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Phenotypic and genetic evaluation of a randombred control population of White Leghorn over 20 generations

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ABSTRACT

Population structure, changes in performance, distribution statistics, heritabilities and genetic and phenotypic correlations among economic traits were studied in a White Leghorn randombred control population over 20 generations. The average number of effective sires and dams were 39.2 and 92.3, providing an effective population size of 183.1. Inbreeding increased at the rate of 0.50% per generation and cumulated to 9.23%. Means of different traits showed wide fluctuations over generations with significant time-trend observed for some traits. These changes could be ascribed to environmental changes as calculated selection differentials for these traits were non-existent. There was no significant change in heritabilities, genetic and phenotypic variances over generations indicating the genetic stability of the line.

Key words: Chicken, Control population, Genetic correlation, Heritability, Inbreeding

Genetically-stable control populations facilitate the exclusion of between – generation variation in performance due to environmental effects and therefore make the assessment of genetic change in selection experiments feasible (Hill 1972). Directional genetic change in the control population may occur through natural or unintentional selection, and also due to genetic drift and inbreeding. The optimum mating designs attempt to minimize these factors in control populations (Hill 1972). Genetic architecture of some control populations, viz. Cornell Control (King *et al.*1959), Athens–Canadian Random bred (Hess 1962) and CARI Control (Johari *et al.*1992) have been described in literature. The present study aimed at evaluation of a White Leghorn Control population in terms of population structure, inbreeding and changes in means, degrees of departures from normality, heritabilities, genetic and phenotypic variances, and genetic correlations over 20 generations.

MATERIALS AND METHODS

The control line was derived from a White Leghorn strain (PL2) which was originally derived from Mychick strain. The line has been maintained as an unselected pedigreed population and had been reproduced through 31 to 49 effective sires, each being mated with 2–3 dams in different generations. Matings among closely related individuals i.e. half - and full-sibs were avoided. The chicks were pedigreed by sire and dam.

The economic traits recorded on each pullet were: age at first egg (ASM), egg number to 40 weeks of age (EN 40), body weights at 20 and 40 weeks of age (BW20 and BW40) and egg weight (EW) based on average of 6–8 eggs measured between 36–40 weeks of age. Derived traits included rate of lay (ROL), egg mass (EM) to 40 weeks of age ratio of 40 to 20 week body weight (ROB) egg weight as% of 40-week body weight (EW%); egg mass per functional day (EMFD) egg production efficiency i.e. egg mass in grams divided by body weight at 40 weeks in grams (EPE) and efficiency index, i.e. egg mass per functional day in grams divided by body weight at 40 weeks in kilograms (EINDEX).

The performance records were adjusted for hatch effects through least-squares analysis (Harvey 1966). Heritabilities, genetic and phenotypic correlations were calculated as per Becker (1984) on hatch–adjusted data. Effective population size (Ne) was calculated as per Gowe *et al.* (1959). Expected rate of inbreeding ("F) was estimated as ½ Ne. The estimates of skewness (G_1) and kurtosis (G_2) were calculated as per Snedecor and Cochran (1980). The changes in means, estimated 't' values for coefficients of skewness and kurtosis, heritabilities and variances were estimated by regression of these statistics on generation numbers, and their significance was tested by t-test (Snedecor and Cochran 1980). The estimates of heritabilities and correlations over generation

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were pooled by weighing the estimate of each generation inversely proportional to its estimate variance.

RESULTS AND DISCUSSION

Population structure and inbreeding: The effective number of male and female breeders alongwith effective population size (Ne), inbreeding coefficients per generation, cumulative inbreeding and the number of pullets tested are given in Table 1. The effective number of sires and dams averaged to be 39.2 and 92.3 respectively per generation which provided an effective population size of 183.1. Such an effective size is considered to be efficient for use in selection studies (Gowe *et al.* 1959).

