RESULTS AND DISCUSSION

A. Components of Variance

Results presented in Tables 1 and 2 indicate that the differences between sires and between dams for 8 and 12 week body weights were statistically highly significant in all generations of random and selected populations. These higher variations in paternal and maternal half-sibs may be attributed to the fact that White Baladi breed of chickens used in this study was not subjected to any method of selection before starting this investigation. One way, therefore, expect higher genetic variations between individuals of this breed.

Significant differences between sires and between dams for dressing percentage were found in most generations of random population. The differences of selected population were, however, not significant in most generations (Table 3). The differences between individuals due to sires and dams for edible meat and blood percentages had no constant significant trend in most generations of random and selected populations (Tables 4 and 5). However, feather percentage showed significant differences in most generations of the two populations (Table 6). It seems, that body weights and feather percentages were characterized with high variations between individuals within generation when compared with edible meat and blood percentages which showed relatively lower variations.

The components of variances due to parental and maternal half-sibs for the studied traits are presented in Tables 7, 8, 9, 10, 11 and 12. The tabulated results indicated higher variances due to dams than those

Table 1: Mean squares of eight week body weight in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
Random population												
Between sires	14	17129.5**	19	31680.2**	19	50925.4**	19	4126.3**	19	10534.2**		
Dams/sires	112	3578.1**	156	7403.2**	147	9252.1**	126	2586.1**	57	6976.8*		
Progeny/dams	407	2163.0	662	3254.6	411	4966.4	294	1722.5	207	4347.2		
Selected population												
Between sires	19	18492.7**	19	26217.1**	19	48687.8**	12	19296.4**	19	12840.5**	18	18275.6***
Dams/sires	163	4153.2**	168	5536.4**	160	10049.7**	85	3674.9**	98	4427.3	98	8256.3**
Progeny/dams	748	1959.6	1146	1947.3	632	5534.8	397	2196.1	264	3798.2	301	4653.2

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

Table 2: Mean squares of twelve week body weight in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
					Random population							
Between sires	14	37215.4**	19	47982.3**	19	75976.7**	19	19923.7**	19	37335.4**		
Dams/sires	111	11588.4**	156	36778.0**	146	12984.9**	123	8472.0*	56	18692.4**		
Progeny/dams	394	5511.4	649	6670.0	375	7599.9	242	6269.1	201	8167.0		
					Selected population							
Between sires	19	31511.8**	19	60836.6**	19	72243.7**	12	83711.2**	19	28584.5**	18	48678.8**
Dams/sires	161	9340.2**	167	13730.3**	158	16125.6**	87	10171.9**	97	10961.7	100	16974.5**
Progeny/dams	633	4235.1	1091	6451.0	558	12072.2	378	6712,4	249	9082.2	287	10810.6

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

Table 3: Mean squares of dressing percentage for twelve week slaughtered males in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
					Random population							
Between sires	14	13.0**	18	11.2**	19	20.0**	19	6.4	19	9.7**		
Dams/sires	93	6.1**	133	6.5*	112	10.4	80	11.8	41	5.7*		
Progeny/dams	123	3.0	208	4.6	108	7.7	62	8.3	81	3.6		
					Selected population							
Between sires	19	1.9	19	20.9**	19	6.0	12	7.4*	19	8.6	18	20.1
Dames/sires	40	4.6	160	6.4*	127	6.4	76	4.2	82	10.0	80	14.9
Progeny/dames	17	3.8	452	5.3	174	6.6	115	3.4	128	8.7	121	12.5

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

Table 4: Mean squares of edible meat percentage for twelve week slaughtered males in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
					Random population							
Between sires	14	10.2**	18	7.2**	19	14.1	19	9.4	19	8.1*		
Dames/sires	93	8.0**	133	5.0**	112	13.8	80	11.1	41	5.4		
Progeny/dames	123	3.8	208	1.2	108	11.0	62	9.4	81	3.9		
					Selected population							
Between sires	19	2.3	19	18.7**	19	4.8	12	4.2	19	5.9	18	23.7**
Dames/sires	40	4.7	160	5.8	127	6.6	76	5.0	82	10.2*	80	14.8**
Progeny/dames	17	5.2	452	5.3	174	7.4	115	4.0	128	7.0	121	9.1

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

Table 5: Mean squares of blood percentage for twelve week slaughtered males in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
Random population												
Between sires	14	0.3	18	1.8**	19	1.2	19	0.5	19	1.8		
Dames/sires	93	0.6	133	0.4*	112	1.7**	80	0.8	41	1.6		
Progeny/dames	123	0.6	208	0.3	108	1.0	62	0.7	81	1.3		
Selected population												
Between sires	19	1.0	19	0.8**	19	0.9	12	1.1*	19	0.5	18	4.2**
Dames/sires	40	0.5	160	0.4	127	0.6	76	0.8**	82	0.5	80	1.7
Progeny/dames	17	0.5	452	0.4	174	0.6	115	0.5	128	0.6	121	1.5

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

Table 6: Mean squares of feather percentage for twelve week slaughtered males in successive generations of random and selected populations.

Generation	F_1		F_2		F_3		F_4		F_5		F_6	
Source of variation	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
Random population												
Between sires	14	2.3	18	5.0**	19	2.6	19	2.2	19	3.8**		
Dames/sires	93	2.5**	133	1.6	112	2.6**	80	1.5	41	2.4		
Progeny/dames	123	1.3	208	1.3	108	1.6	62	1.9	81	1.7		
Selected population												
Between sires	19	2.9*	19	3.5**	19	2.0	12	2.5**	19	1.6*	18	6.2**
Dames/sires	40	2.4*	160	1.7**	127	1.8	76	1.1*	82	1.0	80	3.0**
Progeny/dames	17	0.9	452	1.0	174	1.4	115	0.8	128	0.9	121	1.2

* Significant, $P \leqslant 0.05$

** Significant, $P \leqslant 0.01$

due to sires in majority of the studied traits and in most generations of random and selected populations. In random population; the variances between individuals due to sires and due to dams for eight and twelve weeks body weights, dressing, edible meat, blood and feather percentages; each presented 10.0 vs. 15.3, 9.2 vs. 24.0, 6.02 vs. 20.6. 2.1 vs. 25.6, 3.3 vs. 10.8 and 4.3 vs. 15.4 percentages (means over all generations) of the corresponding phenotypic variances, respectively. While variances between individuals due to sires and due to dams in selected population for the same respective traits, each presented 10.8 vs. 13.5, 11.3 vs. 11.2, 2.5 vs. 8.1, 2.0 vs. 8.8, 7.0 vs. 6.3 and 4.7 vs. 24.0 percentages of the corresponding phenotypic variances. The variations between parental and between maternal half-sibs are supposed to be additive hereditary variability. However, the differences between σ_s^2 and σ_d^2 might be attributed to maternal effects which appeared to be of significant importance for most of the studied traits especially in random population. The maternal influences presented 4.42 vs. 2.82, 17.17 vs. -0.88, 14.41 vs. 4.85, 17.74 vs. 8.66, 10.81 vs. 1.64 and 11.74 vs. 26.41 percentages of the corresponding phenotypic variances for 8 and 12 weeks body weights, dressing, edible meat, blood and feather percentages (means over all generations) of random and selected populations, respectively. There was a trend that differences between individuals due to both sires and dams were relatively higher in most traits of random population than those of selected population. The lower variabilities due to heridity and due to materal influences detected in selected population might be attributed to the effect of selection which reduced the genetic variability between individuals and consequently increased homozygosity of the genetic make-up. Thus, the individuals of the selected population, were genetically and phenotypically more uniform.

Table 7: Estimates of the components of the phenotypic variance and their percentages for eight week body weight in random and selected populations.

