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Some polymorphic protein and enzyme systems of quail*

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ABSTRACT

Existence of distinct polymorphism was identified for haemoglobin, adenylate kinase, adenosine deaminase and esterase-D. Albumin, transferrin, glyoxalase, alkaline phosphatase, amylase and lysozyme showed monomorphism. These observations established the existence of 2 new red cell enzyme maker systems, viz. adenylate kinase and adenosine deaminase. The average heterozygosity calculated was 0.115.

The domestic quail (*Coturnix c. japonica)* is highly variable for several protein and enzyme systems. Recently Cheng and Kumura (1990) described polymorphism for at least 47 proteins and enzymes. The present investigation was carried out to study the polymorphic status of some important enzyme and non-enzymic protein systems in quail.

MATERIALS AND METHODS

Quail germplasm of this Institute was surveyed for electrophoretic variations for 10 enzyme and protein systems. Standard electrophoretic assay techniques were employed for blood proteins in starch-gel (Singh and Singh 1988), red cell enzymes, alkaline phosphatase and amylase in agarose-gel (Harris and Hopkinson 1976, Ogita 1992, Watanabe and Wakasugi 1978) and egg white lysozyme in acrylamide-gel (Sato and Watanabe 1976).

RESULTS AND DISCUSSION

The existance of distinct polymorphism was observed for haemoglobin, esterase-D, adenosine deaminase and adenylate kinase. During electrophoresis haemoglobin resolved as a thick darkly stained band (M) and a faster moving lightly stained component (m). Two phenotypes observed in faster moving minor component confirm the report of Dimri *et al.* (1981). Esterase-D separated out as a broad band along with a lightly stained component moving ahead in the upper half of the gel. The heterozygote individuals revealed a 3 banded phenotype (Fig. 1) similar to that reported earlier by Watanabe *et al.* (1977). Most interesting variation was observed for red cell enzymes adenosine deaminase and adenylate kinase in this flock. The adenosine deaminase bands were identified in the mid-half of the agarose-gel; the heterozygote phenotype showed the presence of 2 bands with slightly different staining site (Fig. 2). The quail adenylate kinase resolved as a thick dark band moving towards the cathode. The heterozygote individuals showed a 2 banded phenotype (Fig. 3).

No individual variations were identified for serum albumin, transferrin, alkaline phosphatase, amylase; egg white lysozyme and red cell glyoxalase. Albumin, alkaline phosphatase and lysozyme showed a single-banded phenotype. Dimri *et al.* (1980) earlier failed to identify any variation for alkaline phosphatase in starch-gel electrophoresis. Both

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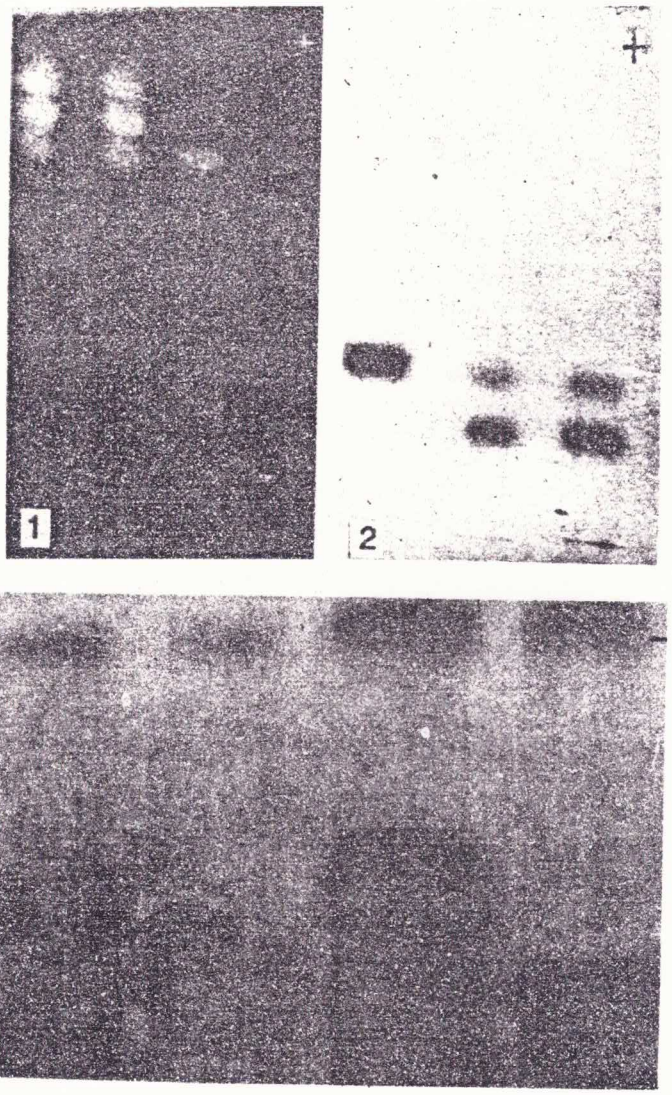

