CHAPTER 4

RESULTS

RESULTS

Among the 40 loci analysed in this study, blood protein polymorphisms were found in 12 loci, namely Albumin **(Alb)**, Amylase **(Amy)**, Alkaline Phosphatase **(Ap)**, Carbonic anhydrase **(Ca)**, Haemoglobin **(Hb)**, Malic enzyme **(Me)**, Malate dehydrogenase **(Mdh)**, NADH-Diaphorase 1 zone 1 **(Dia-1)**, NADH-Diaphorase 1 zone 2 **(Dia-2)**, Purine nucleoside phosphorylase **(Np)**, Transferrin **(Tf)** and X-protein **(Xp)** (Table 5). The electrophoretic phenotypes for these twelve polymorphic loci are shown. The remaining 28 loci were monomorphic as listed in Table 6 and the electrophoretic banding patterns illustrated in Figure 16 and Plates 22 - 49. Further description of relative band positions and staining intensity have been given in the appendix 1. Loci were classified as monomorphic only after scoring at least 25 samples from each population except for Hambantota (Sri Lanka) goat populations where only 10 samples were available. Levene's (1949) correction test has been performed for populations having small sample size. Goat population's identification chart as given in Table 3 indicates the population code numbers used in the gene frequency tables (Table 7).

4.1. Pedigree Studies for the Polymorphic Loci

Although the X^2 test was not carried out due to the small number of progenies per mating type, yet it was possible to prove that all the alleles in the polymorphic loci were codominant and controlled by two autosomal alleles. This is obvious by the fact that each offspring displayed only one of the possible genotypes expected for codominant inheritance. Since the various heterozygotes forms appeared in both the male and female parents and progenies, it can be confirmed that these loci are autosomal.

4.2. Gene frequency

Phenotype and gene frequency obtained at each locus in the 13 goat populations of Southeast Asia, Sri Lanka and Australia are listed in Tables 5 and 7 respectively. The data shows that the allelic distribution is random with wide range of variation; i.e. the allelic frequency distribution for most of the loci is not correlated with their geographical locations. The data also revealed that the frequency distribution was independent from locus to locus.

The presence of null alleles was detected in few of the populations and it was only found in few samples. Hence, the null alleles detected in these loci (Ca, Dia-1 and Dia-2) were not used in the final statistical analysis. However the frequency of phenotypes involving the null alleles is given in the appendix 5.

Comparatively large frequency differences among the goat populations were observed mainly at the Alb, Ap, Ca, Hb, Dia-1, Dia-2, Tf and Xp loci.

4.2.1. Albumin

Three phenotypes were recognized in the present study: Alb A, Alb AB and Alb B. This is in accordance with a genetic hypothesis of two codominant alleles at an autosomal locus: Alb^{A} and Alb^{B} (Watanabe and Suzuki, 1967; Salerno *et al.*, 1968; Tjankov, 1970 and Osterhoff & Ward-Cox, 1970). This plasma system did show less genetic variability, the Alb^{A} allele appeared in high frequency (>0.70) in all the populations, but in Musuan, Hat Yai and Hambantota, it's frequency was lower (<0.68).

Table 5 . Phenotype frequencies of the goat populations examined

ENZYME / PROTEIN GENOTYPE		MALAYSIA			INDONESIA			PHILIPPINES	THAILAND		SRI LANKA			AUSTRALIA
		MARDI/IPT	SABAH	SARAWAK	BOGOR	SULUWESI	MEDAN	MUSUAN	CHENGMAI	HADYAI	S1	S2	S3	N.S.W.
Albumin														
ALB	(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
	A	47	31	42	26	32	29	19	27	12	3	30	28	41
	AB	8	20	27	24	5	21	30	21	24	7	7	3	11
	B	0	-	2	-	11	-	2	2	3	-	-	-	-
Plasma amylase														
AMY	(N)	55	51	71	50	48	50	51	39	39	11	37	31	52
	H	36	39	45	27	32	31	33	25	25	8	23	21	42
	L	19	12	26	23	16	19	17	14	14	3	14	10	10
Alkaline phosphatase														
AP	(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
	FF	39	34	35	46	21	26	23	34	30	7	28	21	37
	00	16	17	36	4	27	24	28	16	9	3	9	10	15
Carbonic anhydrase														
CA	(N)	53	50	64	46	46	50	51	45	39	10	36	31	46
	102	-	-	-	-	-	-	-	-	-	1	0	0	0
	102/100	-	-	-	-	-	-	-	-	-	0	2	0	0
	100	47	45	61	21	24	44	40	38	37	2	32	29	44
	100/98	-	2	3	7	4	-	7	5	2	7	2	0	2
	98	6	3	-	18	20	6	4	2	-	0	0	2	0

* **S1 - HAMBANTOTA** **S2 - WEERAWILLA** **S3 - THAMBUTHEGAMA**

(Contd. Table 5). Phenotype frequencies of the goat populations examined

ENZYME / PROTEIN GENOTYPE		MALAYSIA			INDONESIA			PHILIPPINES	THAILAND		SRI LANKA			AUSTRALIA
		MARDI/IPT	SABAH	SARAWAK	BOGOR	SULUWESI	MEDAN	MUSUAN	CHENG MAI	HAD YAI	S1	S2	S3	N.S.W.
NADH Diaphorase 1 Zone 1														
DIA 1	(N)	55	51	70	50	48	50	49	50	39	10	36	31	52
	102	-	-	-	-	-	-	**2**	-	-	0	0	0	0
	102/100	-	-	-	-	-	-	3	-	-	0	0	0	0
	100	55	46	58	50	48	50	31	42	33	10	36	31	52
	100/98	-	4	6	-	-	-	**2**	**3**	-	0	0	0	0
	98	-	1	6	-	-	-	11	5	6	0	0	0	0
NADH-Diaphorase 1 Zone 2														
DIA 2	(N)	55	49	62	50	48	50	49	50	37	8	35	31	52
	102	-	7	14	9	4	4	7	5	1	0	0	13	32
	102/100	**2**	8	8	10	5	**2**	8	7	7	0	**2**	4	11
	100	52	34	34	31	39	44	34	38	22	8	23	14	9
	100/98	1	-	-	-	-	-	-	-	5	0	8	0	0
	98	-	-	-	-	-	-	-	-	**2**	0	**2**	0	0
Haemoglobin														
HB	(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
	A	43	38	60	46	35	**42**	38	39	33	0	6	0	5
	AB	5	6	-	4	8	6	8	6	4	**3**	8	7	14
	AX	7	7	11	-	-	-	-	-	-	0	0	0	0
	B	-	-	-	-	5	**2**	5	5	**2**	7	**22**	24	33

*** S1 - HAMBANTOTA** **S2 - WEERAWILLA** **S3 - THAMBUTHEGAMA**

(Contd. Table 5). Phenotype frequencies of the goat populations examined

ENZYME / PROTEIN GENOTYPE		MALAYSIA			INDONESIA			PHILIPPINES	THAILAND		SRI LANKA			AUSTRALIA
		MARDI/IPT	SABAH	SARAWAK	BOGOR	SULUWESI	MEDAN	MUSUAN	CHENG MAI	HAD YAI	S1	S2	S3	N.S.W.
Malate dehydrogenase														
MDH	(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
	100	39	31	48	38	25	34	31	31	15	1	14	28	42
	100/98	5	4	8	3	13	9	13	10	11	7	11	0	2
	98	11	16	15	9	10	7	7	9	13	2	11	3	8
Malic enzyme														
ME	(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
	104	-	-	-	-	-	-	-	-	-	-	-	-	2
	102	3	6	3	5	5	2	9	5	3	3	4	8	23
	102/100	7	7	6	3	6	4	1	9	1	1	0	0	5
	100	45	34	54	38	29	34	36	29	3	3	19	13	20
	100/98	-	1	3	-	3	3	1	1	0	0	3	1	1
	98	-	3	3	4	5	7	4	6	3	3	10	1	1
Nucleoside phosphorylase														
NP	(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
	H	33	37	55	55	30	40	28	34	29	7	27	25	26
	L	22	14	16	11	18	10	23	16	10	3	9	6	26

* **S1 - HAMBANTOTA** **S2 - WEERAWILLA** **S3 - THAMBUTHEGAMA**

(Contd. Table 5) Phenotype frequencies of the goat populations examined

ENZYME / PROTEIN GENOTYPE		MALAYSIA			INDONESIA			PHILIPPINES	THAILAND		SRI LANKA			AUSTRALIA
		MARDI/IPT	SABAH	SARAWAK	BOGOR	SULUWESI	MEDAN	MUSUAN	CHENG MAI	HAD YAI	S1	S2	S3	N.S.W.
Transferrin														
TF	(N)	55	51	71	50	48	50	51	50	39	11	37	31	52
	A	12	28	24	23	20	27	17	20	8	11	37	28	36
	AB	24	22	29	29	22	19	26	21	22	-	-	3	12
	AC	-	-	2	2	-	1	3	-	-	-	-	-	-
	AD	1	-	-	-	-	1	-	-	-	-	-	-	-
	B	14	1	15	15	2	2	4	9	9	-	-	-	4
	BC	2	-	-	-	3	-	1	-	-	-	-	-	-
	BD	2	-	1	1	-	-	-	-	-	-	-	-	-
	CD	-	-	-	-	-	-	-	-	-	-	-	-	-
X-Protein														
XP	(N)	55	51	64	50	48	50	51	50	39	10	36	31	52
	X-1	6	8	20	8	7	3	6	9	11	3	10	8	36
	X 1-2	16	7	5	5	6	8	12	8	5	3	2	7	12
	X-2	27	31	34	34	29	33	31	26	23	3	20	13	4
	00	6	5	5	3	6	6	2	7	-	1	4	3	-

* S1 - HAMBANTOTA S2 - WEERAWILLA S3 - THAMBUTHEGAMA

Table 6. List of monomorphic loci investigated.

Loci / Plate No		Abbreviation	Approximate distance traveled from point of insertion (mm)
1. Acid phosphatase	(Plate 22)	Acp	20
2. Adenylate kinase	(Plate 23)	Ak	15
3. Biliverdin reductase	(Plate 24)	Blvr	22
4. 2-3, Diphosphoglyceromutase	(Plate 25)	Dpgm	12
5. Esterase-2	(Plate 26)	Est-2	20
6. Fructose-1,6-diphosphatase	(Plate 27)	Fdp	20
7. Fumarase	(Plate 28)	Fum	25
8. Fructokinase	(Plate 29)	Fk	12
9. Glucose dehydrogenase	(Plate 30)	Gldh	20
10. Glucose phosphate isomerase	(Plate 31)	Gpi	14
11. Glutamate oxaloacetate transaminase	(Plate 32)	Got	18
12. Glutamate pyruvate transaminase	(Plate 33)	Gpt	18
13. α - Glyceraldehhyde -3 - phosphate dehydrogenase	(Plate 34)	GPDH	20
14. Glutathione reductase	(Plate 35)	Gr	25
15. Hexokinase	(Plate 36)	Hk	20
16. Isocitrate dehydrogenase	(Plate 37)	Icd	32
17. Lactate dehydrogenase	(Plate 38)	Ldh	35
18. Mannose phosphate isomerase	(Plate 39)	Mpi	25
19. NADPH - Diaphorase 2	(Plate 40)	NADPH - Dia 2	15
20. Peptidase - A	(Plate 41)	Pep-A	30
21. Peptidase-B	(Plate 42)	Pep-B	45
22. Peptidase - C	(Plate 43)	Pep-C	35
23. Peptidase - D	(Palte 44)	Pep - D	15
24. Phosphoglucomutase-2	(Plate 45)	Pgm-2	20
25. 6-Phosphogluconate dehydrogenase	(Plate 46)	6Pgdh	25
26. Pyruvate kinase	(Plate 47)	Pk	20
27. Sorbitol dehydrogenase	(Plate 48)	Sordh	12
28. Superoxide dismutase	(Plate 49)	Sod	25

