<0.05$) differences in ASM across generations (47.08±0.70 – 49.87±0.7) were consistent with the findings of Adelaja (2012) who reported significant differences in lines of Japanese quails divergently selected for body weight between generations and also the superiority of the F_2 generation (47.08±0.70) over the earlier generations obtained in this study were consistent with the observations of Adelaja (2012) and also explains the increase in egg number from the base (31.85±1.80) generation to the F_2 generation 33.47±1.80). This superiority in ASM also impacts on DLAY (15.93±0.70) and RLAY (2.70±0.10) as obtained in this study and values reported were within the range 25 – 69 day reported (Sezer, 2007) though they were higher than the range of 38 to 42 days of age in Japanese quails reported (Mizutani, 2003), this may be due to differences in genetic make-up and body weight. The importance of early sexual maturity in any farm animal is that it has a longer reproductive life and hence ability to produce more offsprings. Egg weight at 9 weeks reported were lower than the range of 9.10g – 13.50g (Kul and Seker, 2004), but the higher weight obtained in the F_2 coincided with the higher body weight observed in this generation compared to and agreed with the report of Reddish *et al.* (2003) who stated that the high weight group laid larger eggs than the control group.

5.4 Phenotypic Correlation between Growth Traits and Egg Production Traits for the F_1 and F_2 Generation

The trend of positive significant correlation between BW and linear body measures at different ages and growth periods obtained were similar to the reports of Bahie El Deen (1994) and Abdel Fattah (2006). Gehan *et al*. (2010). This may imply that selection for any of these periodic measures in the F_1 and F_2 will lead to corresponding increase in similar measurements at a latter period, consequently, selecting for shank length at 2 weeks will positively influence shank length at six weeks. The non significant association between BW measures at different periods and most egg production traits were at variance with the reports of Minvielle (1998), Brah *et al.,* (2001). and Sezer *et al.,* (2006) and Adelaja (2012) that selection for BW_4 in Japanese quails contributed considerably to the variation observed in most traits, thus correlated response is expected to be high in these traits. This may be due to sample size and differences in the types of birds used for the study. The high negative and significant correlation between ASM and RLAY and DLAY were similar to the findings of Sezer (2007) who reported that estimates of genetic correlation of ASM with weekly body weight ranged from –0.04 to -0.26: Hidalgo *et al.* (2011) who estimated ranges of -0.01 to -0.77 between ASM and Average egg weight for some lines and Aboul-Hassan (2001b) who also reported negative but moderate correlation between ASM and average egg number while it disagreed with Abdel-Mounsef (2005) who reported positive but low correlation between ASM, average egg number and average egg weight implies that an increase in ASM will lead to a decrease in RLAY and DLAY which will consequently impact on EN by decreasing it. Observed positive correlation between ASM and BW at different periods agreed with the report of Abdel-Tawab (2006) describing positive correlation between ASM, body weight and average daily gain.

5.5 Phenotypic Correlations between Glutathione Peroxidase, Haematological Variables and Growth Traits in F_1 and F_2 Generations.

The obtained significant association and coefficients of correlation between Glutathione peroxidase enzyme activities and growth traits in both generations were similar and agreed with the range of 0.20 – 0.58 reported by Gehan *et al*. (2010) for similar relationships in Japanese quail. This trend points to the fact that selecting for increase in glutathione peroxidase enzyme activities in Japanese quail will lead to increase in growth traits especially body weight and shank length. This is in accordance with the findings of Abdel Azim and Farahat (2009). The trend of positive association between Lymphocyte count at different ages and growth traits were similar to the findings of Gehan *et al*. (2010). Significant ($P<0.01$) positive phenotypic correlations estimates that were found between GPx enzymes activity and Lymph at 6 weeks of age with each of BW_2, BW_4, BW_6, GR2-4, SL_2, SL_4 and SL_6 in Japanese quail agrees with (Gehan *et al*., 2010). All other haematological variables indicated varying degrees of significance and direction of association with growth traits at different periods. This is an indication that GPx enzymes activity and blood constituents can be used as prediction indicators to increase and improve growth traits and can also be used in selection programs to improve production and immunological traits of Japanese quail.

5.6 Phenotypic Correlation between Egg Production, Glutathione Peroxidase and Haematological Parameters in F_1 and F_2 Generation.

