

EFFECTIVE MEANS OF PREVENTING
THE SPREAD OF THE
DISEASE



M. V. D. Thesis Submitted
in
POULTRY SCIENCE

BY

Kunja Bihari Mishra

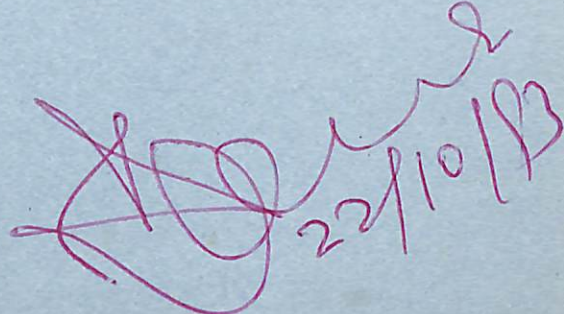
IN
PARTIAL FULFILLMENT OF THE
REQUIREMENTS FOR THE
DEGREE OF MASTER OF SCIENCE

Presented with best
regard to Dr. R. P. Sharma

Babu
21.10.93.
Dr. K. B. Sahu.

Donated by
Dr. K. B. Sharma
Former Director
B. D. P. Hyderabad




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**EFFECTIVENESS OF INDEX SELECTION
PROGRAMME IN SIRE AND DAM
BROILER POPULATIONS**



THESIS

**SUBMITTED IN PARTIAL FULFILMENT OF THE
REQUIREMENTS FOR THE DEGREE OF**

**Master of Veterinary Science
IN
POULTRY SCIENCE**

BY

Kunja Bihari Sahu

TO

**DEEMED UNIVERSITY
INDIAN VETERINARY RESEARCH INSTITUTE
IZATNAGAR-243 122 (U. P.) INDIA**

1993

Dedicated
To My Beloved
Parents

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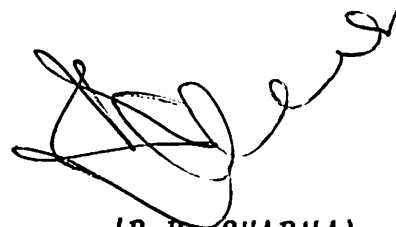
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Dated : 10th Aug' 1993

CERTIFICATE

Certified that the research work embodied in this thesis entitled "EFFECTIVENESS OF INDEX SELECTION PROGRAMME IN SIRE AND DAM BROILER POPULATIONS" submitted by Dr.K.B. Sahu, for the award of Master of Veterinary Science in Poultry Science of Deemed University, Indian Veterinary Research Institute, Izatnagar is the original work carried out by the candidate himself under my supervision and guidance.

It is further certified that Dr.K.B. Sahu has worked for more than 24 months in this Institute and has put in more than 150 days' attendance under me from the date of registration for Master's Degree of University as required under the relevant ordinance.



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CERTIFICATE

Certified that the thesis entitled "EFFECTIVENESS OF INDEX SELECTION PROGRAMME IN SIRE AND DAM BROILER POPULATIONS" submitted by Dr.K.B. Sahu in partial fulfilment of M.V.Sc. Degree in Poultry Science of Deemed University, Indian Veterinary Research Institute, embodies the original work done by the candidate. The candidate has carried out his work sincerely and methodically.

We have carefully gone through the contents of the thesis and are fully satisfied with the work carried out by the candidate, which is being presented by him for the award of M.V.Sc. Degree of this Institute.

It is further certified that the candidate has completed all the prescribed requirements, governing the award of M.V.Sc. Degree of Indian Veterinary Research Institute, Izatnagar.

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Kunja Bihari Sahu

ABBREVIATIONS

4 BW	:	Four week body weight
6 BW	:	Six week body weight
6 BA	:	Six week breast angle
6 SL	:	Six week shank length
EP	:	Egg production to 40 weeks of age
EW	:	Egg weight at 40th week of age
g	:	Gram
kg	:	Kilogram
(°)	:	Notation of degree
cm	:	Centimetre
IU	:	Index unit
Av.	:	Average

!!!

C O N T E N T S

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INTRODUCTION

INTRODUCTION

During the last four decades there has been intensive genetic manipulation for growth rate in broilers, which together with improved environment has resulted in a maximum growth rate of about 2.5 times as 40 years ago. While there is decline in production of other meat, the poultry meat in India realises an average annual growth rate of 7.96 percent after 1980 and is getting the mass preference. As recommended by National Institute of Nutrition, Hyderabad a balanced diet should contain minimum 30 g of egg and 30 g of meat per day. This calls for a nine fold growth in layer sector and 35 times in broiler sector. With an achievement of 200 million broilers in 1992-93, the projection of broiler production for 1995 is 400 million (Devegowda, 1993). With a vast scope of development and in a rising trend of income urbanisation and diet awareness, the breeders need to take it as a challenge to achieve a balance between production and consumption in this developing country.

Breeding of meat type chickens is considered to be a more complex and difficult proposition than breeding of egg type chickens. This is because a broiler breeder is not only to select for broiler traits such as growth rate, viability and feed efficiency of commercial broiler but also for the production and reproduction traits of the parent strains for the viability of operation. Further, undesirable genetic correlation between production and reproduction traits offer limited scope for simultaneous improvement of these traits in the same population. In order to overcome this problem, Smith (1964), Maov and Hill (1966) and Chambers et al (1984) proposed the use of specialized sire and dam lines for production of commercial broilelrs. Accordingly, the sire lines are primarily selected for broiler traits while those of dam lines for production and reproduction traits in addition to broiler traits.

Body weight is the most important trait in broilers, however, several other traits give good support to meet the challenge of modern commercial competition. Such other traits which need improvement are breast angle and shank length in sire line and egg production^{and} egg weight in dam line.

The superiority of an index selection to tandem and independent culling level to optimise genetic gains was shown theoretically by Hazel and Lush (1942), Young (1961) and Finney (1962). Later it was confirmed experimentally by Sen and Robertson (1964) and Avalos and Hill (1981) in *Drosophilla* and Lin (1980) in mice. Since continued genetic improvement of economically important traits is the main emphasis in commercial breeding, the application of selection index theory for a defined breeding goal (H) and available information results in the optimal selection index (I) and maximal expected selection response (Hazel, 1943).

In meat-type chicken, Lerner et al. (1947), Saxena (1976) and Sharma (1981) made theoretical approach to tell that index selection is superior to tandem selection. Although a few experimental works have been reported by Singh (1986) in male and Dev Roy (1986) in female lines while comparing index and tandem selection in meat type chicken, further studies need to be undertaken on similar lines alongwith the comparison between predicted and realised responses to index selection.

The present study was, therefore, planned with the following objectives :

1. To study the change in genetic and phenotypic performance of two broiler populations undergoing index selection alongwith a control population.

2. To study the efficiency in prediction of responses and comparison with realised responses for primary and component traits of indices of both lines.
3. To estimate the genetic drift, sampling variance, co-efficient of variation and inbreeding effects in male and female lines and control population.
4. To study the genetic and phenotypic trend in different traits of the index used in the male and female lines.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

2.1 SELECTION INDEX

Selection index provides a means for selection of several traits simultaneously where in each candidate for selection is given a score which combines important traits, weighted by their relative importance. The method was introduced for multiple trait selection in plants by Smith (1936) using Fisher's (1936) notion of a discriminant function and was developed for animal applications by Hazel (1943). Theoretically, the superiority of index method to maximise genetic gain to tandem and independent culling level has been shown by Hazel and Lush (1942), Young (1961) and Finney (1962). They also reported that since the index selection method is expected to provide rapid improvement of economic value, suitable weight need to be provided to each trait according to its relative importance, its heritability and the genetic and phenotypic correlations between the different traits.

Selection indices have been used for many years particularly in the field of breeding of meat-type chickens. Lerner et al. (1947), Saxena (1976), Sharma et al. (1981), Saxena et al. (1982), Dev Roy et al. (1983), Patro and Singh (1986) did a great deal of theoretical works with the data in meat type chickens. Experimental works have also been reported by Dev Roy et al. (1986, 1988) and Singh et al. (1988, 1989, 1990).

Moreover, the basic index theory has for many reasons been modified during the last 10-25 years. Lin (1978), Ronningen (1979) and Falconer (1981) have reviewed the principles of index selection and their application in different situation.

2.1.1 Basic theory

A comprehensive treatment of the basic theory has been given by Cunningham (1969), Lin (1978), Falconer (1981) and James

(1982). Therefore only the summary of basic theory is presented, largely to establish notation.

The aggregate economic worth of an individual (H) is defined as :

$$H = a_1g_1 + a_2g_2 \dots + a_ng_n$$

where, a_1, a_2, \dots, a_n are the relative economic values and g_1, g_2, \dots, g_n are the breeding values of the traits considered for selection.

The index (I) is defined as :

$$I = b_1x_1 + b_2x_2 \dots + b_nx_n$$

where, b_1, b_2, \dots, b_n are the partial regression coefficients to be calculated and x_1, x_2, \dots, x_n are the phenotypic values of traits considered for index selection.

The partial regression coefficients are so computed that the multiple correlation (r_{H1}) between the aggregate economic worth (H) and the index (I) is maximum. The solution of the index coefficients (b) are obtained by the equation as.

$$\underline{b} = P^{-1}Ga$$

where,

\underline{b} = the vector of the index weighting factors.
 P = the phenotypic variance co-variance matrix
 G = the genetic variance covariance matrix
 \underline{a} = the vector of relative economic values

The following relationship exist from the above definitions :

$$\sigma_I^2 = \underline{b}' \underline{Pb}$$

The variance of aggregate genotype or breeding value is

$$\sigma_H^2 = \underline{a}' \underline{Ga}$$

The correlation between the index and the aggregate genotype is defined as :

$$r_{HI} = \frac{\sigma_I}{\sigma_H} = \sqrt{\frac{\underline{b}' \underline{Pb}}{\underline{a}' \underline{Ga}}}$$

Since, the weighting factors b 's result in the regression of breeding value on index values being unity. i.e. $b_{H1} = 1$, one unit of index is equivalent to one unit of predicted breeding value. Expected selection response for the i th index trait due to selection on I is.

$$\Delta G_i = i \cdot b'_i g_i / \sigma_I \quad (\text{Cunningham, 1969; Lin, 1978})$$

Where, g_i is a column vector of additive covariance between the i th trait and each component trait included in the index, b' is a row vector of the weighting factors used in the index, i is the selection intensity for the index and σ_I is the standard deviation of the index. Cunningham (1969) reported that the index is the best estimate of the candidate's True Breeding Value by the following criteria.

- (i) It maximises r_{HI} , the correlation between the True Breeding Value (H) and the Index (I).
- (ii) It maximises the probability of correctly ranking the candidates on their True Breeding Values.

- (iii) It maximises genetic progress through selection.
- (iv) It minimises the mean squared difference, $(I-H)^2$ between True Breeding Value and Index.

2.1.2 Assumptions required for selection indices

There are assumptions made in constructing and using selection indices (Cunningham, 1969).

- (i) Relative weights are known without error.
- (ii) Relative economic weights remain constant over the range of variation likely to occur for the different traits.
- (iii) Relative economic weights do not change through time.
- (iv) Genetic and phenotypic variances and covariances (Matrices: P, G and C) are known without error.
- (v) Both index and aggregate genotype are normally distributed.

2.1.3 Relative importance of different variables in the index

The most useful measure of the efficiency of the index is the correlation between aggregate genotype and the index values (r_{HI}), since genetic progress from selection is directly proportional to this correlation. The importance of each variable in the index can therefore be measured by the reduction in r_{HI} which would result from dropping that particular variable from the index. This reduction in r_{HI} has generally been calculated by computing a new index from which the variable in question has been excluded, computing the r_{HI} with that original index. A direct alternate method without going through these procedures is given by Cunningham (1969).

2.1.4 Heritability of an index

The squared correlation r_{HI}^2 between selection index (I) and the true breeding value (H) had long been wrongly used as the heritability of an index by the workers (Willham, 1965, Pirchner, 1969). Lin and Allaire (1977) and Nordskog (1978) defined heritability of an index as the regression of genetic index (g) on the selection index. Accordingly heritability of an index,

$$h_I^2 = \frac{b'Gb}{b'Pb}$$

The second method of arriving at heritability of an index is the single trait measurement by sib analysis. Lin (1978) showed that the aforesaid two methods of calculating h_I^2 are equivalent theoretically and yield similar estimates from experimental data. Lin (1979) outlined a procedure for obtaining sampling variance of heritability of an index estimated by regression method. Akbar et al. (1984) reported that the heritability of an index deals with the gains in the genetic index rather than the net merit and the index with higher heritability is not necessarily the index with higher efficiency for improving the net merit.

Singh (1986) reported that the index unit (taken as a trait) with 8 wk B.Wt., 8 B.A., 8 S.L. and 8 K.L. is moderately heritable just like 8 Wk B.Wt. Pooled estimates from sire component were moderate and of similar magnitude both for male and female progeny in index line (0.21 and 0.23).

Patro and Singh (1986) reported the heritability estimates for selection index pooled over 2 generations to be 0.2422 ± 0.0229 in male and 0.5346 ± 0.2394 in female on subjecting the data to half sib analysis, while the corresponding value in regression method are 0.2243 and 0.5149 respectively.

2.1.5 Application of selection index

Hazel (1943) applied the index selection in Swine and reported that the efficiency based on r_{HI} value of the two types of indices were 0.30 and 0.40 respectively.

Selection on the basis of index by various workers has been reported in almost all species of animals. Some of the important experiments in meat type chicken are as follows :

Lerner et al. (1947) constructed several selection indices taking into consideration 12 WK body Wt., shank length, keel length and breast width. They showed 10-14 % more improvement due to selection based on an index than tandem selection.

Abplanalp et al. (1960) reported that the gain in breast width at 12 weeks of age in New Hampshire was 20 % more in index selected line than the line selected on the basis of breast width alone.

Shimizu, et al. (1968) made a comparison between independent culling level and index selection method for the improvement of body weight at 9 weeks of age and egg production in a flock of New Hampshires and reported the index selection method to be efficient compared to independent culling level.

Joubert et al. (1974) constructed selection index incorporating 12 week body weight, breast width and shank length. He observed that arbitrarily choosen economic values and differences in genetic variability influence the selection index in such a way that it was doubtful whether selection indexes would be important in practical breeding operations.

Saxena (1976) constructed selection index in broiler dam line utilising body wt at 10 week of age, egg weight and rate of lay and reported the efficiency of indices as 0.65, 0.64 and 0.46 for

White Cornish, White Rock and New Hampshire dams respectively.

Mohapatra et al. (1983) compared relative efficiency of multi-trait selection indexes with one and three sources of information for each of the component traits using important traits for broilers and observed higher efficiencies for multi-trait multi-source indexes relative to multi-trait indexes involving single source of information.

Sharma et al. (1983) reported that index selection was 35 % more efficient than culling level selection. Also tandem selection was seen to be less efficient than independent culling level for all the traits studied except for hatchability in a dam line of broiler.

Akhtar et al. (1987) compared the three selection methods in White Plymouth flock and reported that index selection (100 %), followed by tandem selection based on 280 day egg production (93.19 %) and independent culling level (88.40%) efficient.

Singh and Singh (1988) calculated the direct and correlated responses expected from single trait selection for traits of economic importance and compared with those of selection indices incorporating these traits. They concluded that the most efficient index to improve all traits is one combining 8 week body wt, age at 1st egg, egg number and egg weight.

Barwal et al. (1993) constructed 16 indices in a White Rock Dam line broiler flock and found index selection to be most efficient to bring about an improvement in most of the component traits when all the traits of economic importance are incorporated to it.

2.1.6 Experimental studies in meat-type chicken

Dev Roy et al. (1986) reported that the correlation between the index and the breeding value was 0.63 and observed the index to be more efficient than tandem by 30 percent for body weight

at 8 week; 42 percent for egg production (40 week) and 55 percent for egg weight.

Dev Roy et al. (1988) working with a dam line broiler population reported that aggregate economic gain was 1.58 percent higher for index selection compared to mass selection.

Singh et al. (1988) reported that progeny of index line of sires were heavier at day old, 4 weeks, 6 weeks and 8 weeks of age and had a higher breast angle and dressing percentage than the line on mass selection.

Singh et al. (1989) reported the ratio of realised to expected selection differential to be 1.01 in multi-trait selection programme for 3 years indicating that natural selection is not important.

Singh et al. (1990) constructed three selection indices incorporating 4 traits (8 wk BW, 8 BA, 8 SL, 8 KL) with different economic weights and observed that the relative efficiency of 3 indices were almost similar and h^2 averaged to 0.65. Further, index selection was found to be 32 % more efficient as compared to individual selection.

2.1.7 Some developments for further use of an index

i) Restricted Selection Index

The idea of restricted selection index was introduced by Kempthorne and Nordskog (1959) and extended by Tallis (1962). The restricted selection index provides a way to manipulate genetic changes in component traits, by holding one or more traits constant while improving others. With this index there are predetermined constraints on genetic response of some traits that partially or completely over-ride the response determined by their economic weights.

Lin (1985) has reviewed selection indices with their constraints.

ii) Family index

Informations from relatives can be utilised to increase the accuracy of selection. Lush (1947) used family mean to aid individual records in making selection. This is called 'family index'.

Osborne (1957) showed that maximum efficiency of selection can be obtained by combining individual, full-sib and half-sib family informations in poultry. The general conclusion was that for low heritable traits this method would be superior to selection based on individual phenotype, but for highly heritable traits individual selection would be superior. Mohapatra et al. (1983) utilised informations on eight week body weight, egg production and percent hatchability with three sources of informations, individual's own performance, full and half-sib average for each trait.

iii) Multistage Selection index

Informations on a few traits become available at an early age while others at later stages. Thus selection can be practised at more than one stages so that selection becomes a continuous process.

Young (1964) presented a multistage index selection procedure for one or more traits available at each of several stages in an individual's lifetime.

Cunningham (1975) examined the efficiency of two stage index selection compared to selection in one stage.

Abdou and Kolstad (1979), Sharma and Mohapatra (1982) and Ayyagiri et al. (1985) studied the advantage of multi-stage selection index in Poultry.

iv) **Weight free selection index**

Elston (1963) developed this index without going through Smith-Hazel index procedure, with the assumption that any individual which fails to meet the minimum standard for any one trait is to be culled. This procedure eliminates the problems of estimating relative economic weights, phenotypic and genetic parameters.

Baker (1974) recommended the use of this index when the index traits have equal importance.

v) **Index in retrospect**

The selection index actually practised in retrospect is called "index in retrospect" (Dickerson et al., 1954) Allaire and Henderson (1966) presented the computation of retrospective index in matrix notation. The various indices described above are derived before selection begins, whereas index in retrospect is obtained after conclusion of selection.

vi) **Base index**

Williams (1962) suggested the use of base index, in which the economic weights are used directly as index weights instead of index computed from estimated parameters.

The main difference between Smith-Hazel index and base index is that the former maximises the correlation between H and I, while the later maximises the correlation between H and g (genetic index). Subsequently regression of (H) on Smith-Hazel index (I) is unity while that on base index is less than unity which explains why the estimated index should be more efficient than the base index, unless estimation error is large enough to reverse theoretical expectations.

Comstock (1977), James (1982) presented a great deal of work relating to base index.

vii) Non-linear index selection

Theoretically, a selection index can be a linear or non-linear function of observable traits. However, it has almost always been assumed that the net merit of an individual is a linear combination of genetic values, each weighted by relative economic values.

Smith (1967) transformed the composite traits to a logarithmic scale so that the effect of component traits becomes linear.

Wilton et al. (1968) developed an index for net merit which included squares and cross products of these traits. This has been called 'quadratic index'.

2.2 GENETIC AND PHENOTYPIC PARAMETERS

2.2.1 Heritability

The heritability is a measure of the variability of the character considered between individuals differing in their additively genetic values relative to the total variability between individuals. It is the most important parameter of a population and in a breeding experiment the importance of heritability lies in its predictive role expressing the reliability of phenotypic value as a guide to the breeding value.

Lush (1940) defined heritability in narrow sense as the regression of additive genetic variance on total phenotypic variance. Falconer (1960) defined heritability in similar way as regression of breeding value on phenotypic value.

The heritability in the broad sense is defined as the portion of the total variance caused by the total genetic differences (Lush, 1940).

The notation h^2 is given to heritability itself not for its square. The symbol derives from Wright (1931) terminology where h stands for the corresponding ratio of standard deviation.

Heritability is expressed on a scale from 0 to 1.0. Heritability may be expressed as low (<0.10) medium (0.11 to 0.30) and high (>0.30).

Estimation of heritability

Several methods have been described in the literature to estimate the heritability by Lerner (1950), Kempthorne (1957) and Falconer (1960). The methods which have been commonly used to estimate the heritability of traits in poultry are the paternal or maternal half sibs correlation, full-sibs correlation and the regression of offspring on parent. Estimates of heritability are subjected biases by the genotype environmental interactions, dominance variance, epistatic variance, maternal effects, selection of sires or dams, non random mating and environmental variation. If dominance and epistasis are sources of genetic variance in the population, heritability estimates from the dam as well as full-sib component would be inflated (Cockerham, 1954). Maternal effect, if exists for the trait, will be included in the dam components. In other words, heritability based on sire components would be a more reliable estimate of additive genetic variance than any involving the dam component.

The common statistical model used for chicken for estimation of heritability from variance component analysis is that of King and Henderson (1954) and the interpretations of these variance components in chicken are given by Lerner (1958) and Dickerson (1960).

Short term selection experiments appear to be very efficient to estimate the genetic parameters both for selected and correlated traits. Although errors in measuring genetic from phenotypic mean become trivial as they become spread over several generations of selection, the random genetic drift in selected line accumulates (Hill, 1971).

Standard error of heritability

The standard error of heritability provides the precision of the estimate. Standard error of heritability estimates are uncomfortably large unless the number of individuals measured are fairly large (Falconer, 1981).

Dickerson (1960) and Falconer (1981) presented various formula to calculate standard errors of heritabilities of offspring on one or on both parents and sib correlation methods.

The heritability estimates for different traits as available in the literature are summarised in Tables 2.1 to 2.6.

2.2.2 Correlation

The relationship between two traits in statistical term is expressed by correlation. The association between the two characters that can directly be observed is the phenotypic correlation which may be due to genetic and environmental causes or due to combination of both factors.

Falconer (1981) has enumerated the chief reasons for which correlated characters are of interest.

- (i) In connection with the genetic causes of correlation through the pleiotropic action of genes : pleiotropy is a common property of major genes, but we have as yet had little occasion to

Table 2.1 Heritability estimates from literature for 4 week body weight

Source of data	Year	Breed	Sex	h^2_S	h^2_D	h^2_{S+D}	2b
Siegel	1963a	WR	C	-	-	-	0.47
	1963b	WR	M	-	-	-	0.43
			F	-	-	-	0.53
			C	-	-	-	0.48
Saikia	1973	WR	C	0.34	-	-	-
		WC	C	0.45	-	-	-
		NH	C	0.30	-	-	-
Saxena	1976	WC	M	0.39	0.38	0.38	-
			F	0.33	0.44	0.38	-
		WR	M	0.46	0.50	0.48	-
			F	0.39	0.46	0.42	-
		NH	M	0.37	0.50	0.44	-
			F	0.42	0.45	0.43	-
			C	0.24	-	-	-
Dev Roy <u>et al.</u>	1983	WR	M	0.16	-	-	-
			F	0.34	-	-	-
			C	0.24	-	-	-
Gill and Verma	1983	PR	C	0.53	-	-	-
Chamber <u>et al.</u>	1984	Syn	C	0.55	-	-	-
Dev Roy	1986	WC	M	0.69	-	-	-
			F	0.41	-	-	-
		WR	M	0.27	-	-	-
			F	0.28	-	-	-
Ramappa <u>et al.</u>	1986	IC-2	C	0.10	-	-	-
		IR-2	C	0.14	0.26	0.20	-
		Control	C	0.27	-	-	-
		IC-3	C	0.12	0.23	0.18	-
		Control	C	0.40	-	-	-
Kumar <u>et al.</u>	1988	WR	C	0.10	0.34	0.22	-
		WC	C	0.18	0.22	0.22	-
Wang <u>et al.</u>	1991	Syn	C	0.38	-	-	-
Average				0.33	0.38	0.34	0.48

Table 2.2 Heritability estimates from literature for 6 week body weight

Source of data	Year	Breed	Sex	h^2_S	h^2_D	h^2_{S+D}	2b
EL-Ibiary & Shoffner Meritt	1951	NH	M	0.13	-	0.38	-
			F	0.40	-	0.28	-
	1966	Meat Control	M	0.39	0.92	0.53	0.51
			F	0.46	0.61	0.44	0.46
			C	0.40	0.72	0.46	0.46
Saxena	1976	WC	M	0.38	0.42	0.40	-
			F	0.40	0.18	0.29	-
		WR	M	0.44	0.51	0.48	-
			F	0.25	0.31	0.28	-
		NH	M	0.58	0.47	0.53	-
			F	0.64	0.45	0.55	-
Aksoy	1980	NH	C	0.50	0.55	0.52	-
Gill and Verma	1983	PR	C	0.76	-	-	-
Dev Roy <u>et al.</u>	1983	WR	M	0.22	-	-	-
			F	0.37	-	-	-
			C	0.25	-	-	-
Chamber <u>et al.</u>	1984	Syn	C	0.63	-	-	-
Cahaner and Krinsky	1985	WR	M	0.47	-	-	-
			F	0.48	-	-	-
Reddy	1988	IC-3	M	0.40	-	-	-
			F	0.33	-	-	-
Singh <u>et al.</u>	1988	Syn	C	0.99	-	-	-
Wang <u>et al.</u>	1991	Syn	C	0.41	-	-	-
Average				0.47	0.51	0.43	0.48

Table 2.3 Heritability estimates of breast angle

Source of data	Year	Breed	Sex	h^2_S	h^2_D	h^2_{S+D}	2b
Lerner <u>et al.</u>	1947	NH (12 week)	C	0.13	0.29	0.21	-
Conkov <u>et al.</u>	1970	WC (8 week)	M	0.23	-	-	-
			F	0.63	-	-	-
		WR (8 week)	M	0.42	-	-	-
		F	F	0.10	-	-	-
Saxena	1976	WC (8 week)	M	0.53	0.35	0.44	-
			F	0.43	0.13	0.28	0.28
		WR (8 week)	M	0.59	0.39	0.48	-
			F	0.66	0.44	0.55	0.25
		NH (8 week)	M	0.67	0.50	0.59	-
			F	0.77	0.41	0.59	0.23
Ulaganathan <u>et al.</u>	1981	WC (8 week)	C	0.64	-	-	-
		WR (8 week)	C	0.81	-	-	-
Mishra <u>et al.</u>	1984	Cornish (8 week)	C	0.44 $\pm .14$	-	-	-
Sharma <u>et al.</u>	1984	Meat type (8 week)	M	0.09 ± 0.02	-	-	-
			F	0.16 ± 0.09	-	-	-
Singh	1986	IC-3 (8 week)	M	0.33	-	-	-
			F	0.29	-	-	-
Champati <u>et al.</u>	1987	Cornish (8 week)	M	0.59 ± 0.19	-	-	-
			F	0.53 ± 0.18	-	-	-
Reddy	1988	Cornish (6 week)	M	0.38	-	-	-
			F	0.35	-	-	-
Choudhary	1992	Syn (6 week)	M	-0.01 ± 0.1	-	-	-
Average				0.42 ± 0.12	0.35	0.49	0.25