The inbreeding coefficient per generation in the control line varied between 0.39 and 0.58% in different generations with cumulative value of 9.23% over 20 generations. Similar rates of inbreeding were reported by Gowe *et al.* (1959), Johari *et al.* (1992) and Brah *et al.* (1993) in their respective controls. The expression for calculation of expected level of inbreeding is based on random mating among selected individuals (Gowe *et al.*1959). Since matings among closely related individuals in the present experiment were avoided, the actual level of inbreeding was expected to be somewhat lower than the figures recorded in Table 1. The low level of inbreeding in the present study implied, not the factor of much significance in depressing the performance and reducing the genetic variability in the economic traits.

Nordskog *et al.* (1974) pointed out two important sources of variability between generations: sampling error of measurement and genetic drift. An approximate estimate of the ratio of the drift variance (σ^2_d) to variance due to sampling errors of measurement (σ^2_e) is given by M/N_e (Nordskog *et al.* 1974) where M is the number of pullets tested per generation and N_e is effective population size. The ratio was (1.66) obtained using the figures given in Table 1, thus the drift variance was about 0.66 times more important than sampling variance among the individuals tested in a given generation. Nevertheless, the drift variance in absolute terms was expected to be small as the effective population size was large.

Changes in means and distribution statistics: Means for different traits over generations are presented in Fig.1, while the regression coefficients of means on generation numbers (b±SE) are given in Table 2. The means varied widely over generations for all the traits presumably due to variability in climatic, managemental, sub-clinical disease conditions and nutrition over generations. The regression coefficients were statistically significant for EN40, ASM, BW20, BW 40, EM, EPE, ROB and EW% which implied that significant time-trends existed for these traits. Of the 6 basic traits, age at sexual maturity and egg number improved; egg weight remained static and BW20 increased, while BW40 declined. Since no selection was practiced in the control line, variability between generations could be ascribed to changes in

Table 1. Effective number of sires, dams, population size and inbreeding coefficient

Generations	No. of pullets tested (N)	Effective number		Effective population size (N_e)	Inbreeding coefficient (%)	
		Sires (N_m)	Dams (N_f)		Per gen.	Cumulative
1.	214	36	64	161.7	0.54	0.54
2.	286	31	80	146.4	0.56	1.10
3.	424	40	110	190.3	0.43	1.53
4.	315	40	99	188.0	0.44	1.97
5.	349	40	102	179.1	0.44	2.40
6.	288	40	98	187.8	0.44	2.84
7.	301	40	90	186.8	0.45	3.29
8.	196	40	93	186.6	0.45	3.74
9.	266	37	77	170.1	0.50	4.24
10.	330	40	110	190.3	0.43	4.67
11.	319	39	104	185.0	0.44	5.11
12.	427	39	95	183.0	0.45	5.56
13.	394	40	110	190.3	0.43	5.99
14.	154	40	78	182.3	0.47	6.46
15.	141	36	54	157.1	0.58	7.04
16.	328	38	104	180.7	0.45	7.49
17.	218	39	87	181.0	0.46	7.95
18.	158	40	94	186.8	0.45	8.40
19.	349	49	95	223.0	0.39	8.78
20.	213	39	101	184.2	0.44	9.23
Average	303.5	39.2	92.3	183.1		

Table 2. Regression coefficients (b±SE) from first to fourth degree statistics on generation number

Trait	b±SE			
	Mean	CV	t_1	t_2
EN 40	0.91*	–0.41*	0.18*	–0.018
	±0.37	±0.09	±0.07	±0.12
ASM (d)	–1.32*	0.04	–0.14	–0.06
	±0.25	±0.04	±0.09	±0.16
BW20(g)	6.97*	0.04*	0.05	–0.03
	±2.5	±0.04	±0.05	±0.04
BW 40 (g)	–4.66*	0.09*	–0.02	–0.08
	±1.81	±0.03	±0.06	±0.06
EW 40 (g)	0.07	0.03*	0.06	–0.07
	±0.04	±0.009	±0.06	±0.06
ROL (%)	–0.04	–0.3*	0.22	–0.03
	±0.24	±0.09	±0.11	±0.29
EM (g)	52.4*	–0.43*	0.21	–0.08
	±18.4	±0.09	±0.081	±0.1
EPE	0.05*	–0.034	0.24	–0.03
	±0.01	±0.09	±0.06	±0.07
EI	0.11	–0.24*	0.31	–0.22
	±0.08	±0.07	±0.08	±0.16
ROB	–0.012*	0.05	–0.06	–0.22
	±0.0031	±0.05	±0.12	±0.2
EMPFD (g)	0.02	–0.33*	0.25	–0.12
	±0.12	±0.09	±0.09	±0.21
EW%	0.02*	0.08*	–0.07	–0.29
	±0.006	±0.03	±0.07	±0.14

