PROSPECTS FOR IMPROVING PERFORMANCE OF TWO TANZANIAN CHICKEN ECOTYPES THROUGH SELECTION

BY

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ABSTRACT

A study was carried out to evaluate the possibility of improving the performance among two chicken ecotypes of Tanzania viz. *Kuchi* and Tanzania *Medium* through selection. The study involved evaluation of their genetic potential, estimation of genetic parameters for various traits, and determining optimal breeding strategies for their improvement through selection. Furthermore, prospects for using Marker Assisted Selection (MAS) for some traits were also investigated. Results indicated that *Kuchi* had significantly higher body weights ($P < 0.001$), better feed conversion ratio ($P < 0.05$), and laid eggs with higher weights ($P < 0.05$) than *Medium* ecotype. On the other hand, *Medium* ecotype was superior in terms of egg production and attained sexual maturity earlier than *Kuchi* ($P < 0.05$). However, differences between ecotypes with respect to other egg quality traits and primary antibody response (primary humoral immune response) against Newcastle disease virus (NDV) vaccine were not significant ($P > 0.05$). Moderate to high heritability estimates were obtained for various traits in both ecotypes. The estimates varied from 0.22 to 0.53 for *Kuchi*, and 0.23 to 0.61 for *Medium* ecotype, with most of the corresponding estimates between the two ecotypes being close to each other. Genetic (r_g) and phenotypic (r_p) correlations in both ecotypes were highest among body weights (i.e. $r_g = 0.60$ to 0.93 and $r_p = 0.54$ to 0.78; $r_g = 0.53$ to 0.80 and $r_p = 0.44$ to 0.72, under intensive and extensive management systems, respectively), and were lowest (i.e. around 0.10 and below, ranging from negative to positive) among primary antibody response against NDV vaccine and production traits, and among eggshell thickness, egg shape index and other production traits. The magnitude of heritability estimates obtained in this study permit improvement of performance of these ecotypes through selection. As *Kuchi* chickens were shown to be superior to *Medium* ecotype in terms of body weight, and converse was true for egg production. Therefore, it was recommended to put emphasis for further improvement in body weights in *Kuchi*, and egg production in *Medium* ecotype. Depending on a breeding scenario, results from simulation studies indicated that it would take between 5 to 11 generations of selection for achieving pre-defined desired gains in various traits. The corresponding years of selection varied from 3 to 12 years. There were some LEI0258 microsatellite alleles (a microsatellite located within MHC B region) which had significant effect on primary antibody response against NDV vaccine (alleles of 205 and 307bp) and body weight (allele of 307bp), hence showing good prospects for using MAS for further improvement of these traits.

DECLARATION

I, JAMES LWELAMIRA, do hereby declare to the SENATE of Sokoine University of Agriculture that this thesis is my own original work and that it has not been submitted for a degree award in any other University.

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The above declaration is confirmed

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DEDICATION

To my father, the late ELIAS LWELAMIRA, and my mother, YUSTINA RWIZA.

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LIST OF ABBREVIATIONS AND SYMBOLS

μ	Micron
μg	Microgramme
μl	Microlitre
μM	Micromolar
mM	Millimolar
°C	Degrees Celcius
%	Percent
Ab	Antibody response against NDV vaccine
ADRI	Animal Diseases Research Institute, Dar-es-Salaam, Tanzania
AFE	Age at first egg (age at sexual maturity)
ARC	Agriculture Research Council, South Africa
Bwt8	Body weight at 8 weeks of age
Bwt12	Body weight at 12 weeks of age
Bwt16	Body weight at 16 weeks of age
Bwt20	Body weight at 20 weeks of age
CP	Crude Protein
DANIDA	Danish International Development Agency
DIAS	Danish Institute of Agricultural Science
DNA	Deoxyribonucleic acid
dNTP	Deoxynuccloside tri-phosphate
d	days

EDTA	Ethylene Diamine Tetraacetic Acid
EN	Egg number
EN-90	Egg number in the first 90 days after sexual maturity
FCE	Frequency of cracked eggs
ESI	Egg shape index
EW	Egg weight
FAO	Food and Agriculture Organisation
FCR	Feed conversion ratio
g	Gram
Gen	Generations of selection
GLM	General Linear Model
GPB	Gain per bird
HA	Haemagglutination
HD	Hen day egg production
HI	Haemagglutination Inhibition
IPB	Intake (of feed) per bird
Kcal	Kilocalories
Kg	Kilogram
Lsmean	Least square mean
MAS	Marker assisted selection
ME	Metabolizable Energy
MHC	Major Histocompatibility Complex

Min	Minute
MOAC	Ministry for Agriculure and Co-operatives (Tanzania)
ND	Newcastle Disease
NDV	Newcastle disease virus
PCR	Polymerase Chain Reaction
PHSL	Improving Health and Productivity of Smallholder Livestock in East Africa
REML	Restricted Maximum Likelihood
RVAU	The Royal Veterinary and Agricultural University (Copenhagen, Denmark)
RIR	Rhode Island Red
SAS	Statistical Analysis Systems
s.e	Standard error
SG	Egg specific gravity
SRBC	Sheep Red Blood Cells
STH	Shell thickness
SUA	Sokoine University of Agriculture (Morogoro, Tanzania)
WL	White leghorn
wk	week

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background information

Animal protein intake in developing countries including Tanzania has been very low compared to the recommended level (Delgado *et al.*, 1998 cited by Pedersen, 2002; Nielsen *et al.*, 2003). Due to their short generation intervals, chickens have high potential to offset this problem of low protein intake. Local chickens dominate the chicken industry in developing countries. It has been estimated that more than 70% of rural households in developing countries keep local chickens (Aini, 1990; MOAC, 1997). Reasons such as source of income, low input requirement in terms of land, feed and labour, lack of religious or social restrictions, and its frequent use in traditional matters (i.e. dowry, traditional ceremonies, sacrifices, gifts) are the major reasons for most rural families to keep local chickens (Yongolo, 1996; Tadelle *et al.*, 2003b; Acamovic *et al.*, 2005; Muchadeyi *et al.*, 2005). Furthermore, local chickens are popular for their tastier meat and eggs (Aganga *et al.*, 2003; Yang and Jiang, 2005), and they have been favourably associated with the ability to adapt to harsh environments prevailing in the Tropics (Horst, 1981; Katule, 1990; Acamovic *et al.*, 2005).

As more than 85% of people in developing countries reside in rural areas (Mcleewas, 1989), in which most of them are keeping local chickens, it is obvious that putting an emphasis on local chickens would have an immediate impact on animal protein intake in developing countries.

Low genetic potential and high prevalence of diseases such as Newcastle disease are among of the major factors limiting productivity of the local chickens in the Tropics. That means developing a genetically superior stock in terms of productivity and disease resistance would have a significant impact on this sector. Imported exotic genotypes are high yielding and could be used in high input-high output enterprises; however, they do not survive well under tropical conditions (Horst, 1981, 1991; Pedersen, 2002; Demeke, 2003). In this regard, various crossbreeding programs between local chickens and improved (exotic) chickens have been initiated in various tropical countries including Tanzania.

Crossbreeding programs aimed at combining desirable features from these two diverse genetic groups i.e. high productivity from exotic genotypes and high adaptability from local chicken genotypes (Katule, 1990). In the beginning, these programs yielded promising results. However, thereafter they became unsustainable due to unreliable supply and high costs of acquiring and maintaining exotic breeding cocks, reduced broodiness and ability to evade predation by the crossbred birds, incompatibility of genotypes with farmers' breeding objectives and production systems (Tadelle *et al.*, 2000; Udo *et al.*, 2001; Kosgey, 2004; Njenga, 2005). Furthermore, crossbreeding programs are also threatened by the current global move on conservation of indigenous genetic resources which campaigns against genetic dilution of indigenous genetic resources. Therefore, there is a need for looking for an alternative approach for genetic improvement such as development of synthetic breeds and selection within local chickens. Genetic improvement through selection within local chickens seems to be an attractive option because they are believed to be well adaptive to local environment.

For genetic improvement through selection to be successful the population under consideration should have a relatively high genetic level/potential for the traits of interest compared to other populations available for choice, and sufficient variations for the traits have to be available (Bentsen, 1990; Gjerde, *et al.*, 2002; Rutten, 2005). Genetic level guarantee a certain level of production. The genetic variation enables the breeder to select the genetically best animals to serve as parents for the next generation, and thereby increase the genetic level of the population. The larger the difference between the genetic levels of the selected parents and the population mean, the larger the eventual response to be achieved (Falconer and Mckay, 1996; Rutten, 2005). In this regard, limited information is available for most of the traits for Tanzania local chickens. For example, results from random sampling of mature birds from villages done in a previous study by Lawrence (1998) in Tanzania indicated *Kuchi* (a chicken ecotype native to the drier parts of north west Tanzania) to be superior to other ecotypes with respect to body weight. However, with the exception to some ecotypes, no systematic study has been carried out to evaluate its average body weights at different ages and under different management systems (Lawrence, 1998; Msoffe *et al.*, 2001; Msoffe, 2003). Similarly that applies to most of the egg traits in different chicken ecotypes in Tanzania.

Estimates of genetic parameters are important in the designing of optimal breeding programs through selection (Conington *et al.*, 2001; Sakata *et al.*, 2004; Rutten, 2005; Thompson *et al.*, 2005; Zehadaran *et al.*, 2005b). Although immense literature exist with regard to genetic parameters of different traits in chickens and other poultry species, however, it is well known that these parameters are a property of a population under a specific environment and for that period it was estimated (Falconer and Mckay 1996; Skorupski *et al.*, 1996; Pakdel, 2004). Therefore, there is a need of estimating these parameters in Tanzania local chicken if a viable genetic improvement program through selection for the population is to be designed.

Improving disease resistance in poultry by direct selection or by selection for immune response may hardly be feasible due to quantitative nature of these traits, their low to moderate heritability, and the difficulties associated with obtaining reliable measurements. In this situation, marker assisted selection (MAS) is expected to be a more effective breeding approach (Yonash *et al.*, 2000). A group of genes called Major Histocompatibility Complex (MHC), has been demonstrated by many workers to be associated with immune response and disease resistance (Lillehoj *et al.*, 1986; Heller *et al.*, 1991; Dunnington *et al.*, 1992; Juul-Madsen *et al.*, 2002; Liu *et al.*, 2002; Parmentier *et al.*, 2004; Xu *et al.*, 2005; Boonyanuwat *et al.*, 2006; Fulton *et al.*, 2006). Results from these studies further showed Restriction Fragment Length Polymorphism (RFLP), and microsatellites linked to this region (i.e LEI0258 in chickens) to be promising DNA markers in characterizing MHC genes. Identifying marker alleles associated with superiority is important before MAS can be used. Using MHC-RFLP, results from some of MHC studies revealed that marker alleles associated with superiority vary depending on population under consideration i.e. background genome. Therefore there is a need for identifying alleles associated with superiority in a population of interest before MAS can be used to improve immunocompetence of that population. Past research on local chicken MHC in Tanzania (Lawrence, 1998) and other countries such as Bolivia and India (Baelmans *et al.*, 2005) has only tested the presence of different MHC haplotypes using specific alloantisera. Similarly apply for Brazilian local chickens using LEI0258 microsatellite (Lima-Rosa *et al.*, 2005). However no study has been carried out to identify MHC alleles/haplotypes responsible for either high or low immune responses (a pre-requisite for MAS) in the local chicken populations of Tanzania.

1.2 Objectives

Based on the above background information, this study was carried out with the following objectives.

(i) To evaluate the genetic potential and estimate phenotypic and genetic parameters for various traits of local chickens managed both on-farm and on-station.

(ii) To determine the optimal breeding strategy for genetic improvement of local chickens through selection by evaluating various breeding scenarios.

(iii) To identify LEI0258 microsatellite alleles (a microsatellite located within MHC B region) associated with performance particularly antibody response (humoral immune response) against Newcastle disease virus vaccine in local chickens.

flock size of 2-20 and 2-58 birds of mixed age and sex was reported in Tanzania by Melewas (1989) and Mwalusanya (1998), respectively.

Local chickens dominate the chicken industry in Tanzania and other developing countries. It has been estimated that over 80% of the total fowl population in Africa comes from the village flock (MOAC, 1997; Tadelle *et al.*, 2003a; Fayeye *et al.*, 2005; Illango *et al.*, 2005). In Asia, the figure has been estimated at 50-80% (Aini, 1990; Minh *et al.*, 2004). Moreover, it has been noted that most of the chicken meat and eggs consumed in these countries come from this sector (Permin and Pederson, 2000). This trend will continue in a number of years to come due to preference of most people to products from local chickens, unavailability of improved stock, lack of capital and technical know how (Crawford, 1992; Pedersen, 2002; Aganga *et al.*, 2003; Theerachai *et al.*, 2003).

2.2 Chicken ecotypes

The term breed refers to a group of interbreeding animals with common gene pool that have similar appearances and usually developed by deliberate selection. Breeds of chickens have their description carefully laid down and each breed has its own standards and register (Crawford, 1984). Used in this context, it is very difficult to classify local chickens into breeds due to heterogeneous nature of the populations. Scavenging local chickens exhibit wide variations in plumage colours, comb types, skin and shank colour, body conformation, as well as in performance (Payne 1990; Horst and Mathur, 1992; Lawrence, 1998; Msoffe, 2003; Fayeye *et al.*, 2005; Njenga, 2005). Furthermore, some of these chickens also contain major genes that are useful to adaptability to tropical environment. The genes include naked neck (Na), frizzled feathers (F), dwarf (dw), silky (h), genes for slow feathering (K), non-inhibitor (id), fibromelanosis (Fm) and peacomb (P) (Horst, 1988, 1991). Advantages associated with these genes are summarised in Table 2.1.

Local chickens are therefore better described as ecotypes rather than a breed meaning they originate from different eco-climatic regions of a country. Example, *Tilili*, *Horro*, *Chefe*, *Jarso* and *Tepi* of Ethiopia (Tadelle *et al.*, 2003a). *Kuchi*, *Shingamagazi*, *Ching'wekwe*, *Morogoro- medium*, *Unguja*, *Pemba and Tanga* of Tanzania (Lawrence, 1998; Gwakisa *et al.*, 1994; Msoffe, 2003), *Fulani* local chickens (native to the drier parts), local chickens of *Derived Savanna*, *Guinea Savanna* and *Rain Forest* of Nigeria (Fayeye *et al.*, 2005; Adedokun and Sonaiya, 2001), *Large Baladi*, and *Betwil* of Sudan (Mohammed *et al.*, 2005). Results from some of these studies have shown some of these local chickens ecotypes to differ considerably in terms of some production parameters especially body weight.

Table 2.1 Major genes in local chicken populations with side effects on tolerance to tropical conditions

Gene	Mode of inheritance	Direct effects	Indirect effects
dw: dwarf	Recessive, sex-linked, multiple allelic	Reduction of body size by 10-30%	Reduced metabolism, improved fitness and disease tolerance
Na: naked neck	Incomplete dominance	Loss of neck feathers, reduction of pterlae width, reduction of secondary feathers	Improved ability for convection, reduced embryonic liveability (Hatchability), improved adult fitness
F: frizzle	Incomplete dominance	Curling of feathers, reduced feathering	Decreased fitness under temperate conditions, improved ability for convection
h: silky	Recessive	Lack of hamuli on the barbules, delicate shafts, long barbs at contour feathers	Improved ability for convection
K: slow feathering	Dominant, sex-linked, multiple allelic	Delay of feathering	Reduced protein requirement, reduced fat deposition during juvenile life, increased heat loss during early growth, reduced viability
id: non-inhibitor	Recessive, sex-linked, multiple allelic	Dermal melanin deposition in the skin and shanks	Improved ability for radiation from shanks and skin
Fm:fibro-melanosis	Dominant with multi-factorial modifiers	Melanin deposition: all over the body; sheaths of muscles and nerves, tendons, mesenterium; blood vessel walls	Protection of skin against UV radiation, improved radiation from the skin, improved pack-cell volume and plasma protein
P: peacomb	Dominant	Change of skin structure; compact comb size; reduction of pterlae width; development of breast ridges	Improved ability for convection, increased frequency of breast blisters.

Source: Horst (1988)

2.3 Productivity of local chickens

Despite the fact that local chickens dominate the poultry industry in almost all developing countries (Aini, 1990; Tadelle *et al.*, 2003a; Fayeye *et al.*, 2005; Illango *et al.*, 2005), and play significant role in the nutrition of people both in urban and rural areas in these countries (Crawford, 1992; Chen *et al.*, 1993; Pedersen, 2002; Aganga *et al.*, 2003; Theerachai *et al.*, 2003), they have been blamed for their poor performance in a number of production related traits when compared to the improved exotic birds (Pedersen, 2002). This section reviews performance of local chickens for various traits that are either directly or indirectly associated with the economic return from a poultry enterprise.

2.3.1 Growth performance

2.3.1.1 Growth rate and body weight

Growth performance is an important trait of economic importance in chickens as it determines at what age the bird would attain the market weight. Most studies (Nwosu *et al.*, 1984; Wilson *et al.*, 1987; Katule and Mgheni, 1990; Mwalusanya, 1998; Safalaoh, 1998; Pedersen, 2002; Demeke, 2003; Msoffe, 2003; Nhleko *et al.*, 2003; Tadelle *et al.*, 2003a; Gondwe and Wollny, 2005; Njenga, 2005) have reported poor growth rate for local chickens. Depending on sex and the period of assessment, average growth rate of local chickens has been estimated to range from 2.6 to 14.2, and 2.8 to 10.2g/day under intensive and extensive (Free-range) management systems, respectively. This growth rate is far too low when compared to that of more than 20g/day for the improved meat type chickens. As a result of this poor growth rate, local chickens have been associated with low body weight.

As with growth rate, a wide range of values for average body weights of local chickens at various ages has been reported in the literature. Average body weights regardless of sex under intensive management system has been estimated to range from 241 to 610g; 375 to 1211g; 802 to 1600g; and 972 to 2100g for body weights at 8, 12, 16 and 20 weeks of age, respectively (Jain *et al.*, 1977; Nwosu *et al.*, 1984; Katule and Mgheni, 1990; Ali, 1995; Engku and Noraziah, 1996 cited by Ramlah, 1996; Safalaoh, 1998; 2001; Adedokun and Sonaiya, 2001; Ndengwa *et al.*, 2001; Pedersen, 2002; Demeke, 2003; Tadelle *et al.*, 2003a; Leotarakul *et al.*,1997 and Choprakan, 1988 cited by Theerachai *et al.*, 2003; Segura-Correa *et al.*, 2004; ARC, 2005; Fayeye *et al.*, 2005; FAO, 2005). Much lower values were reported under extensive management system. The corresponding values under extensive system have been estimated to lie between 152 to 464g; 353 to 729g; 800 to 1065g; and 848 to 1300g, respectively (Ramlah and Shukor, 1987; Pedersen, 2002; Tadelle and Ogle 1998, cited by Tadelle *et al.*, 2003a; Demeke, 2003; Sall, 1990 cited by Sonaiya and Swan, 2004; Gondwe and Wollny, 2005; Sandra, 2005).

The above reported values are far too low when compared to body weights of broilers which can attain average body weight of nearly 2kg within 8 weeks of age under intensive system (Pedersen, 2002). However, growth performance of the improved exotic chickens under extensive and semi extensive system was noted to deteriorate drastically when compared to local chickens hence the gap in performance between the two genotypes is much reduced (Ali, 1995; Demeke, 2003). Reduced ability to withstand harsh conditions under free-range system i.e. feed shortage, high prevalence of diseases, external and internal parasites by the improved exotic breeds have been pointed out to be the major reason for the above observations (Tadelle *et al.*, 2000; Demeke, 2003).

With regard to mature body weight, most of the studies encountered have reported mature weights of local chicken under extensive management and which are based on random sampling of mature birds from rural households. Mature body weights were reported to range from 1 to 2.5 kg for hens and 1.2 to 3.3 kg for cocks (Kuit *et al.*, 1986; Wilson *et al.*, 1987; Minga *et al.*, 1989; Gunaratne *et al.*, 1992; Sonaiya, 1992; Lawrence, 1998; Msoffe *et al.*, 2001; Mwalusanya *et al.*, 2002; Mohammed *et al.*, 2005; Njenga, 2005; Nthimo, 2005). However, somewhat higher ranges were reported by Aganga *et al.* (2000) in Botswana in which they found average weight of mature males to be 2.2 kg (range of 1.0 to 3.9) and for female to be 2.0 (range of 1.0 to 3.0 kg). Regarding chicken ecotypes under the current study, mean mature body weights for *Kuchi* and *Medium* ecotypes were reported to be 2.71 and 1.9kg for males, and 1.8 and 1.1kg for females, respectively (Lawrence, 1998).

2.3.1.2 Feed utilization efficiency

Feed cost accounts for more than 75% of total costs in poultry industry (Austic and Nesheim, 1990). Birds that utilize feed more efficiently are preferred in poultry enterprises in order to realize the increased economic return. Feed utilization efficiency for growth of local chickens has been demonstrated in many studies to be poor. While feed efficiency (Feed: gain ratio) has been estimated to be around 2 or below for fast growing broilers (Safalaoh, 1998; Beaumont *et al.*, 1998), and around 3 for slow growing broilers (N'dri *et al.*, 2006), values ranging from 4.9 to 5.5 were reported for Ethiopian local chickens by Tadelle *et al.* (2003a). Somewhat higher values were reported for local chickens of Zimbabwe by Pedersen (2002) (7.7), and egg type chickens by Demeke (2004) (6.6) and Pedersen (2002) (7.1). On the contrary, although poor, Safalaoh (1998) reported a rather small margin in differences in feed utilization efficiency for growth between Malawi local chickens and broilers. He reported feed utilization efficiency to be 2.2, 2.67 and 2.7 for fast growing broilers, Black Australorp (A dual purpose breed), and Malawi local chickens, respectively. No study has reported this trait in the studied local chicken ecotypes i.e. *Kuchi* and *Medium* ecotype.

2.3.2 Egg production and related traits

2.3.2.1 Age at sexual maturity

Age at sexual maturity is another important trait of economic importance as it is directly associated with productive period. Most of the studies have reported delayed age at sexual maturity by local chickens when compared to the improved egg type chickens. A study conducted by Adedokun and Sonaiya (2001) in Nigeria has shown average age at sexual maturity measured as age at first egg of different Nigerian local chicken ecotypes under intensive management to vary from 157 and 165 days with an average of 161 days. A value that lies within this range was reported by Choprakarn *et al* (1998) in Thailand. On the other hand, Akinokun (1990) cited by Adedokun and Sonaiya (2001). and Khalil *et al.* (2004) reported slightly higher values. They reported values of 170 and 168 days in Nigeria and Saudi Arabia local chickens, respectively. A much lower value (153 days). and a much higher value of 203 was reported in Ethiopian and Indian local hens by Demeke (2004) and Sah *et al.* (1985), respectively. Although no literature found reporting this trait for the two studied chicken ecotypes, Katule and Mgheni (1990) reported relatively higher value (197 days) for a mixture of local chicken ecotypes of Tanzania (i.e a mixture of chickens from different agro-ecological zones). The estimates above are to some extent higher than those values reported for egg type chickens. Egg type chickens were reported to reach sexual maturity at 18-22 weeks of age. This corresponds to age at sexual maturity of 126- 154 days (Pedersen, 2002).

When considering age at sexual maturity under extensive management, much higher values have been reported. Studies carried out by several workers independently in different countries have shown age at sexual maturity for local chickens including *Medium* ecotype of Tanzania to have ranged from 6 to 9 months (Kuit *et al.*, 1986; Wilson *et al.*, 1987: Minga *et al.* 1989; Sonaiya, 1992; Gunaratne *et al.*, 1992; Mwalusanya *et al.*, 2002; Aganga *et al.*, 2003).

2.3.2.2 Egg production

Egg number for a given period of laying, in other words laying rate expressed as percentage is also a trait of economic importance in poultry enterprise. Results from various places have shown average laying rate of local chickens under both intensive and extensive management to be low. Studies conducted in various countries have indicated average laying rate of local chickens to be less than 60%. Akinokun (1990) cited by Adedokun and Sonaiya (2001) has reported average egg number for a period of 8 months of Nigerian local chickens to be 100 eggs per bird, which corresponds to a laying rate of about 42%. Choprakarn *et al.* (1998) obtained a value close to this figure for Thailand local chickens assessed between 21-60 weeks of age. They obtained a value of 41%. These values are also within the range reported by Mohammed *et al.* (2005) for Sudanese local chickens in their early period of laying under intensive management. The authors reported values to range from 38.57 to 48.57%. Values slightly lower than those reported above were also revealed in a number of studies. Pedersen (2002) working with Zimbabwean local chickens found a laying rate of 36%. Similarly, values close to this were reported by Demeke (2004) in Ethiopian local chickens. Fairly higher values have been reported by Katule and Mgheni (1990) in Tanzania (in a mixture of different chicken ecotypes), Adedokun and Sonaiya (2001) in Nigeria, and Khalil *et al.* (1998) in Saudi Arabia. While Katule and Mgheni (1990) and Khalil *et al.* (2004) reported average egg production within the first 90 days of production to be 52 eggs per bird, which corresponds to a laying rate of about 58%, Adedokun and Sonaiya (2001) found average egg production in the Nigerian chicken ecotypes which corresponds to laying rates varying between 44.7 and 55%. No research has reported values for this trait separately for each of the two studied ecotypes.

The values reported in the literature above clearly indicate laying rate of local chickens is low when compared to that for improved egg type chickens, which have an average laying rate of more than 60% (Pedersen, 2002; Demeke, 2004; Khalil *et al.*, 2004).

With regard to egg production under extensive system, extremely low annual production levels have been reported in different studies. In Tanzania Minga *et al.* (1989) and Mwalusanya (1998) observed an annual egg production rate from 66 to 78 eggs in 3-4 clutches with a clutch size of 12-18 eggs. These values for egg number correspond to an annual laying rate of 18- 21%. Similar low egg production levels under extensive systems have been observed in other countries such as Nigeria (Sonaiya, 1990), Mali (Kuit *et al.*, 1986 and Wilson *et al*, 1987), Botswana (Aganga *et al.*, 2003), and Malaysia (Jalaludin, 1992).

2.3.2.3 Egg weight

Egg weight is one of the most important traits as far as external egg quality traits are concerned. Egg weight for local chicken is generally accepted to be low when compared to the improved egg type birds. While average egg weight for egg type chickens has been reported to be 50g and above (Katule and Mgheni 1990; Chen *et al.*, 1993; Sabri *et al.*, 1999; Islam *et al.*, 2001; Pedersen, 2002; Khatkar *et al.*, 1994; Anderson *et al.*, 2005), most of the studies reported values lower than 50g for average egg weight of local chickens under intensive management system.

Katule and Mgheni (1990) working with a mixture of some Tanzania chicken ecotypes reported a value of 38.2g. Furthermore, studying different chicken ecotypes of Tanzania separately, Msoffe (2003) reported a value of 42g for most of the ecotypes including *Medium* ecotype, while that for *Kuchi* ecotype was 44g. Average egg weights of 40.7 g, 39g, 40g were reported for local chickens of Nigeria (Fayeye *et al.*, 2005), Bangladesh (Islam *et al.*, 2001), and Zimbabwe (Pedersen, 2002), respectively. Values within this range were also reported by Dutta (1993) for *Miri* (one of the chicken ecotype) in India under intensive systems of management. In contrast, higher value of 49g was presented in a study by Chen *et al.* (1993) in Taiwan local chickens. Interestingly, when the literature reporting average egg weight for local chickens under extensive management (free-range) was examined closely, values more or less similar to those under intensive management were reported (Minga *et al.*, 1989; Mwalusanya, 1998; Wilson *et al.*, 1987).

2.3.2.4 Eggshell quality

Eggshell quality is another important external egg quality trait as it affects both hatchability and number of intact eggs reaching the market. Eggshell quality embodies characteristics such as shell thickness, shell weight, specific gravity, shell strength, and resistance to breakage (Washburn *et al.*, 1981; Poggenpoel, 1986; Brah *et al.*, 1991; Khatkar *et al.*, 1994; Sabri *et al.*, 1999; Narushin and Romanov, 2002). Studies have shown that thin-shelled eggs are associated with weakening of the embryos and poor hatchability. A study conducted by Bennet (1992) had shown hatchability of thin shelled eggs to be 3-9% lower than the thicker shelled eggs. Furthermore, both reduction in hatchability and weakening of the embryo of the thin-shelled eggs were noted by Peebles and Brakes (1987). For better results of hatchability, eggshell thickness of not less than 32μ has been recommended (Khan *et al.*, 2004; Bao, 1978, cited by Khang and Ogle, 2004; Mohammed *et al.*, 2005).

Thin-shelled eggs and other shell quality traits were also associated with the increased amount of broken/cracked eggs during marketing, hence increased economic loss (Peebles and Brakes, 1987; Chen *et al.*, 1993; Sabri *et al.*, 1999; Islam *et al.*, 2001; Dunn *et al.*, 2005; Fayeye *et al.* 2005; Mohammed *et al.*, 2005). In the beginning, these traits were ignored in poultry breeding programs, but later on, as results of increased economic loss due to broken eggs were being reported, most of the breeders were triggered to think of incorporating these traits in poultry breeding programs (Engström *et al.*, 1986; Poggenpoel, 1986).