Generation	Components of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	374.7	345.0	2163.0	13.0	12.0	75.0
F_2	560.4	891.7	3254.6	12.0	18.9	69.1
F_3	1414.6	1273.9	4966.4	18.5	16.6	64.9
F_4	60.5	296.5	1722.5	2.9	14.3	82.8
F_5	181.4	784.2	4347.2	3.4	14.8	81.8
Average				10.0	15.3	74.7
			Selected population			
F_1	300.3	439.1	1959.6	11.1	16.3	72.6
F_2	303.5	512.8	1947.3	10.9	18.6	70.5
F_3	935.1	1022.7	5534.8	12.5	13.6	73.9
F_4	403.3	301.6	2196.1	13.9	10.4	75.7
F_5	431.0	205.7	3798.2	9.7	4.7	85.6
F_6	416.6	1051.9	4653.2	6.8	17.2	76.0
Average				10.8	13.5	75.7

Table 8: Estimates of the components of the phenotypic variance and their percentages for twelve week body weight in random and selected populations.

Generation	Components of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	705.7	1511.4	5511.4	9.1	19.6	71.3
F_2	140.8	6555.5	6670.0	1.1	49.0	49.9
F_3	2288.2	1705.4	7599.9	19.7	14.7	65.6
F_4	571.7	845.5	6269.1	7.4	11.0	81.6
F_5	1045.4	3199.4	8167.0	8.4	25.8	65.8
Average				9.2	24.0	66.8
			Selected population			
F_1	521.5	1159.1	4235.1	8.8	19.6	71.6
F_2	724.0	1079.6	6451.0	8.7	13.1	78.2
F_3	1510.9	1002.8	12072.2	10.4	6.8	82.8
F_4	1988.4	747.5	6712.4	21.0	8.0	71.0
F_5	927.2	641.0	9082.2	8.7	6.0	85.3
F_6	1406.5	1896.9	10810.6	10.0	13.4	76.6
Average				11.3	11.2	77.5

Table 9: Estimates of the components* of the phenotypic variance and their percentages for dressing percentage in random and selected populations .

Generation	Component of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	0.410	1.509	2.980	8.4	30.8	60.8
F_2	0.213	0.858	4.578	3.8	15.2	81.0
F_3	0.754	1.546	7.677	7.6	15.5	76.9
F_4	0.000	2.258	8.333	0.0	23.0	77.0
F_5	0.522	0.944	3.610	10.3	18.6	71.1
Average				6.0	20.6	73.4
			Selected population			
F_1	0.000	0.702	3.814	0.0	18.7	81.3
F_2	0.452	0.317	5.293	7.5	5.2	87.3
F_3	0.000	0.000	6.580	0.0	0.0	100.0
F_4	0.187	0.390	3.398	4.7	9.8	85.5
F_5	0.000	0.612	8.731	0.0	6.7	93.3
F_6	0.376	1.150	12.545	2.7	8.1	89.2
Average				2.5	8.1	89.4

* Negative estimates considered zero.

Table 10: Estimates of the components* of the phenotypic variance and their percentages for **edible meat percentage in random and selected** populations .

Generation	Components of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	0.087	2.005	3.812	1.5	34.0	64.5
F_2	0.055	1.667	1.186	1.9	57.3	40.8
F_3	0.000	1.569	10.999	0.0	12.5	87.5
F_4	0.000	1.111	9.417	0.0	10.8	89.2
F_5	0.341	0.671	3.949	6.9	13.5	79.6
Average				2.1	25.6	72.3
			Selected population			
F_1	0.000	0.000	5.196	0.0	0.0	100.0
F_2	0.408	0.124	5.332	7.0	2.1	90.9
F_3	0.000	0.000	7.390	0.0	0.0	100.0
F_4	0.000	0.421	4.047	0.0	9.6	90.4
F_5	0.000	1.504	7.021	0.0	18.7	81.3
F_6	0.596	2.753	9.063	4.8	22.2	73.0
Average				2.0	8.8	89.2

* **Negative estimates considered zero.**

Table 11: Estimates of the components* of the phenotypic variance and their percentages for blood percentage in random and selected populations .

Generation	Components of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	0.000	0.007	0.565	0.0	1.2	98.8
F_2	0.068	0.051	0.318	15.5	11.7	72.8
F_3	0.000	0.357	1.038	0.0	26.5	73.5
F_4	0.000	0.042	0.722	0.0	5.8	94.2
F_5	0.018	0.130	1.314	1.2	8.9	89.9
Average				3.3	10.8	85.9
			Selected population			
F_1	0.145	0.000	0.530	22.7	0.0	77.3
F_2	0.013	0.016	0.378	3.1	4.0	92.9
F_3	0.019	0.013	0.607	2.9	2.1	95.0
F_4	0.008	0.154	0.483	1.3	23.9	74.8
F_5	0.003	0.000	0.584	0.6	0.0	99.4
F_6	0.206	0.137	1.458	11.4	7.6	81.0
Average				7.0	6.3	86.7

* **Negative estimates considered zero.**

Table 12: Estimates of the components* of the phenotypic variance and their percentages for feather percentage in random and selected populations .

Generation	Components of variance			Percent of components		
	σ_s^2	σ_d^2	σ_w^2	σ_s^2	σ_d^2	σ_w^2
			Random population			
F_1	0.000	0.547	1.340	0.0	29.4	70.6
F_2	0.177	0.110	1.310	11.1	6.9	82.0
F_3	0.000	0.553	1.640	0.0	25.5	74.5
F_4	0.036	0.000	1.947	2.1	0.0	97.9
F_5	0.179	0.336	1.666	8.2	15.4	76.4
Average				4.3	15.4	80.3
			Selected population			
F_1	0.039	1.219	0.942	1.8	55.4	42.8
F_2	0.054	0.208	0.963	4.4	17.0	78.6
F_3	0.005	0.191	1.414	0.3	11.9	87.8
F_4	0.076	0.171	0.773	7.4	16.8	75.8
F_5	0.042	0.063	0.895	4.2	6.3	89.5
F6	0.227	0.843	1.229	9.9	36.7	53.4
Average				4.7	24.0	71.3

* Negative estimates considered zero.

B. Heritabilities

Heritability is a static value which describes a certain population in terms of observed phenotypic variance due to differences between individuals in their heredity (Lush, 1948). It can be narrowly defined as the ratio of the additive genetic variance to the total phenotypic variance. The heritability estimates is an exceedingly important figure since it determines the amount of gain which selective breeding can accomplish and the magnitude of which dictates the most effecient selection method. Heritability estimates is, also, helpful in making any decisions regarding the type of mating system that will permit the fastest and best improvement in the characters under selection.

Estimates of heritability for the studied traits of random and selected populations are presented in Tables 13, 14, 15, 16, 17 and 18. It was found that estimates of 8 and 12 week body weights (Tables 13 and 14), dressing (Table 15) and feather (Table 18) percentages were higher than those of edible meat and blood percentages (Table 16 and 17) in both populations. Means of full-sibs heritabilities over all generations in random and selected populations for 8 and 12 week body weights, dressing and feather percentages were 0.505 vs. 0.486, 0.664 vs. 0.447, 0.525 vs. 0.201 and 0.390 vs. 0.573, respectively. While those of edible meat and blood percentages were 0.552 vs. 0.211 and 0.278 vs. 0.261, respectively. It seems that 8 and 12 weeks body weights, dressing and feather percentages were relatively highly heritable traits and, therefore, must be considered in selection programme. Similar results were obtained by Goodman and Godfrey (1956), Siegel and Essary (1959), Goodman (1973) and Kumar and Acharya (1980).

Table 13: Heritability estimates (± standard errors) for eight week body weight in random and selected populations.

Generation	h^2_s	h^2_d	$h^2_{(s+d)}$
		Random population	
F_1	0.520 ± 0.238	0.479 ± 0.168	0.499 ± 0.151
F_2	0.476 ± 0.199	0.758 ± 0.156	0.617 ± 0.132
F_3	0.739 ± 0.286	0.666 ± 0.175	0.702 ± 0.173
F_4	0.116 ± 0.115	0.570 ± 0.233	0.343 ± 0.141
F_5	0.137 ± 0.106	0.590 ± 0.304	0.364 ± 0.189
Average	0.398	0.613	0.505
		Selected population	
F_1	0.445 ± 0.182	0.651 ± 0.139	0.548 ± 0.119
F_2	0.439 ± 0.176	0.742 ± 0.125	0.591 ± 0.112
F_3	0.499 ± 0.199	0.546 ± 0.140	0.523 ± 0.126
F_4	0.556 ± 0.266	0.416 ± 0.163	0.486 ± 0.161
F_5	0.389 ± 0.190	0.186 ± 0.209	0.287 ± 0.121
F_6	0.272 ± 0.177	0.687 ± 0.234	0.480 ± 0.159
Average	0.433	0.538	0.486

Table 14: Heritability estimates (± standard errors) for twelve week body weight in random and selected populations.

