Effect of the Slow (K) or Rapid (k^+) Feathering Gene on Growth Performance and Skeletal Dimensions of Broiler Chickens Selected for Cut up Carcass Value

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Abstract: An experiment was undertaken to evaluate the impact of slow/rapid feathering sex linked-gene on growth performance and certain skeletal dimensions in a broiler flock under selection for breast and thighs weight with imposing restriction against low value portions of carcass over 3 generations. Analysis of variance for all factors involved demonstrated that k^+k^+/k^+W genotypes are significantly superior than K-/KW for BW at 1 and 14 day with reverse results for BW (42 days), BrL, ShW and DSC ($p<0.05$). Inter sex t-test comparisons revealed significant superioty of k^+k^+ males for BW (1 day) and GW (28-42 days). The K- females showed significant greater ShW and DSC. Inter family analysis revealed significant superiority of k^+k^+/k^+W genotypes for BW (1 day) in 3 families. In one family, GW (1-42 days) was significantly greater for slow feathered birds while in 2 other families the same birds showed significant greater means for GW (28-42 days) ($p<0.05$). The slow feathered birds demonstrated significantly greater means for BrA in 3 families and BrI in 2 families ($p<0.01$). Inter family and inter females t-test comparisons showed significant superiority of KW genotypes for BW (14 days) in 3 families and for BrA, BrI, ShL and ShW in 4 other distinct families. Considering KW vs k^+W in an ANOVA for female's data revealed consistent superioty of the fast feathered females (k^+W) for all growth related traits (except for BW at 28 days) as well as CW. Mean BrL and ShL were significantly greater for slow feathered females while they were inferior for DSC. It is concluded that to incorporate fast feathering gene (k^+) in broiler breeding plans would be of positive economic outcome in commercial broiler production.

Key words: Broiler chickens, growth, feathering rate, skeletal dimensions

INTRODUCTION

In many breeds of chicken, the primary and secondary feathers of a newly hatched bird project well beyond the down and wing coverts whereas in others this is not the case. Serebrovsky (1992) attributed the character to a single pair of sex-linked genes. Warren (1925) verified this important construal and Hertwing and Rittershaus (1929) assigned the K gene symbol to the locus. Later on many reports appeared in the literature to converse the locus exhaustively (Somes and Jakowski, 1974; Walker and Somes, 1979; Harris *et al.*, 1984).

Poultry producers are particularly interested in the economical impact of the K locus. Moreover, the sex of newly hatched chicken can be determined by their rate of feathering when the parents have the genotypes k^+/k^+ and K/W for sires and dams, respectively. The influence of the locus on broilers as well as layers growth, mortality (Lowe and Garwood, 1981; Lowe and Merkley, 1986; Merkley and Lowe, 1988) and disease resistance (Somes and Jakowski, 1974; Harris *et al.*, 1984) were intensively investigated, however, no consistent accordance in the

results achieved. Earlier reports mainly confirmed the priority of k^+k^+/k^+W (fast feathered) birds over the alternative genotypes. They generally attributed this supremacy to the adequate feather cover and its insulative role that aids in thermoregulation, especially in cooler climates. They also extended the advantages of the fast feathered birds to the ability of flying on the roosts at an earlier age, therefore, getting some measure of protection against predators and against the risk of crowding on the floor in corners of a brooder house (Warren and Payne, 1945; Hutt, 1949; Hurry and Nordskog, 1953). However, few pioneers reported that there are no significant differences for fast- or slow-feathered birds with respect to growth performance (Godfery and Farnsworth, 1952). Since 1960s, many works showed that the influence of sex-linked feathering gene is diverged (Sheridan and McDonald, 1963; Goodman and Muir, 1965) in either sexes (Merkery and Lowe, 1986) and populations; and it is a locus carrying a major gene with wide impact on whole organism (Walker and Somes, 1979; Dunnington and Siegel, 1986; Katanbaf *et al.*, 1988; Chambers *et al.*, 1994; Leeson and Walsh, 2004 a, b; Zerehdaran *et al.*, 2004).

However, many recent reports are collectively still of ambiguous results on which genotype (k^+k^+/k^+W vs. $K-/KW$) has to be launched in commercial broiler flocks? where min differences in bird's performance are imperative when applied to the vacant production costs and profit limits. Therefore, this study was carried out to further investigate the effect of major gene K compared to its allele on growth performance and certain skeletal dimensions in an experimental colored broiler flock.