Some studies conducted under intensive management systems have indicated eggshell thickness for local chickens to be superior to that of exotic birds. Furthermore, differences between different populations of local chickens were also noted. A study conducted by Arad and Malder (1982) in Sudan has shown average shell thickness for Sudanese local chickens to be 37μ when compared to 31.3μ for White Leghorn under similar management conditions. In the same country, Mohammed *et al.* (2005) found average shell thickness to range from 34.3- 36.2μ for some different Sudanese chicken ecotypes. Values within this range were also reported in Bangladesh local chickens (Islam *et al.*, 2001), and crosses between Bangladesh local chickens (*Hilly* type) with either Rhode Island Red or Fayoumi (exotic breeds) (Khan *et al.*, 2004). In contrast, in a similar study by Islam *et al.* (2001), the authors found shell thickness for Shaver Redbro (exotic chickens) to be 30-34μ. Chen *et al.* (1993) working with Taiwan's local chickens reported a slightly higher value (38μ). In addition, in their study they found no significant difference between Taiwan's local chickens and Single comb White Leghorns (egg type birds). On the other hand, much higher values were reported by Fayeye *et al.* (2005) (58μ), and Anderson *et al.* (2005) (46 to 47μ) in Fulani local chickens of Nigeria, and some strains of White Leghorns, respectively.

In perusal of the literature encountered, no article has reported values for eggshell thickness or other eggshell quality traits for local chickens under extensive management. However, studies conducted for the egg type chickens have shown that birds under extensive management always have thicker eggshells than those under intensive management (Hughes, 1985; Mostert *et al.*, 1995 cited by Miao *et al.*, 2004).

2.3.2.5 Egg shape index

Egg shape index is also a frequently measured external egg quality trait. Egg shape index measured as the ratio of maximum width of the eggs to egg length (Chen *et al.*, 1993) determines the degree of broadness of the egg. Although egg shape index is not a serious issue as far as marketing of eggs from local chickens in developing countries is concerned, eggs with deformed shape are likely to be sold at lower price than normal eggs. Futhermore, eggs of normal shape have been reported to hatch more successfully than those shaped abnormally (Narushin and Romanov, 2002). Egg shape index ranging from 69-76% has been recommended as optimal (Eshwaraish, 1988 cited by Ali, 2002; Smith, 2001, cited by Khang and Ogle, 2004).

Few studies have estimated egg shape index for local chicken populations. Chen *et al.* (1993) reported average egg shape index for Taiwan's local chickens under intensive management conditions to be 73% which was not significantly different from that of Single Comb White Leghorn hens (Egg type chickens). A similar value was obtained by Brah *et al.* (1991) for some strains of White Leghorn in India. However, a slightly higher value (74%) was reported by Khatkar *et al.* (1994) in some other strains of White Leghorn in India, while Anderson *et al.* (2005) have shown it to vary from 72 to 75% again in some White Leghorn strains. Average egg width and length that corresponds to a bit higher egg shape index (76%) was noted in a study by Choprakarn *et al.* (1998) in local chickens of Bangladesh. Egg shape index for crossbred birds between Bangladesh local chickens (*Hilly* type) and either Rhode Island Red (RIR x *Hilly*) or Fayoumi (*Hilly* x Fayoumi) was also reported for the birds under semi scavenging system (Khan *et al.*, 2004). The values were 72 and 79% for *Hilly* x Fayoumi and RIR x *Hilly*, respectively. Limited information is available with regard to this parameter for local chicken populations from the African continent. An experiment carried out in Nigeria (Fayeye *et al.*, 2005) for *Fulani* local chickens under intensive management revealed a much lower value for egg shape index. From the measurements obtained in their experiment, average egg shape index was calculated to be 68%, which is slightly lower than the recommended range. In contrast, higher values than this (72 to 80%) were reported in Kenya (another country in Africa) by Njenga (2005) for local chickens from Coastal areas of the country. Unfortunately, no literature has been encountered which reports the value for this trait for local chicken under extensive management. However, the above wide variations between different genotypes under intensive management for egg shape index demonstrates strong genetic basis for the inheritance of this trait.

2.3.3 Immune responses

Reduced productivity of local chickens due to high prevalence of diseases is well known (Alexander, 2001; Otim, 2005). Among many diseases of poultry endemic in Tanzania and other developing countries, Newcastle disease (ND) has been reported to be the most important (Minga *et al.*, 1989; Rahman *et al.*, 2002; Illango *et al.*, 2005; Otim, 2005). When Newcastle disease strikes, 60 to 100% of chickens in a household can be lost (Yongolo, 1996; Alexander, 2001; Acamovic *et al.*, 2005). Newcastle is an acute rapidly spreading viral disease of domestic poultry characterised by respiratory signs, nervous manifestations and diarrhoea. This disease is an obnoxious killer and is of economic importance in poultry industry since it affects all age categories of chickens (Awan *et al.*, 1994; Al-Garib *et al.*, 2003). Although the strategy of mass vaccination has largely been an effective control of the Newcastle disease, combining vaccination programs and development of genetically resistant stocks will further maximize protection of the chickens from the disease.

The existence of strong relationship between antibody levels in the blood and tolerance of an individual against the pathogen that triggered production of such antibodies has been reported in animals. The antibody level following antigenic challenge (humoral immune response) i.e. challenge with vaccine against disease pathogen of interest has therefore been extensively used as an indicator of immunocompetence of an individual against the disease under study (Dunnington *et al.*, 1992; Yonash *et al.*, 2000; Al-Garib *et al.*, 2003). Furthermore, humoral immune response to non specific multi-determinant complex antigens e.g. sheep red blood cells (SRBC) has also been used as an indication of natural immunity status in poultry (Miller *et al.*, 1997; Zhou *et al.*, 2002; Siwek *et al.*, 2003).

Studies to assess humoral immune response of local chickens against Newcastle disease virus (NDV) vaccine have been carried out by several workers under intensive management system. A study by Msoffe (2003) using different chicken ecotypes from Tanzania reported average antibody titres measured by Haemagglutionation Inhibition test (HI $\log_2$) to range from 4.5-6 for primary immune response assessed two weeks post vaccination. Values within this range were also reported in a preceding experiment by Gwakisa *et al.* (1994). Slightly higher values than those reported above were reported by Lwelamira and Katule (2004), who found average antibody titres at the same period of measurement to range from 5.7-6.4 for Tanzania local chickens and their reciprocal crosses with RIR, and much higher values (7.0) were reported by Otim (2005) in Ugandan local chickens.

2.3.4 Mortality rates

Good survival rate is an important parameter as far as overall output and hence profit in poultry enterprise is concerned. High survival rates ensure substantial number of birds reach the marketing age, and the presence of the replacement stock. Poor chick survival under extensive management has been noted by several researchers to be among the problems hindering further expansion of local chickens in developing countries. Chick mortality in a household under free range conditions may vary from 0 to 100% with an average of 30% and more with most of it occuring in the first few weeks of life. Mwalusanya *et al.* (2002) reported average chick mortality under free range conditions up to 10 weeks of age in Tanzania local chickens to be 40%, while Gunaratne (1993) estimated it to be 65% in Sri-Lanka local chickens. Pedersen (2002) found chick mortality up to 12 weeks of age in Zimbabwean local chickens under village conditions to be 45%, which was close to 41% reported for Botswana local chickens by Mushi *et al.* (2005). In another study, Kondombo *et al.* (2005) working with local chicken of Burkina Faso reported chick mortality up to 8 weeks of age under extensive management to be 31.7%. Identified causes for high chick mortality under on-farm conditions were mainly predation, high prevalence of diseases and parasites, and poor nutrition (Mwalusanya *et al.*, 2002; Pedersen, 2002; Dakpogan, 2005; Mushi *et al.*, 2005). Compared to exotic chickens under this management system, relatively higher mortality rate has been recorded. Gondwe and Wollny (2003) reported somewhat high mortality rates in Black Australorp compared to Malawian local chickens (14.4 vs 11.3%) in the first five weeks after being introduced to extensive management conditions at 9 weeks of age. Similarly, Demeke (2003) observed relatively higher mortality rate in White Leghorn than in Ethiopian local chickens (13.9 vs 5.6%) introduced to village conditions from 10 days to 8 weeks of age.

With regard to mortalities under intensive management, relatively low values have been reported. On average, mortality rate from day old up to around 12 weeks of age may vary from 0 to 24% (Pedersen, 2002; Demeke, 2003; Tadelle *et al.*, 2003a; Lwelamira and Katule, 2004). However, when compared to exotic chickens, much lower ranges (mortality rates < 10%) even up to a point of lay have been frequently reported in literature (Farooq *et al.*, 2002; Pedersen, 2002; Demeke, 2003).

2.4 Genetic improvement of chickens

The phenotype of an individual is usually determined by its genetic make up and the environment in which it is subjected e.g. plane of nutrition (Falconer and McKay, 1996). Hence, genetic manipulation can have a direct effect on the performance of a population. Genetic potential of a population can easily be improved through either selection, crossbreeding, crossbreeding followed by selection or vice versa (Katule, 1991; Ali *et al.*, 2000). As far as the current study is concerned, much of the effort in this section is put in reviewing genetic improvement of chickens through selection.

2.4.1 Crossbreeding

The increased performance of crossbred animals is a result of heterosis. Heterosis is caused by dominance, overdominance, and epistatic gene action. The magnitude of heterosis depends on the degree of genetic differences between populations and the nature of the trait under consideration. A significant improvement in the performance of local chickens as a result of crossing local chickens with exotic chickens has been demonstrated in various studies (Katule, 1990; Ali *et al.* 2000; Padhi *et al.*, 2004; Segura-Correa *et al.*, 2004; Sunder *et al.*, 2005). Results from these studies have shown growth rate, total egg production and egg size for local chickens to improve significantly following crossbreeding with specialized exotic chickens. These studies aimed at tapping high production potential of exotic breeds, and tolerance to harsh environment of local chickens so as to have chicken populations that perform well in free-range systems.

2.4.2 Selection

The basis for selection in breeding programmes is utilization of potential benefits associated with additive gene action (i.e. many genes influencing a trait and acting in an additive manner). Selective breeding has been applied successfully to improve production of many livestock species, especially in the last half century. The ability to distinguish between desirable and undesirable breeding animals has increased and the knowledge to deploy these animals efficiently in breeding programs has been developed. Therefore, dramatic changes in performance in the livestock species have been achieved. For example, in the Netherlands broiler chickens were noted to grow three times faster to marketable weight on half the amount of food of the vintage broiler since the 1950s (Havestein *et al.*, 1994; McKay *et al.*, 2000).

2.4.3 Phenotypic and genetic parameters

Genetic parameters (i.e heritabilities, phenotypic and genetic correlations) are indispensable for the design and optimisation of breeding programs (Kosgey, 2004; Pakdel, 2004; Rutten, 2005; Zerehdaran *et al.*, 2005b). Studies conducted by several workers revealed genetic parameters to differ with populations and environment in which they are estimated (Falconer and McKay, 1996; Skorupski *et al.*, 1996; Siegel and Wolford, 2003). For example, in most cases it can be found that genetic and phenotypic correlations among various traits in different populations to be similar in direction but different in magnitude. A review on estimates of genetic parameters for various important traits in poultry production is presented in this section.

2.4.3.1 Heritability estimates

A large volume of literature existing on heritability estimates for various traits in chickens have mainly been estimated in chicken populations developed for specific purposes such as egg or meat production. Next to chickens, Japanese quail is another poultry species in which heritability estimates for different traits particularly body weight has been extensively studied. Due to their short generation intervals, Japanese quails have been preferred by many researchers as model animals in studying inheritance of different traits in poultry (Resende *et al.*, 2005; Vali *et al.*, 2005). Few studies have been carried out in other poultry species such as turkeys, muscovy ducks, and guinea fowls (Mudra *et al.*, 1993; Sacco *et al.*, 1994; Hu *et al.*, 1999).

2.4.3.2 Heritability estimates for body weights

An immense number of studies have been carried out to estimate heritabilities for body weights in chickens. Based on sire, dam, and sire plus dam components of variance, most studies have reported heritability estimates for juvenile body weight in exotic chickens to lie between 0.24 and 0.85; 0.30 and 0.99; 0.25 and 0.80, respectively (Jaap *et al.*, 1962; Jain *et al.*, 1980; Sørensen *et al.*, 1980; Singh and Singh, 1981; Kumar *et al.*. 1988; Shadap *et al.*, 1990; Brah *et al.*, 1991; Jilani *et al.*, 2005; Sivaraman *et al.*, 2005). Similarly, values within this range were reported for some Japanese and Chinese local breeds of chickens based on sib correlation analyses (Luo *et al.*, 1991 cited by Jiang and Groen, 2000; Okamoto *et al.*, 2003), unimproved local chickens of Iran (Kamali, *et al.*, 1995), and unimproved local chickens of Nigeria and Cameroon (Asuquo and Nwosu, 1987; Oluyemi and Oyenugu, 1974, and Akinokun, 1971, cited by Asuquo and Nwosu, 1987; Manjeli *et al.*, 2003; Ebangi and Ibe, 1994 cited by Manjeli *et al.*, 2003). Furthermore, using animal model of linear mixed model procedures, heritability estimates for juvenile body weight in broilers were reported to range from 0.20 to 0.67 with most studies reporting values above 0.25 (Fleming *et al.*, 1997; Lopez and Quaas, 1997; Morris, 1996 cited by Morris and Pollot, 1997; Beaumont *et al.*, 1998; Mignon-Grasteau *et al.*, 1998; Mignon-Grasteau *et al.*, 1999; Buitnehuis, 2003; Pakdel, 2004; Zerehdaran *et al.*, 2004). Similarly, with the exception of the study by Prado-Gonzalez *et al.* (2003) in Mexican local chickens (*Creole* chickens), in which a much lower value (0.00) was reported, a study by Norris and Ngambi (2006) also reported values close to this range (0.22 to 0.41) for heritability estimates for juvenile body weights in one of the South African local chicken strain (*Venda* chickens) using animal model of linear mixed model procedures.

Heritability estimates for mature body weight were also estimated in some studies specifically for egg type birds. Based on either sire. dam. sire plus dam component of variances or animal model. as in the case of juvenile body weights. heritability estimates ranging from moderate to high (i.e. 0.24 and above) were also reported in most of the studies (Kolstad, 1980; Sørensen *et al.*, 1980; Shadap *et al.*, 1990; Brah *et al.*, 1991; Hagger, 1994; Akbaş *et al.*, 2002; Buitenhuis, 2003). In contrast, few studies have reported heritability estimates for other traits related to growth performance such as daily gain and feed conversion ratio (FCR) (van Kaam *et al.*, 1999; Beaumont *et al.*, 1998; Okamoto *et al.*, 2003). In these studies values ranging from 0.13 to 0.54 were reported.

2.4.3.3 Heritability estimates for egg production and related traits

Age at sexual maturity

As with body weight, most studies to estimate genetic parameters for egg production and related traits have mostly used improved breeds of chickens under intensive management. Based on sib correlation analyses, studies by Akbaş *et al.* (2002), Bednarczyk *et al.* (2000), Brah *et al.* (1991), Jain *et al.* (1980), Shadap *et al.* (1990), Pi *et al.* 1999 cited by Jiang and Groen (2000), Liljedahl and Weyde (1980), Kolstad (1980), Sørensen *et al.* (1980), and Jilani *et al.* (2005) reported values ranging from 0.24 to 0.70, with most of the estimates in these studies being 0.30 and above. Likewise, a study by Khalil *et al.*(2004). Lundén *et al.* (1993), and Nirasawa *et al.* (1998) also reported relatively high estimates (0.55, 0.65 and 0.61 to 0.62, respectively) for this trait in White Leghorn hens when animal model of linear mixed models procedures was used as estimation method. Discrepant results were shown by some values of Sang *et al.* (2006) (0.12 to 0.32) in Korean local chickens estimated from animal model of linear mixed models procedures.

Egg production

Similar to age at first egg, a wide range of heritability estimates for egg production/laying rate have been reported in literature under intensive management system. However, despite of the wide range reported, using either sib-correlation analysis or animal model of linear mixed models procedures, most of the studies estimated it to be of low to moderate scale. Based on sib correlation analyses, heritability estimates for egg production in 200 to 360 days have been reported to range from 0.05 to 0.54 in egg type chickens (Jaffé, 1966; Jain *et al.*, 1980; Engström *et al.*, 1986; Singh *et al.*, 1989), and from 0.10 to 0.38 in Chinese local breeds of chickens (Luo *et al.*, 1991 and Li *et al.*, 1998 both cited by Jiang and Groen, 2000). Using animal model of linear mixed models procedures, estimates ranging from 0.31 to 0.54 were reported in egg type chickens (Nurgiartiningsih *et al.*, 2002; Khalil *et al.*, 2004; Morris, 2005).

Heritability estimates varying from 0.20 to 0.70 were reported for egg production in egg type chickens between age at sexual maturity to 38-42 weeks of age estimated from sib correlation analyses (Singh *et al.*, 1972; Liljedahl and Weyde, 1980; Kolstad, 1980; Sørensen *et al.*, 1980; Brah *et al.*, 1991; Ahmad *et al.*, 1993; Berdnarczyk *et al.*, 2000; Akbaş *et al.*, 2002). Using animal model of linear mixed models procedures, the estimates were reported to range from 0.09 to 0.50 (Lundén *et al.*, 1993; Besbes *et al.*, 1991 cited by Wei and van der Werf, 1993; Hagger, 1994; Francesch *et al.*, 1997; Nirasawa *et al.*, 1998; Sang *et al.*, 2006), with most of these studies conducted in egg type chickens. Moreover, studies by Khalil *et al.* (2004) using animal model of linear mixed models procedures in the crosses between Saudi Arabia local chickens and White Leghorns, and Singh and Hussani (1978) using sib correlation analyses in White Leghorn reported heritability estimates in the first 90 days after sexual maturity to be 0.31 and to vary from 0.08 to 0.78, respectively. Similarly, heritability estimates of 0.27 between 18 to 25 weeks of age, and 0.37 to 0.53 between 26 to 30 weeks of age were reported in White leghorns by Sabri *et al.* (1999) using sib correlation analyses, and Wei and van der Werf (1993) using animal model of linear mixed models procedures, respectively. In general, despite of the wide range of the estimates reported, most of the studies above reported the values of 0.40 and below.

Egg weight

Heritability estimates for egg weight in chickens have also been reported by a number of studies under intensive management system. In these studies, values ranging from 0.27 to 0.85 with most of the estimates being 0.40 and above have been reported for egg type chickens using both sib correlation analyses (Goodman and Jaap, 1961; Jaffé, 1966; Singh *et al.*, 1972; Kolstad, 1980; Liljedahl and Weyde, 1980; Sørensen *et al.*, 1980; Potts and Washburn, 1985; Engström *et al.*, 1986; Poggenpoel, 1986; Singh *et al.*, 1988; Shadap *et al.*, 1990; Brah *et al.*, 1991; van Druden and Groot, 1992; Ahmad *et al.*, 1993; Chen *et al.*, 1993; Khatkar *et al.*, 1994; Sabri *et al.* 1999; Dunn *et al.*, 2005, Jilani *et al.*, 2005), and animal model of linear mixed models procedures (Lundén *et al.*, 1993; Wei and van der Werf, 1993; Fransceesch *et al.*, 1997; Lopez and Quaas, 1997; Hartmann *et al.*, 2000; Nurgiartiningsih *et al.*, 2002; Dunn *et al.*, 2005; Zhang *et al.*, 2005). In contrast, low values ranging from 0.06 to 0.13 were reported by Sang *et al.* (2006) in Chinese local breeds of chickens using animal model.

Limited information is available on heritability estimates for this trait and other egg traits in unimproved local chicken populations. In a study by Chen *et al.* (1993), based on maternal half-sib correlation analysis, a value within the above range was estimated for unimproved Taiwanese local chickens, however, a much lower value (0.07) was obtained from paternal half-sib correlation.

Shell thickness and egg shape index

Like other traits of economic importance in poultry industry, which have been reviewed in the preceding sections, extensive studies on inheritance of eggshell thickness and other traits related to eggshell quality have been carried out. Results from these studies have indicated the existence of substantial additive genetic variance in most of the chicken populations studied as revealed by moderate to high heritability estimates.

Researches by Poggenpoel (1986), Mohapatra *et al.* (1985) and Khatkar *et al.* (1994), have generally estimated values for heritability for eggshell thickness from sib-correlation analyses to range from 0.31 to 0.69 in egg type chickens, while Chen *et al.* (1993) reported it to be 0.28 in Taiwanese local chickens. Furthermore, using animal model of mixed models procedures, Zhang *et al.* (2005) and Nirasawa *et al.* (1998) reported values that lie within that range in egg type chickens (0.34 to 0.45). Heritability estimate for egg specific gravity, eggshell weight, eggshell strength, and frequency of cracked shells (another measure eggshell quality), and even eggshell colour have also been reported by many researchers to have moderate to high heritabilities. For example, with the exception of a few studies by Zhang *et al.* (2005) and Potts and Washburn (1985) for eggshell strength, in which much low values (i.e below 0.25) were reported. On average most of the studies have reported heritability estimates for these measures of eggshell quality to range from around 0.30 to 0.86 (Kolstad, 1980; Sørensen *et al.*, 1980; Engström *et al.*, 1986; Brah *et al.*, 1991; van Druden and Groot, 1992; Wei and van der Werf, 1993; Besbes *et al.*, 1991 cited by Wei and van der Werf, 1993; Khatkar *et al.*, 1994; Nirasawa *et al.*, 1998; Sabri *et al.*, 1999; Zhang *et al.*, 2005). Moderate to high heritability estimates (0.23 to 0.57) were also noted for egg shape index in a considerable number of studies in egg type chickens (Mishra *et al.*, 1986; Brah *et al.*, 1991; Maan *et al.*, 1983 cited by Chen *et al.*, 1993; Khatkar *et al.*, 1992 cited by Khatkar *et al.*, 1994; Dunn *et al.*, 2005; Zhang *et al.*, 2005). On the other hand values of 0.16 and 0.23 were reported by Mishra *et al.* (1986) and Chen *et al.* (1993) in Red Cornish (broilers), and unimproved Taiwanese local chickens, respectively.

2.3.3.4 Heritability estimates for antibody response (Humoral immune response)

Genetic control of humoral immune response in chickens and other poultry species has been investigated in a remarkable number of studies. Using different types of antigens, it has been shown in these studies that both additive and non-additive gene action are important in the inheritance of this trait. Studies by Siegel and Gross (1980), Pinard *et al.* (1992) and Martin *et al.* (1990) estimated realized heritability for primary antibody response to SRBC in chicken lines selected for either high or low antibody response to this antigen to range from 0.17 to 0.44; 0.21 to 0.25, and 0.25 to 0.23, respectively. In contrast, a higher value (0.61) was reported by Sarkar *et al.* (1999). Furthermore, using the same type of antigen and animal models of linear mixed models procedures for estimating heritability, work by Bovenhuis *et al.* (2002) and Pinard *et al.* (1992) reported heritability estimates to be 0.18 and 0.31, respectively. In contrast, Yonash *et al.* (1996) estimated values ranging from 0.42 to 0.44 using *Escherichia coli* vaccine as an antigen. Again using SRBC, and other types of antigens such as vaccines to Newcastle disease virus, *Pasteurella multocida*, *Mycoplasma gallisepticum*, and *Escherichia coli*, heritability estimates varying from 0.00 to 0.60 with most estimates being 0.40 and below. Such estimates were reported in commercial chickens by a substantial number of studies when sib correlation analyses were employed (Peleg *et al.*, 1976; van der Zijpp and Leenstra, 1980; Soller *et al.*, 1981; Gyles *et al.*, 1986; Kim *et al.* 1987; Cheng *et al.*, 1991; Kumar, 2002; Sivaraman *et al.*, 2005). Similar observations were in a study by Lwelamira and Katule (2004) (0.27 to 0.39) in a mixture of some Tanzania chicken ecotypes, and their reciprocal crosses with RIR. Furthermore, Genetic parameters for secondary humoral immune responses were also estimated in some studies. In a similar study by Lwelamira and Katule (2004) the values for secondary humoral immune responses were reported to range from 0.18 to 0.28.

2.4.3.5 Phenotypic and genetic correlations among various traits of economic importance

As stated earlier, estimates of genetic and phenotypic correlations are another important genetic parameters in design of optimal breeding schemes. As a result, extensive research has been carried to estimates these parameters in different populations of chickens and other related species such as Japanese quail, and to a lesser extent in turkeys, muscovy ducks, guinea fowls, and pheasants (Mudra *et al.*, 1993; Rizzi *et al.*, 1994; Rodenburg *et al.*, 2003; Pakdel, 2004; Hu *et al.*, 2004; Zerehdaran *et al.*, 2004; Resende *et al.*, 2005). As with heritabilities, genetic and phenotypic correlations among traits in chickens have largely been estimated in improved breeds/strains of chickens. In these studies, genetic correlations have largely been estimated from additive variance/covariances derived from either sire or sire plus dam components of variances/covariances, or animal model of mixed models procedures, and phenotypic correlations from total variance and covariances (Becker, 1984; Gilmour *et al.* 1999).

(i) Correlations among body weights

Both genetic and phenotypic correlations among body weights in chickens measured at different ages have been shown by many authors to be positive, and range from moderate to high (Table 2.2). It is also evident from this table that high estimates were obtained when either sib correlations analyses or animal model were used as estimation methods. Similar observations were also noted in Japanese quail (Resende *et al.*, 2005; Adeogun and Adeoya, 2004; Vali *et al.*, 2005), Guinea fowls (Mudra *et al.*, 1993), and in pheasants (Rizzi *et al.*, 1994).

Table 2.2 Genetic and phenotypic correlations (in parentheses) among body weights

Trait pair	Genotype	Value	Method	Author/s
Bwt8-Bwt42	Layers (Strain U)	0.68(0.59)	S	Sørensen *et al.* (1980)
Bwt8-Bwt42	Layers (Strain D)	0.84(0.64)	S	-do-
Bwt20-Bwt40	WL	0.77, 0.55	S, D	Srivastava *et al.* (1993)
Bwt20-Bwt40	WL(Meyer)	0.67(0.43)	S	Kumararaj *et al.* (1995)
Bwt20-Bwt40	WL(Forsgate)	0.61(0.66)	S	-do-
Bwt6-Bwt8	Plymouth Rock	0.97(0.74)	S	Gill and Verma (1983a)
Bwt6-Bwt16	WL	0.64(0.50)	S	Sosama and Singh (1979)
Bwt4-Bwt8	White rock, White cornish	0.37, 0.89, 0.78	S, D, S+D	Kumar *et al.* (1988)
Bwt8-Bwt10	New Hampshire	1.00(0.91)	S	Singh and Singh (1981)
Bwt8-Bwt12	Ya x Local x Gold Link	0.54(0.70)	S	Asuquo and Nwosu (1987)
Bwt8-Bwt16	-do-	0.74(0.56)	S	-do-
Bwt8-Bwt20	-do-	0.52(0.44)	S	-do-
Bwt12-Bwt16	-do-	1.00(0.75)	S	-do-
Bwt12-Bwt20	-do-	0.22(0.54)	S	-do-
Bwt3-Bwt10	Local, RIR & Crosses	0.47(0.35)	S	Lwelamira & Katule (2004)
Bwt7-Bwt9	White Plymouth rock	0.98	AM	Zerehdaran *et al.* (2005a)
Bwt5-Bwt7	White Plymouth rock	0.94(0.88)	AM	Zerehdaran *et al.* (2004)
Bwt3-bwt7	White Plymouth rock	0.65	AM	van Kaam *et al.* (1999)
Bwt4-Bwt5	Broilers	0.87(0.88)	S	Sivaraman *et al.* (2005)
Bwt5-Bwt6	Broilers	0.43(0.65)	S	-do-
Bwt5-Bwt6	Broilers	0.80(0.76)	S	-do-
Bwt4-Bwt8	Broilers	0.78	S+D	Kumar (2004)
Bwt8-Bwt16	Broilers	0.77(0.64)	S	Jaap *et al.* (1962)
Bwt8-Bwt24	Broilers	0.36(0.33)	S	-do-
Bwt16-Bwt24	Broilers	0.60(0.57)	S	-do-

Bwt = Body weight to the respective week of age indicated by numbers; WL= White Leghorn; RIR = Rhode Island Red; S, D, S+D, AM= Estimates (genetic correlations) calculated from sire, dam and sire plus dam components of (co)variance, and animal model of mixed models procedures, respectively.

(ii) Correlations among egg traits

Values ranging from negative to positive have been reported for genetic and phenotypic correlations between age at first egg (i.e. age at sexual maturity) and egg number. However, in general, most of the studies reported correlations to range from low to highly negative (Table 2.3). In contrast, values ranging from low to moderately positive were reported by a good number of studies among age at sexual maturity and egg weight, and shell quality (Table 2.3).