Generation	h^2_s	h^2_d	$h^2_{(s+d)}$
		Random population	
F_1	0.365 ± 0.199	0.782 ± 0.205	0.574 ± 0.151
F_2	0.042 ± 0.112	1.962 ± 0.271	1.002 ± 0.160
F_3	0.790 ± 0.301	0.588 ± 0.176	0.689 ± 0.179
F_4	0.298 ± 0.170	0.440 ± 0.242	0.369 ± 0.158
F_5	0.337 ± 0.282	1.031 ± 0.349	0.684 ± 0.253
Average	0.366	0.961	0.664
		Selected population	
F_1	0.353 ± 0.162	0.784 ± 0.163	0.568 ± 0.121
F_2	0.351 ± 0.143	0.523 ± 0.109	0.437 ± 0.093
F_3	0.414 ± 0.168	0.275 ± 0.132	0.335 ± 0.110
F_4	0.842 ± 0.367	0.316 ± 0.146	0.579 ± 0.201
F_5	0.348 ± 0.185	0.241 ± 0.225	0.295 ± 0.156
F_6	0.399 ± 0.208	0.538 ± 0.222	0.468 ± 0.163
Average	0.451	0.446	0.447

Table 15: Heritability estimates (± standard errors) for dressing percentage in random and selected populations.

Generation	h_s^2	h_d^2	$h^2_{(s+d)}$
		Random population	
F_1	0.335 ± 0.252	1.232 ± 0.379	0.783 ± 0.245
F_2	0.151 ± 0.136	0.608 ± 0.283	0.379 ± 0.168
F_3	0.302 ± 0.213	0.620 ± 0.393	0.461 ± 0.239
F_4	0.000 ± 0.000	0.853 ± 0.575	0.426 ± 0.326
F_5	0.412 ± 0.365	0.744 ± 0.484	0.578 ± 0.350
Average	0.240	0.811	0.525
		Selected population	
F_1	0.000 ± 0.000	0.622 ± 1.201	0.311 ± 0.684
F_2	0.298 ± 0.136	0.209 ± 0.152	0.254 ± 0.324
F_3	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000
F_4	0.188 ± 0.188	0.392 ± 0.375	0.290 ± 0.226
F_5	0.000 ± 0.000	0.262 ± 0.383	0.131 ± 0.222
F_6	0.107 ± 0.167	0.327 ± 0.386	0.217 ± 0.231
Average	0.099	0.302	0.201

It is clear, also, that estimates of heritability for all traits in selected population were lower than those in random population. These results agree with the established theory which indicates that heritability decreases during the course of selection due to loss of genetic variation by fixation of genes and also because of increasing homozygosity from inbreeding.

The estimates of heritability from the dam component of variance were much higher than those derived from the sire component of variance for the majority of the studied traits in both populations. The mean of estimates of heritability over all generations derived from each sire and dam components of variances in random population were 0.398 vs. 0.613, 0.366 vs. 0.961, 0.240 vs. 0.811, 0.082 vs. 1.023, 0.134 vs. 0.422 and 0.168 vs. 0.612 for 8 and 12 week body weights, dressing, edible meat, blood and feather percentages, respectively. While the respective heritabilities in selected population were 0.433 vs. 0.538, 0.451 vs. 0.446, 0.099 vs. 0.302, 0.078 vs. 0.343, 0.272 vs. 0.250 and 0.186 vs. 0.960. The estimates from the sire component are supposed to include all the additive plus a fraction of additive interactions, while those derived from the dam component involve all additive, all dominance, epestasis and all maternal effects. However, Siegel (1962) estimated higher heritability values from sire component (0.26) than that from dam component (0.14) for feather development at 8 weeks of age in White Plymouth Rock, indicating sex linked infleunces which did not show in the present study.

Table 16: Heritability estimates (± standard errors) for edible meat percentage in random and selected populations.

Generation	h_s^2	h_d^2	$h^2_{(s+d)}$
		Random population	
F_1	0.059 ± 0.169	1.359 ± 0.409	0.709 ± 0.242
F_2	0.075 ± 0.171	2.293 ± 0.373	1.184 ± 0.224
F_3	0.000 ± 0.000	0.500 ± 0.426	0.250 ± 0.239
F_4	0.000 ± 0.000	0.422 ± 0.589	0.211 ± 0.333
F_5	0.275 ± 0.318	0.541 ± 0.485	0.408 ± 0.337
Average	0.082	1.023	0.552
		Selected population	
F_1	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000
F_2	0.278 ± 0.126	0.085 ± 0.146	0.182 ± 0.101
F_3	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000
F_4	0.000 ± 0.000	0.377 ± 0.392	0.188 ± 0.220
F_5	0.000 ± 0.000	0.706 ± 0.400	0.353 ± 0.232
F_6	0.192 ± 0.219	0.887 ± 0.400	0.540 ± 0.252
Average	0.078	0.343	0.211

Table 17: Heritability estimates (± standard errors) for blood percentage in random and selected populations.

Generation	h_s^2	h_d^2	$h_{(s+d)}^2$
		Random population	
F_1	0.000 ± 0.000	0.046 ± 0.370	0.023 ± 0.202
F_2	0.620 ± 0.274	0.468 ± 0.242	0.544 ± 0.190
F_3	0.000 ± 0.000	1.024 ± 0.426	0.512 ± 0.240
F_4	0.000 ± 0.000	0.219 ± 0.597	0.110 ± 0.331
F_5	0.050 ± 0.254	0.355 ± 0.500	0.202 ± 0.328
Average	0.134	0.422	0.278
		Selected population	
F_1	0.858 ± 0.518	0.000 ± 0.000	0.429 ± 0.607
F_2	0.126 ± 0.084	0.158 ± 0.156	0.142 ± 0.094
F_3	0.117 ± 0.118	0.082 ± 0.301	0.100 ± 0.172
F_4	0.051 ± 0.169	0.956 ± 0.414	0.504 ± 0.245
F_5	0.023 ± 0.096	0.000 ± 0.000	0.012 ± 0.188
F_6	0.457 ± 0.262	0.305 ± 0.352	0.381 ± 0.236
Average	0.272	0.250	0.261

Table 18: Heritability estimates (± standard errors) for feather percentage in random and selected populations.

Generation	h^2_s	h^2_d	$h^2_{(s+d)}$
		Random population	
F_1	0.000 ± 0.000	1.160 ± 0.406	0.580 ± 0.233
F_2	0.442 ± 0.210	0.274 ± 0.252	0.358 ± 0.171
F_3	0.000 ± 0.000	1.009 ± 0.426	0.504 ± 0.244
F_4	0.072 ± 0.179	0.000 ± 0.000	0.036 ± 0.303
F_5	0.328 ± 0.336	0.616 ± 0.485	0.472 ± 0.341
Average	0.168	0.612	0.390
		Selected population	
F_1	0.071 ± 0.490	2.216 ± 0.929	1.144 ± 0.612
F_2	0.175 ± 0.115	0.680 ± 0.188	0.428 ± 0.117
F_3	0.013 ± 0.102	0.474 ± 0.319	0.244 ± 0.181
F_4	0.297 ± 0.239	0.672 ± 0.376	0.484 ± 0.238
F_5	0.167 ± 0.174	0.252 ± 0.367	0.209 ± 0.222
F_6	0.395 ± 0.305	1.467 ± 0.411	0.931 ± 0.281
Average	0.186	0.960	0.573

C. Genetic, Environment and Phenotypic Correlations

Pleiotropy is the genetic cause of correlations; however, linkage can be a cause of transient correlations, especially in populations derived from crosses between divergent strains. Pleiotropy is the property of a gene which affects two or more characteristics. Thus, the segregated gene causes simultaneous variation in the characters it affects. The extent to which two characters are influenced by the same genes is expressed by degree of correlation arising from pleiotropy. However, correlation resulting from pleiotropy is overall, or net, effect of all of the segregating genes that affect both character (Falconerl 1967). Genetic correlation can, also, be induced by artificial selection in such a way that improvement in one character will cause simultaneous changes in other characters in time. The environment is a cause of correlation in a way that two characters can be influenced by the same differences of environmental conditions. Environmental correlation includes deviations due to environment togeather with non-additive genetic deviations. Hence, the phenotypic correlation ($r_{P_{XY}}$) between the two traits X and Y in terms of path coefficients is:

$$r_{P_{XY}} = h_X \, r_{G_{XY}} \, h_Y + e_X \, r_{E_{XY}} \, e_Y$$

Thus, high estimates of heritability for each trait means that the phenotypic correlation is determined chiefly by genetic correlation, otherwise, the environmental correlation is the most important. The genetic and environmental correlations between any two traits in the present study were calculated from the information based on the sire, dam and full-sib components of variances.