Table 2.4 Heritability estimates from literature for shank length

Source of data	Year	Breed	Sex	h^2_S	h^2_D	h^2_{S+D}	2b
Merritt	1968	Meat type (63 days)	M	0.38	0.84	-	-
			F	0.46	0.54	-	-
Aggarwal	1975	Pure bred (10 weeks)	M	0.30	0.83	0.57	-
			F	0.68	0.63	0.65	-
		Cross bred (10 weeks)	M	0.48	0.68	0.58	-
			F	0.40	0.76	0.58	-
Saxena	1976	WC (8 week)	M	0.30	0.70	0.50	-
			F	0.28	0.46	0.37	0.29
		WR (8 week)	M	0.25	0.70	0.47	-
			F	0.26	0.67	0.46	0.28
		NH (8 week)	M	0.42	0.66	0.54	-
			F	0.26	0.71	0.49	0.25
Mishra <u>et al.</u>	1984	Cornish (8 week)	C	0.45 + .15	-	-	-
Sharma <u>et al.</u>	1984	Meat type (8 week)	M	0.10 + .02	-	-	-
			F	0.05 + .07	-	-	-
Singh	1986	Meat type (8 week)	M	0.30	-	-	-
			F	0.31	-	-	-
Champati <u>et al.</u>	1987	Meat type (8 week)	M	0.49 + .19	-	-	-
			F	0.40 + .16	-	-	-
Reddy	1988	Cornish (6 week)	M	0.59 +0.75	-	-	-
			F				
Choudhury	1992	Syn (6 week)	M	0.08 +0.13	-	-	-
Average				0.35 +0.02	0.68	0.52	0.27

Table 2.5 Heritability estimates from literature for egg production

Source of data	Year	Criterion of measurement	h^2_S	h^2_D	h^2_{S+D}	2b
Hicks	1958	AV. of 3 yrs. E.P.	-	-	0.23	-
Merritt	1968	% EP to 500 age	0.19	0.26	-	-
		Survivors EP.	0.21	0.30	-	-
Shalev	1970	% EP 190 days age				
		to 3 mths	0.20	-	-	-
Saxena	1976	EP to 280 days age				
		WC	0.18	0.47	0.32	0.28
		WR	0.26	0.55	0.40	0.25
		NH	0.27	0.24	0.25	0.25
Reddy and Siegel	1977	% hen day prodn of normal eggs	-	-	0.24	-
Sharma	1981	EP to 300 days age	0.26	-	-	-
		AV. of 4 strain				
Balachandran and Ulaganathan	1989	40 wks E.P.				
		IR-2	0.17	-	-	-
		IR-3	0.37	-	-	-
Average			0.23	0.36	0.29	0.26

Table 2.6 Heritability estimates from literature for egg weight

Source of data	Year	h^2_S	h^2_D	h^2_{S+D}	2b
Jaap <u>et al.</u>	1962	0.60	-	-	-
Siegel	1963	-	-	0.63	-
Hale and Clayton	1965	0.49	0.58	-	-
Merritt	1968	0.83	0.52	-	-
Shalev	1970	0.50	-	-	-
Saxena	1976	0.37	0.60	0.48	0.49
		0.56	0.67	0.62	0.54
		0.47	0.53	0.50	0.51
Aksoy	1980	0.42	0.63	0.52	-
Sharma	1981 Pooled	0.13	-	-	-
Kataria	1985	0.32	0.31	0.27	-
		0.23	0.60	0.30	-
		0.55	0.50	0.26	-
Dev Roy	1986	0.27	-	-	-
		0.30	-	-	-
		0.45	-	-	-
Mishra <u>et al.</u>	1986	0.13	0.99	-	-
Balachandran and Ulaganathan	1989	0.31	-	-	-
		0.43	-	-	-
Barwal <u>et al.</u>	1993	0.14	-	-	-
Average		0.39	0.59	0.45	0.51

consider its effects in quantitative genetics.

- (ii) In connection with changes brought about by selection : it is important to know how a change in one character will cause simultaneous changes in other characters.
- (iii) In connection with natural selection : the relationship between metric character and fitness is the primary agent that determines the genetic properties of that character in a natural population.

Falconer (1981) stated that genetic and environmental correlation may be different in magnitude and sometimes different in direction.

The theory of genetic correlation has been discussed in detail by Hazel (1943), Lerner (1950) and Falconer (1981). The genetic correlations between the traits are caused mostly by pleiotropy. Another transient cause may be linkage of genes controlling the traits. Detailed discussions on the variance of genetic correlation have been presented by Reeve (1955) and Robertson (1959).

The correlations are calculated as numerical values on a scale from -1.0 to +1.0. Falconer (1960) reported that a number of factors such as genotype environmental interactions, dominance and epistatic interactions, maternal effects, sampling etc. may be responsible for biased estimates of genetic correlations.

Estimation of genetic correlation

The genetic correlation estimated from half-sib component of variance and co-variance will approximately closely a genetic correlation in the "narrow sense" (Becker, 1964). A genetic correlation computed from full sibs may contain a correlation between dominance effects and maternal effects and therefore, may not be as

relevant as the correlations derived from half-sib data for prediction of correlated response (Pirchner, 1983).

As compared to estimation of the error of heritability, the error of genetic correlation is more difficult to compute and formulas are still more complicated. If genetic correlations and heritabilities are estimated from the same set of data, the errors of the former are considerably larger than errors of heritability estimates (Pirchner, 1983).

Genetic and phenotypic correlation co-efficients among different traits of broiler available in literature are presented in Tables 2.7 to 2.13.

2.3 RELATIVE ECONOMIC WEIGHTS

The economic value of a trait is defined as the amount of profit gained for every unit increase in that trait.

Hazel and Lush (1942) suggested to calculate the relative economic value for each class of animals from time to time and place to place. Hazel (1943) defined the linear selection objective in a linear index as the sum of the products of the additive genetic values of the component traits and their economic weights.

Hogsett and Nordskog (1958) presented a procedure to calculate the economic weights of the traits in farm animals from direct market and farm price analysis. They assigned relative economic weights to egg weight, body weight and rate of lay as 1.14, -2.86 and 1.00 respectively. Moav (1966) assessed the dependence of broiler profits on the reproductive performance of parent stocks and the efficiency of meat production by progeny. Pasternak and Shalev (1967) indicated that an increase of 30 gm of broilers body weight was found to save one day in broiler raising. On these assumptions the arrived relative economic weights were 1.0, 210.0 and 2.33 for 1 gm body weight, 1 kg body weight and 1% egg rate respectively.

Table 2.7 Genetic, phenotypic and environmental correlations between body weights at various ages from literature

Source of data	Year	Criterion	Breed	Sex	r_G	r_P	r_E
Martin <u>et al</u>	1953	3 wk-6 wk	NH	C	0.91	0.83	0.76
		3 wk-9 wk		C	0.83	0.73	0.77
Horton and McBridge	1964	4 wk-8 wk	NH	M	0.47	-	-
				F	0.49	-	-
Merrit	1966	6 wk-9 wk	Meat control	M	0.05	0.84	-
				F	0.90	0.81	-
Pym and Nicholas	1979	5 wk-9 wk	Meat	M	0.82	0.79	-
			type	F	0.79	0.74	-
Sharma	1981	Day old- 8 week	-	M	0.41	-	-
				F	0.36	-	-
Dev Roy <u>et al.</u>	1983	4 wk-6 wk	WR	M	0.89	0.76	-
		4 wk-8 wk		F	0.98	0.79	-
		6 wk-8 wk		M	0.75	0.66	-
				F	0.96	0.71	-
		6 wk-8 wk		M	0.92	0.84	-
				F	1.01	0.82	-
Aman and Becker	1983	6 wk-7 wk		C	0.58	-	-
Chambers <u>et al.</u>	1984	4 wk-6 wk	Syn	C	1.03	0.77	-
		4 wk-8 wk		C	0.80	0.67	-
		6 wk-8 wk		C	1.00	0.93	-
Kumar <u>et al.</u>	1988	day old-4 wk		C	-0.49	-	-
		4 wk-8 wk		C	0.37	-	-
Poulose <u>et al.</u>	1988	4 wk-8 wk	Dwarf broiler	C	0.83	-	-
Singh <u>et al.</u>	1988	day old-6 wk	Syn	C	0.11	0.08	-
Choudhary	1992	4 wk-6 wk	Syn	C	1.34	0.69	-
Average					0.68	0.73	0.77

Table 2.8 Genetic, phenotypic and environmental correlations between body weight and shank length from literature

Source of data	Year	Criterion	Breed	Sex	r_G	r_P	r_E
Lerner, <u>et al.</u>	1947	Body wt-S.L (12 wk)	NH	C	0.99	-	-
Merritt	1968	Bwt-S.L (9 wk)	Meat type	M	-	0.77	-
				F	-	0.75	-
Saxena	1976	Bwt-S.L (10 wk)	WC	M	0.31	0.44	0.70
				F	0.42	0.65	0.94
			WR	M	0.50	0.67	0.99
				F	0.39	0.54	0.74
			NH	M	0.45	0.71	1.17
				F	0.42	0.37	0.32
Unni <u>et al.</u>	1977	Bwt-S.L	WC	M	-	0.91	-
				F		0.86	-
Mishra <u>et al.</u>	1984	Bwt-S.L (8 wk)	Cornish	C	0.41	0.61	-
					± 0.23	± 0.02	-
Champati <u>et al.</u>	1987	Bwt-S.L (8 wk)	White	M	0.58	0.59	-
			cornish		± 0.17	± 0.001	
				F	0.47	0.45	-
					± 0.20	± 0.03	
Reddy	1988	4 BW-6 Wk SL	RC	M	0.86	0.44	-
				F	0.38	0.44	-
Choudhary	1992	Bwt-S.L (6 wk)	Syn	M	0.75	0.45	-
Average					0.53	0.60	0.81
					± 0.20	± 0.02	

Table 2.9 Genetic, phenotypic and environmental correlations between body weight and breast angle from literature

Source of data	Year	Criterion	Breed	Sex	r_G	r_P	r_E
Lerner <u>et al.</u>	1947	B.Wt.-B.A.(12 wk)	NH	C	0.10	0.13	0.16
Siegel	1962b	B.Wt.-B.A.(8 wk)	Meat type	M	0.51	-	-
				F	0.53	-	-
Saxena	1976	B.Wt.-B.A.(10 wk)	WC	M	0.55	-	-
				F	0.58	-	-
			WR	M	0.58	-	-
				F	0.43	-	-
			NH	M	0.50	-	-
				F	0.41	-	-
Sharma	1981	B.Wt.-B.A.(8 wk)	Meat type	C	0.57	0.31 to	-
					0.72	0.40	
Mishra <u>et al.</u>	1984	B.Wt.-B.A.(8 wk)	RC	F	0.49	0.74	-
					± 0.20	± 0.02	
Champati <u>et al.</u>	1987	B.Wt.-B.A.(8 wk)	WC	M	0.29	0.53	-
					± 0.02	± 0.03	
				F	0.21	0.38	-
					± 0.23	± 0.03	
Reddy	1988	4BW-6 Wk BA	RC	M	0.72	0.39	-
				F	0.42	0.24	-
Choudhary	1992	B.Wt.-B.A.(6 wk)	Syn.	M	1.30	-0.30	-
Average					0.51	0.30	0.16
					± 0.32	± 0.03	

Table 2.10 Genetic and phenotypic correlations between breast angle and shank length from literature

Source of data	Year	Criterion	Breed	Sex	r_G	r_P
Lerner <u>et al.</u>	1947	At 12 wk	NH	C	0.14	0.38
Aggarwal	1975	At 10 wk	Meat type	M	0.51	0.75
				F	0.30	0.30
Saxena	1976	At 10 wk	WC	M	0.29	0.46
				F	0.46	0.53
			WR	M	0.60	0.73
				F	0.34	0.55
			NH	M	0.57	0.68
				F	0.78	0.55
Sharma	1981	At 8 wk	Pooled	M	0.66	0.39
			(4 strain)	F	0.27	0.20
Mishra <u>et al.</u>	1984	8 wk	Red	C	0.46	0.34
			Cornish		+0.18	+0.02
Choudhary	1992	6 wk	Syn	M	>1	0.01
Average					0.49	0.45
					+0.18	+0.02

Table 2.11 Genetic and phenotypic correlations between body weight and egg production from literature

Source of data	Year	Criterion	r_G	r_P
McClung	1958	8 wk BW - 4 month EP	-0.04	-
Jaap <u>et al.</u>	1962	8 wk BW - EP to 46 wks	0.15	0.03
Merritt	1968	42nd BW - H.H. Production	-0.16	-0.01
		63 d BW - H.H. Production	-0.37	-0.03
Shalev	1970	8 wk BW - rate of EP	-0.50	-0.35
Saxena	1976	10 wk BW- EP 180 d	-0.33	-0.32
			-0.19	-0.19
			-0.21	-0.20
Sharma	1981	8 wk BW - EP to 300 d	-0.13	0.02
Singh <u>et al.</u>	1988	6 wk BW - EP to 40 wk	0.47	-0.02
Average			-0.13	-0.19

Table 2.12 Genetic and phenotypic correlations between body weight and egg weight from literature

Source of data	Year	Criterion	r_G	r_P
Jaap <u>et al.</u>	1962	8 wk BW - EW at 30 wk	0.25	0.08
Friar <u>et al.</u>	1962	8 wk BW - EW	0.011	0.145
Merritt	1968	40 d BW - EW	0.15	0.18
		60 d BW - EW	0.20	0.19
Shalev	1970	8 wk BW - E.W.	0.45	0.35
Saxena	1976	10 wk BW - EW at 40 wk	0.57	0.60
			0.47	0.58
			0.33	0.45
Sharma	1981	8 wk BW - EW at 300 d	0.49	0.03
Kataria	1985	8 wk BW - EW at 40 wk	0.45	0.23
			0.43	0.52
			0.17	0.09
Average			0.33	0.29

Table 2.13 Genetic and phenotypic correlations between egg production and egg weight

Source of data	Year	Criterion	r_G	r_P
Hogsett and Nordskog	1958	Winter EP - March EW	-0.79	-0.14
Jaap <u>et al.</u>	1962	46 wk EP - 30 wk EW	-0.58	-
Merrit	1968	300 d EP - EW	-0.39	-0.13
Shalev	1970	3 month EP - EW	-0.30	-0.05
Saxena	1976	280 EP - EW	-0.31	-0.18
Sharma	1981	300 d EP - EW	-0.91	-0.01
Dev Roy	1986	40 wk EP - EW	-0.24	-0.12
			-0.67	-0.10
			-0.52	-0.16
Hazary	1988	40 wk EP - 32 wk EW	-0.43	-0.28
Balachandran and Ulaganathan	1989	40 wk EP - EW	-0.06	-0.16
			-0.19	-0.11
Average			-0.45	-0.13

Pease et al. (1967) showed that an error upto $\pm 50\%$ in the economic value of any one trait reduced the efficiency of the index less than 2% while errors upto 100% could reduce the efficiency only upto 4%.

These results were confirmed by Vandepitte and Hazel (1977) with additional traits and an extended range of changes in the economic weights. Large changes ($\pm 200\%$) in some traits, however, are shown to have substantial losses in efficiency and the losses were asymmetrical.

Kotaiah and Renganathan (1980) suggested that the direction of the economic weights assigned to the different traits entering into an index was more important than their relative magnitude. Sharma (1981) calculated two sets of economic weights assuming a target demand on an integrated broiler enterprise and also considering the performance of the flock and market price. Saxena et al. (1982) derived relative economic values considering farm profit as suggested by Hogsett and Nordskog (1958). The relative economic weights were 3.05 per 100 gm of 10 week body weight, 1.0 for rate of lay and 2.20 for egg weight in White Rocks and corresponding values in New Hampshires were 3.05, 1.00 and 1.48.

Shalev and Pasternak (1983) calculated relative economic weights of all traits affecting the profitability of a broiler enterprise.

Smith (1983) reported that moderate losses in efficiency may be incurred through changes in the economic weights. Larger losses in efficiency occur when (1) important traits are omitted and unimportant traits are given importance, or (2) when the direction of selection is reversed for an important trait.

Akbar et al. (1986) developed a systematic procedure to calculate relative economic values of the traits in the breeding objective from bio-economic function in commercial broilers.

2.4 CONTROL POPULATION

The observed changes in selected populations may result from genetic changes and environmental fluctuations. Of the various methods used for the genetic progress in poultry, the most common is the use of the unselected control populations through which the common environmental variance is eliminated.

The design of various control populations, problems related to use of controls and their importance has been well documented (Gowe et al., 1959b; Hill, 1972a,b). Gowe et al. (1959a) discussed the three important functions of control population as mentioned below.

- (a) To assess the magnitude of short term fluctuation in environment and to furnish a means of correction.
- b) To maintain genetic consistency over a period of time thereby enabling the evaluation of long term trends in the environment.
- c) To serve as a gene pool with known genetic parameters for use as base material in selected experiments.

Hill (1972a,b) discussed the value of a control with other methods as a means of measuring of genetic change in selected populations, and also considered many aspects of the design of control populations to maximise the effective breeding number and thus to minimise random genetic drift.

Thiyagasundaram (1984) has presented the detailed account of designs and advantages of maintaining the randombred pedigree-bred and repeat mating controls along with other methods of keeping genetic controls with particular reference to poultry.

Hill (1980) has discussed the necessity of elimination of common environmental variance. However, he advocated to have a stable control to estimate the actual responses.

Blair and Pollack (1984) described the detail methods with appropriate examples to estimate the genetic trend in a selected population with and without a control population.

Behaviour of control populations of meat type chicken

The first poultry meat control strain (Ottawa meat control population) started in 1955 by crossing within three commercials and one pure strain. From 1958, this population was reproduced annually by use of 80 male and 240 female parent (Merritt, 1968). During the year 1959-63 regressions of means on years were negative and non-significant for males and females for body weights at 6, 9, 21 and 44 wks (except for 21 wks in males) and also for breast angle, keel length and shank length.

Siegel (1978) discussed the performance of Athens Canadian randombred control population which was maintained for 20 generations to measure the environmental trend. The regression of 56-day body weight on generations were -1.8 ± 1.5 for males and -2.0 ± 1.48 for females and showed that phenotypic time trends over 20 generations were not important for juvenile body weight in random breeding population.

Singh et al. (1981) reported a positive but non-significant regression of 24.9 gm per generation for 8 week body weight for a random control population of 198 per generation.

Chambers et al. (1984) constituted an unselected control population from commercial stocks suitable for modern broiler breeding programmes. This population was synthesized from 16 commercial broiler parent stocks. Chambers (1987) described the performance of five generation of a random breeding sire strain control (ARC strain 20) developed with five sire time stocks in 1978 and of three selected strains derived from this base population.

2.5 POPULATION SIZE

The resources available for carrying out any poultry breeding programme is limited. Exorbitant cost of feed and managerial component compels the breeder to design a breeding plan, in respect to size of population so as to maximise the rate of genetic improvement by judicious use of resources.

During past 30 years, the population size and its importance in selection experiments has been well felt for two definite reasons.

- 1) In small populations genetic drift is very important source of variation among selected lines, causing not only variation in mean response (Hill, 1971) but also variation within the line additive genetic variance (Avery and Hill, 1977).
- 2) The artificial selection in small populations results in the chance loss of some desirable alleles, and thus results in a decreased limit to selection (Robertson, 1960).

Hill (1980) discussed the variation of response of artificial selection and the suitable size of the population to achieve a large portion of the response prediction in short term.

2.5.1 Effective population size

Effective population size, N_e , is the number of individuals that would give rise to calculated sampling variance, or rate of inbreeding, if they are bred in the manner of the idealised population (Falconer, 1981).

The relation is $N_e = 1/2 \Delta F$

Where, ΔF = rate of inbreeding.

Wright (1940) gave the formula for calculation of effective number of parents.

$$N_e = \frac{4 N_m N_f}{(N_m + N_f)}$$

Where,

The effective sires and dams (N_m and N_f) is defined as the number of progeny surviving to breeding age.

Gowe et al. (1959b) suggested a different formula for arriving at effective population size because of the possibility of each parent contributing unequal number of progeny. The formula included a term for variance of family size to arrive at effective population size. They also suggested a formula for arriving at the effective population size in a random-bred control.

Jones et al. (1968) reported a linear decline in cumulative response as the population size decreases. Bowman (1984) observed that selecting fewer parents leads to a greater rate of inbreeding, which will be not desirable. In meat type chicken selection experiment, the greatest rate of genetic gain may be predicted from a design with a population size of either 500 or 1250.

2.5.2 Inbreeding

Long-term unidirectional selection promotes development of homozygosity for favourable alleles. The expression can be derived term of the effective number by means of which the state of dispersion of the gene frequencies could be expressed as the coefficient of inbreeding. Falconer (1981) defined coefficient of inbreeding as the probability of any individual being an identical allele by descent. Wright (1931) provided the necessary formula for calculation of the expected increase in inbreeding coefficient in a random mating population which is as follows :

$$\Delta F = \frac{1}{8N_m} + \frac{1}{8N_f}$$

Where, N_m and N_f refer to the number of males and females used as parent.

Nordskog (1978) suggested that the predicted rate of increase in inbreeding using the N_e calculated as per Gowe et al. (1959b) was more close to that of actual pedigree.

Nordskog and Hardiman (1980) considered the importance of certain limiting factors including effects of inbreeding depression and natural selection on artificial selection for improvement in poultry. They showed that when N_e is less than 20, efficiency of selection may be reduced from 10 to 50%, depending on the trait selected. For relatively large populations with say $N_e = 250$, the loss of selection efficiency is 3-4 percent.

On perusal of the results in literature it can be concluded that inbreeding tends to reduce fitness. The results express consensus among poultry breeders that reproduction and survival, the major components of fitness, decline on inbreeding. So to eliminate the effects of inbreeding depression in selection studies, Hill (1980) suggested few alternatives:

- i) The use of only lines with large effective size in short-term experiments and minimise inbreeding by maximum avoidance of mating relatives.
- ii) To maintain control population with the same increment in inbreeding as the selected population so that the comparison between them should be free of inbreeding effects and
- iii) To maintain replicate lines and if necessary, replicate control population and make two way crosses as required to estimate response at the end of experiment.

Burrows (1984) suggested the avoidance of mating between relatives in a selection programme as there is possibility of inbreeding depression and restriction of genetic diversity available for further selection due to enhanced drift effect.

2.6 GENETIC DRIFT

The genetic drift occurring from the change of gene frequency from sampling is random in the sense that its direction is unpredictable, but its magnitude can be predicted in terms of variance of change (Falconer, 1981).

Wright (1952) described the theoretical consequences of genetic drift in terms of gene frequencies. Later those were extended to quantitative traits by Hill (1972).

Hill (1980) reviewed all previous work on variation in response to selection and concluded the most appropriate formula for drift variance and measurement error variance for selected and control lines.

Genetic drift results from random variation in genetic response to selection. The drift variation in any generation and is retained in all following generations because it has a genetic basis. In poultry genetic drift has been studied experimentally. Foster and Thompson (1980) divided a pedigreed control strain into three lines which were maintained genetically distinct over nine generations. Results suggested that discernible genetic drift had occurred in several traits. Singh (1986) predicted the total drift variance over three generations of selection in mass, index and control lines. The result showed that in male progeny of mass and control line for 8 week body weight, the drift variance were 113.52 and 113.97. The corresponding values in female progeny were 71.98 and 76.39.

For index unit, the total predicted drift variance for males were 66.56 and 142.43 in index and control lines. The corresponding values in female progeny were 48.85 and 113.53.

2.7 SELECTION DIFFERENTIAL

Falconer (1960) defined the selection differential (S) as the mean phenotypic value of the individuals selected as parents, expressed as a deviation from the population mean, that is from the

mean phenotypic value of all the individuals in the parental generation before selection was made.

Falconer (1960) distinguished between the expected and effective selection differential as the individual parents do not contribute equally to the offspring generation. When more extreme phenotypes are selected and they are less fertile, the natural selection is considered working against artificial selection.

Falconer (1981) suggested that if the selection applied to males and females differs, the values of S and i to be used are the unweighted means for the two sexes i.e.

$$S = \frac{1}{2} (S_m + S_f)$$

and

$$i = \frac{1}{2} (i_m + i_f)$$

The intensity of selection (i) is defined as the selection differential in phenotypic standard deviation unit $S/6_p$. Pleiotropy can cause serious over-estimation of the intensity of selection on a single trait. Selection on phenotypically correlated traits and directional selection can also bias estimation of selection intensity upward.

Hill (1977) discussed the effect of family and correlated structure as selection differentials. He viewed that the influence of family structure becomes negligible as the population size increases, unless only a few individuals are selected as parents.

In meat type chickens, several studies have shown that the effective selection differentials were not significantly different from expected selection differentials showing that natural selection has exerted little influence as response to artificial selection (Siegel, 1962; Saxena, 1976, Marks, 1983; Kataria, 1985; Singh et al 1989).

2.8 RESPONSE TO SELECTION

The response to selection (R) may be defined as the difference in mean phenotypic value of the offspring of selected parents and the whole of the parental generation before selection.

Quantitative genetic theory provides a statistical formula for prediction of expected response of the population to selection. This prediction is strictly valid only for single generation because the expected response per generation, ΔG is dependent on three component, the heritability (h^2), the intensity of selection (i) and the phenotypic standard deviation of the selection criterion (σ_p)

$$\text{So } \Delta G = i h^2 \sigma_p$$

Dickerson (1961) reported that the expected rate of improvement from selection depends upon selection intensity at each generation, degree of heritability and generation interval.

Marks and Britten (1978) reviewed the selection experiments and concluded that major genes were the first to be influenced by selection followed by additive action of minor genes in the later stages of selection programme.

Hill (1980) categorised selection experiments as short and long terms. The short term experiments are essentially of five generations or less and are aimed mainly for estimation of genetic parameters and to compare rates of response in alternative breeding programmes.

Gifford and Baker (1982) discussed the effect of intense artificial selection on genetic variability and selection responses. For a given character in a particular population, more intense selection is expected to increase the response since the frequency of favourable genes affecting that character will increase more rapidly.

Response to juvenile body weight in meat type chicken

Goodfrey and Goodman (1955) reported improvement of 277 g for 6 week body weight and 594 g for 12 week body weight from five generation of within line selection.