Table 2.3 **Genetic and phenotypic correlations (in parentheses) among age at first egg, egg number, egg weight and shell quality**

Trait I	Trait 2	Genotype	Value	Method	Author/s
AGE AT FIRST EGG (AFE) - EGG No.					
AFE	EN (280d)	WL	-0.74, -0.40	S, D	Srivastava *et al.* (1993)
	EN(40wk)	WL (PL1)	-0.13 (0.12)	S+D	Brah *et al.* (1991)
	EN(40wk)	WL (PL2)	0.09 (0.01)	S+D	-do-
	EN (40wk)	WL (Forsgate)	-0.72 (-0.68)	S	Thangaraju and Ulaganathan (1990)
	EN (40wk)	WL (Meyer)	-0.34 (-0.58)	S	-do-
	EN (90d)	Saudi local x WL	-0.39	AM	Khalil *et al.* (2004)
	EN (280d)	Saudi local x WL	-0.36	AM	-do-
	EN(22-40wk)	Brown layers	-0.29 (-0.43)	S+D	Akbaş *et al.* (2002)
	EN(90d)	WL	0.02 (-0.16)	S	Singh & Hussani (1978)
	EN(350d)	WL	-0.09 (0.16)	S	Jain *et al.* (1980)
	EN (42wk)	Layers	-0.52(-0.56)	S	Kolstad (1980)
	EN (42wk)	Layers (Strain U)	-0.72(-0.58)	S	Sorensen *et al.*(1980)
	EN (42wk)	Layers (Strain D)	-0.76(-0.56)	S	-do-
AGE AT FIRST EGG (AFE) - EGG WEIGHT					
AFE	EW(40wk)	WL	0.24, 0.44	S, D	Srivastava *et al.* (1993)
	EW (32-38wk)	WL (PL1)	0.02 (-0.01)	S+D	Brah *et al.* (1991)
	EW(40wk)	WL (Forsgate strain)	0.78 (0.27)	S	Thangaraju & Ulaganathan (1990)
	EW(40wk)	WL (Meyer strain)	-0.02 (-0.05)	S	-do-
	EW(34wk)	WL	0.15 (0.09)	S+D	Poggenpoel (1986)
	EW(35-38wk)	Layers	-0.02(0.04)	S	Kolstad (1980)
	EW(39-40wk)	Layers (Strain U)	0.14(0.04)	S	Sorensen *et al.* (1980)
	EW(39-40wk)	Layers (Strain D)	0.08 (0.04)	S	-do-
	EW(300d)	Chinese local chickens	0.13	S	Luo et al. 1991 cited by Jiang and Groen (2000)
	EW(500d)	-do-	0.31	S	-do-
AGE AT FIRST EGG (AFE) - SHELL QUALITY					
AFE	STH (34wk)	WL	0.15(0.09)	S+D	Poggenpoel (1986)
	SG(34wk)	WL	0.09(0.06)	S+D	-do-
	SG(35-38wk)	Layers	0.12(0.03)	S	Kolstad (1980)
	SG(39-40wk)	Layers (Strain U)	-0.08(-0.03)	S	Sorensen *et al.* (1980)
	SG(39-40wk)	Layers (Strain D)	0.04(0.08)	S	-do-
	SG(32-38wk)	WL (PL1)	0.23(-0.01)	S+D	Brah *et al.* (1991)
	SG(32-38wk)	WL (PL2)	-0.01(0.01)	S+D	Brah *et al.* (1991)
	SG(26-54wk)	WL	-0.61(-0.03)	S+D	Sabri *et al.* (1999)

AFE= Age at first egg; EN, EW, STH, SG = Egg number, egg weight, shell thickness, and egg specific gravity, respectively, measured at different weeks (wk) and days (d) of age indicated in the brackets; WL = White leghorn; S, S+D, AM= Estimates (genetic correlations) calculated from sire and sire plus dam components of (co)variance, and animal model of mixed models procedures, respectively.

Genetic and phenotypic correlations among egg number and other egg traits such as egg weight, shell quality and egg shape index, and among egg weight and the last two egg traits were also reported in a remarkable number of studies (Table 2.4 and 2.5). On average, correlations among egg number and egg weight, egg number and shell quality were reported by majority of the studies to range from low to moderately negative. On the other hand, correlation between egg number and egg shape index was reported by Jaap *et al.* (1962) to be low and positive. Estimates ranging from low negative to low positive were reported by a relatively large proportion of authors for correlations among egg weight and shell quality traits, and egg shape index (Table 2.5). A limited number of studies have reported correlations among shell quality and egg shape index. Results from these studies indicated values ranging from lowly positive to highly negative (Table 2.5).

Table 2.4 Genetic and phenotypic correlations (in parentheses) among egg number, egg weight, shell quality and egg shape index

Trait 1	Trait 2	Genotype	Value	Method	Author/s
EGG No.-EGG WEIGHT					
EN (280d)	EW	WL	-0.21, -0.19	S, D	Srivastava *et al.* (1993)
EN (40wk)	EW(40wk)	WL (Forsgate)	-0.59(-0.25)	S	Thangaraju& Ulaganathan (1990)
EN (40wk)	EW(40wk)	WL	-0.107 to -0.49	S	Ahmad *et al.* (1993)
EN(First 30d)	EW(28-33wk)	WL	-0.19 to -0.33	AM	Nurgiartiningsih *et al.* (2002)
EN(300d)	EW(300d)	Chinese local chickens	-0.01 to -0.46	S	Luo *et al.* (1991) cited by Jiang and Groen (2000)
EN(39wk)	EW(39wk)	Layers	-0.19 to -0.22	AM	Francesch *et al.* (1997)
EN(40wk)	EW(40wk)	RIR x WPR	-0.27 (-0.16)	AM	Hagger (1994)
EN (42wk)	EW(39-40wk)	Layers (Strain U)	-0.32, (-0.12)	S	Sorensen *et al.* (1980)
EN (42wk)	EW(39-40wk)	Layers (Strain D)	-0.17, (-0.11)	S	-do-
EN(40wk)	EW(32-38wk)	WL (PL1)	-0.34 (-0.14)	S+D	Brah *et al.* (1991)
EN(40wk)	EW(32-38wk)	WL (PL2)	-0.13 (-0.15)	S+D	Brah *et al.* (1991)
EN(40wk)	EW(40wk)	Broilers	-0.49	AM	Lopez and Quaas (1997)
EGG No- SHELL QUALITY, EGG SHAPE INDEX					
EN(500d)	STH (34wk)	WL	-0.16 (-0.09)	S+D	Poggenpoel (1986)
EN(26-54wk)	SG (26-54wk)	WL	-0.10 (0.02)	S+D	Sabri *et al.* (1999)
EN(68-80wk)	FCE (68-80wk)	WL	-0.28 (-0.88)	S+D	Engström *et al.* (1986)
EN (42wk)	SG(35-38wk)	Layers	-0.03(-0.01)	S	Kolstad (1980)
EN (42wk)	SG(39-40wk)	Layers (Strain U)	-0.13(-0.05)	S	Sørensen *et al.* (1980)
EN (42wk)	SG(39-40wk)	Layers (Strain D)	-0.27(-0.12)	S	Sorensen *et al.* (1980)
EN/year	SG(32-33wk)	WL (strain A1)	-0.03(0.01)	S	Jaffé (1966)
EN/year	SG(32-33wk)	WL(strain A2)	-0.23(-0.06)	S	Jaffé (1966)
EN (46wk)	ESI (30wk)	White Gold	0.12(0.07)	S	Jaap *et al.* (1962)

EN, EW, STH, SG, ESI, FCE = Egg number, egg weight, shell thickness, egg specific gravity, egg shape index, and frequency of cracked eggs, respectively, measured at different weeks (wk) and days (d) of age indicated in the brackets; WL = White leghorn; WPR = White Plymouth Rock; RIR = Rhode Island Red; S, D, S+D; AM= Estimates (genetic correlations) calculated from sire, dam and sire plus dam components of (co)variance, and animal model of mixed models procedures, respectively.

Table 2.5 Genetic and phenotypic correlations (in parentheses) among egg weight, shell quality and egg shape index

Trait 1	Trait 2	Genotype	Value	Method	Author/s
EGG WEIGHT – SHELL QUALITY, EGG SHAPE INDEX					
EW(39-40wk)	SG(39-40wk)	Layers (Strain U)	0.15(0.00)	S	Sørensen *et al.* (1980)
EW(39-40wk)	SG(39-40wk)	Layers (Strain D)	-0.13(-0.08)	S	-do-
EW(35-38wk)	SG(35-38wk)	Layers	-0.02(-0.06)	S	Kolstad (1980)
EW(26-54wk)	SG(26-54wk)	WL	-0.16(-0.167)	S+D	Sabri *et al.* (1999)
EW(32-33wk)	SG(32-33wk)	WL (strain A1)	-0.27(0.01)	S	Jaffé (1966)
EW(32-33wk)	SG(32-33wk)	WL(strain A2)	0.22(-0.06)	S	Jaffé (1966)
EW(32-38wk)	SG(32-38wk)	WL(PL1)	0.05(0.03)	S+D	Brah *et al.* (1991)
EW(32-38wk)	SG(32-38wk)	WL(PL2)	-0.83(-0.25)	S+D	Brah *et al.* (1991)
EW(40wk)	STH(40wk)	WL	0.16	S+D	Mohapatra *et al* (1985)
EW(34wk)	STH(34wk)	WL	0.22	S+D	Poggenpoel (1986)
EW(68-80wk)	FCE (68-80wk)	WL	-0.22(-0.07)	S+D	Engström *et al* (1986)
EW(38-40wk)	STH(38-40wk)	WL (PL1)	0.27(0.23)	S+D	Khatkar *et al.* (1994)
EW(38-40wk)	STH(38-40wk)	WL (PL2)	0.27(0.16)	S+D	-do-
EW(38-40wk)	ESI(38-40wk)	WL (PL1)	0.18 (-0.047)	S+D	-do-
EW(38-40wk)	ESI(38-40wk)	WL (PL2)	0.047(-0.027)	S+D	-do-
EW(32-38wk)	ESI(32-38wk)	WL (PL1)	-0.17(0.15)	S+D	Brah *et al.* (1991)
EW(32-38wk)	ESI(32-38wk)	WL (PL2)	-0.15(-0.06)	S+D	Brah *et al.* (1991)
EW(34wk)	ESI(34wk)	Taiwan local	-0.04	S	Chen *et al.* (1993)
EW(38-40wk)	ESI(38-40wk)	WL (PL1)	0.18(-0.047)	S+D	Khatkar *et al.* (1994)
EW(38-40wk)	ESI(38-40wk)	WL (PL2)	0.047(-0.027)	S+D	Khatkar *et al.* (1994)
EGG SHAPE INDEX - SHELL QUALITY					
ESI(38-40wk)	STH(38-40wk)	WL (PL1)	-0.113(0.054)	S+D	Khatkar *et al.* (1994)
ESI(38-40wk)	STH(38-40wk)	WL (PL2)	0.21(0.12)	S+D	Khatkar *et al.* (1994)
ESI(34wk)	STH(34wk)	Taiwan local	-058(0.24)	S	Chen *et al.* (1993)
ESI(32-38wk)	SG(32-38wk)	WL (PL1)	-0.07(0.11)	S+D	Brah *et al.* (1991)
ESI(32-38wk)	SG(32-38wk)	WL (PL2)	-0.90(-0.34)	S+D	Brah *et al.* (1991)

EW, STH, SG, ESI, FCE = Egg weight, shell thickness, egg specific gravity, egg shape index, and frequency of cracked eggs, respectively, measured at different weeks (wk) and days (d) of age indicated in the brackets; WL = White leghorn; S, S+D= Estimates (genetic correlations) calculated from sire and sire plus dam components of (co)variance, respectively.

(iii) Correlations among body weights and egg traits

Studies to estimate genetic and phenotypic correlations among body weights and egg traits have also been carried out extensively. Values ranging from highly negative to highly positive were reported for correlations between body weight and age at first egg with most of the authors reporting values between moderately negative to lowly positive (Table 2.6). Furthermore, with the exception to some few studies, correlations among body weight and egg number generally ranged from low to moderately negative. Hu *et al.* (2004) working with muscovy ducks reported a moderate negative genetic correlation between body weight and egg number. In comparison, as opposed to egg number, results from various studies summarized in Table 2.7 show that many workers reported correlations between body weight and egg weight in chickens to range from moderate to highly positive. Values ranging from low to moderate, positive to negative, were reported for correlations between body weight and shell quality, and egg shape index (Table 2.7).

Table 2.6 Genetic and phenotypic correlations (in parentheses) among body weights, age at first egg, and egg number

Trait 1	Trait 2	Genotype	Value	Method	Author
BODY WEIGHT-AGE AT FIRST EGG (AFE)					
Bwt(20wk)	AFE	WL	-0.08, -0.09	S, D	Srivastava *et al.* (1993)
Bwt(20wk)	-do-	WL(Meyer)	-0.12(-0.24)	S	Kumararaj *et al.*(1995)
Bwt(40wk)	-do-	WL(Meyer)	-0.06(0.136)	S	-do-
Bwt(20wk)	-do-	WL(Forsgate)	0.013 (-0.27)	S	-do-
Bwt(40wk)	-do-	WL(Forsgate)	0.70(0.012)	S	-do-
Bwt(20wk)	-do-	WL(Forsgate)	-0.37(-0.25)	S	Thangaraju and Ulaganathan, (1990)
Bwt(20wk)	-do-	WL(Meyer)	0.63 (-0.18)	S	-do-
Bwt(SM)	-do-	Brown layers	-0.42(-0.60)	S+D	Akbaş *et al.* (2002)
Bwt(42wk)	-do-	layers	-0.05(-0.02)	S	Kolstad (1980)
Bwt(8wk)	-do-	Layers (Strain U)	-0.09(-0.07)	S	Sorensen *et al.* (1980)
Bwt(8wk)	-do-	Layers (Strain D)	0.04(0.01)	S	-do-
Bwt(42wk)	-do-	Layers (Strain U)	-0.08(0.00)	S	Sorensen *et al.* (1980)
Bwt(42wk)	-do-	Layers (Strain D)	0.05(0.05)	S	-do-
BODY WEIGHT-EGG No.					
Bwt(40wk)	EN(40wk)	Brown layers	-0.034	S+D	Akbaş *et al.* (2002)
Bwt(20wk)	EN(280d)	WL	0.10. 0.25	S, D	Srivastava *et al.* (1993)
Bwt(wk12)	EN(90d)	WL	0.37(0.07)	S	Singh and Hussani (1978)
Bwt(20wk)	EN(40wk)	WL(Forsgate)	0.55(0.35)	S	Thangaraju and Ulaganathan. (1990)
Bwt(40wk)	EN(40wk)	RIR x PMR	-0.036 (-0.018)	AM	Hagger (1994)
Bwt(42wk)	EN(42wk)	Layers	-0.05(-0.02)	S	Kolstad (1980)
Bwt(8wk)	EN(42wk)	Layers (Strain U)	-0.02(0.00)	S	Sorensen *et al.* (1980)
Bwt(8wk)	EN(42wk)	Layers (Strain D)	-0.05(-0.03)	S	-do-
Bwt(42wk)	EN(42wk)	Layers (Strain U)	0.09(-0.01)	S	-do-
Bwt(42wk)	EN(42wk)	Layers (Strain D)	-0.06(-0.02)	S	-do-
Bwt(20wk)	EN(40wk)	Layers	-025(-0.23)	S	Neelam *et al.* (2003)
Bwt(20wk)	EN(40wk)	Layers (Crosses)	-0.22(-0.01)	S	Neelam *et al.* (2003)
Bwt(Juvenile)	EN (HD%)	Broilers	-0.20	AM	Koerhuis and Mckay (1996)

Bwt, EN = Body weight and egg number, respectively, measured at different weeks (wk), and days (d) of age indicated in brackets; SM = Sexual maturity; HD = Hen day egg production; AFE = Age at first egg; WL = White leghorn; RIR = Rhode Island Red; PMR = Plymouth Rock; S, D, S+D; AM= Estimates (genetic correlations) calculated from sire, dam and sire plus dam components of (co)variance, and animal model of linear mixed models procedures, respectively.

Table 2.7 Genetic and phenotypic correlations (in parentheses) among body weights, egg weight, shell quality and egg shape index

Trait 1	Trait 2	Genotype	Value	Method	Author
BODY WEIGHT-EGG WEIGHT					
Bwt(20wk)	EW(32-38wk)	WL(PL1)	0.62(0.35)	S+D	Brah *et al.* (1991)
Bwt(20wk)	EW(32-38wk)	WL(PL2)	0.17(0.11)	S+D	-do-
Bwt(40wk)	EW(32-38wk)	WL(PL1)	0.73(0.17)	S+D	-do-
Bwt(40wk)	EW(32-38wk)	WL(PL2)	0.01(0.18)	S+D	-do-
Bwt(20wk)	EW(40wk)	WL(Meyer)	0.05(0.14)	S	Thangaraju and Ulaganathan (1990)
Bwt(40wk)	EW(40wk)	RIR x PMR	0.29(0.24)	AM	Hagger (1994)
Bwt(42wk)	EW(35-38wk)	Layers	0.46(0.35)	S	Kolstad (1980)
Bwt(8wk)	EW(39-40wk)	Layers (Strain U)	0.36(0.30)	S	Sorensen *et al.* (1980)
Bwt(8wk)	EW(39-40wk)	Layers (Strain D)	0.44(0.29)	S	-do-
Bwt(42wk)	EW(39-40wk)	Layers (Strain U)	0.36(0.35)	S	-do-
Bwt(42wk)	EW(39-40wk)	Layers (Strain D)	0.60(0.39)	S	-do-
Bwt(32wk)	EW(32-33wk)	WL (strain A1)	0.48(0.29)	S	Jaffé (1966)
Bwt(32wk)	EW(32-33wk)	WL(strain A2)	0.49(0.36)	S	Jaffé (1966)
Bwt(6wk)	EW(40wk)	Broilers	0.21	AM	Lopez and Quaas (1997)
BODY WEIGHT-SHELL QUALITY, EGG SHAPE INDEX					
Bwt(20wk)	ESI(32-38wk)	WL(PL1)	-0.17(0.15)	S+D	Brah *et al.* (1991)
Bwt(20wk)	ESI(32-38wk)	WL(PL2)	-0.15(-0.06)	S+D	-do-
Bwt(40wk)	ESI(32-38wk)	WL(PL1)	0.08(-0.28)	S+D	-do-
Bwt(40wk)	ESI(32-38wk)	WL(PL2)	0.29(0.11)	S+D	-do-
Bwt(32wk)	SG(32-33wk)	WL (strain A1)	-0.11(-0.08)	S	Jaffé (1966)
Bwt(32wk)	SG(32-33wk)	WL(strain A2)	0.24(0.07)	S	Jaffé (1966)
Bwt(8wk)	SG(39-40wk)	Layers (Strain U)	-0.07(-0.02)	S	Sorensen *et al.* (1980)
Bwt(8wk)	SG(39-40wk)	Layers (Strain D)	-0.06(-0.02)	S	-do-
Bwt(42wk)	SG(39-40wk)	Layers (Strain U)	0.01(-0.05)	S	-do-
Bwt(42wk)	SG(39-40wk)	Layers (Strain D)	0.01(-0.09)	S	-do-
Bwt(42wk)	SG(35-38wk)	Layers	-0.19(-0.06)	S	Kolstad (1980)

Bwt, EW, SG, ESI = Body weight, egg weight, egg specific gravity, and egg shape index, respectively, measured at different weeks (wk) of age indicated in the brackets; WL = White leghorn; S, S+D, AM= Estimates (genetic correlations) calculated from sire, and sire plus dam components of (co)variance, and animal model of linear mixed models procedures, respectively.

(iv) Correlations among antibody response (humoral immune response) and productivity

Correlations among humoral immune response and productivity specifically body weight have been reported by several studies. In these studies values ranging from low positive to low negative have been reported, with most of the authors reporting them to be negative. Values ranging from 0.06 to –0.13 have been reported by Lwelamira and Katule (2004) in a mixture of different Tanzania chickens ecotypes and their reciprocal crosses with RIR for primary antibody response against Newcastle disease virus (NDV) vaccine. Similar observations were noted by Sivaraman et al. (2005) in broilers for primary antibody response against SRBC. Values ranging from 0.09 to –0.12 were reported in Turkeys by Sacco et al. (1994) for primary antibody response against NDV vaccine and Pasteurrela multocida vaccine. Considering the correlation between humoral immune response and other production traits, a study by Chao and Lee (2003) in Taiwan local chickens indicated phenotypic correlation between antibody response against SRBC and age at sexual maturity, egg weight and egg production to vary from -0.027 to -0.038, -0.027 to -0.05, and -0.046 to -0.063, respectively.

2.5 Selection indices

2.5.1 Smith-Hazel index

Total economic value of an animal always depends on several traits. Hence, considering several economically important traits simultaneously during selection is of prime importance. One way of achieving this is through use of selection indices. Several selection indices have been developed by a number of authors. The first paper on selection index was given by Smith (1936) for multi-trait selection in plant populations. Later on, Hazel (1943) developed essentially the same index to apply in animal populations. Generally, the above indices (Smith-Hazel index) estimate the value of an individual for an aggregate genotype (H), which is expressed in financial terms in linear form of additive genetic merits for component traits, weighted by their relative economic values. The economic value of a trait can be defined as the change in the profit of the farm, as a consequence of one unit of change in the genetic merit of the trait considered when other traits held constant (Nordskog, 1986; Kosgey, 2004; Gicheha *et al.*, 2005;). Although widely used, one of the major difficulties of applying Smith-Hazel index, is that of determining relative economic values of various traits. Many animal and plant breeders find it difficult to express the relative importance of various traits in an economic sense (Pesek and Baker, 1969; Baker, 1974; Yamada *et al.*, 1975; Itoh and Yamada, 1986; Silva *et al.*, 1998; Helmink *et al.*, 2003; Kanis *et al.*, 2005). The difficulties arise as a result of the following reasons:

i. Large volume of data is required for obtaining accurate estimates for economic values.

ii. Economic situations may change with time and location (Hazel *et al.*, 1995). They may change easily with external factors and the change in the population mean by selection. Therefore, even though an accurate economic assessment is made, inaccurate relative weights may likely result after selection.

iii. No records exist in some production systems (i.e extensive systems in the tropics) (Kosgey 2004; Bosso. 2005; Menge *et al.*. 2005).

iv. There are several traits such that one can hardly assess their importance, i.e. body conformation, disease resistance (Nordskog, 1986; Helmink *et al.*, 2003; Kanis *et al.*, 2005).

v. Desirability views of breeders, producers, marketing dealers and consumers are often quite different by locality. Breeder's view for economically optimal genotype is often different.

vi. It is very logical and desirable to improve a population mean linearly toward the economically optimal level. But economical environment tend to shift with time and balance between demand and supply. (Hazel *et al.* 1995; Yadav *et al.*, 2005).

2.5.2 Restricted gain indices

Practical animal breeders frequently confront situations where genetic gains in the component traits should be controlled. For example, when a trait has already achieved an optimum level, breeders will usually design to keep that level while maximizing genetic gains in other important traits. If antagonistic correlations exist between traits restriction should be imposed on the genetic gains in order to avoid undesirable correlated responses. In an endeavour to solve these problems, Kempthorne and Nordskog (1959) consequently developed a method called 'restricted index selection'.

In their index, the change in aggregate genotype is maximized under the restriction of zero-gain on a component trait. Their principles were summarized in a review by Brascamp (1984). Furthermore, the much simpler technique to obtain the restricted selection index as that of Kempthorne and Nordskorg (1959) was presented by Abe *et al.* (1969), and Cunningham *et al.* (1970). The method of Kempthorne and Nordskog (1959) was further modified by several authors, e.g Tallis (1962) developed a restricted selection index in which a given trait could be changed to a pre-specified level while other traits are improved as much as possible. On the other hand, the index with inequality constraints, and the index with proportionality constraints were developed by Rao (1962) and Harville (1975), respectively. Developing methods for constructing restricted selection indices has not ended there. More recently, Lin (2005a, b) devised a method for construction of selection indexes with multiple restrictions. However, the problem of restricted selection indexes is the reduction of genetic gain, and correlation between the index (I) and the aggregate genotype (H) when compared to the unrestricted selection indices i.e. Smith-Hazel index (Akhatar *et al.*, 1993; Chakravarty and Rath, 1990; Singh *et al.*, 2001). As with Smith-Hazel Index, restricted gain indexes also require the presence of economic values of individual traits in a breeding goal (aggregate genotype).

2.5.3 Desired gain indices

In a situation where economic values of individual traits in a breeding goal are not available or difficult to estimate, desired gain indices have been suggested (Pesek and Baker, 1969; Baker, 1975; Yamada *et al.*, 1975; Kaushik and Khanna, 2003; Kanis *et* *al.*, 2005; Suzuki *et al.*, 2005; Singh and Sinha, 2006). Desired gain indices are also useful for controlling genetic gains in component traits in the index, i.e. when a certain trait is at optimal level and want to keep that level while improving other traits (Campo and Valesco, 1989; Mukai *et al.*, 1989; Nomura *et al.*, 2001; 2002). A selection index for attaining pre-determined desired genetic gain which does not require defining aggregate genotype and estimation of relative economic values of component traits was first developed by Pesek and Baker (1969), and later by Yamada *et al.* (1975) as described by Yamada (1995).

2.6. Role of molecular genetics in poultry breeding

Identification of genes controlling a particular trait offers an opportunity for accurately screening superior individuals and hence hastening genetic gain when incorporated into the breeding programmes (i.e. Marker assisted selection (MAS)). MAS is very useful in improving sex limited traits such as egg production, in traits with low to medium heritability, and in traits which are difficult to obtain reliable measurements e.g. immunocompetence traits (Yonash *et al.*, 2000). As a result several studies have been initiated for the genome-wide searches for regions or genes associated with economic traits (Yonash *et al.*, 2001; Zhou *et al.*, 2002; Yunis *et al.*, 2002; Deeb and Lamont, 2003; Kramer *et al.*, 2003; Zhou and Lamont, 2003). This genome-wide search has been in two general categories of phenotypic traits: (1) growth and reproduction and (2) immunoresponsiveness and disease resistance.

A group of genes called Major Histocompatibility Complex (MHC) (B region) has been identified to be associated with immune responses, resistance and susceptibility to numerous pathogens (Dunnington *et al.*, 1992; Juul-Madsen *et al.*, 2002; Liu *et al.*, 2002; Zekarias *et al.*, 2002; Taylor, 2004; Joiner *et al.*, 2005; Lavi *et al.*, 2005; Xu *et al.*, 2005; Boonyanuwat *et al.*, 2006), as well as productivity (Abplanalp *et al.*, 1992; Lundén *et al.*, 1993). Chicken MHC, initially identified as B blood group system (Briles *et al.*, 1950); is composed of two regions, the B and *Rfp*-Y regions which segregate independently of each other (Miller *et al.*, 1994; Juul-Madsen *et al.*, 1997; Thoraval *et al.*, 2003) and are located on a microchromosome 16 (Miller *et al.*, 1996).

The MHC B region codes for three classes of cell surface antigens. These are the B-F and B-L, and these are equivalent to the mammalian class I and class II antigens, and B-G which is absent in mammalian MHC (Lamont and Dieter, 1990; Lamont, 1993). *Rfp*-Y region codes for cell surface antigens similar to that of class I and II. Genes in *Rfp*-Y cluster were reported to have lower expression and seemed to be less polymorphic than the genes in the MHC B system cluster (Miller *et al.*, 1996; Afanassieff *et al.*, 2001).

Polymorphism of the genes at MHC region has been studied using serological methods (Lillehoj *et al.*, 1986; Lawrence, 1998; Juul-Madsen *et al.*, 2006a), and molecular approaches such as Restriction fragment length polymorphism (RFLP) (Yonash *et al.*, 2000; Emara *et al.*, 2002; Iglesias *et al.*, 2004; Boojanuwat *et al.*, 2006), Single strand conformation polymorphism (Goto *et al.*, 2002), DNA sequence (Sung *et al.*, 1993; Miller *et al.*, 2004), Sequence-specific polymerase chain reaction (SS-PCR) (Livand and

Ewald, 2005), and Microsatellites i.e LEI0258 (Dalgaard *et al.*, 2005; Lima-Rosa *et al.*, 2005; Fulton *et al.*, 2006; Schou *et al.*, 2006). Although variability at MHC B region were associated with immune responses, susceptibility and resistance to some pathogens, and productivity, results from some of these studies have shown that the expression of the marker alleles vary depending on the background genome (i.e. interactions between markers and the background genome). This implies that an allele identified to be associated with superiority in a particular population would not necessarily be associated with superiority in another population. Therefore, looking for alleles associated with superiority in a population of interest before MAS can be instituted is of paramount importance.

CHAPTER THREE

3.0 MATERIAL AND METHODS

3.1 Study site and chicken ecotypes used

The study was conducted at Sokoine University of Agriculture poultry research unit, Morogoro, Tanzania and two nearby villages (i.e. Kauzeni and Mgambazi). The place is located at an altitude of about 525m, above sea level. The relative humidity at the location is about 81%, while the monthly mean and maximum temperatures are 18.7 and 30.1^{0} C, respectively. The area has annual mean rainfall of 846mm.