Table 7 . Numbers of animal assayed (N) and allele frequencies for 12 polymorphic loci

	Population												
Locus	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13
ALB													
(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
A	.927	.804	.782	.760	.760	.790	.667	.750	.615	.650	.905	.952	.894
B	.073	.196	.218	.240	.240	.210	.333	.250	.385	.350	.095	.048	.106
AMY													
(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
H	.409	.520	.394	.320	.427	.380	.333	.420	.397	.500	.378	.435	.558
L	.591	.480	.606	.680	.573	.620	.667	.580	.603	.500	.622	.565	.442
AP													
(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
F	.464	.422	.289	.470	.250	.310	.255	.450	.526	.450	.514	.435	.462
00	.536	.578	.711	.530	.750	.690	.745	.550	.474	.550	.486	.565	.538
CA													
(N)	53	50	64	46	46	50	53	45	39	10	36	31	46
102	.000	.000	.000	.000	.000	.000	.000	.000	.000	.100	.028	.000	.000
100	.887	.920	.977	.533	.533	.880	.849	.849	.974	.974	.944	.935	.978
98	.113	.080	.023	.467	.467	.120	.151	.151	.026	.026	.028	.065	.022
HB													
(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
A	.891	.872	.923	.960	.812	.900	.824	.840	.897	.150	.278	.113	.231
B	.045	.059	.000	.040	.188	.100	.176	.160	.103	.850	.722	.887	.769
X	.064	.069	.077	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
ME													
(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
104	.00	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.038
102	.118	.186	.186	.130	.167	.080	.186	.190	.141	.350	.112	.112	.490
100	.882	.745	.745	.790	.698	.750	.726	.680	.744	.350	.569	.569	.443
98	.000	.069	.069	.080	.135	.170	.088	.130	.115	.300	.319	.319	.029

(Contd.)

Table 7 . Numbers of animal assayed (N) and allele frequencies for 12 polymorphic loci

	Population												
Locus	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13
MDH													
(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
100	.755	.647	.732	.790	.656	.797	.735	.720	.526	.450	.542	.903	.827
98	.245	.353	.268	.268	.344	.230	.265	.280	.474	.550	.458	.097	.173
NP													
(N)	55	51	71	50	48	50	51	50	39	10	36	31	52
H	.364	.480	.528	.530	.385	.550	.333	.430	.500	.450	.500	.565	.288
L	.636	.520	.472	.470	.615	.450	.667	.570	.500	.550	.500	.435	.712
DIA1													
(N)	55	51	70	50	48	50	49	50	39	10	36	31	52
102	.000	.000	.000	.000	.000	.000	.071	.000	.000	.000	.000	.000	.000
100	1.000	.941	.871	1.000	1.000	1.000	.684	.870	.846	1.000	1.000	1.000	1.000
98	.000	.059	.129	.000	.000	.000	.245	.130	.154	.000	.000	.000	.000
DIA2													
(N)	55	49	62	50	48	50	49	50	37	8	35	31	52
102	.018	.224	.298	.280	.135	.100	.224	.170	.122	.000	.029	.484	.721
100	.973	.776	.776	.720	.865	.900	.776	.830	.757	1.000	.800	.516	.279
98	.009	.000	.000	.000	.000	.000	.000	.000	.122	.000	.171	.000	.000
TF													
(N)	55	51	71	50	48	50	51	50	39	11	36	31	52
A	.446	.765	.556	.680	.604	.750	.618	.610	.610	1.000	1.000	.952	.808
B	.509	.235	.423	.290	.323	.230	.343	.370	.370	.000	.000	.048	.192
C	.018	.000	.014	.030	.042	.010	.039	.020	.020	.000	.000	.000	.000
D	.027	.000	.007	.000	.031	.010	.000	.000	.000	.000	.000	.000	.000
XP													
(N)	55	51	64	50	48	50	51	50	39	10	36	31	52
1	.218	.206	.343	.200	.188	.120	.196	.200	.346	.400	.306	.258	.808
2	.527	.618	.563	.710	.594	.560	.618	.470	.654	.400	.569	.371	.192
00	.255	.176	.094	.090	.218	.320	.186	.330	.000	.200	.125	.371	.000

The gene frequency of Alb^{A} allele ranged from 0.615 (Hat Yai) to 0.952 (Thambuthegama) as shown in Table 7. The zymogram of the gel is shown in Plate 10 and the schematic representation of the electrophoretic banding patterns in Figure 4.

To further support the genetic hypothesis of two codominant alleles, the inheritance of Alb phenotypes was observed in the available 24 families as shown in Table 8. The distribution of the genotypes among the offspring is sufficient to support the genetic interpretation for the albumin phenotypes.

4.2.2. Amylase

Using cellulose acetate electrophoresis, two phenotypes of Amy were found : Amy H and Amy L, their genetic control being to two autosomal alleles, Amy^{H} and Amy^{L}, with dominance of Amy H. The zymogram of the gel is shown in Plate 11 and the schematic representation of the electrophoretic banding patterns in Figure 5.

The study did not reveal much differences existing in the overall gene frequency data for the locus, but there is a tendency for the allele Amy^{L} (>0.50) to predominate in most of the goat populations except in Sabah (0.48) and New South Wales (0.44) as shown in Table 7.

Family studies have supported the interpretations of genetic control being due to two autosomal alleles as shown in Table 9.

Plate 10. Zymogram of Albumins.

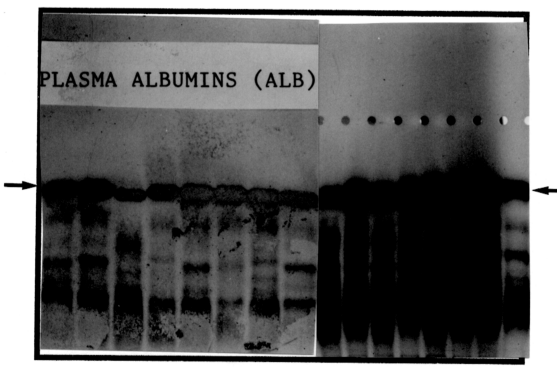


Plate 11. Zymogram of Amylase.

From Left to Right

Amylase phenotypes : L H H L H L H H

Figure 4. Schematic representation of albumin.

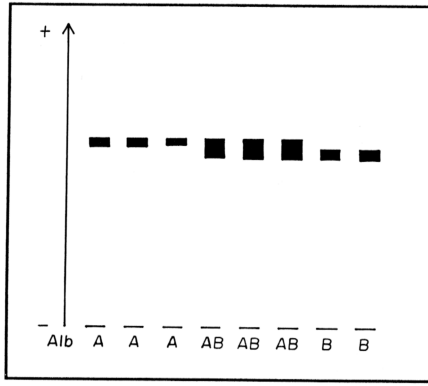


Figure 5. Schematic representation of amylase.

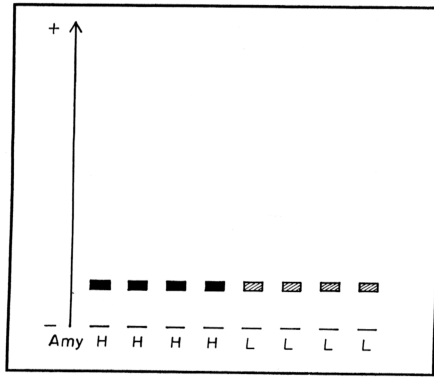


Table 8. Distribution of Albumin phenotypes among offspring

Mating Types	No. of Matings	Progeny Type A	AB	B
A X A	16	23	0	0
A X AB	8	8	4	0

Table 9. Distribution of Amylase phenotypes among offspring

Mating Types	No. of Matings	Progeny Type H	L
H x H	12	17	1
H x L	9	7	4
L x L	2	0	3

4.2.3. Alkaline phosphatase

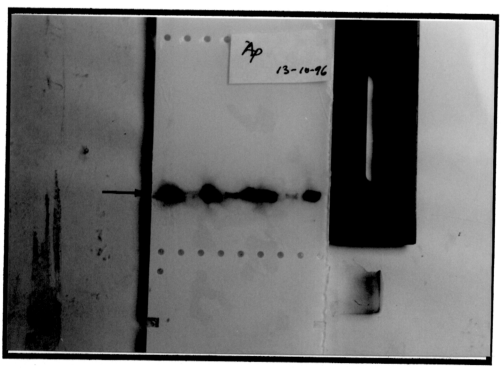
Two phenotypes of Alp were found: Alp F and Alp O, their genetic control being due to two autosomal alleles , Alp^F and Alp^O, with the dominance of Alp^F. To further support the genetic hypothesis of the two autosomal alleles Alp^F and Alp^O, a family study supports the hypothesis as shown in Table 10. The zymogram for the locus is shown in Plate 12 and the schematic representation of the electrophoretic banding patterns in Figure 6. The Alp^O allele seems to predominate (>0.53) but in Hat Yai and Weerawilla goat populations, the frequency was lower (<0.49) as shown in Table 7.

4.2.4. Carbonic anhydrase

The electrophoretic patterns observed is shown diagrammatically in Figure 7 and Plate 13. Five phenotypes were observed in red cell carbonic anhydrase. The three commonest phenotypes observed Ca 100/100, Ca 100/98 and Ca 98/98 have been identified in almost all the populations and the rarest phenotypes were Ca 102/102 and Ca 102/100. They are attributed to the three common alleles : Ca^{102}, Ca^{100} and Ca^{98} in homozygous and heterozygous combinations. The family study also supports the genetic control by one autosomal locus with two codominant alleles as shown in Table 11.

There is a significant difference noted at the Ca locus, the Ca^{100} allele appeared generally in high frequency for all the populations (>0.80), but in Bogor, Ujung Pandang and Hambantota goat populations, the frequency was 0.53, 0.53 and 0.55 respectively (Table 7). The Ca^{102} allele was only observed for the first time in two of the populations in Sri Lanka, i.e. Hambantota and Weerawilla in Sri Lanka.

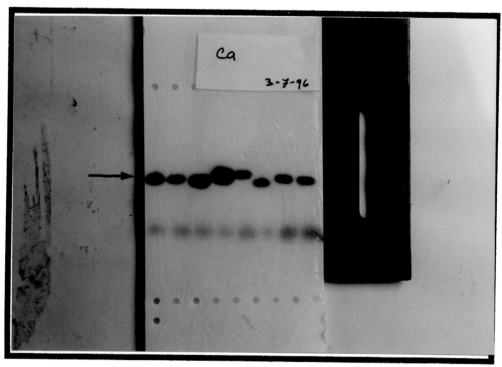
Plate 12. Zymogram of Alkaline Phosphatase



From Left to Right

Alkaline Phosphatase phenotypes: **H L H L H H L H**

Plate 13. Zymogram of Carbonic Anhydrase.



From Left to Right

Carbonic anhydrase phenotypes : **100 100 100/98 102/100 102 98 100 100**

Figure 6. Schematic representation of alkaline phosphatase.

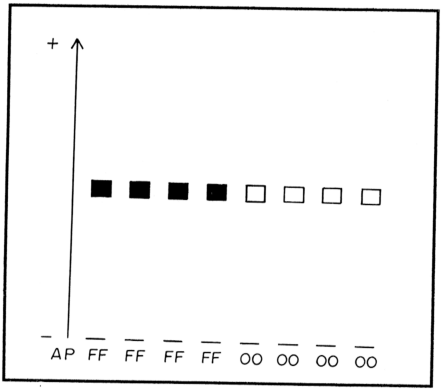


Figure 7. Schematic representation of carbonic anhydrase.

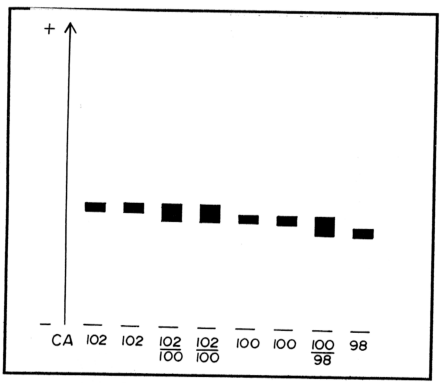


Table 10. Distribution of Alkaline phosphatase phenotypes among offspring.