environmental conditions. In order to rule out the effect of unintentional selection, which may have occurred due to sampling, selection differentials for different traits were calculated. Selection differential were close to zero for different traits implying the absence of selection in the control population. Gowe *et al.* (1959) and Kinney and Lowe (1968) reported significant time-trend for sexual maturity and egg production while Johari *et al.* (1992) did not observe any

Table 3. Regression coefficients (b±SE) of heritabilities and variances on generation number

Trait	b±SE		
	h^2	V_P	V_A
ASM	0.005±0.007	–1.21±2.2	–1.3±1.47
EN 40	–0.010±0.006	–6.09*±2.32	–5.42*±2.18
BW 20	–0.014±0.011	199.26*±80.1	–0.82±148.4
BW 40	–0.016±0.010	225.5±120.6	–226.2±264.2
EW 40	–0.005±0.012	0.11*±0.03	–0.009±0.131
ROL	–0.001±0.007	–5.82*±1.45	–1.78±1.37
EM	–0.013±0.007	–15615*±5993	–17155.5*±6411
EPE	0.001±0.009	–0.0007±0.003	–0.001±0.004
EI	0.002±0.009	–0.45*±0.18	–0.15±0.22
RBW (%)	0.007±0.008	–0.0002±0.0003	0.000005±0.00014
EMPFD	–0.007±0.007	–1.61*±0.37	–0.76±0.41
EW%	–0.004±0.010	0.004*±0.001	0.0008±0.0013

Table 4. Sire and dam component heritabilities over different time periods

Trait	Generations	Heritability	
		Sire	Dam
ASM	1–4	0.270±0.130	0.780±0.170
	5–12	0.140±0.009	0.173±0.103
	13–20	0.305±0.0910	0.285±0.124
	Pooled	0.142±0.009	0.319±0.072
EN 40	1–4	0.140±0.110	0.690±0.170
	5–12	0.138±0.064	0.237±0.105
	13–20	0.102±0.084	0.289±0.131
	Pooled	0.138±0.055	0.339±0.074
BW 20	1–4	0.540±0.160	0.890±0.170
	5–12	0.210±0.100	0.564±0.115
	13–20	0.3850±0.106	0.585±0.136
	Pooled	0.213±0.001	0.640±0.078
BW 40	1–4	0.440±0.150	0.830±0.170
	5–12	0.337±0.090	0.728±0.115
	13–20	0.385±0.112	0.946±0.019
	Pooled	0.371±0.064	0.939±0.019
EW 40	1–4	0.450±0.140	0.770±0.170
	5–12	0.469±0.095	0.545±0.105
	13–20	0.396±0.105	0.520±0.132
	Pooled	0.439±0.063	0.580±0.074
ROL	1–4	0.180±0.100	0.300±0.150
	5–12	0.016±0.054	0.191±0.105
	13–20	0.084±0.072	0.031±0.127
	Pooled	0.062±0.040	0.165±0.071
EM	1–4	0.150±0.120	0.720±0.170
	5–12	0.188±0.009	0.324±0.109
	13–20	0.075±0.084	0.626±0.071
	Pooled	0.187±0.009	0.556±0.056
EPE	1–4	0.140±0.120	0.690±0.170
	5–12	0.208±0.069	0.224±0.100
	13–20	0.243±0.091	0.124±0.057
	Pooled	0.207±0.050	0.191±0.048
EI	1–4	0.210±0.100	0.260±0.140
	5–12	0.039±0.060	0.195±0.106
	13–20	0.131±0.076	0.056±0.126
	Pooled	0.010±0.043	0.168±0.070
RBW	1–4	0.290±0.110	0.450±0.150
	5–12	0.237±0.069	0.079±0.093
	13–20	0.373±0.091	0.076±0.120
	Pooled	0.288±0.049	0.150±0.066
EMPFD	1–4	0.230±0.100	0.330±0.150
	5–12	0.047±0.059	0.268±0.112
	13–20	0.091±0.074	0.071±0.127
	Pooled	0.093±0.042	0.217±0.073
EW%	1–4	0.410±0.130	0.460±0.150
	5–12	0.250±0.010	0.513±0.108
	13–20	0.325±0.098	0.430±0.134
	Pooled	0.282±0.001	*0.476±0.073*