The genetic interpretion of these correlations can be derived from the following table in terms of genetic covariance:

Component of covariance	cov_A	cov_D	cov_{AA}	cov_{AD}	cov_{DD}	cov_{AAA}	cov_E
cov_s	1/4	0	1/16	0	0	1/64	0
cov_d	1/4	1/4	3/16	1/8	1/16	7/64	0
cov_w	1/2	3/4	3/4	7/8	15/16	7/8	1
$cov_s + cov_d$	1/2	1/4	1/4	1/8	1/16	1/8	0
$cov_w - 2cov_s$	0	3/4	5/8	7/8	15/16	27/32	1
$cov_w - 2cov_d$	0	1/4	3/8	5/8	13/16	42/64	1
$cov_w - cov_s - cov_d$	0	1/2	1/2	6/8	7/8	6/8	1

Where:

cov_s = covariance due to sire.

cov_d = covariance due to dam.

cov_w = covariance due to progeny/ ~~dams~~/sires.

cov_A = covariance of additive effects.

cov_D = covariance of dominance effects.

cov_E = covariance of environmental effects.

Thus, the genetic correlation based on sire components (r_{G_s}) has no dominance effects, but it includes 1/4 of additive interaction. While the genetic correlation based on dam components (r_{G_d}) involves all the dominance effects and 3/4 additive interaction plus various amounts of epistasis in its estimation. The correlation based on full sibs ($r_{G_{s+d}}$) has 1/2 of the dominance deviations and 1/2 additive interaction plus some fraction of epestatic deviations. The environmental correlation based on sire components (r_{E_s}), on the otherhand, contains 3/4 dominance and 5/8 additive interaction plus more amounts of epestasis. The estimate based on dam component (r_{E_d}) contains 1/4 dominance and 3/8 additive interaction plus less amount of epestasis than in (r_{E_s}). The environmental correlation based on full sibs components contains 1/2 of the dominance effects and 1/2 of the additive interaction plus greater amounts of epestasis.

Genetic correlations based on sire, dam and full sib components along with the phenotypic correlations among the studied traits for random and selected populations are presented in apendices A1 to A22, respectively. The means of genetic and phenotypic relationships over all generations are presented in Tables 19 and 20, respectively.

Most of the genetic correlation coefficients among the studied traits based on sire components are, in general, positively higher than those obtained from dam components in random and selected populations; indicating that sires inhereted their linked and/or pleiotropic genes additively to most of the traits.

The estimates of genetic association between 8-week body weight and each of the other traits are generally positively higher in random population than in selected population; indicating that selection reduced the genetic variabilities among the studied traits. However, the genetic and phenotypic relationships between 8 and 12 weeks body weights, are positively higher in both random and selected populations. The genetic

Table 19: Genetic and phenotypic correlations* among six traits in random population.

Traits	8-week body weight	12-week body weight	Dressing %	Edible meat %	Blood %	Feather %
		Genetic correlations based on sire components.				
8 week		0.584	0.862	0.478	0.242	0.476
12 week	1.132		0.717	-0.015	0.462	0.267
Dressing %	0.363	-0.167		-0.013	0.028	0.343
Edible meat %	0.307	-0.248	0.883		-0.302	0.151
Blood %	-0.165	-0.438	-0.650	-0.025		0.002
Feather %	0.103	0.206	0.062	-0.160	-0.075	
	Genetic correlations based on dam components.					
		Genetic correlations based on full-sib components.				
8 week		0.999	0.419	0.260	-0.503	0.156
12 week	0.722		-0.004	0.212	-0.358	0.111
Dressing %	0.161	0.212		0.884	0.042	-0.017
Edible meat %	-0.010	0.063	0.734		0.319	-0.183
Blood %	-0.001	0.013	-0.091	-0.197		-0.056
Feather %	0.175	0.275	-0.135	-0.165	-0.130	
	Phenotypic correlations based on full-sib components.					

* Correlation coefficients are over-all means of five generations.

Table 20: Genetic and phenotypic correlations* among six traits in [illegible] selected population.

Genetic correlations based on sire components.

Traits	8-week body weight	12-week body weight	Dressing %	Edible meat %	Blood %	Feather %
8 week		0.510	-0.095	-0.155	0.015	0.543
12 week	0.176		-0.007	-0.010	-0.400	0.513
Dressing %	-0.130	0.228		-0.277	0.061	-0.447
Edible meat %	0.271	-0.177	-0.020		-0.293	0.203
Blood %	-0.374	-0.649	-0.359	-0.104		0.462
Feather %	-0.503	0.306	-0.153	-0.199	0.026	

Genetic correlations based on dam components.

Genetic correlations based on full-sib components.

8 week		0.368	-0.162	0.070	0.101	-0.186
12 week	0.525		0.361	-0.107	0.097	0.059
Dressing %	0.020	0.154		-0.243	-0.334	-0.254
Edible meat %	-0.032	0.088	0.853		-0.143	-0.142
Blood %	0.013	-0.016	-0.089	0.006		-0.045
Feather %	0.057	0.171	-0.068	-0.032	-0.313	

Phenotypic correlations based on full-sib components.

* Correlation coefficients are over-all means of six generations.

estimates based on sire, dam and full sibs components are 0.584, 1.132 and 0.999 in random population, respectively (Table 19). While those respective estimates in selected population are 0.510, 0.176 and 0.368 (Table 20). This means that traits of body weights are additively highly correlated traits. Thus, one may expect, that genes affect 8 week body weight may themselves affect 12 week body weight. These results are in agreement with those of Merritt (1966), Nestor et. al.(1966), Saeki et. al. (1969), El-Hossari and Ragab (1970), Siegel (1970), Singh and Singh (1979) and Ahlawat et. al. (1980). Also, higher genetic correlations, based on sire components, were obtained between feather development and each of 8 and 12 week body weights. However, the estimates were higher in selected than in random population. The coefficients between feather percentage and each of 8 and 12 week body weights are 0.543 and 0.513 in selected population; while the respective estimates in random population are 0.476 and 0.267 (Tables 19 and 20). These results indicate that body weight is genetically correlated with feather development. Therefore, improving body weight by selection will simultanously followed by an improvement in feather development through fixation of genes affecting these traits.

The genetic correlations based on sire components, between dressing percentage and each of 8 (-0.095) and 12 (-0.007) week body weights were lowerly negative in selected population and highly positive in random population (0.862 and 0.717, respectively) indicating that selection for heavier 8 week body weight did not accompanied by higher dressing percentage. However, the genetic (0.884) and phenotypic (0.734) correlations between dressing percentage and edible meat were positively higher in random population. Also, higher positive phenotypic (0.853) and negative genetic (-0.243) correlations were obtained between these two traits in selected populations. This indicates that higher dressing percentage will be associated with higher percentage of edible meat. These results are nearly similar to those of Tosovsky and Jandac (1975) and Singh (1979).