Mating Types	No. of Matings	Progeny Type F	O
F x F	6	7	0
F x O	3	4	2
O x O	2	0	3

Table 11. Distribution of Carbonic anhydrase phenotypes among offspring.

Mating Types	**No. of Matings**	**Progeny Type**		
		100	**100/98**	**98**
100 x 100	24	30	0	0
100 x 100	4	2	3	0
98 x 98	1	0	0	1

4.2.5. Haemoglobin

Four phenotypes were observed in the haemoglobin gels: Hb AA, Hb AB, Hb BB and Hb AAx. The nomenclature used in this study is as designated by Huisman (1970) and Hasima (1986). The three common phenotypes of the Hb AA, AB and BB are controlled by two codominant autosomal alleles: Hb^{A} and Hb^{B} (Huisman, 1970). The zymogram of gel is shown in Plate 14 and the schematic representation of the electrophoretic banding patterns is shown in Figure 8.

The mode of inheritance of hemoglobin was established from the available 17 families of different mating types combinations (Table 12). The results confirmed presence of two codominant autosomal alleles: Hb^{A} and Hb^{B} as reported earlier by Huisman (1970).

The frequency of Hb^{A} allele was presumably very high in all the Southeast Asian goats populations (>0.80) but for Hambantota, Weerawilla, Thambuthegama and New South Wales, the frequency of allele Hb^{B} was much higher (>0.70) than the allele Hb^{A}. The existence of Hb^{X} allele was only observed in the Malaysian goat population but was present in a low frequency as shown in Table 7.

4.2.6. Malic enzyme

Eight phenotypes were observed in the present study. The five common phenotypes Me 102/102, Me 102/100, Me 100/100, Me 100/98 and Me 98/98 have been identified in almost all goat populations. They are attributed to three common alleles, Me^{102}, Me^{100} and Me^{98} in homozygous and heterozygous combinations. The phenotype Me 104/104 was only detected in 2 individuals of the New South Wales goat populations

and hence the rarest allele is *Me* ^{104}. The zymogram of the gel and schematic representation of the banding patterns are shown in Plate 15 and Figure 9 respectively.

The family sample were analysed in an attempt to study the mode of inheritance of malic enzymes phenotypes. Results from the 25 available mating pairs (Table 13) showed that the observed phenotypes of the offspring were consistent with the hypothesis that Me phenotypes observed are coded for by an autosomal locus with three codominant alleles.

Allele *Me* ^{100} seems to be the most commonest allele in all the goat populations (frequency > 0.50) but in New South Wales goat population Me ^{102} was known to be higher than allele *Me* ^{100}.

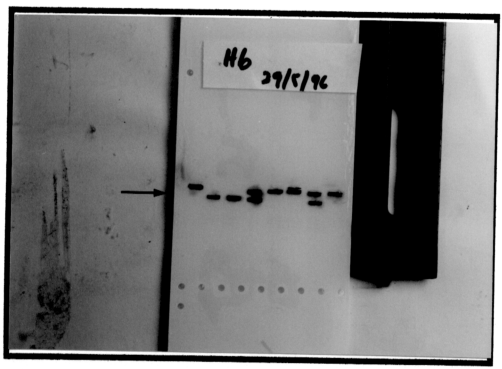
4.2.7. Malate dehydrogenase

Genetic variants for malate dehydrogenase for the goats have not been reported earlier. In this study, it was observed that there are three distinct phenotypes. The two homozygous types, the faster Mdh 100/100 and the slower Mdh 98/98 showed a major band and a minor band each. The heterozygous phenotype Mdh 100/98 had three bands of which the middle band is most intense. The zymogram of the gel and the schematic representation of the banding patterns is shown in Plate 16 and Figure 10 respectively.

Family studies were done for this system and the distribution of the progeny phenotypes in Table 14 was very close to the Mendelian expectations, assuming that codominant alleles were involved. Hence, the Mdh phenotypes were controlled by two autosomal alleles *Mdh* ^{100} and *Mdh* ^{98}.

Allele Mdh 100 seems to be the most commonest allele among the populations, frequency ranging from 0.450 (Hambantota) to 0.903 (Thambuthegama) as shown in Table 7.

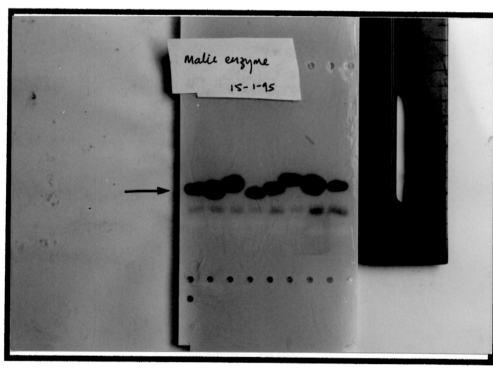
Plate 14. Zymogram of Haemogobin.



From Left to Right

Haemoglobin phenotypes : **A B B AB A AX AB A**

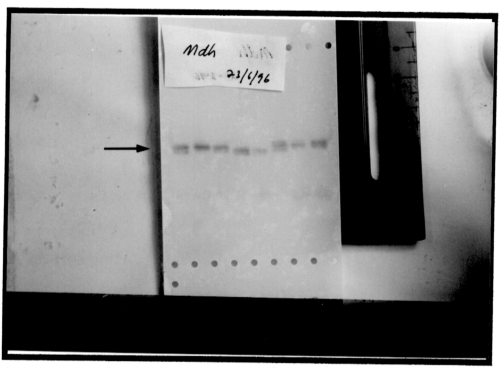
Plate 15. Zymogram of Malic Enzyme.



From Left to Right

Malic enzyme phenotypes : **100 100/98 102 98 100 104 102/100 100**

Plate 16. Zymogram of Malate Dehydrogenase.



From Left to Right

Malate dehydrogenase phenotypes : 100/98 100 100 98 98 100/98 100 100

Figure 8. Schematic representation of haemoglobin.

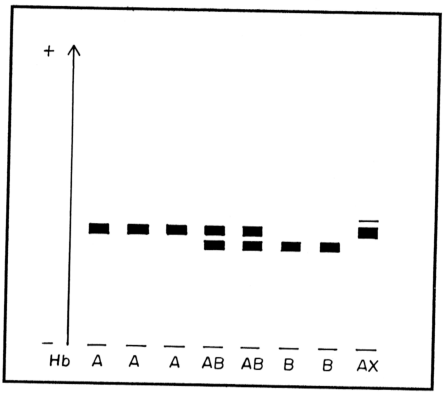


Figure 9. Schematic representation of malic enzyme.

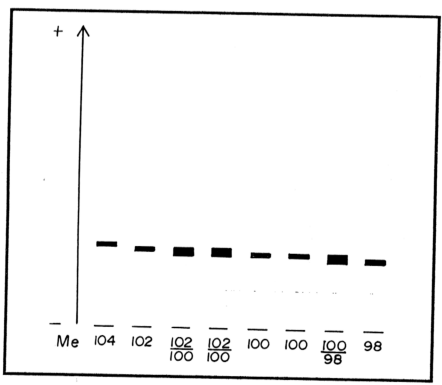


Table 12. Distribution of Haemoglobin phenotypes among offspring

Mating Types	No. of Matings	Progeny Type		
		A	AB	B
A x A	10	12	0	0
A x AB	3	2	1	0
AB x AB	2	2	1	0
B x B	2	0	0	2

Table 13. Distributions of Malic enzyme phenotypes among offspring

Mating Types	No of Mating	Progeny Types				
		102	102/100	100	100/98	98
102 x 102	1	2	0	0	0	0
102 x 100	4	0	5	0	0	0
100 x 100	9	0	0	15	0	0
98 x 98	1	0	0	0	0	1
102/100 x 100	8	0	5	7	0	0
102/100 x 102/100	2	0	2	1	0	0

Table 14. Distribution of Malate dehydrogenase phenotypes among offspring

Mating Types	No. of Matings	Progeny Type		
		100	100/98	98
100 x 100	16	25	0	0
100 x 98	4	0	4	0
100/98 x 100	1	0	1	0
100/98 x 98	4	0	3	1

4.2.8. Purine Nucleoside Phosphorylase

With the available family sample size of 20, two phenotypes of Np with same electrophoretic mobility were found: Np H (strongly stained band) and Np L (weakly stained band). To further support the hypothesis, a simple spectrophotometric assay has been done as a measure of correlation between the high intensities of the bands with high enzyme activities (Sekaran *et al.*, 1989). Weakly stained bands on gels showed low enzyme activities when measured spectrophotometrically as in Table 15. Family studies (Table 16) support the hypothesis that the variation noticed is due to two allomorphic genes, one specifying high activity (Np^{H}) and the other low activity (Np^{L}). The zymogram and the schematic representation of the banding is shown in Plate 17 and Figure 11.

Not much of difference exist in the overall gene frequency between population but the study shows there is a tendency for the Np^{L} allele to predominate except in Sarawak. Bogor, Medan and Thambuthegama goat populations (frequency < 0.50). Differences among populations were greater with allele Np^{L} ranging from 0.435 to 0.712 as shown in Table 7.

Plate 17. Zymogram of Purine Nucleoside Phosphorylase.

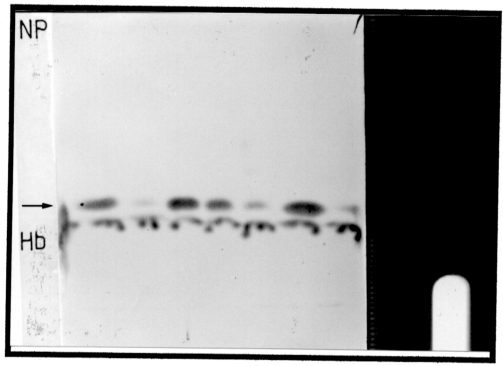


Figure 10. Schematic representation of malate dehydrogenase.

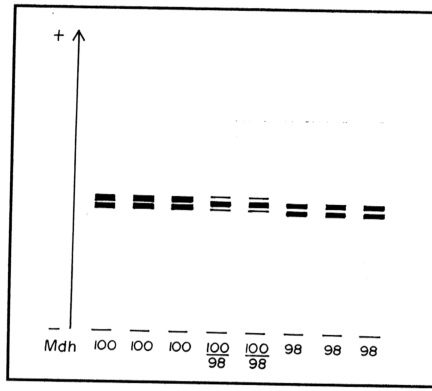


Figure 11. Schematic representation of nucleoside phosphorylase.

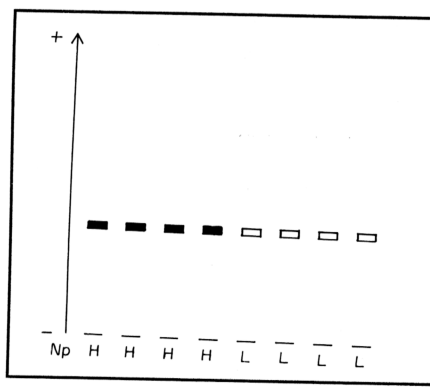


Table 15. Spectrophotometric assay of Nucleoside phosphorylase activity

Electrophotometric score	No of samples used	Activity (umol/min/g haemoglobin)
H	15	0.04 - 0.06
L	15	0.002 - 0.004

Table 16. Distribution of Nucleoside phosphorylase phenotypes among offspring.

Mating types	No of Matings	Progeny Type H	L
H x H	10	15	0
H x L	8	8	4
L x L	2	0	3

4.2.9. NADH Diaphorase 1

Band patterns are demonstrated in two different zones i.e. NADH-Dia 1-zone 1 (will be known as NADH Dia-1) and NADH-Dia 1-zone 2 (will be known as NADH-Dia 2). Both these loci have been examined extensively for the first time. The notation used for naming the allele were suggested in the earlier chapter on methods.

