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Biochemical gene profile of an Aseel population*

S.K. PAL, HARPREET SINGH, V.K. SAXENA[1] and D.P. SINGH

Central Avian Research Institute, Izatnagar - 243 122

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ABSTRACT

Evaluation of gene determined electrophoretic variability in Aseel revealed existence of distinct polymorphism for ovalbumin, ovoglobulin G_2 and G_3, transferrin, alkaline phosphatase, amylase and adenosine deaminase. Haemoglobin, albumin, adenylate kinase, esterase-D, glyoxalase and lysozyme showed monomorphism. The study established existence of a new marker system *viz.*, adenosine deaminase in Aseel. The average heterozygosity was calculated to be 0.126.

Gene determined electrophoretic variations detected for a number of proteins and enzymes have been extensively utilised as marker genes for characterisation and estimation of genetic variability within and between domestic fowl germplasms of Asian and Mediterranean origin (Singh, 1987; Grunder, 1990). But only limited information is available regarding native chicken germplasms of the Indian subcontinent. Investigation of indigenous domestic fowl germplasm by Baker *et al.* (1971) and Singh (1986) have revealed polymorphism at several serum and egg white protein and enzyme loci. Similar observations were also reported for native fowl of Sri Lanka and Bangladesh (Hashiguchi *et al.*, 1986; Okada *et al.*, 1988). The present investigation deals with evaluation of electrophoretic status of hitherto unreported protein and enzyme systems in Aseel breed.

* Part of the Ph.D. dissertation of the first author approved by the Deemed University, I.V.R.I., Izatnagar.

1 Scientist, Department of Goat Genetics & Breeding, C.I.R.G., Makhdoom, Mathura - 281 122.

MATERIALS AND METHODS

Aseel population maintained at this institute was studied for two blood protein systems *viz.*, albumin (Alb) and haemoglobin (Hb); six enzyme systems *viz.*, adenylate kinase (Ak), adenosine deaminase (Ada), esterase - D (Es - D) and glyoxalase (Glo) in red cells and alkaline phosphatase (Akp) and amylase (Amy) in serum, and five egg white protein and enzyme systems *viz.*, ovalbumin (Ov), transferrin (Tf), Ovoglobulin G_2 and G_3 and lysozyme (Ly).

Standard electrophoretic procedures were employed for red cell and serum enzymes in agarose - gel (Ogita 1962; Harris and Hopkinson, 1976; Watanabe and Wakasugi, 1978) and blood and egg white proteins in starch - gel media (Singh, 1986). Lysozyme was studied in acrylamide - gel electrophoreses (Sato and Watanabe, 1976).

RESULTS AND DISCUSSION

Haemoglobin and lysozyme showed monmorphism. This observation is in agreement with the

earlier reports of Singh (1986) for Aseel and Kadaknath breeds. Electrophoretic variations for haemoglobin and lysozyme are very rare among chicken. Except the mutant reported among Japanese Bantam, all other haemoglobin variants observed among chicken stock were of fairly recent common ancestory (Washburn, 1976). Similarly, the existence of lysozyme polymorphism has been recorded in only one Polish Bantam flock (Baker *et al.*, 1971).

Individual variations were also not detected for adenylate kinase, esterase - D and glyoxalase. Esterase-D phenotype was identified as two equally staining bands resolving very close to each other but glyoxalase showed presence of a thick dark staining band accompanied by a faster moving weak component. During electrophoresis all these proteins/ enzymes migrated anodically, except the adenylate kinase which showed cathodal mobility.

Existence of distinct polymorphism was observed for adenosine deaminase, alkaline phosphatase, amylase, ovalbumin, transferrin (conalbumin) and G_2 and G_3 ovoglobulin components. The adenosine deaminase separated out as a broad dark stained band along with a faint minor band in the upper half of the agrose gel. The heterozygote phenotype had two dark stained bands (Fig. 1). The slow migrating alkaline phosphatase phenotype was identified as a single lightly stained band, while fast phenotype (Akp^f) showed presence of an intensely staining slow and a fast moving component. These variations are similar to that reported earlier by Tamaki (1975). The amylase activity was observed in three different zones. The zone-I was

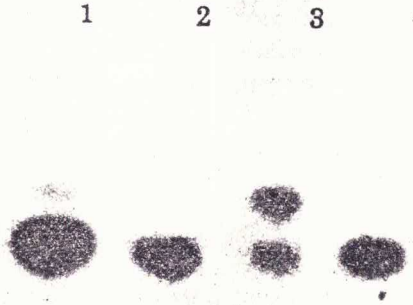

Fig. 1. Zymogram showing adenosine deaminase phenotypes: 1-AA, 2-AA, 3-AB, 4-AA.

represented by anodically migrating components showing maximum activity. Three electrophoretic phenotypes were identified in this zone. Both ovalbumin and transferrin (conalbumin) revealed two phenotypes (Fig. 2). The Ov-AA and Tf-AA phenotypes were predominant in this population.