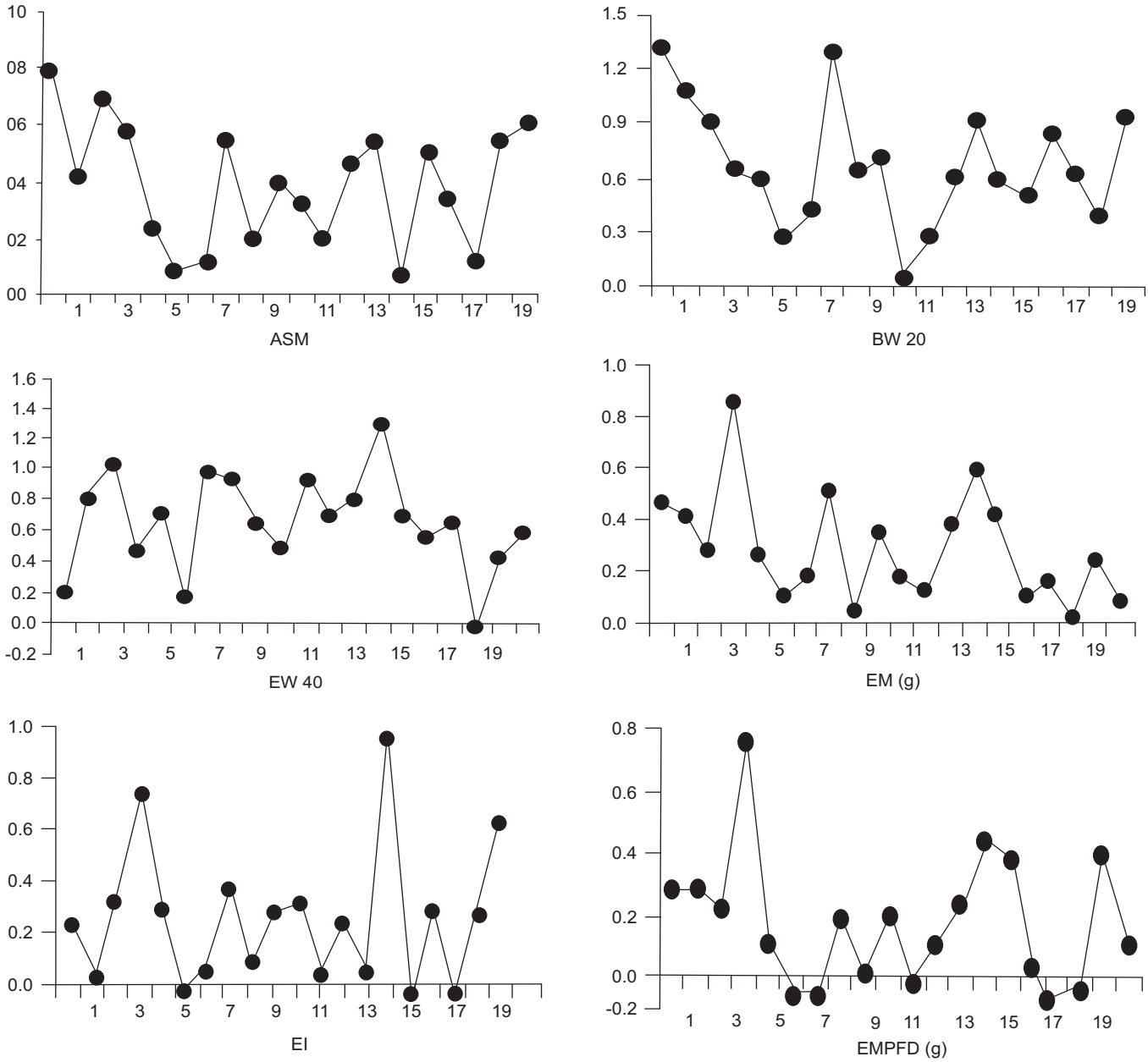

Fig. 1. Means of various growth, egg production and efficiency traits over 20 generations

such time-trend in CARI control population.