MATERIALS AND METHODS

An experimental colored broiler flock was used over three generations to evaluate the response to selection for breast and thighs weight with imposing restriction against low value portions of carcass. The methodology used in the selection program is described in detail by Khosravinia *et al.* (2006). The day-old chicks were wing banded, distinguished for fast or slow feathering and randomly allocated in the pens placed in a naturally ventilated open shed (with 0.9 m^2 bird^{-1} density). The average effective population size and number of progenies in each generation was 545 and 1250, respectively. Corn and soybean meal based starter (22% CP, 3100 kcal ME kg^{-1} 1-14 days) and grower (20% CP, 3100 kcal ME kg^{-1} 15-42 days) diet as well as water were provided *ad libitum* under round the clock lighting regime.

Individual body weight from day old up to 42 days of age was recorded biweekly. Breast characteristics including Angle (BrA; at 35 days), Length (BrL; at 41 days) and Width (BrW; at 41 days) were measured with 0.2, 0.1 and 0.01 mm precision, respectively. Shank Length (ShL) and Width (ShW) along with drumstick circumference (DSC; at the most fleshy point) were measured with 0.01 mm accuracy at 35 days. Breast measurements were then used to establish a breast index (BrI) in order to estimate the breast volume as below:

$$BrI = [BrW \times Sin (180° - 0.5\ BrA) \times 0.5\ BrW] \times 0.33\ BrL$$

Random samples of the birds were weighed and slaughtered to evaluate the carcass weight and yield at 42 days.

Data were subjected to analysis of variance (ANOVA) or t-test comparisons using the General Linear Model (GLM) and t-test procedures of Statistical Analysis System (SAS Institute, 1998), respectively, to study the influence of generation, genetic group, sex and rate of feathering as fixed effects along with sire and live body weight (42 days) as random effects as well as the interaction between fixed effects on variables concerned. Body weight (42 days) as a continuous variable was incorporated in the models and used to analyze the carcass allied traits. All data expressed in percentage were subjected to *arc sin* transformation prior to analysis. Means for each fixed effect and significant interactions were separated using Duncan's Multiple Range Test.

RESULTS

The primary statistics for the concerned variables and the assigned symbols are presented in Table 1. Growth related traits had greater variability, represented by a higher Coefficient of Variation (CV), as bird's age advances. The external body measurements (except breast dimensions) showed greater variability than body weight and gain at various ages.

Results from ANOVA for all fixed and random effects using nearly 3000 records, demonstrated a significant superiority of k^+k^+/k^+W genotypes over $K-/KW$ for *BW* at 1 and 14 days. However, the reverse results observed for BW (42 days). The slow feathering genotypes showed consistent greater means for all skeletal dimensions, but the differences were only significant for BrL, ShW and DSC ($p<0.05$) (Table 2).

Inter sex t-test comparisons revealed highly significant superioty of k^+k^+ genotype over $K-$ in male birds for BW (1 day) and GW (28-42 days). Similarly, k^+ bearing female chicks showed greater means for all growth related traits, however, the difference was only significant for BW (1 day) ($p<0.05$). Among the skeletal dimensions studied, there were significant differences between

Table 1: Primary statistics[1] for growth allied variables and body measurements

Variable[2]	Symbol	N	Mean	Standard error	CV
Body weight (g; 1 day)	BW (1 day)	2951	40.00	0.071	9.634
Body weight (g; 14 day)	BW (14 day)	2949	210.94	1.023	10.32
Body weight (g; 28 day)	BW (28 day)	2956	634.14	1.629	13.97
Body weight (g; 42 day)	BW (48 day)	2978	1186.25	3.287	15.12
Gain weight (g; 1-42 days)	GW (1-42 days)	2951	1145.00	3.280	15.54
Gain weight (g; 28-42 days)	GW (28-42 days)	2956	552.15	2.255	12.21
Carcass weight (g)	CW	2853	783.25	2.222	15.16
Carcass yield (%)	CY	2924	74.80	0.026	1.88
Breast Length (cm)	BrL	2977	108.49	0.133	6.68
Breast Width (cm)	BrW	2977	51.38	0.090	9.52
Breast Angle (Degree)	BrA	2977	84.64	0.134	8.62
Breast Depth (mm)	BrD	2977	18.92	0.032	9.26
Breast index	BrI	2976	326.82	1.590	26.47
Shank length (cm)	ShL	2975	81.57	0.263	17.61
Shank Width (mm)	ShW	2966	9.99	0.053	29.03
Drum stick circumference (mm)	DSC	2970	36.74	0.103	15.26

[1]: Basic statistics were calculated by MEANS procedure of SAS software (SAS Institute, 1998), [2]: All variables have been recorded at 42 days of age, [3]: LVP = Low Value Portion (including neck, rack, saddle and wings)

sexes. In females, the *K*- males showed greater ShW and DSC. Mean ShL was significantly higher for the fast feathered birds but the reverse results observed for DSC (Table 3).