Jaap et al. (1962) selected a line for 8 week weight from a randambred population of White Gold meat-type fowls and reported gain in body weight at 8 weeks of age as 240gm and 190gm in males and females respectively.

Urban and kaatz (1979) studied the effect of intense selection in genetic gain in broiler breeding stock. An increase of 70 percent in body weight at 8 weeks of age was recorded after 15 generations of selection.

McCarthy and Siegel (1983) reviewed the genetical and physiological effects of selection in meat-type poultry. They concluded that prolonged selection for increased body weight of meat-type chicken produced continuous response with little evidence of depletion of genetic variance in growth rate.

Singh et al (1990) assessed the direct responses for seven generations of mass selection for 8wk. Body weight and index selection with Body weight, Breast angle, Shank length and Keel length as component trait at 8 weeks at age. The realised gains in actual units per generation in 8 wk body wt. in male progeny of MSL and ISL were 75.14 and 78.03 g, respectively, whereas the corresponding gains in female progenies were 67.05 and 72.43 g.

2.9 REALISED HERITABILITY

Student (1934) introduced the concept of realised heritability and defined the same as the ratio between response and selection differential. Falconer (1954) defined realised heritability

as the regression of response on cumulative selection differential.

Hill (1971, 1972,b) gave a detailed discussion of the factors influencing the precision on variance of realised heritability estimates from single trait selection experiments. These included population size, family size, selection intensity, number of generation of selection and the parameter themselves.

Pirchener (1981) reported that when epistasis, dominance and common environmental effects are unimportant, heritabilities from sib correlations should be similar to realised heritabilities.

Siegel (1962) reported realised heritability of 0.3 for eight week body weight from a short term selection involving four generations only.

Pym and Nicholls (1979) obtained an estimate of 0.37 for heritability of 5 to 9 week gain during five generations of selection from a broad based broiler strain.

Kataria (1985) reported realised heritabilities, computed from regression of response on cumulative selection differentials. The values for males and females respectively were 0.54 and 0.79 for White Rock 0.43 and 0.45 for White Cornish and 0.47 and 0.56 for New Hampshire breeds after two generation of selection.

Singh (1986) calculated realised heritability of 8 week body weight and of index unit during selection of mass and index selected lines for three generations from regression of responses on cumulative selection differentials and results are as follows:

	<u>Male</u>	<u>Female</u>
Mass Line	0.16±0.17	0.28±0.14
Index Line	0.22±0.05	0.36±0.05

2.10 EFFICIENCY IN PREDICTED AND REALIZED RESPONSES

Harris (1964) studied the influence of the magnitude of the sampling error on the estimates of the heritabilities and genetic correlation on the quality of prediction of response in index selection and observed that the losses increase when the heritabilities are low and genetic correlations are negative.

Caballero (1989) indicated the decrease in the agreement between realised and predicted progress due to poor parameter estimates and also due to change in the magnitude of the estimates as selection proceeds due to genetic drift or selection itself.

Singh et al (1992) studied the efficiency in predicted and realised responses in male and female progeny of meat type chicken for 3 generation of selection and found a close agreement in the efficiencies as indicated below:

Traits	Male/Efficiency in %	Female/Efficiency in %
-----	-----	-----
8 WW (g)	92	95
8 BA (°)	94	88
8 SL (cm)	100	100
8 KL (cm)	100	94
8 IU (unit)	96	97

MATERIALS AND METHODS

MATERIALS AND METHODS

3.1 HISTORY OF THE FLOCK

Two purebred broiler strains, Red Cornish (IC-3) and White Plymouth Rock (IR-3) maintained at the Experimental Broiler Farm of Central Avian Research Institute, Izatnagar (U.P.) served as the foundation stock for this study. The strain, Red Cornish is characterised by golden red plumage with single or pea comb and the Rock strain with white plumage and single comb. Red Cornish (IC-3) and white plymouth Rock (IR-3) strains were imported during the year 1972 and maintained thereafter as pedigreed closed flock separately and subjected to selection for high body weight at 8 weeks of age. The chicks hatched out during October to December, 1987 from both stocks separately constituted the base population for this study.

3.2 MODE OF SELECTION AND TRAITS UNDERTAKEN

In the present study multi-trait index selection was practised incorporating body weight at 4 and 6 weeks of age, breast angle and shank length both measured at 6th week separately for both sexes in IC-3 strain (sire line). In the case of IR-3 strain which is identified as a dam line, the traits included in the index were 4 and 6 week body weight for males and 4 and 6 week body weight, egg production to 40 weeks of age and egg weight at 40th week of age for females. All the indices were developed utilizing data from the base generation.

All the lines were reproduced during winter season in each generation. The number of males and females selected in each line and in each generation alongwith the number of progeny are given in the Table 4.1.

The data utilized in the present study was the part of an ongoing project at Central Avian Research Institute, Izatnagar (U.P.). Three generation data including that of base generation has been utilized in this study. However the 4th generation data has been used only for a limited purpose for calculating response.

3.3 MATING STRUCTURE

Within strain and generations, matings were at random with the restriction that mating of individuals having parents in common were avoided to reduce the rate of inbreeding.

3.4 CONTROL POPULATION

The pedigreed control population used in the present study was originated from IC-3 strain during 1980 and maintained as a control line in order to find out environmental fluctuations.

The number of males and females in control line with number of progeny reproduced in each generation are given in Table 4.1. In all the generations the choice of parents and their mating was random with the only restriction that birds having parents in common were avoided with the obvious reason of minimising inbreeding. Artificial insemination in a ratio of 1:2 was practised twice a week utilising fresh semen to produce the fertile eggs by keeping males and females in individual cages. The control line was maintained by randomly selecting one male and two females from each sire family. The traits as measured in selected lines were also measured in control line.

3.5 HATCHING AND MANAGEMENT

The pedigreed chicks in both selected and control lines were taken out in 3 to 5 hatches in different generations with an interval of 10 days between two consecutive hatches. The breeding birds of the selected lines were kept in single sire pens in a ratio of one male to 7-8 females. Artificial insemination was used in all four generations to reproduce chicks in control line.

Hatchable eggs after collection were cleaned and stored in egg cooler for 10 days prior to selection. Only the settable eggs were chosen for hatching and were sorted out sire-wise within the line before setting

in the incubator. The candling was done on 18th day of incubation and after removing the infertile and dead germs all the good hatchable eggs were transferred to hatcher.

The chicks were removed from the hatcher on 22nd day of incubation, pedigreed by sire and placed in floor pens under hover type brooders in deep litter houses. All the chicks were under continuous light until 42 days of age. The chicks were vaccinated with Marek's disease vaccine and F_1 R.D. vaccine on the day of the hatch. At 4th weeks of age the booster dose of F_1 R.D. vaccine was given. Then at 8th weeks of age the birds were vaccinated with R_2 B strain of R.D. vaccine. The feeding and other managerial conditions were kept identical in both selected and in control lines as far as possible within a generation. The birds were fed broiler starter ration upto 6-weeks of age, grower ration from 7-20 weeks and a layer ration thereafter. Restricted feeding was practised between 7 to 20 weeks of age twice a week. While the males and females of IC-3 strain and males of IR-3 and control line were kept on litter all through in a generation, the females of IR-3 and control population were kept at 20 weeks of age in individual cages after eliminating pullets with mistaken identity due to loss of wing bands and individual egg production upto 280 days was recorded. Since some females die before completion of the experiment in each generation, only those birds which have provided complete information were considered for the study.

4.6 MEASUREMENT OF TRAITS

(1) Body weights : The body weights at 4 week and 6 week of age were measured by Yamato and Salter balance to the nearest of 5 to 10 g accuracy.

(2) Breast angle : The breastometer was used to record breast angle in degrees at 6 weeks of age. It was placed at a point about 10 to 12 mm. posterior to the anterior edge of keel bone for measuring breast angle.

(3) Shank length : A vernier callipers was used to measure shank length at 6 week of age to the nearest of 0.1 cm. accuracy. The jaws of callipers was placed between the hock and carpal joint to measure shank length.

(4) Egg production : Egg production in dam line (IR-3) was recorded upto 40 weeks of age by keeping them in individual laying cages.

(5) Egg weight : The average weight of three consecutive eggs laid during 40th week of age of each female was recorded in IR-3 strain with 0.1 g in accuracy.

✓ 3.7 STATISTICAL ANALYSIS

All statistical analysis were carried out in DCM, PS-386 computer at Central Avian Research Institute, Izatnagar (U.P.).

✓ 3.7.1 Correction for hatch effect

Since chicks were hatched in more than one hatches in each of the generation and preliminary analysis revealed significant differences among hatches, the data were corrected for hatch effects by fitting least square constants as per Harvey (1966), separately for each sex within the strain in each generation.

The following mathematical model was used for adjustment of hatch effects.

$$Y_{ij} = \mu + h_i + e_{ij}$$

Where,

$$\begin{aligned} Y_{ij} &= \text{the observation of } j^{\text{th}} \text{ progeny of } i^{\text{th}} \text{ hatch.} \\ \mu &= \text{common overall population mean.} \\ h_i &= \text{effect of the } i^{\text{th}} \text{ hatch.} \\ e_{ij} &= \text{random error assumed to be normally and} \\ &\quad \text{independently distributed with mean 0 and variance} \\ &\quad \sigma_e^2. \end{aligned}$$

✓ 3.7.2 Mean and its standard error

The mean, standard error and co-efficient of variation for each trait was computed using the formula :

$$\bar{Y} = \frac{\sum_{i=1}^n Y_i}{n}$$

$$S.E. = \sqrt{S^2/n}$$

$$C.V. \% = S/\bar{Y} \times 100$$

Where,

\bar{Y} = mean
 Y_i = measurement of a trait on i^{th} individual
 n = number of individuals measured

$$S^2 = \frac{\sum Y_i^2 - \frac{(\sum Y_i)^2}{n}}{n - 1}$$

✓ 3.7.3 Estimation of genetic parameters

✓ 3.7.3.1 Heritability

Heritability of each trait was computed on the data adjusted for hatch effects using sire component analysis of variance as per King and Handerson (1954). Heritabilities of all the traits of selected populations and only of broiler traits of control population were initially estimated within sex/line/generation basis and then pooled over generation within the line and sex to obtain pooled estimates as per Enfield et al. (1966). In females of control population the heritabilities of egg production (upto 40 weeks of age) and egg weight (at 40th week of age) were not calculated due to small sample size at adult stage.

✓ For half-sib (sire) families

The heritabilities for index units and component traits were computed from sire component of variance. The statistical model used for heritability estimation was :

$$Y_{ij} = \mu + S_i + e_{ij}$$

Where,

- Y_{ij} = the observation of a trait on j^{th} progeny of the i^{th} sire
- μ = population mean
- S_i = effect of i^{th} sire
- and e_{ij} = the residual environmental and genetic deviation including dam effects

The analysis of variance table for calculation of heritability was as follows :

Analysis of variance

Source of variation	d.f.	S.S.	M.S.S.	E.M.S.
Between sires	S-1	SS_s	MS_s	$\sigma^2_s + K \sigma^2_w$
Progeny within sires	n.-S	SS_w	MS_w	σ^2_w

Where,

- S = total number of sires
- n. = total number of progeny
- K = average number of progeny per sire
- σ^2_s = sire component of variance
- and σ^2_w = error component of variance.

The value of 'K' was calculated from the following formula:

$$K = \frac{1}{(S-1)} \left(n. - \frac{\sum n_i^2}{n.} \right)$$

Computation formulas

Source of variation	Sum of Squares	Mean square
Correction term (C.T.)	$Y_{..}^2$	-
Between sires	$\sum_i \frac{n_i Y_i^2}{n} - CT.$	$SS_s / (S-1) = MS_s$
Progeny within sires	$\sum_i \sum_k \frac{n_i Y_{ik}^2}{n_i} - \sum_i \frac{Y_i^2}{n_i}$	$SS_w / n.-S = MS_w$

Estimation of σ_s^2 and σ_w^2

$$\sigma_w^2 = \frac{MS_w}{MS_s - MS_w}$$

$$\sigma_s^2 = \frac{\frac{1}{4} \sigma_s^2}{\sigma_s^2 + \sigma_w^2}$$

The standard errors of heritability were calculated as per Dickerson (1960) as follows :

$$S.E. (h_s^2) = \frac{4}{\sqrt{\frac{2}{k^2} \left[\frac{MS_s^2}{S-1} + \frac{MS_w^2}{n.-S} \right]}}$$

3.7.3.2 Correlations

The genetic and phenotypic correlations were estimated from variance and covariance component analysis as per Becker (1964). Variance component analysis was the same as used in the estimation of heritability.

Covariance components were estimated from covariance Table as follows:

Analysis of covariance

Source of variation	d.f.	S.C.P.	M.C.P.	E.M.C.P.
Between sires	S-1	SCP_s	MCP_s	$Cov_w + K Cov_s$
Progeny within sires	n.-S	SCP_w	MCP_w	Cov_w

Computational formulas

Source	Sum of cross products	Mean cross products
Correction term (C.T.)	$\frac{X_{..} \cdot Y_{..}}{n}$	-
Between sires	$\sum_i \frac{X_{i.} \cdot Y_{i.}}{n_i} - C.T.$	$SCP_s / S - 1 = MCP_s$
Progeny within sires	$\sum_i \sum_j \frac{X_{ij} \cdot Y_{ij}}{n_i} - C.T.$	$SCP_w / (n - S) = MCP_w$

Where, X and Y are the two traits whose correlations is to be estimated, K was the same as used for estimation of variance components. The genetic correlation between X and Y were then estimated from sire components of variance and covariance as follows:

$$r_G(XY) = \frac{Cov_S(XY)}{\sqrt{\sigma^2_{S(X)} \sigma^2_{S(Y)}}}$$

The standard error of genetic correlations was obtained as per Robertson (1959).

$$\text{S.E. of } r_G = \frac{1 - r_G^2}{\sqrt{2}} \sqrt{\frac{\text{S.E. } h^2_{(x)} \cdot \text{S.E. } h^2_{(y)}}{h^2_{(x)} h^2_{(y)}}}$$

The phenotypic correlations were calculated as follows :

$$r_{P(XY)} = \frac{\text{Cov}_S + \text{Cov}_W}{\sqrt{(\sigma^2_{S(x)} + \sigma^2_{W(x)}) (\sigma^2_{S(y)} + \sigma^2_{W(y)})}}$$

The standard error of phenotypic correlations were obtained as per Goulden (1962)

$$\text{S.E. } r_P = \frac{1 - r_P^2}{n - 2}$$

* 3.7.3.3 Pooling of parameters

Heritabilities, genetic and phenotypic correlations were initially calculated within sex-line generation basis and then pooled over generations within sex and line by weighting each estimate with the inverse of its variance to provide pooled estimates as per the formula suggested by Enfield et al. (1966). For pooling of heritabilities and their standard errors the formula used as as follows :

$$\begin{aligned} \text{Pooled heritability} &= \frac{\sum_{i=1}^n \frac{h^2}{(\text{S.E.}_i)^2}}{\sum_{i=1}^n \frac{1}{(\text{S.E.}_i)^2}} \\ \text{S.E. of pooled heritability} &= \sqrt{\frac{1}{\sum_{i=1}^n \frac{1}{(\text{S.E.}_i)^2}}} \end{aligned}$$

Genetic and phenotypic correlations were also pooled similarly.

✓ 3.7.4 Estimation of selection differential

✓ A. Expected selection differential

The deviation of mean of the selected individuals from the population mean is defined as the expected selection differentials.

$$S = \bar{X}_{\text{Selected}} - \bar{X}_{\text{population}}$$

✓ B. Standardized selection differential

Expected selection differential divided by phenotypic standard deviation is the standardised selection differential.

$$i = \frac{S}{\sigma_p}$$

Since the selection was applied to males and females separately, it has been calculated as per Falconer (1981).

$$S = \frac{1}{2} (S_m + S_f)$$

$$i = \frac{1}{2} (i_m + i_f)$$

✓

✗ C. Effective selection differential

The expected selection differential was weighted for the number of progeny produced by each sire and dam.

$$\text{Effective } S = S_E = \frac{\sum x_i n_i}{\sum n_i} - \bar{X}_p$$

Where,

X_i is the observation on the i^{th} sire
 n_i is the number of progeny of the i^{th} sire
 \bar{X}_p is population mean.

The effect of natural selection over artificial selection was calculated from the ratio of effective selection differential to expected selection differential (Falconer, 1960).

3.7.5 Effective population size and rate of inbreeding

The effective population size, N_e in each parental generation for the selected group was computed as per the formula described by Wright (1940).

$$N_e = \frac{4N_m \cdot N_f}{N_m + N_f}$$

For control line N_e was calculated as per formula suggested by Gowe et al. (1959b) as:

$$N_e = \frac{16 N_m \cdot N_f}{3N_f + N_m}$$

Where,

N_m and N_f are the numbers of male and female breeders respectively.

The increase in co-efficient of inbreeding per generation (rate of inbreeding) for selected group due to finite population size was calculated as per Wright (1931) using the following formula.

$$\Delta F = \frac{1}{8N_m} + \frac{1}{8N_f} = \frac{N_m + N_f}{8 N_m \cdot N_f}$$

Where,

N_m and N_f are the number of male and female parents respectively, which had progeny surviving upto 6 weeks of age for broiler traits.

For control line inbreeding co-efficient per generation was computed as suggested by Gowe et al. (1959b).

$$\Delta F = \frac{3}{32N_m} + \frac{1}{32N_f}$$

† 3.7.6 Construction of selection index

Sire line (IC-3)

The general outline of the selection index applicable to the present study incorporating four broiler traits is as follows:

Linear selection index :

$$I = \sum_{i=1}^4 b_i x_i = \underline{X}' \underline{b}$$

Aggregate genotype : $H \sum_{i=1}^4 a_i g_i = \underline{g}' \underline{a}$

Where,

$\underline{X}' = (x_1 \ x_2 \ \dots \ x_4)$ = a row vector of known phenotypic values

$\underline{g}' = (g_1 \ g_2 \ \dots \ g_4)$ = a row vector of unknown genetic values

$\underline{a}' = (a_1 \ a_2 \ \dots \ a_4)$ = a row vector of known relative economic values, and

$\underline{b}' = (b_1 \ b_2 \ \dots \ b_4)$ = a row vector of index coefficients to be computed.

Selection of optimum index coefficients was given by:

$$\underline{b} = P^{-1} G \underline{a}$$

The variance of the index (σ_I^2), the variance of aggregate genotype (σ_H^2) and the correlation of the index and aggregate genotype (r_{HI}) were calculated as :

$$\begin{aligned} \sigma^2_{6I} &= \underline{b}' P \underline{b} \\ \sigma^2_{6H} &= \underline{a}' G \underline{a} \\ r_{HI} &= \frac{\sigma^2_{6I}}{\sigma_{6I} \sigma_{6H}} = \frac{\sigma_{6I}}{\sigma_{6H}} \end{aligned}$$

Heritability of the index was calculated as per Nordskog (1978).

$$h^2_I = \frac{\underline{b}' G \underline{b}}{\underline{b}' P \underline{b}}$$

+ Expected response from selection index

The expected response to selection R_I from the use of index selection was obtained as

$$R_I = \bar{i} \sqrt{(\underline{b}' P \underline{b})} = \bar{i} \sigma_{6I}$$

Where,

- \bar{i} = intensity of selection
- \underline{b}' = a row vector of 4 index coefficients
- P = phenotypic variance and covariance matrix (4x4)
- σ_{6I} = standard deviation of index.

The genetic gain in the i^{th} index trait due to selection on I

was calculated as:

$$\Delta G_i = \underline{g}_i' \underline{b} (i/\sigma_{6I})$$

Where,

\underline{g}_i' is the i^{th} row vector of genetic variance covariance matrix.

The genetic responses due to selection of pullets in dam line for egg production and egg weight was calculated by multiplying in these formulae by 0.5 since regression of offspring on single parent is half of the heritability (Falconer, 1981). Further, the index unit was taken as single trait and the expected genetic response has been calculated as $i\sigma_p h^2$ as per Singh (1986), where h^2 and σ_p has been calculated from the sire component of variance and covariance analysis.

The value of each variate in the index which is the percent reduction in the efficiency on dropping that trait from the index was obtained as :

$$100 - \sqrt{\frac{b'Pb - (b_i)^2/W_{ii}}{b'Pb}} \times 100 \quad (\text{Cunningham, 1969}).$$

Where,

- W_{ii} = the diagonal element of P^{-1}
 b_i = the weighting factor of the i^{th} trait to be dropped.
 $b'Pb$ = variance of the index.

Dam line (IR-3)

The same procedure of selection was carried out in Dam line females as in sire line but the males of this line were selected using the index with two traits, i.e. 4 week body weight and 6 week body weight.

✓ 3.7.7 Realized phenotypic response (R_p) from selection index

Realized phenotypic response (R_p) per generation for the selection index units and of the component traits were estimated by regression of generation means on generation number.

✓ 3.7.8 Realized genetic response (R_g) from selection index

Realized genetic response (R_g) to selection for selection index units and of the component traits were estimated as follows :

$$R_g = (S_n - C_n) - (S_o - C_o)$$

Where,

S and C represent selected and control lines respectively and subscript represent the generation number.

Rates of response were calculated as per regression of cumulative response on generation number.

The formula used for regression of y and x was:

$$b_{yx} = \frac{\frac{\sum xy - (\sum x)(\sum y)}{n}}{\frac{\sum x^2 - (\sum x)^2}{n}}$$

Where,

y = Control deviation of selected trait (dependent variate)

x = Generation number (independent variate)

n = Number of observations

✗ The standard error of regression coefficient was calculated as given below:

$$S.E. (b) = \sqrt{\frac{\left[\frac{\sum y^2 - (\sum y)^2}{n} \right] - b \left[\frac{\sum xy - (\sum x)(\sum y)}{n} \right]}{(n-2) \left[\frac{\sum x^2 - (\sum x)^2}{n} \right]}}$$

The coefficient of regression calculated was tested for its statistical significance using t-test where,

$$t = b / S.E. (b) \text{ with } (n-2)$$

degree of freedom where there are 'n' pairs of observations.

✗ 3.7.9 Expected drift variance and sampling error measurement

Drift variance and sampling errors are major causes of variable response in a selection experiment. In this study these were estimated from the information on population parameters.

The drift variance and sampling error variance were calculated as per Hill (1972 and 1980) for selected and control lines using the formulae:

$$\sigma_{dx}^2 = \frac{t \times h^2 (1 - h^2) \sigma_p^2}{N_e}$$

$$\sigma_{dc}^2 = \frac{t \times \sigma_A^2}{K_e}$$

$$\sigma_{ex}^2 = \frac{(1 - h^2)}{M_e} \sigma_p^2$$

$$\sigma_{ec}^2 = \frac{\sigma_p^2}{J_e}$$

Where,

σ_{dx}^2 = total drift variance in selected line

σ_{dc}^2 = total drift variance in control line

σ_{ex}^2 = sampling error variance in selected line

σ_{ec}^2 = sampling error variance in control line

t = at 't' generation of selection

σ_A^2 = additive genetic variance

σ_p^2 = phenotypic variance of trait

h^2 = heritability of the trait

N_e	=	effective population size in selected line
M_e	=	number of individual scored each generation in selected line
K_e	=	effective population size in control line
J_e	=	number of individual scored each generation in control line

The drift variance in an index score per generation was estimated as per Hill (1980) as

$$(\sigma_d^2) = \frac{t \times h^2 (1 - r_{HI}^2) \sigma_P^2}{N_e}$$

Where,

h^2	=	heritability of index unit
r_{HI}	=	correlation between index and breeding value
σ_P^2	=	variance of the index unit
N_e	=	effective population size
t	=	generation number

✓ 3.7.10 Realized heritability

Realized heritabilities h_R^2 were estimated by regression of standard cumulative response on standardised cumulative selection differential for the selected traits (Manson, 1973). In the same manner regression coefficient of the component traits of indices were calculated. ✓

✗ PREDICTED AND REALIZED GENETIC REGRESSION

The formula used for the calculation of predicted genetic regression in this selection experiment was as per Kinney et al. (1970).

$$\int G_T G_C \times \frac{h_T}{h_C} \times \frac{\sigma_{PT}}{\sigma_{PC}}$$

Where,

$\int G_T G_C$ is the genetic correlation between trait T and criterion of selection.

h_T is the square root of heritability of trait T

σ_{PT} is phenotypic standard deviation of selection

h_C is the square root of heritability of criterion of selection

and σ_{PC} is the phenotypic standard deviation of criterion of selection.

✓ Realized genetic regression was obtained by dividing genetic gain in component traits with the direct gain in the index unit.

✓ Efficiency in predicted (P) and realized (R) response through 3 generations of index selection in male and female progeny was calculated as follows:

$$\text{Efficiency (E \%)} = \frac{(P - R)}{P} \times 100$$

Where,

P = predicted response on three generations of selection

R = realized response on three generations of selection ✓

RESULTS

RESULTS

4.1 EFFECTIVE POPULATION SIZE AND RATE OF INBREEDING

The effective number of sires and dams and expected increase in inbreeding (rate of inbreeding) in each generation for selected and control lines are presented in Table 4.1. The effective number of sires were considered as those which had progeny surviving upto six weeks of age in IC-3 and upto the completion of forty weeks of age in IR-3 and control line.

The average effective number of sires per generation were 33.75, 32 and 43.75 in IC-3, IR-3 and control line respectively. The effective number of dams averaged over generations were 201.25, 223.25 and 86.25 in IC-3, IR-3 and control line respectively. The average effective number of parents per generation were 116.25, 111.95 and 199.77 in IC-3, IR-3 and control line respectively.

The expected percent increase of inbreeding per generation were 0.44, 0.45 and 0.25 in IC-3, IR-3 and control line respectively. The cumulative inbreeding over three generations of selection in percentage were 1.76 in IC-3, 1.80 in IR-3 and 1.00 in control population. This however, was considered to be the upper limit since full and half-sib matings were avoided in all the lines.

4.2 HATCH EFFECTS

Since chicks were hatched out in more than one hatches in all the genetic groups studied and the preliminary analysis revealed significant hatch differences (Tables 4.2, 4.3 and 4.4) the data were subjected to least square analysis for correction of hatch effects as per Harvey (1966). The subsequent analysis were carried out with hatch corrected data.