The environmental relationships between the studied traits in each of random and selected population are presented in Tables 21 and 22, respectively. The genetic and environmental correlations, based on full sibs, between 8 and 12 week body weights and between 12 week body weight and each of dressing, edible meat, blood and feather percentages; also, between dressing percentage and each of edible meat and blood percentage, both associations are positive in sign in random and selected populations. This means that these traits may arise either because the traits are genetically correlated owing to common sources of genetic variation, or, because they developed in a common environment or both. The genetic and the environmental correlations among the other traits are different in signs either in random and selected populations. A difference in sign between the two correlations shows that genetic and environmental sources of variation affect the characters through different physiological mechanisms.

Table 21: Environmental correlations* among six traits in random population .

Traits	8-week body weight	12-week body weight	Dressing %	Edible meat %	Blood %	Feather %
Env. correlations based on sire components.						
8 week		0.388	-0.086	-0.179	-0.116	0.101
12 week	0.066		0.179	0.143	0.002	0.432
Dressing %	0.206	1.429		0.662	0.013	-0.104
Edible meat %	0.117	0.520	0.772		-0.021	-0.124
Blood %	0.178	0.314	0.805	0.361		-0.252
Feather %	0.187	0.515	-0.141	0.040	-0.208	
Environmental correlations based on dam components.						
Env. correlations based on full-sib components.						
8 week		0.362	-0.164	-0.118	-0.116	0.133
12 week			0.126	0.139	-0.081	0.784
Dressing %				0.960	0.134	-0.127
Edible meat %					0.049	0.098
Blood %						-0.265
Feather %						

* Correlation coefficients are over-all means of five generations.

Table 22: Environmental correlations* among six traits in selected population .

Traits	8-week body weight	12-week body weight	Dressing %	Edible meat %	Blood %	Feather %
		Env. correlations based on sire components.				
8 week		0.610	0.008	-0.094	-0.016	0.074
12 week	0.645		0.167	0.017	-0.008	-0.079
Dressing %	0.033	0.025		0.900	-0.184	0.086
Edible meat %	-0.308	-0.076	1.036		-0.017	-0.174
Blood %	0.022	0.009	-0.106	-0.169		-0.360
Feather %	0.414	0.108	0.177	0.203	-0.300	
	Environmental correlations based on dam components.					
		Env. correlations based on full-sib components.				
8 week		0.628	0.131	-0.147	-0.008	0.282
12 week			0.117	-0.026	0.055	0.206
Dressing %				0.948	-0.150	0.381
Edible meat %					-0.077	0.303
Blood %						-0.512
Feather %						

* : Correlation coefficients are over-all means of six generations.

D. Response of Selection

The significances of differences between random and selected populations and between generations of selection for the studied traits are presented in Tables 23, 24 and 25. It is shownfrom these results that there were highly significant differences between populations and between generations in all traits. The means of the studied traits for males, females and males & females in each generation of random and selected populations are presented in Tables 26, 27 and 28. The results indicated that males, females and males & females were heavier in selected population than in random population for 8 and 12 weeks body weights. The increase (means of over all generations) in 8 week body weight of males, females and males & females of selected population was 52.9, 35.6 and 48.6 grams, respectively (Table 26). While, the respective increase in 12 week body weight was 111.0, 59.3 and 95.7 grams (Table 27). However, percentages of dressing, edible meat, blood and feather were almost equal in both random and selected populations (Table 28). Awad (1978) in his studies of selection for 8 week body weight in chickens found that 8 week feather score of the selected line was 17.6 percent higher than the control.

The realized and expected genetic gain for 8 week body weight due to mass selection over 6 generations are presented in Tables 29, 30, 31, 32, 33 and 34. The results indicated that the White Baladi breed of chicken responded significantly, in general, to selection in most generations. However, the progress was retarded at the fourth generation of selection; after which the birds responded again to selection during the fifth and sixth generations. The realized progress for each of F_1,

Table 23: Populations and generations mean squares of the studied traits.

Source of variations	8-week body weight		12-week body weight		Dressing %		Edible meat %		Blood %		Feather %	
	df	MS	df	MS	df	MS	df	MS	df	MS	df	MS
Population	1	10199975.1**	1	16538099.2**	1	885.7**	1	1502.4**	1	7168.8*	1	4084.8**
Generations	4	12757647.1**	4	15265849.0**	4	625.5**	4	303.5**	4	3266.0	4	73525.3**
Error	6622	6307.6	6214	13197.1	2593	7.8	2593	8.0	2593	1361.5	2593	160.5

* Significant, $P \leq 0.05$

** Significant, $P \leq 0.01$

Table 24: Generations mean squares of eight and twelve week body weight for males, females and males + females of random and selected populations.

8 week body weight

Source of variations	Males		Females		Males + females	
	df	MS	df	MS	df	MS
Random population						
Generations	4	1775117.1**	4	1579488.6**	4	3354044.8**
Error	1408	5101.6	1258	3991.2	2670	4572.8
Selected population						
Generations	6	6569232.6**	6	5990266.5**	6	12552628.5**
Error	2589	4151.1	2305	3710.4	4900	3947.1

12 week body weight

Random population						
Generations	4	3076705.4**	4	2362620.1**	4	5453378.1**
Error	1348	12198.5	1192	9255.5	2544	10802.5
Selected population						
Generations	6	10671287.9**	6	9232736.7**	6	19905456.1**
Error	2449	10374.0	2137	8606.2	4592	9555.1

** Significant, $P \leqslant 0.01$

Table 25: Generations mean squares of dressing, edible meat, blood and feather percentages in males of random and selected populations.

Source of variations	Dressing %		Edible meat %		Blood %		Feather %	
	df	MS	df	MS	df	MS	df	MS
Random population								
Generations	4	1040.8**	4	1023.5**	4	3370.4**	4	38433.1**
Error	1131	6.9	1131	7.0	1131	82.1	1131	186.1
Selected population								
Generations	6	967.8**	6	711.0**	6	2521.0	6	32224.5**
Error	1909	6.9	1909	6.8	1909	1822.1	1909	171.7

* Significant, P ≤ 0.01

Table 26: Means (± standard **errors**)of males, females and males + females for eight week body weight in successive generations of random and selected populations*.

Generation	Males		Females		Males + females	
	No.	Mean	No.	Mean	No.	Mean
			Random population			
F_1	279	277.3 ± 3.2 a	255	274.2 ± 3.4 a	534	276.0 ± 2.3 a
F_2	406	445.6 ± 3.5 b	432	380.3 ± 3.2 b	838	411.9 ± 2.4 b
F_3	295	521.3 ± 5.7 b	283	433.9 ± 4.5 b	578	478.5 ± 3.6 b
F_4	228	421.0 ± 3.1 b	212	359.5 ± 3.0 b	440	391.0 ± 2.2 b
F_5	204	492.3 ± 5.2 b	80	460.0 ± 7.7 b	284	471.9 ± 4.3 b
Average		431.5		381.6		405.9
			Selected population			
F_0	279	277.3 ± 3.2 a	255	274.2 ± 3.4 a	534	276.0 ± 2.3 a
F_1	446	443.3 ± 2.5 be	485	361.7 ± 2.3 b	931	400.8 ± 1.7 bcd
F_2	661	517.6 ± 2.1 cf	673	443.4 ± 1.9 b	1334	480.2 ± 1.4 d
F_3	412	757.9 ± 4.3 d	400	622.6 ± 4.3 c	812	691.1 ± 3.0 e
F_4	245	355.3 ± 3.1 ab	250	322.1 ± 3.7 a	495	338.6 ± 2.4 ab
F_5	272	444.2 ± 4.1 ce	110	391.1 ± 6.1 b	382	428.9 ± 3.4 cd
F_6	280	595.5 ± 4.8 f	138	505.4 ± 6.3 d	418	565.9 ± 3.8 f
Average		484.4		417.2		454.5

* Means within a trait within a classification followed by the same litter do not differ significantly from each other, otherwise they do differ significantly at $P \leqslant 0.05$.

Table 27: Means (± standard errors) of males, females and males + females for twelve week body weight in successive generations of random and selected populations*.