Significant ($p<0.05$) positive correlation between GPx_6 and $LYMP_6$ in the F_1 and $LYMP_9$ in the F_2 agreed with the findings of Gehan *et al*., (2010), while all other associations between GPx Lymph in both generations differed from this trend. Positive association between GPx enzyme activity and ASM obtained in both generations indicates that selecting for increase in enzyme concentration and activity in Japanese Quail will lead to decrease in age at which sexual maturity

is attained and consequently impact positively on egg production as evidenced by the positive association between enzyme activity at the sixth and ninth week and most other egg production measures in the two generations, studies by El-Full *et al*. (2010) in different breeds of chickens showed that birds with higher enzyme activity had better egg production performance compared to birds with lower enzyme activity. correlations amongst other haematological traits showed no definite pattern and were wide and varying in both magnitude and direction, but some of these agreed with the correlation coefficients among some blood parameters in chickens as reported by El Safty *et al.*, (2004) and Abdel Azim and Farahat (2009).

Correlation among blood parameters and GPx enzymes activity indicated pleiotropic effects and consequently performing selection in any of the two traits may lead to change on the other trait, but further research is needed to support that hypothesis.

5.7 Heritability Estimates (±standard error) of Body Length, Body Weight, Shank Length and Growth Rate for F_1 and F_2 Generation.

The moderate to high estimates of heritability obtained for BW(0.4±0.12 – 0.55±0.1) in both generations of this study at different ages indicates that considerable improvement in this trait could be achieved through efficient selection programmes, however selection response for body weight are expected to be high. The BW at two, four and six weeks of age seems to be highly heritable in quails. Similar trends were reported by EL Fiky (1991) also these estimates were within the range of heritability for growth traits estimated by several investigators (Saatci *et al.,* 2002 and Abdel Fattah, 2006).Similar conclusion could be drawn with regards to shank length with obtained estimates agreeing with the range of 0.20 -0.70 reported by (Gehan *et al*., 2010) and also a wide range of heritability estimates for growth traits have been reported by many researchers (Farahat, 1998; Bahie El–Deen, 1999; Aboul–Hassan *et al.,* 1999; Aboul-Hassan 1997 and 2000 and 2001 b; El–Fiky *et al.,* 2000a and b; Abdel-Fattah, 2006; El–Fiky, 2005;

Abdel-Mounsef, 2005; Vali *et al.*, 2008; Abdel-Tawab, 2006). These authors studied body weight at different ages and used different methods to estimate the heritability. Thus, heritability estimates reported for body weight would be expected to vary in diverse genotypes and under different environments.

Abdel-Seoud, (2008) had observed that discrepancies between heritability estimates for a particular trait should be considered the norm rather than the exception. The uniqueness of the population, the selection environment, and the period and length of selection (Generations), all can have a pronounced effect on the magnitude of the heritability estimate. (Aboul-Hassan, 1997).

5.8 Heritability Estimate (±standard error) of Glutathione Peroxidase Activity, Hematological Parameters and Egg Production Traits.

Estimates obtained for GPx enzymes activity at six and nine weeks in both generations were similar to those reported by Gehan *et al*. (2010) as 0.45, 0.55 and 0.51 for sire, dam and sire+dam variance components, it also agreed with the estimates of 0.47 reported for GPx activity in pigs (Lingass *et al*., 1991) and indicates that it is possible to increase GPx levels in blood plasma of Japanese quails.

Though certain estimates were lower, the general estimates obtained for blood constituents were comparable to the range of 0.25 – 0.76 reported by (Gehan *et al*., 2010) and they were also in agreement with those obtained in chickens by AbdelLatif, (2001) and El Dlebshany *et al.*, (2009). The estimates for heritability of GPx and blood constituents in Japanese quail lead to conclusion that a considerable improvement in this traits could be achieved through efficient selection programme, however selection response for GPx and blood constituents are expected to be large. Based on the obtained heritability estimates, the analyzed traits seemed to be able to respond to selection at variable intensities.