4.2.9.1. NADH-Dia 1-zone 1 (Dia-1):

The most common phenotype is designated NADH-Dia -1 100/100, while the faster one was called NADH-Dia 1 102/102 and the slower one designated as NADH-Dia -1 98/98. The heterozygotes observed were designated as NADH-Dia-1 102/100 and NADH-Dia -1 100/98. Hence, they are attributed to three common alleles *Dia-1* ^{102}, *Dia-1*^{100} and *Dia-1* ^{98}, in homozygous and heterozygous combinations. The zymogram and the schematic representation of the banding patterns is shown in Plate 18 and Figure 12 respectively.

In family studies (Table 17) it was observed that no progeny possessed any NADH-Dia-1 variants unless possessed by either or both the parents. The distribution of progeny phenotypes was very close to the Mendelian distribution, assuming that codominant alleles were involved. It is, therefore, concluded that the NADH-Dia-1 type is controlled by codominant alleles.

No variation was observed for the locus in the MARDI/IPSR, Bogor, Ujung Pandang, Medan, Hambantota, Weerawilla, Thambuthegama and New South Wales goat populations but the locus was polymorphic in other populations. Allele *Dia-1*^{100} was the most commonest allele with frequency ranging from 0.684 to 1.0 and allele *Dia -1* ^{102} and *Dia-1* ^{98} detected infrequently.

4.2.9.2. NADH-Diaphorase 1 zone 2 (Dia-2):

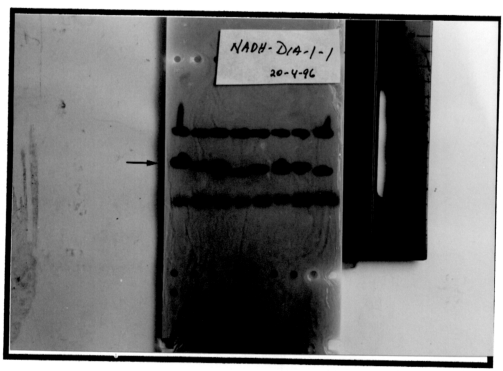
Similarly, the most common phenotype is designated as NADH-Dia-2 100/100, whereby the faster one designated as NADH-Dia-2 102/102 and the slower one designated as NADH-Dia-2 98/98. The heterozygotes observed were designated as NADH-Dia-2 102/100 and NADH-Dia-2 100/98.

Hence, they are attributed to three common alleles *Dia-2* ^{102}, *Dia-2*^{100} and *Dia-2*^{98} in homozygous and heterozygous combinations. The zymogram and the schematic representation of the banding patterns is shown in Plate 19 and Figure 13 respectively.

To further support the hypothesis that the loci is controlled by codominant alleles, a family study is done from the available 23 families. The distribution of the progeny phenotypes in Table 18 was very close to the Mendelian distribution assuming that codominant alleles were involved. The phenotypic distribution rules out any sex linkage for red cell NADH-Diaphorase because heterozygous genotypes were present in both sexes, thus the autosomal locus was controlled by two codominant alleles. It was also observed from the matings that there was a chance deviation for the mating types between *Dia-2 100/100 x Dia-2 102/100* which produced more heterozygotes than homozygotes. This could be probabbly due to phenotypic disassortative mating which acts opposite to assortative mating in that it tends to maintain heterozygosity.

The existence of *Dia-2* ^{100} allele was observed significantly in high frequency ranging from 0.516 (Thambuthegama) to 0.973 (MARDI/IPSR). Differences among populations were greater for this allele. In the New South Wales goat population, allele *Dia -2* ^{102} was higher with gene frequency of 0.721.

Plate 18. Zymogram of NADH - Diaphorase 1 zone 1.



From Left to Right
(lower zone)

NADH-Dia 1 zone 1 phenotypes : **102 100 100/98 98 100 102/100 102 100**

Plate 19. Zymogram of NADH - Diaphorase 1 zone 2.

From Left to Right
(upper zone)

NADH-Dia 1 zone 2 phenotypes : **102 100 100 102/100 98 100/98 100 102**

Figure12. Schematic representation of NADH-Diaphorase 1 zone 1.

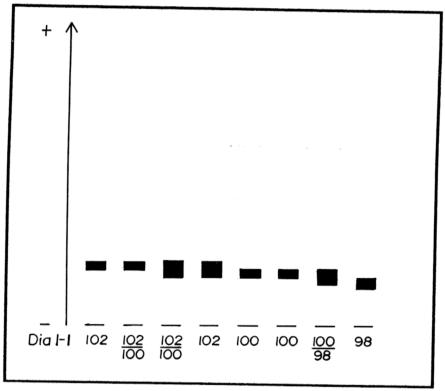


Figure 13 . Schematic representation of NADH-Diaphorase 1 zone 2.

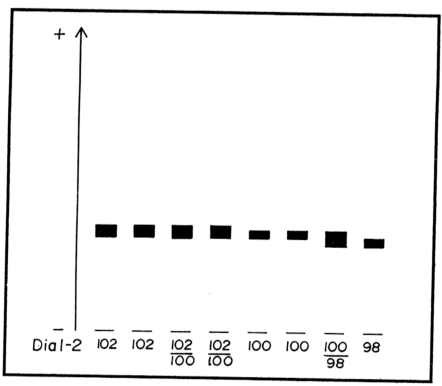


Table 17. Distribution of NADH-Dia -1 phenotypes among offspring.

Mating Types	No of Matings	Progeny Type		
		100	100/98	98
100 x 100	21	31	0	0
100 x 100/98	1	1	1	0

Table 18. Distribution of NADH -Dia -2 phenotypes among offspring

Mating Types	No of Matings	Progeny Type		
		102	102/100	100
100 x 100	9	0	0	12
100 x 102/100	8	0	8	1
102 x 102/100	3	2	0	2
102/100 x 102/100	2	0	2	2
102 x 102	1	2	0	0

4.2.10. Transferrin

Eight phenotypes were observed in the present study: Tf AA, Tf AB, Tf AC, Tf AD, Tf BB, Tf BC, Tf BD and Tf CD. From the available family data as shown in Table 19, it could be demonstrated that the three common phenotypes observed Tf AA, Tf AB and Tf BB are genetically controlled by two codominant alleles Tf^A and Tf^B. Studies by Osterhoff and Ward-Cox (1970) Watanabe and Suzuki (1973) and Shotake *et al.*, (1986) have indicated the presence of four transferrin alleles (Tf^A, Tf^B, Tf^C and Tf^D) in different goat breeds of the world.

In the present study, it could be established at the moment that the Tf locus is genetically controlled by four codominant alleles (Tf^A, Tf^B, Tf^C and Tf^D). Three of the alleles Tf^A, Tf^B *and* Tf^C were earlier detected in the goat populations of Southeast Asia. The Tf^D allele is reported for the first time in this region but it is found in a low frequency in populations of MARDI/IPSR (0.27), Sarawak (0.007), Bogor (0.031) and Medan (0.10).

Transferrin allele Tf^A was the most commonest in all populations (frequency > 0.55) except for MARDI/IPSR in which the frequency of allele Tf^B was higher (frequency > 0.509). In two of the Sri Lankan goat populations i.e. at Hambantota and Weerawilla, no variation was detected for the locus.

Differences among populations for the gene frequency were greater for allele Tf^A (0.445 to 1.0) as shown in Table 7. The zymogram of the gel and schematic representation of the banding patterns is illustrated in Plate 20 and Figure 14 respectively.

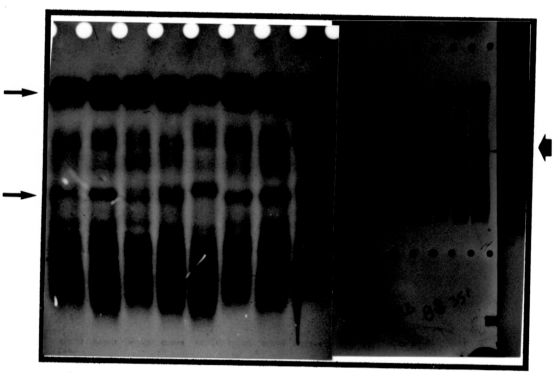
4.2.11. X-Protein

Tucker and Clarke (1980) suggested polymorphisms of an unidentified red cell protein in goats analogous to sheep "X" protein. This polymorphism was later confirmed by Tucker *et al.*, (1983) and Hasima *et al.*,(1986) by starch gel electrophoresis.

In the present study four phenotypes were observed Xp-1-1, Xp 1-2, Xp-2-2 and Xp OO. With limited family data from available 10 families as shown in Table 20, it tends to confirm that the locus is controlled by two codominant alleles. Since the effects of Xp^1 and Xp^2 alleles are both expressed in the heterozygotes, they must be codominant and that of Xp^O is recessive, gene frequencies were calculated using the formula for genotype frequencies established for ABO blood group system (Gardner and Snustad, 1981). The zymogram of the gel and the schematic representation of banding patterns is shown in Plate 21 and Figure 15 respectively.

The frequency of allele Xp^2 seems to be high in all the populations (frequency > 0.50) but in the New South Wales goats population the allele Xp^1 was observed to be higher (0.808) as shown in Table 7. The presence of the null alleles was detected infrequently in low frequency among the populations

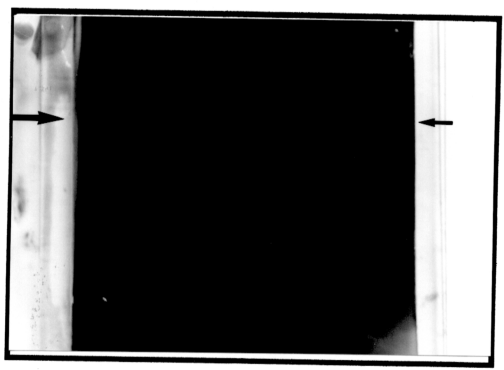
Plate 20. Zymogram of Transferrin.



From Left to Right

Transferrin phenotypes: AC AB A B A A AD A AB B AB A B B AD AD

Plate 21. Zymogram of X-Protein.



From Left to Right

X-protein phenotypes : 00 X-1 00 X1-2 X-1 X-1 00 X1-2 00 X-1 X-1 X-2 X-1

Figure 14. Schematic representation of transferrin.

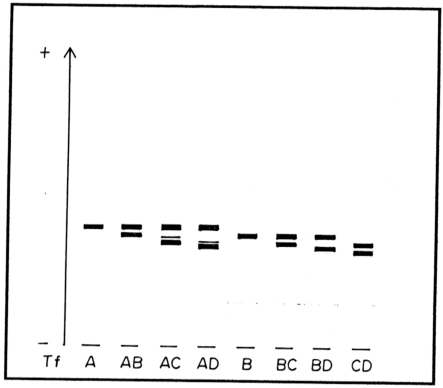


Figure 15. Schematic representation of X-Protein.

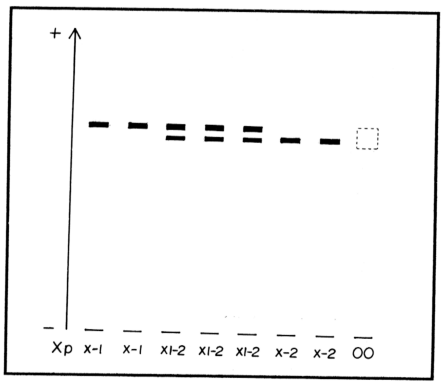


Table 19. Distribution of Transferrin phenotypes among offspring

Mating Types	No of Matings	Progeny Type A	AB	B
A x A	2	4	0	0
A x AB	6	3	4	0
B x AB	3	0	4	1
A x B	1	0	1	0
AB x AB	16	10	11	1

Table 20. Distributions of X-protein phenotypes among offspring.