The study involved two chicken ecotypes from four regions of Tanzania (Table 3.1 and Figure 1). The study targeted local chickens from Mwanza and Shinyanga region in the northern parts of the country; Singida and northwest parts of Morogoro region close to Dodoma region in central part of the country. Results from random sampling of mature local birds from villages done in previous studies (Lawrence, 1998; Yongolo, M.G.S. (2003), personal communication) indicated that chickens from Mwanza and Shinyanga regions (*Kuchi*) were relatively high in weight while those from Singida and northwest part of Morogoro regions (*Medium*) were of medium weight. While *Kuchi* ecotype are located in the specified areas in the respective regions and they are few in number, *Medium* ecotype are found everywhere in the specified regions and they are large in number. A sample of chickens from *Medium* ecotype is indicated in Plate 1, while that for *Kuchi* ecotype is indicated in Plate 2 and 3.

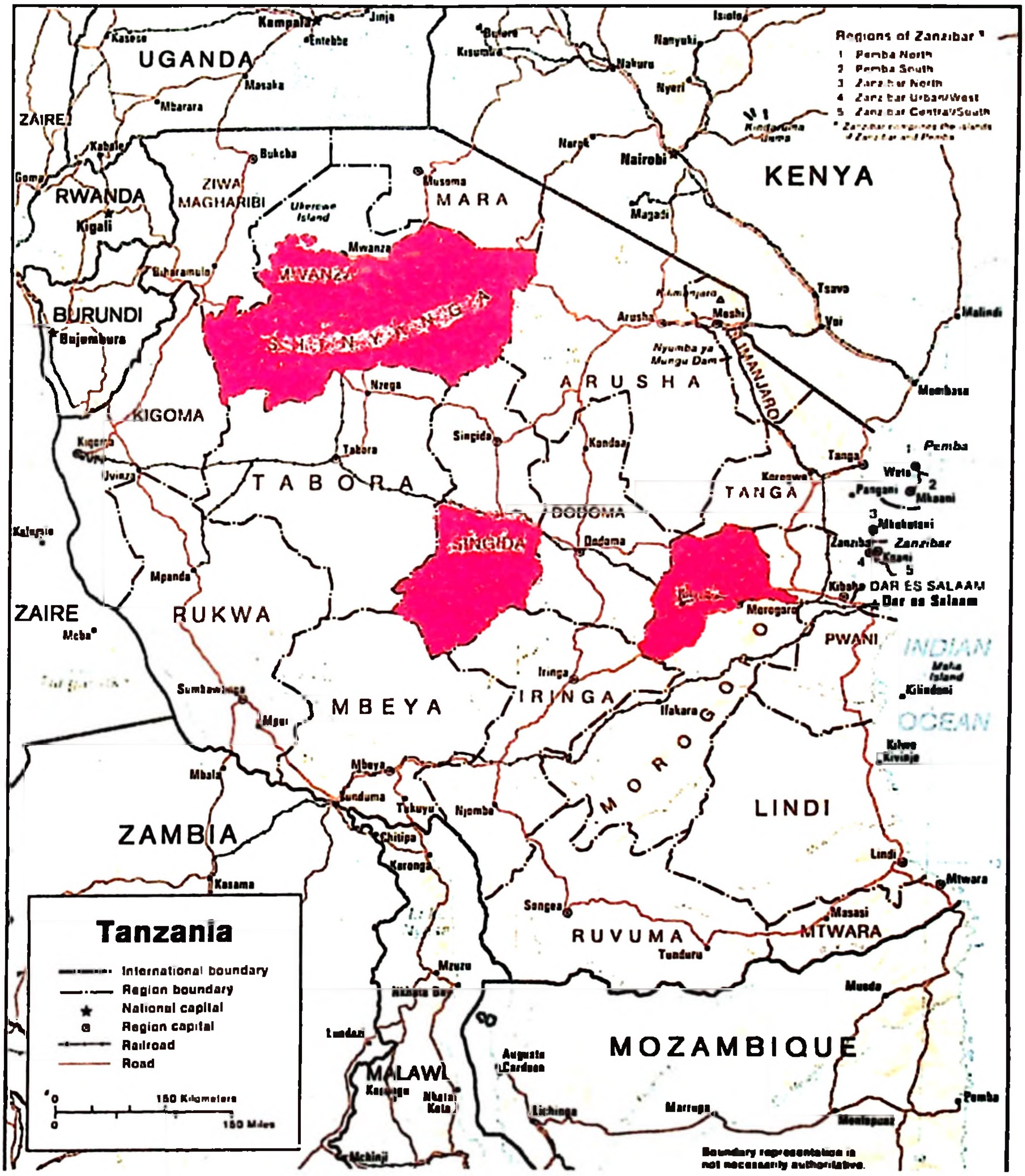
Table 3.1 Sampling area for parent stock

Location	Ecotype	
	Kuchi	***Medium***
Region	Mwanza, Shinyanga	Morogoro, Singida
Districts	Mwanza:Sengerema, Geita, Ngudu	Morogoro: Kilosa (Gairo)
	Shinyanga: Shinyanga rural	Singida: Singida rural

Plate 1. *Medium* ecotype cock (on the left) and hens (on the right)

Plate 2. An attendant holding a hen (on the left) and a cock (on the right) from *Kuchi* ecotype

Plate 3. A researcher holding a cock from *Kuchi* ecotype



Key:

🟥 Sampled areas

Figure 1. **Map of Tanzania showing location where chicken were sampled**

3.2 Studies carried out

This work involved three main studies. The first one involved on-station and on-farm evaluation of the performance and estimation of genetic parameters for two chicken ecotypes viz. *Kuchi* and Tanzania Medium (*Medium*) found in Tanzania. The second study involved using the obtained genetic parameters from the first study in designing and evaluation of various breeding scenarios/schemes for improving performance of these ecotypes through selection. The last study involved examination of the possibilities of using Marker assisted selection (MAS) in selection programs in local chickens by evaluating the association between LEI0258 (a microsatellite located at MHC B region) microsatellite alleles and performance.

3.3 Study I

3.3.1 Experimental materials

3.3.1.1 Sampling of the parent stock

A total of 70 cocks and 405 hens were randomly collected from four regions of Tanzania (Table 3.1 and 3.2). All together 34 cocks and 185 hens, 36 cocks and 220 hens were collected for *Kuchi* and *Medium* weight ecotypes, respectively. After accounting for mortalities, 32 cocks and 175 hens, 30 cocks and 180 hens were available for experiment for *Kuchi* and *Medium* ecotypes, respectively (Table 3.2). During collection, birds were vaccinated against ND two weeks before collection. Furthermore, upon arrival on-station, they were put into isolation for 3 to 4 weeks before being taken to the experimental houses. While in isolation they were given antihelmintics, coccidiostats and observed for disease symptoms. Moreover, to ensure protection of young chicks from Gumboro, parents stocks were also vaccinated against Gumboro before being transferred to the experimental pens.

Table 3.2 Sample size of parent stock

Variable	*Kuchi*			*Medium*		
	Mwanza	Shinyanga	Total	Morogoro	Singida	Total
No of cocks (males)	20	14	34	27	9	36
No of hens (females)	112	73	185	119	101	220
Mortality-cocks	2	-	2	5	1	6
Mortality-hens	7	3	10	38	2	40
No. of cocks available for expt.[1]			32 (24)			30(27)
No. of hens available for expt.[2]			175			180

[1] Figures in parentheses are number of cocks used for experiment

[2] All dams were used for experiment.

3.3.1.2 Mating, data structure and management of the birds for on-station trial

The study was carried out both on-station and on-farm. While all hens available were used for on-station experiment, only 24 and 27 cocks from *Kuchi* and *Medium* ecotype respectively were used in this study (Table 3.2). Cocks were mated to hens of their own ecotype chosen randomly, and number of hens per cock in each ecotype ranged from 5 to 8. Average number of hens per cock was 7.2 and 6.7, for *Kuchi* and *Medium* ecotype, respectively. Before mating, hens were rested without a cock for a period of three weeks in order to ensure that upon mating, a known/planned cock has fertilized the eggs. Mating was done repeatedly after every one week with mating and egg collection period lasting for three days and one week, respectively in each cycle. After every mating, transferring of hens to individual battery cages was done with the purpose of identifying and marking the eggs from each hen before incubation in order to keep track on pedigree. A total of 1468 chicks were produced in eleven hatches with 645 and 823 being chicks from *Kuchi* and *Medium* ecotypes, respectively. Upon hatching, not all hens possessed chicks, therefore the chicks above were the progeny of 163 and 175 hens for *Kuchi* and *Medium* ecotypes, respectively. Hatched chicks were tagged and housed in floor pens up to 12 weeks of age. Thereafter they were transferred to individual cages. In addition, while in floor pens a total of 120 birds from batch No.6 at the age of 5 weeks were randomly chosen from the two ecotypes (i.e. 60 birds from each ecotype) and subjected to a feed utilization trial up to 12 weeks of age. In this trial, 60 birds from each ecotype were randomly allocated to four pens with two pens for each sex and each pen containing 15 birds.

Birds were fed a starter ration (20% CP and 2800 Kcal ME/kg) from day old to 8th week of age, growers ration (16% CP and 2750 Kcal ME/kg) from 9th to 16th week of age, and layers ration (17%CP and 2700 Kcal ME/kg) from 17th week of the age to the rest of the period. Parent stock was also fed the same layers ration. Water was supplied on *ad libitum* basis. Furthermore, birds were vaccinated against Gumboro disease when they were about 10 to 14 days of age, and also due to the experimental set-up they were first vaccinated against Newcastle disease when they were 4 weeks of age, and vaccinations were repeated three weeks post vaccination, and later on after every three months.

3.3.1.3 Mating, data structure and management of the birds for on-farm trial

After the end of mating and hatching period in on-station experiment, the parent stock was taken to the field for on-farm experiment. The study involved two villages viz. Kauzeni and Mgambazi. A total of 285 hens from the two ecotypes (139 and 146 hens from *Medium* and *Kuchi* ecotypes, respectively), and 46 cocks (22 cocks being from *Kuchi*, and 24 cocks being from *Medium* ecotype) were supplied to 68 farmers i.e. 30 and 38 farmers from Mgambazi and Kauzeni, respectively. Criteria for the choice of the farmers were that the farmer was supposed to participate in construction of a chicken house, which could accommodate at least 6 adult birds on individual compartments.

Parent stocks were vaccinated against ND and Gumboro two weeks and one week, respectively before being taken to the field. Initially each farmer was supplied with two hens from each ecotype (4 hens per farmer), however due to fertility problems some farmers were given up to 5 hens. Average number of hens per cock was 6.6 and 5.8 for *Kuchi* and *Medium* ecotypes, respectively. Before being taken to the field hens were also mated to the respective cocks for 1 week. Upon arrival to the field, the birds were placed in individual compartments and confined. Furthermore, three to four nearby farmers were supplied with two cocks one from each ecotype and the cocks were circulated to those farmers. Mating arrangements in the field were in such a way that each cock continued to mate hens which it had mated on-station. To ensure this, those nearby farmers were supplied with hens in which the cocks they were mated on station were the circulating cocks.

While in confinement, hens were let to lay and incubate and hatch their eggs. During mating, incubation and hatching periods, birds were supplied with water and layers ration (17% CP and 2700 Kcal ME/kg) on *ad libitum* basis. At this period parent stocks were also given antihelmintics (*Kukuzole*®) and broad spectrum antibiotics (OTC-plus®) regularly (prophylactic treatments) according to manufacturer instructions, and their bodies/houses were dusted with pesticides (*Dudu-dust*®) to control external parasites. After hatching chicks were tagged and hens continued to stay in confinement with their chicks for a period of ten days. While in confinement the birds were fed chick starter as that used in on-station trial. The purpose of confining chicks in the early days of their lives was to minimize mortalities due to predation. After the end of confinement period birds were freed and chicks left to move out (scavenging) with their mothers. At this stage birds were depending entirely on scavenging feed. Hatching was done in two phases. Phase I covered the period from early April to mid-May, 2005, and Phase II from early June to early August, 2005. A total of 554 and 690 chicks from *Kuchi* and *Medium* ecotypes were hatched. As with on-station trial, not all hens in the experiment produced chicks. Therefore the above chicks were progeny of 101 and 112 hens for *Kuchi* and *Medium* ecotype, respectively. The vaccination regimes for chicks were as in the on-station trial.

3.3.2 Parameters studied

3.3.2.1 Mortality, body weight and feed utilization efficiency

Body weights were recorded on all individuals at 8, 12, 16 and 20 weeks of age and mortalities were recorded for the entire experimental period both on-station and on-farm. Feed utilization efficiency (on-station) was evaluated in 120 individuals from batch no. 6 from 5 to 12 weeks of age. In this aspect, feed utilization efficiency was assessed as the ratio between average total feed intake per bird (IPB) for the above specified period to average total weight gain per bird (GPB) in that period i.e. Feed Conversion Ratio (FCR) (Beaumont *et al.* 1998; Safalaoh, 1998; Pedersen, 2002; Tadelle *et al.*, 2003a; Demeke, 2004).

3.3.2.2 Laying performance and related traits

Hens were further assessed for age at sexual maturity, egg production, egg weight, shell thickness and egg shape index for the on-station trial. Age at sexual maturity was measured by age at first egg in days, and egg production by egg number in the first 90 days from sexual maturity. Egg weight, shell thickness and egg shape index was recorded on each individual hen as the average of 3 to 4 eggs from 33rd to 36th weeks of age. A micrometer screw gauge was used to measure a shell thickness. In each egg, shell thickness was recorded as the average of three readings taken from three different sites on the egg i.e. at the equator (middle), broad and narrow ends as it has been suggested in previous studies (Jaffé, 1966; Khatkar *et al.*, 1994; Mohammed *et al.*, 2005). Egg shape index were measured according to Brah *et al.* (1991), Chen *et al.* (1993) and Smith (2001) as the ratio of egg width to length (in %). Egg width and length were measured by a vernier calliper.

3.3.2.3 Antibody response (humoral immune response) against NDV vaccine

The chicks were vaccinated with Newcastle disease virus vaccine (La Sota) according to manufacturer instructions at the age of 4 weeks and antibody levels were assessed just prior and two weeks post vaccination. Blood from each chick was collected from wing vein using syringes. Samples were titrated for Newcastle disease virus (NDV) specific antibodies by the microtitre method of the haemagglutination inhibition (HI) test (Allan and Gough, 1974) using NDV antigen. Four haemagglution (HA) units were used and twofold serial dilutions of sera added with a starting dilution of 1:2. The titres were expressed in $\log_2$ form of the highest dilution causing HI. Since antibody titre prior to vaccination were almost zero in nearly all chicks, then only antibody titre two weeks post vaccination (primary antibody response) was considered in subsequent analyses.

3.3.3 Statistical analyses

3.3.3.1 Descriptive statistics and least squares analyses of variances

All data including those for antibody titre were checked for skewness using SAS (2000) UNIVARIATE procedure and found to conform to normal distribution. The data were then subjected to descriptive statistical analyses and least squares analyses of variances using the SAS (2000). General Linear Model (GLM) procedure using statistical Models 1 and 2 for antibody titre and body weights for on-station and on-farm trials. respectively. Furthermore, statistical Models 3 and 4 were used for feed utilization efficiency data and egg production and related traits for on-station trial, respectively. However, since some of the fixed effects in some traits were found to be non-significant, data set for these traits were re-analysed without two way interactions between these effects and other fixed effects in the model. (i.e. analysed using reduced models). In this regard, all the two way interactions between fixed effects were dropped from the model in the final analysis of antibody titre data on-station. A similar process was applied to two way interactions between village and other fixed effects for body weights on-farm, all two way interactions between fixed effects for antibody titre on-farm, two way interaction between fixed effects for feed intake per bird in feed utilization efficiency trial, and two way interactions between fixed effects for egg production and related traits.

The general models are shown below:-

$Y_{ijkl} = \mu + H_i + G_j + C_k + (HG)_{ij} + (HC)_{ik} + (GC)_{jk} + e_{ijkl}$..............Model 1

Where:

Y_{ijkl} = observation of l^{th} individual from k^{th} sex, j^{th} genotype and i^{th} hatch;

μ = underlying constant in every observation Y_{ijkl};

H_i = fixed effect of i^{th} hatch ($i = 1..11$);

G_j = fixed effect of j^{th} genotype ($j = 1..2$);

C_k = fixed effect of k^{th} sex ($k = 1..2$);

$(HG)_{ij}$ = interaction between hatch and genotype;

$(HC)_{ik}$ = interaction between hatch and sex;

$(GC)_{jk}$ = interaction between genotype and sex;

e_{ijkl} = random effect peculiar to each individual distributed as $NID(0, \sigma_e^2)$.

$Y_{ijklmn} = \mu + V_i + F_{ij} + M_k + G_l + C_m + (VM)_{ik} + (VG)_{il} + (VC)_{im} + (MG)_{kl} + (MC)_{km} + (GC)_{lm} + e_{ijklmn}$...Model 2

Where:

Y_{ijklmn} = observation of n^{th} individual from m^{th} sex, l^{th} genotype, k^{th} hatching month in i^{th} village and j^{th} farm;

μ = underlying constant in every observation Y_{ijklmn};

V_i = fixed effect of i^{th} village ($i = 1..2$);

F_{ij} = fixed effect of j^{th} farm within i^{th} village ($j = 1..65$);

M_k = fixed effect of k^{th} hatching month ($k = 1..5$);

G_l = fixed effect of l^{th} genotype ($l = 1..2$);

C_m = fixed effect of m^{th} sex ($m = 1..2$) ;

$(VM)_{ik}$= interaction between village and hatching month;

$(VG)_{il}$ = interaction between village and genotype;

$(VC)_{im}$ = interaction between village and sex;

$(MG)_{kl}$ = interaction between hatching month and genotype;

$(MC)_{km}$ = interaction between hatching month and sex;

$(GC)_{lm}$ = interaction between genotype and sex;

e_{ijklmn} = random effect peculiar to each individual distributed as $NID(0, \sigma_e^2)$.

$Y_{ijk} = \mu + G_i + C_j + (GC)_{ij} + e_{ijk}$ ....Model 3

Where:

Y_{ijk} = observation of k^th replication from i^th genotype and j^th sex;

μ = underlying constant in every observation Y_{ijk};

G_i = fixed effect of i^th genotype ($i = 1..2$);

C_j = fixed effect of j^th sex ($j = 1..2$);

$(GC)_{ij}$ = interaction between genotype and sex;

e_{ijk} = random effect peculiar to each individual distributed as $NID(0, \sigma_e^2)$.

$Y_{ijk} = \mu + H_i + G_j + (HG)_{ij} + e_{ijk}$ ....Model 4

Where:

Y_{ijk} = observation of k^th individual from j^th genotype and i^th hatch;

μ = underlying constant in every observation Y_{ijk};

H_i = fixed effect of i^th hatch ($i = 1..11$);

G_j = fixed effect of j^th genotype ($j = 1..2$);

$(HG)_{ij}$ = interaction between hatch and genotype;

e_{ijk} = random effect peculiar to each individual distributed as $NID(0, \sigma_e^2)$.

3.3.3.2 Estimation of phenotypic and genetic parameters

(i) Heritabilities

Heritabilities based on sire variance components were calculated within each genetic group using equation 1 as suggested by Falconer and McKay (1996) and their standard errors were approximated according to Becker (1984). The variance components for calculating heritabilities were estimated using the restricted maximum-likelihood (REML) method from VARCOMP procedures of SAS (2000). The data sets for each genotype were analysed with model 5 for antibody response (titres) and body weights on-station, model 6 for laying performance and related traits on-station, and model 7 for antibody response and body weights on-farm. An estimate was considered to be significant if is higher than twice its standard error.

$$h^2_s = \frac{4\,\sigma^2_s}{\sigma^2_s + \sigma^2_d + \sigma^2_e} \quad \text{.......................................Equation 1}$$

where σ^2_s, σ^2_d, σ^2_e, are sire, dam, and error variance components, respectively.

$$Y_{ijklm} = \mu + H_i + C_j + S_k + D_{kl} + (HC)_{ij} + e_{ijklm} \quad \text{........................Model 5}$$

Where:

Y_{ijklm} = record of mth individual from ith hatch, jth sex, and lth dam mated to kth sire;

μ = underlying constant in every observation Y_{ijklm};

H_i = fixed effect of ith hatch;

C_j = fixed effect of jth sex;

S_k = random effect of kth sire, *NID* $(0, \sigma_S^2)$;

D_{kl} = random effect of lth dam mated to kth sire, *NID* $(0, \sigma_D^2)$;

$(HC)_{ij}$ = interaction between hatch and sex;

e_{ijklm} = random effect peculiar to each individual distributed as *NID*$(0, \sigma_e^2)$.

$Y_{ijkl} = \mu + H_i + S_j + D_{jk} + e_{ijkl}$..Model 6

Where:

Y_{ijkl} = observation of l^{th} individual from i^{th} hatch, and k^{th} dam mated to j^{th} sire;

μ = underlying constant in every observation Y_{ijkl};

H_i = fixed of i^{th} hatch;

S_j = random effect of j^{th} sire, *NID* $(0, \sigma_S^2)$.

D_{jk} = random effect of k^{th} dam mated to j^{th} sire, *NID* $(0, \sigma_D^2)$;

e_{ijkl} = random effect peculiar to each individual distributed as *NID*$(0, \sigma_e^2)$.

$Y_{ijklmno} = \mu + V_i + F_{ij} + M_k + C_l + S_{im} + D_{mn} + (VM)_{ik} + (VC)_{il} + (MC)_{kl}$
$+ e_{ijklmno}$..Model 7

Where:

$Y_{ijklmno}$ = observation of o^{th} individual from i^{th} village, j^{th} farm within i^{th} village, k^{th} hatching month, l^{th} sex, and n^{th} dam mated to m^{th} sire within i^{th} village;

μ = underlying constant in every observation $Y_{ijklmno}$;

V_i = fixed effect of i^{th} village;

F_{ij} = Fixed effect of j^{th} farm within i^{th} village;

M_k = fixed effect of k^{th} hatching month;

C_l = fixed effect of l^{th} sex;

S_{im} = random effect of m^{th} sire within i^{th} village, *NID* $(0, \sigma_S^2)$.

D_{mn} = random effect of n^{th} dam mated to m^{th} sire, *NID* $(0, \sigma_D^2)$.

$(VM)_{ik}$ = interaction between village and hatching month;

$(VC)_{il}$ = interaction between village and sex;

$(MC)_{kl}$ = interaction between hatching month and sex;

$e_{ijklmno}$ = random effect peculiar to each individual distributed as *NID*$(0, \sigma_e^2)$.

(ii) Phenotypic and genetic correlations among different traits

Phenotypic and genetic correlations between traits were calculated from variance and covariance components. The variance components were estimated using the REML method of the VARCOMP procedures of SAS (2000). Again, Model 5, 6 and 7 were used. Covariance components (σxy) of two traits, x and y, for example, were calculated by using equation 2:

$$\sigma_{xy} = \frac{\sigma^2_{x+y} - \sigma^2_x - \sigma^2_y}{2} \quad \text{..Equation 2}$$

where σ^2_{x+y} is the variance of the individual sums of the two traits, and σ^2_x and σ^2_y are the variances of x and y, respectively. Genetic covariances were calculated by using sire components of variance, multiplied by 4, in equation 2. Phenotypic correlations (r_p) were calculated by

$$r_p = \frac{\sigma_{xy}}{\sigma_x . \sigma_y} \quad \text{..Equation 3}$$

where σ_x and σ_y were phenotypic standard deviations of traits x and y, respectively. Genetic correlations (r_g) were estimated by using the calculated genetic covariances together with sire standard deviations of x and y, multiplied by 4 in equation 3. Standard errors for the estimates were approximated according to Becker (1984) and an estimate was considered to be significant if its magnitude was higher than twice the standard error of the estimate.

(iii) Genetic correlation between the same trait measured in two environments (i.e. genotype by environment (G x E) interaction)

For the traits which were measured in two environments i.e. body weight and antibody response (humoral immune responses), genetic correlations for the same trait measured in two environments were also estimated within each genetic group (ecotype). The correlations were estimated using equation 4 proposed by Robertson (1959) as applied by Sorensen (1977).

$$\sigma^2_{S \times E} = \frac{(\sigma_{A1} - \sigma_{A2})}{2} + \sigma_{A1} . \sigma_{A2} . (1 - r_g) \quad \text{................Equation 4}$$

Where, $\sigma^2_{S \times E}$ = Sire by environment interaction component of variance;

σ_{A1} = square root of additive genetic variation in environment 1;

σ_{A2} = square root of additive genetic variation in environment 2;

r_g = genetic correlation between the same trait measured in two environments.

The interaction component of variance was estimated using MIXED procedure of SAS (2000) using statistical model 8. Additive genetic variances in respective environments were estimated based on sire components of variances as per Falconer and Mckay (1996). MIXED procedures of SAS (2000) were also used to estimate sire components of variances using statistical model 9. Before analyses data were adjusted for significant effect of other fixed factors such as hatch (on-station environment), hatching month and farm (on-farm environment) using GLM procedures of SAS (2000).

$$Y_{ijkl} = \mu + C_i + E_j + S_k + (ES)_{jk} + e_{ijkl} \text{.....................................Model 8}$$

Where:

Y_{ijkl} = record of l^{th} individual from i^{th} sex, j^{th} environment, and k^{th} sire;

μ = overall mean;

C_i = fixed effect of i^{th} sex;

E_j = fixed effect of j^{th} environment;

S_k = random effect of k^{th} sire, $NID\ (0,\ \sigma_S^2)$.

$(ES)_{jk}$ = random interaction effect of sire and environment;

e_{ijkl} = random effect peculiar to each individual distributed as $NID(0,\ \sigma_e^2)$.

$Y_{ijk} = \mu + C_i + S_j + e_{ijk}$..Model 9

Where:

Y_{ijkl} = record of k^{th} individual from i^{th} sex and j^{th} sire;

μ = overall mean;

C_i = fixed effect of i^{th} sex;

S_j = random effect of j^{th} sire, $NID\ (0,\ \sigma_S^2)$;

e_{ijk}= random effect peculiar to each individual distributed as $NID(0,\ \sigma_e^2)$.

3.4 Study II

This study involved evaluation of various breeding scenarios/schemes for improving the performance of the studied chicken ecotypes through selection by simulation. In this aspect, informations obtained in study I were used in computation of various breeding scenarios.

3.4.1 Comparison of various breeding scenarios/ schemes

Various breeding scenarios were designed and compared through simulation. These scenarios were compared in terms of gain per generation, number of generations required to achieve the desired performances, and correlated responses. For the scenarios which involved single trait selection based on own performance, response per generation and correlated responses were calculated according to Falconer and Mckay (1996) using equation 5 and 6, respectively. Furthermore, since relative economic weights for various traits were not available, those scenarios where more than one trait were considered, desired gain selection indices were used. The desired gain indices were constructed according to Yamada *et al.* (1975) as applied in subsequent studies (Gill and Verma, 1983b; Hazary *et al.*, 1998; Nishida *et al.*, 2001; Noda *et al.*, 2002; Kaushik and Khanna, 2003). Therefore, gain per generation, correlated responses and number of generations required to achieve the desired perfomances in multi-trait selection were computed as per Yamada *et al.* (1975).

$$R = ih^2\sigma_P \text{..........} \text{Equation 5}$$

Where, R = response to selection per generation;

i = intensity of selection;

h^2 = heritability estimate;

σ_P = phenotypic standard deviation.

$$CR_Y = r_A \frac{\sigma_{AY}}{\sigma_{AX}} R_X \text{..........} \text{Equation 6}$$

Where, CR_Y = Correlated response on trait Y following selection for trait X;

r_A = genetic correlation;

σ_{AY} = additive genetic standard deviation for trait Y;

σ_{AX} = additive genetic standard deviation for trait X;

R_X = response to selection for trait X;

Use of index I in selection usually involves calculation of weighting factors **b** for traits to be used as selection criteria (equation 7).

$I = b' X$ ....Equation 7

Where:

I= Selection index;

b = n x 1 vector of weighting factors;

X = 1 x n vector of source of information, usually phenotypic measurements on candidate for selection or its relatives.

In the present study, information source (X) was individual own performance for immune response and body weight, and fullsib averages for egg production and related traits.

Based on the Yamada index, **b** in the present study was calculated as:

$b = (G' R)^{-1}Q$ ....Equation 8

Where:

G = n x m genetic variance-covariance matrix of the traits used as selection criteria and traits in the breeding objectives;

Q = m x 1 vector of intended genetic changes for m traits assigned by breeder;

R = n x n matrix of Wrights coefficient of relationship.

Desired genetic changes for various traits (i.e. **Q**) were calculated as the difference between desired and observed means (Yamada *et al.*, 1975; Kaushik and Khanna, 2003; Suzuki *et al.*, 2005). Furthermore, based on Yamada index, expected genetic gains per generations in all k traits under study (i.e. direct and correlated responses) including m traits in the breeding objectives were calculated using equation 9.

$$\Delta G^{*\prime} = \frac{i_I}{\sigma_I} . b'RG^{*} \quad \text{..........Equation 9}$$

Where:

i_I = intensity of selection based on the index;

σ_I = standard deviation of the index calculated as shown in equation 10;

ΔG^* = k x 1 vector of genetic gains per generation in k traits:

G^* = n x k genetic variance-covariance matrix.

$$\sigma_I = \sqrt{(b' P b)} \quad \text{..........Equation 10}$$

Where **P** is an n x n phenotypic variance-covariance matrix.