Inter family analysis (using pooled data over sexes) for 8 larger half sib families (on average n = 27) revealed an average 1 g significant superiority in BW (1 day) for $k^+k^+/$ k^+W bearing birds over their sibs with the alternative feathering genotypes for leg measurements

in either genotype (*K-/KW*) for BW (1d) in 3 families. In one family, GW (1-42 days) was significantly greater for slow feathered birds (1158 vs. 1118 g) while in two other families the birds of the same genotypes showed greater GW (28-42 days) by 7.26 and 3.91% (p<0.05; Table 4). With respect to skeletal dimensions, the slow feathered birds demonstrated greater BrA in 3 families by 2.91, 4.14 and 4.19% and a significant supremacy over the fast feathered birds for BrI in 2 families by 13.09 and 1.475% (p<0.01; Table 4).

Inter family and inter females t-test comparisons for 7 larger half sib families showed significant superiority of *KW* genotypes over k^+ sibs for BW (14d) in 3 families by 2.21, 6.34 and 8.29% (p<0.05; Table 5). The BrL was significantly higher for the fast feathered females in one family (106 vs. 103 mm). In 4 distinct families, the slow feathered females showed greater values for BrA, BrI, ShL and ShW by 5.16, 7.14, 3.77 and 4.54%, respectively (Table 5).

Considering feathering rate as a fixed effect (*KW* and k^+W) in the ANOVA model to analyze the female's data revealed a consistent superiority of the fast feathered females (k^+W) over the slow feathered ones (*KW*) for all growth related traits as well as CW. Except for BW at day 28, the means for all traits were significantly greater in k^+W genotypes. Compared to the fast feathered females, mean BrL and ShL were significantly higher f or the slow feathered ones (Table 6). On the contrary, the fast feathered females showed a significantly greater mean for DSC (Table 6).

Table 2: Partial ANOVA results for fixed effects of sex, Feathering Rate (FR) and their interactions derived form general model used[1]

	Feathering genotype		F-test results			
Variables[2]	*K*-	k^+k^+	Sex	FR	Sex×FR	BW (6w)
BW (g; 1 day)	39.54[b]	40.38[a]	**	**	ns	
BW (g; 14 day)	209.63a	212.04[a]	**	**	ns	-
BW (g; 28 day)	637.09[a]	631.98[b]	**	**	ns	-
BW (g; 42 day)	1175.00[b]	1198.00[a]	**	ns	ns	-
GW (g; 1-42 days)	1157.88[a]	1134.38[b]	**	ns	ns	-
GW (g; 28-42 days)	562.14[a]	543.81[b]	**	ns	ns	-
CW (g)	790.90[a]	776.90[a]	*	ns	ns	**
CY (%)	74.83[a]	74.75[a]	ns	*	ns	**
BrL (mm)	108.72[a]	108.28[a]	**	*	ns	-
BrW (mm)	51.48[a]	51.30a	**	ns	ns	-
BrA (Degree)	84.83[a]	84.56[a]	ns	ns	ns	-
BrD (mm)	18.93[a]	18.91[a]	**	ns	ns	-
BrI	329.57[a]	324.38[a]	**	ns	ns	-
SL (mm)	82.09[a]	81.14[a]	**	ns	ns	-
SW (mm)	10.14[a]	9.86[b]	**	ns	ns	-
DSC (mm)	37.33[a]	36.25[b]	**	ns	ns	-

[1]: $Y_{ijkl} = \mu + GEN_i + GG_j + G(S) k + Se_l + FR_m + (\text{all interactions}) + b (BW_i - BW) + e_{ijklmn}$ where μ; flock mean and GEN_i, GG_j, SE_l and RF_m are the fixed effects of ith, jth, lth and mth generation, genetic group, sex and rate of feathering, respectively. $G(S)_k$ BW and e_{ijklm} are represent the random effects of kth sire, mean live body weight (6w) and the residual error, respectively, [2]: Variables are introduced in Table 1, [a-b]: Within raw and for each effect, values with different letter differ significantly (p<0.01), **: p<0.01, *: p<0.05, [ns]: Non significant