Mating Types	No of Matings	Progeny Type 1	1-2	2	00
1 x 1	4	5	0	0	1
1 x 1-2	5	3	6	0	0
1 x 2	1	0	1	0	0

Plate 22. Zymogram of Acid Phosphatase.

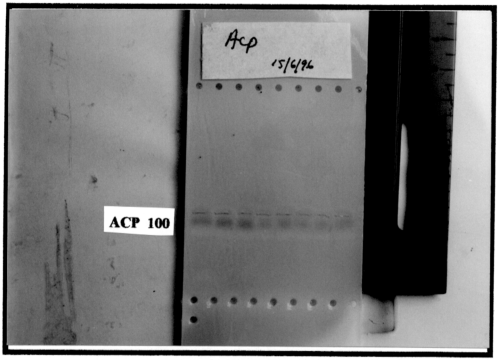


Plate 23. Zymogram of Adenylate Kinase.

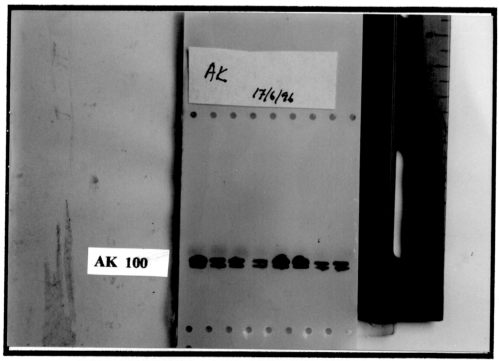


Plate 24. Zymogram of Biliverdin Reductase.

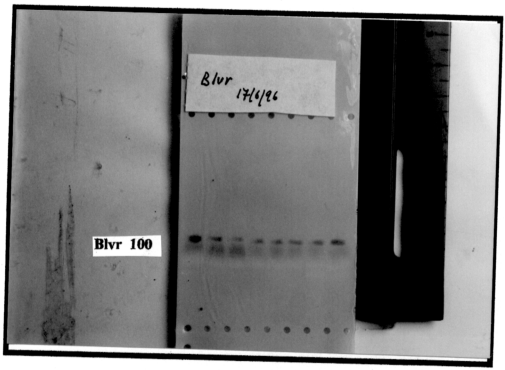


Plate 25. Zymogram of 2-3,Diphosphoglyceromutase.

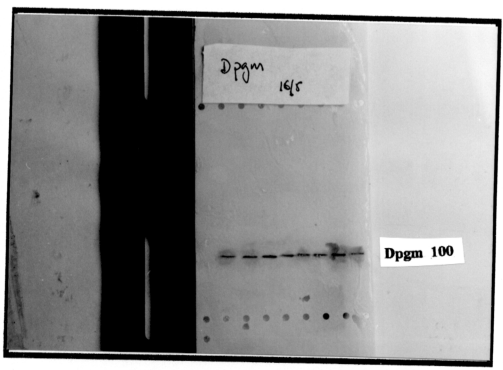


Plate 26. Zymogram of Esterase-2.

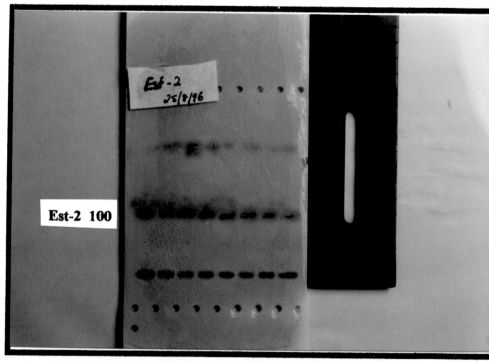


Plate 27. Zymogram of Fructose 1,6-diphosphatase.

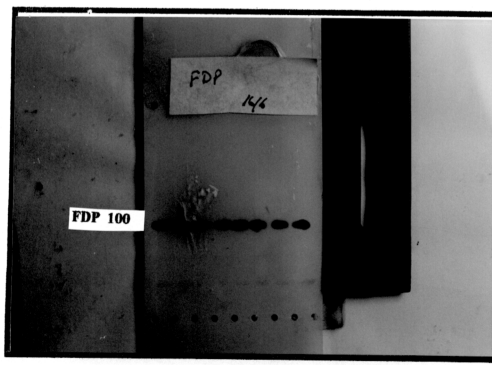


Plate 28. Zymogram of Fumarase.

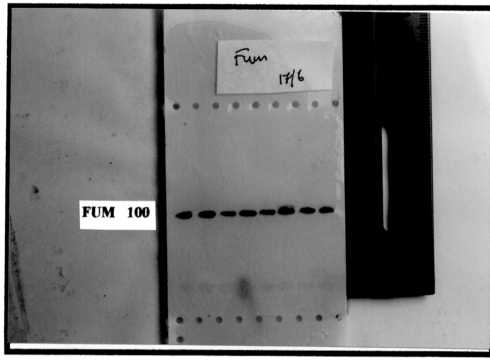


Plate 29. Zymogram of Fructokinase.

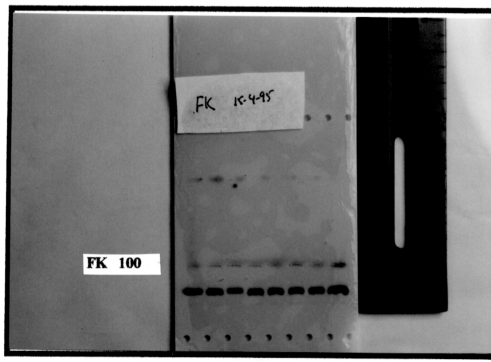


Plate 30. Zymogram of Glucose dehydrogenase.

Plate 31. Zymogram of Glucose Phosphate Isomerase.

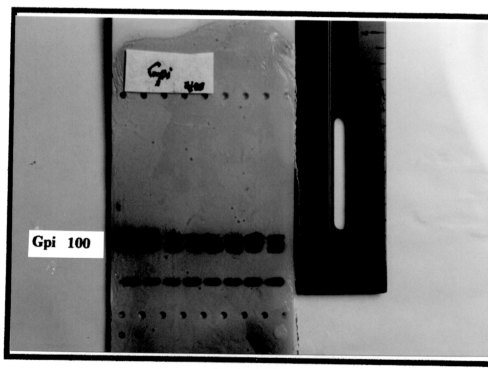


Plate 32. Zymogram of Glutamate Oxaloacetate Transaminase.

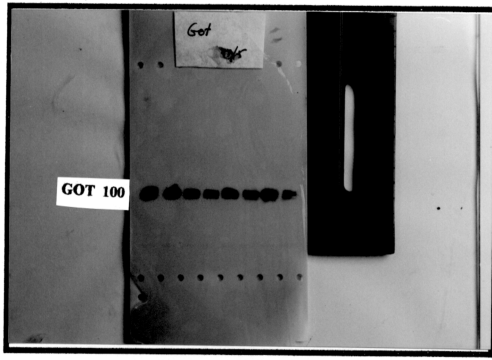


Plate 33. Zymogram of Glutamate Pyruvate Transaminase.

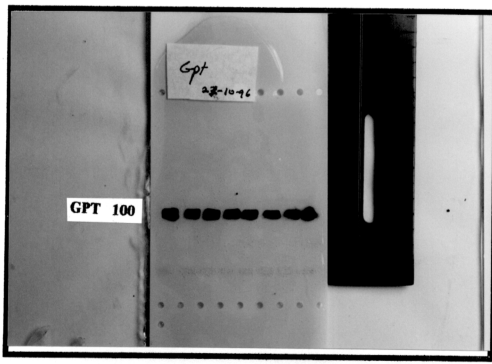


Plate 34. Zymogram of α -Glyceraldehyde-3-Phosphate Dehydrogenase

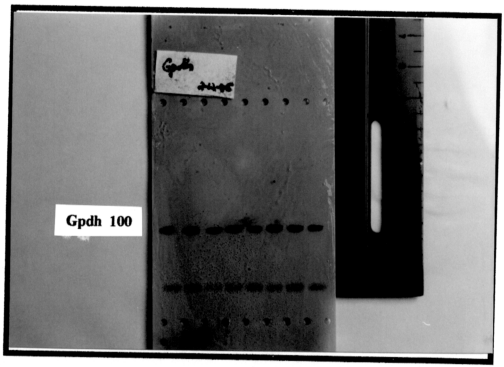


Plate 35. Zymogram of Glutathione Reductase.

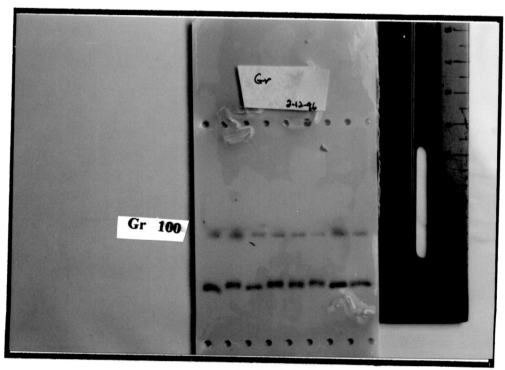


Plate 38. Zymogram of Lactate Dehydrogenase.

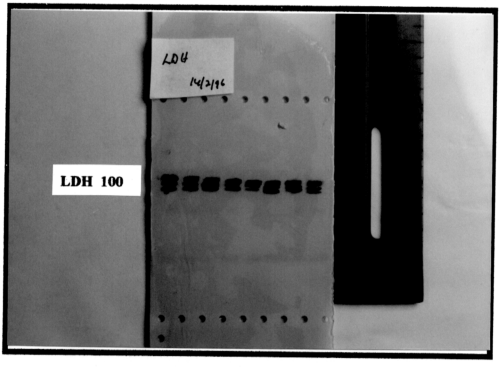


Plate 39. Zymogram of Mannose Phosphate Isomerase.

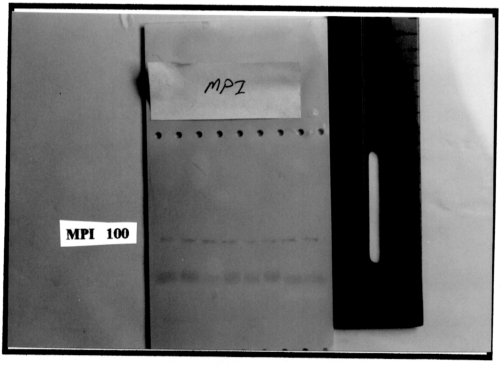


Plate 40. Zymogram of NADPH - Diaphorase 2.

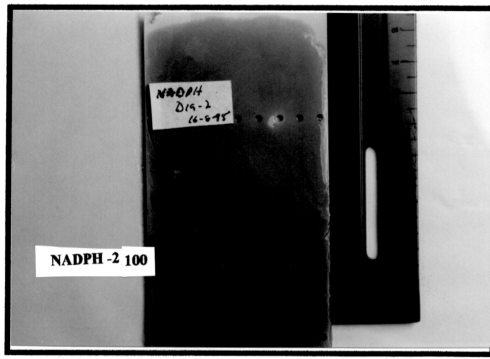


Plate 41. Zymogram of Peptidase - A.

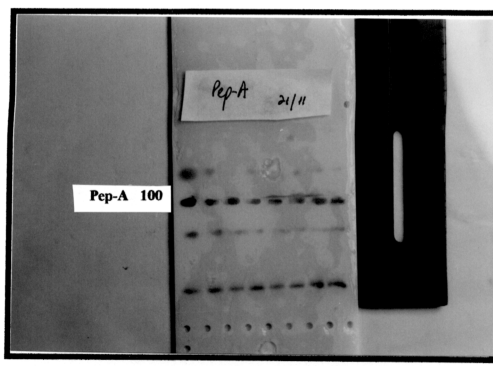


Plate 42. Zymogram of Peptidase - B.