The number of generations q required to attain the pre-defined breeding objectives was calculated using equation 11 (Yamada *et al.*, 1975; Kaushik and Khanna, 2003). All matrix equations were solved using Interactive Matrix Language (IML) procedures of SAS (2000).

$$q = \frac{\sigma_I}{i_I} = \frac{\sqrt{(b' P b)}}{i_I} \quad \text{..........Equation 11}$$

3.4.2 Population structure and selection intensities

Specification of a population structure is an important step in simulation of breeding programs through selection (Pakdel, 2004; Zerehdaran *et al.*, 2005b). This helps on decisions about selection intensities to be used. Therefore this section presents population structures and selection intensities assumed during simulation on the two management systems.

3.4.2.1 On-station

In simulating genetic improvement through selection under intensive management, in the present work it was assumed that in each generation 40 best males are randomly mated to 240 best females with a mating ratio of one male to six females. Number of progeny per dam obtained in the current experiment under intensive management was around 4 and 5 for *Kuchi* and *Medium* ecotypes, respectively. However, the average number of progeny per dam could be increased by increasing the number of hatches, and improving hatchability (i.e. current hatchability of fertile eggs for the parent stock was 63% for *Kuchi* and 66% for *Medium* ecotypes) by improving egg storage conditions before hatching (Abdou *et al.*, 1990; Ruiz and Lunam, 2002). Furthermore, since the parent stock collected from field consisted of mature birds, in which some of them were likely to be too old for good laying performance, hence the average laying rate for these parent stock were low (around 35%) compared to that of around 50% obtained in the current study for their offspring, in which all of them were young (i.e. in their early period of laying). Hence by involving young mature breeding females in the breeding program as would be the case in the current simulation work, it would more likely result into increased number of progeny per dam. Moreover, since hatchability under artificial incubation is known to be negatively affected by the age of the dam (Tona *et al.*, 2001), therefore by involving relatively young mature hens as breeding females, would result into increased hatchability and hence the number of offspring per dam.

Based on the above facts, in the current simulation it was assumed that on average each female produces 10 progeny, with 5 chicks of each sex (i.e. in total there would be 2400 chicks). Taking into account mortality/loss of about 10% by the time birds are selected and mated, then the total number of birds available for selection would be 2400 – (2400 x 0.10) = 2160 (i.e. 1080 birds for each sex). Therefore, by selecting around 40 best males and 240 best females in each generation would lead to the proportion selected of about 3.7 and 22.2 % for males and females, respectively (i.e. average selection intensity of 1.78). Proportions selected (%) were transformed into selection intensity (i) using a Table by Falconer and Mackay, (1996). This average selection intensity is within the range of that of around 1.5 to 2 mostly used in commercial chicken breeding (Ameli, 1991; Su *et al.*, 1997).

3.4.2.2 On-farm

In simulating selection under this management system it was assumed that 100 farmers (households) are involved in the program, and each household keeps 2 to 3 breeding females. Furthermore, it was assumed that, in total in each generation 40 best males and 240 best females are selected, and each cock saves 2-3 households (i.e. a mating ratio of one male to 4 to 9 females). In the current study the average number of progeny per dam obtained under field condition was around 6. Therefore, 240 hens are expected to produce 1440 progeny in total with 720 birds of each sex. Taking into account the mortality rate/loss of about 33% by the time birds are selected and mated (i.e. average loss of 2 chicks per hen), then the number of birds available for selection would be 240 x 4 = 960 (i.e. 480 chicks of each sex). The chosen percent mortality/loss was based on the obtained percent mortality/loss up to 12 weeks of age of about 30% under the settings of the current study under field conditions, and further assuming that once a chick reachies the age of 12 weeks stands a high chance to survive to maturity and breed when regular control of outbreak of major diseases under field conditions specifically Newcastle disease are in place. Therefore, after accounting for mortalities/loss, selection of 40 best cocks and 240 best females in each generation would result into proportions selected of about 8.3% and 50% for males and female, respectively (i.e.

average selection intensity of 1.35). Proportions selected (%) were transformed into selection intensity (i) using a Table by Falconer and Mackay, (1996).

3.5 Study III

This study involved evaluation of the association of LEI0258 microsatellite alleles (a microsatellite located within MHC B region) with antibody response (humoral immune response) and productivity in the two chicken ecotypes studied. Although all chicks were assessed for primary antibody response against Newcastle disease virus vaccine, this experiment used samples from 85 and 88 individuals randomly picked from five batches/hatches on station for *Kuchi* and *Medium* ecotypes, respectively.

3.5.1 DNA isolation and MHC haplotyping

For each chicken, DNA was isolated from 200µl packed cells from EDTA- stabilized blood using a salt protocol, as described by Juul-Madsen *et al.* (1993). The MHC haplotypes were determined by PCR-based genotyping of the LEI0258 microsatellite locus (Dalgaard *et al.*, 2005; Lima-Rosa *et al.*, 2005; Fulton *et al.*, 2006; Schou *et al.*, 2006). The PCR amplification from genomic DNA was carried out in 25µl reaction volumes using standard buffer (Amersham) containing 0.05µM of each primer (the forward primer having been labelled with fluorescein). 0.4 mM of each dNTP. 1.5mM $MgCl_2$ and 1unit of *Taq* DNA polymerase (Amersham). After an initial 5 min of denaturation at 94 °C, the amplication went through 25 cycles of denaturation at 94 °C for 1 min, annealing at 56 °C for 1min and extension at 72 °C for 2 min. The amplification was completed with a final extension for 10 min at 72 °C. The amplicons were measured by electrophoresis on a denaturing polyacrylamide gel in an ALF DNA sequencer® (Amersham) to detect allelic polymorphism. A mixture of 10 fluorescein-labelled fragments of 50-500 bp (Amersham) was used as a size marker. Furthermore, DNA samples from three well-characterised lines of White Leghorn homozygous for the MHC haplotypes B13, B19 and B21 (Miller *et al.*, 2004) were included on a gel as control samples. The different MHC haplotypes were finally classified according to the repeat motif of the LEI0258 microsatellite (Fulton *et al.*, 2006).

3.5.2 Statistical analyses

Since the distribution of different alleles were almost similar in the two ecotypes, the data for the two ecotypes were pooled together, and six most frequent alleles in both ecotype (i.e. 205, 215,234, 307, 321, and 345 bp size alleles) were chosen for the association study.

The traits considered were primary antibody response against NDV vaccination, and body weight at 16 weeks of age. Egg production and related traits were not included in the association analysis as there were very few observations per allele for statistical analyses in nearly all the alleles considered. For each band (allele), all individuals were scored as a carrier (1) or non carrier (0) of the allele. Then single band analysis was carried out to determine the association of each band with the traits considered by regression analysis using REG procedures of SAS (2000). In this analysis it was assumed that the mode of gene action for these alleles is complete dominance (Schou *et al.*, 2006). Furthermore, before analysis data were adjusted for the fixed effects of ecotype, sex and hatch using GLM procedures of SAS (2000).

CHAPTER FOUR

4.0 RESULTS AND DISCUSSION

4.1 Body weights and feed utilization efficiency

4.1.1 Body weights at various ages

Least squares analyses of variances for body weights at various ages are presented in Appendix 1 and 2. Least square means along with their standard errors are presented in Table 4.1 and 4.2. Results from analyses of variances indicate that there was a significant effect of hatch, sex and ecotype on body weights under intensive management ($P<0.001$). Futhermore, most of the interactions between these main effects were not significant ($P> 0.05$).

Regarding body weights under extensive management system, as with body weights under intensive management, results for analyses of variances indicate that body weights under extensive management were also significantly influenced by ecotype and sex ($P< 0.001$). In addition, effect of farm and hatching month were also significant ($P<0.01$). Effect of village and various interactions included in the statistical models were not significant ($P> 0.05$).

Table 4.1 **Body weights under intensive management (on-station) summarized by sex and ecotype**

Sex	Trait	*Kuchi*			*Medium*		
		N	Lsmeans ± s.e	Range	N	Lsmeans ± s.e	Range
M	Bwt8 (g)	279	540.7 ± 3.20	280-748	368	457.4 ± 2.33	231-615
	Bwt12 (g)	278	1025.6± 5.80	701-1460	365	845.5 ± 4.51	586-1175
	Bwt16 (g)	274	1448.5± 6.10	1035-2060	360	1240.2 ± 4.90	991-1720
	Bwt20 (g)	270	1706.2± 6.87	1295-2318	360	1512.0±6.10	1186-2040
F	Bwt8 (g)	317	438.4 ± 2.50	242-662	395	350.1 ± 1.85	202-545
	Bwt12 (g)	315	883.2 ± 5.56	655-1316	393	705.6 ± 3.53	478-1013
	Bwt16 (g)	312	1339.2 ± 5.92	1048-1804	391	1124.9± 4.26	836-1634
	Bwt20 (g)	310	1586.8 ± 6.21	1296-2053	388	1382.1± 4.57	1070-1906
M+F	Bwt8 (g)	596	489.6 ± 2.28	242-748	763	403.7 ± 1.67	202-615
	Bwt12 (g)	593	954.4 ± 4.14	655-1460	758	775.6 ± 3.20	478-1175
	Bwt16 (g)	586	1393.9 ± 4.52	1035-2060	751	1182.5 ± 3.54	836-1720
	Bwt20 (g)	580	1646.5 ± 4.87	1295-2318	748	1447.1 ± 4.36	1070-2040

M, F and M+F= Males, females and both males and females, respectively; Bwt8, Bwt12, Bwt16, and Bwt20 = Body weights at 8, 12, 16, and 20 weeks of age, respectively.

Table 4.2 Body weights under extensive management (on-farm) summarized by sex and ecotype

Sex	Traits	*Kuchi*			*Medium*		
		N	Lsmeans ± s.e	Range	N	Lsmeans ± s.e	Range
M	Bwt8 (g)	201	374.9±3.94	190-518	248	305.0±3.01	178-421
	Bwt12 (g)	195	739.1±7.36	470-987	238	630.1±5.84	450-864
	Bwt16 (g)	190	1023.5±9.40	735-1329	230	897.2±7.40	752-1253
	Bwt20 (g)	186	1240.2±10.24	902-1567	215	1097.5±9.36	858-1419
F	Bwt8 (g)	203	320.1±3.50	180-509	266	240.9±2.40	171-407
	Bwt12 (g)	197	631.7±7.23	454-920	254	531.0±4.71	425-831
	Bwt16 (g)	192	924.5±8.31	731-1281	244	793.60±6.04	697-1226
	Bwt20 (g)	187	1135.2±9.60	870-1470	223	994.10±8.04	817-1406
M+F	Bwt8 (g)	404	347.5±2.84	180-518	514	273.0±1.98	171-421
	Bwt12 (g)	392	685.4±5.34	454-987	492	580.5±3.71	425-864
	Bwt16 (g)	382	974.0±6.40	731-1329	474	845.4±5.23	697-1253
	Bwt20 (g)	373	1187.7±7.28	870-1567	438	1045.8±6.75	817-1419

M, F and M+F= Males, females and both males and females, respectively; Bwt8, Bwt12, Bwt16, and Bwt20= Body weights at 8, 12, 16, and 20 weeks of age, respectively.

The results show that males were heavier than females in all body weight measurements under both management systems (Table 4.1 and 4.2). This was not unexpected as sexual dimorphism in body weight and growth traits in avian species is well known (Larzul *et al.*, 2000; Vali *et al.*, 2005). Results further show that *Kuchi* was heavier than *Medium* ecotype under both management systems. Average body weights over both sexes under intensive management for *Kuchi* and *Medium* ecotypes were 490 and 404g; 954 and 776g; 1394 and 1183g; 1647 and 1447g, for body weights at 8, 12, 16 and 20 weeks of age, respectively. The corresponding values under extensive management were 348 and 273g; 685 and 581g; 974 and 845g; 1188 and 1046g, respectively, meaning that body weights for *Medium* ecotype were 80 to 89 percent of that of *Kuchi* under both management systems, and there was a significant reduction (of 24 to 27 percent) in body weights in both ecotypes under extensive management system. Low body weights under extensive management could be attributed to hash environment (i.e. feed shortages, high prevalence of diseases and parasites) that is usually prevailing under such system (Magwisha *et al.*, 2002; Horning *et al.*, 2003; Rosa dos Anjos, 2005).

The superiority of *Kuchi* over *Medium* ecotype in terms of body weight demonstrated in the present study supports the results of previous study by Lawrence (1998) done in random samples of mature birds from villages, in which mean mature body weights for *Kuchi* and *Medium* ecotypes were reported to be 2708 and 1850g for males, and 1828 and 1108g for females, respectively. Furthermore, comparing results of the present study and previous reports in literature, average body weight at 8 weeks of age age for *Kuchi* (490g) and *Medium* ecotype (404g) are higher than the values below 400g repoted by local chickens of Nigeria and Ethiopia (Adedokun and Sonaiya, 2001; Demeke, 2003; Fayeye *et al.*, 2005), but lower than that of 600g reported for local chickens of Mexico (Segura-Correa *et al.*, 2004).

Concerning average body weight at 12 weeks of age under intensive management, the estimates for *Kuchi* obtained in the present study (954g) over both sexes is close to the average weight of 973g by Engku and Noraziah cited by Ramlah (1996) in Malaysian local chickens, but higher than the reported figures of 775g (Manjeli *et al.*, 2003), 600g (Nwosu *et al.*, 1984; Adedokun and Sonaiya, 2001), and 375 to 510g (Tadelle *et al.*, 2003a) for local chickens of Cameroon, Nigeria, and Ethiopia, respectively. In contrast, the current average weight of 776g for *Medium* ecotype is in the middle of the above given range from the literature. Regarding average body weight at 16 weeks of age under intensive management, the current figures for *Kuchi* and *Medium* ecotypes of 1394 and 1183g, respectively averaged over both sexes are higher than the mean weight of 802g (Nwosu *et al.*, 1984) obtained for local chickens of Nigeria. On the other hand, while the average value for *Medium* ecotype is at lower end of the range (1136 to 1520g) reported for local chickens Thailand, Malaysia and South Africa (Ramlah, 1996; Theerachai *et al.*, 2003; ARC, 2005), the average value for *Kuchi* is at middle of this range.

Concerning body weight at 20 weeks of age under intensive management, lower value (1000g and below) than those obtained in both ecoypes in the current study was reported for Nigerian local chickens (Nwosu *et al.*, 1984; Adedokun and Sonaiya, 2001). In constrast, in a study by ARC (2005) in some strains of South Africa local chickens, the values ranging from 1600 to 2000g averaged over both sexes, which are in close agreement with the results of the present study for *Kuchi* were reported for average body weight at 20 weeks of age. Furthermore, in line with the results of the present study for *Medium* ecotype, average body weight at 20 weeks of age under intensive management varying from 1300 to 1500g were reported for Vietnamese local chickens (FAO, 2005).

As with intensive management, significant number of studies have also reported the performance of local chicken under extensive management. With regard to average body weight at 8 weeks of age over both sexes, Pedersen (2002) and Sandra (2005) working independently both reported the value of 250g for Zimbabwean and Malawian local chickens, respectively, which are generally close to the current findings for *Medium* ecotype (273g) but lower than the value obtained for *Kuchi* (348g). However, the current value for *Kuchi* is comparable to the results by Ramlah and Shukor (1987) for Malaysian local chickens under village conditions.

Concerning measurement of body weights at later ages under extensive management, apart from mature body weight, relatively few studies have reported average body weights at more than 8 weeks of age for local chickens. Average body weights at 12 weeks of age regardless of sex were reported to be 631 and 640g, for Burkina Faso (Sall, 1990 cited by Sonaiya and Swan, 2004) and Zimbabwean local chickens (Pedersen, 2002), respectively. These values are in between the weights for *Kuchi* (685g) and *Medium* (581g) ecotypes obtained in the present study. On the other hand, the weights obtained by Sall (1990) cited by Sonaiya and Swan (2004) (860g), and Pedersen (2002) (1000g) for body weight at 16 weeks of age were much close to corresponding weight for *Medium* (845g) ecotype and *Kuchi* (974g), respectively.

Regarding average body weight at 20 weeks of age, the values of 1300g (Ramlha and Shukor, 1987) for Malaysian, and 1000g (Pedersen, 2002) for Zimbabwean local chickens under extensive management tend to concur with the current findings for *Kuchi* (1188g) and *Medium* (1046g) ecotypes respectively.

In general, although *Kuchi* had higher body weights than *Medium* ecotype, the results obtained in the present study for both ecotypes are not far from those reported in literature. As with other local chickens in other developing countries both ecotypes still had poor growth rate when compared to the improved stocks. It can be seen from the current results that, on average, substantial body weight that can be marketed i.e. body weight of 1kg and above (Pedersen, 2002; Theerachai *et al.*, 2003; Acamovic *et al.*, 2005) in both ecotypes and sexes were attained at about 16 and 20 weeks of age under intensive and extensive management systems, respectively. This imply that market weight in the studied local chicken populations is attained at a rather late ages compared to 8 weeks of age for meat type chickens, and 12 weeks for the crosses between local chickens and meat type chickens (Ali *et al.*, 2000; Pedersen, 2002; Theerachai *et al.*, 2003) under intensive management. Marketable body weight for these ecotypes could probably be further improved to enhance market value, or let them to be attained at earlier age following genetic improvement through selection. However this will depend on the existence of substantial additive genetic variation in these populations with regard to body weight. As *Kuchi* already had higher body weight compared to *Medium* ecotype, to start with *Kuchi* could be a good avian genetic resource to start with.

4.1.2 Feed utilization efficiency

Feed intake and feed utilization efficiency were evaluated under intensive management. These traits were only recorded in chicks from batch No.6 from 5th to 12th weeks of age. Results from Table 4.3 and analyses of variance in Appendix 3 indicate that *Kuchi* had unfavourably higher (by 4.2%) but non significant (P>0.05) feed intake compared to

Medium ecotype, but had significantly higher body weight gain (P< 0.01) and feed utilization efficiency (P< 0.05) (i.e.FCR for *Kuchi* was 5.6 vs 6.3 for *Medium* ecotype). Similar results apply to males when compared to females. Differences between ecotypes in feed utilization efficiency were also reported in Ethiopian local chickens by Tadelle *et al.* (2003a). In general, the current findings on feed utilization efficiency in both ecotypes were poor and consistent with the range reported in literature for local chickens indicating that the birds were not selected for meat production (Pedersen, 2002; Demeke, 2003; Tadelle *et al.*, 2003a). Since growth performance and body weight are in most cases usually favourably correlated with feed utilization efficiency (Siegel and Wolford, 2003; Zhang and Aggrey, 2003; N'dri *et al.*, 2006), selection for improved body weight would ultimately result into improved feed utilization efficiency.

Table 4.3 Feed utilization efficiency and related parameters summarized by genotype and sex for the period from 5 to 12 weeks of age (Lsmeans±s.e)

Genotype	Sex	IPB (g)	GPB (g)	FCR
Kuchi	Male	2659.0 ± 35.6	507.5± 5.8	5.3 ± 0.12
	Female	2620.0 ± 35.6	444.0± 5.8	5.9 ± 0.12
	Both	2639.5 ± 25.2	475.8± 4.1	5.6 ± 0.09
Medium	Male	2577.0 ± 35.6	422.5± 5.8	6.1 ± 0.12
	Female	2487.5 ± 35.6	385.5± 5.8	6.4 ± 0.12
	Both	2532.3 ± 25.2	404.0± 4.1	6.3 ± 0.09

IPB = Feed intake per bird, GPB = Gain per bird and FCR = Feed conversion ratio

4.2 Egg production and related traits

Analyses of variance for egg production and related traits are presented in Appendix 4. Table 4.4 shows the average performance for egg production traits in each of the two ecotypes. Results from analysis of variance indicate the existence of significant differences between ecotypes with respect to age at sexual maturity (P< 0.01), egg number ($P<0.05$), and egg weight ($P<0.01$). Differences between ecotypes with regard to shell thickness and egg shape index were not significant ($P>0.05$). The effect of hatch only affected ($P<0.05$) egg shape index.

Table 4.4 Egg production and related traits (Lsmeans ± s.e) summarized by ecotype

Genotype	Trait	Lsmeans ± s.e	Minimum	Maximum
Kuchi	**Age at sexual Maturity (N= 300)**			
	Age at first egg (Days)	173.2 ± 0.80	142	236
	Egg number and egg quality (N= 296)			
	Egg Number (90-Days)	44.5 ± 0.46	23	78
	Egg weight (g)	45.0 ± 0.24	35	54
	Shell thickeness (µ)	37.3 ± 0.18	30	55
	Egg shape index (%)	74.8 ± 0.25	68	86
Medium	**Age at sexual maturity (N = 381)**			
	Age at first egg (Days)	167.92 ± 0.74	145	232
	Egg number and egg quality (N= 373)			
	Egg Number (90-Days)	48.9 ± 0.48	31	77
	Egg weight (g)	42.4 ± 0.18	34	53
	Shell thickeness (µ)	37.3 ± 0.20	32	54
	Egg shape index (%)	74.1 ± 0.29	65	85

Medium ecotype tended to attain sexual maturity relatively earlier by 5 days than *Kuchi* (173 days vs 168 days), however, findings from both ecotypes are still within the range of 153 to 203 days reported in literature for unimproved local chickens in other countries (Sah *et al.*, 1985; Demeke, 2004). Despite the fact that *Medium* ecotype matured earlier than *Kuchi*, its average egg weight was noticeably lower than that of *Kuchi* (42g vs 45g) (Table 4.4). Compared to the previous studies, the value obtained in

Medium ecotype for egg weight is very close to those of 40g given by Fayeye *et al.* (2005), Pedersen (2002), and Islam *et al.* (2001) for local chickens of Nigeria, Zimbabwe and Bangladesh, respectively. Furthermore, the results coincide with the values by Msoffe (2003) for some of the chicken ecotypes in Tanzania including *Medium*, but lower than the average weight of 49g obtained by Chen *et al.* (1993) in Taiwan local chickens. On the other hand, the average egg weight for *Kuchi* of 45g obtained in the present study falls in the middle of the range reported in these previous studies.

Although by small margin, the average egg number in the first 90-days of laying was significantly higher in *Medium* ecotype than in *Kuchi* (49 vs 45). These figures correspond to laying intensities of 54% and 50% for *Medium* ecotype and *Kuchi*, respectively. Katule and Mgheni (1990) and Khalil *et al.* (2004) working with a mixture of some chicken ecotypes of Tanzania, and Saudi Arabia local chickens, respectively both reported egg number in an early period of laying that corresponds to a laying intensity of 58%, which are substantially higher than the current values. However, the current values in both ecotypes are within the range of 40 to 55% derived for local chickens of Sudan (Mohammed *et al.*, 2005), Nigeria (Adedokun and Sonaiya, 2001), and Thailand (Choprakarn *et al.*, 1998), but appreciably higher than the values of 36% derived from the studies by Pedersen (2002) and Demeke (2003), in Zimbabwean and Ethiopian local chickens, respectively.

With regard to eggshell thickness and egg shape index, as stated earlier, analyses of variances revealed no significant differences between ecotypes. The average egg shape indices for *Kuchi* and *Medium* ecotype were 75 and 74%, respectively. The estimates are within the range of 72 to 80% reported by Njenga (2005) for some Kenyan chicken ecotypes, and Khan *et al.* (2004) for crosses between Bangladesh local chickens and RIR and *Fayoumi*, but higher than the value of 58% given by Fayeye *et al.* (2005) for Nigerian local chickens.

Average shell thickness in both ecotypes in this study was approximately 37 μ. The value is on the upper side of the range (34 to 37 μ) reported for Sudanese local chickens (Arad and Malder, 1982; Mohammed *et al.*, 2005), and very close to the value of 38 μ presented by Chen *et al.* (1993) in Taiwan local chickens, but lower than the value of 58 μ obtained for Fulani local chickens in Nigeria by Fayeye *et al.* (2005).

In general, results for egg production and related traits obtained in the present study were in agreement with most of the values reported in literature for unimproved local chickens. Furthermore, as with other studies their laying performance and egg weight and age at sexual maturity were generally poor when compared to those reported for egg type chickens (laying rate of more than 60%, egg weight of around 50g and more, and age at sexual maturity of 126 to 154 days) (Katule and Mgheni, 1990; Pedersen, 2002; Anderson *et al.*, 2005). However, their average egg shape indices were not very different from those reported in egg type chickens (Chen *et al.*, 1993; Khatkar *et al.*, 1994; Anderson *et al.*, 2005). With regard to shell thickness, values both higher and lower than the current estimates in both ecotypes were reported in egg type chickens

(Brah *et al.*, 1991; Chen *et al.*, 1993; Anderson *et al.*, 2005). In addition, the values for average shell thickness and egg shape index obtained for both ecotypes in this study were also within the range recommended in literature by several authors (Smith, 2001; Eshwaraish, 1988 cited by Ali, 2002; Bao, 1978 cited by Khang and Ogle, 2004; Khan *et al.*, 2004; Mohammed *et al.*, 2005). Therefore, based on the results of the present study, as shell thickness and egg shape index were shown to be optimal, selection programmes geared at improving genetic potential for egg production and related traits in the studied ecotypes should be based on improving egg number, egg weight and age at sexual maturity. However, as with body weight, this will depends on the existence of substantial additive genetic variation for these traits in the two ecotypes for selection to be effective. Moreover, as *Medium* ecotype was somewhat superior to *Kuchi* with respect to these traits, this ecotype could be a good avian genetic resource to start with.

4.3 Antibody response (humoral immune response) and mortality rates

4.3.1 Primary antibody response against NDV vaccine

Least squares analyses of variances for primary antibody response against NDV vaccination for the studied chicken ecotypes are presented in Appendix 5. Least square means are shown in Table 4.5. Results from analysis of variance reveal that there was no significant difference between ecotypes and sexes with respect to antibody response (P>0.05) both under intensive and extensive management systems, suggesting no differences between the two ecotypes and sexes in relation to fitness against Newcastle disease. Furthermore, effect of all other main factors and interactions included in statistical model under intensive management were also not significant (P> 0.05).

Regarding other main factors and interactions included in statistical model under extensive management, most of them were not significant ($P > 0.05$).

Mean HI antibody titre ($\log_2$) under intensive management over both sexes in both ecotypes was 5.0. Moreover, it can be noted from Table 4.5 that mean antibody titres in both ecotypes under extensive management system were slightly lower than that from intensive management, to some extent reflecting stressful nature of extensive management to the wellbeing of chickens (Magwisha *et al.*, 2002; Hørning *et al.*, 2003; Otim, 2005; Rosa dos Anjos, 2005). Mean antibody titres over both sex in both ecotypes were 4.8. Although no article has been encountered reporting primary humoral immune response in chicks under extensive management, the values obtained in this study under both management systems and ecotypes are within the range reported by Msoffe (2003) under intensive management. In that study, as opposed to the results of the current study, differences between other chicken ecotypes found in Tanzania including *Medium ecotype* were found. Average HI antibody titres ($\log_2$) at the same period of assessment post vaccination were reported to range from 4.5 to 6. However, all the values for average antibody titres (HI $\log_2$) obtained in the present study were lower than that of 5.7 to 6 (HI $\log_2$) by Lwelamira and Katule (2004) in a mixture of different Tanzania chicken ecotypes and their reciprocal crosses with RIR, and the value of 7 (HI $\log_2$) derived from a study by Otim (2005) in Ugandan local chickens under intensive management. The observed differences could partly be attributed to differences in genotypes involved.

Table 4.5 Antibody titre (HI titre $\log_2$) against NDV vaccine in chicks summarized by management system, ecotype and sex

Management	Ecotype	Sex	N	Lsmeans±s.e
Intensive	*Kuchi*	Male	285	4.97±0.06
		Female	321	5.03±0.06
		Both	606	5.00±0.04
	Medium	Male	371	5.10±0.05
		Female	400	5.00±0.05
		Both	771	5.05±0.04
Extensive	*Kuchi*	Male	213	4.81±0.07
		Female	217	4.76±0.08
		Both	430	4.79±0.06
	Medium	Male	261	4.80±0.07
		Female	277	4.84±0.07
		Both	538	4.82±0.05

4.3.2 Mortalities

Results from Table 4.6 show that percent survivals up to 12 weeks of age were 91.9 and 70.2% for *Kuchi*, and 92.2 and 72.3% for *Medium* ecotype under intensive and extensive management systems, respectively. This corresponds to percent loss of about 8.1 and 29.1% for *Kuchi*, and 7.8 and 27.7% for *Medium* ecotype, respectively. Differences between ecotypes in both management systems were not significant (P> 0.05). Causes of chick loss under extensive management were mainly diseases (42%) and predators (33%), while under intensive management system, apart from diseases (36%), cannibalism mainly at the age of 4 weeks and above also contributed a significant loss of 29% (Fig. 2 and 3). Visible disease symptoms before chicks died under extensive management system were mainly swollen head, lesions in the head, diarrhoea (gastrointestinal problems), emaciation/weakening, and sometimes respiratory signs, while under intensive management it was mainly diarrhoea (gastrointestinal problems).

Futhermore, a few chicks from extensive management system were sampled for further laboratory analysis at SUA and some of them were found to have worms.