The regression of CV on generation numbers (Table 3) was statistically significant for most of the traits with the exception of ASM, BW20 and ROB. The CV's decreased over generations for EN40, ROL, EM, EPE, EINDEX and EMFD, which indicate that the changes in environmental conditions over generations tended to make the line more uniform for these traits. However, for BW40, EW40 and EW% the CV's increased over generations. These inconsistent changes for different traits could partly be due to changes associated with means over generations (scale effects).

The departures from normality of distribution for different traits were quantified by the estimated values for coefficients of skewness (t_1) and kurtosis (t_2). The regression coefficients of estimated 't' values on generation numbers are given in Table 2. Egg number showed a significant increase in departure from normality in the form of skewness. None of the other 5 basic traits showed any statistically significant changes in the degree of departures from normality of distribution over generations. The ROB and EW% did not depict changes in the shape of their distribution while other derived-traits depicted significant increase in departures from normality in the form of skewness. The reasons for changes due to departures from normality could be attributable to non-genetic factors as the control line did not experience a

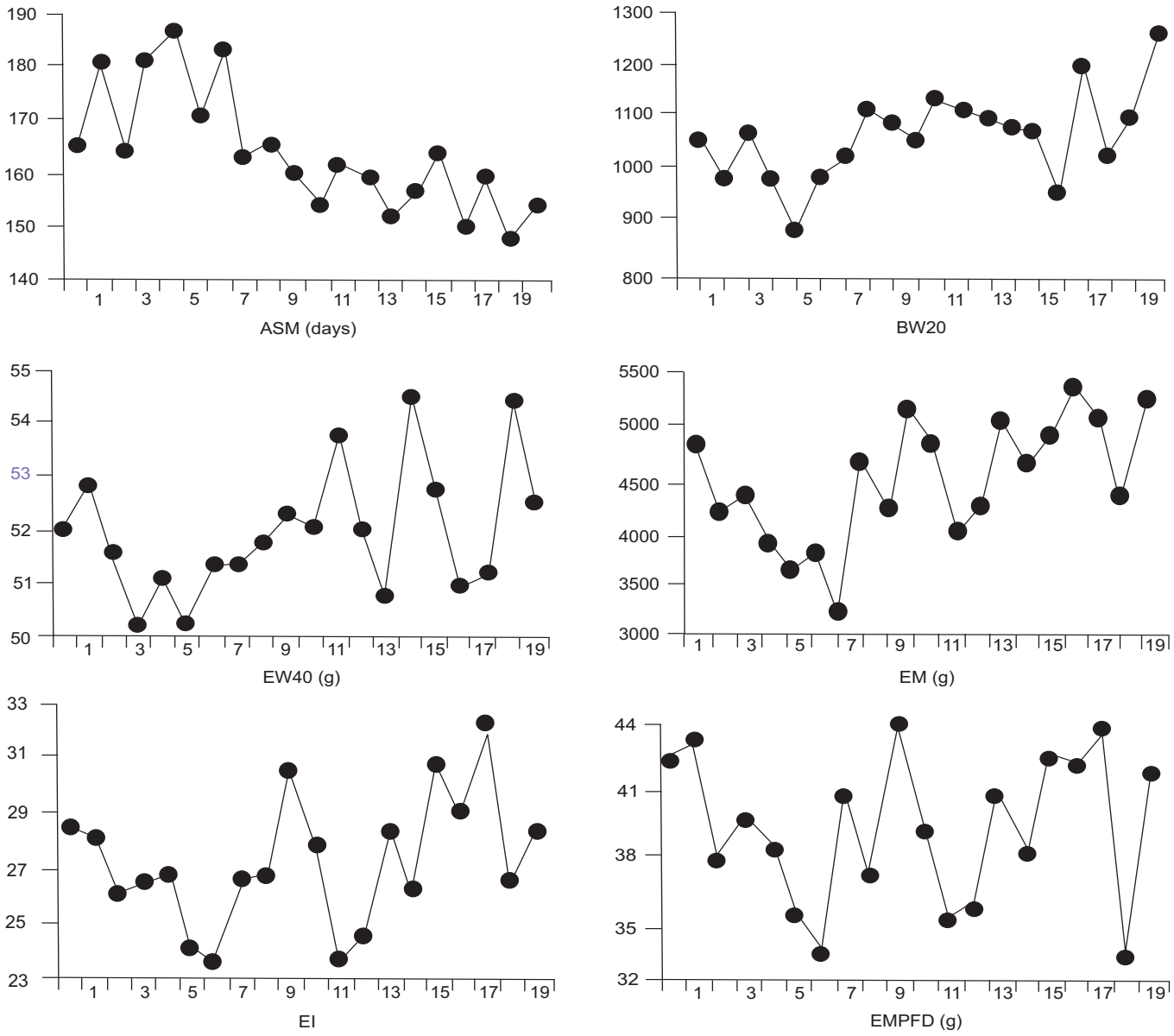

Fig. 2. Heritabilities of various growth, egg production and derived traits over 20 generations

genetic change as indicated by the absence of selection differentials.

Heritabilities, variances and genetic correlations: The regression estimates of half-sib heritabilities, additive-genetic and phenotypic variances on generation numbers are presented in Table 4. The half-sib estimates of heritability for different traits over generations are presented in Fig. 2. The h^2 estimates varied widely over generations, mainly because of sampling nature of inheritance and the population size per generation was small. However, there were no significant time-trends in half-sib heritabilites over generation numbers but the changes in the additive genetic variances