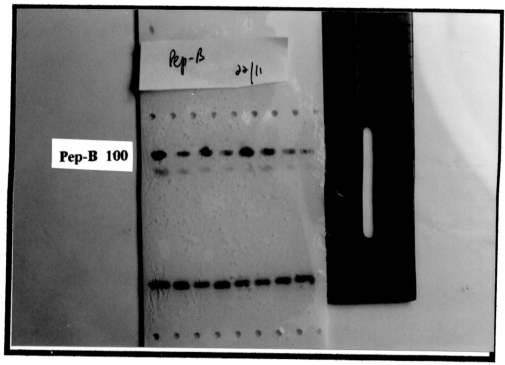


Plate 43. Zymogram of Peptidase - C.

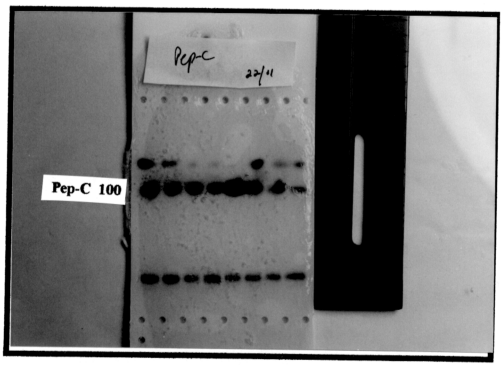


Plate 44. Zymogram of Peptidase - D.

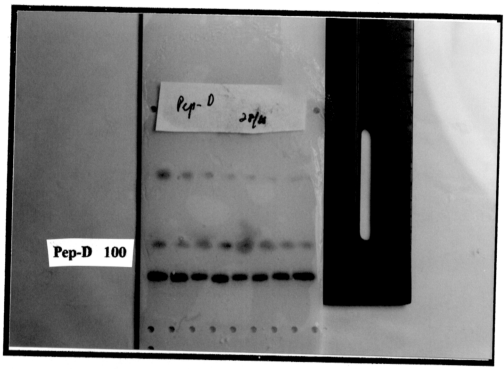


Plate 45. Zymogram of Phosphoglucomutase - 2.

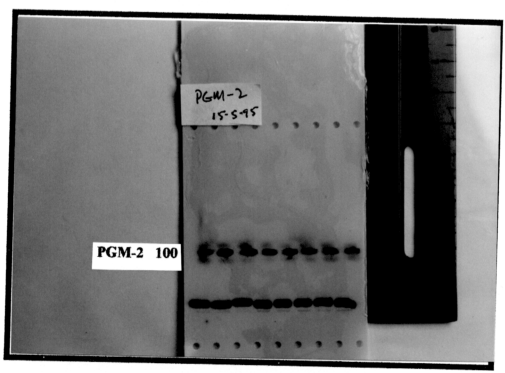


Plate 46. Zymogram of 6-Phosphogluconate Dehydrogenase.

Plate 47. Zymogram of Pyruvate Kinase.

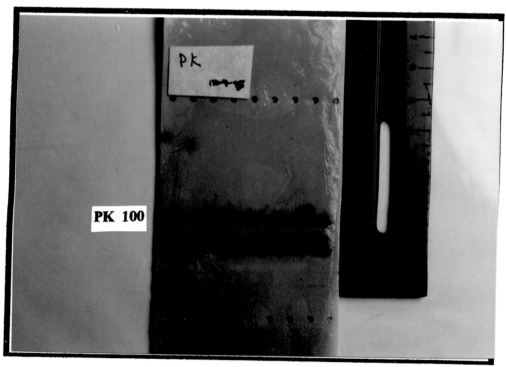


Plate 48. Zymogram of Sorbitol Dehydrogenase.

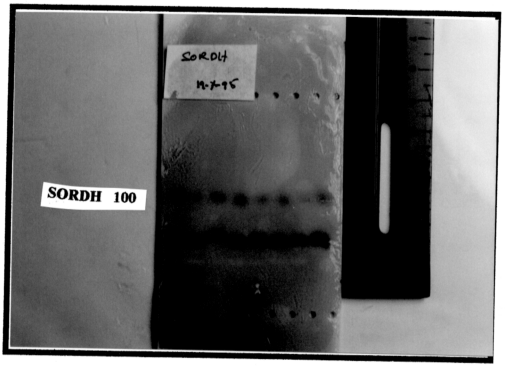


Plate 49. Zymogram of Superoxide Dismutase.

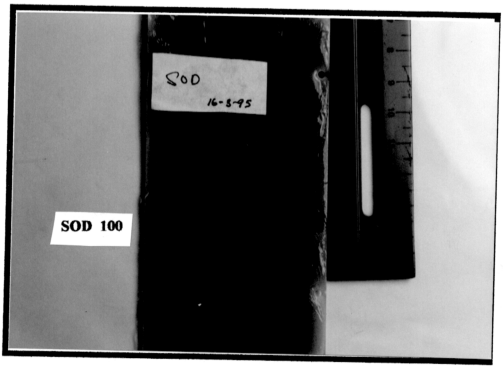
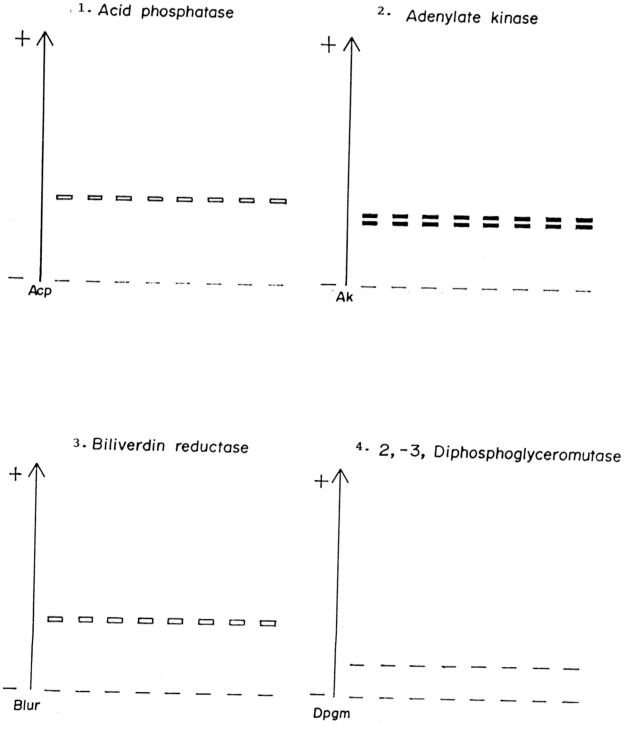
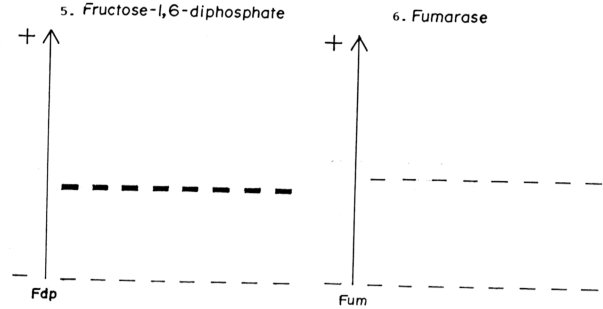
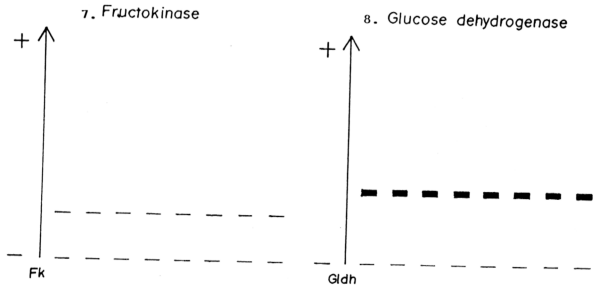


Figure 16. Schematic representations of the monomorphic loci.

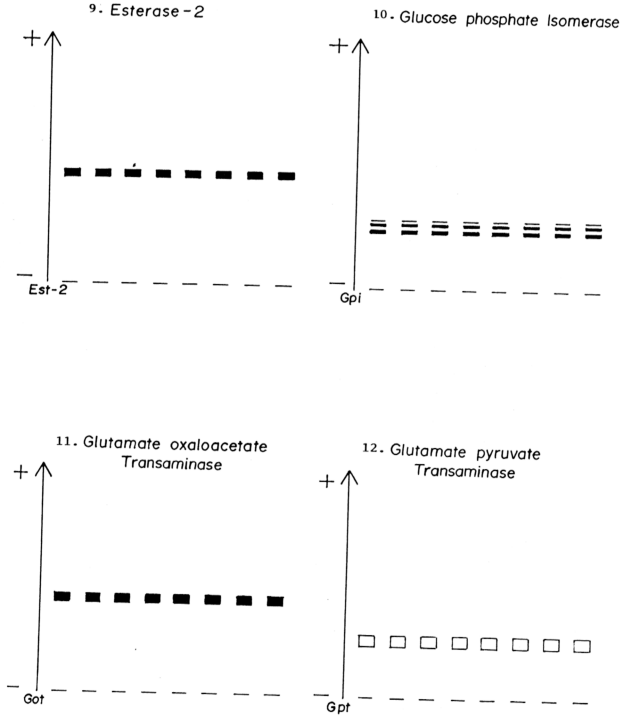


Cont'd Figure 16. Schematic representations of the monomorphic loci.

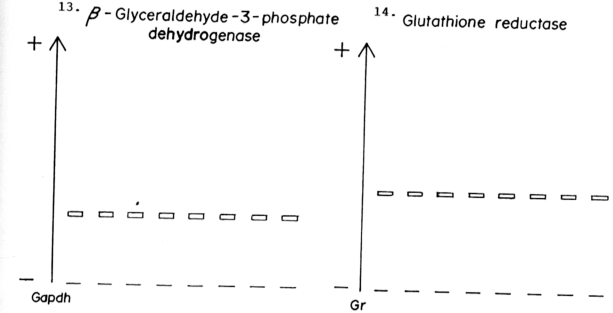


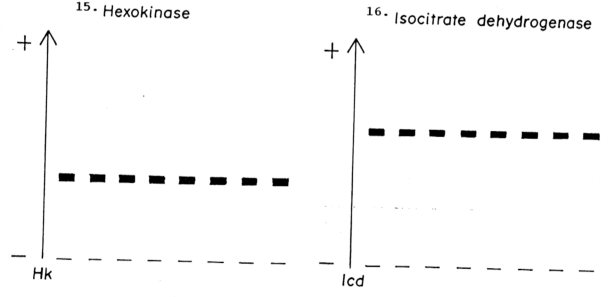


Cont'd Figure 16. Schematic representations of the monomorphic loci.

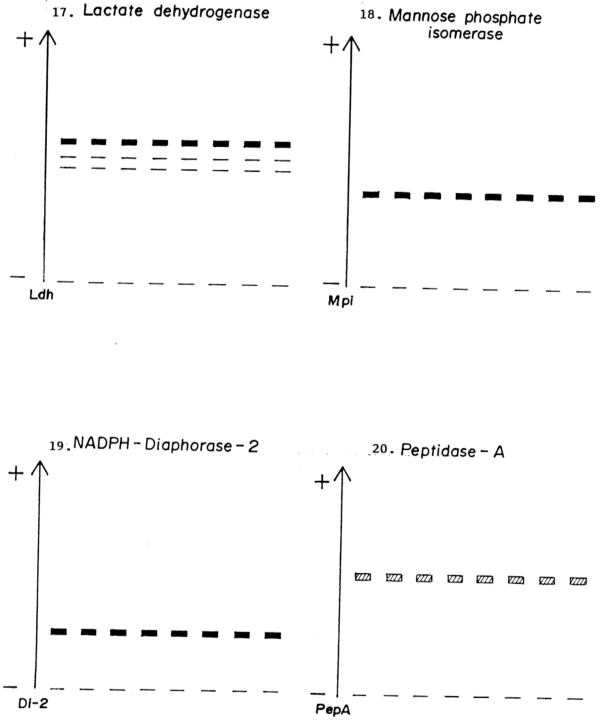


Cont'd Figure 16. Schematic representations of the monomorphic loci.