Compared to the previous studies, the percent loss/mortalities under intensive management are within the range (0 to 24%) reported in literature (Nwosu *et al.*, 1984; Pedersen, 2002; Demeke, 2003; Tadelle *et al.*, 2003a; Lwelamira and Katule, 2004). Regarding the values under extensive management, despite of the confinement of the chicks in the first ten days of their lives in the current experiment, percent loss/mortality rate were only reduced by a small margin when compared to some other previous studies. For example, mortality rate up to 12 weeks of age under extensive management without early confinement of birds were reported to be 45% for Zimbabwean local chickens (Pedersen, 2002), and 41% for Botswana local chicks (Mushi *et al.*, 2005) compared to the values close to 30% obtained in the current experiment under the same age. This could pose a threat to breeding programmes under extensive management. Hence, confinement of chicks for a bit longer period before being released to the field and regular disease control regimes seem to be required.

Table 4.6 Cumulative survival/ mortalities up to 12 weeks of age summarized by management system and ecotype

Management	Ecotype	N	No. Died/Lost	% Died/lost	No. Survived	% Survived	χ^2 - Value
Intensive	*Kuchi*	645	52	8.1	593	91.9	0.041^{NS}
	Medium	823	64	7.8	759	92.2	
Extensive	*Kuchi*	554	161	29.1	393	70.9	0.289^{NS}
	Medium	690	191	27.7	499	72.3	

NS= Non-sigificant (P> 0.05)

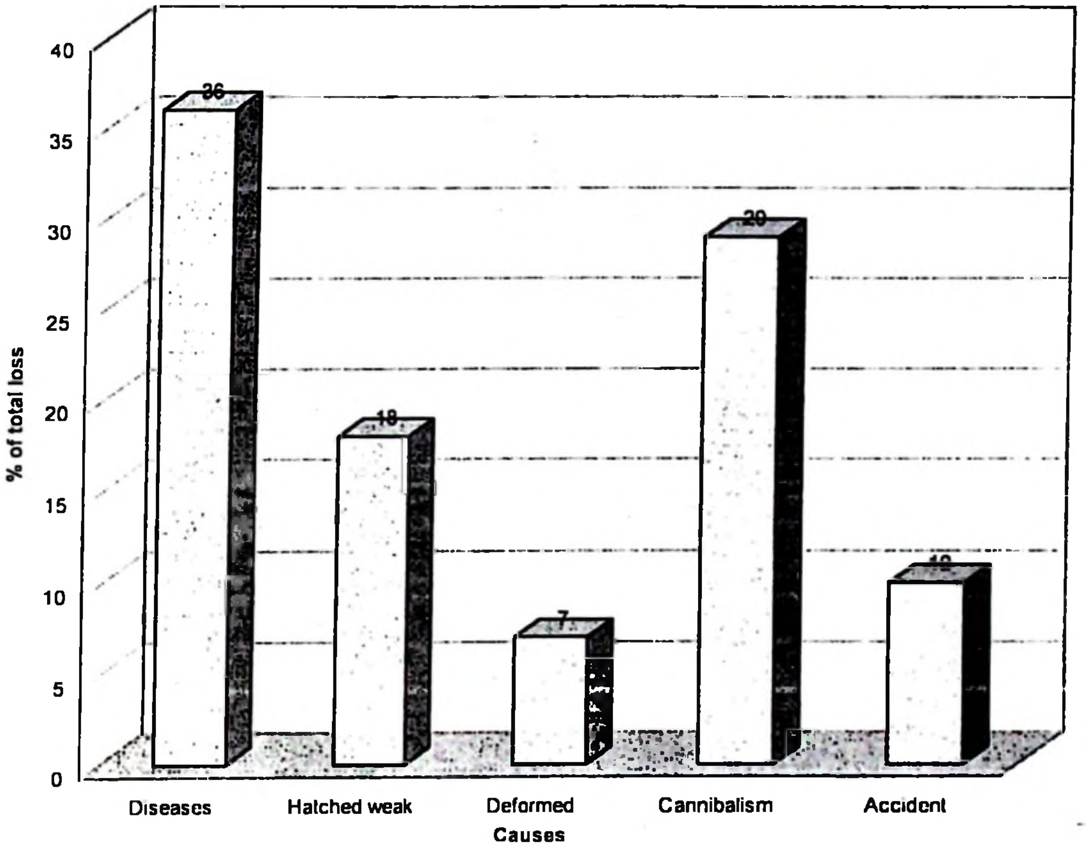


Figure 2. **Causes of chick loss under on-station management**

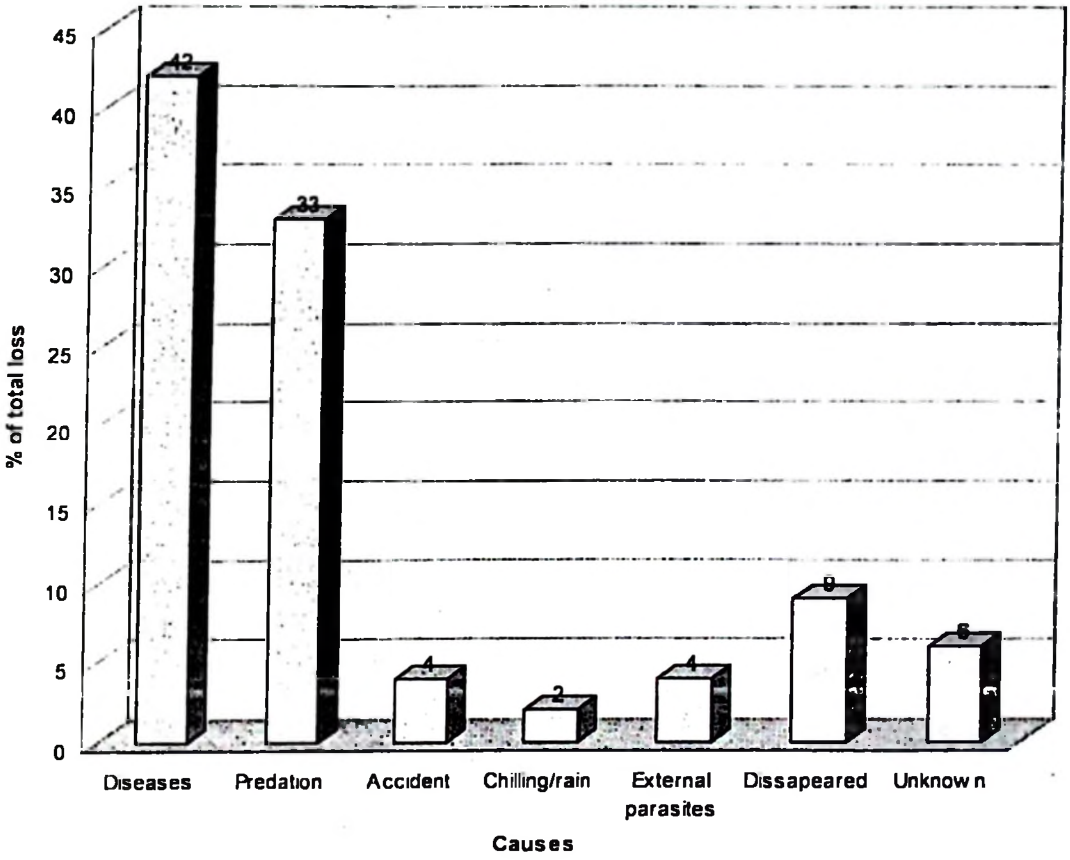


Figure 3. Causes of chick loss under on-farm management

4.4 Phenotypic and genetic parameters

4.4.1 Heritability estimates

Heritabilites for body weights at various ages, egg production and related traits, and primary antibody response against NDV vaccine were estimated in the present study. While heritabilities for body weights and primary antibody response against NDV vaccine were estimated both under intensive and extensive management, heritabilities for egg production and related traits were only estimated under intensive management.

4.4.1.1 Body weights

Results for heritability estimates based on paternal half sib correlation for body weights are presented in Table 4.7. In general, the results indicate that heritability estimates varying from moderate to moderately high were obtained for body weights in the present study with corresponding estimates between the two ecotypes being close to each other. Furthermore, these heritability values were also found to be significant (i.e values higher than twice their standard errors). The estimates under intensive management ranged from 0.38 to 0.45 and from 0.39 to 0.43, for *Kuchi* and *Medium* ecotype, respectively. The corresponding estimates in all body weights measurements under extensive management system were lower than those under intensive system, reflecting relatively high environmental influences under on farm conditions. The estimates under this management system varied from 0.30 to 0.39 and from 0.31 to 0.38 for *Kuchi* and *Medium* ecotypes, respectively. Relatively high environmental influences on the performance of an individual under extensive management were also reported in previous studies in cattle (Bosso, 2005), and sheep (Roden *et al.*, 2003).

Table 4.7 Heritability estimates (± s.e) for various body weights computed for each ecotype in the two management systems

Management	Trait	*Kuchi*	*Medium*
Intensive	Bwt8	0.38 ± 0.10	0.39 ± 0.09
	Bwt12	0.41 ± 0.07	0.43 ± 0.10
	Bwt16	0.44 ± 0.08	0.42 ± 0.08
	Bwt20	0.45 ± 0.09	0.43 ± 0.07
Extensive	Bwt8	0.30 ± 0.13	0.31 ± 0.12
	Bwt12	0.34 ± 0.12	0.36 ± 0.14
	Bwt16	0.37 ± 0.11	0.35 ± 0.10
	Bwt20	0.39 ± 0.12	0.38 ± 0.11

Although heritability estimates under extensive management were relatively low, the magnitude of the estimates obtained in both management systems and ecotypes shows that there is a substantial additive genetic variation for the traits to respond adequately upon selection under both management systems. However, according to Falconer and Mckay (1996), selection based on individual own performance (mass selection) is expected to be a bit more efficient under intensive management compared to extensive management. Furthermore, based on similar argument, as heritability estimates obtained between the two ecotypes were almost similar, no differences are expected between ecotypes.

Results from the current study also revealed somewhat generally higher heritability estimates in later than early ages particularly in *Kuchi* (Table 4.7), suggesting mass selection could be a bit more efficient in later ages compared to early ages. This could be attributed to higher environmental influences in early ages such as maternal effects compared to later ages. This observation supports earlier findings by Manjeli *et al.* (2003) in Cameroon local chickens, Resende *et al.* (2005) in Japanese quail, Shadap *et al.* (1990) and Brah *et al.* (1991) in White Leghorn strains and Amer (1964) in Fayoumi. However, the results contradict the report by Asuquo and Nwosu (1987) in Nigerian local chickens, Sivaraman *et al.* (2005) in broilers, and Aggrey and Cheng (1994) in Japanese quail in which no clear trends were observed.

Although no report has so far been encountered in literature reporting heritability estimates for body weights under extensive management conditions, however, most of the estimates obtained in the present study in the two ecotypes which vary from 0.38 to 0.45 under intensive management, and from 0.30 to 0.39 under extensive management are within the ranges described in literature under intensive management. The estimates are in the middle of the range (0.30 to 0.63) of paternal halfsib estimates reported for local chickens of Nigeria, Cameroon and dual-purpose breeds of China between 6 to 20 weeks of age (Asuquo and Nwosu, 1987; Jiang and Groen, 2000; Manjeli *et al.*, 2003), and that of 0.43 to 0.80 (most estimates under intensive management) for broilers (Jaap *et al.*, 1962; Sivaraman *et al.*, 2005). The results also concur with range of animal model of linear mixed models procedures estimates of 0.30 to 0.59 for juvenile body weight reported in broilers (Beaumont *et al.*, 1998; van Kaam *et al.*, 1999; Zerehdaran *et al.*, 2004), and that of 0.22 to 0.40 for juvenile body weight in one of the South African local chicken (*Venda strain*) (Norris and Ngambi, 2006).

4.4.1.2 Egg production and related traits

(i) Egg number

Heritabilities for age at sexual maturity, egg number, egg weight, shell thickness, and egg shape index estimated from paternal halfsib correlations among the two local chicken ecotypes under intensive management are presented in Table 4.8. Results indicate that all heritability values for egg production and related traits obtained in the present study to be significantly different from zero (i.e. estimates were higher than twice their standard errors). Results from Table 4.8 also indicate that moderate heritability estimates were obtained in the present study for egg number with the estimates being around 0.30 in both ecotypes, indicating the possibility of improving the trait in both ecotypes through selection.

Table 4.8 Heritability estimates for egg production and related traits calculated for each ecotype

Trait	*Kuchi*	*Medium*
AFE	0.42 ± 0.10	0.52± 0.11
EN-90	0.31 ± 0.05	0.32 ± 0.06
EW	0.43 ± 0.08	0.50 ± 0.07
STH	0.53 ± 0.11	0.61 ± 0.13
ESI	0.48 ± 0.13	0.52 ± 0.10

AFE= Age at first egg, EN-90= Egg number in the first 90 days after sexual maturity, EW= Egg weight, STH= Shell thickness, ESI= Egg shape index

As with other egg traits, most of the heritability estimates for egg number reported in literature are from egg type chickens i.e. White Leghorn. However the estimates obtained in the present study are in good agreement with a number of studies. Computed from paternal halfsib correlations, heritability of similar magnitude were reported in egg type chickens by Sabri *et al.* (1999) (0.27), Akbaş *et al.* (2002) (0.31), and Liljedahl and Weyde (1980) (0.30). Several workers also estimated heritabilities for egg production and related traits using animal model of mixed models procedures. In some of these studies heritability estimates of 0.29 (Hagger. 1994) and 0.31 to 0.33 (Morris. 2005) in egg type chickens; and 0.24 to 0.36 (Sang *et al.*, 2006) in Korean local chickens, which are generally consistent with the present estimates were reported.

(ii) Age at sexual maturity

Results from present study indicate that heritability estimates for age at sexual maturity for *Kuchi* and *Medium* ecotypes were 0.42 and 0.52, respectively, suggesting the trait in both ecotypes to be moderately highly heritable, hence good scope for improving it in both ecotypes through selection. Apart from being relatively highly heritable compared to egg number, results also show that there was a notable difference between ecotypes in favour of *Medium* ecotype. This implies that there is a relatively higher additive genetic variation in *Medium* ecotype compared to *Kuchi* for this trait, hence relatively high potential for response to mass selection (Falconer and McKay, 1996).

The heritability estimate for *Kuchi* falls in the middle of range of values reported in literature of 0.37 to 0.50 estimated from paternal half sib analysis in egg type chickens (Kolstad, 1980; Sorensen *et al.*, 1980; Shadap *et al.*, 1990; Brah *et al.*, 1991). In constrast, the estimate for *Medium* ecotypes is at the high end of the range reported by Nurgiartiningsih *et al.* (2002) (0.39 to 0.54) in egg type chickens. In addition, heritability estimates for egg weight in *Kuchi* obtained in the current study is also consistent with those of Singh *et al.* (1988) (0.41), and the range reported by Khatkar *et al.* (1994) (0.27 to 0.43) in egg type chickens estimated from paternal halfsib analyses. On the other hand, the estimate for *Medium* ecotype also agrees closely with the values in egg type chickens of 0.52 by Dunn *et al.* (2005) and the range of 0.47 to 0.52 by Wei and van der Werf (1993) from paternal halfsib analyses.

Regarding other egg quality traits studied, heritabilities for shell thickness (0.53; 0.61) and egg shape index (0.48; 0.52) obtained in the present study, for *Kuchi* and *Medium* ecotypes, respectively, tend to fall in the upper ends of the range published in literature of 0.28 to 0.69 for shell thickness, and 0.23 to 0.57 for egg shape index (Mohapatra *et al.*, 1985; Mishra *et al.*, 1986; Poggenpoel, 1986; Brah *et al.*, 1991; Chen *et al.*, 1993; Maan *et al.*, 1983 cited by Chen *et al.*, 1993; Khatkar *et al.*, 1994; Nirasawa *et al.*, 1998; Dunn *et al.*, 2005; Zhang *et al.*, 2005). With regard eggshell thickness, the current estimates in both ecotypes are in accordance with the range of 0.36 to 0.69 given by Khatkar *et al.* (1994) in egg type chickens obtained from paternal halfsib correlations analyses. Regarding egg shape index, heritability estimates for this trait in both ecotypes agree with the range (0.37 to 0.57) reported by Brah *et al.* (1991) in egg type chickens also estimated from paternal halfsib correlation analyses.

4.4.1.3 Antibody response (humoral immune response) against NDV vaccine

Results for heritability estimates for primary antibody response against NDV vaccine in the two ecotypes are shown in Table 4.9. Moderate heritability estimates were obtained in each of the two ecotypes in both management systems. Results further show all the estimates were significant and the corresponding estimates in the two ecotypes were close to each other. Furthermore, the values under extensive management tended to be lower than those under intensive management. The estimates for *Kuchi* and *Medium* ecotypes under intensive management were 0.27 and 0.29, respectively, and the corresponding estimates under extensive management were 0.22 and 0.23. Moderate heritability estimates obtained in the present study with regard to this trait suggests that adequate additive genetic variation exist for the studied populations to be considered for selection.

Few studies have estimated genetic parameters for humoral immune response in local chickens. Furthermore, no reports were found in literature reporting primary humoral immune response against NDV vaccine in local chickens under extensive management. However, all estimates obtained in the present study are generally in good agreement with the estimates reported in literature by several authors in different breeds of poultry, and type of antigens under intensive management. The current estimates under intensive management (0.27 and 0.29) fall within the range of 0.27 to 0.39 by Lwelamira and Katule (2004), 0.25 to 0.41 by Soller *et al.* (1981), and 0.31 to 0.60 by Peleg *et al.* (1976) estimated from paternal halfsib analyses for humoral immune response against NDV vaccine in chickens. With the exception to the study by Lwelamira and Katule (2004), in which a mixture of different Tanzania chicken ecotypes and their reciprocal crosses with RIR were used, other studies used egg type chickens. In contrast, current estimates under extensive management (0.22 and 0.23) are slightly lower than the low ends of the above given ranges.

The current estimates in both management systems are also within the range of 0.00 to 0.34 reported in previous studies based on paternal halfsib analyses (Gyles *et al.*, 1986; Kim *et al.*, 1987; Kumar *et al.*, 2002; Sivaraman *et al.*, 2005), animal model of linear mixed models procedures estimates of 0.18 to 0.31 (Pinard *et al.*, 1992; Bovenhuis *et al.*, 2002) for humoral immune response against SRBC in exotic chickens.

Table 4.9 Heritability estimates for primary antibody response against NDV vaccine computed for each ecotype under the two management systems

	Ecotype	
Management system	*Kuchi*	*Medium*
Intensive	0.27 ± 0.06	0.29 ± 0.05
Extensive	0.22 ± 0.08	0.23 ± 0.08

4.4.2 Genetic and phenotypic correlations

In addition to heritabilities, other genetic and phenotypic parameters such as genetic (r_g) and phenotypic (r_p) correlations among various traits were also estimated. As with heritabilites, the estimates were done both on-station and on-farm (intensive and extensive management systems, respectively). Since egg production and related traits were not recorded under extensive management, again as with heritabilities, estimates of genetic and phenotypic correlations under extensive management involved only body weights and immune responses. Results for genetic and phenotypic correlations among various traits studied are given in Tables 4.10, 4.11 and 4.12.

Table 4.10 Genetic (above diagonal) and phenotypic (below diagonal) correlations for on-station *Kuchi* chickens

.	Ab	Bwt8	Bwt12	Bwt16	Bwt20	AFE	EN-90	EW	STH	ESI
Ab	.	-0.11	-0.09	-0.10	-0.07	-0.02	-0.04	-0.01	-0.04	0.10
Bwt8	-0.08	.	0.80	0.72	0.60	-0.15	-0.06	0.20	0.06	0.05
Bwt12	-0.05	0.68	.	0.78	0.69	-0.18	-0.13	0.25	-0.04	0.11
Bwt16	-0.04	0.65	0.68	.	0.93	-0.22	-0.18	0.22	-0.06	0.08
Bwt20	-0.07	0.54	0.60	0.74	.	-0.20	-0.23	0.34	-0.05	0.05
AFE	-0.03	-0.04	-0.14	-0.18	-0.16	.	-0.19	0.32	-0.01	0.10
EN-90	-0.02	-0.02	-0.10	-0.13	-0.18	-0.16	.	-0.19	-0.13	0.01
EW	-0.00	0.10	0.13	0.17	0.25	0.12	-0.13	.	-0.04	0.05
STH	0.05	0.09	-0.04	-0.07	-0.00	0.03	-0.17	-0.05	.	0.09
ESI	0.05	0.04	0.08	0.03	-0.01	0.11	0.04	0.08	0.08	.

Ab= Antibody response (humoral immune response) against NDV vaccine; Bwt8, Bwt12, Bwt16 and Bwt20= Body weight at 8, 12, 16 and 20 weeks of age, respectively; AFE= Age at first egg; EN-90 = Egg number in the first 90 days after sexual maturity, EW= Egg weight; STH= Shell thickness; ESI= Egg shape index.

Table 4.11 Genetic (above diagonal) and phenotypic (below diagonal) correlations for on-station *Medium* chickens

.	Ab	Bwt8	Bwt12	Bwt16	Bwt20	AFE	EN-90	EW	STH	ESI
Ab	.	-0.08	-0.10	-0.11	-0.07	-0.04	-0.04	-0.05	0.01	0.08
Bwt8	-0.05	.	0.90	0.83	0.66	-0.03	-0.11	0.13	0.03	0.05
Bwt12	-0.09	0.67	.	0.88	0.73	-0.12	-0.13	0.25	-0.07	0.02
Bwt16	-0.08	0.69	0.78	.	0.86	-0.21	-0.16	0.23	-0.04	-0.02
Bwt20	-0.07	0.64	0.69	0.76	.	-0.23	-0.21	0.30	-0.06	0.04
AFE	-0.03	0.03	-0.09	-0.13	-0.19	.	-0.15	0.22	0.02	0.06
EN-90	-0.04	-0.04	-0.11	-0.10	-0.12	-0.14	.	-0.14	-0.03	0.10
EW	-0.06	0.09	0.24	0.20	0.25	0.15	-0.11	.	-0.02	0.06
STH	-0.03	0.04	-0.06	-0.02	-0.07	-0.05	-0.04	0.02	.	0.03
ESI	0.04	-0.01	0.07	-0.00	0.03	0.02	0.08	0.10	0.05	.

Table 4.12 Genetic (above diagonal) and phenotypic (below diagonal) correlations for on-farm *Kuchi* and *Medium* chickens

Genotype		Ab	Bwt8	Bwt12	Bwt16	Bwt20
Kuchi	Ab	.	-0.09	-0.05	-0.06	-0.02
	Bwt8	-0.05	.	0.74	0.59	0.53
	Bwt12	-0.02	0.53	.	0.71	0.67
	Bwt16	-0.08	0.47	0.60	.	0.70
	Bwt20	-0.03	0.44	0.56	0.64	.
Medium	Ab	.	-0.08	-0.10	-0.04	-0.05
	Bwt8	-0.07	.	0.78	0.75	0.63
	Bwt12	-0.06	0.67	.	0.80	0.78
	Bwt16	-0.03	0.65	0.72	.	0.75
	Bwt20	-0.03	0.57	0.67	0.65	.

Ab= Antibody response (humoral immune response) against NDV vaccine; Bwt8, Bwt12, Bwt16 and Bwt20 = Body weight at 8, 12, 16 and 20 weeks of age, respectively

4.4.2.1 Correlations among body weights

Results show that the correlations among body weights were generally high and positive. The estimates for genetic correlations under intensive management varied from 0.60 to 0.93, and 0.66 to 0.90, for *Kuchi* and *Medium* ecotypes, respectively (Table 4.10 and 4.11), and their standard errors were calculated to vary from 0.15 to 0.20, and 0.17 to 0.24, respectively, indicating the estimates to be significantly different from zero. The corresponding phenotypic correlations varied from 0.54 to 0.74, and 0.64 to 0.78, respectively (Table 4.10 and 4.11), and their standard errors from 0.19 to 0.24, and 0.12 to 0.20, again indicating the estimates to be significantly different from zero. Although high, most estimates under extensive management were relatively lower compared to the corresponding estimates under intensive management. The genetic correlations ranged from 0.53 to 0.74; 0.63 to 0.80, and the phenotypic correlations from 0.44 to 0.64; 0.57 to 0.72, for *Kuchi* and *Medium* ecotypes, respectively. (Table 4.12). The corresponding standard errors of the estimates for genetic correlations were calculated to ranged from 0.18 to 0.22; 0.21 to 0.25, and for phenotypic correlations from 0.16 to 0.20; 0.19 to 0.22, for *Kuchi* and *Medium* ecotypes, respectively, implying the estimates to be significant. In addition, results further reveal that genetic correlations were higher than phenotypic correlations, and consistent with studies by Sivaranam *et al.* (2005) and Jaap *et al.* (1962). Results also indicate that correlations among adjacent weights generally tended to be relatively higher than distant weights, indicating adjacent body weights to be controlled by nearly the same set of genes and environmental conditions. Compared to the estimates from other studies reported in literature, the current estimates in both ecotypes agree with most of the previous reports in which values varying from 0.33 to unity were reported (Jaap *et al.*, 1962; Asuquo and Nwosu 1987; Lwelamira and Katule, 2004; Zerehdaran *et al.*, 2005a, 2004; Sivaranam *et al.*, 2005). High positive correlation among body weights obtained in the present study imply that selection for one body weight measurement could result into substantial correlated responses in the others.

4.4.2.2 Correlations among egg traits

(i) Egg number and egg weight

Results for genetic and phenotypic correlations among egg traits are presented in Tables 4.10 and 4.11. Results show that genetic and phenotypic correlations between egg number and egg weight obtained in present study in both ecotypes were unfavourable but low. Estimated genetic and phenotypic correlations between egg number and egg weight in *Kuchi* were -0.19 and -0.13, respectively, and corresponding estimates in *Medium* ecotype were -0.14 and -0.11. Calculated standard errors for the respective correlations were 0.06 and 0.04; 0.04 and 0.03, for *Kuchi* and *Medium* ecotypes, respectively, showing that the obtained correlations were significantly different from zero. The magnitude and direction of correlations obtained in the present study between these traits indicate moderately low antagonistic genetic relationship exists between egg number and egg weight in both ecotypes.

Compared to previous studies, the estimates in both ecotypes are generally within the range reported by Ahmad *et al.* (1993) (r_g = -0.107 to -0.49) and Sørensen *et al.* (1980) (r_g = -0.17 to -0.32; r_p = -0.11 to -0.12), and Brah *et al.* (1991) (r_g = -0.13 to 0.34, r_p = -0.14 to -0.15), in egg type chickens; and the estimates by Luo *et al.* (1991) cited by Jiang and Groen (2000) (r_g = -0.01 to -0.46) in Chinese local chickens, but lower than the estimates by Thanguraju and Ulaganathan (1990) (r_g = -0.59, r_p = -0.25) in one of the White Leghorn strain (Forsgate), with genetic correlations being estimated from either sire or sire plus dam components of variance and covariance. Furthermore, the estimate for genetic correlation in *Kuchi* coincides with the lower end of the estimates reported in literature (r_g = -0.19 to -0.46) in egg type chickens and broilers using animal model of mixed models procedures (Hagger, 1994; Francesch *et al.*, 1997; Lopez and Quaas, 1997; Nurgiartiningsih *et al.*, 2002).

(ii) Age at first egg and egg number

Results from the present study revealed favourable but moderately low genetic (r_g = -0.19 for *Kuchi*, and r_g = -0.15 for *Medium* ecotype) and phenotypic (r_p = -0.16 for *Kuchi*, and r_p = -0.14 for *Medium* ecotype) correlations between age at first egg and egg number, indicating birds that are genetically inclined to attain sexual maturity earlier to some extent tend to be associated with high egg number. Corresponding standard errors of the estimates for genetic correlations were computed to be 0.06 and 0.04, and for phenotypic correlations to be 0.03 and 0.04, for *Kuchi* and *Medium* ecotypes, respectively, revealing that the estimates were significant.

Compared to other studies, the estimates are within the ranges reported by Singh and Hussani (1978), Jain *et al.* (1980) and Brah *et al.* (1991) in which values below 0.20 in absolute terms ranging from positive to negative were reported. However the current estimates are substantially lower than the estimates by Srivastava *et al.* (1993) (r_g = -0.40 to -0.74), Thangaraju and Ulaganathan (1990) (r_g = -0.72, r_p = -0.68), Kolstad (1980) (r_g = -0.52, r_p = -0.56) and Sorensen *et al.* (1980) (r_g = -0.72 to -0.76, r_p = -0.56 to -0.58), with genetic correlations being obtained from sire, dam or sire plus dam components of variance and covariance, and the estimates by Khalil *et al.* (2004) (r_g = -0.36, r_p = -0.39) in crosses between Saudi Arabia local chickens and White Leghorn using animal model of mixed models procedures.

(iii) Age at first egg and egg weight

Results from the present study shows that moderate positive genetic correlations were found between age at first egg and egg weight. The corresponding phenotypic correlations were also positive but low. The estimates were 0.32 and 0.12 in *Kuchi*, and 0.22 and 0.15 in *Medium* ecotype, for genetic and phenotypic correlations, respectively. Moderate positive genetic correlations between age at first egg and egg weight suggests that selection for reduced age at first egg could lead to reduction in egg weight. Calculated standard errors of the estimates (s.e for r_g = 0.11 and for r_p = 0.04; s.e for r_g = 0.07 and for r_p = 0.05, for *Kuchi* and *Medium* ecotypes, respectively) revealed the values to be significantly different from zero.