over generations showed significant change for EM only. The phenotypic variances exhibited significant changes over generation for EN40, BW20, EW, ROL, EM, EI, EMFD and EW%. However, the direction of changes in phenotypic and additive variance for several traits were in similar direction which made the h^2 to be fairly stable over generations.

In order to assess the type of gene action and to critically examine the changes in h^2, the estimates from full-sib analysis, pooled for 1–4, 5–12 and 13–20 generations, are given in Table 4. Of the 6 basic traits, the sire-component heritabilities for EN, BW40 and EW varied much lesser over the 3 time periods implying the lack of changes in genetic architecture. For ASM, BW20, BW40, ROL, EI, ROB, EM and EW%, the sire-component estimates in the mid-period were lower than in the first – and the last-periods. The h^2 for

Table 5. Estimate of genetic correlation among different traits over different time periods

Trait combination		Generations			Pooled
		1–4	5–12	13–20	
	BW 20	–0.30±0.10	–0.38±0.11	–0.13±0.11	–0.014
	BW 40	0.12±0.11	0.27±0.11	0.43±0.09	0.012
	EW 40	0.04±0.12	0.19±0.11	0.16±0.11	0.03
	ROL	–0.23±0.15	–0.88±0.25	0.19±0.21	–0.05
	EM	–0.70±0.07	–1.00±0.0	–0.74±0.08	–0.0001
EN40 with:	BW 20	0.32±0.11	0.34±0.12	0.33±0.13	0.02
	BW 40	0.12±0.12	–0.15±0.11	–0.22±0.13	–0.06
	EW 40	0.05±0.13	–0.41±0.10	–0.53±0.10	–0.01
	ROL	0.79±0.07	1.02±0.11	0.56±0.20	0.004
	EM	0.94±0.02	0.91±0.03	0.79±0.08	0.0003
BW 20 with:	BW 40	0.78±0.04	0.74±0.04	0.71±0.05	0.0008
	EW 40	0.41±0.09	0.32±0.08	0.54±0.07	0.005
	ROL	0.22±0.13	0.26±0.24	0.80±0.07	0.006
	EM	0.43±0.09	0.54±0.10	0.74±0.07	0.004
BW 40 with:	EW 40	0.48±0.08	0.47±0.06	0.57±0.06	0.003
	ROL	0.30±0.13	–0.03±0.22	0.27±0.17	0.038
	EM	0.26±0.12	0.12±0.12	0.16±0.14	0.029
EW with:	ROL	0.15±0.19	–0.87±0.06	–0.62±0.13	–0.004
	EM	0.39±0.11	0.11±0.11	0.37±0.12	0.015
ROL with	EM	0.77±0.07	0.96±0.04	0.25±0.31	0.001

derived traits showed greater changes between time-periods but did not depict any consistent pattern. Pooled over generations, the sire-component heritabilities were lower for EN40, ASM, ROL, EM, EPE, EI and EMFD and moderate to high for BW20, BW40, EW, ROB and EW%.