Table 4.1. Effective number of sires and dams and expected rate of inbreeding (ΔF) in selected and control lines

Line	Gen.	Sires (N_m)	Dams (N_f)	N_e	ΔF
IC-3	S ₀	45	180	150.32	0.003326
	S ₁	30	211	105.06	0.004759
	S ₂	30	208	104.87	0.004767
	S ₃	30	206	104.75	0.004773
	Av.	33.75	201.25	116.25	0.004406
	Cumulative ΔF				0.017625
IR-3	S ₀	38	266	133.00	0.003759
	S ₁	30	209	104.93	0.004765
	S ₂	30	207	104.81	0.004770
	S ₃	30	211	105.06	0.004759
	Av.	32	223.25	111.95	0.004513
	Cumulative ΔF				0.018053
Control	C ₀	44	81	198.68	0.002516
	C ₁	43	86	196.57	0.002543
	C ₂	45	90	206.65	0.002419
	C ₃	43	88	197.21	0.002535
	Av.	43.75	86.25	199.77	0.002502
	Cumulative ΔF				0.010010

Table 4.2 Mean squares from analysis of variance to test hatch effects for various broiler traits in different lines and generations (males)

Lines	Gen.	Source of variation	d.f.	MEAN SQUARE			
				4 BW (g)	6 BW (g)	6 BA (°)	6 SL (cm)
IC-3	S ₀	Between hatches	4	81960.65**	1478393.00**	183.01**	15.72**
		Error	927	6235.17	16339.12	20.82	0.17
	S ₁	Between hatches	2	1778971.00**	1827343.00**	10884.51**	29.77**
		Error	862	5140.94	13291.80	23.38	0.09
	S ₂	Between hatches	4	266471.60**	310445.70**	2732.05**	24.73**
		Error	1272	5325.61	15151.90	23.55	0.15
	S ₃	Between hatches	3	380449.70**	307550.20**	1097.39**	90.59**
		Error	1067	5803.09	15553.70	22.04	0.11
IR-3	S ₀	Between hatches	3	343209.90**	1212577.00**	-	-
		Error	937	3487.81	10276.82	-	-
	S ₁	Between hatches	2	412703.30**	692460.90**	-	-
		Error	863	3354.08	9897.38	-	-
	S ₂	Between hatches	2	112536.80**	133472.30**	-	-
		Error	1172	3847.25	8592.72	-	-
	S ₃	Between hatches	3	376123.20**	949457.80**	-	-
		Error	1385	4541.94	12730.50	-	-
Control	C ₀	Between hatches	2	65792.64**	83958.19**	98.31**	8.90**
		Error	276	4216.98	11303.40	12.13	0.19
	C ₁	Between hatches	2	165510.10**	141909.00**	3698.80**	10.79**
		Error	314	3193.92	9741.35	23.37	0.08
	C ₂	Between hatches	3	12197.00*	102205.00**	779.86**	5.40**
		Error	434	4149.51	9957.50	26.14	0.27
	C ₃	Between hatches	2	67251.30**	98453.15**	108.34**	9.15**
		Error	198	3842.71	14523.42	18.36	0.24

* P / 0.05;

** P / 0.01

Table 4.3 Mean squares from analysis of variance to test the hatch effects for various broiler traits in different lines and generations (females)

Lines	Gen.	Source of variation	d.f.	MEAN SQUARES			
				4 BW (g)	6 BW (g)	6 BA (°)	6 SL (cm)
IC-3	S ₀	Between hatches	4	72640.64**	834590.90**	451.02**	10.23**
		Error	872	4924.12	9635.80	17.69	0.13
	S ₁	Between hatches	2	1293095.00**	1419784.00**	8877.27**	25.55**
		Error	879	4515.45	11116.20	23.48	0.11
	S ₂	Between hatches	4	262453.40**	326721.20**	3230.14**	21.11**
IR-3	S ₃	Error	1112	5052.02	13510.30	23.55	0.15
		Between hatches	3	242186.30**	178229.90**	637.76**	66.28**
	S ₀	Error	913	4978.27	9930.02	22.42	0.11
		Between hatches	3	168666.30**	449441.10**	-	-
	S ₁	Error	857	3442.31	7004.60	-	-
		Between hatches	2	263817.30**	513772.40**	-	-
	S ₂	Error	924	2923.35	7793.03	-	-
		Between hatches	2	106626.80**	128426.00**	-	-
	S ₃	Error	1142	3658.34	8498.83	-	-
		Between hatches	3	321165.40**	535671.40**	-	-
Control	C ₀	Error	1365	3923.36	9140.38	-	-
		Between hatches	2	69977.06**	58383.89**	72.68*	9.01**
	C ₁	Error	279	4424.48	9803.87	18.16	0.17
		Between hatches	2	112304.80**	149753.00**	3388.15**	5.83**
	C ₂	Error	292	3004.82	8906.57	24.18	0.10
		Between hatches	3	53197.32**	60936.27**	1158.77**	6.55**
	C ₃	Error	496	4459.27	9357.74	24.94	0.19
		Between hatches	2	54927.28**	44325.42*	1025.30**	8.25**
		Error	184	4281.35	8732.51	14.26	0.15

* P \leq 0.05; ** P \leq 0.01

Table 4.4 Mean squares from analysis of variance to test hatch effects for various production traits in different lines and generations (females)

Lines	Gen.	Source of variation	d.f.	Mean Squares	
				E.P.	E.W.
IR-3	S ₀	Between hatches	3	3026.99**	640.20**
		Error	378	263.49	17.48
	S ₁	Between hatches	2	134.94	8.32
		Error	466	323.68	20.03
	S ₂	Between hatches	2	1431.39**	200.31**
		Error	403	252.79	16.58
	S ₃	Between hatches	3	4023.38**	612.97**
		Error	524	295.27	15.25
Control	C ₀	Between hatches	2	459.04	0.59
		Error	92	394.25	21.80
	C ₁	Between hatches	2	449.46*	1.22
		Error	111	115.40	11.45
	C ₂	Between hatches	3	80.72	2.94
		Error	92	50.77	7.32
	C ₃	Between hatches	2	501.32**	1.52
		Error	100	98.29	6.31

* P / 0.05; ** P / 0.01

4.3 MEANS, STANDARD ERROR AND COEFFICIENT OF VARIATION

Body weights

Tables 4.5 and 4.6 present the least square means of various broiler traits in IC-3, IR-3 and control population.

The means of 4 week body weight of males in IC-3, IR-3 and control line over generations varied from 492.08 g to 530.21 g, 480.01 g to 501.25 g and 390.27 g to 394.9 g, respectively. While the corresponding variation of mean values in females were from 438.66 g to 479.87 g, 426.73 g to 459.54 g and 352.70 g to 357.25 g. The regression of progeny means on generation number of IC-3, IR-3 and control lines were 9.85 ± 10.07 , 3.72 ± 7.72 and -0.48 ± 7.59 respectively with corresponding values in females 9.38 ± 11.54 , 7.35 ± 8.14 and -1.02 ± 6.57 . In selected lines the percent coefficient of variance showed a declining and no marked change was observed in control line.

The least square means ^{of 6 weeks body weight} in males of IC-3, IR-3 and control line over generations (Tables 4.5 and 4.6) varied from 1021.16 g to 1073.0 g, 967.28 g to 990.50 g and 797.03 g to 796.80 g respectively. While the corresponding variation of mean values in females were from 874.72 g to 927.94 g, 836.94 g to 865.31 g and 691.46 g to 667.79 g. The regression coefficients in males of IC-3, IR-3 and control line were 25.08 ± 29.10 , 13.66 ± 17.92 and 3.05 ± 17.37 respectively and corresponding values in females were 21.24 ± 17.36 , 13.36 ± 16.07 and -5.58 ± 12.68 . The coefficient of variations were less in selected lines compared to control lines.

Breast angle at 6th weeks of age

The least square means as presented in Tables 4.5 and 4.6 for breast angle at 6 weeks of age envisage the change of mean values in IC-3 and control line males from 65.23° to 64.60° and 63.05° to 56.90° respectively over the generations. In case of females the

Table 4.5 Means along with standard errors, coefficients of variation and phenotypic regressions in males for different broiler traits in selected and control lines

Traits	Lines	GENERATIONS				b±S.E.
		S_0/C_0	S_1/C_1	S_2/C_2	S_3/C_3	
		n $\bar{x} \pm S.E.$	n $\bar{x} \pm S.E.$	n $\bar{x} \pm S.E.$	n $\bar{x} \pm S.E.$	
4 BW (g)	IC-3	931 492.08±2.58 (16.01)	865 544.50±2.43 (13.15)	1277 528.65±2.03 (13.78)	1071 530.21±2.32 (14.35)	9.85±10.07
	IR-3	941 480.01±2.00 (12.80)	866 513.23±1.96 (11.28)	1175 486.70±1.78 (12.53)	1389 501.25±1.80 (13.45)	3.72± 7.72
	Control	279 390.27±3.90 (16.57)	317 421.72±3.16 (13.35)	438 403.00±3.06 (15.92)	201 394.91±4.78 (17.16)	-0.48± 7.59
						25.08±29.10
6 BW (g)	IC-3	932 1021.16±4.17 (12.49)	865 923.74±3.91 (12.06)	1277 1019.04±3.43 (12.46)	1071 1073.00±3.80 (11.60)	13.66±17.92
	IR-3	941 967.28±3.29 (10.46)	866 905.00±3.37 (10.98)	1175 971.95±2.96 (10.43)	1389 990.50±3.02 (11.37)	13.66±17.92
	Control	279 797.03±6.34 (13.29)	317 730.66±5.52 (13.46)	438 761.80±4.75 (13.05)	201 796.80±7.42 (13.17)	3.05±17.34
						0.03± 0.64
6 BA (°)	IC-3	932 65.23±0.15 (6.96)	865 62.57±0.16 (7.72)	1277 64.75±0.14 (7.48)	1071 64.60±0.14 (7.26)	-1.92± 0.86
	Control	279 63.05±0.21 (5.50)	317 57.77±0.27 (8.34)	438 57.03±0.24 (8.93)	201 56.90±0.29 (7.27)	-0.03± 0.26
	IC-3	932 6.48±0.01 (6.39)	865 5.58±0.01 (5.52)	1277 6.62±0.01 (5.99)	1071 6.03±0.01 (5.70)	-0.20± 0.10
	Control	279 5.98±0.03 (7.41)	317 5.34±0.02 (5.21)	438 5.47±0.03 (9.64)	201 5.27±0.02 (6.67)	13.51±13.63
Index unit	IC-3	932 1215.75±3.50 (8.80)	865 1174.93±3.34 (8.52)	1277 1239.42±2.96 (8.55)	1071 1239.38±3.27 (8.62)	3.84± 2.96
	IR-3	941 310.24±1.07 (10.61)	866 301.62±0.95 (10.23)	1175 312.51±0.96 (10.55)	1389 319.40±0.91 (10.64)	-15.39±11.57
	Control*	279 1051.73	317 988.22	438 997.76	201 997.25	1.32± 2.72
	Control**	279 254.70	317 244.82	438 255.74	201 255.46	

Figures in parenthesis are coefficients of variation

Control* - Index unit calculated with control means using same b-values of IC-3 for 4-traits

Control** - Index unit calculated with control means using same b-values of IR-3 for 2 traits

Table 4.6 Means along with standard errors, coefficients of variation and phenotypic regressions in females for different broiler traits in selected and control lines

Traits	Lines	GENERATIONS					b±S.E.
		S/C_0	S/C_1	S/C_2	S/C_3		
		n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$		
4 BW (g)	IC-3	877 438.66±2.36 (15.96)	882 496.03±2.26 (13.53)	1117 466.22±2.12 (15.22)	917 479.87±2.32 (14.67)	9.38±11.54	
	IR-3	861 426.73±1.99 (13.79)	927 464.71±1.77 (11.63)	1145 439.77±1.78 (13.74)	1369 459.54±1.69 (13.60)	7.35± 8.14	
	Control	282 352.70±3.95 (18.79)	295 378.83±3.18 (14.42)	500 355.03±2.97 (18.75)	187 357.25±4.25 (16.28)	-1.02± 6.57	
6 BW (g)	IC-3	877 874.72±3.31 (11.20)	882 825.33±3.54 (12.76)	1117 878.02±3.47 (13.21)	917 927.94±3.29 (10.72)	21.24±17.36	
	IR-3	861 836.94±2.84 (9.97)	927 783.33±2.89 (11.26)	1145 831.83±2.72 (11.08)	1369 865.31±2.58 (11.03)	13.36±16.07	
	Control	282 691.46±5.88 (14.27)	295 635.23±5.48 (14.8)	500 650.39±4.31 (14.83)	187 667.79±7.57 (15.52)	-5.58±12.63	
6 BA (°)	IC-3	877 63.71±0.14 (6.59)	882 60.87±0.16 (7.96)	1117 62.36±0.14 (7.76)	917 62.23±0.16 (7.59)	-0.29± 0.60	
	Control	282 61.62±0.25 (6.89)	295 56.13±0.28 (8.73)	500 53.90±0.22 (9.23)	187 52.84±0.32 (8.23)	-2.86± 1.12	
	IC-3	877 6.09±0.01 (6.0)	882 5.33±0.01 (6.28)	1117 6.24±0.01 (6.25)	917 5.72±0.01 (5.75)	-0.02± 0.22	
6 SL (cm)	Control	282 5.65±0.02 (7.43)	295 5.04±0.02 (6.44)	500 5.25±0.02 (9.23)	187 5.17±0.02 (5.29)	-0.12± 0.11	
	IC-3	877 338.00±1.78 (15.65)	882 373.51±1.93 (15.37)	1117 343.15±1.77 (17.26)	917 384.25±1.83 (14.42)	8.93±10.39	
	Control	282 257.68	295 266.43	500 248.05	187 255.46	-2.00± 4.37	

Figures in parenthesis are coefficients of variation

values change from 63.71° to 62.23° and 61.62° to 52.84° in IC-3 and control line respectively. The regression coefficients in males of IC-3 and control line were 0.03 ± 0.64 and -1.92 ± 0.86 respectively and the corresponding values in females were -0.29 ± 0.60 and -2.86 ± 0.12 . The percent coefficient of variation showed lower values in selected line than control line indicating the presence of less variability in IC-3.

Shank length at 6 weeks of age

The least square means for shank length in males of IC-3 and control line at 6 weeks of age has been presented in Tables 4.5 and 4.6. The shank length varied from 6.48 cm to 6.03 cm and 5.98 cm to 5.27 cm over the generations in IC-3 and control lines respectively, while the corresponding variation of mean values in females were from 6.09 cm to 5.72 cm and 5.65 cm to 5.17 cm. The phenotypic regression in males of IC-3 and control line were -0.03 ± 0.26 and -0.20 ± 0.10 respectively. While in females the regression values were -0.02 ± 0.22 and -0.12 ± 0.11 .

The percent coefficient of variation showed low values in general in IC-3 in comparison to control line.

Egg production upto 40 weeks of age

On perusal of Table 4.7 it is evident that the least square means for egg production (in number) to 40 weeks of age in females of IR-3 and control line varied from 54.10 to 53.8 and 50.35 to 41.6 respectively over S_0 to S_2 generation of selection. The regression of generation means on generation number was found to be -0.78 ± 1.82 for IR-3 and -3.58 ± 1.42 for control line. The percent C.V. was found to be more in different generations in IR-3 than in control line.

Egg weight at 40th week of age

The least square means for egg weight at 40th week of age are tabulated in Table 4.7. The change in means in females of

Table 4.7 Means along with standard errors, coefficients of variation and phenotypic regressions in females for index used and for different component traits of the index in adult stage in selected and control lines

Traits	Lines	GENERATIONS				b±S.E.
		S_0/C_0	S_1/C_1	S_2/C_2	S_3/C_3	
		n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$	n $\bar{X} \pm S.E.$	
4 BW (g)	IR-3	382 428.43±2.68 (12.22)	469 467.82±2.01 (9.28)	406 442.48±2.25 (10.28)	528 461.23±2.11 (10.52)	7.31± 8.36
	Control	92 355.50±4.74 (12.80)	114 379.45±4.44 (13.59)	96 358.02±5.34 (14.63)	103 359.82±4.79 (13.52)	-0.76± 6.03
6 BW (g)	IR-3	382 838.45±3.17 (7.41)	469 789.25±2.70 (7.42)	406 833.43±3.15 (7.62)	528 866.23±3.11 (8.24)	12.75±14.93
	Control	92 693.73±8.18 (11.30)	114 636.55±6.38 (10.71)	96 651.47±8.49 (12.77)	103 669.81±8.81 (13.35)	-5.68±12.89
EP (no.)	IR-3	382 54.10±0.82 (29.88)	469 60.93±0.82 (29.14)	406 54.04±0.78 (29.15)	528 53.80±0.73 (31.17)	-0.78± 1.82
	Control	92 50.35±2.04 (38.90)	114 50.84±0.99 (20.93)	96 41.25±0.71 (16.99)	103 41.60±0.75 (18.25)	-3.58± 1.42
EW (g)	IR-3	382 55.79±0.21 (7.46)	469 56.21±0.20 (7.92)	406 57.80±0.20 (7.02)	528 57.44±0.19 (7.60)	0.65± 0.25
	Control	92 52.60±0.47 (8.75)	114 52.27±0.31 (6.41)	96 51.98±0.27 (5.12)	103 50.86±0.37 (7.52)	-0.55± 0.14
Index unit	IR-3	382 1590.80±0.83 (1.01)	469 1573.09±0.83 (1.14)	406 1595.37±0.78 (0.99)	528 1626.70±0.73 (1.03)	12.70± 7.93
	Control	92 1391.33	114 1322.94	96 1282.25	103 1298.17	-32.02±13.49

* P < 0.05

IR-3 and control line were 55.79 g to 57.44 g and 52.60 g to 50.86 g respectively from S_0 to S_2 generation of selection and the corresponding phenotypic regression coefficients were 0.19 ± 0.25 and -0.55 ± 0.14 . The C.V.% was found to be not much different in IR-3 and control line.

Index unit

The mean index units in different generations in the four indices are presented in Tables 4.5, 4.6 and 4.7. In males of IC-3 and IR-3 the mean values changed from 1215.75 to 1239.28 and 310.24 to 319.40 respectively over three generations of selection, however the respective variation in values in females were 259.28 to 300.74 and 1590.80 to 1626.70. The regression of mean index units over generation number in males of IC-3 and IR-3 were 13.51 ± 13.63 and 3.84 ± 2.96 respectively. The corresponding values in females were 8.93 ± 10.39 and 12.70 ± 7.93 .

4.4 GENETIC AND PHENOTYPIC PARAMETERS

4.4.1 Heritability

The heritability estimates along with their standard errors of various economic traits for the selected and control lines are presented in Table 4.8 for broiler traits and in Table 4.9 for production traits. The heritabilities were estimated initially from sire component of variance and then pooled over generations within lines and sex as per Enfield et al. (1966) to obtain the pooled estimates.

Body weight

The pooled estimates (h_s^2) for 4 week body weight in males were 0.414 in IC-3, 0.251 in IR-3 and 0.412 in control population, while the corresponding values in females were 0.272, 0.314 and 0.550, respectively in three lines (Table 4.8).

Table 4.8 Heritability estimates (h_s^2) of various broiler traits in selected and control lines

Line	Gen.	4 B.W.		6 B.W.		6 B.A.		6 S.L.		Index Unit	
		M	F	M	F	M	F	M	F	M	F
IC-3	S ₀	0.388	0.264	0.408	0.209	0.506	0.249	0.296	0.099	0.514	0.313
		+0.111	+0.093	+0.114	+0.084	+0.129	+0.091	+0.096	+0.064	+0.130	+0.101
		-0.435	-0.234	-0.485	-0.428	-0.201	-0.261	-0.263	-0.170	-0.457	-0.360
	S ₁	+0.133	+0.091	+0.143	+0.131	+0.084	+0.097	+0.098	+0.077	+0.137	+0.118
		-0.428	-0.335	-0.467	-0.330	-0.387	-0.232	-0.215	-0.334	-0.485	-0.349
		+0.122	+0.106	+0.129	+0.105	+0.113	+0.084	+0.077	+0.106	+0.133	+0.109
	Pooled	0.414	0.272	0.447	0.290	0.319	0.245	0.251	0.212	0.486	0.338
		+0.069	+0.055	+0.073	+0.058	+0.059	+0.052	+0.051	+0.044	+0.076	+0.062
		-0.020	-0.035	-0.030	-0.061	-0.059	-0.008	-0.041	-0.118	-0.015	-0.025
	b±S.E.	+0.016	+0.038	+0.027	+0.092	+0.142	+0.012	+0.014	+0.037	+0.018	+0.017
IR-3	S ₀	0.185	0.288	0.210	0.358	-	-	-	-	0.216	-
		+0.077	+0.100	+0.082	+0.113	-	-	-	-	+0.083	-
		-0.281	-0.348	-0.167	-0.248	-	-	-	-	-0.175	-
	S ₁	+0.102	+0.114	+0.077	+0.093	-	-	-	-	+0.079	-
		-0.331	-0.315	-0.347	-0.381	-	-	-	-	-0.182	-
		+0.098	+0.095	+0.101	+0.109	-	-	-	-	+0.077	-
	Pooled	0.251	0.314	0.244	0.321	-	-	-	-	-0.190	-
		+0.052	+0.059	+0.049	+0.058	-	-	-	-	+0.045	-
		-0.073	-0.013	-0.069	-0.012	-	-	-	-	-0.017	-
	b±S.E.	+0.013	+0.027	+0.064	+0.070	-	-	-	-	+0.014	-
Control	C ₀	0.322	0.665	0.382	0.413	0.259	0.103	0.593	0.472	-	-
		+0.191	+0.234	+0.200	+0.204	+0.182	+0.157	+0.226	+0.212	-	-
		-0.650	-0.221	-0.618	-0.134	-0.804	-0.516	-0.270	-0.236	-	-
	C ₁	+0.219	+0.172	+0.216	+0.159	+0.236	+0.211	+0.168	+0.175	-	-
		-0.765	-0.942	-0.723	-0.856	-0.691	-0.572	-0.271	-0.244	-	-
		+0.200	+0.208	+0.196	+0.200	+0.192	+0.169	+0.138	+0.122	-	-
	Pooled	0.412	0.550	0.574	0.413	0.544	0.365	0.329	0.283	-	-
		+0.099	+0.115	+0.117	+0.106	+0.115	+0.100	+0.096	+0.090	-	-
		-0.221	-0.138	-0.170*	-0.222	-0.216	-0.235	-0.161	-0.144	-	-
	b±S.E.	+0.061	+0.336	+0.038	+0.289	+0.190	+0.103	+0.060	+0.070	-	-

* P < 0.05

Table 4.9 Heritability estimates (h^2_s) of various production traits (females)

Line	Gen.	E.P.	E.W.	Index unit
IR-3	S_0	0.535±0.187	0.461±0.177	0.594±0.195
	S_1	0.305±0.137	0.127±0.098	0.323±0.140
	S_2	0.315±0.148	0.185±0.122	0.192±0.124
	Pooled	0.360±0.088	0.195±0.070	0.313±0.084
	b ± S.E.	-0.110±0.069	-0.138±0.113	-0.201±0.049

The pooled estimates (h^2_s) for 6 week body weights were slightly higher than the corresponding estimates for 4 week body weight except the males of IR-3 and females of control line. The pooled estimates were 0.447, 0.244 and 0.574 for males and 0.290, 0.331 and 0.413 for females in IC-3, IR-3 and control population respectively (Table 4.8).

Shank length

On perusal of the Table 4.8 it is revealed that the pooled heritability estimates of shank length at 6 weeks of age were 0.251 and 0.329 in the males of IC-3 and control line respectively while the corresponding values in females were 0.212 and 0.283.

Egg production

The Table 4.9 displays the heritability estimates for egg number upto 40 weeks of age in IR-3. The heritability in the base generation was 0.535 and it reduced in subsequent two generations to 0.305 and 0.315, respectively. The pooled estimate was found to be 0.36.

Egg weight

The pooled estimate of heritability in IR-3 was 0.195 (Table 4.9). In the base generation the estimate was 0.461 and it reduced to 0.127 and 0.185 in subsequent two generations.

Index unit

On perusal of the Tables 4.8 and 4.9 it is revealed that the pooled heritability estimates of index unit were 0.486 to 0.190 in males of IC-3 and IR-3 respectively while the corresponding values in females were 0.338 and 0.313.

4.4.2 Time trend in heritability estimates

Time trends in heritability estimates have been presented in Table 4.8 and 4.9. It is observed that the trend was positive for four and six week body weight in both sexes and in both the selected lines and the unselected control population. However, for breast angle and shank length and also for index unit, no definite trend could be established. While it was negative for breast angle in both sexes in IC-3, it was positive in control population. In case of shank length it was negative for breast angle in both sexes in IC-3 - and it was positive in control population. In case of shank length it was negative for both the sexes in control and in males of IC-3 strain. For index unit the trend was found to be negative in case of males in both the selected strains and also in IR-3 females over three generations of selection, while in IC-3 females the trend was lowly positive. For egg production and egg weight in IR-3 strain the time trend was found to be negative, so was the trend in index unit.

4.4.3 Correlations

The genetic and phenotypic correlations were estimated from sire component of variance and covariance utilizing variance and covariance component analysis. Correlations were initially estimated within sex, line and generation basis and pooled over generations as per Enfield et al. (1966).

Four week body weight and six week body weight

Four week body weight was seen to be high and positively and significantly correlated with six week body weight both on genetic and phenotypic levels (Table 4.10A) in both selected and the unselected control populations and in all the three generations under study. The pooled estimates of genetic correlations in males were 0.940, 0.974 and 0.938 in IC-3, IR-3 and control line respectively, while the respective values in females were 0.975, 0.965 and 0.732. However, the corresponding pooled estimates of phenotypic correlations in males were 0.791, 0.831 and 0.810 and in case of females the values were 0.764, 0.818 and 0.784,

Table 4.10 Genetic and phenotypic correlations between broiler and production traits

Lines	Gen.	r_g		r_p	
		----- M ----- F		----- M ----- F	
IC-3	S_0 S_1 S_2 Pooled	>1 0.924±0.117** 0.948±0.080** 0.940±0.066**	0.958±0.105** 0.883±0.232** 0.980±0.039** 0.975±0.036**	0.747±0.008** 0.752±0.008** 0.824±0.005** 0.791±0.003**	0.717±0.010** 0.748±0.009** 0.789±0.006** 0.764±0.004**
IR-3	S_0 S_1 S_2 Pooled	0.957±0.120** 0.468±1.007 0.977±0.043** 0.974±0.040**	0.975±0.051** 0.836±0.328* 0.926±0.132** 0.965±0.047**	0.812±0.006** 0.654±0.012** 0.860±0.004** 0.831±0.003**	0.783±0.007** 0.679±0.011** 0.849±0.004** 0.818±0.003**
Control	C_0 C_1 C_2 Pooled	>1 0.938±0.072** 0.938±0.072** 0.938±0.072**	0.732±0.415 >1 >1 0.732±0.415	0.673±0.020** 0.800±0.011** 0.383±0.008** 0.810±0.006**	0.498±0.003** 0.722±0.016** 0.821±0.008** 0.784±0.006**
IC-3	(B) 4 BW x 6 BA				
IC-3	S_0 S_1 S_2 Pooled	0.716±0.380 0.675±0.608 0.723±0.402 0.711±0.250**	0.415±0.979 0.278±1.145 0.378±0.946 0.357±0.584	0.388±0.020** 0.426±0.020** 0.431±0.016** 0.417±0.010**	0.236±0.260** 0.397±0.020** 0.494±0.015** 0.419±0.010**
Control	C_0 C_1 C_2 Pooled	0.310±1.353 0.701±0.335* 0.478±0.470 0.612±0.267*	-0.099±1.672 0.768±0.532 0.767±0.245** 0.752±0.220**	0.304±0.042** 0.455±0.031** 0.352±0.031** 0.382±0.019**	0.284±0.043** 0.480±0.031** 0.401±0.027** 0.407±0.018**
IC-3	(C) 4 BW x 6 SL				
IC-3	S_0 S_1 S_2 Pooled	0.868±0.235** 0.736±0.461 0.598±0.667 0.819±0.199**	0.387±1.478 0.583±0.959 0.650±0.561 0.581±0.449	0.443±0.018** 0.528±0.016** 0.533±0.013** 0.501±0.008**	0.447±0.019** 0.432±0.019** 0.633±0.011** 0.555±0.008**
Control	C_0 C_1 C_2 Pooled	0.589±0.683 0.800±0.378* 0.760±0.381* 0.773±0.249**	0.435±0.538 >1 0.632±0.512 0.554±0.399	0.488±0.031** 0.415±0.033** 0.319±0.033** 0.410±0.018**	0.372±0.038** 0.390±0.036** 0.371±0.028** 0.376±0.019**
IC-3	(D) 6 BW x 6 BA				
IC-3	S_0 S_1 S_2 Pooled	0.622±0.470 0.739±0.491 0.751±0.357* 0.712±0.246**	0.485±0.991 0.610±0.635 0.379±0.950 0.526±0.465	0.465±0.018** 0.542±0.016** 0.493±0.014** 0.501±0.009**	0.300±0.024** 0.525±0.016** 0.515±0.015** 0.481±0.009**

Contd...