Table 3: Inter-sex comparisons (t-test) for variables considered by the fixed effect of feathering genotype (k^+k^+ vs *K*- in males and k^+W vs *KW* in females)

	Males			Females		
Variables[1]	k^+k^+	*K*-	T-value	k^+Y	*KY*	T-value
BW (g; 1day)	40.83	39.70	5.4614**	40.07	39.34	3.6701**
BW (g; 14 day)	218.72	216.11	0.9628[ns]	207.45	201.67	1.8796[ns]
BW (g; 28 day)	667.64	665.10	0.5226[ns]	607.67	603.08	1.839[ns]
BW (g; 42 day)	1266.31	1279.88	1.4214[ns]	1113.79	1100.08	1.8898*
GW (g; 1-42 d)	1223.69	1238.15	1.5199[ns]	1073.26	1060.56	1.75123
GW (g; 28-42 d)	598.67	615.38	2.5641**	506.75	497.49	1.7693[ns]
CW (g)	835.80	843.60	1.2019[ns]	735.70	727.10	1.7220[ns]
CY (%)	75.03	74.99	0.4428[ns]	74.56	74.62	0.8367[ns]
BrL (mm)	111.74	111.49	0.6535[ns]	105.93	105.36	1.7767[ns]
BrW (mm)	52.45	52.25	0.7183[ns]	50.51	50.55	0.1748[ns]
BrA (Degree)	84.62	84.95	0.7996[ns]	84.52	84.46	0.1820[ns]
BrD (mm)	19.32	19.17	1.4237[ns]	18.63	18.64	0.1616[ns]
BrI	349.37	349.00	0.0750[ns]	307.29	306.37	0.2379[ns]
SL (mm)	83.78	84.79	0.9533[ns]	79.34	78.81	2.0513*
SW (mm)	10.30	10.46	2.4342*	9.56	9.76	1.0059[ns]
DSC (mm)	37.65	38.51	3.1792**	35.29	35.91	2.0700

[1] Variables are introduced in Table 1, **: p<0.01, *: p<0.05, [ns] Non significant

Table 4: Inter-family comparisons (t-test results) for variables considered by the fixed effect of feathering genotype (k^+k^+ or k^+W vs K- or KW) irrespective of sex

	T-values for selected families							
Variables	1	2	3	4	5	6	7	8
BW (g; 1 day)	0.4166ns	0.4732ns	0.8489ns	0.1049ns	2.0998*	2.0321*	2.3686*	1.1437ns
BW (g; 14 day)	0.2176ns	0.0541ns	0.2641ns	0.7553ns	1.9668ns	1.0668ns	1.6572ns	0.1608ns
BW (g; 28 day)	0.1135ns	0.0223ns	0.1720ns	0.7342ns	1.6263ns	0.3700ns	0.3534ns	0.5166ns
BW (g; 42 day)	0.6556ns	0.0365ns	1.9167ns	0.7331ns	0.4136ns	1.4243ns	0.4181ns	1.0206ns
GW (g; 1-42 days)	0.6500ns	0.0481ns	2.0300*	0.7381ns	0.3648ns	1.3520ns	0.3493ns	0.9842ns
GW (g; 28-42 days)	0.5266ns	0.0019ns	2.9420**	0.3995ns	0.6303ns	1.9777*	0.0963ns	1.5085ns
CW (g)	0.4341ns	1.2564ns	0.1106ns	0.0523ns	0.0082ns	1.7829ns	0.4873ns	0.4841ns
CY (%)	0.4643ns	1.7480ns	1.2658ns	0.5290ns	1.2857ns	0.4126ns	0.0690ns	1.3444ns
BrL (mm)	1.0207ns	1.1528ns	0.5437ns	0.1483ns	0.9738ns	1.6223ns	1.6223ns	0.2387ns
BrW(mm)	1.6660ns	0.7131ns	1.8819ns	1.0793ns	0.0603ns	1.4417ns	1.4417ns	0.0801ns
BrA (Degree)	1.1082ns	0.6989ns	2.3150*	1.3748ns	0.8993ns	3.0481**	3.0481**	1.5990ns
BrD (mm)	1.5638ns	0.4005ns	0.0896ns	0.4873ns	0.7363ns	0.2980ns	0.2980ns	0.6384ns
BrI	1.7253ns	0.8131ns	1.9269ns	1.1734ns	0.2932ns	2.8645**	2.8645**	0.5630ns
SL (mm)	1.0791ns	0.3506ns	0.5363ns	0.0212ns	0.1242ns	0.1845ns	0.1845ns	1.6087ns
SW (mm)	1.6568ns	0.4867ns	1.2546ns	1.6706ns	0.3565ns	1.2785ns	1.2785ns	1.3414ns
DSC (mm)	0.5564ns	0.4236ns	1.2302ns	0.9801ns	0.1666ns	1.2934ns	1.2934ns	0.7623ns