The dam-component estimates were consistently higher than sire-component estimates for BW20, BW40, EW and EM. Pooled across all the generations the h^2 were 1.5 to 3 time higher than h^2 for these traits which implied the existence of dominance-deviation and/ or maternal effects for these traits. On generation-pooled basis, the dam-component yielded higher h^2 than the sire-component for ASM, EI, EMFD and EW% also. The dam-component estimates varied between the 3 time periods but did not depict any consistent pattern of change. These observations coupled with those given in Table 4 explicitly showed the lack of changes in genetic and phenotypic variability over generations.

The estimates of heritabilities reported herein are in fair agreement with those reported in the literature for body weight, egg weight and sexual maturity but are on the higher side for egg number and rate of lay (Fairfull and Gowe 1990). The reason for higher heritabilities for main components of layer productivity i.e. egg number and laying rate could be the lack of selection for these traits for a number of years, and also due to break up of epistatic combinations created in the selected line due to continuous selection.

The estimates of genetic correlations for each of the 3 time periods for the seven important traits of productivity are presented in Table 5. The signs of the genetic correlation between different traits were, in general, similar over the three periods. There were, however, changes in the magnitude of the correlations over the 3 time periods but the changes did not depict a clear cut pattern implying the lack of changes in genetic covariability as well. The lack of significant changes observed for means, heritabilites and genetic variances, and genetic correlation in the WLH control line used here implied that the population remained genetically stable during the course of 20 generations. The level of inbreeding was low, so little consequence in causing any significant inbreeding depression.

REFERENCES

Becker W A. 1984. *Manual of Quantitative Genetics* 4th edn., Academic Enterprises, Pullman, W A, USA.

Brah G S, Chaudhary M L, Sandhu J S. 1993.Evaluation of a randombred control population of layer chicken. *Indian Journal of Poultry Science* **32**: 23–27.

Fairfull R W and Gowe R S. 1990. Genetics of egg production in chickens. *Poultry Breeding and Genetics*. Pp. 705–60. (Ed) Crawford R D. Elsevier, Amsterdam.

Gowe R S, Johnson A S, Downs J H, Gibson R, Mountain W F, Strain J H and Tinney B F. 1959. Environment and poultry breeding problems. 4. The value of a randombred control strain in a selection study. *Poultry Science* **38**: 443–82.

Harvey W R. 1966. *Least-square analysis of data with unequal subclass numbers.* United States Department of Agriculture, Agricultural research science and education administration.

Hess C W. 1962. Randombred populations of the Southern Regional poultry breeding project. *World Poultry Science Journal* **18**: 147–52.

Hill W G. 1972. Estimation of genetic changes. 1. General theory and design of control populations. *Animal Breeding Abstract* **40**: 1–5.

Johari D C, Kataria M C, Sharma D, Singh D P and Gopal R. 1992. Evaluation of randombred control population of White Leghorn. 1. Economic traits. *Indian Journal of Poultry Science* **27**: 6–9.

Kinney T B and Lowe P C. 1968. Genetic and phenotypic variation in the Regional red controls over nine years. *Poultry Science* **47**: 1105–10.

King S C, Carson J R and Doolittle D P. 1959. The Connecticut and Cornell Randombred populations of chickens. *World's Poultry Science Journal* **15**: 139–59.

Nordskog A W, Tolman H S, Asey D W and Lin C Y. 1974. Selection in small populations of chickens. *Poultry Science* **53**: 1188–1219.

Snedecor G W and Cochran W G. 1980. *Statistical Methods*. 7th edn. The Iowa State University Press, Ames, Iowa.