Generation	Males		Females		Males + females	
	No.	Mean	No.	Mean	No.	Mean
Random population						
F_1	273	484.0 ± 5.4 a	247	457.6 ± 5.5 a	520	471.5 ± 3.8 a
F_2	402	663.1 ± 6.4 ab	423	557.0 ± 4.9 ab	825	609.4 ± 4.0 ab
F_3	283	777.9 ± 6.5 b	258	640.8 ± 6.6 b	541	712.4 ± 4.6 b
F_4	197	768.3 ± 8.5 b	188	618.1 ± 6.1 b	385	695.5 ± 4.5 b
F_5	197	758.9 ± 8.4 b	80	730.8 ±10.3 b	277	740.4 ± 6.7 b
Average		690.4		600.9		645.8
Selected population						
F_0	273	484.0 ± 5.4 a	247	457.6 ± 5.5 a	520	471.5 ± 3.8 a
F_1	389	672.8 ± 4.1 b	425	603.7 ± 3.5 b	814	636.9 ± 2.7 b
F_2	640	753.2 ± 3.7 b	638	630.7 ± 3.5 b	1278	691.9 ± 2.5 b
F_3	374	1121.5 ± 6.6 c	362	860.4 ± 5.9 c	736	993.5 ± 4.4 c
F_4	238	733.5 ± 6.8 b	240	613.9 ± 5.6 b	478	673.2 ± 4.4 b
F_5	268	719.6 ± 6.4 b	98	617.7 ±10.0 b	366	692.3 ± 5.4 b
F_6	273	1125.5 ± 7.0 c	133	837.1 ±10.8 c	406	1031.3 ± 5.9 c
Average		801.4		660.2		741.5

* Means within a trait within a classification followed by the same litter do not differ significantly from each other, otherwise they do differ significantly at $P \leqslant 0.05$.

Table 28: Means (± standard error) of dressing, edible meat, blood and feather percentages for twelve week slaughtered males in successive generations of random and selected populations*.

Gen.	No.	Dressing %	Edible meat %	Blood %	Feather %
		Random population			
F_1	231	56.2 ± 0.1 a	67.6 ± 0.2 a	4.0 ± 0.5 a	5.2 ± 0.9 ab
F_2	360	57.6 ± 0.1 ab	68.2 ± 0.1 a	3.7 ± 0.3 a	4.8 ± 0.7 a
F_3	240	57.9 ± 0.2 ab	67.4 ± 0.2 a	4.6 ± 0.7 a	7.1 ± 1.0 bc
F_4	162	61.5 ± 0.2 b	72.6 ± 0.3 b	4.3 ± 0.7 a	7.1 ± 1.0 bc
F_5	142	61.4 ± 0.2 b	71.2 ± 0.2 ab	3.6 ± 1.0 a	7.6 ± 1.2 c
Average		58.9	69.4	4.0	6.4
		Selected population			
F_0	231	56.2 ± 0.1 ab	67.6 ± 0.2 ab	4.0 ± 0.5 a	5.2 ± 0.9 bc
F_1	77	54.5 ± 0.2 b	65.0 ± 0.2 b	4.6 ± 0.9 a	5.8 ± 1.7 abc
F_2	632	56.9 ± 0.1 bc	67.3 ± 0.1 bc	4.1 ± 0.3 a	4.7 ± 0.4 c
F_3	321	59.0 ± 0.1 acd	68.6 ± 0.1 acd	4.6 ± 0.4 a	7.2 ± 0.7 a
F_4	204	56.5 ± 0.1 ab	66.3 ± 0.1 ab	4.2 ± 0.6 a	6.6 ± 0.7 ab
F_5	230	57.0 ± 0.2 ab	67.5 ± 0.2 ab	4.8 ± 0.5 a	6.3 ± 0.7 abc
F_6	220	61.5 ± 0.3 d	71.4 ± 0.2 d	4.0 ± 0.9 a	6.9 ± 1.4 a
Average		57.4	67.7	4.3	6.1

* Means within a trait within a classification followed by the same litter do not differ significantly from each other, otherwise they do differ significantly at $P \leq 0.05$.

F_2, F_3, F_4, F_5 and F_6 generations was 124.9, 79.4, 210.9, -352.5, 90.3 and 137.0 grams for males & females, respectively. The results, also, indicated that the realized genetic gain was much higher than the corresponding expected genetic gain in most generations. The respective expected genetic gain for males & females was 15.1, 16.6, 18.5, 28.0, 16.8 and 6.0 grams. The realized heritability values within each generation of selection were, therefore, larger than the estimated heritabilities. However, when the progress due to selection was averaged over generations (Table 35), the realized progress for males & females (48.4 grams) was nearly equal to the expected genetic gain (44.1 grams). Also, the corresponding realized heritability (0.537) was nearly equal to the estimated heritability (0.489).

These results indicate that selection for improving body weight of White Baladi breed which contains considerable amount of additive variance is unlikely to reach a selection limit in the foreseeable future. In other words, the response pattern of absolute weights from generations 1 to 6 suggests that this breed of chicken did not reach an apparent selection plateau for 8 week body weight. Thus, more genetic improvement in body weight could be expected by further generations of selection. If the genetic gain reached the level of selection plateau after a long term of selection; this would be due to cessation of genetic changes, the causes of which might be due to;

(1) The exhaustion of genetic variability as a result of selection and inbreeding.

(2) Natural selection counteracting the effectiveness of artificial selection.

(3) The establishment of a negative genetic correlation between selected traits and fitness.

Table 29: Realized and expected genetic gain due to selection for 8 week body weight from F_0 to F_1 generations.

Basis of selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_0 generation	279	277.3	255	274.2	534	275.9
Selected breeders.	20	374.0	184	298.7	204	306.1
Mean of F_1 generation.	446	443.3	485	361.7	931	400.8
Realized selection differential.		96.7		24.5		30.2
Realized progress.		166.0		87.5		124.9

Basis for calculating expected genetic gain	Estimated h^2	Expected genetic gain		
		$\Delta\overline{G}_{g_m}$	$\Delta\overline{G}_{g_f}$	$\Delta\overline{G}_{g_{m+f}}$
Sire components	0.520	25.1	6.4	15.7
Dam components	0.479	23.2	5.9	14.5
Sire+dam comp.	0.499	24.1	6.1	15.1
Realized h^2		h^2_s	h^2_d	h^2_{s+d}
		1.717	3.571	4.136

Table 30: Realized and expected genetic gain due to selection for 8 week body weight for F_1 to F_2 generations.

Basis for selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_1 generation.	446	443.3	485	361.7	931	400.8
Selected breeders.	20	590.8	190	414.3	210	431.1
Mean of F_2 generation.	661	517.6	673	443.4	1334	480.2
Realized selection differential.		147.5		52.6		30.3
Realized progress.		74.3		81.7		79.4

Basis of calculating expected genetic gain	Estimated h^2	Expected genetic gain		
		$\Delta\overline{G}_{g_m}$	$\Delta\overline{G}_{g_f}$	$\Delta\overline{G}_{g_{m+f}}$
Sire components	0.445	32.8	11.7	13.5
Dam components	0.651	48.0	17.1	19.7
Sire+dam comp.	0.548	40.4	14.4	16.6
Realized h^2		h^2_m	h^2_f	h^2_{m+f}
		0.504	1.553	2.620

Table 31: Realized and expected genetic gain due to selection for 8 week body weight from F_2 to F_3 generations.

Basis for selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_2 generation.	661	517.6	673	443.4	1334	480.2
Selected breeder.	20	639.3	184	497.6	204	511.5
Mean of F_3 generation	412	757.9	400	622.6	812	691.1
Realized selection differential		121.7		54.2		31.1
Realized progress		240.3		179.2		210.9

Basis of calculating expected genetic gain	Estimated	Expected genetic gain		
	h^2	$\triangle\bar{G}g_m$	$\triangle\bar{G}g_f$	$\triangle\bar{G}g_{m+f}$
Sire components	0.439	26.7	11.9	13.7
Dam components	0.742	45.2	20.1	23.3
Sire+dam comp.	0.591	36.0	16.0	18.5
Realized h^2		h^2_m	h^2_f	h^2_{m+f}
		1.975	3.306	6.738

Table 32: Realized and expected genetic gain due to selection for 8 week body weight from F_3 to F_4 generations.

