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GENETIC DIVERGENCE AMONG GUINEAFOWL VARIETIES*

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ABSTRACT

Genetic divergence among six genetic groups of guineafowl was studied using Mahalanobis D^2 statistics. Growth and conformation traits included were body weight at hatch, 4, 8 and 12 weeks, keel length, shank length and breast angle at 12 weeks and serum lysozyme level at 8 weeks of age. Contribution of various traits to the total genetic divergence ranged from 9.26 to 17.96%. Breast angle contributed maximum (17.96%) followed by 12-week body weight (17.04%). The 6 genetic groups were clubbed into 3 clusters using Trocher's method. The inter- and intra-cluster distances were estimated.

Guineafowl (*Numida meleagris*) has a considerable traditional popularity as an alternate poultry species. This hardy poultry species has hitherto received very limited attention of geneticists and breeders. Present study is a preliminary attempt to evaluate genetic divergence and similarities among guineafowl varieties using discriminant function and D^2 statistics.

MATERIALS AND METHODS

The genetic groups used in the analysis included 38 White slow feathering (GG 1), 50 White rapid feathering (GG 2), 64 Lavender slow feathering (GG 3), 52 Lavender rapid feathering (GG 4), 66 Pearl slow feathering (GG 5) and 122 Pearl rapid feathering birds.

Released from blood platelets, lysozyme, is widely distributed in the body and has a direct role in basic defence mechanism (Jolles and Jolles, 1984). Accordingly, serum lysozyme level was also included and was estimated as per the method of Sato and Watanabe (1976). Records on body weights at hatch, 4, 8 and 12 weeks, and keel length, shank length and breast angle at 12 weeks and serum lysozyme level at 8 weeks were analysed by least-squares method (Harvey, 1966) to study the variation among different genetic groups. Duncan's multiple range test as modified by Kramer (1957) was used to study the difference among the least-squares means. The genetic distances among the different genetic groups were estimated by Mahalanobis D^2 statistics.

Table 1. Analysis of variance forbody weight, conformation traits and serum lysoyme level

Sources of variation	df	Mean sum of squares							
		Lysozyme level at 8 wk	Body weights at				Conformation trait at 12 wk		
			Hatch	4 wk	8 wk	12 wk	SL*	KL$^{\#}$	BA$^{\$}$
Between genetic groups	5	1.38**	51.51**	7669.36**	111251.42**	118119.65**	6.65**	8.99**	23.60**
Error	386	0.16	4.84	822.98	7912.81	9948.32	0.32	0.36	18.46

** $P \leq 0.01$. *SL: shank length. #KL: keel length. \$ BA: breast angle.

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Table 2. Means and standard error of different traits

Genetic group	N	Lysozyme level at 8 wk	Mean ± SE						
			Body weights at				Conformation traits at 12 wk		
			Hatch	4 wk	8 wk	12 wk	SL*	KL*	BA$
GG 1	38	1.05^a ±0.06	25.15^a ±0.35	198.85^a ±4.65	546.31^a ±14.43	881.57^a ±16.18	6.76^a ±0.09	8.61^a ±0.09	40.05^b ±0.69
GG 2	50	1.39^b ±0.05	22.53^e ±0.27	172.50^e ±3.59	449.37^e ±11.11	786.25^e ±12.46	6.32^d ±0.07	7.89^d ±0.07	39.53^c ±0.59
GG 3	64	1.13^d ±0.04	23.93^b ±0.27	178.18^d ±3.53	454.84^d ±10.94	794.60^d ±12.27	6.13^e ±0.07	7.70^e ±0.07	38.60^d ±0.52
GG 4	52	1.17^c ±0.05	25.04^a ±0.31	191.20^b ±4.05	499.20^b ±12.57	856.80^b ±14.10	6.62^b ±0.08	8.35^b ±0.08	40.44 ±0.60
GG 5	66	1.43^a ±0.05	23.65^{cd} ±0.30	182.30^c ±3.97	480.00^c ±12.33	829.61^c ±13.83	6.41^c ±0.09	8.10^c ±0.08	40.00^b ±0.59
GG 6	122	1.15^d ±0.03	23.59^d ±0.19	168.52^f ±2.59	422.90^f ±8.05	767.37^f ±9.03	5.91^f ±0.05	7.59^f ±0.05	39.77^b ±0.38

Means with same superscript do not differ significantly ($P \leq 0.05$).
*SL: Shank length; *KL : Keel length; $ BA: breast angle.

RESULTS AND DISCUSSION

The results of analysis of variance are presented in Table 1 and the means along with standard error for the various traits are presented in Table 2.

Although no definite trend for body weights, conformation traits and lysozyme level regarding feathering type (slow and rapid) could be observed, the slow feathering birds in pearl and white varieties had higher values of body weights and conformation traits whereas in lavender variety, the rapid feathering birds were heavier and had longer body measurements. However lysozyme concentration was higher in rapid feathering birds in white and lavender varieties and in slow feathering birds in pearl variety.

Table 3. Relative contribution of economic traits to total divergence

Characters	Rank total	Contribution %
Lysozyme level at 8 weeks	60	11.11
Body weight at hatch	50	9.26
Body weight at 4 weeks	51	9.44
Body weight at 8 weeks	61	11.29
Body weight at 12 weeks	92	17.04
Shank length	67	12.42
Keel length	62	11.48
Breast angle	97	17.96
Total	540	100.00

The rank totals which provided the basis for estimation of relative contribution of different traits to total genetic divergence along with the percentage contribution of the various traits are given in Table 3. The relative contribution of each character to the total genetic distance (D^2) between each pair of genetic groups was ranked according to the D^2 due to each character (Thiyaga Sundaram *et al.*, 1982).

Table 4. D^2 values of 6 genetic groups

Genetic groups	1	2	3	4	5	6
1	0	0.56	4.42	2.50	3.04	4.14
2		0	2.67	1.14	1.84	2.48
3			0	0.68	1.59	1.43

Table 5. Average inter- and intra-cluster distances (D)

Cluster	I	II	III
I	0.668	1.695	1.196
II		0.747	1.638
III			0.827

The contribution of different traits to the genetic divergence ranged from 9.26 to 17.96%. Breast angle contributed maximum (17.96%) followed by 12-week weight (17.04%).

The D^2 values for different traits among 6 genetic groups have been presented in Table 4. Trocher's method of clustering revealed 3 clusters: GG 5 and GG 6 formed cluster I, GG 1 and GG 2 cluster II and GG 3 and GG 4 cluster III.

The average intra- and inter-cluster distance (D) are presented in Table 5. Cluster I had the minimum intracluster distance whereas cluster III had the maximum. Clusters I and III were more closer than any other combination.

In a contemporary study, Pal *et al.* (1992) using similar genetic groups and body weights, conformation traits and serum alkaline phosphatase level also revealed 3 clusters, viz. clusters I (GG 1, GG 2 and GG 4), II (GG 5 and GG 6) and III (GG 3). However, in the present analysis, lysozyme when included in place of serum alkaline phosphatase, influenced the clustering pattern.

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