Table 4.10 contd...

1	2	3	4	5	6
Control	C ₀	0.732±0.258**	0.293±1.880	0.515±0.031**	0.430±0.034**
	C ₁	0.744±0.301*	0.937±0.200**	0.550±0.025**	0.637±0.021**
	C ₂	0.658±0.353	0.790±0.231**	0.432±0.027**	0.466±0.027**
	Pooled	0.718±0.171**	0.870±0.151**	0.500±0.016**	0.539±0.014**
(E) 6 BW x 6 SL					
IC-3	S ₀	0.748±0.411	0.529±1.365	0.572±0.014**	0.564±0.015**
	S ₁	0.656±0.553	0.460±0.943	0.553±0.015**	0.487±0.017**
	S ₂	0.625±0.616	0.712±0.482	0.577±0.012**	0.620±0.011**
	Pooled	0.694±0.290*	0.647±0.409	0.568±0.007**	0.576±0.007**
Control	C ₀	0.642±0.522	0.404±0.863	0.390±0.041**	0.374±0.038**
	C ₁	0.575±0.719	0.741±1.036	0.426±0.033**	0.459±0.034**
	C ₂	0.869±0.226**	0.622±0.540	0.388±0.029**	0.402±0.027**
	Pooled	0.825±0.200**	0.589±0.418	0.401±0.019**	0.413±0.018**
(F) 6 BA x 6 SL					
IC-3	S ₀	0.375±0.745	0.040±1.773	0.256±0.024**	0.111±0.030**
	S ₁	0.354±0.151*	-0.093±1.387	0.245±0.026**	0.256±0.025**
	S ₂	0.152±1.044	0.037±1.104	0.308±0.019**	0.422±0.017**
	Pooled	0.311±0.536	-0.003±0.776	0.277±0.012**	0.322±0.012**
Control	C ₀	0.550±0.562	0.037±1.941	0.205±0.025**	0.242±0.046**
	C ₁	0.577±0.643	-0.188±1.214	0.269±0.041**	0.325±0.040**
	C ₂	0.472±0.741	0.692±0.532	0.312±0.031**	0.353±0.029**
	Pooled	0.539±0.367	0.393±0.472	0.251±0.017**	0.322±0.020**
(G) 4 BW x EP					
IR-3	S ₀	-	0.212±1.341	-	0.026±0.050
	S ₁	-	0.320±0.955	-	0.009±0.046
	S ₂	-	0.517±1.099	-	-0.123±0.056*
	Pooled	-	0.039±0.634	-	-0.021±0.280
(H) 4 BW x EW					
IR-3	S ₀	-	0.068±1.479	-	0.081±0.047
	S ₁	-	0.576±1.028	-	0.060±0.044
	S ₂	-	0.561±1.276	-	0.016±0.049
	Pooled	-	0.455±0.704	-	0.053±0.027*
(I) 6 BW x EP					
IR-3	S ₀	-	0.268±0.797	-	0.045±0.049
	S ₁	-	0.178±1.056	-	-0.034±0.048
	S ₂	-	-0.503±1.170	-	-0.170±0.058**
	Pooled	-	0.066±0.558	-	-0.040±0.029

Contd...

Table 4.10 contd...

1	2	3	4	5	6
(J) 6 BW x EW					
IR-3	S ₀	-	0.070±0.906	-	0.047±0.049
	S ₁	-	-0.138±1.544	-	0.061±0.043
	S ₂	-	0.882±0.432*	-	0.032±0.048
	Pooled	-	0.701±0.384	-	0.047±0.026
(K) EP x EW					
IR-3	S ₀	-	-0.106±0.849	-	-0.031±0.053
	S ₁	-	-0.321±1.560	-	0.118±0.041**
	S ₂	-	-0.371±1.315	-	0.073±0.041
	Pooled	-	-0.208±0.648	-	0.065±0.026*
(L) IU x 4 BW					
IC-3	S ₀	>1	0.978±0.047**	0.900±0.003**	0.908±0.003**
	S ₁	0.972±0.045**	0.901±0.210**	0.899±0.003**	0.902±0.003**
	S ₂	0.975±0.039**	0.972±0.052**	0.918±0.002**	0.915±0.003**
	Pooled	0.973±0.029**	0.973±0.034**	0.909±0.001**	0.908±0.002**
IR-3	S ₀	0.979±0.059**	0.716±0.658	0.909±0.003**	0.326±0.035**
	S ₁	0.763±0.564	0.620±0.641	0.823±0.006**	0.240±0.035**
	S ₂	0.844±0.318**	-0.021±1.829	0.793±0.005**	0.293±0.035**
	Pooled	0.972±0.058**	0.642±0.445	0.869±0.002**	0.286±0.029**
(M) IU x 6 BW					
IC-3	S ₀	0.967±0.049**	0.962±0.089**	0.914±0.003**	0.874±0.004**
	S ₁	0.974±0.040**	0.983±0.029**	0.915±0.003**	0.915±0.004**
	S ₂	0.982±0.028**	0.958±0.079**	0.929±0.002**	0.931±0.002**
	Pooled	0.977±0.020**	0.978±0.026**	0.922±0.001**	0.918±0.002**
IR-3	S ₀	0.991±0.011**	0.684±0.438	0.981±0.001**	0.579±0.022**
	S ₁	0.928±0.227**	0.661±0.601	0.968±0.001**	0.467±0.025**
	S ₂	0.932±0.214**	0.207±1.828	0.984±0.001**	0.460±0.027**
	Pooled	0.991±0.010**	0.659±0.347	0.977±0.001**	0.511±0.014**
(N) IU x 6 BA					
IC-3	S ₀	0.785±0.271**	0.570±0.750	0.640±0.012**	0.421±0.020**
	S ₁	0.793±0.409	0.629±0.647	0.700±0.010**	0.593±0.014**
	S ₂	0.823±0.261**	0.528±0.786	0.676±0.009**	0.609±0.012**
	Pooled	0.802±0.170**	0.582±0.415	0.676±0.006**	0.571±0.008**
(O) IU x 6 SL					
IC-3	S ₀	0.788±0.328*	0.306±1.485	0.605±0.013**	0.327±0.023**
	S ₁	0.711±0.489	0.356±1.101	0.605±0.013**	0.308±0.023**
	S ₂	0.584±0.660	0.505±0.714	0.641±0.010**	0.513±0.015**
	Pooled	0.737±0.252**	0.438±0.555	0.621±0.007**	0.422±0.011**

Contd...

Table 4.10 contd...

1	2	3	4	5	6
(P) IU x EP					
IR-3	S ₀	-	0.863±0.198**	-	0.812±0.010**
	S ₁	-	0.852±0.326**	-	0.841±0.007**
	S ₂	-	0.735±0.690	-	0.768±0.012**
	Pooled	-	0.852±0.164**	-	0.819±0.005**
(Q) IU x EW					
IR-3	S ₀	-	0.139±0.808	-	0.207±0.041**
	S ₁	-	-0.236±1.609	-	0.340±0.031**
	S ₂	-	0.319±1.672	-	0.306±0.035**
	Pooled	-	0.103±0.662	-	0.296±0.020**

* P \leq 0.05;** P \leq 0.01

respectively.

Four week body weight and six week breast angle

The correlations between 4 week body weight and 6 week breast angle are summarised in Table 4.10B. The pooled genetic and phenotypic correlations in both the sexes of IC-3 and control line were positive and significant except in the female of control population on genetic scale where it was negative but non-significant. In the males the genetic correlations were 0.711 and 0.612 in IC-3 and control line respectively and in females the respective values were 0.357 and 0.752. The phenotypic correlations in males of IC-3 and control line were 0.417 and 0.382 respectively while in the females the values were 0.419 and 0.407.

Four week body weight and six week shank length

The genetic and phenotypic correlations between 4. week body weight and shank length have been summarised in Table 4.10C. The correlations in both the scales were significant and positive. The pooled genetic correlations in males were 0.819 and 0.773 in IC-3 and control line respectively while the respective values in females were 0.581 and 0.554. The pooled over generation phenotypic correlations were 0.501 and 0.410 in males of IC-3 and control line respectively while the respective values in females were 0.551 and 0.376.

Six week body weight and six week breast angle

Positive and significant correlations were found between 6 week body weight and 6 week breast angle in all the cases (Table 4.10D) except the values in IC-3 females were non-significant but positive. The pooled genetic correlations in males were 0.712 and 0.718 in IC-3 and control line respectively while the respective values for females were 0.501 and 0.5. The corresponding phenotypic correlations in males were 0.526 and 0.870 and in females were 0.481 and 0.539 respectively.

Six week body weight and six week shank length

The pooled genetic correlations between 6 week body weight with 6 week shank length were significant and positive and the values were 0.694 and 0.825 in males of IC-3 and control line respectively. While the respective values in females were 0.647 and 0.589 (Table 4.10E). The pooled phenotypic correlations were found to be 0.568 and 0.401 in the males of IC-3 and control line while the respective values in females were 0.576 and 0.413. These values were highly significant.

Six week breast angle and six week shank length

The pooled genetic correlations between 6 week breast angle and 6 week shank length in males of IC-3 and control line were 0.311 and 0.539 respectively. While the values in females were - 0.003 and 0.393 (Table 10F). The corresponding phenotypic correlations significant and in males were 0.277 and 0.251 while for females the values were 0.322 and 0.322 respectively.

Four week body weight and egg production

The pooled genetic correlations between 4 week body weight with egg production to 40 week of age in IR-3 was 0.039 and the corresponding phenotypic correlation was -0.021 (Table 4.10G). However, both the estimates were non-significant.

Six week body weight and egg weight

On perusal of the Table 4.10H it is revealed that the pooled genetic correlation between 4 week body weight and egg weight at 40th week was 0.455 and corresponding phenotypic correlation was 0.053 in IR-3 strain. The pooled estimate in phenotypic scale was significant.

Six week body weight and egg production

The genetic and phenotypic correlations between 6 week body weight and egg production upto 40 weeks of age in IR-3 varied

from positive to negative in different generations and were non-significant. The pooled estimates were found to be 0.066 and -0.04 on genetic and phenotypic scale respectively (Table 4.10I).

Six week body weight and egg weight

The pooled genetic and phenotypic correlations between 6 week body weight and egg weight at 40th weeks of age in IR-3 strain were found to be 0.166 and 0.048 (Table 4.10J) and estimates were non-significant in both the scale.

Egg production and egg weight

The correlation between egg production to 40 weeks of age and egg weight at 40th week of age was found to be negative and non-significant in genetic scale in all the generation under study. So was with the pooled estimates on genetic scale. However, on phenotypic scale it was negative in base generation and varied positively in both of the subsequent generations and also on pooled estimates on phenotypic scale (Table 4.10K). The pooled estimates was lowly positive and significant.

Index unit and four week body weight

The pooled as well as generation wise genetic and phenotypic correlations between index unit and 4 week body weight were found to be positive and highly significant for both the strain and sexes under study except in IR-3 females in which the values were positive and non-significant. The pooled estimates in males were 0.973 and 0.972 in IC-3 and IR-3 strain respectively while the respective values in females were 0.973 and 0.624 (Table 4.10L). The corresponding phenotypic correlations in males were 0.909 and 0.869 while in females the values were 0.908 and 0.286 respectively.

Index unit with six week body weight

The pooled genetic correlations between 6 week body weight and index unit in males were 0.977 and 0.991 of IC-3 and IR-3 strain respectively while in case of females the respective values

were 0.978 and 0.659. The values were significant in all the cases except in females of IR-3 in genetic scale (Table 4.10M). The pooled phenotypic correlations in males were 0.922 and 0.977 in IC-3 and IR-3 respectively while the values for females were 0.918 and 0.511. Similar trend was observed in both the strain and in all the generations under study.

Index unit and six week breast angle

The pooled genetic correlations between index unit and 6 week breast angle in males and females were 0.802 and 0.582 respectively of IC-3 and corresponding pooled phenotypic correlations were found to be 0.676 and 0.571 (Table 4.10N). The estimates were significantly differing from zero.

Index unit and six week shank length

On perusal of the Table 4.10 O it is revealed that the pooled genetic correlations between index unit and 6 week shank length in males and females were 0.737 and 0.438 respectively in IC-3 - while the corresponding values for pooled phenotypic correlation were 0.621 and 0.422. The estimates excepting in genetic scale in females were significant in both the scale.

Index unit and egg production

The correlations between index unit and egg production to 40 weeks of age were found to be high and positive on both genetic and phenotypic scale in all three generations. The pooled over generation estimates also behaved in similar fashion. All the estimates were significant except at the genetic level in S_2 generation in IR-3 (Table 4.10P).

Index unit and egg weight

The Table 4.10Q displays the results of correlations between index unit and egg weight at 40th week of age in IR-3. The pooled genetic and phenotypic correlations were 0.103 and 0.296

respectively. The estimates in phenotypic scale were only positive.

4.5 SELECTION INDEX

Four multi-trait selection indices (one for each sex in each strain) were developed utilizing the information of base generation. The variance covariance matrices utilized have been presented in Table 4.11.

4.5.1 Relative economic weights

Since the traits used for the construction of selection indices were dissimilar for sire and dam line even though traits like 4 week body weight and 8⁶ week body weight were considered in both the lines, separate sets of relative economic weights were calculated for sire and dam lines.

The details of calculation procedures were as follows:

a) Sire line

The broiler traits such as 4 BW, 6 BW, 6 BA and 6 SL were considered for construction of selection indices in both the sexes. The indices were designed to maximise net genetic economic gain and indirectly gains in body weights, breast angle and shank length. This is equivalent to saying that economic values of body weight on arbitrarily being choosen as one and same economic worth would be assumed for breast angle and shank length. The reasoning adopted here was similar to that of Lerner et al. (1947) and Abplanalp et al. (1960). The relative economic weights have been tabulated in Table 4.11.

b) Dam line

From a priori of information of flock performance it was consiered that a breeder hen would lay 150 settable eggs in one year period. Considering 77% hatchability and 5% mortality while attaining

Table 4.11 Variance and covariance matrices and relative economic weights used for construction of indices in both the lines

Lines	Sex	"P" matrix				"G" matrix				"a"
		4 B.W.	6 B.W.	6 B.A.	6 S.L.	4 B.W.	6 B.W.	6 B.A.	6 S.L.	
IC-3	Male	6231.96	7533.10	139.58	14.52	2420.80	4016.21	114.44	9.66	1
			16327.99	271.36	30.37		6653.72	164.79	13.81	1
				20.82	0.49			10.53	0.28	1
		Sym			0.17	Sym			0.05	1
	Female	4916.63	4927.39	69.57	11.48	1300.14	1546.68	31.39	1.60	1
			9616.72	123.79	20.25		2006.14	45.57	2.73	1
				17.65	0.17			4.40	0.01	1
		Sym			0.13	Sym			0.01	1
IR-3	Male	4 B.W.	6 B.W.	E.P.	E.W.	4 B.W.	6 B.W.	E.P.	E.W.	
		3756.87	5021.45			695.88	1167.47			1
		Sym	10172.91			Sym	2138.56			1
	Female	2744.32	1989.67	21.67	17.79	406.32	970.43	50.69	3.85	1
			3868.30	45.22	12.09		1786.98	134.31	8.43	1
				262.50	-2.10			140.38	-3.56	10.82
		Sym			17.40	Sym			8.02	16.64

6 weeks of age, the total number of chicks available would be 110. One gram increase in dam 6 weeks body weight would result 0.3 g increase in 6 week body weight of progeny resulting an increase of 33 g of live weight. The cost of 33 g of live weight of progeny @ Rs.18.00 per kg would be Rs.0.59. For gaining 33 g of live weight the chicks would consume 72.6 g of feed with 1:2.2 FCR. The cost of 72.6 g of feed @ of Rs.3.50 per kg would be Rs.0.25. So the economic weight on increase in one gram in dam 6 week b.wt. would be Rs.0.34. Similar economic values as for 4 week body weight was assigned as estimated for 6 week body weight as per assumption discussed during calculation of economic weight in sire line.

From the priori of information it was assumed that one egg would fetch 0.73 chick (Hatchability and mortality of chick being discussed). The cost of 0.73 chick @ Rs.6.00 per chick would be Rs.4.38. To lay one egg the breeder hen would require 200 g of feed costing Rs.0.70 @ Rs.3.50 per kg. So, the net gain on increase of one egg would be Rs.3.68.

Hatching egg size has been known to influence broiler weight in a positive linear manner (Tindell and Morris, 1964; Merritt and Gowe, 1965). For each one gram increment of egg weight, the broiler weight increases by at least 5 g at 6 week of age. Under this assumption weight of 110 probable chicks per dam at 6 weeks of age would be $110 \times 5 = 550$ g live weight of progeny. The cost of 550 g of live weight @ Rs.18.00 per kg would be Rs.9.90. For gaining 5 gram body weight at 6 weeks of age the requirement of feed for 110 chicks would be 1.21 kg with 1:2.2 FCR. The cost of the feed would be Rs.4.24 @ Rs.3.50 per kg. So the economic value for 1 g increase in egg weight would be Rs.5.66.

The assumption used in sire line for calculating economic values in the males, was also adopted in males of dam line for 4 week body weight and 6 week body weight. The relative economic weights have been presented in Table 4.11.

4.5.2 Genetic economic weights (b-values)

Genetic economic weights of the component traits of the indices are presented in Table 4.12. It is evident from the table that shank length received highest positive weights while 6 week body weight the lowest in case of the index used for males of IC-3. However, in IC-3 female index the shank length received the negative weighting factor. In the index used for males of IC-3, the genetic economic weights were 0.6294, 0.3223, 5.8935 and 29.7050 for 4 BW, 6 BW, 6 BA and 6SL respectively, while the corresponding values in the index for females were 0.4509, 0.2096, 1.8065 and -38.9065.

The IR-3 males were selected by use of an index with two traits body weight at 4 and 6 weeks of age. The genetic economic weights were 0.1772 and 0.2328 for 4 and 6 week body weight respectively. The index weighting factors for females of IR-3 strain were obtained incorporating 4 and 6 week body weight, egg production upto 40 weeks of age and egg weight at 40th week of age. The genetic economic weighting factors were -0.1429, 1.1515, 6.1633 and 6.3295 respectively for the traits undertaken in the females.

Efficiency of the index

The r_{HI} values for different indices ranged from 0.4577 to 0.7807 (Table 4.12). The efficiency of the index was highest for IR-3 female followed by the index used for IC-3 male. The efficiency of index was found to be lowest for IR-3 males.

4.5.3 Statistical properties of selection indices

The statistical properties of indices used in IC-3 and IR-3 have been shown in Table 4.13. The ratio of the square of efficiency and heritability of indices (by regression method) ranged from 0.97 to 1.00.

Table 4.12 Genetic economic weightages (b), relative efficiency (r_{HI}) and expected aggregate genetic worth ($i \hat{G}_I$) of indices

Lines	Sex	"b" values									
		4 B.W.	6 B.W.	6 B.A.	6 S.L.	E.P.	E.W.	\hat{G}_I	\hat{G}_H	$i \hat{G}_I$	r_{HI}
IC-3	Male	0.6294	0.3223	5.8935	29.7050	-	-	100.21	133.13	127.76	0.7527
	Female	0.4509	0.2096	1.8065	-38.9065	-	-	45.06	81.03	57.45	0.5560
IR-3	Male	0.1772	0.2328	-	-	-	-	32.91	71.89	52.42	0.4577
	Female	-0.1429	1.1515	-	-	6.1633	6.3295	125.70	160.99	200.24	0.7808

Table 4.13 Statistical properties of selection indices, variances, correlations and heritabilities of indices

Source of data	Lines	Sex	$V(I) = b'Pb$	$V(H) = a'Ga$	$V(K) = b'Gb$	R_{HI}^2	h_I^2	R_{HI}^2/h_I^2
Base generation	IC-3	M	10042.04	17723.59	5875.73	0.57	0.58	0.98
		F	2030.95	6565.86	657.86	0.31	0.32	0.97
	IR-3	M	1083.06	5168.17	224.07	0.21	0.21	1.00
		F	15800.49	25917.78	9367.26	0.61	0.61	1.00

Reduction in efficiency of indices due to omission of traits

The percent reduction in the efficiencies of indices on omission of traits have been presented in Table 4.14. In case of IC-3 - males, the reduction percentage in efficiency of the index if the trait would have dropped from the index was 5.57 for 4 BW, 2.94 for 6 BW, 2.85 for 6BA and 0.51 for 6 SL. However, the respective values in females were 12.72, 4.20, 1.29 and 3.43. In the index used for males of IR-3 the reduction percentage in efficiencies were 1.87 and 9.10 for 4 BW and 6 BW respectively while in the index for females of IR-3 the reduction percentage in efficiency due to omission of traits were 0.12, 10.76, 39.10 and 2.21 for 4 BW, 6 BW, EP and EW respectively.

4.5.4 Expected genetic gain

The expected genetic gain in aggregate genotype (ΔH) per generation by use of different indices are presented in Table 4.12. The highest gain per generation was in the index used for females of IR-3 and the lowest was in the index used for males of the same strain. The genetic gains in aggregate genotype were 127.76 and 57.45 in the males and females of IC-3 respectively while corresponding values in IR-3 were 52.42 and 200.24.

4.6 SELECTION DIFFERENTIALS

The response to selection in a component trait in index method is a function of standardised selection differential, genetic economic weights, genetic variance and covariance matrix and standard deviation of the index. From the genetic point of view, it is therefore, essential to measure the standardised selection differential to observe the response in a selection experiment.

The expected and effective selection differentials were calculated in each generation in IC-3 and IR-3 for the index unit and for the component traits Tables 4.15 and 4.16. The average of ratios of effective selection differential and expected selection differential

Table 4.14 Reduction in efficiency of indices due to omission of traits

Lines	Sex	Traits	Percent reduction in the efficiency of the index
IC-3	M	4 B.W.	5.57
		6 B.W.	2.94
		6 B.A.	2.85
	F	6 S.L.	0.51
		4 B.W.	12.72
		6 B.W.	4.20
		6 B.A.	1.29
		6 S.L.	3.43
	M	4 B.W.	1.87
		6 B.W.	9.10
IR-3	F	4 B.W.	0.12
		6 B.W.	10.76
		E.P.	39.10
	F	E.W.	2.21

Table 4.15 Expected and effective selection differentials and selection intensities for index unit and component traits in sire line (IC-3)

Traits	Gen.	Males (S_m)		Females (S_f)		$1/2 (S_m + S_f)$		Eff./Exp.	\bar{p}		Selection intensities			
		Exp.S.D.	Eff.S.D.	Exp.S.D.	Eff.S.D.	Exp.S.D.	Eff.S.D.		Males	Females	Males(i_m)	Females(i_f)	Avg. (i)	
Index unit	S_0	195.45	191.34	33.35	37.34	114.40	114.34	0.999	106.98	52.87	1.826	0.630	1.228	
	S_1	175.72	175.00	45.60	49.73	110.66	112.36	1.015	100.10	57.40	1.755	0.794	1.275	
	S_2	193.79	-	48.44	-	126.08	-	-	105.97	59.22	1.828	0.818	1.323	
	Av.	188.32	183.71	42.46	43.53	117.04	113.35	1.007	104.35	54.59	1.803	0.747	1.275	
4 B.M.	S_0	133.78	130.01	61.00	61.79	97.39	95.90	0.985	78.78	70.01	1.698	0.871	1.285	
	S_1	128.93	131.25	58.10	61.83	93.52	96.54	1.032	71.60	67.11	1.801	0.866	1.334	
	S_2	121.35	-	71.58	-	96.47	-	-	72.85	70.95	1.666	1.009	1.293	
	Av.	128.02	130.63	63.56	61.81	95.79	96.22	1.009	74.41	69.36	1.722	0.915	1.304	
6 B.M.	S_0	216.51	210.00	87.06	85.55	151.78	147.77	0.974	127.54	97.96	1.697	0.888	1.293	
	S_1	202.53	203.98	91.02	101.46	146.77	152.72	1.040	115.10	105.31	1.759	0.864	1.312	
	S_2	231.33	-	110.38	-	170.85	-	-	122.90	115.98	1.994	0.951	1.473	
	Av.	216.79	206.99	96.15	93.51	156.47	150.25	1.007	121.85	106.72	1.817	0.901	1.359	
6 B.A.	S_0	4.97	4.93	1.93	1.94	3.45	3.44	0.997	4.54	4.20	1.095	0.459	0.777	
	S_1	3.66	3.21	3.77	3.55	3.72	3.38	0.908	4.83	4.85	0.758	0.777	0.767	
	S_2	5.37	-	2.17	-	3.77	-	-	4.84	4.84	1.109	0.448	0.778	
	Av.	4.67	4.07	2.62	2.75	3.65	3.41	0.953	4.74	4.63	0.987	0.561	0.774	
6 S.L.	S_0	0.41	0.43	0.41	0.41	0.41	0.42	1.024	0.41	0.37	0.990	1.123	1.057	
	S_1	0.26	0.26	0.14	0.15	0.20	0.21	1.050	0.31	0.34	0.844	0.418	0.631	
	S_2	0.32	-	0.28	-	0.30	-	-	0.40	0.40	0.808	0.718	0.763	
	Av.	0.33	0.35	0.28	0.28	0.30	0.32	1.037	0.37	0.37	0.881	0.753	0.817	

Table 4.16 Expected and effective selection differentials and selection intensities for index unit and component traits in dam line (IR-3)

Traits	Gen.	Males (S_m)		Females (S_f)		$1/2 (S_m + S_f)$		Eff./Exp.	\bar{p}		Selection intensities		
		Exp.S.D.	Eff.S.D.	Exp.S.D.	Eff.S.D.	Exp.S.D.	Eff.S.D.		Males	Females	Males(i_m)	Females(i_f)	Avg. (i)
Index unit	S_0	64.96	63.72	95.72	97.13	80.30	80.77	1.005	32.92	125.51	1.973	0.758	1.366
	S_1	63.69	65.24	145.45	143.11	104.57	104.18	0.996	30.86	132.92	2.063	1.094	1.578
	S_2	74.11	-	128.51	-	101.31	-	-	32.96	114.81	2.248	1.119	1.835
	Av.	67.59	64.48	123.22	120.12	95.39	92.48	1.001	48.37	124.42	2.106	0.990	1.593
4 B.W.	S_0	111.90	115.19	29.92	27.12	70.91	71.16	1.004	61.44	52.35	1.821	0.572	1.197
	S_1	103.20	102.58	19.35	18.62	61.28	60.60	0.989	57.89	43.89	1.783	0.446	1.115
	S_2	126.13	-	30.83	-	78.48	-	-	60.98	45.49	2.068	0.678	1.373
	Av.	113.74	108.89	26.70	22.87	70.22	65.88	0.997	60.10	47.24	1.891	0.565	1.228
6 B.W.	S_0	191.88	190.34	49.66	51.44	120.77	120.89	1.001	101.17	62.13	1.897	0.799	1.348
	S_1	195.00	199.43	43.46	44.27	119.23	121.85	1.022	99.37	58.56	1.962	0.742	1.352
	S_2	222.50	-	70.48	-	146.49	-	-	101.37	63.51	2.195	1.110	1.653
	Av.	203.13	194.89	54.53	47.86	128.83	121.39	1.012	100.64	61.40	2.018	0.884	1.451
E.P.	S_0	-	-	6.00	6.04	6.00*	6.04*	1.006	-	16.17	-	0.371	0.371
	S_1	-	-	14.84	13.49	14.84*	13.49*	0.909	-	17.76	-	0.836	0.836
	S_2	-	-	8.14	-	8.14*	-	-	-	15.75	-	0.517	0.517
	Av.	-	-	9.66	9.76	9.66*	9.76*	0.958	-	16.56	-	0.575	0.575*
E.M.	S_0	-	-	0.76	0.76	0.76*	0.76*	1.000	-	4.16	-	0.183	0.183
	S_1	-	-	1.03	1.05	1.03*	1.05*	1.019	-	4.45	-	0.231	0.231
	S_2	-	-	0.25	-	0.25*	-	-	-	4.06	-	0.062	0.062
	Av.	-	-	0.68	0.91	0.68*	0.91*	1.010	-	4.23	-	0.159	0.159*

* Selection differential available only in females

were 1.007 in IC-3 and 1.001 in IR-3 for index unit.