[1]: Variables are introduced in Table 1, **: $p<0.01$, *: $p<0.05$, ns: Non significant

Table 5: Inter-family and inter-female comparisons (t-test results) for variables considered by the fixed effect of feathering genotype (k^+W vs KW)

	T-values for selected families						
Variables[1]	1	2	3	4	5	6	7
BW (g; 1 day)	0.9162ns	0.9162ns	1.3834ns	0.8748ns	0.8748ns	0.5203ns	0.9162ns
BW (g; 14 day)	0.2419ns	0.2419ns	0.0018ns	2.1190*	2.1190*	2.3269*	0.2419ns
BW (g; 28 day)	0.0649ns	0.0649ns	1.3102ns	1.3038ns	1.3038ns	0.1683ns	0.0649ns
BW (g; 42 day)	0.0913ns	0.0913ns	1.0698ns	1.7270ns	1.7270ns	0.2303ns	0.0913ns
GW (g; 1-42 d)	0.1249ns	0.1249ns	1.0345ns	1.6962ns	1.6962ns	0.4113ns	0.1249ns
GW (g; 28-42 days)	0.0634ns	0.0634ns	0.5443ns	1.0199ns	1.0199ns	0.1874ns	0.0634ns
CW (g)	2.0478ns	0.0182ns	1.7142ns	0.7401ns	0.4873ns	0.4841ns	2.0572ns
CY (%)	2.0723ns	0.7059ns	0.3288ns	0.2951ns	0.0690ns	1.3444ns	0.3442ns
BrL (mm)	0.1945ns	0.1945ns	1.6915ns	2.0385*	1.0009ns	1.2363ns	0.1945ns
BrW(mm)	0.7755ns	0.7755ns	1.5871ns	0.8531ns	0.6877ns	0.2476ns	0.7755ns
BrA (Degree)	0.4141ns	0.4114ns	1.4576ns	1.4110ns	2.7303**	1.7507ns	0.4141ns
BrD (mm)	0.7083ns	0.7083ns	0.4648ns	0.0204ns	1.1844ns	0.8646ns	0.7083ns
BrI	0.7158ns	0.7158ns	2.0554*	1.2882ns	1.1404ns	0.8733ns	0.7158ns
SL (mm)	0.2724ns	0.2724ns	0.6734ns	0.8002ns	2.5505*	0.5659ns	0.2724ns
SW (mm)	0.2859ns	0.2859ns	2.2315*	0.8732ns	1.0023ns	0.8333ns	0.2859ns
DSC (mm)	1.2011ns	1.2011ns	0.9263ns	1.2425ns	0.1689ns	0.0178ns	1.2011ns

[1]: Variables are introduced in Table 1, *: $p<0.05$, ns: Non significant

Table 6: Partial ANOVA results for fixed effect of Feathering Rate (FR) based on data corrected for all fixed and random effects in the general model used[1]

	Feathering genotype for females		F-test results
Variables[2]	KY	k^+Y	for sex
BW (g; 1 day)	39.35b	40.07a	0.0001**
BW (g; 14 day)	201.67b	207.45a	0.0834ns
BW (g; 28 day)	603.38a	607.68a	0.0979ns
BW (g; 42 day)	1102.30b	1117.42a	0.9984ns
GW (g; 1-42 days)	1060.57b	1073.26a	0.5907ns
GW (g; 28-42 days)	497.49b	506.75a	0.6287ns
CW (g)	730.80b	737.53a	0.5246ns
CY (%)	74.63a	74.57a	0.2551ns
BrL (mm)	105.36b	105.93a	0.6777ns
BrW(mm)	50.55a	50.51a	0.0588ns
BrA (Degree)	84.46a	84.52a	0.5461ns
BrD (mm)	18.64a	18.63a	0.1401ns
BrI	306.37a	307.29a	0.1065ns
SL (mm)	78.81b	79.34a	0.0082**
SW (mm)	9.76a	9.57a	0.6233ns
DSC (mm)	35.91a	35.29b	0.5322ns