Using sib correlation analyses, studies by Srivastava *et al.* (1993) in White leghorns, and Luo *et al.* (1991) cited by Jiang and Groen (2000) in Chinese local chickens also reported moderate positive genetic correlations (0.24, and 0.13 to 0.31, respectively), which were comparable to results of the current study. On the other hand, lower values than the present estimates, ranged from positive to negative (r_g = -0.02 to 0.15, r_p = - 0.01 to 0.09) were reported by Sørensen *et al.* (1980), Kolstad (1980), Poggenpoel (1986), Brah *et al.* (1991), and much higher values (r_g = 0.78, r_p = 0.27) were given by Thangaraju and Ulaganathan (1990) also in egg type chickens.

(iv) Other correlations among egg production and related traits

Other correlations coefficients (both genetic and phenotypic) among egg production and related traits were all low in both ecotypes with most of the estimates being below 0.10 in absolute terms, indicating selection for improving either of the trait in a pair would not have an effective correlated response on the other. Furthermore, their computed standard errors for the estimates ranged from 0.03 to 0.07 with most of the estimates being lower than twice their standard errors (i.e. not significantly different from zero). Compared to the previous works, the estimates are mostly in the range reported in earlier studies in egg type chickens (Engstöm *et al.*, 1986; Poggenpoel, 1986; Brah *et al.*, 1991; Khatkar, *et al.*, 1994; Sabri *et al.*, 1999), and some results of Chen *et al.* (1993) in Taiwanese local chickens, in which genetic correlations were estimated from either sire or sire plus dam components of variance/covariance.

4.4.2.3 Correlations among body weight and egg traits

(i) Body weight and egg weight

Genetic and phenotypic correlations among body weights and egg production and related traits are presented in Table 4.10 and 4.11. With regard to correlation between body weight and egg weight, results generally indicate that low to moderately positive correlations were obtained both in *Kuchi* (r_g = 0.20 to 0.34, r_p = 0.10 to 0.25) and *Medium* ecotype (r_g = 0.13 to 0.30, r_p = 0.09 to 0.25), indicating that selection for improving juvenile body weight in both ecotypes could be associated with an increased egg weight. Standard errors of the for genetic correlations varied from 0.05 to 0.09 in *Kuchi* ; 0.03 to 0.06 in *Medium* ecotype and for phenotypic correlations from 0.04 to 0.10 for *Kuchi* and from 0.03 to 0.08 for *Medium* ecotype with the estimates being significant.

Consistent with the findings of the present study, Sørensen *et al.* (1980), Brah *et al.* (1991), and Thangaraju and Ulaganathan (1990) also found favourable positive correlations (r_g = 0.05 to 0.62; r_p = 0.11 to 0.35) between juvenile body weight and egg weight in egg type chickens. Similarly, between mature body weight and egg weight (Jaffé, 1966; Kolstad, 1980; Sørensen *et al.*, 1980; Brah *et al.*, 1991) (r_g = 0.01 to 0.73, r_p = 0.17 to 0.39). In these studies, genetic correlations were estimated from sib correlation analyses (i.e. sire, and sire + dam components of variance/covariance). Furthermore, using animal model of mixed models procedures, moderate positive correlations between body weight and egg weight were also reported by Hagger (1994) (r_g = 0.29, r_p = 0.24), and Lopez and Quaas (1997) (r_g = 0.21).

(ii) Body weights and egg number

With regard to egg number, the correlations with body weight were unfavourable. Estimated genetic correlations were all negative and varied from low to moderate. The estimates for genetic correlation varied from -0.06 to -0.23 in *Kuchi* and their standard errors from 0.04 to 0.11; -0.11 to -0.21 in *Medium* ecotype and their standard errors from 0.05 to 0.08. Corresponding phenotypic correlations in both ecotypes were also unfavourably negative but all low, ranging from -0.02 to -0.18

in *Kuchi* and their standard errors from 0.04 to 0.07; -0.04 to -0.12 in *Medium* ecotype and their standard errors from 0.03 to 0.05. Most of the estimates were significant.

Low to moderate negative genetic correlations suggest that selection for improving genetic merit for juvenile body weights could results into low to moderate negative correlated response in egg number. In general, results of the current study accord well with the estimates of -0.02 to -0.25 for genetic correlations, and –0.01 to –0.23 for phenotypic correlations reported in studies by Kolstad (1980), Sørensen *et al.* (1980), Thanguraju and Ulagnathan (1990), Akbaş *et al.* (2002) and Neelam *et al.* (2003) in egg type chickens, with genetic correlations being estimated from sib correlation analyses. Likewise, the current estimates also agree with animal model of linear mixed models estimates by Koerhuis and Mckay (1996) (r_g = -0.20) and Hagger (1994) (r_g = -0.04, r_p = -0.018), reported for broilers and egg type chickens, respectively. However, the present observations contradicts the findings by Srivastava *et al.* (1993), Singh and Hussani (1978), and some results of Thanguraju and Ulagnathan (1990) and Sørensen *et al.* (1980) in egg type chickens in which low to moderate positive correlations (r_g = 0.10 to 0.55, r_p = 0.00 to 0.35) were reported, with genetic correlation being obtained from sib correlation analyses.

(iii) Body weight and age at first egg

Estimated genetic correlation between body weight and age at first egg in the current study for *Kuchi* and *Medium* ecotypes varied from -0.15 to -0.22, and -0.03 to -0.23, respectively, and their associated standard errors from 0.06 to 0.09, and 0.04 to 0.09, respectively. Corresponding phenotypic correlations were all weak and varied from -0.04 to -0.18 and 0.03 to -0.19, respectively, and their associated standard errors from 0.02 to 0.07, and 0.03 to 0.06, respectively. Compared to previous studies, variable estimates have been presented in literature with estimates varying from moderately negative to highly positive (r_g) or negative (r_p) (r_g =-0.37 to 0.70, r_p = -0.24 to -0.60) for correlations between both juvenile body weight and mature body weight and age at sexual maturity, with genetic correlations being obtained from sib correlation analyses (i.e. sire, dam, and sire + dam components of variance/covariances) (Kolstad, 1980; Sørensen *et al.*, 1980; Thangaraju and Ulaganathan, 1990; Srivastava *et al.*, 1993; Kumararaj *et al.*, 1995; Akbaş *et al.*, 2002). However the current estimates agree with the range of moderately negative to lowly positive reported by most of these studies.

(iv) Body weight and egg shape index and shell thickness

Both genetic and phenotypic correlations between body weights and shell thickness and egg shape index in the two ecotypes were all low, ranging from negative (for most correlations with shell thickness) to positive (for most correlations with egg shape index). Estimated genetic and phenotypic correlations for *Kuchi* varied from -0.06 to 0.11, and -0.07 to 0.09, respectively, and in *Medium* ecotypes from -0.07 to 0.08, and -0.07 to 0.07, respectively, with most of the coefficients being very low (i.e. below 0.10 in absolute terms), indicating that selection for increased genetic merits for juvenile body weight would have little or no influence on these traits. Standard errors of the estimates for genetic and phenotypic correlations for *Kuchi* varied from 0.03 to 0.07, and 0.04 to 0.09, and for *Medium* ecotype from 0.04 to 0.07, and 0.03 to 0.10, respectively, with nearly all the correlations being not significantly different from zero.

Compared to other studies, unfortunately few articles have been encountered in literature reporting genetic and phenotypic correlations between body weight and egg shape index (Brah *et al.*,1991), and egg shell quality (Jaffé, 1966; Kolstad, 1980; Sorensen *et al.*, 1980), with genetic correlations being estimated from sire and sire plus dam components of (co)variance. Furthermore, with regard to shell quality, as opposed to current study, egg specific gravity (another measure of shell quality) was used instead of shell thickness; however, most of the estimates reported coincide well with the current estimates in which shell thickness was used. Sørensen *et al.* (1980) reported genetic and phenotypic correlations between both juvenile body weight and mature body weight with egg specific gravity to be less than 0.10, while in the other two studies genetic and phenotypic correlations between egg specific gravity and mature body weight were estimated to be -0.19 and -0.06 (Kolstad, 1980), and to vary from -0.11 to 0.24, and -0.08 to 0.07 (Jaffé, 1966), respectively. Regarding egg shape index, Brah *et al.* (1991) working with some populations of White Leghorns estimated correlations between juvenile and adult body weight with egg shape index. and some of the estimates obtained were also as low as the results of the present study.

4.4.2.4 Correlations between antibody response (humoral immune response) and productivity

Correlations between primary antibody responses against NDV vaccine and production traits are given in Tables 4.10, 4.11, and 4.12. Results indicate that primary antibody response against NDV vaccine in each of the two ecotypes was unfavourably correlated with most of the production traits in both management systems. However, the estimates were too low to result into significant reduction in primary humoral immune response following selection for improved genetic merits for these production traits. Most estimates were around -0.10 and below, and they were non-significant (i.e.standard errors varied from 0.03 to 0.08). Most correlations reported in the literature between antibody response and production are between the trait and body weight (Sacco *et al.*, 1994; Lwelamira and Katule, 2004; Sivaraman *et al.*, 2005), with few studies reporting it with other production traits i.e. egg production, egg weight and age at sexual maturity (Chao and Lee, 2001). In these studies correlation coefficients of almost similar magnitude as those in the present study were reported.

4.4.3 Genetic correlations between the same traits measured in two environments

Genetic correlations for the same traits measured in the two environments (i.e intensive and extensive management) such as primary antibody response against NDV vaccine and body weights were also estimated in the current study. Results from Table 4.13 indicate that genetic correlations for antibody response were 0.72 and 0.75. while for body weights they ranged from 0.75 to 0.76, and 0.79 to 0.85, for *Kuchi* and *Medium* ecotypes, respectively. According to Robertson (1959) and Mulder and Bijma (2005) classifications, in which a value of genetic correlation equal to or above 0.80 (i.e ≥ 0.80) is considered to have no substantial/biologically important G x E interactions, with the exception to body weight for *Medium* ecotype at 8, 12, and 16 weeks of age, all other genetic correlations indicating substantial G x E interaction. Significant G x E interactions for body weights were also reported by several authors in broilers. Sørensen (1977) reported a genetic correlation for body weight at 5 weeks of age for broilers under high and low protein diets to be 0.33. Similarly, in an experiment by Pakdel (2004) studying the effect of cold stress on Ascites (a disease associated with high growth rates in broilers) in broilers reported a genetic correlation between body weight at 6 weeks of age for broilers measured under normal and cold stress to be 0.56. Substantial G x E interaction were also reported for egg production and related traits by Mukherjee (1980) in egg type chickens evaluated in Berlin, Germany (Temperate climate) and Kuala Lumpur, Malaysia (Tropical environment) with genetic correlations between the same trait in the two environments ranged from 0.41 to 0.64.

The existence of significant G x E interaction for the same trait measured in two environments indicates that different sets of genes and involved in the expresses of the traits in the two environments (Sørensen, 1977; Hohenboken, 1985; Togashi *et al.*, 2001; Lin and Togashi, 2002; Kolmodin, 2003; Mulder and Bijma, 2005; Charo-Karisa, 2006). Hence improvement obtained in one environment would not be fully realized in another environment where G x E interaction is significant. Furthermore, the degree of seriousness of the problem of G x E interactions also depends on the extent of variability between the environments under consideration, the more similar the environments are, the less the problem of G x E (Buvanendran and Petersen, 1980; Sorensen, 1999; Kolmodin, 2003).

Therefore, breeding programs that consider G x E interactions (i.e. environment specific breeding programs), or modification of the environments (i.e. management) to reduce the differences between environments under consideration could be required to minimize the problem of G x E interactions.

Table 4.13 Genetic correlations among immune responses and body weights measured in two environments (i.e Intensive and extensive management)

Trait	Ecotype	
	Kuchi	***Medium***
Ab	0.72	0.75
Bwt8	0.75	0.80
Bwt12	0.76	0.83
Bwt16	0.75	0.85
Bwt20	0.75	0.79

Ab= Antibody response (humoral immune response) against NDV vaccine; Bwt8, Bwt12, Bwt16 and Bwt20= Body weight at 8, 12, 16 and 20 weeks of age, respectively

4.5 Breeding strategies for improving performance of *Kuchi* and *Medium* ecotypes

In this section various breeding scenarios (Tables 4.14, 4.17 and 4.20) for improving the performance of these ecotypes have been compared. Based on the performance of these ecotypes in study I (i.e. *Kuchi* showed good prospects for body weight and *Medium* for egg production), emphasis was put on improving body weight for *Kuchi* and egg production and related traits for *Medium* ecotype together with primary antibody response against NDV vaccine (i.e. humoral immune response). Since egg production and related traits were not recorded under on-farm management, breeding scenarios for improving performance of *Medium* ecotype were designed for intensive management conditions. Selection index coefficients for those breeding scenarios which involved use of selection indices are presented in Appendix 6.

Intended performances /improvement and hence desired gains (a pre-requisite for using Yamada index) for traits ear-marked for improvement in various breeding scenarios in Tables 4.14, 4.17, and 4.20 are presented in Tables 4.15, 4.18, and 4.21. These intended performances were chosen in such a way that they are within the capacity of the population as shown by performance of some individuals in an environment under consideration. Furthermore, the chosen intended performances were close to the performance of the crosses between local and exotic birds (Ali *et al.*, 2000; Theerachai *et al.*, 2003). In addition, the chosen intended performance for body weight also depended on weight at which a chicken can be marketed.

When assessing body weight much further, based on maximum weight possible under the respective manangement system, possibility of attaining a body weight of at least 1kg (market weight) at 8 weeks under intensive management and 8 or 12 weeks of age under extensive management were non-existent. Moreover, since heritability estimates for body weights were relatively higher in later ages compared to earlier ages, and good genetic and phenotypic correlation existed between body weights, correlated responses are anticipated. Therefore, body weight at 16 weeks of age (Bwt16) was chosen as the target body weight in various breeding scenarios where body weight was considered. Furthermore, based on the capacity of the population (*Kuchi*), body weight at 16 weeks of age was also chosen as it is possible to target much higher weights in a breeding objective (i.e. above 1.5kg under intensive conditions, and hence chickens would be fetching good prices) compared to body weights at 8 and 12 weeks of age, and at earlier age than at 20 weeks of age.

4.5.1 Genetic improvement of *Kuchi* for meat production under intensive management

Responses per generation in various traits resulting from various breeding scenarios for *Kuchi* under intensive management presented in Table 4.14 are shown in Table 4.16. Predicted direct response to selection in 16wk body weight under intensive management ranged from 70 to 87 g per generation, with maximum response being achieved when selection is based on single trait selection for body weight at 16 wk of age. Gain per generation for a particular trait is always expected to increase when an antagonistic trait with that trait is removed from the index or not considered for selection (i.e. egg number and antibody response in relation to body weight in the present case) (Pakdel, 2004).

Dropping or ignoring egg number in the breeding program (scenario 3 and 4) resulted into a significant drop in egg production (i.e. 1 egg per generation) which is undesirable.

Table 4.14 Breeding scenarios for *Kuchi* under intensive management

Scenario	Ab	Bwt16	EN-90
1	+	+	0
2	-	+	0
3	+	+	-
4	-	+	-

Ab= Antibody response (humoral immune response), Bwt16 = Body weight at 16 weeks of age, EN-90 = Egg number in the first 90 days after sexual maturity

+ = A trait is improved, 0 = A trait is held constant, - = A trait is dropped from the index

Table 4.15 Observed and desired mean and desired gain for *Kuchi* under intensive management system

Trait	Unit	Observed mean	Desired mean	Desired change	Percentage change (%)
Ab	HI (log_2)	5.0	6	1	20
Bwt16	Gram	1394	1800	406	29

Ab= Antibody response (humoral immune response), Bwt16= body weight at 16 weeks of age

Table 4.16 Direct and correlated responses per generation resulting from various breeding scenarios for on-station *Kuchi* chickens

Sc	Ab	Bwt8	Bwt12	Bwt16	Bwt20	AFE	EN-90	EW	STH	ESI	Gen
1	(0.17)	23.80	48.31	(69.92)	70.31	-2.50	(0.00)	0.50	-0.24	0.39	5.80
2	-0.07	28.18	56.42	(81.12)	80.83	-2.65	(0.00)	0.58	-0.22	0.28	5.00
3	(0.18)	24.96	51.58	(74.83)	76.31	-2.21	-0.95	0.63	-0.19	0.39	5.43
4	-0.07	29.57	60.12	(86.66)	87.43	-2.37	-0.97	0.71	-0.16	0.29	4.69

Sc = Scenario; Gen= number of generations required to achieve the desired gains; Ab= Antibody response (humoral immune response) (HI log_2) ; Bwt8, Bwt12, Bwt16, and Bwt20 = body weights at 8, 12, 16, and 20 weeks of age in gram, respectively; AFE= age at first egg (days), EN-90= egg number in the first 90 days after sexual maturity, EW= egg weight (g) ; STH= shell thickness (μ); ESI= egg shape index (%).

Figures in parentheses are direct response to selection (i.e. traits included in the index), while those out of parentheses are correlated responses (i.e. traits not included in the index).

Results from Table 4.16 also reveal that all breeding scenarios considered for *Kuchi* on-station predicted to result into favourable correlated responses in other body weight measurements (24-87g per generation), egg weight (0.5 to approximately 1g per generation), and age at sexual maturity (- 2 to -3 days per generation) with little change on egg shell thickness and egg shape index. Dropping antibody response (humoral immune response) from the index will result into a slight deterioration of this trait. Based on the knowledge of genetic correlations between these traits obtained in the present study as supported by other previous works (Sørensen *et al.*, 1980; Gill and Verma, 1983b; Srivastava *et al.*, 1993; Kumararaj, 1995; Koerhuis and Mckay ,1996; Akbaş *et al.*, 2002; Chao and Lee, 2003; Lwelamira and Katule, 2004; Sivaraman *et al.*, 2005; Zerehdcran *et al.*, 2005), the direction and magnitude of correlated responses obtained in the current simulation work are not surprising.

Compared to gain per generation achieved in previous studies for selection for body weights it is difficult to make direct comparison due to differences in either selection procedures employed, selection intensities used, or age at which the body weight is intended to be improved. In a study by Su *et al.* (1997) in broilers, gain per generation for body weight at 6 wk of age under intensive management of about 45g based on mass selection was reported. On the other hand Bhusan *et al.* (1998) reported predicted gain per generation in broilers resulting from selection based on indices incorporating body weight at 6 and 8 weeks of age and feed utilization parameters to range from 12 to 15g per generation. In contrast, using similar traits, response of up to 56g per generation were reported in broilers by Singh *et al.* (2000).

Considering the mean body weight at 12 wk of age for *Kuchi* averaged over both sexes of 954g under intensive management obtained in the present study (Table 4.1), and correlated responses for 12 wk of age of around 280g after the entire period of selection (i.e gain per generation x number of generations required to achieve the desired gain) in almost all breeding scenarios considered, the expected average body weight at 12 wk of age after completion of the selection process is estimated to be 1234g. Furthermore, considering local chickens in the tropics are starting to be marketed when their average body weight is around 1kg and above (Pedersen, 2002; Theerachai *et al.*, 2003; Acamovic *et al.*, 2005), therefore after selection, *Kuchi* can start to be marketed at 12 wk of age under intensive management, and at 16 wk of age they would be having a weight of more than 1500g (i.e. 1800g) (Table 4.15) and hence fetching higher prices.

Results from the present study also show that the number of generations required to achieve the desired gains ranged from 5 to 6 generations (Table 4.16). Based on the observations of the current study, assuming the activities of mating, collection of eggs, incubation and hatching; rearing of birds from day old to sexual maturity; and recording of egg production for a period of 3 months after sexual maturity for birds from all hatches/batches lasting for about 2, 6, and 5 (i.e. 2 + 3) months, respectively, this would lead to a generation interval of 13 months (i.e. 2 + 6 + 5) for breeding scenario 1 and 2 (where apart from improving body weight, egg number is also held constant), and 8 months (i.e. 2 + 6) for breeding scenario 3 and 4 (where control of correlated response in egg number is ignored). Hence, to attain the desired gain in body weight it would require 6.3, 5.4, 3.6, and 3.1 years of selection for breeding scenario 1, 2, 3, and 4, respectively. Although few years are required to attain the desired gain in body weight for breeding scenario 3 and 4, and they are cheap in terms of recording, however, these breeding scenarios are predicted to result into noticeable drop in egg number (approximately 1 egg per generation). Therefore, given the situation where resources are available, it could be better to use those breeding scenarios which control response in egg number (i.e. breeding scenario 1 and 2). Since apart from improving body weight, humoral immune response against NDV vaccine is also improved in breeding scenario 1, this breeding strategy could be recommended at the expense of one more year of selection relative to breeding scenario 2. Although majority of farmers in tropics rear their chickens under extensive management (MOAC, 1997; Tadelle *et al.*, 2003a; Fayeye *et al.*, 2005), the stock obtained from improving this ecotype under intensive management can benefit those farmers who would be able to shift from current system of management to at least semi-intensive system of management.

4.5.2 Genetic improvement of *Kuchi* for meat production under extensive management

Five breeding scenarios were considered under this management system as indicated in Table 4.17. Due to the presence of genotype by environment interactions observed in the current study for body weight, some breeding scenarios (1 and 2) were designed to predict response on farm (extensive management) as a result of selection under intensive management. Since apart from genetic correlation between the same trait measured in the two environments, data structure in the current study didn't allow estimation the corresponding phenotypic correlations, and both genetic and phenotypic correlation between different traits (i.e. trait 1 and trait 2) measured two different environments; and further that egg production was not recorded under on-farm conditions. Therefore, it was not possible to calculate the correlated responses for body weight under field conditions based on index selection under intensive management (i.e. those scenarios in the preceding section where body weight was improved while egg number was held constant or antibody response was also improved). Hence the predicted responses under extensive management resulting from selection under intensive management were from single trait selection for 16 week body weight based on individual own performance. Furthermore, since egg production and related traits were not recorded on-farm (extensive conditions), genetic improvement under extensive management didn't involve those situations/scenarios where body weight was improved while controlling response in egg number as it was in some cases for on station improvement.

Table 4.17 Breeding scenarios for improving performance of *Kuchi* on-farm (extensive management)

Scenario	Description
1	Selection for improving body weight at 16 weeks of age done on-station and the improved stock (both males and females) is taken to the field (on-farm) after the end of selection.
2	Selection for improving body weight at 16 weeks of age done on-station and only improved males are taken to the field in each generation.
3	Selection is done both in males and females under farm conditions for improving both antibody response (humoral immune response) against NDV vaccine and body weight at 16 weeks of age.
4	Selection is done both in males and females under farm conditions for improving body weight at 16 weeks of age.
5	Selection is done only in males under farm conditions for improving body weight at 16 weeks of age.

Table 4.18 Observed and desired mean and desired gain for *Kuchi* under extensive management system

Trait	Unit	Observed mean	Desired mean	Desired change	Percentage change (%)
Ab	HI (log_2)	4.8	6	1.2	25
Bwt16	Gram	974	1300	326	34

Ab= Antibody response (humoral immune response), Bwt16= body weight at 16 weeks of age

Table 4.19 Response to selection for body weight at 16 weeks of age on-farm for *Kuchi* (gain per generation in trait units)

Scenario	Bwt16 (g)	Generations
1	68.14	4.78
2	34.07	9.57
3	53.42	6.10
4	64.80	5.03
5	43.97	7.41

Based on genetic correlations between the same trait measured in the two environments obtained in the present study, results from Table 4.19 indicate that on-station single trait selection for body weight at 16 weeks of age predicted to yield an on-station response of around 87g per generation would be associated with a correlated response of about 68g per generation under extensive management (scenario 1). This is close to the response of 65g per generation obtained for single trait selection for body weight at 16 weeks of age carried out in both males and females under farm/extensive conditions (scenario 4), but higher that the response of 53g per generation obtained when apart from body weight, antibody response was also considered for selection under farm conditions (Scenario 3). Furthermore, in a breeding scenario where only improved cocks from the station (intensive management i.e. elite nucleus) are taken to the field as breeding males as suggested by Horst (1981), and Mukherjee (1990) (scenario 2), or selection for improving body weight at 16 weeks of age under extensive conditions is done only on males (scenario 5), it was predicted to result into appreciably lower genetic responses per generation (i.e. 34 and 44g, respectively) than those obtained in all other breeding scenarios investigated. Considering the average body weight over both sexes of 974g at 16 week of age under extensive management obtained in the present study (Table 4.2), breeding scenarios 1, 2, 3, 4 and 5 would be expected to attain the desired average body weight of 1300g under extensive management (Table 4.18) after 4.78, 9.57, 6.10, 5.03, and 7.41 generations of selection, respectively (Table 4.19). By assuming mating, egg laying and incubation and hatching by the hen under extensive conditions takes approximately 2 months (i.e. 1 month for mating and egg laying, and 21 days for incubation and hatching), and age at sexual maturity under this management system is reached at around 8 months of age (Wilson *et al.*, 1987; Minga *et al.* 1989; Sonaiya, 1992; Gunaratne *et al.*, 1993; Mwalusanya *et al.*, 2002; Aganga *et al.*, 2003), which would lead to a generation interval of around 10 months for breeding scenario 3, 4 and 5. Further assuming a generation interval of about 8 months (i.e. 2 months for mating, egg collection, and hatching + 6 months for attaining sexual maturity under intensive system) for breeding scenario 1 and 2, it would require 3.2, 6.4, 5.1, 4.2, and 6.2 years of selection for breeding scenario 1, 2, 3, 4, and 5, respectively for achieving the desired gain.

Breeding scenario 1 and 2 are more convenient (cheap and easy to institute) compared to the other breeding scenarios, however, the problem of these breeding scenarios are reduced fitness under extensive management, and to a large extent in breeding scenario 1 (Horst, 1981; Mukherjee, 1990, 1992; Demeke, 2003). Doing selection under farm (extensive) conditions has the advantage of minimizing a problem of fitness under this management system i.e. loss of scavenging habit (scenarios 3, 4, and 5). However, the success of breeding scenarios under extensive conditions requires close supervision on record keeping under farm conditions which could be too involving and expensive. The problem could be more serious in breeding scenario 3 and 4 where both males and females are selected compared to breeding scenario 5 where only males are selected. Despite of being too involving and expensive, results from Table 4.19 also indicate breeding scenario 3 and 4 to have reasonably high genetic gain per generation. Therefore, in situation where resources are available for carrying out selection program under on-farm conditions, breeding scenario 3 could be recommended as it improves both body weight and humoral immune response to ND which is usually a serious problem under field conditions (Minga *et al.*, 1989; Yongolo, 1996; Alexander, 2001; Ilango *et al.*, 2005; Otim, 2005) at the expense of one more year of selection relative to breeding scenario 4. In a situation where resources are a problem, breeding scenario 5 or 2 could be advised depending on the magnitude of the problem. However, to achieve the desired gain in body weight, approximately one more year of selection would be required in both breeding scenarios relative to breeding scenario 3. If the problem of resources is not very severe, breeding scenario 5 could be a selection scheme of choice as it is expected to be associated with more fitness under farm conditions compared to breeding scenario 2.

4.5.3 Genetic improvement of *Medium* ecotype for egg production and related traits under intensive management

Breeding strategies for improving the performance of *Medium* ecotypes were concentrated on improving egg production and related traits together with antibody response (humoral immune response). Since egg production and related traits were not recorded under extensive management, it was not possible to design and evaluate various breeding strategies geared at improving performance of these traits under extensive system of management. Therefore, the current simulation is based on improving the performance of this ecotype under intensive management.

Breeding scenarios designed for improving performance of *Medium* ecotype under intensive management are presented in Table 4.20. Results from Table 4.22 show that the number of generations required for achieving the desired gains in various breeding scenarios ranged from 8 to 11 generations, which are higher than those obtained in various breeding scenarios for achieving the desired gains in *Kuchi* under intensive management. Again by assuming a generation interval of 13 months as in some breeding scenarios for *Kuchi* under intensive management (i.e. 2 months for mating, egg collection, incubation and hatching; 6 months for rearing birds to sexual maturity, 5 months for egg recording for chicks from all hatches), the required number of generations to achieve the desired gains in breeding scenario 1, 2, 3, 4, 5, 6, 7, and 8 would correspond to 11.5, 11.2, 11.2, 11.5, 8.8, 8.4, 8.4, and 8.7 years of selection, respectively.

Table 4.20 Breeding scenarios/selection indices for *Medium* ecotype under intensive management

Scenario	Ab	Bwt16	AFE	EN-90	EW
1	+	0	+	+	+
2	-	0	+	+	+
3	-	-	+	+	+
4	+	-	+	+	+
5	+	0	+	+	0
6	-	0	+	+	0
7	-	-	+	+	0
8	+	-	+	+	0

Ab= Antibody response (humoral immune response); Bwt16 = Body weight at 16 weeks of age; EN-90 = Egg number in the first 90 days; EW = Egg weight; AFE= age at first egg
+ = A trait is improved, 0 = A trait is held constant, - = A trait is dropped from the index

Table 4.21 Observed and desired mean and desired gain for *Medium* ecotype under intensive management

Trait	Unit	Observed mean	Desired mean	Desired change	Percentage change (%)
Ab	HI ($\log_2$)	5.1	6	0.9	18
EN-90	No.	49	68	19	39
EW	Gram	42	50	8	19
AFE	Days	168	154	-14	8

Ab= Antibody response (humoral immune response), Bwt16= body weight at 16 weeks of age, EN-90= egg number in the first 90 days, EW= egg weight, AFE= afe at first egg.