The average standardised selection differential $\frac{1}{2} (i_m + i_f)$ in three generation ranged from 1.228 to 1.323 in IC-3 and 1.366 to 1.835 in IR-3 for the criterion of selection. The corresponding average values were 1.275 and 1.593 respectively.

4.7 GENETIC DRIFT AND SAMPLING ERROR

The genetic drift and sampling error component of variance of response were calculated for the index units of different indices and for the component traits of the indices and presented in Tables 4.17 and 4.18.

The predicted drift variance over three generations of selection (36_d^2) for index units in males of IC-3 and IR-3 were 59.46 and 4.30 respectively. The respective values in female progenies were 19.05 and 52.69. The sampling error (6_e^2) per generation for index units in males of IC-3 and IR-3 were 5.46 and 0.79 respectively while in females the respective values were 2.21 and 24.80.

The ratio ($6_d^2/6_e^2$) of index units was found to be 3.63 and 1.81 in males of IC-3 and IR-3 respectively and the respective values in females were 2.87 and 0.71.

The ratio of genetic drift per generation and sampling error in the component traits of indices in selected and control lines were also calculated. For 4 week body weight the ratios were 3.691, 2.451 and 0.8835 in males of IC-3, IR-3 and control line respectively while for females the respective ratios were 2.218, 1.252 and 1.2018. For 6 week body weight the ratios for males of IC-3, IR-3 and control line were 3.984, 2.381 and 0.8733 while the respective values in females were 2.266, 1.2804 and 0.7475. The ratio of genetic drift per generation and sampling error variance of 6 BA in males of IC-3 and control line were 2.842 and 1.0101, however, the respective values in females were 1.998 and 0.6809. For shank length at 6 weeks of age

Table 4.17 Genetic drift and sampling error variance of response of index units in sire and dam lines based on three generations of selection

Specified parameters	Sire line		Dam line	
	M	F	M	F
Heritability pooled (h_s^2)	0.486	0.338	0.190	0.313
Average phenotypic variance (σ_p^2)	11026.22	3166.26	1069.26	16109.36
Squared correlation between index and breeding value (r_{HI}^2)	0.57	0.31	0.21	0.61
Effect population size per generation (N_e)	116.25	116.25	111.95	111.95
Individuals scored per generation (M_e)	1036.25	948.25	1092.75	446.25
Total drift variance for three generation of selection ($3\sigma_d^2$)	59.46	19.05	4.30	52.69
Sampling error (σ_e^2)	5.46	2.21	0.79	24.80
Ratio of σ_d^2/σ_e^2	3.63	2.87	1.81	0.71

Table 4.18 Genetic drift and sampling error variance of component traits of indices in selected and control lines over three generations of selection

Lines	Traits	SEX				RATIO = Per Gen. drift/ Sampling error	
		Male		Female		Male	Female
		Genetic drift	Sampling error	Genetic drift	Sampling error		
IC-3	4 B.W.	33.73	3.05	24.83	3.73	3.691	2.218
	6 B.W.	95.86	8.02	58.49	8.24	4.984	2.266
	6 B.A.	0.125	0.015	0.101	0.017	2.778	1.980
	6 S.L.	0.00065	0.00010	0.00056	0.00010	2.167	1.867
IR-3	4 B.W.	19.41	2.64	13.11	3.49	2.451	1.252
	6 B.W.	53.22	7.45	23.97	6.24	2.381	1.280
	E.P.	-	-	1.706	0.397	-	1.432
	E.W.	-	-	0.0764	0.0328	-	0.776
Control	4 B.W.	32.92	12.42	45.90	12.73	0.884	1.202
	6 B.W.	87.51	33.40	66.34	29.58	0.873	0.748
	6 B.A.	0.200	0.066	0.143	0.070	1.010	0.681
	6 S.L.	0.00036	0.00060	0.00025	0.00050	0.200	0.167
	E.P.	-	-	0.52600	0.64690	-	0.271
	E.W.	-	-	0.03010	0.04290	-	0.234

in males of IC-3 and control line the ratios were 2.166 and 0.2 respectively and in females the respective values were 1.866 and 0.1666. For egg production upto 40 weeks of age the ratio of genetic drift and sampling error was 1.432 and 0.2710 in IR-3 and control line respectively while the respective values for egg weight at 40th week of age were 0.777 and 0.2338.

4.8 REALISED AND PREDICTED GENETIC GAIN AND EFFICIENCY (%)

The realised genetic gains were calculated by regression of control deviated means over generations (Tables 4.19 and 4.20 and Figs. 4.1 to 4.6).

The realised gains per generation in males of IC-3 were 28.90 (IU) 10.33 g, 22.04 g, 1.95° and 0.77 cm for index unit, 4 BW, 6 BW, 6 BA and 6 SL respectively while the respective values in females were 10.93 (IU), 10.40 g, 26.82 g, 2.56° and 0.10 cm. However, the prediction for genetic gain per generation in males of IC-3 were 64.660 (IU) 48.089 g, 76.990 g, 2.490° and 0.173 cm for index unit, 4BW, 6BW, 6BA and 6 SL respectively and the respective values in females were 24.346 (IU), 25.600 g, 30.948 g, 3.022° and 0.129 cm. The efficiency percentage in prediction in different traits in males of IC-3 ranged from 21.48 to 98.26 and in females from 40.63 to 77.51 (Table 4.19).

The realised gains per generation in males of IR-3 (Table 4.20) were 2.52 (IU), 4.20 g and 10.62 g for index unit, 4 BW and 6 BW respectively while in females the values were 44.71 IU), 8.06 g, 18.44 g, 2.81 (no.) and 1.20 g for index unit, 4 BW, 6 BW, EP and EW respectively. The corresponding values for predicted gains per generation in males were 9.758 (IU), 19.13 g, 34.10 g and in females were 62.366 (IU), 17.693 g, 35.486 g, 3.544 (no.) and 0.552 g. The efficiency percentage in prediction in different traits in males ranged from 21.96 to 31.14 while in females the range was 45.55 and 217.39.

4.9 REALISED AND PREDICTED GENETIC REGRESSIONS

The realised and predicted genetic regression of component traits of indices in selected lines were calculated as per Kinnev et al. (1970) (Table 4.21).

Table 4.19 Realised and predicted genetic gain and efficiency per generation in index units and in component traits of sire line (IC-3)

Sex	Traits	Genetic gain		Efficiency (%)
		Realised	Predicted	
Male	Index unit	28.90± 7.08	64.660	44.69
	4 B.W. (g)	10.33± 2.51	48.089	21.48
	6 B.W. (g)	22.04±12.69	76.990	28.62
	6 B.A. (°)	1.95± 0.48	2.490	78.31
	6 S.L. (cm)	0.17± 0.18	0.173	98.26
Female	Index unit	10.93± 6.24	24.346	44.89
	4 B.W. (g)	10.40± 4.98	25.600	40.63
	6 B.W. (g)	26.82± 4.78*	30.948	86.66
	6 B.A. (°)	2.56± 0.39*	3.022	84.71
	6 S.L. (cm)	0.10± 0.15	0.129	77.51

* $P < 0.05$

Table 4.20 Realised and predicted genetic gain and efficiency per generation in index units and in component traits of dam line (IR-3)

Sex	Traits	Genetic gain		Efficiency (%)
		Realised	Predicted	
Male	Index unit	2.52±1.11	9.758	25.82
	4 B.W. (g)	4.20±4.35	19.130	21.96
	6 B.W. (g)	10.62±6.77	34.100	31.14
Female	Index unit	44.71±7.17*	62.366	71.68
	4 B.W. (g)	8.06±2.84	17.693	45.55
	6 B.W. (g)	18.44±2.75*	35.486	51.96
	E.P. (No.)	2.81±1.09	3.544	79.28
	E.W. (g)	1.20±0.16*	0.552	217.39

* $P \leq 0.05$

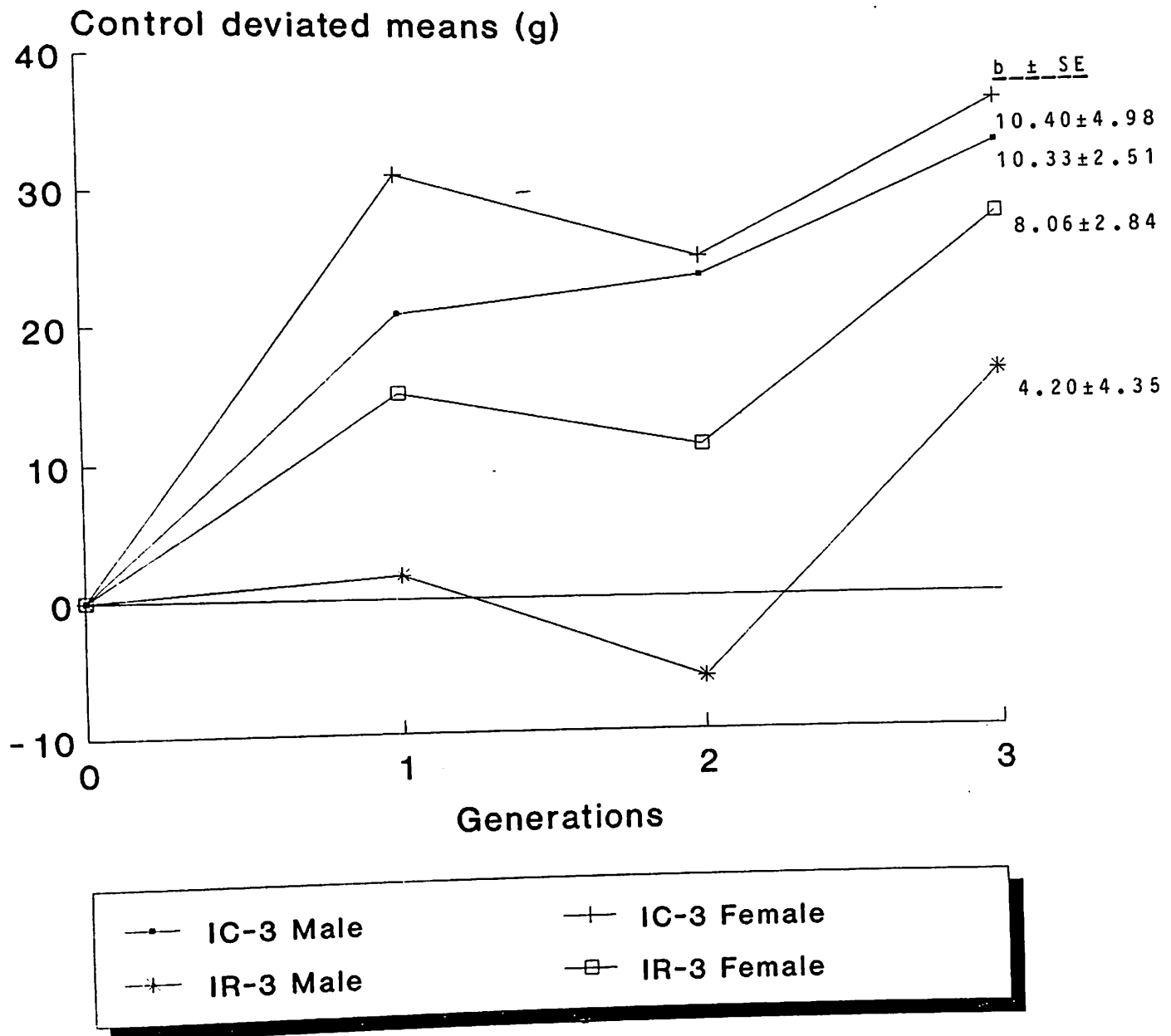


Fig. 4.1: Realised responses on 4-week body weight due to index selection in both the lines (sex-wise).

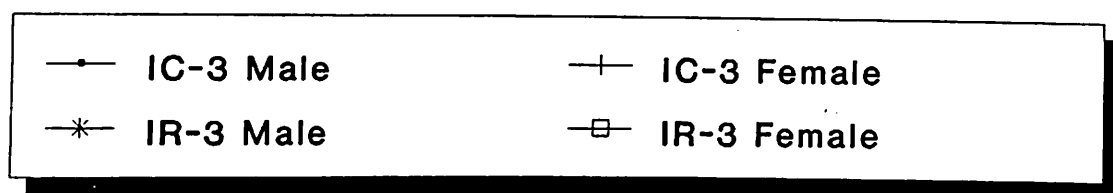
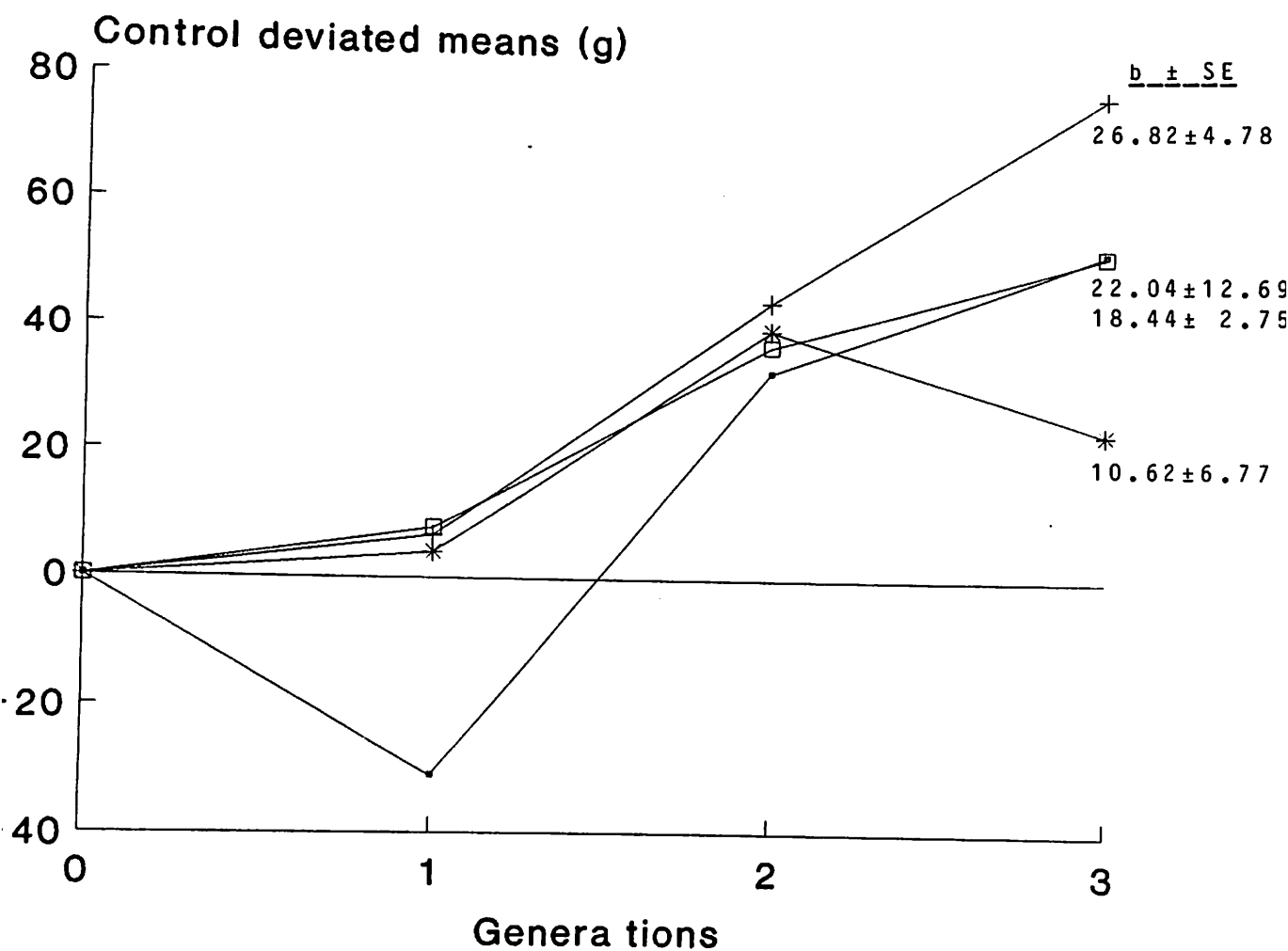


Fig. 4.2 : Realised responses on 6-week body weight due to index selection in both the lines (sex-wise).

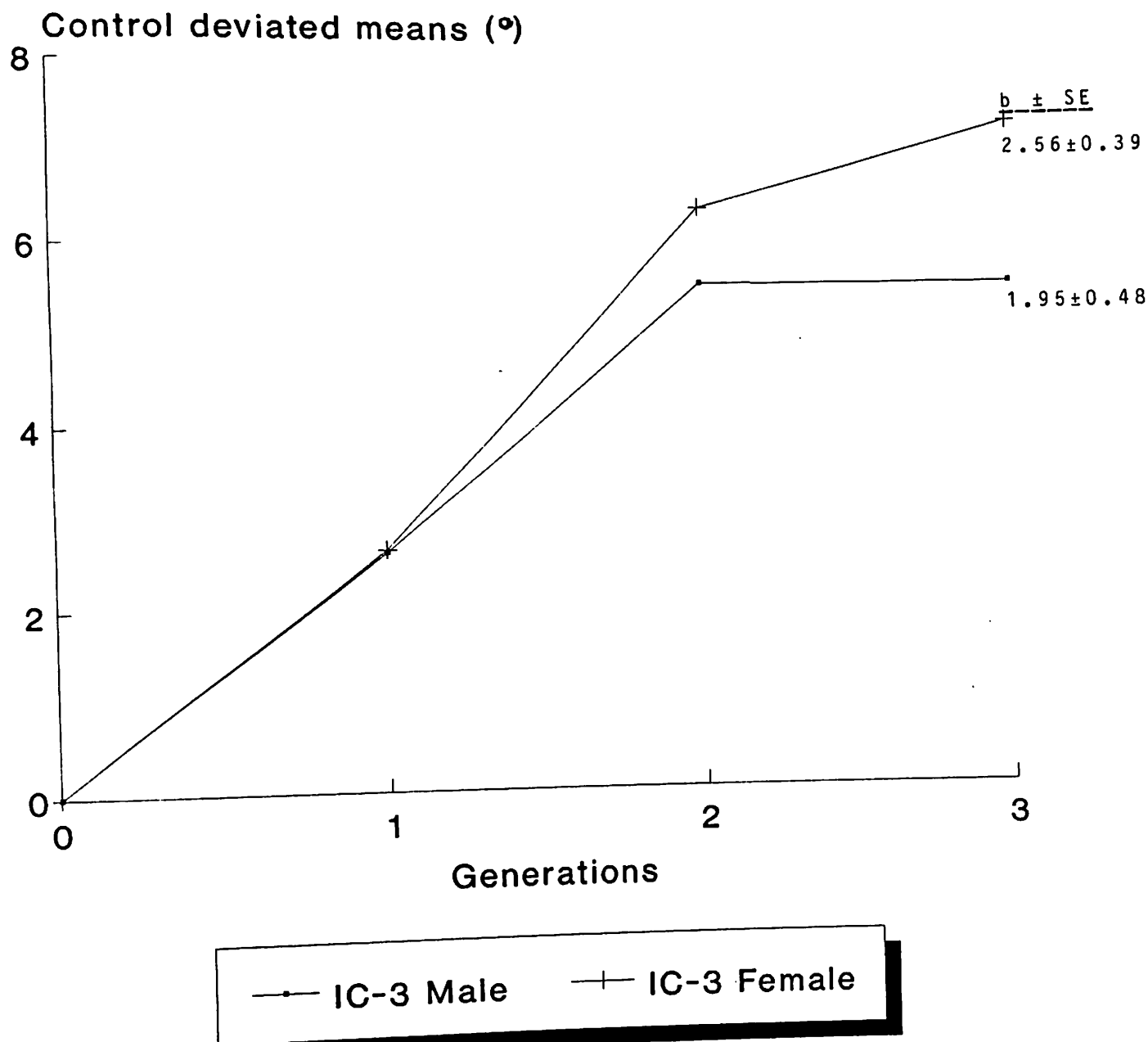


Fig. 4.3: Realised responses on 6-week breast angle due to index selection in IC-3 (sex-wise).