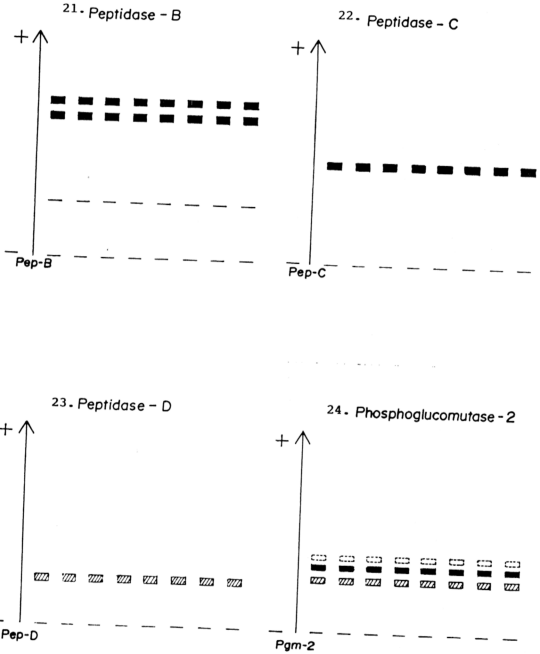




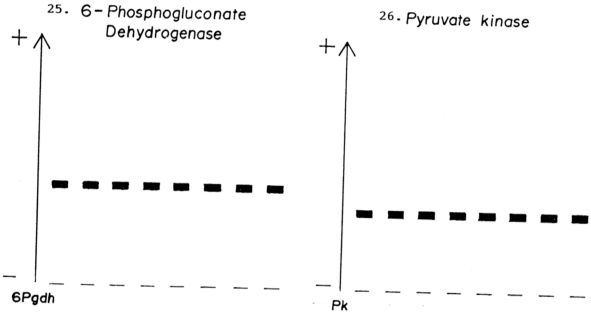
Cont'd Figure 16. Schematic representations of the monomorphic loci.

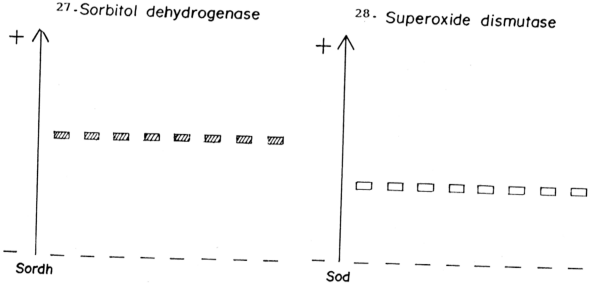


Cont'd. Figure 16. Schematic representations of the monomorphic loci.



Cont'd Figure 16. Schematic representations of the monomorphic loci.





4.3. Null and Rare Alleles

In the present study several null and rare alleles were found to be present in certain populations (Table 21). In the case of null alleles only two types were observed i.e. null alleles of alkaline phosphatase (Ap^{oo}) and X-Protein (Xp^{O}). Null alleles for alkaline phosphatase were present in all the populations and it's frequency ranged from 0.474 to 0.750 (Hat Yai - Ujung Pandang). The proportion of null alleles for each population ranged from 8% to 56.25% (Bogor- Ujung Pandang).

In the case of null allele of X-protein , only two populations indicated the absence of this allele i.e. Hat Yai and New South Wales. In rest of the populations the frequencies ranged from 0.090 to 0.371 (Bogor - Thambuthegama).The proportion of null alleles for this locus in each population except Hat Yai and New South Wales was very low and it ranged from 3.92% to 14.0% (Musuan - Chengmai).

Out of the twelve polymorphic loci examined, only four loci showed the presence of some rare alleles in them. These are NADH-Dia 1 zone 2 (allele 98), Hb (allele A^{X}), Me (allele 104) and Tf (allele D). The distribution of gene frequencies for NADH-Dia-1 zone 2 of allele 98 was 0.009 for MARDI/IPSR, 0.122 for Hat Yai and 0.171 for Weerawilla. Only the three Malaysian goat populations showed the existence of the rare allele *Hb* A^{X} with frequencies of 0.064 for MARDI/IPSR, 0.069 for Sabah and 0.077 for Sarawak (Table 21).

Of all the goat populations analysed only two samples from the Australian population of New South Wales demonstrated the existence of the very rare allele Me^{104} at 0.038 frequency. Another very rare allele in this region, the Tf^{D} allele was

Table 21. Distribution of Null and Rare alleles among the 13 populations examined.

ENZYME / PROTEIN GENOTYPE		MALAYSIA			INDONESIA			PHILIPPINES	THAILAND		SRI LANKA			AUSTRALIA
		MARDUPT	SABAH	SARAWAK	BOGOR	SULUWESI	MEDAN	MUSUAN	CHENG MAI	HAD YAI	S1	S2	S3	N.S.W.
Null alleles														
Alkaline Phosphatase	(N)	55	51	71	50	48	50	51	50	39	10	37	31	52
	Observed	16	17	36	4	27	24	28	16	9	3	9	10	15
(Ap^{00})	Gene Freq	0.536	0.578	0.711	0.530	0.750	0.690	0.745	0.550	0.474	0.55	0.486	0.565	0.538
	Percentage	29.09	33.33	50.70	8.00	56.25	48.00	54.90	32.00	23.08	0	24.32	32.26	28.85
											30.0			
X-Protein	Observed	6	5	5	3	6	6	2	7	0	0	4	3	0
(Xp^{00})	Gene Freq	0.255	0.176	0.094	0.090	0.218	0.320	0.186	0.330	0		0.125	0.371	0
	Percentage	10.90	9.80	7.04	6.00	12.50	12.00	3.92	14.00	0	1	10.80	9.60	0
											0.20			
											0			
											9.09			
Rare alleles														
NADH-Dia1 zone 1	(N)	55	51	64	50	48	50	51	50	39	10	36	31	52
	Observed	1	0	0	0	0	0	0	0	7	0	10	0	0
allele 98	Gene Freq	0.009	0	0	0	0	0	0	0	0.122	0	0.171	0	0
Haemoglobin														
	Observed	7	7	11	0	0	0	0	0	0	0	0	0	0
allele Hb A^X	Gene Freq	0.064	0.069	0.077	0	0	0	0	0	0	0	0	0	0
Malic enzyme														
	Observed	0	0	0	0	0	0	0	0	0	0	0	0	2
allele Me^{104}	Gene Freq	0	0	0	0	0	0	0	0	0	0	0	0	0.038
Transferrin														
	Observed	3	0	1	1	0	1	0	0	0	0	0	0	0
allele Tf^D	Gene Freq	0.027	0	0.007	0.031	0	0.010	0	0	0	0	0	0	0

* S1 - HAMBANTOTA S2 - WEERAWILLA S3 - THAMBUTHEGAMA

noted in low frequencies at 0.027 in MARDI/IPSR, 0.007 in Sarawak , 0.031 in Bogor and 0.010 in Medan (Table 21).

4.4. Genetic Variability

If the frequency of the most common allele at a locus does not exceed 0.95, the locus is defined as ***polymorphic***. The genetic variability within populations were quantified by measuring the proportion of polymorphic loci, the expected proportion of heterozygosity per individual and effective number of alleles per locus.

Table 22 gives the measures of genetic variability at 40 loci within each populations. Allele frequencies for the polymorphic loci (Table 7) show substantial differences among populations, but the same allele was the most common in all populations except for six loci (Amy, Ap, Hb, Np, Tf and Xp). Amy^{L} was most common in eleven populations, but had a slightly lower frequencies in Sabah (0.480) and New South Wales (0.442). Alp^{O} was most common in eleven populations too, but has lower frequencies in Hat Yai (0.474) and Weerawilla (0.486). Hb^{A} was the most common allele in all Southeast Asian goats ranging from 0.812 to 0.960 but had significantly lower frequencies for the goat populations of Sri Lanka and Australia ranging from 0.113 to 0.278.

Differences among populations were greater for Np (Np^{L} range of 0.435 to 0.712) and for Tf (Tf^{A} range of 0.445 to 1.0, with Tf C not present in six populations and Tf^{D} not present in nine). The Tf^{D} allele is reported here for the first time in Southeast Asian goats. Although at low frequency in any one population, it is widespread throughout the region (Table 7).

The percentage of polymorphic loci were in the range of 22.5 to 30.0 %, the mean heterozygosity values range from 0.118± 0.061 to 0.311± 0.105 and the effective

number of alleles per locus ranges from 1.3 ± 0.1 to 1.4 ± 0.1 in all goat populations (Table 22). Thambuthegama goat population has a lower proportion of polymorphic loci compared to other locations. This is due to the fact that the three polymorphic loci (Mdh, Np and Dia 1-2) in the Thambuthegama goat population contain significantly higher frequencies of variants than in the other populations.

It can be seen that the observed heterozygosity is lowest for Thambuthegama (0.118 ± 0.061) and highest for Hambantota (0.311 ± 0.105), but is not significantly different among populations. For all populations except Hambantota it is seen that the observed heterozygosity is less than expected. Mean observed and expected heterozygosity values have been presented in Table 22.

Table 22. Measures of Genetic variability at 40 loci in each populations

Population	Effective No of allele per Locus	Percentage of Loci polymorphic	Mean Heterozygosity	
			Observed	Expected
MARDI/IPSR	1.4 ± 0.1	25.0	0.162 ± 0.056	0.250 ± 0.064
SABAH	1.4 ± 0.1	30.0	0.193 ± 0.046	0.320 ± 0.044
SARAWAK	1.4 ± 0.1	27.5	0.176 ± 0.047	0.328 ± 0.0.56
BOGOR	1.4 ± 0.1	25.0	0.181 ± 0.061	0.325 ± 0.057
UJUNG PANDANG	1.4 ± 0.1	27.5	0.167 ± 0.044	0.380 ± 0.058
MEDAN	1.4 ± 0.1	27.5	0.164 ± 0.053	0.276 ± 0.047
MUSUAN	1.4 ± 0.1	30.0	0.252 ± 0.067	0.397 ± 0.028
CHENGMAI	1.4 ± 0.1	30.0	0.208 ± 0.046	0.366 ± 0.044
HAT YAI	1.4 ± 0.1	27.5	0.259 ± 0.071	0.378 ± 0.044
HAMBANTOTA	1.3 ± 0.1	22.5	0.311 ± 0.105	0.311 ± 0.097
WEERAWILLA	1.4 ± 0.1	25.0	0.139 ± 0.039	0.297 ± 0.077
THAMBUTHEGAMA	1.3 ± 0.1	22.5	0.118 ± 0.036	0.257 ± 0.074
NEW SOUTH WALES	1.3 ± 0.1	25.5	0.150 ± 0.034	0.276 ± 0.059

4.5. Deviations from Hardy-Weinberg Proportions

The overall trend of an observed deficiency of heterozygotes may be further analysed in more detail by testing the significance of deviations of the observed genotype frequencies from the expected under Hardy-Weinberg equilibrium. The usual chi-square goodness-of-fit test was performed and expected frequencies for small samples were calculated using Levene's (1949) formula.

4.5.1. MARDI/IPSR

Five loci Alb, Hb, Me, Dia-2 and Tf show no significant departures from Hardy-Weinberg equilibrium (Table 23). Two loci (Ca and Mdh) and to a lesser extent Me, Tf and Xp show observed deficiencies of heterozygotes (Table 24).

4.5.2. SABAH

Four loci Alb, Hb, Dia-1 and Tf show no significant departures from Hardy-Weingberg equilibrium (Table 23). Five loci (Ca, Me, Mdh, Dia-2 and Xp) and to a lesser extent (Dia-1) showed observed deficiencies of heterozygotes (Table 24).