Estimates for ASM (0.29± 0.11 – 0.30±0.07) as obtained in this study were low to moderate and within the same range of 1.35 - 0.42 reported (Bahie El-Deen, (1991); El-Fiky *et al.* (2000a); Aboul-Hassan (2001b); Tawefeuk (2001) and Abdel-Mounsef (2005). EWT_9 and EN_9 estimates also agreed with estimates in Japanese quail reported in literature which ranged between (0.05 and 0.88) and (0.01 and 0.17), respectively (Aboul-Hassan and El-Fiky, 1995; Minvielle *et al.* 1997; Abdel-Mounsef, 2005 and Hidalgo *et al.,* 2011) the lower estimates for Egg weight however is a reflection of greater non-additive genetic variance and variance due to common environment. Reports about Generational differences concerning these traits are scanty. The estimate for rate of lay in both generations were lower than 0.77 reported for early sexually maturing Japanese female quails but comparable to 0.23 and 0.48 for the medium and late maturing types as reported by Bahie El-Deen *et al*. (2008) and since the ASM value obtained for this study fell within the medium sexual maturity class described by these authors, there is likelihood that selection on the basis of ASM will also produce good response to selection in RLAY.

CHAPTER SIX

6.0 SUMMARIES, CONCLUSIONS AND RECOMMENDATIONS

6.1 Summaries

- A study was designed to evaluate sexual dimorphism in growth, haematological and glutathione peroxidase enzyme activity and also egg production characteristics in the base, F_1 and F_2 generations of Japanese quail.
- A total of 100 day old chicks that fed diet containing 26% CP and 2741 ME Kcal/Kg at 4 weeks of age, and then were introduced to breeder diets containing 24%CP and 2900 ME Kcal/kg forty five (45) females and fifteen (15) males were randomly selected and matined at a ratio of 1male: 3 females.
- Fertile eggs were collected and marked according to sire number and incubated for 16 days. The hatched chicks were marked according to sire brooded.
- Growth traits were measured at two, four and six weeks of age. Growth rate during the periods of 2, 4 and 6 weeks were calculated.
- Blood samples were collected at 6 and 9 weeks of age from sample birds to evaluate glutathione peroxidase in plasma and other haematological variables. Egg production traits (age at sexual maturity, egg number at 9 weeks, egg weight at 9 weeks, days in lay and rate of lay) were recorded.
- Obtained data were subjected to one-way analysis of variance to calculate Phenotypic correlation between growth, haematological, enzyme activity and egg production variables. Heritability estimate were also determined in the F_1 and F_2 generation.
- GPx enzymes activity and blood plasma constituents were positively correlated with growth traits and egg production traits. Correlation between GPx and bodyweight in F_1

(0.56), GPx and shank length in F_1 (0.36), GPx and bodyweight in F_2 (0.41), GPx and shank length in F_2 (0.44). Correlation between GPx and age at sexual maturity in F_1 (0.16) GPx and egg weight in F_1 (0.17), GPx and EN in F_1 (0.19), GPx and ASM in F_2 (0.18), GPx and EWT in F_2 (0.18), GPx and EN in F_2 (0.19). Correlation between GPx and WBC F_1 (0.22) GPX and LYMP in F_1 (0.12), GPx and WBC in F_2 (0.19), GPx and LYMP in F_2 (0.19). The correlations between the enzyme activities and production traits obtained in this study especially the correlations between the enzyme activities of body weight and egg production suggest that, this selection could be used to improve performance and disease resistance.

- Heritability of Glutathione peroxidase based on sire variance is high. (F_1 0.51, F_2 0.55). This indicates that there are higher chances of passing the gene from the parent to the next generation. Also the higher the heritability the higher gain in selection response.
- The level of glutathione peroxidase activities were higher in females than in males (Females 12.75u/g Males 12.18u/g),

6.2 Conclusion

- GPx enzymes activity and blood plasma constituents are positively correlated with growth traits and egg production traits, Therefore selection for either (GPx enzymes Blood constituents) may lead to improvement in the other traits (Growth and Egg traits).
- Correlation among blood parameters and GPx enzymes activity indicates that estimates of one of these parameters could be use as a good indicator to other traits
- Heritability of Glutathione peroxidase based on sire variance is high. (F_1 0.51, F_2 0.55). This indicates that there are higher chances of passing the gene from the parent to the next generation. Also the higher the heritability the higher the gain in selection response.
- The levels of glutathione peroxidase activities were higher in females than in males (Females 12.75u/g Males 12.18u/g). Therefore there is sexual dimorphism between males and females in gluthione peroxidace.

1.3 Recommendation

In view of the positive correlation between glutathione peroxidase, egg production and growth traits, further research should be done with a larger data size so as to clearly establish these blood biochemical factors as indicator to improve productive and reproductive traits in Japanese quail.

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