Table 4.22 **Direct and correlated responses per generation resulting from various breeding scenarios/ selection indices for on-station *Medium* chickens**

Sc	Ab	Bwt8	Bwt12	Bwt16	Bwt20	AFE	EN-90	EW	STH	ESI	Gen
1	(0.09)	-1.26	0.74	(0.00)	2.26	(-1.32)	(1.79)	(0.76)	-0.06	0.28	10.60
2	-0.01	-1.25	0.72	(0.00)	2.08	(-1.35)	(1.84)	(0.77)	-0.06	0.22	10.36
3	-0.02	0.41	4.00	4.00	6.04	(-1.36)	(1.84)	(0.78)	-0.07	0.22	10.31
4	(0.09)	-0.19	2.85	2.58	4.81	(-1.32)	(1.80)	(0.76)	-0.06	0.28	10.58
5	(0.11)	-0.33	0.15	(0.00)	-1.17	(-1.72)	(2.34)	(0.00)	-0.05	0.26	8.13
6	-0.012	-0.29	0.11	(0.00)	-1.52	(-1.80)	(2.44)	(0.00)	-0.06	0.19	7.79
7	-0.01	-1.05	-1.37	-1.82	-3.32	(-1.81)	(2.45)	(0.00)	-0.06	0.19	7.75
8	(0.11)	-1.72	-2.58	-3.35	-4.50	(-1.74)	(2.37)	(0.00)	-0.05	0.26	8.04

Sc = Scenario; Gen= number of generations required to achieve the desired gains; Ab= Antibody response (humoral immune response) (HI $\log_2$) ; Bwt8, Bwt12, Bwt16, and Bwt20= body weights at 8, 12, 16, and 20 weeks of age in gram, respectively; AFE= age at first egg (days), EN-90= egg number in the first 90 days after sexual maturity, EW= egg weight (g) ; STH= shell thickness (μ); ESI= egg shape index (%).

Figures in parentheses are direct response to selection (i.e. traits included in the index), while those out of parentheses are correlated responses (i.e. traits not included in the index).

It can also be seen in Table 4.22 that gain per generation in various breeding scenarios for egg number and age at first egg was around 2 eggs, and -1 to -2 days, respectively, with little change in shell thickness and egg shape index. In situations where egg weight was also improved (scenario 1, 2, 3, and 4), gain per generation for this trait ranged from 0.76 to 0.78g. As with body weight, it is difficult to directly compare responses per generation obtained in the present study and those from other studies due to differences in either selection methods or selection intensities used. However the response obtained in the present study would definitely be lower than selection based on single trait as selection for antagonistic traits (i.e. egg weight and egg number) are always expected to lower the magnitude of genetic response (Pattanayak and Patro, 1995; Pakdel, 2004).

For example, values ranging from 1.2 to 2.2g per generation in egg weight, which are much higher than the response predicted in the present study were reported for single trait selection for egg weight in Scandinavian egg type chickens (Kolstad, 1980; Sorensen *et al.*, 1980; Liljedahl and Weyde, 1980;).

Results from Table 4.22 further show that in breeding scenarios where either body weight (which is antagonistic to egg number), or humoral immune responses are dropped from the selection index, it was predicted to result into slight changes in these traits and in number of generations required to achieve the desired gains (i.e. efficiency). This could be attributed to the favourable relationship existing between age at first egg and egg weight with body weight, which were also included in the indices, and low genetic correlation between humoral immune response and production traits revealed in previous sections of this study.

The purpose of breeding programs in the current study as far as *Medium* ecotype is concerned was mainly to improve egg production and related traits together with antibody response (humoral immune response) against ND vaccination. It could also be desirable to improve these traits without affecting other important traits negatively i.e. decrease in body weight. Since, dropping of body weight into indices that involve all three egg traits (i.e. AFE, EN-90, EW) didn't result into significant change per generation in this trait, the breeding scenarios given for *Medium* ecotype (Table 4.20) could logically concentrate on those which ignore body weight from the index (i.e scenarios 3, 4, 7 and 8). Apart from some egg production and related traits, humoral immune response against NDV vaccine is also improved in breeding scenario 4 and 8. Furthermore, since eggs from local chickens can be marketed with the current low egg weight without a problem (Msoffe, P.L.M. 2006 and Mlozi, M.R.S, 2006, personal communication), then the two selection indices (4 and 8) could be breeding scenarios of choice among the four breeding scenarios above (i.e. those ignoring body weight in the index). However, for breeding scenario 4 it would require approximately 3 more years of selection to achieve the desired gains compared to breeding scenario 8. Therefore, the choice among these two scenarios will depend on availability of resources.

As stated earlier, although majority of farmers in the tropics reside in rural areas, breeding programs for improving egg production under intensive management can benefit those farmers who are ready to shift from extensive system of management to semi- intensive system of management as this will reduce the magnitude of genotype by environment interactions (Sørensen, 1999; Ali, 2002; Kolmodin ,2003).

4.6 Prospects for using MAS for further improvement

Possibility for using MAS for further improvement of some traits (i.e. antibody response against NDV vaccine) was investigated in the present study. The study targerted the MHC B region which is known to be associated with immune response, susceptibility and resistance to some pathogens, and productivity. Polymorphism at MHC B region was studied using the LEI0258 microsatellite which is located at this region (Dalgaard *et al.*, 2005; Lima-Rosa *et al.*, 2005; Fulton *et al.*, 2006; Schou *et al.*, 2006).

4.6.1 LEI0258 microsellite allele frequencies in the two Tanzania chicken ecotypes

Results from the current study revealed that 22 and 23 alleles of LEI0258 were identified in *Kuchi* and *Medium* ecotype, respectively (Fig. 4 and 5). In a study by Schou *et al.* (2006) in local chickens of Vietnam, and Lima-Rosa *et al.* (2005) in local chickens of Brazil a total of 19 and 15 alleles were identified in their populations, respectively using the same microsatellite, which are lower than the number obtained in the current study. However, the number of alleles in these studies including the current work are much higher than those reported for commercial breeds such as Lohman Silver Line (3 alleles) (Fink *et al.*, 2005), and in Lohaman brown line (5 alleles) (Schou *et al.*, 2006). As in most cases local chicken are kept under free range conditions in which a variety of diseases are prevalent compared to intensive management in which commercial chickens are kept (Pinard-van der Laan, 2002), the observed increased number of alleles in free range local chickens in the present study and the study by Lima-Rosa *et al.* (2005) and Schou *et al.* (2006) are not surprising. Increased polymorphism at MHC increases their ability to respond to various disease antigens and hence high chance of surviving in their environments. Furthermore, apart from rearing environment, reduced polymorphism at MHC in commercial chickens is also likely being contributed by selection for productivity, as opposed to the outbred populations.

Results from current study also revealed high level of heterozygosity in the studied populations, in which proportion of heterozygous individuals in *Kuchi* and *Medium* ecotypes were 88.2 and 86.4%, and the difference between the two ecotypes was not significant (P> 0.05) (Table 4.23). These values are in close agreement with that of 91% reported by Schou *et al.* (2006) in one population of Vietnamese local chickens, but higher, than those of 50% and 75% reported by Lima- Rosa *et al.* (2005) in two populations of Brazilian local chickens, typed using the same microsatellite. As reviewed by Wegner *et al.* (2004), MHC heterozygocity seems to be advantageous in MHC mediated disease resistance due to increased diversity of antigens capable of being presented to T cells. Therefore the frequency of heterozygocity at the MHC is expected to be higher in outbred populations exposed to all kinds of infectious agents as observed in the current study. The reduced degree of heterozygocity observed reported for Brazilian local chickens reported by Lima-Rosa (2005) compared to the results of the current study could probably be attributed to relatively low antigenic diversity prevailing in the environments in which these chickens have been evolved compared to the populations used in the current study (i.e. *Kuchi* and *Medium*). This is also reflected in the degree of polymorphism (number of alleles), in which lower number of alleles (15) were reported in the Brazilian chickens compared to 22 and 23 alleles found in the present study for *Kuchi* and *Medium* ecotypes, respectively.

Table 4.23 Frequency of homozygous and heterozygous individuals summarized by ecotype

Status	***Kuchi* (n = 85)**		***Medium* (n = 88)**	
	Frequency	**%**	**Frequency**	**%**
Homozygous	10	11.8	12	13.6
Heterozygous	75	88.2	76	86.4

χ^2 value = 0.136, P> 0.05

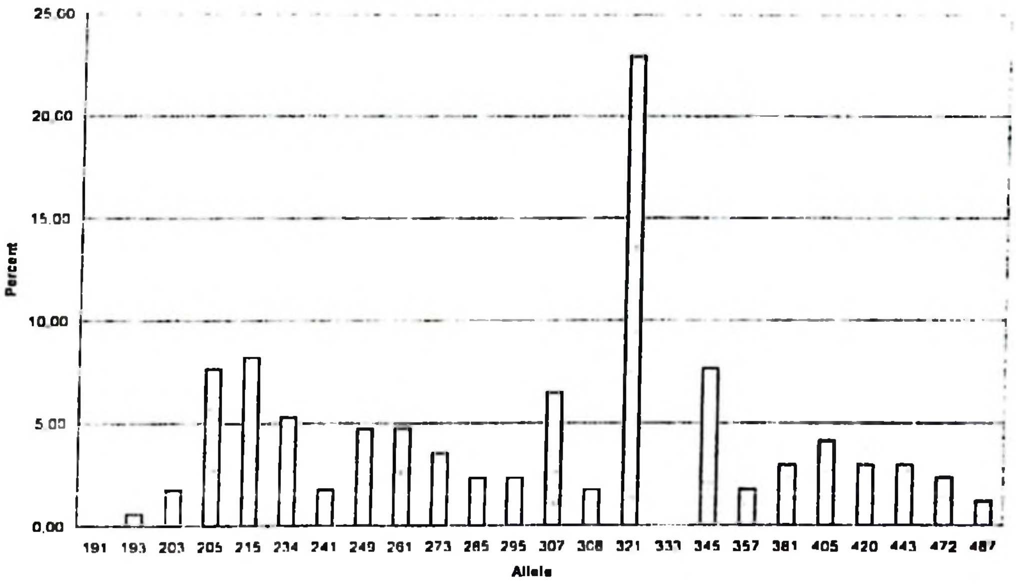


Figure 4. Allele frequencies in *Kuchi* ecotype

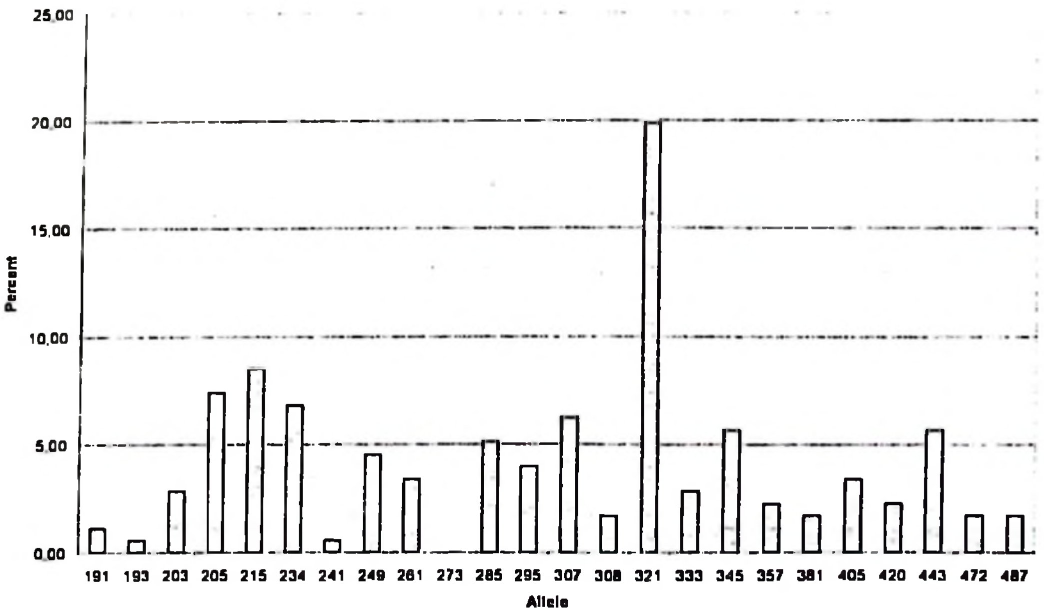


Figure 5. Allele frequencies in *Medium* ecotype

4.6.2 Association of LEI0258 microsatellite alleles with primary antibody response and body weight in the studied local chickens

Association between LEI0258 and the performance was also evaluated in the current study. Since, distribution of the different alleles among the two studied ecotypes were very similar (Fig. 3 and 4), the data for the two ecotypes were pooled together and six most frequent alleles in both ecotypes (i.e. 205, 215,234, 307, 321, and 345 bp size alleles) were chosen for the association analysis.

Choosing the most frequent alleles was based on the concept that for a random mating population, at a particular locus, frequency of a certain allele in a population is expected to be increased by natural selection if it plays a significant role in the survival of the individuals in the environment (Jeffery and Bangham, 2000; Sabeti *et al.*, 2002; Saunders *et al.*, 2002; Verrelli *et al.*, 2002).

Results from Table 4.24 indicate that the alleles 205bp and 307bp to be of special interest. The allele 205bp were significantly positively associated with the elevated primary antibody responses against NDV vaccine ($P<0.001$), while the allele 307bp was significantly negatively associated with this trait ($P<0.05$). Significant influence of LEI0258 microsatellite alleles on fitness parameters in chickens were also demonstrated in a study by Schou *et al.* (2006) in which the allele 276bp which is not found in the populations under current study was found to be associated to resistance to some species of worms in Vietnamese local chickens. Results from Table 4.24 further show that body weight was only influenced by the allele 307bp in which its presence was associated with the increased body weight at 16 weeks of age. Association of some alleles of microsatellites located within MHC region with performance were also reported in other livestock species such as sheep (Bot *et al.*, 2004).

Despite of presence of significant association between some of the alleles and the performance in the present study, however, results for R^2 in Table 4.24 indicate that the proportion of total phenotypic variance explained by these alleles is too low (i.e. less than 0.10). Using RFLP, studies by Yonash *et al.* (1999; 2000) also reported low proportion of total phenotypic variation that is explained by single MHC allele/band with regard to primary antibody response to Escherichia Coli, SRBC, and NDV vaccination in broilers. Low R^2 could be due to the fact antibody response (humoral immune response) and body weights are controlled by many loci, and some of these loci map outside the MHC region (Yonash *et al.*, 2000, 2001; Zhou and Lamont, 2003).

Due to low total phenotypic variation explained by significant alleles, incorporating these markers in breeding programs would results into marginal additional response. By considering the current method used for MHC typing in terms of time used, its involvement, and sometimes associated costs in relation to expected additional response, their use in developing countries could be limited to few livestock research centres which have enough resources. However, for livestock research centres with limited resources could use the technology by either forging a link/collaboration with centres with enough resources, or use other methods of MHC typing which are quick, cheap and less involving such as serological method (Lawerence, 1998; Juul-Madsen *et al.*,2006a) and Mannual Microsatellite MHC typing (Msoffe, 2003). However, regarding serological method, currently available alloantisera have been derived from inbred lines of commercial chickens i.e White Leghorn (Baelmans *et al.*, 2005; Fulton *et al.*, 2006). Inbred lines contain a limited combination of BG, BF and BL genes. In contrast, in outbred populations (i.e local chickens), novel alleles and combinations of alleles exist. Therefore, available alloantisera might not be able to identify all the existing haplotypes in local chickens (i.e some chickens may not show reaction to any of the available haplotype specific antisera) as it has been demonstrated in a study by Lawrence (1998) and Baelmans *et al.* (2005). Therefore, developing alloantisera that can adequately type the populations of local chickens is inevitable if serological method is to be used. To start with, haplotypes/groups obtained from LEI0258 microsatellite typing can be used in initial development of serological reagents using procedures described by Juul-Madsen *et al.* (2006b).

Table 4.24 Association between LEI0258 microsatellite alleles and body weight at 16 weeks of age and primary antibody response against NDV vaccine

Trait	Allele (bp)	β	S.E	Sign.	R^2
Ab	205	1.34	0.26	0.000	0.082
	215	0.03	0.27	0.900	
	234	-0.10	0.29	0.730	
	307	-0.92	0.29	0.001	0.028
	321	0.08	0.18	0.652	
	345	-0.16	0.28	0.557	
Bwt16	205	21.53	46.19	0.641	
	215	-65.32	46.94	0.165	
	234	-18.80	50.07	0.708	
	307	135.33	49.51	0.007	0.002
	321	-12.40	31.17	0.691	
	345	-7.41	48.01	0.877	

β = Regression coefficient, S.E = Standard error, Sign. = Significance, R^2 = R – Square.

CHAPTER FIVE

5.0 CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

Based on the results of the present study, the following conclusions were drawn:

(i) Production performance of both ecotypes was generally poor when compared to that of improved stocks, and was not different from what has been reported in literature for unimproved local chickens in other developing countries, and hence their performance need to be improved.

(ii) *Kuchi* was superior to *Medium* ecotype in terms of body weight, egg weight and feed utilization efficiency (i.e. FCR), while *Medium* ecotype was superior to *Kuchi* in terms of age at sexual maturity and egg number. Therefore *Kuchi* showed good prospects for further improvement in body weight, and *Medium* ecotype for further improvement in egg production. No significant differences between ecotypes with respect to eggshell thickness and egg shape index were observed.

(iii) There was no significant difference between ecotypes with respect to primary antibody response (humoral immune response) against NDV vaccine and hence fitness to Newcastle disease.

(iv) Based on heritability estimates, substantial additive genetic variation existed for all the traits studied and would therefore adequately respond to selection.

(v) Genetic and phenotypic correlations among traits in both ecotypes were highest among body weights, and were lowest among antibody response against NDV vaccine and production traits, and among eggshell thickness, egg shape index and other production traits. Furthermore, unfavourable correlations also existed between some production traits e.g. body weight and egg number.

(vi) About 3 to 6 years of selection would be required for improving Bwt16 either singly or together with antibody response in *Kuchi* from their current levels to the desired averages of 1300g under extensive management and 1800g under intensive management, and antibody response of around 6 (HI $\log_2$) in both management systems. Eight to 12 years of selection would be required for improving either AFE and EN-90 or together with EW or antibody response or both of them from their current level in *Medium* ecotype under intensive management to the desired averages of 154 days, 68 eggs, 50g, and 6 (HI $\log_2$), respectively.

(vii) Significant associations existed between some LEI0258 microsatellite alleles and antibody response against NDV vaccine and body weight, hence prospects for using MAS for further improvement of these traits.

5.2 Recommendations

(i) Breeding programs for improving performance of local chickens through selection should be initiated. To start with, *Kuchi* could be used for further improvement in body weight, and *Medium* ecotype for further improvement in egg production.

(ii) Selection indices which control gain in some traits should be used to counteract undesirable correlated responses.

(iii) Since high number of generations and hence years of selection are required for achieving desired gain in some breeding scenarios, apart from merits associated with these scenarios (i.e. correlated responses), the choice of breeding scenarios should also consider the availability of resources.

(iv) For the wider use of MAS in breeding programs in developing countries, methods for MHC typing which are quick, less involving and cheap i.e. serological method and manual microsatellite MHC typing are encouraged.

(v) Further studies on association between MHC haplotypes and phenotype should be carried out to explore other components of immune system which are also involved in immune response to Newcastle disease. Furthermore, other diseases which are also a problem to local chickens (i.e. Coccidiosis, Infectious Coryza, Fowl typhoid and Fowl cholera) should be considered. More studies are required to correlate prospective MHC haplotypes/groups with different diseases to further investigate relationship between MHC and diseases.

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APPENDICES

Appendix 1: Analyses of variance for on-station body weights

Weight at 8 wk of age

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	306819.016	30681.902	5.90	<.0001
Genotype	1	1953524.631	1953524.631	375.35	<.0001
Sex	1	2840202.678	2840202.678	545.71	<.0001
Hatch*Genotype	10	145022.927	14502.293	2.79	0.0020
Hatch*Sex	10	40008.753	4000.875	0.77	0.6593
Genotype*Sex	1	1336.679	1336.679	0.26	0.6124
Error	1325	6896102.60	5204.61		
Total	1358	14145634.78			

Weight at 12 wk of age

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	317359.320	31735.932	4.51	<.0001
Genotype	1	8792626.775	8792626.775	1249.62	<.0001
Sex	1	5166005.115	5166005.115	734.20	<.0001
Hatch*Genotype	10	134357.196	13435.720	1.90	0.0593
Hatch*Sex	10	73546.387	7354.639	1.05	0.4025
Genotype*Sex	1	219.347	219.347	0.03	0.8599
Error	1317	9266708.07	7036.22		
Total	1350	28013025.30			

Weight at 16 wk of age

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	305538.60	30553.86	3.70	<.0001
Genotype	1	12252146.71	12252146.71	1484.88	<.0001
Sex	1	3225573.83	3225573.83	390.92	<.0001
Hatch*Genotype	10	88477.80	8847.78	1.07	0.3804
Hatch*Sex	10	64620.13	6462.01	0.78	0.6452
Genotype*Sex	1	1273.45	1273.45	0.15	0.6945
Error	1303	10751381.63	8251.25		
Total	1336	31454569.47			

Weight at 20 wk of age

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	277617.67	27761.77	3.15	0.0005
Genotype	1	10657773.20	10657773.20	1208.63	<.0001
Sex	1	3934573.01	3934573.01	446.19	<.0001
Hatch*Genotype	10	108163.40	10816.34	1.23	0.2689
Hatch*Sex	10	63167.01	6316.70	0.72	0.7097
Genotype*Sex	1	9306.92	9306.92	1.06	0.3045
Error	1294	11410596.55	8818.08		
Total	1327	30991488.51			

Appendix 2: Analyses of variance for on-farm body weights

Body weight at 8 weeks of age

Source	DF	SS	MS	F-value	Pr > F
Village	1	779.6504	779.6504	0.18	0.6727
Farm (village)	65	783203.2690	12049.2811	2.76	<.0001
Hmonth	4	43980.7818	10995.1954	2.52	0.0400
Genotype	1	721090.3625	721090.3625	165.11	<.0001
Sex	1	436036.1934	436036.1934	99.84	<.0001
Hmonth*Genotype	4	19352.2210	4838.0552	1.12	0.3520
Hmonth*Sex	4	12837.8310	3209.457	0.74	0.5682
Genotype*Sex	1	14965.6834	14965.6834	3.43	0.0645
Error	836	3651049.5484	4367.284		
Total	917	6707666.375			

Hmonth= hatching month

Body weight at 12 weeks of age

Source	DF	SS	MS	F-value	Pr > F
Village	1	1607.812	1607.812	0.25	0.6171
Farm (village)	65	912755.659	14042.395	2.19	<.0001
Hmonth	4	106573.706	26643.427	4.16	0.0025
Genotype	1	1195772.711	1195772.711	186.47	<.0001
Sex	1	1332784.101	1332784.101	207.84	<.0001
Hmonth*Genotype	4	28071.407	7017.852	1.094	0.3596
Hmonth*Sex	4	23479.669	5869.917	0.92	0.4571
Genotype*Sex	1	1390.398	1390.398	0.22	0.6420
Error	802	5142987	6412.70		
Total	883	11113287.45			

Body weight at 16 weeks of age

Source	DF	SS	MS	F-value	Pr > F
Village	1	1421.745	1421.745	0.21	0.6466
Farm (village)	65	1254660.413	19302.468	2.85	<.0001
Hmonth	4	108033.86	27008.466	3.99	0.0032
Genotype	1	1634363.196	1634363.196	241.35	<.0001
Sex	1	1478019.032	1478019.032	218.26	<.0001
Hmonth*Genotype	4	46067.404	11516.851	1.70	0.1471
Hmonth*Sex	4	27222.810	6805.703	1.01	0.4030
Genotype*Sex	1	10021.061	10021.061	1.48	0.2238
Error	774	5241440	6771.886		
Total	855	12566532.36			

Body weight at 20 weeks of age

Source	DF	SS	MS	F-value	Pr > F
Village	1	2801.106	2801.106	0.39	0.5332
Farm (village)	65	1299709.805	19995.535	2.77	<.0001
Hmonth	4	85374.836	21343.709	2.96	0.0192
Genotype	1	1898209.402	1898209.402	263.11	<.0001
Sex	1	1670970.765	1670970.765	231.61	<.0001
Hmonth*Genotype	4	35373.641	8843.410	1.23	0.2980
Hmonth*Sex	4	7975.885	1993.971	0.28	0.8930
Genotype*Sex	1	5197.869	5197.869	0.72	0.3960
Error	729	5259358	7214.48		
Total	810	13002184.81			

Appendix 3: Analyses of variance for feed utilization efficiency (on-station) from 5 to 12 weeks of age

Gain per bird (GPB)

Source	DF	SS	MS	F-value	Pr > F
Genotype	1	10296.13	10296.13	59.22	0.0015
Sex	1	5050.13	5050.13	29.04	0.0057
Genotype*Sex	1	351.13	351.13	2.02	0.2283
Error	4	695.50	173.88		
Total	7	16392.875			

Feed intake per bird (IPB)

Source	DF	SS	MS	F-value	Pr > F
Genotype	1	23005.13	23005.13	4.22	0.1016
Sex	1	8256.13	8256.13	1.52	0.3127
Error	5	27233.63	5446.73		
Total	7	58494.875			

Feed Conversion ratio (FCR)

Source	DF	SS	MS	F-value	Pr > F
Genotype	1	0.980	0.980	9.56	0.0365
Sex	1	0.796	0.796	7.73	0.0439
Genotype*Sex	1	0.045	0.045	0.44	0.5438
Error	4	0.410	0.103		
Total	7	2.231			

Appendix 4: Analyses of variances for laying performance and related traits for on- station chickens

Age at first egg (AFE)

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	3676.389046	367.638905	1.00	0.4431
Genotype	1	2803.634735	2803.634735	7.61	0.0058
Error	669	246528.961	368.50		
Corrected Total	680	265957.8972			

90-days egg number (EN-90)

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	4929.337347	492.93373	1.42	0.1643
Genotype	1	1585.335267	1585.335267	4.55	0.0372
Error	657	228889.6	348.39		
Corrected Total	668	233292.8191			

Egg weight (EW)

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	704.2148613	70.421486	0.81	0.6191
Genotype	1	594.2069921	594.2069921	6.86	0.0087
Error	657	56891.5618	86.593		
Corrected Total	668	59092.30792			

Shell thickness (STH)

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	514.1082798	51.41082798	1.31	0.2185
Genotype	1	0.2775959	0.2775959	0.01	0.9326
Error	657	25754.61	39.200		
Corrected Total	668	26250.96263			

Egg shape index (ESI)

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	498.5294072	49.8529407	1.93	0.0385
Genotype	1	6.9406139	6.9406139	0.27	0.6043
Error	657	16972.74	25.83		
Corrected Total	668	17606.72646			

Appendix 5: Analyses of variances for antibody response (humoral immune response) (HI $\log_2$) for on-station and on- farm chickens

Primary antibody response on-station

Source	DF	SS	MS	F-value	Pr > F
Hatch	10	20.46063321	2.04606332	1.70	0.0751
Genotype	1	0.73875377	0.73875377	0.61	0.4330
Sex	1	0.07268403	0.07268403	0.06	0.8059
Error	1364	1646.235	1.21		
Corrected Total	1376	1665.352215			

Primary antibody response on-farm

Source	DF	SS	MS	F-value	Pr > F
Village	1	4.2697564	4.2697564	4.06	0.0482
Farm (village)	65	116.9633417	1.7994360	1.71	0.0060
Hmonth	4	0.7689822	0.1922455	0.18	0.9402
Genotype	1	0.0839118	0.0839118	0.08	0.7739
Sex	1	0.0169525	0.0169525	0.02	0.8973
Error	895	940.5426	1.051		
Total	967	1056.214876			

Hmonth = hatching month

Appendix 6: Selection index coefficients

Ecotype	Management system	Scenario	Ab	Bwt16	AFE	EN-90	EW
Medium	On-station	1	3.397	-0.008	-0.333	1.597	3.573
		2	-	-0.012	-0.360	1.543	3.552
		3	-	-	-0.320	1.593	3.382
		4	3.505	-	-0.303	1.633	3.461
		5	3.315	0.008	-0.140	1.516	0.549
		6	-	0.004	-0.167	1.463	0.529
		7	-	-	-0.182	1.445	0.587
		8	3.209	-	-0.170	1.481	0.659
Kuchi	On-station	1	4.473	0.083	-	0.529	-
		2	-	0.080	-	0.463	-
		3	4.347	0.080	-	-	-
	On-farm	3	4.214	0.058			

Ab= Antibody response (humoral immune response); Bwt16 = Body weight at 16 weeks of age; EN-90 = Egg number in the first 90 days; EW = Egg weight; AFE= age at first egg