Basis for selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_3 generation.	412	757.9	400	622.6	812	691.1
Selected breeder.	13	954.2	102	717.9	115	744.7
Mean of F_4 generation.	245	355.3	250	322.1	495	338.6
Realized selection differential		196.3		95.3		53.6
Realized progress		-402.6		-300.5		-352.5

Basis Of calculating expected genetic gain	Estimated h^2	Expected genetic gain		
		$\Delta\bar{G}_{g_m}$	$\Delta\bar{G}_{g_f}$	$\Delta\bar{G}_{g_{m+f}}$
Sire components	0.499	49.0	23.8	26.7
Dam components	0.546	53.6	26.0	29.3
Sire+dam comp.	0.523	51.3	24.9	28.0
Realized h^2		h^2_m	h^2_f	h^2_{m+f}
		-2.051	-3.256	-6.576

Table 33: Realized and expected genetic gain due to selection for 8 week body weight from F_4 to F_5 generations.

Basis of selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_4 generation	245	355.3	250	322.1	495	338.6
Selected breeder.	20	459.3	132	360.1	152	373.1
Mean of F_5 generation.	272	444.2	110	391.1	382	428.9
Realized selection differential		104.0		38.0		34.5
Realized progress.		88.9		69.0		90.3

Basis of calculating expected genetic gain	Estimated	Expected genetic gain		
	h^2	$\Delta\overline{G}_{g_m}$	$\Delta\overline{G}_{g_f}$	$\Delta\overline{G}_{g_{m+f}}$
Sire components	0.556	28.9	10.6	19.2
Dam components	0.416	21.6	7.9	14.4
Sire+dam comp.	0.486	25.3	9.2	16.8
Realized h^2		h^2_m	h^2_f	h^2_{m+f}
		0.855	1.816	2.617

Table 34: Realized and expected genetic gain due to selection for 8 week body weight from F_5 to F_6 generations.

Basis of selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of F_5 generation.	272	444.2	110	391.1	382	428.9
Selected breeder.	7	575.7	43	429.4	50	449.9
Mean of F_6 generation.	280	595.5	138	505.4	418	565.9
Realized selection differential.		131.5		38.3		21.0
Realized progress.		151.3		114.3		137.0

Basis of calculating expected genetic gain	Estimated	Expected genetic gain		
	h^2	$\Delta\overline{G}\,g_m$	$\Delta\overline{G}\,g_f$	$\Delta\overline{G}\,g_{m+f}$
Sires components	0.389	25.6	7.4	8.2
Dams components	0.186	12.2	3.6	3.9
Sire+dam comp.	0.287	18.9	5.5	6.0
Realized h^2		h^2_m	h^2_f	h^2_{m+f}
		1.151	2.984	6.524

Table 35: Over all means of realized and expected genetic gain due to selection for 8 week body weight.

Basis of selection	Males		Females		Males + females	
	No.	Mean(gm)	No.	Mean(gm)	No.	Mean(gm)
Mean of preceeding generations.	2315	465.9	2173	402.5	4488	435.9
Selected breeder.	100	598.9	835	453.0	935	526.0
Mean of succeeding generations.	2316	519.0	2056	441.1	4372	484.3
Realized selection differential.		133.0		50.5		90.1
Realized progress.		53.1		38.6		48.4

Basis of calculating expected genetic gain	Estimated	Expected genetic gain		
	h^2	$\Delta\bar{G}\,g_m$	$\Delta\bar{G}\,g_f$	$\Delta\bar{G}\,g_{m+f}$
Sire components	0.475	31.6	12.0	42.8
Dam components	0.503	33.4	12.7	45.3
Sire+dam comp.	0.489	32.5	12.3	44.1
Realized h^2		h^2_s	h^2_d	h^2_{s+d}
		0.399	0.764	0.537

(4) The emerging increase of non-additive gene effects which do not comply to ordinary selection procedures (Lush, 1951; Falconer, 1953; Lerner, 1954; Tebb, 1957 and Kan et. al.,(1959). However, Siegel (1962) reported that natural selection was a minor factor in influencing the short term response to artificial selection for 8 week body weight in chickens.

Results presented in Tables 29, 30, 31, 32, 33 and 34, also, indicated that males responded effectively to selection than females within each generation of selection. The over all mean of realized progress (53.1 vs. 38.6 grams) and the expected genetic gain (32.5 vs. 12.3 grams) in males were, therefore, higher than those of females, respectively (Table 35). Again, the estimated (0.475 vs. 0.399) and the realized (0.503 vs. 0.764) heritabilities were nearly equal in males and females, respectively. One may expect that males would respond largely to selection than females, since males were subjected to intensive selection pressure (5.5%) than that of females (51.5%). Similar results were reported by Jaap et. al. (1962), Jaap (1966) and Siegel (1970).

The cessation of genetic progress in the fourth generation might be due to the effect of environmental influences which were not reasonably suitable for the flock to the extent that the birds did not respond effictivelly to selection pressure.

E. Correlated Response

Lerner (1961) discussed the theory of correlated response in such a way that the origin of correlation between traits may be responsible for either pleiotropy or linkage. Its rationale is rather simple. Different allels or blocks may have net affects of various kinds on traits X and Y. Thus, some may increase both X and Y, others increase X and decrease Y, and so forth. The full list of possible combinations and their fate under simultaneous selection for plus expressions of both X and Y is as follows:

	Effect on X	Effect on Y	Fate under selection
1.	+	+	Fixation
2.	+	0	
3.	0	+	
4.	-	-	Elimination
5.	-	0	
6.	0	-	
7.	+	-	Continued segregation
8.	-	+	

Although originally in this model X and Y were not correlated (assuming equal frequencies of all eight kinds of units), by the time only types 7 and 8 are left segregating in the gene pool a negative correlation between X and Y has been established. Continued selection for X will then inevitably lead to a correlated response in Y and vice versa. Such respose can have grave consequences in the selection for multiple objectives. In addition to pleiotropy and linkage, correlated responses may be the result of association of loci and blocks located on different chromosomes. In particular, systems of correlations between selection coefficient of independently transmitted genes based on gene interactions may produce short-range correlated responses. Common origin of independent allels in a population of hyprid derivation may cause temporary correlations. Any kind of non-random segregation can have a similar effect.

Correlated response may be either obligate or facultative. The first type is particularly important when the response takes the form of decreased fitness. This consequence of selection obtains when:

(a) selection for character, which initially may not be a major component of fitness, is continued for a long time;

(b) a major fitness component which is subjected to selection has an intermediate optimum;

(c) selection is directed to a metric trait in the direction opposite to the sign of the correlation between it and fitness.

If selection for a character not a major component of fitness, inbreeding may in part be responsible for the reduction in fitness.

The correlated response between the selected character of 8 week body weight and each of body weight, dressing, edible meat, blood and feather percentages at 12 week of age within each generation of selection are presented in Tables 36, 37, 38, 39 and 40. The tabulated results indicated that the change in 8 week body weight due to selection was associated positively with a change of about 45, 13 and 11 grams in 12 week body weight based on sire, dam and sire & dam components of

Table 36: Correlated response between 8 and 12 week body weights in selected population.

Generation	Sire	Dam	Sire + Dam
F_0	24.9619	32.8242	23.2305
F_1	20.7291	18.7036	7.5136
F_2	23.3409	59.3444	20.1436
F_3	95.1320	-31.5556	4.0516
F_4	29.3533	23.8557	15.7398
F_5	78.7388	- 6.4820	4.5142
F_6	42.9811	- 3.7351	0.5141
Average	45.034	13.279	10.815

Table 37: Correlated response between 8 week body weight and 12 week dressing percentage in selected population.