Figs 1-3. 1. Quail esterase-D zynogram. 2. Quail adenosine deaminase zynogram. 3. Quail adenylate kinase zynogram.

serum transferrin and red cell glyoxalase resolved as 2 banded phenotype. Amylase bands were identified in 3 different zones but individual variations were not identified.

Electrophoretic variation pattern for 2 regulatory enzymes of red cells, viz. adenylate kinase (EC 2.7.4.3) and adenosine deaminase (EC 3.5.4.4) established the existence of 2 more maker systems for this species (Table 1). Preliminary observations suggested genetic control through codominant alleles but detailed pedigreed investigations are desired.

High comparative variability of domestic quail vis-a-vis closely related galliform species for the amount of genetically interpretable protein variations is well established. This

Table 1. Polymorphic status of protein and enzyme systems

Systems	Source	N	Phenotype			Gene frequencies	
			A	AB	B	A	B
Protein systems							
Albumin	Serum	30	30	0	0	1.00	0.00
Haemoglobin	RBC	30	21	99	0	0.85	0.15
Transferrin	Serum	30	0	0	80	0.60	1.00
Enzyme systems							
Adenosine deaminase	RBC	26	17	9	0	0.82	0.18
Adenylate kinase	RBC	26	20	6	0	0.88	0.12
Alkaline phosphatase	Serum	25	25(s)	-	0	1.00(s)	-
Amylase-1	Serum	25	25	0	0	1.00	0.00
Esterase-D	RBC	26	19	7	0	0.086	0.14
Glyoxylase	RBC	28	28	0	0	1.00	0.00
Lysozyme	Egg white	22	22	0	0	1.00	0.00

higher variability was a consequence of bringing together of formerly isolated populations during early domestication (Baker and Manwell 1975).

Population characterization through quantitation of biochemical genetic variations showed high degree of average heterozygosity (H-0.090-0.285) for different domestic quail populations (Baker and Manwell 1975, Kimura *et al.* 1983). The average heterozygosity (H-0.115) observed in the present study was within the above reported range. A comparative genetic study of 2 wild quail populations by Kimura *et al.* (1983) showed the existence of polymorphism in 15 out of 31 loci in 1 and 13 out of 30 loci in another population. Maeda *et al.* (1980) reported 30% reduction in heterozygosity for a population selected for 47 generations for body weight (4 weeks) as compared to the unselected control line. The possibility of fixation of alleles during intense selection for growth was suggested. The basic germplasm for the presently investigated quail population was obtained from the University of California, Davis in 1974. Subsequently more stocks were imported from Korea and Germany (Panda 1989). This population has also undergone intensive selection for body weights during the last 2 decades. It is most likely that similar factors might also be operating and thereby relatively low heterozygosity levels are detected.

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