The allelic frequencies of the protein and enzyme systems are presented in the Table 1. The gene frequency estimates for alkaline phosphatase, ovalbumin, transferrin, G_2 and G_3 ovoglobulin components are in agreement with the earlier study of Singh (1986). These estimates for amylase and adenosine deaminase are also comparable with that reported for White Leghorn by Watanabe and Suzuki (1977) and Grunder and Hollands (1978), respectively. Since no comparative studies could be undertaken, the presently used allelic designation for adenosine deaminase are tentative.

Nei (1978) observed that average hetrozygosity and genetic distance estimates obtained from large number of loci instead of large number of individuals per locus provide unbiased estimates particularly when the total number of gene to be examined is fixed. The number of individuals to be examined depends largely on the level of heterozygosity; more individual should be examined when heterozygosity is high. The proportion of polymorphism (P) and average heterozygosity (H) calculated for Aseel were 0.46 and 0.126, respectively. Birds harbour relatively low average polymorphism and average heterozygosity (Ayala, 1982). The presently observed average polymorphic loci (P) and average heterozygosity (H) values are within the range reported for avian species.

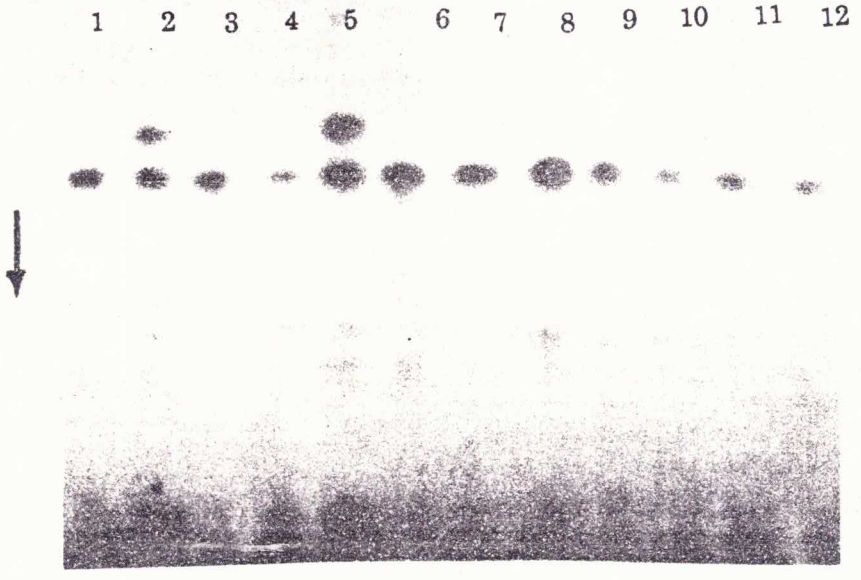

Fig. 2. Electrophoretogram showing transferrin phenotypes :

Table 1. Status of protein and enzyme polymorphism in Aseel

Locus	Enzyme code No.	Observed phenotype				Allele frequency	
		N	A	AB	B	A	B
Hb	—	30	30	0	0	1.00	0.00
Alb	—	30	0	0	30	0.00	1.00
Ov	—	30	20	10	0	0.84	0.16
Tf (con)	—	30	21	9	0	0.85	0.15
G_2	—	30	1	6	23	0.14	0.86
G_3	—	30	19	6	5	0.73	0.27
Ak	2.7.4.3	28	28	0	0	1.00	0.00
Es-D	3.1.1.1	28	28	0	0	1.00	0.00
Akp	3.1.3.1	25	S-20		F-5	0.90(s)	0.10(F)
Amy I	3.2.1.1	20	18	2	0	0.95	0.05
Ly	3.2.1.17	25	25	0	0	1.00	0.00
Ada	3.5.4.4	25	18	7	0	0.86	0.14
G10	4.4.1.5	26	26	0	0	1.00	0.00

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