[1]: $Y_{ijkl} = \mu + GEN_i + GG_j + G(S)k + FR_l + $ (all interactions) $+ b(BW_i - BW) + e_{ijklm}$ where μ; flock mean and GEN, GG and RF are the fixed effects of ith, jth and lth generation, genetic group, sex and rate of feathering, respectively. $G(S)_k$ and e_{ijklm} are represent the random effects of kth sire and the residual error, respectively, [2]: Variables are introduced in Table 1, a-b: Within raw and for each effect, values with different letter differ significantly ($p<0.01$), **: $p<0.05$, ns: Non significant

DISCUSSION

Results from various analytical models applied (Table 2-6) show that the fast feathering genotypes are generally superior to the alternate genotypes with respect to the early growth performance. These findings are in fair accordance with the results reported by the other researchers (Warren and Payne, 1945; Hutt, 1949; Jull, 1952; Plumart and Mueller, 1954; Dunnington and Siegel, 1986). Such a primacy could be reasoned out by the presence of adequate feather cover and consequently the insulative role of feathers which aids the fast feathered birds in thermoregulation. This greater covering of the body affords fast feathering genotypes (k^+k^+/k^+W) lower requirement of energy for maintenance of body temperature and thus leaves more energy available for growth. However, there are many reports in contradiction with the results obtained where the slow feathered birds showed equal (Godfery and Farnsworth, 1952; Sheridan and McDonald, 1963; Lowe and Garwood, 1981) or even greater (Merkery and Lowe, 1988) growth capabilities even at early ages compared to the fast feathered birds. Differences in experimental populations and protocols used may have contributed to these contradictory results, indicating that this area warrants further investigation.

The results from the current study demonstrate the greater means for most of the skeletal dimensions in the slow feathered birds (Table 2, 3 and 6). Reports on comparison between feathering genotypes for skeletal dimensions or body measurements are scanty to further converse the matter. Moreover, the primacy of a feathering genotype over the other seems to be diverged by sex (Table 3). These results in agreement with the findings of Walker and Somes (1979), Dunnington *et al.* (1987) and Katanbaf *et al.* (1988) reveal that the K gene is a mutation with broad influence on whole organism growth and that its effects could not be interpreted independently from sex associated factors. The substantial alliance among sex related factors and feathering genotypes has been verified by many reports (Lowe and Garwood, 1981; Zerehdaran *et al.*, 2004).

To further interpret the impacts of sex associated feathering loci it could be verified that results from whole data set analysis, sex wise and inter family comparisons are diverged for individual traits and even for a single trait at various ages. These observations reveal that the loci influences growth of the whole organism through out the bird's life much beyond on its impact in accelerating the growth of the feathers and its consequential isolative advantages (Siegel and Dunningham, 1987; Chambers *et al.*, 1994). Many researchers attributed the impact of feathering loci on growth of chicken to the deviated nutrient requirements in genotypes relevant (Moran, 1981; Deschutter and Leeson, 1986; Kafri *et al.*, 1986; Weinberg *et al.*, 1986; Zelenka *et al.*, 1992;

Fosta *et al.*, 2001; Pakdel *et al.*, 2002; Leeson and Walsh, 2004 a, b). The debates are specifically focused on amino acid requirements of the young birds (Deschutter and Leeson, 1986), particularly for cystine. Moran (1981) and Engler *et al.* (1985) reported a slightly higher sulfur amino acid requirements of females than males due to differences between sexes in the rate of feathering. With respect to fast vs. slow feathering, they discussed that with increasing demands for uniformity of market broilers; there is an increasing need to account for variation in rate of feathering in order to evaluate amino acid requirements accurately.

From the results obtained it could be concluded that; there are no concrete reason to believe K and k^+ alleles have identical impact on growth performance. Although the effect of the genes K, k^+ assumed to be equal or constant, the genetic background with which they interact are not identical in either sexes and from an individual, family and flock to the other. Diverged results for impact of this locus on growth performance could be attributed to two reasons. Firstly, over the generations, bird's genetic make up constantly changing due to genetic selection and nutritional advances. Secondly, it is not clear that all genotypic combinations involving the K, k^+ genes were used in all previous studies or that the performances of homozygotes and hetrozygotes were measured separately. In today's efficient, competitive and swiftly changing broiler industry, small differences in bird's performance especially at early ages (e.g., 0.1% in feed conversion or 1.0% in body weight) are imperative when applied to current production costs and profit margins. Therefore, incorporating the fast feathering gene (k^+) with a reasonable influence on early growth performance would be of positive economic outcome in commercial broiler production.

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