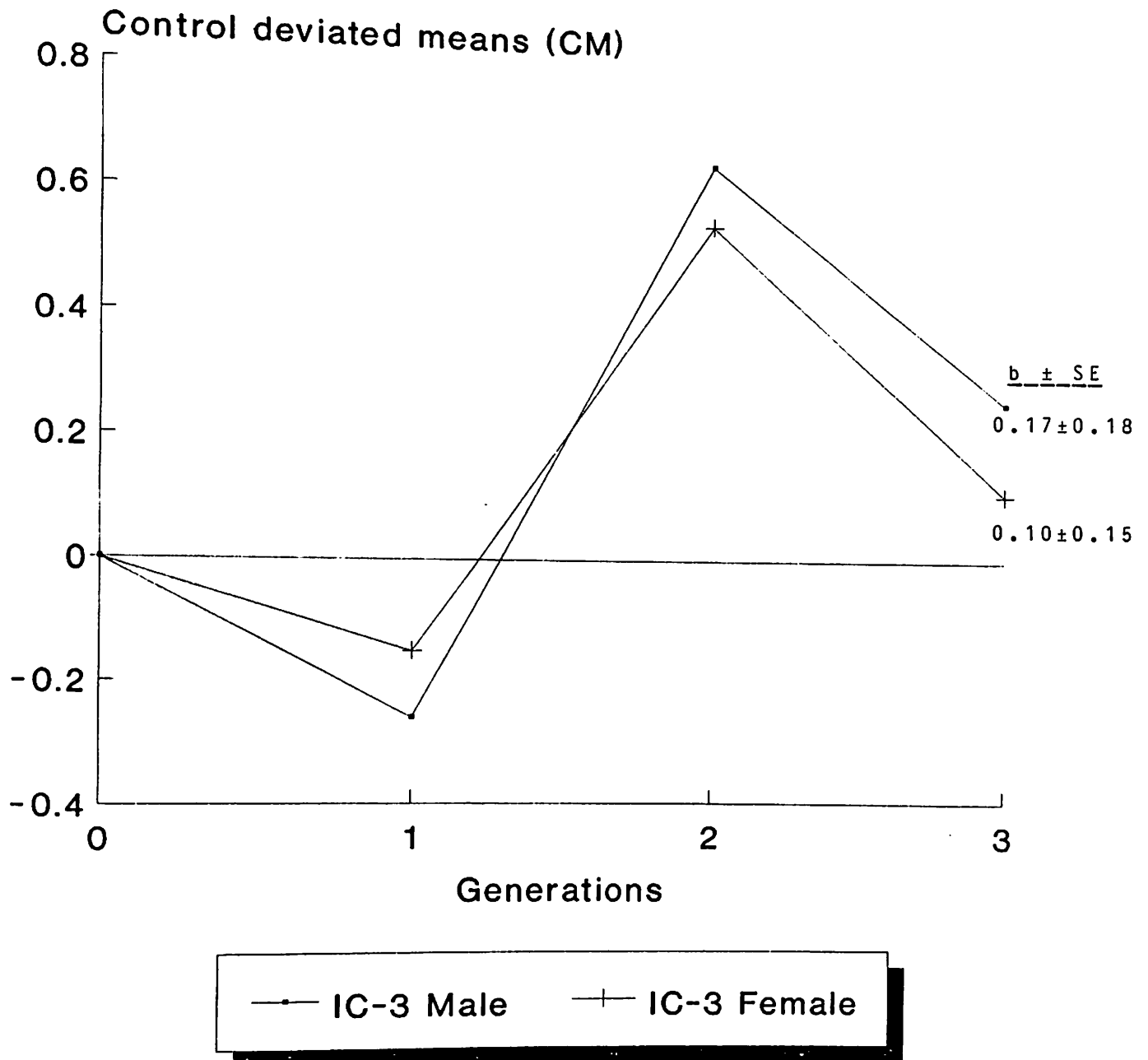


Fig. 4.4 : Realised responses on 6-week shank length due to index selection in IC-3 (sex-wise)

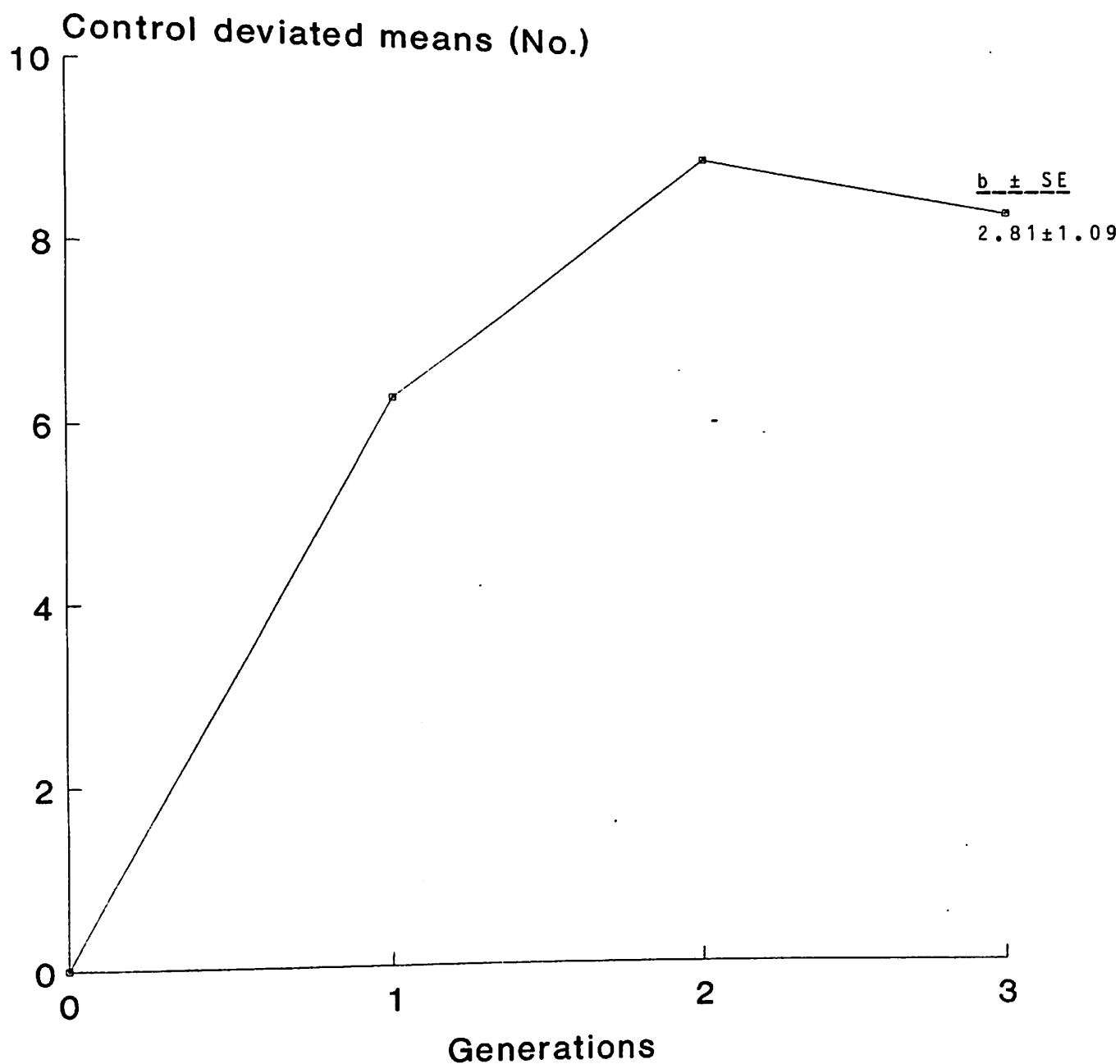


Fig. 4.5 : Realised response on egg production to 40 weeks of age due to index selection in IR-3.

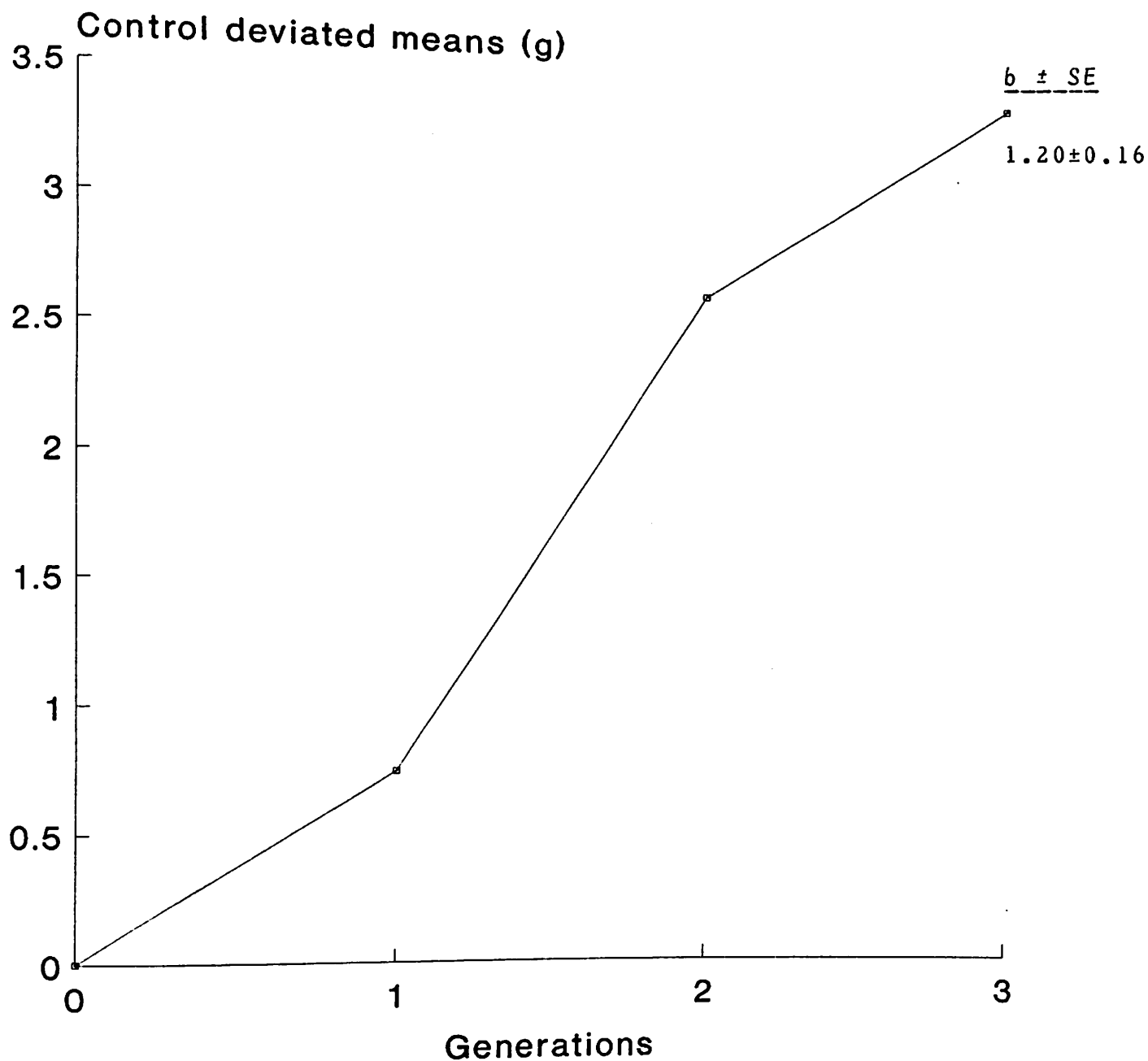


Fig. 4.6 : Realised response on egg wt.
at 40th week of age due to index
selection in IR-3.

Table 4.21 Realised and predicted genetic regressions for component traits of the indices in sire and dam lines

Sex	Traits	Sire line (IG-3)		Dam line (IR-3)	
		Realised	Predicted	Realised	Predicted
Male	4 B.W. (g)	0.3574	0.6404	1.6660	2.0810
	6 B.W. (g)	0.7626	1.0940	4.0476	3.5038
	6 B.A. (°)	0.0675	0.0295	-	-
	6 S.L. (cm)	0.0058	0.0019	-	-
Female	4 B.W. (g)	0.9515	1.0714	0.1803	0.2374
	6 B.W. (g)	2.5788	1.7057	0.4124	0.3293
	6 B.A. (°)	0.2461	0.0406	-	-
	6 S.L. (cm)	0.0096	0.0023	-	-
	E.P. (No.)	-	-	0.0628	0.1216
	E.W. (g)	-	-	0.0268	0.0040

The realised genetic regression in IC-3 males were 0.3574 g, 0.7626 g, 0.0675° and 0.0058 cm for 4 BW, 6 BW, 6 BA and 6 SL respectively while the respective values in females were 0.9515 g, 2.5788 g, 0.2461° and 0.0096 cm. The corresponding prediction of genetic regression were 0.6404 g, 1.0940 g, 0.0295° and 0.0019 cm for males and 1.0714 g, 1.7057 g, 0.0406° and 0.0023 cm in females.

The realised genetic regression in IR-3 males were 1.660 g and 4.0476 g for 4 BW and 6 BW and in females the values were 0.1803 g, 0.4124 g, 0.0628 (no) and 0.0268 g for 4 BW, 6 BW, EP and EW respectively. The corresponding predicted values were 2.081 g and 3.5038 g in males and 0.2374 g, 0.3293 g, 0.1216 (no.) and 0.0040 g in females.

4.10 REALISED HERITABILITY

In the present study the realised heritabilities of principal trait (index unit) were calculated by regression of standardised cumulative response on standardised cumulative selection differentials as per Manson (1973).

On perusal of the Table 4.22 it is revealed that in males and females of IC-3, the realised heritabilities of index units were 0.222 ± 0.056 and 0.049 ± 0.019 respectively. The corresponding pooled estimates from half-sib method were 0.486 ± 0.076 and 0.338 ± 0.062 (Table 4.8).

In IR-3 males and females, the realised heritabilities of index units were 0.155 ± 0.085 and 0.215 ± 0.042 respectively and the corresponding pooled estimates of heritabilities from half-sib method were 0.190 ± 0.045 and 0.313 ± 0.084 (Tables 4.8 and 4.9).

Table 4.22 Realised heritability estimates of index units and regression coefficients of component traits in sire and dam line

Lines	Sex	Traits					
		Index unit	4 B.W.	6 B.W.	6 B.A.	6 S.L.	E.P. E.W.
IC-3	M	0.222±0.056	0.104±0.024	0.146±0.077	0.534±0.132	0.799±0.699	-
	F	0.049±0.019	0.112±0.055	0.183±0.052	0.799±0.699	0.427±0.528	-
IR-3	M	0.155±0.085	0.072±0.015	0.071±0.049	-	-	-
	F	0.215±0.042	0.136±0.046	0.212±0.034	-	-	0.151±0.194 1.639±0.194

DISCUSSION

DISCUSSION

5.1 EFFECTIVE POPULATION SIZE AND RATE OF INBREEDING

The most convenient way of dealing with any particular deviation from idealised breeding structure is to express the situation in terms of the effective number of breeding individuals or the effective population size. This refers to the number of individuals that give rise to calculated sampling variance, or rate of inbreeding, if they are bred in the manner of the idealised population. The effective number of sires, effective number of dams and effective population size for each generation as well as averaged over generation in selected and control lines are presented in Table 4.1.

Gowe et al. (1959) and King et al. (1954) have discussed vividly the implication of effective population size especially in selection experiments. Nordskog et al. (1967) also reported that effective population size is very important in determining response to selection and to reduce the coefficient of inbreeding. Nicholas (1980) suggested that in order to be fairly certain that observed response will be quite close to expected response over a small number of generations, quite a large population is required. Since the coefficient of inbreeding is inversely proportional to response to selection, it is essential that effective population size should be fairly large and stable over generations. The coefficient of inbreeding for the selected and control lines are presented in Table 4.1. The estimates however, may be considered as upper limit, since full-and half-sib matings were deliberately avoided.

Effective population size in different lines in the present study were quite high as compared to values reported by Saxena (1976) and Kataria (1985), in short-term selection experiments. However, the values are quite similar in comparison to values as reported by Dev Roy (1986) and Singh (1986).

Shoffner (1948), Wilson (1948) and Nordskog et al. (1974) have reported the effects of inbreeding on economic traits in poultry. The general conclusion that can be drawn from the studies is that inbreeding should be kept at the minimum during the selection to maximise the response with reasonably good size of effective population as in the present study. In the present investigation the expected cumulative inbreeding was very much similar to the findings of Singh (1986) and Dev Roy (1986) in short term selection experiments.

5.2 HATCH DATE EFFECTS

There are enough reports in the literature to suggest that most of the economic traits in poultry are affected by date of hatch. Bohren et al. (1952) obtained a systematic effect of hatch date on early egg weight. Skaller (1954) reported that the hatch effects are of considerable importance in egg production. Similar reports were made by earlier workers suggesting significant hatch date effects on economic traits in chicken (King and Henderson, 1954; Aggarwal, 1975; Saxena, 1976; Sharma, 1981; Dev Roy, 1986 and Barwal et al., 1993).

The results obtained in this study presented the same general trend of significant effect of hatch date (Tables 4.2 to 4.4). All the data were therefore corrected for hatch effects following procedure of Harvey (1966) on an intra-line/intra-generation basis for males and females.

5.3.1 Means, standard errors and coefficient of variation

The generation and sex wise means for different selected and unselected traits separately are presented in Tables 4.5 to 4.7.

It is evident from the tables that in selected lines the mean values of broiler and production traits have shown substantial

increase in positive direction and it might be due to index selection which helped for accumulation of genes of traits considered. No marked change in mean values in controls were seen over the generations. Body weight and conformation traits exhibited higher values in males than females irrespective of line. The broiler traits were of higher mean values in IC-3 than IR-3, and the controls had lower value than the selected line. The production traits in IR-3 had higher mean values than the corresponding values in control.

Since the individuals scored per generation were quite large in selected lines, the magnitude of standard errors of means were low in those lines, while in control the standard errors of means of different traits were relatively high. It is because the standard error of means are inversely proportional to the individuals scored.

The percent coefficient of variation in general were higher in controls in all the traits under study than the corresponding values in the selected lines. This might be due to existence of more of genetic variability in controls than the selected lines. It is also evident from the tables that in most of the traits in selected lines the C.V.% were showing a decreasing trend from S_0 to S_3 generation as expected which might be due to exhaustion of genetic variability in successive generations of selection.

5.3.2 Phenotypic time trend

Phenotypic changes exhibited by index selected lines along with means of random control population for index units and for component traits are given in Tables 4.5 to 4.7. The results revealed that the realised phenotypic responses were non-significant for all the traits as evident from non-significant regression of generation means on generation number. Substantial phenotypic changes in index units were observed in positive direction in each of the sex of selected lines. In general, the phenotypic regression of component traits of the indices in selected lines were in positive direction except in shank length in males and both breast angle and shank length in females in IC-3.

In IR-3 the phenotypic regression value at egg production to 40 weeks of age was lowly negative.

5.4 GENETIC AND PHENOTYPIC PARAMETERS

5.4.1 Heritability estimates

Falconer (1960) pointed out that the estimates of heritability computed from sire component of variance is most reliable as it is least augmented by environment sources of variation. However, Lerner (1950) was of the opinion that sire component estimates might not be reliable as they were based on smaller degrees of freedom.

Since the degrees of freedom associated with the between sire component in ANOVA were quite high in the present study (Tables 4.8 and 4.9). The heritabilities were estimated from sire component of variance using variance component analysis.

Falconer (1981) reported that small populations maintained long enough for an appreciable amount of fixation of genes to have taken place are expected to show lower heritabilities than large populations. More variable environmental conditions of management reduce the heritability, while more uniform increase it. So any value of heritability of a given trait refers to a particular population under particular condition.

Kinney and Shoffner (1967) suggested that the pooled estimates would be preferable for use over single generation estimates as they were associated with small standard errors.

Four week body weight

The pooled estimates revealed that 4 week body weight was moderately to highly heritable (Table 4.8). The pooled heritability estimates ranged from 0.251 to 0.414 in males and 0.272 to 0.550 in females in different lines.

The review of literature showed a similar variation in the estimates of heritability. The average of the estimates reported was 0.33 (Table 2.1). Higher estimates of heritability was reported by Gill and Verma (1983), Wang et al. (1991). The heritability estimates obtained in this investigation were smaller in magnitude than some of the estimates reported in literature but agreed fairly well with those reported by Saikia (1973), Dev Roy et al. (1983) and Ramappa et al. (1986).

Six week body weight

The review of literature for heritability of six week body weight revealed that the trait is moderate to highly heritable. The average of the estimates reported based on sire component of variance was 0.47 (Table 2.2).

In the present study the pooled estimates for 6 week body weight ranged from 0.244 to 0.574 in males and 0.290 to 0.413 in females (Table 4.8). These values were in good agreement with those reported by Saxena (1976), Aksoy (1980), Dev Roy et al. (1983), Reddy (1988) and Wang et al. (1991).

Six week breast angle

Heritability estimates pooled over generations for breast angle ranged from 0.319 to 0.544 in males and 0.245 to 0.365 in females in different lines (Table 4.8).

The review of literature revealed many reports on heritability estimates of breast angle at 8 weeks of age and the average value reported was 0.42 (Table 2.3).

The estimates in the present study are in good agreement to the earlier reports of Reddy (1988), however, they defer to the reports of Choudhary (1992). The heritability estimate of this trait can be taken to be moderate to highly heritable.

Six week shank length

The pooled heritability estimates were moderate to high for shank length at six weeks of age and the range in different lines were 0.251 to 0.329 in males and 0.212 to 0.283 in females (Table 4.8). Similar to the case of breast angle the review of literature reveal very scanty report even though a sizable reports are available for heritability of shank length at 8 weeks of age (Table 2.4). However, the estimates in the present study are lower to the earlier report of Reddy (1988) and higher to the report of Choudhary (1992).

Egg production

The review of literature reveal the average heritability of egg production to be 0.23 (Table 2.5). The pooled estimate of heritability of egg production was 0.36 (Table 4.9) and is higher than the reports available in literature. Higher genetic variability may be attributed to the fact that no earlier selection was made for egg number in this line (IR-3). However, the estimates agreed fairly well with the values reported by Jerome et al. (1956), Aksoy (1980) and Balachandran and Ulaganathan (1989).

Egg weight

The estimate of heritability pooled over generation for egg weight was moderate in this study (Table 4.9).

The review of literature indicate the average estimate of heritability from sire component of variance to be 0.39 (Table 2.6). The estimate in the present study is in good agreement with the report of Sharma (1981), Mishra et al. (1986) and Barwal et al. (1993).

Index unit

The heritability values presented in Tables 4.8 and 4.9 revealed that index unit was moderate to highly heritable. The magnitude of pooled estimates ranged from 0.19 to 0.486 in males and 0.313 to 0.338 in females in different lines.

Although no reports of heritability estimates are available for index unit incorporating the traits undertaken in the present study for a suitable comparison, Singh (1986) reported moderate heritability of index unit incorporating body weight, breast angle, shank length and keel length all measured at 8 weeks of age. Similar report for female line index was reported by Dev Roy (1986) incorporating 8 week body weight, Egg production to 40 weeks of age and egg weight at 40th weeks of age.

5.4.2 Time trend in heritability estimates

The time trend in heritability estimates serves the purpose of assessing the changes in genetic variability. Changes in genetic variance due to selection is conditioned by the genetic constitution of the base population.

On perusal of the Tables 4.8 and 4.9 it is revealed in the present investigation that the time trend pattern of heritability over generations was not consistent. Similar results are also reported by Singh (1986) and Dev Roy (1986) in short term selection experiments in meat type chickens.

Maloney et al. (1963) reported no change in the heritability estimates in a selection experiment for increased body weight over 10 generations of selection, although there was a reduction in phenotypic variance.

However, Maloney et al. (1967) reported a reduction of heritability at the rate of -1.0 ± 2.7 per cent and an increase of 2.4 ± 1.4 per cent per generation in males and females respectively

for 12 week body weight in the last 10 generations of a fifteen year experiment.

Siegel and Cherry (1981) reported an inconsistent change in heritability of 8 week body weight in the high weight line and a progressive reduction in additive genetic variance in low weight line in first 10 generations of a long term experiment.

5.4.3 Correlation

The genetic and phenotypic correlations in the present investigation were estimated utilizing sire component of variance and covariance analysis method within sex/line/generation and then pooled over generations within each sex and line to have a precised estimate.

Four week and six week body weight

The association between four and six week body weight was seen to be positive and very high, almost nearing unity, irrespective of line and sex and significant on both genetic and phenotypic scale suggesting that most of the genes that influence four week body weight were also influencing inheritance of six week body weight (Table 4.10A).

The pooled estimates in different lines both on genetic and phenotypic scale were in good agreement with those reported in literature (Saxena, 1976; Dev Roy et al., 1983; chambers et al., 1984; Singh, 1986 and Choudhary, 1992).

The high positive association between these two traits indicate that selection in one can bring about simultaneous improvement in the other trait.

Four week body weight and breast angle at 6 weeks of age

Moderate to high positive and significant correlations between 4 week body weight and 6 week breast angle both at genetic

and phenotypic levels were in all the cases except at genetic level in females of IC-3, in which it was non-significant but positive (Table 4.10B). Reddy (1988) also reported positive genetic and phenotypic correlations between these two traits.

Positive genetic correlation of 4 week body weight with breast angle at 6 weeks of age would suggest that selection for 4 week body weight would bring simultaneous improvement in both 4 week body weight and 6 week breast angle.

Four week body weight and shank length at six weeks of age

The genetic and phenotypic correlations between four week body weight and 6 week shank length were seen to be positive and significant except at genetic level in females in which it was non-significant (Table 4.10C).

Reddy (1988) also reported positive genetic and phenotypic correlations between these two traits. Unni et al. (1977), Mishra et al. (1984) and Champati et al. (198.) reported positive correlation between body weight and shank length at 8 weeks of age.

Body weight and breast angle at six weeks of age

It was observed that the correlations between body weight and breast angle at six weeks of age both at genetic and phenotypic levels were positive and significant (Table 4.10D).

Reddy (1988) and Choudhary (1992) reported similar positive correlations between these two traits.

The high magnitude of pooled genetic correlations between these two traits suggest that selection in any one of the traits can bring about improvement in other trait concomitantly.

Body weight and shank length at six weeks of age

On perusal of the Table 4.10E it is observed that significantly high positive correlations both at phenotypic and genetic scale existed between body weight and shank length at six weeks of age except in females on genetic scale in which it was positive and non-significant.

The results of the present study fairly agreed with the earlier reports of Reddy (1988) and Choudhary (1992).

Breast angle and shank length at six weeks of age

The phenotypic correlations between shank length and breast angle at six weeks of age were positive and significant but moderate in magnitude. The corresponding values on genetic level were positive but non-significant in all the lines (Table 4.10F).

The results in the present study agree well to the reports of Reddy (1988). However, Choudhary (1992) reported higher estimates on phenotypic scale and lowest estimates on genetic scale in comparison to the estimates obtained in the present study.

Juvenile body weight and egg production

The pooled phenotypic correlation between body weights at both 4 and 6 weeks of age with egg production were negative and non-significant. However, at genetic level the males were lowly positive and non-significant (Tables 4.10G and 4.10I).

The review of literature indicate the correlation coefficients between juvenile body weight and egg production at phenotypic and genetic levels to be negative and averaged -0.13 and -0.19 respectively (Table 2.11).

The results in the present study are in close agreement with the reports of earlier workers (Jaap et al., 1962 and Singh et al., 1988). (Table 2.11).

However, they defer a little to the reports of McClung (1958), Shalve (1970) and Sharma (1981).

The positive but low genetic correlation in the present study might be due to no prior selection for egg production in the flock other than the present study.

Juvenile body weight and egg weight

The association between four week body weight and egg weight has been found to be positive both as genetic and phenotypic scale. Also correlation between six week body weight and egg weight was found to be positive (Tables 4.10H and 4.10J). The results in the present study are comparable to that of the reports available in the literature (Jaap et al., 1962; Friar et al., 1962; Kataria, 1985 and Dev Roy, 1986).

Egg production and egg weight

There appeared to be an inverse relationship between egg production and egg weight even though lowly positive correlation was there at phenotypic level (Table 4.10K). The reports of earlier worker indicate the general trend of negative association between these two traits both at genetic and phenotypic level the average values being -0.45 and -0.13 (Table 2.13).

The results obtained in this study as well as those reported in literature (Shalev, 1970; Saxena, 1976 and Dev Roy, 1986) indicate that egg weight would decline as a consequence to selection for high egg production.

Most of the reports indicate negative phenotypic association between these two traits as observed in the base

generation. However, the positive association provided support to the findings of Sharma (1981), Kataria (1985) and Dev Roy (1986).

Index unit and other component traits

Positive and moderate to high correlations both at genetic and phenotypic level between index unit and each of component trait of indices in both the sexes of the selected lines were observed in the present study (Table 4.10L to 4.10Q).

The results are in good agreement with the earlier reports (Singh, 1986 and Dev Roy, 1986) who conducted short-term experiments and found the association of index unit with its component traits as positive.

Since, multi-trait selection indices are designed for over-all improvement in aggregate economic worth of the individual the positive correlation of index unit with each of its component trait in this study justifies the effectiveness of selection programme in desired direction.

5.5 CONTROL POPULATION

Phenotypic responses realised in a population as a result of selection over a period of time, may be due to environmental factors such as management, feeding regimes, health control measures, climate etc. and as a result of actual changes in the genetic merit of the population. Evaluating the effectiveness of a selection programme therefore, requires that environmental changes be monitored to assess the rate of genetic improvement. One of the most common method utilized for measuring the environmental trend in a selection experiment is to maintain simultaneously an unselected control population.

Lerner (1950) briefly discussed the value of control strains and suggested probable ways to separate out the

environmental effect from generation means. Since then several methods have been described in literature.

Dickerson (1955) also recognised the need for genetically constant populations to measure the actual time trends due to environment. Gowe et al. (1959) discussed several types of controls for the measurement of genetic responses. Most of these have been presented in a review by Hill (1972).

Gowe et al. (1959) presented a detailed analysis of the results for one particular flock of control population and concluded that a pedigreed randombred control was preferable over the non-pedigreed randombred control in the selection experiments in chicken. In the present study a pedigreed randombred control line developed from IC-3 strain in the year 1980 and maintained thereafter was used to measure the time trend in environment during the course of index selection programme.