Generation	Sire	Dam	Sire + Dam
F_0	0.4716	0.3028	0.2608
F_1	0.4075	0.0858	0.0243
F_2	0.2341	0.2914	0.1143
F_3	0.3554	-0.3544	0.1480
F_4	0.0511	-0.1479	-0.0589
F_5	-0.2268	0.0623	-0.0010
F_6	0.0546	-0.2584	-0.0318
Average	0.193	0.099	0.065

Table 38: Correlated response between 8 week body weight and 12 week edible meat percentage in selected population.

Generation	Sire	Dam	Sire + Dam
F_0	0.3220	0.5131	0.3674
F_1	0.1758	0.1256	0.0542
F_2	-0.3873	0.4948	0.0924
F_3	0.0450	0.0597	0.0229
F_4	0.3201	0.2022	-0.0389
F_5	0.0255	0.0603	0.0186
F_6	-0.3432	0.6273	0.0722
Average	0.0230	0.2980	0.0840

Table 39: Correlated response between 8 week body weight and 12 week blood percentage in selected population.

Generation	Sire	Dam	Sire + Dam
F_0	0.0930	-0.0087	0.0092
F_1	0.2891	0.1467	-0.0719
F_2	-0.1771	-0.3148	-0.1137
F_3	0.2711	0.1027	0.0658
F_4	0.0710	-0.1316	-0.0481
F_5	-0.0257	0.1616	0.0423
F_6	-0.3293	0.2341	0.0223
Average	0.0270	0.0270	-0.0130

Table 40: Correlated response between 8 week body weight and 12 week feather percentage in selected population.

Generation	Sire	Dam	Sire + Dam
F_0	-0.0663	0.0157	-0.0007
F_1	-0.5465	0.1665	-0.0080
F_2	0.2457	0.0705	-0.0112
F_3	0.3983	-1.2089	-0.0285
F_4	0.0594	0.0898	0.0507
F_5	0.3225	-0.1819	-0.0241
F_6	1.3404	-0.1636	0.0100
Average	0.2510	-0.1730	-0.0020

variances, respectively (Table 36). Thus, one may conclude that genes or blocks of polygenes intermingled along the chromosome which cause an increase in 8 week body weight may also cause an increase in 12 week body weight. Seigel (1963 a) reported that changes in 8 week body weight were positively associated with changes in 4, 24 and 38 week body weights. Similar results were also obtained in turkey by Johanson and Asmundson (1957) who stated that 8 week body weight was positively correlated with 12 week body weight.

The expected gain in each percentage of dressing, edible meat, blood and feather at 12 weeks of age were rather small (Tables 37, 38, 39 and 40). Similar results were found by Frairs and Tiku (1969) who reported that the percentage gain from selection for weight at 12 weeks of age was small in the eviscerated weight.

In general, the expected genetic gain calculated from the sire component of variance was higher than that derived from the dam component of variance in all the studied traits. This indicate that sires contriputed largely to the changes either in selected or unselected traits. Previously it was found that the genetic correlations among the studied traits based on sire components were generally positively higher than those obtained from dam components; which indicate that sires inherited their linked genes additively to most of the studied traits especially those genes affect both 8 and 12 week body weights.

Correlated response of the unselected characteristics with moderate heritability estimates was found when the genetic correlation with the selected trait was large, but not when it was low. When there is no reduction in general fitness, a low heritability can mask the effect of a large genetic correlation; while a moderate to high heritability has little inhibtory influence on the associated response when the genetic correlations is large (Seigel, 1963 a). In addition two different approaches to the theory underlying correlated responses have been developed. One, on a purely qualitative basis, derives from Mather's theory of polygenic inheritance (Wigan and Mather, 1942; Mather and Harrison, 1949). If metric traits are conditioned by polygenic systems organized in blocks, it is to be expected that polygenes concerned in the variability of one trait are intermingled along the chromosome with those determining variability of another. Selection directed towards increasing frequencies of certain blocks will then also affect the frequencies of allels linked to them, thus generating correlated response. The other treatment of the question is a quantitative one and is rooted in the theory of genetic correlation developed by Smith (1936) and by Hazel (1943) from the respective fundamental formulations of biommetrical genetics of Fisher and of Wright. The exposition of the subject here combines features of both approaches.

SUMMARY

This study was carried out to evaluate genetic parameters and to estimate response of mass selection for 6 generations to improve body weight in a native breed of White Baladi chickens. A total number of 20 males and 200 females was taken at random for the original population. Each male was mated with 10 females in individual breeding pen. Two hatches were obtained from the same parents. The first hatch made up the selected population and the second hatch made up the random-bred population. At 8 weeks of age, mass selection based on body weight applied on the progeny of each generation of the selected population in such a way that the heaviest 20 males and 200 females were selected. The pedigreed randombred population was reproduced each generation along with the selected population. However, the 20 males used as parents were chosen at random, one male from each previous sire. Each male within each population was mated to 10 females with only a restriction that no full or half sib mating was avoided to prevent inbreeding depression. On hatch, all produced chicks were wing-banded to keep their pedigree and weighed at 8 and 12 weeks of age. Males of each generation of selected and randombred populations were slaughtered at 12 weeks of age to evaluate dressing, edible meat, blood and feather percentages.

The collected data were adjusted for sex effect within population and generation and were statistically analysied by the application of nested design with unequal number of subclasses. Tests of significance for the differences between means of populations and between generations were done according to Duncan's Multiple Range Test.

Heritabilities of the studied traits as well as Genetic, environmental and phenotypic correlations among the traits were estimated on the basis of sire, dam and sire + dam components of variances. The expected genetic gain per generation of selection; also, the expected correlated response were derived from the three components of variances.

The obtained results can be summarized as follows:

Heritability estimates for 8 and 12 week body weights, dressing and feather percentages were larger than those of edible meat and blood percentages; indicating that the first four traits were highly heritable.

Heritability estimates for all traits in the selected population were lower than those in random population; indicating that selection decreased genetic variations through fixation of genes.

Heritabilities estimated from the dam component were much higher than those derived from the sire component for the majority of the studied traits in both populations; indicating the presence of maternal effects.

Most of the genetic correlations among the studied traits based on sire components were generally positively higher than those obtained from dam components in both populations; indicating that sires inhereted their linked and/or pleiotropic genes additively to most of the traits.

The genetic relationships between 8 week body weight and each of the other traits were positively higher in random population than in selected population; indicating that selection reduced the genetic variabilities among the studied traits.

Higher genetic correlations were obtained between 8 and 12 week body weights; also, between feather percentage and each of 8 and 12 week body weights; indicating that improving body weight by selection will be followed by improving feather development.

The genetic correlations between dressing percentage and each of 8 and 12 week body weights were lowerly negative in selected population and highly positive in random population; indicating that selection for heavier 8 week body weight did not accompany by higher dressing percentage.

The genetic and the phenotypic associations between dressing percentage and edible meat were positively higher in both populations; indicating that correlations between those two traits were automatic.

Results, also, indicated that males, females and males + females were heavier in selected population than in random population for 8 and 12 week body weights; indicating that the White Baladi breed of chickens responded largely to selection for improving body weights. However, percentages of dressing, edible meat, blood and feather were almost equal in both populations.

The average of realized progress over all generations for males + females (48.4 grams) was nearly equal to the expected genetic gain (44.1 grams). Also, the corresponding realized heritability (0.537) was nearly equal to the estimated heritability (0.489). However, the realized genetic gain was much higher than the corresponding expected genetic gain within each generation of selection; indicating that selection for improving body weight of White Baladi breed which contains considerable amount of additive variance is unlikely to reach a selection limit in the forseeable futures.

The results, also, indicated that males responded effectively to selection than females; this was due to intensive selection pressure subjected to males (5.5%) than that of females (51.5%).

The results, also, showed that the change in 8 week body weight due to selection was associated positively with a change of about 45, 13 and 11 grams in 12 week body weight based on sire, dam and sire + dam components of variances, respectively. However, the correlated response of each percentage of dressing, edible meat, blood and feather at 12 weeks of age was rather small. This indicated that correlated response of the unselected traits with moderate heritability estimates was found when the genetic correlation with the selected trait was large, but not when it was low.