The means of index units and its component traits of control line in various generations have been presented in Tables 4.5, 4.6 and 4.7. The regression of generation means on generation numbers in control were statistically non-significant, suggesting that early fluctuations in control were the random variation of the environment. The mean values in different traits of the control line as presented in the aforesaid tables along with the selected lines in various generation also showed a non-significant regression on generation numbers.

The non-significant reduction in the means in different traits in control was probably the effect of relaxation of selection.

Hill (1980) suggested that in short term selection experiments sampling errors associated with estimating genetic mean might be more important than drift variance. In the current study (Table 4.17) the ratio of per generation drift variance (6_d^2) and the

sampling error of measurement of means (6_e^2) in control line ranged from 0.2 to 1.01 in males and 0.234 to 1.202 in females while the corresponding ratio in selected lines ranged from 2.167 to 4.984 in males and 0.776 to 2.266 in females. This indicated that drift variances were more in selected lines than control line.

Singh (1986) also found similar result while evaluating his control population. It is, therefore, logical to assume that the deviations of selected lines from the control line are unbiased estimates of genetic changes resulting from selection.

5.6 SELECTION INDEX

The selection indices used in the present investigation were of conventional type (Hazel, 1943 and Cunningham, 1969).

5.6.1 Validity of parameters of the indices

Hazel (1943) developed the selection index for application in animal breeding in terms of heritabilities and correlations. Selection index can also be computed utilizing the variances and covariances instead of heritabilities and correlations. While both forms of index require same assumption and informations, and give the same index values, use of variance and covariance is more straight forward and easier to handle computationally and less subjected to rounding errors (Cunningham, 1969). As such the variances and covariances were utilized for the construction of index in the present study.

The genetic and phenotypic variances and covariances from the base generation were used to establish the indices (Table 4.11). Separate indices developed for males and females in both the selected lines and the same and respective indices were used throughout the period of selection. Hill (1971) concluded that changes in genetic variances are likely to occur only if there is much inbreeding or there are genes with a large effect on the quantitative traits under selection. Short term selection experiments of less than

five generations durations are not likely to show changes in genetic variance and covariance. In the present study since the inbreeding was kept to the minimum and the duration of selection was only for three generations it was logical to assume that the variances and covariances did not change much during the course of selection, thus the same indices line-wise and sex-wise were used throughout the period of selection.

5.6.2 Relative economic weights

The indices developed for both sexes of sire line (IC-3) utilizing the parameters of base generations were designed for maximum gain in body weight based on combined measurements of body weight at 4 and 6 weeks of age and breast angle and shank length both measured at 6 weeks of age.

The relative economic weights assigned to the traits under study in IC-3 were arbitrarily chosen (Table 4.11) adopting the reasoning advocated by Lerner et al. (1947), Abplanalp et al. (1960), Sharma (1981) and Singh (1986). Similar assumption was adopted while allotting economic weights in IR-3 males.

For the index of the females of dam line (IR-3) the estimations of relative economic weights were done from the empirical consideration taking the loss or gain due to unit change in the trait under consideration (Table 4.11) as per Hogsett and Nordskog (1958) and Dev Roy (1986).

5.6.3 Index coefficients (b-values)

The index coefficients for the component traits of the four indices corresponding to each of the sex in both the selected lines are presented in Table 4.12. In the indices developed for each sex in IC-3, all the component traits received positive index coefficients, except the shank length in the female which had negative coefficient. Singh (1986) also reported the negative b-value for shank length.

The indices utilized in IR-3 in each sex also received positive index weighting factors except in the case of 4-week body weight in the index for females which had negative coefficient. Sharma (1981) and Saxena et al. (1982) reported negative index coefficient for 8 week body weight and 10 week body weight respectively in the indices developed incorporating body weight, EP and EW. Since, the index coefficients were well in agreement with the earlier studies, they were utilized to maximise the genetic worth of the lines.

5.6.4 Efficiency of the indices

The correlation (r_{HI}) between index and breeding values gives a measure of the efficiency of an index, the greater the correlation the better is the index as a predictor of breeding value (Falconer, 1981). The r_{HI} values in the different indices (Table 4.12) were quite high except in the case of males of IR-3 which incorporated only two traits viz., 4 B.W. and 6 B.W. However, the efficiency ranged from 0.4577 to 0.7808. Saxena et al. (1982) constructed indices for New Hampshire and White Rock strain and the r_{HI} values were 0.46 and 0.64, respectively. Dev Roy (1986) reported r_{HI} for selection index constructed for short term experiment as 0.6705. Since, incorporation of traits solely depends upon the choice of breeder and the efficiency is directly proportional to the number of traits incorporated in the index, a valid comparison cannot be made. Since, the r_{HI} values were in good agreement with the earlier reports, the indices were expected to bring about desired genetic improvement in respective lines and sex.

5.6.5 Statistical properties of selection indices

Henderson (1963), Nordskog (1978) and Singh (1986) discussed some very important statistical properties of an index of multiple traits.

Some statistical properties, viz., the variances, $V_{(I)}$, $V_{(H)}$ and $V_{(K)}$ were first computed, from which r_{HI}^2 and heritability of index were derived from four selection indices (Table 4.13) developed in the present study. Differences in $V_{(K)}$ values were reflected not only by differences in r_{HI}^2 , but also by difference in heritability of indices as one would expect because these are strongly correlated. Taking the four indices into consideration, the value of r_{HI}^2 ranged from 0.21 to 0.61, which implies that 21 to 61 per cent of variance in economic merit (H) were predictable from the different indices in selection programme in both the lines. However, the h_I^2 also ranged from 0.21 to 0.61 which implies that 21 to 61 per cent of the indices themselves, when considered as performance indices were of genetic origin. The ratios of r_{HI}^2/h_I^2 ranged from 0.97 to 1.00.

The findings of statistical properties of selection indices were in accordance with the conclusions reported by Nordskog (1978) and Singh (1986).

5.6.6 Value of variates

Reduction in the efficiency due to exclusion of a particular component trait from the index was calculated as per Cunningham (1969).

In the present study omission of 40 week egg production from the index for IR-3 females would have resulted maximum reduction in efficiency (39.10%) of index (Table 4.14).

Sharma (1981) and Dev Roy (1986) also reported maximum reduction in the efficiency due to omission of egg production from the index.

Saxena (1976), Das (1982) and Barwal (1993) constructed selection indices incorporating various traits in poultry. They reported varying degrees of efficiencies for the different indices and also observed that exclusion of one or more traits from the index

reduced the efficiencies as seen in present study.

5.6.7 Expected genetic gains in indices

The expected genetic gains in aggregate genotype (ΔH) per generation by use of different indices are presented in Table 4.12. The expected aggregate genetic worth were quite substantial and in desired direction. Since the average selection intensities were different for both the lines and also there were differences in constituent traits of the indices, no comparison was made between the indices.

5.7 SELECTION DIFFERENTIALS

The expected and effective selection differentials and selection intensities (i) along with phenotypic standard deviations for criteria of selection are presented in Tables 4.15 and 4.16. Also presented in these tables are the expected and effective selection differentials for component traits of indices.

5.7.1 Primary selection differentials

The criterion of selection throughout the study was index unit. In the sire line (IC-3) the average of expected and effective selection differentials of S_0 and S_1 generation for index unit were 112.53 and 113.35 respectively. The corresponding values in IR-3 were 92.43 and 92.47 (Tables 4.15 and 4.16). The ratios of effective and expected selection differential was 1.007 in IC-3 and 1.001 in IR-3 indicating the natural selection was unimportant during the course of study for this criterion.

Das (1982) reported from his multi-trait index selection study in layer type chickens, that natural selection favoured to some extent the artificial selection during S_0 and disfavoured during S_1 generation when selection was made for total score.

Singh (1986) and Dev Roy (1986) reported that natural selection did not hinder the artificial selection in their short term

selection study on index score in IC-3 and IR-3 strains as observed in the present study.

5.7.2 Correlated selection differentials

The selection differentials for correlated traits are presented in Tables 4.15 and 4.16 for IC-3 and IR-3 strain respectively. The purpose of computing selection differential in component traits of the indices was to assess the influence of selection criterion on the correlated selection differential.

In the sire line (IC-3) the average standardised secondary selection differentials in the component traits of the indices were very high in magnitude for 4 week body weight ($1.304 \sigma_p$), 6 week body weight ($1.359 \sigma_p$), breast angle ($0.0774 \sigma_p$) and shank length ($0.817 \sigma_p$) at 6 weeks of age. Since, positive selection intensities were observed in all the traits under study it was assumed that realised responses for four traits would be better in magnitude which could result in increase in economic worth of the individuals. The natural selection favoured the artificial selection in all the traits except in shank length. The results in this investigation were in good agreement with Singh (1986). In the dam line (IR-3) the average standardised secondary selection differentials in the component traits of the indices were high in magnitude except in egg weight which was low but positive ($0.159 \sigma_p$). The selection intensities for other traits were ($1.228 \sigma_p$) for 4 week body weight ($1.451 \sigma_p$) for 6 week body weight and ($0.575 \sigma_p$) for egg production to 40 weeks of age. It was expected for an improvement in all the component traits in IR-3 in desired direction.

The natural selection favoured artificial selection for all the traits except for egg production to 40 weeks of age in which it slightly hindered the artificial selection.

A conclusion can be arrived that natural selection did not hinder, in general the artificial selection in the index units and also in component traits in the present study. Similar reports were also available (Singh (1986) in a short term index selection experiment.

5.8 GENETIC DRIFT AND SAMPLING ERROR

The theory of artificial selection is based on the assumption that population size is infinite (Falconer, 1960). However, selection is practised in populations having finite number of individuals. As a result of small population size, random drift causes changes in gene frequencies which may result not only variation in mean of response (Hill, 1971) but also variation within line additive genetic variance (Avery and Hill, 1977).

Vasquez and Bohren (1982) indicated that small effective population size tends to reduce the response to selection and the realised heritability and this could be partly attributed to genetic drift. The changes due to drift are cumulative, any change in one generation being carried on as the starting point for the change in the next generation. Often, the drift will be of significant size in control population because it is generally reproduced from smaller number of individuals due to economic necessity.

Since, in many selection experiments, control and selected strains are derived from a single line, direct evidence for existence of genetic drift is not readily available in literature. However, genetic drift variance can be predicted from the theoretical expectations before experimentation.

Similarly, errors in estimation of mean (sampling error) are always present and can also be measured in advance. The magnitude of sampling error variance can be reduced by increase in size of the test population and it does not accumulate over generations.

In order to study the importance of genetic drift and sampling error variance, in control and selected lines, the values were predicted as per Hill (1972 and 1980).

The predicted total drift variance over three generations of selection in males of IC-3 for index units and for component traits are presented in Tables 4.17 and 4.18. The values for sampling error variance are also presented along with drift variance in the aforesaid tables. In general the ratio of per generation drift to sampling error in males and females of selected lines for component traits of indices were 3.31 to 4.16 times greater than the ratio in control line as was expected (Table 4.18). The results obtained in this study revealed that drift variance and sampling error variances in selected and control lines were of smaller magnitude, since effective population size and progeny scored per generation in each line were fairly large enough to minimise these effects considerably.

The results of this investigation were in good agreement with the report of Singh (1986).

5.9 REALISED AND PREDICTED GENETIC GAINS AND PERCENT EFFICIENCY

The average realised genetic gains from three generations of selection in index units and in component traits of the indices are presented in Tables 4.19 and 4.20 for IC-3 and IR-3 respectively. Figs. 4.1 and 4.6 explain the magnitude and pattern of improvement over generations in component traits due to index selection. Positive and significant realised genetic gains were found in body weight and breast angle in females of IC-3 and in index unit, 6 week body weight and egg weight at 40 week of age in females of IR-3. However, positive and non-significant but substantial genetic gains were also observed in all other traits in the present study in both the lines. There are no reports available in literature for comparison of the realised genetic gains in index units incorporating the traits

undertaken were not similar to the traits considered in this study. However, Singh (1986), Dev Roy (1986) and Singh (1992) obtained positive realised genetic gains in index units and also in component traits of the indices in a short term index selection programmes, but all the traits undertaken in this study. However, Singh (1986), Dev Roy (1986) and Singh (1992) obtained positive realised genetic gains in index units and also in component traits of the indices in a short term index selection programmes, but all the traits undertaken were not similar to traits considered in this study.

The average predicted genetic responses corresponding to the realised responses are presented in Tables 4.19 and 4.20. On perusal of the tables it could be seen that predicted genetic responses were of higher magnitude for index scores and also for component traits of indices except for egg weight in IR-3 females. The realised and predicted direct and correlated responses were positive and in same direction for all the traits under study.

The efficiency in prediction of index score was 44.69% for males and 44.89% for females in IC-3 while corresponding values in IR-3 were 25.82% and 71.68%. In the component traits of indices the efficiency (%) ranged from 21.48% to 98.26% in IC-3 and from 21.96% to 217.39% in IR-3.

Various reasons are available in literature relating to the non-agreement of predicted responses to the realised one. Harris (1964) reported that continued index selection might shift the initial genetic parameters and thus may contribute to deviations of expected responses. Siegel (1968²) reported that the large discrepancy in predicted and realised correlated responses might be due to genotype-environment interaction. Over-estimation of expected genetic change to realised genetic change as observed in case of index unit and other component traits except egg weight in IR-3 strain in the present study might be due to inclusion of non-additive genetic effect in estimation of genetic parameter (Dickerson, 1955). Higher realised response than expected responses as obtained for egg

weight in the present study in IR-3 have also been reported by Kinney and Shoffner (1967) and EL Housoni and Royub (1971). The results in the present study are in good agreement with the report of Dev Roy (1986), who found the variation of efficiency (%) in prediction from 33.23% for 96.47% in the component traits in an index selection programme in meat type chicken. Saxena (1976) did not find a definite trend between expected and realised correlated responses for various broiler and production traits. However, Singh (1986) reported a close agreement between predicted and realised response in index unit and the component traits in a short term selection experiment.

5.10 REALISED AND PREDICTED GENETIC REGRESSIONS

The realised genetic regressions are of special interest because they are computed directly from observed responses (Bohren et al., 1970) and indicate the trend in correlated responses per unit change achieved in the trait of selection.

In the present study, the predicted and realised genetic regressions of the component traits on the respective index units were calculated as per Kinney et al. (1970).

The predicted and realised regressions for component traits of indices in each of the sex in IC-3 and IR-3 are presented in Table 4.21. A comparison of realised and predicted genetic regression values in both males and females of IC-3 indicated fair agreement for all the traits studied indicating that selection for index score would change the body weights at 4-, 6-weeks of age and breast angle and shank length at 6 weeks of age in the expected direction. Similar result was obtained in IR-3 in both the sexes for all the traits studied.

Singh (1986) also obtained similar agreement between expected and realised genetic regression as observed in the present study in BW, BA, SL and KL all measured at 8 week of age in his short term selection index experiment in meat type chickens.

5.11 REALISED HERITABILITY

The realised heritability estimated as regression of cumulative response on cumulative selection differential for the principal trait of selection, provides the most empirical description of effectiveness of selection. It also allows comparison of different experiments even when the selection intensities are not the same.

There are various methods available in literature for estimation of realised heritability. In the present study, since, separate indices were used for each of the sex in both the lines, the suitable method in such situation was by regression of standardised cumulative response on standardised cumulative selection differential as proposed by Manson (1973).

Singh (1986) and Dev Roy (1986) reported no change in realised heritabilities computed either by the method of Falconer (1960) or Manson (1973).

In sire line (IC-3) the realised heritability of index unit in males and females were 0.222 ± 0.056 and 0.049 ± 0.019 , respectively, while the corresponding values in IR-3 were 0.115 ± 0.085 and 0.215 ± 0.042 (Table 4.22). Singh (1986) reported realised heritability of index unit to be 0.22 ± 0.05 in males and 0.36 ± 0.05 in females incorporating body weight, breast angle, shank length and keel length at 8 weeks of age in his index in a short term selection programme.

Dev Roy (1986) reported the realised heritability of index unit to be 0.20 ± 0.05 in males and 0.30 ± 0.07 in females incorporating 8 week body weight, egg production to 40 weeks of age and egg weight at 40 weeks of age in a short-term selection study. The comparison could have been more precised had the information been available in the literature for the traits undertaken in this study.

SUMMARY

SUMMARY

Growing demand of broiler all around the globe, has forced the breeders and planners to evolve the optimum strategy for the high juvenile growth rate with viability of the operation. For the genetic improvement of economically important traits, the application of selection index theory for a defined breeding goal (H) and available information results in the optimal selection index (I) and maximal selection response. Although a few reports from experimental studies on selection index in meat type chicken are available, a study in similar line along with the comparison between predicted and realised responses to index selection can be of paramount help to the poultry industry.

The investigation reported in this thesis was, therefore, undertaken with the following objectives:

1. To study the change in genetic and phenotypic performance of two broiler populations undergoing index selection with a control population.
2. To study the efficiency in prediction of responses and comparison with realised responses for primary and component traits of indices of both lines.
3. To estimate the genetic drift, sampling variance, co-efficient of variation and inbreeding effects in male and female lines and control population.
4. To study the genetic and phenotypic trend in different traits of the index used in the male and female lines.

In order to achieve these objectives, two purebred broiler strains, IC-3 and IR-3 which were subjected to selection for high body weight at 8 week of age for 16 years, were utilized. A pedigreed randombred control population, originated from IC-3 strain

during 1980 was maintained as a control line simultaneously to monitor the genetic progress in the selection programme. The chicks hatched out during October to December, 1987 from the three stocks separately constituted the base population for this study. Three generation data including that of base generation have been utilized in this study. However, the 4th generation data have been used for the sole purpose of calculation of response. While, pen mating in the ratio of one male to seven to eight females was practised in selected lines, artificial insemination utilizing one male to two females was done in control line. Full and half-sib matings were deliberately avoided to keep the rate of inbreeding at the minimum.

The multi-trait index selection was practised incorporating body weight at 4 and 6 weeks of age, breast angle and shank length both at 6 weeks of age separately for both the sexes in IC-3 strain. However, the traits included in the index for males of IR-3 were 4 and 6 week body weight and in case of IR-3 females the traits were 4 and 6 week body weight, egg production to 40 weeks of age and egg weight at 40th week of age. All the indices were developed utilizing data from the base generation and same indices were used in respective sex and line throughout the study. The relative efficiencies of various indices utilized in this study ranged from 45.77 to 78.08 per cent which were effective enough to bring about improvement in genetic economic worth.

The average number of effective sires and dams respectively per generation were 33.75 and 210.25 in IC-3, 32 and 223.25 in IR-3 and 43.75 and 86.25 in control line. The effective population size was 116.25 in IC-3, 111.95 in IR-3 and 199.77 in control line. The inbreeding coefficient increased by 1.76, 1.80 and 1.0 per cent in IC-3, IR-3 and control line during the three generations of selection study.

Hatch effects were found to be significant for most of the traits and in all the lines. The data, therefore, were corrected for hatch effects by fitting least square constants before detailed analysis.

The heritability estimates computed from sire component of variance and pooled over generations in IC-3 males were 0.414, 0.447, 0.319, 0.251 and 0.486 for 4-, 6-week body weight, breast angle and shank length at 6 weeks of age and index unit respectively. The respective values in IC-3 females were 0.272, 0.290, 0.245, 0.212 and 0.338. In IR-3 males the pooled estimates were 0.251, 0.244 and 0.190 for 4-, 6-week body weight and index units respectively whereas the values for IR-3 females were 0.314, 0.321, 0.360, 0.195 and 0.313 for 4-, 6-week body weight, egg production to 40 weeks of age, egg weight at 40th week of age and index unit respectively. The pooled estimates for control line males were 0.412, 0.574, 0.544 and 0.329 for 4-, 6-week body weight, breast angle and shank length at 6-weeks of age. The corresponding values in females of control population were 0.550, 0.413, 0.365 and 0.283 respectively.

The genetic and phenotypic correlations of component traits showed a trend similar to those reported in literature. The genetic correlations between index unit and the component traits of the indices were positive and ranged from moderate to high in magnitude. This indicated that index selection would bring about positive changes in all the constituent traits of the respective indices. The phenotypic correlations were smaller in magnitude than the corresponding genetic correlations.

The average mid-parent selection intensities over the generations for index units were $1.275 \sigma_p$ in IC-3 and $1.593 \sigma_p$ in IR-3. - Comparison of effective and expected selection differentials for the selection criteria revealed no differences in general in the lines under selection indicating that natural selection did not interfere with artificial selection during the course of the present study.

The predicted drift variance over three generations of selection for index units were small in magnitude. Also the sampling error per generation was found to be small in magnitude. The ratio of drift variance to sampling error per generation for index units were 3.63 and 1.81 in males of IC-3 and IR-3 respectively. The

corresponding values in females were 2.87 and 0.71. For the component traits of indices the ratio of per generation drift variance to sampling error in general were higher in selected lines than the control line which indirectly implies the stability of control population.

Realised heritabilities of index units, the criterion of selection in both the sexes of the two selected lines were calculated. In males the estimates were 0.222 ± 0.056 in IC-3 and 0.155 ± 0.085 in IR-3. The corresponding estimates in females were 0.049 ± 0.019 and 0.215 ± 0.042 which implies the effectiveness of selection in desired direction.

The phenotypic time trends of means of index units and constituent traits over the generation were estimated. In the selected lines for most of the traits the trend was positive and non-significant. However, the phenotypic gains were substantial. In control line also the regression of generation means over generation number were non-significant implying stability of the control population.

The average realised and predicted genetic gains from three generations of selection in index units and in component traits of indices were estimated. Positive and significant realised gains were found for body weight and breast angle at 6 weeks of age in females of IC-3 and for index unit, 6 week body weight and egg weight at 40th week in females of IR-3. However, positive and substantial realised gains were also obtained in all other traits under study in both the lines. The average realised genetic gains in index unit, 4-, 6-week body weight, breast angle and shank length at 6 weeks of age in IC-3 - were 28.90 IU, 10.33 g, 22.04 g, 1.95° and 0.17 cm respectively in males and 10.93 IU, 10.40 g, 26.82 g, 2.56° and 0.10 cm in females. The average realised genetic gains in IR-3 were 2.52 IU for index unit, 4.20 g for 4 week body weight and 10.62 g for 6 week body weight in males and in females the gains were 44.71 IU for index unit, 8.06 g for 4 week body weight, 18.44 g for 6 week body weight, 2.81 (no.) for egg production to 40 weeks of age and 1.20 g for egg weight. The

average predicted genetic responses were higher in magnitude than the realised responses for index units and also for component traits of indices in both the lines for egg weight in IR-3.

From the results of the present study which is pertaining to three generations of selection it can be concluded that:

- * A non-significant phenotypic time trend for all the economic traits in control population suggests stability of pedigreed random-bred control population which is effective to monitor the genetic progress.
- * Comparison of effective and expected selection differentials indicated that natural selection was not important in the present study.
- * In short term selection study drift variance is unimportant if the effective population size is maintained.
- * Positive and moderate to high genetic correlation of index units with its constituent traits in sire and dam lines indicate the effectiveness of index selection method to bring about improvement in its component traits in desired direction.
- * The multi-trait selection index is efficient in bringing about substantial improvement in component traits and thereby maximising the aggregate genetic economic worth in sire and dam lines of meat type chicken.

लघु सारांश

दो शुद्ध नस्ली मांसज कुक्कुट की प्रजातियों आईसी 3 और आई आर 3 में तीन वशावलियों तक बहुगुणी सूचकांक चयन हेतु अध्ययन किया गया। आईसी 3 के सूचकांकों में समावेशित गुण 4 बी 0 डब्ल्यू 0, 6 बी 0 डब्ल्यू 0, 6 बी 0 ए 0 और 6 एस 0 स्ल 0, तथा आई आर 3 में समावेशित गुण 4 बी 0 डब्ल्यू 0, 6 बी 0 डब्ल्यू 0, 30 पी 0 और 30 डब्ल्यू 0 थे। आनुवांशिक प्रगति का गति जानने के लिए साथ में एक मानक वशावली भी रखी गई। दोनों प्रजातियों के प्राथमिक और सम्बद्ध गुणों के सूचकांकों हेतु लब्ध प्रातिवेदनो की प्रयुक्त क्षमता को ऑक्लैत व्युत्पन्न माना गया।

सम्पूर्ण अध्ययन में 45.77 से 78.08 तक दक्षता वाले आधारीय वशावली के ऑक्लैडो से निर्मित चार सूचकांकों का उपयोग किया गया। चयन काल की अवधि में आई सी 3, आई आर 3 तथा मानक वशावली में अतः प्रजनन गुणांक क्रमशः 1.76, 1.80 तथा 1.0 प्रतिशत बढ़ गया। चयनित और मानक वशावली में सम्बद्ध गुणों का मिश्रित वशागतत्व आकलन प्रकाशित मानों के अनुरूप थे। सूचकांक ईकाईयाँ सामान्य से उच्च वंशागत थी। आनुवांशिक और लक्षण प्ररूपी सहसम्बन्ध प्रकाशित मानों के समान ही थे। सूचकांक ईकाई और उसके सम्बन्ध गुणों में अनात्मक तथा सामान्य से उच्च आनुवांशिक सहसम्बन्ध पाये गये। अध्ययन काल में कृत्रिम चयन में प्राकृतिक चयन का व्यवधान नहीं था। वर्तमान अध्ययन में अपवादित प्रसरण तथा प्रतिचयन-त्रुटि महत्वहीन रहे। नर आई सी 3 में औसत लब्ध आनुवांशिक लाभ 28.90 आई यू 0 और 4 बी 0 डब्ल्यू 0, 6 बी 0 डब्ल्यू 0, 6 बी 0 ए 0 तथा 6 एस 0 स्ल 0 की सूचकांक ईकाईयाँ क्रमशः 10.33 ग्रा 0 22.04 ग्रा 0, 1.95⁰ तथा 0.17 से 0 मी 0 थी। मादाओं में समकक्ष मान क्रमशः 10.93 आई यू 0, 10.40 ग्रा 0 26.82 ग्रा 0, 2.56⁰ तथा 0.10 से 0 मी 0 थे। आई आर 3 नरों में सूचकांक ईकाई, 4 बी 0 डब्ल्यू 0 तथा 6 बी 0 डब्ल्यू 0 क्रमशः 2.52 आई यू 0, 4.20 ग्रा 0 और 10.62 ग्रा 0, तथा मादाओं में 44.71 आई यू 0, 8.06 ग्रा 0 व 18.44 ग्रा 0 थे। इनके आतिरेक्त मादाओं में 30 पी 0 2.81 और 30 डब्ल्यू 0 1.2 ग्रा 0 थे। प्राथमिक तथा सम्बद्ध गुणों के आकलन की दक्षता 21.48 से 217.39 प्रतिशत पायी गयी।

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