4.5.3. SARAWAK

No significant departure from Hardy-Weinberg equilibrium was seen for four loci (Alb, Ca, Hb and Tf) in this goat population (Table 23). Significant deficiencies of heterozygotes for five loci (Me, Mdh, Dia-1, Dia-2 and Xp) and to a lesser extent for (Tf) were observed (Table 24).

4.5.4. BOGOR

In this goat population, no significant departure (Table 23) from Hardy-Weinberg equilibrium is observed for two loci (Hb and Tf). On the other hand, significant deficiencies of heterozygotes is observed (Table 24) for five loci (Ca, Me, Mdh, Dia-2 and Xp) and to a lesser extent in Tf in this goat population.

4.5.5. UJUNG PANDANG

Only one locus i.e. Tf shows no significant departure from Hardy-Weinberg equilibrium (Table 23). Significant deficiencies of heterozygotes were observed for seven loci (Alb, Ca, Hb, Me, Mdh, Dia-2 and Xp) and to a lesser extent (Tf) as shown in Table 24.

4.5.6. MEDAN

Three loci Alb, Tf and Xp seem to be in Hardy-Weinberg equilibrium (Table 23). Five loci (Ca, Me, Mdh, Dia-2 and Xp) and to a lesser extent Hb showed significant deficiencies of heterozygotes (Table 24).

4.5.7. MUSUAN

For this goat population of the Philippines, only two loci (Tf and Xp) showed no significant departures from Hardy-Weinberg equilibrium (Table 23). Four loci (Ca, Me, Dia-1, Dia-2) showed significant deficiencies of heterozygotes (0.40) as shown in Table 24.

4.5.8. CHENGMAI

In the Chengmai goat population, four loci (Alb Ca, Tf and Xp) showed no significant departures from the Hardy-Weinberg equilibrium (Table 23). Deficiencies of heterozygotes are significant at six loci (Hb, Me, Mdh, Dia-1, Dia-2 and Xp) and to a lesser extent for Ca and Tf (Table 24).

4.5.9. HAT YAI

In the Hat Yai goat population, no significant departures from Hardy-Weinberg equilibrium is observed for three loci (Ca, Dia-2 and Tf) as shown in Table 23. Significant deficiencies of heterozygotes is observed at Me and Xp loci and to a lesser extent at 3 loci (Hb, Mdh and Dia-2) as shown in Table 24.

4.5.10. HAMBANTOTA

At the Hambantota goat population of Sri Lanka. three loci namely Ca, Hb and Mdh showed no significant departures from Hardy-Weinberg equilibrium (Table 23). One locus (Mdh) and another (Xp) to a lesser extent showed observed deficiencies of heterozygotes (Table 24).

4.5.11. WEERAWILLA

Three loci (Alb, Ca and Dia-2) in the Weerawilla goat population showed no significant departures from Hardy-Weinberg equilibrium (Table 23) and significant observed heterozygotes deficiencies (Table 24) were seen for Hb, Me, Xp and to a lesser extent at Mdh and Dia-2 loci.

4.5.12. THAMBUTHEGAMA

No significant departures from Hardy-Weinberg equilibrium were seen for three loci (Alb, Hb and Tf) in the Thambuthegama goat population of Sri Lanka (Table 23). Significant observed deficiencies of heterozygotes were seen at Ca, Mdh, Dia-2 and to a lesser extent at Me and Xp (Table 24).

4.5.13. NEW SOUTH WALES

In the goat population of the Australian Feral goats from New South Wales, Hardy-Weinberg equilibrium was seen for three loci namely Alb, Ca and Tf (Table 23). Significant deficiencies of observed heterozygotes were seen at two loci (Me and Mdh) and to a lesser extent at Hb, Dia-2 and Xp as shown in Table 24.

From Table 23, it could be illustrated that one locus (Me) and to a lesser extent Ca, Mdh, Dia-2 and Xp showed consistent observed deficiencies of heterozygotes. Only Tf showed no significant departures from Hardy-Weinberg equilibrium in any of the goat populations except for Hambantota and Weerawilla where the locus was known to be homozygous.

Table 23. Summary of results of Chi-square test for deviations from Hardy-Weinberg Equilibrium in each population

Locus / Locality	Alb	Hb	Ca	Me	Mdh	Dia-1	Dia-2	Tf	Xp
MARDI / IPSR	0.294	57.337	0.750	9.219	32.510		0.029	2.330	61.975
	(1)	(1)	(3)	(1)	(1)	HOMO	(3)	(6)	(3)
	(0.588)	(0.000)	(0.861)	(0.002)	(0.000)		(0.999)	(0.887)	(0.000)
SABAH	2.861	30.251	0.996	58.133	35.971	5.406	14.633	1.847	75.152
	(1)	(1)	(3)	(3)	(1)	(1)	(1)	(1)	(3)
	(0.091)	(0.000)	(0.802)	(0.000)	(0.000)	(0.020)	(0.000)	(0.174)	(0.000)
SARAWAK	0.826	0.024	0.452	58.458	37.006	28.302	27.302	4.221	114.710
	(1)	(1)	(1)	(3)	(1)	(1)	(1)	(6)	(3)
	(0.363)	(0.876)	(0.501)	(0.000)	(0.000)	(0.000)	(0.000)	(0.647)	(0.000)
BOGOR	4.745	22.892	0.064	85.569	35.122		13.347	8.505	84.734
	(1)	(1)	(1)	(3)	(1)	HOMO	(1)	(3)	(3)
	(0.000)	(0.000)	(0.800)	(0.0000)	(0.0000)		(0.000)	(0.037)	(0.000)
UJUNG PANDANG	27.490	31.000	10.606	42.548	8.117		16.149	71.478	70.621
	(1)	(1)	(1)	(3)	(1)	HOMO	(1)	(6)	(3)
	(0.000)	(0.000)	(0.001)	(0.000)	(0.004)		(0.001)	(0.000)	(0.000)
MEDAN	3.340	54.069	6.364	44.392	12.815		33.496	0.931	59.822
	(1)	(1)	(1)	(3)	(1)	HOMO	(1)	(6)	(3)
	(0.000)	(0.000)	(0.012)	(0.000)	(0.001)		(0.000)	(0.988)	(0.000)
MUSUAN	5.042	11.380	11.380	90.417	6.506	56.265	14.633	1.954	73.632
	(1)	(1)	(1)	(3)	(1)	(3)	(1)	(3)	(3)
	(0.025)	(0.001)	(0.001)	(0.000)	(0.011)	(0.000)	(0.000)	(0.000)	(0.000)

UPPER ROW = Chi Square values

MIDDLE ROW = Degrees of Freedom (No of alleles - 1)

LOWER ROW = Probability level (P) (Population in equilibrium when $P > 0.05$)

Homo = Locus Homozygous

Amy, Ap and Np not included as genotype frequencies were estimated assuming Hardy-Weinberg equilibrium.

(Contd.)

Table 23. Summary of results of Chi-square test for deviations from Hardy-Weinberg Equilibrium in each population

Locus / Locality	Alb	Hb	Cn	Me	Mdh	Dia-1	Dia-2	Tf	Xp
CHENGMAI	0.612 (1) (0.434)	7.606 (1) (0.006)	16.472 (1) (0.000)	53.034 (3) (0.000)	13.347 (1) (0.000)	29.200 (1) (0.000)	13.645 (1) (0.000)	3.618 (3) (0.306)	69.853 (3) (0.000)
HAT YAI	3.223 (1) (0.073)	7.606 (1) (0.006)	8.922 (1) (0.003)	26.309 (3) (0.000)	7.809 (1) (0.005)	42.092 (1) (0.000)	6.800 (3) (0.079)	0.525 (1) (0.469)	20.890 (1) (0.000)
HAMBANTOTA	2.423 (1) (0.120)	22.473 (3) (0.000)	0.199 (1) (0.656)	18.073 (3) (0.000)	1.314 (1) (0.252)	HOMO	HOMO	HOMO	20.611 (3) (0.000)
WEERAWILLA	0.342 (1) (0.559)	0.092 (3) (0.993)	7.737 (1) (0.005)	64.570 (3) (0.000)	5.726 (1) (0.017)	HOMO	47,023 (6) (0.000)	HOMO	68.600 (3) (0.000)
THAMBUTHEGAMA	0.053 (1) (0.819)	40.702 (1) (0.000)	0.424 (1) (0.515)	26.033 (1) (0.000)	36.655 (1) (0.000)	HOMO	17.820 (1) (0.000)	0.053 (1) (0.819)	44.494 (3) (0.000)
NEW SOUTH WALES	0.656 (1) (0.418)	0.011 (1) (0.916)	3.340 (1) (0.916)	135.386 (6) (0.000)	41.062 (1) (0.000)	HOMO	12.287 (1) (0.000)	3.795 (1) (0.051)	3.795 (1) (0.051)

UPPER ROW = Chi Square values

MIDDLE ROW = Degrees of Freedom (No of alleles - 1)

LOWER ROW = Probability level (P) (Population in equilibrium when P > 0.05)

Homo = Locus Homozygous

Amy, Ap and Np not included as genotype frequencies were estimated assuming Hardy-Weinberg equilibrium.

Table 24. Summary of results of Coefficients for heterozygotes deficiencies in each loci for each goats population

Locus / Locality	Alb	Hb	Ca	Me	Mdh	Dia-1	Dia-2	Tf	Xp
MARDI / IPSR	8 (7.486) (0.069)	0 (10.743) (-1.000)	12 (11.110) (0.080)	7 (11.569) (-0.395)	5 (20.560) (-0.757)	HOMO	3 (2.963) (0.012)	29 (30.046) (-0.035)	16 (28.771) (-0.444)
SABAH	20 (16.238) (0.232)	2 (7.434) (-0.731)	13 (11.871) (0.095)	8 (20.881) (-0.617)	4 (20.881) (-0.830)	4 (23.525) (-0.830)	8 (17.237) (-0.536)	22 (18.535) (+0.187)	7 (24.822) (-0.718)
SARAWAK	27 (24.404) (+0.106)	3 (2.953) (0.016)	11 (10.220) (0.076)	9 (21.851) (-0.588)	8 (28.028) (-0.715)	6 (15.799) (-0.620)	9 (26.171) (-0.656)	32 (36.589) (-0.125)	5 (35.157) (-0.858)
BOGOR	24 (18.424) (+0.303)	7 (23.154) (-0.698)	4 (3.879) (+0.031)	3 (17.808) (-0.832)	3 (16.758) (-0.821)	HOMO	10 (20.364) (-0.509)	25 (22.859) (-0.094)	5 (21.182) (-0.764)
UJUNG PANDANG	5 (19.611) (-0.754)	4 (24.084) (-0.834)	8 (14.779) (-0.459)	9 (22.642) (-0.603)	13 (21.884) (-0.406)	HOMO	5 (11.358) (-0.560)	22 (25.611) (-0.141)	6 (24.084) (-0.751)
MEDAN	21 (16.758) (0.253)	0 (10.611) (-1.001)	6 (9.091) (-0.340)	7 (20.313) (-0.655)	9 (17.889) (-0.497)	HOMO	2 (9.091) (-0.780)	21 (19.414) (0.082)	8 (21.131) (-0.621)
MUSUAN	30 (22.891) (+0.311)	7 (12.921 (-0.458)	8 (14.970) (-0.466)	2 (22.208) (-0.910)	13 (20.050) (-0.352)	5 (23.144) (-0.352)	8 (17.237) (-0.536)	30 (25.713) (+0.167)	12 (21.465) (-0.441)

UPPER ROW = OBSERVED HETEROZYGOTES

MIDDLE ROW = EXPECTED HETEROZYGOTES

LOWER ROW = LEVEL OF HETEROZYGOTES DEFICIENCIES OR EXCESS.
SIGNIFICANT OBSERVED DEFICIENCIES OF HETEROZYGOTES (-) AND
SIGNIFICANT OBSERVED EXCESS OR HETEROZYGOTES (+).

HOMO = LOCUS HOMOZYGOTES

Amy, Ap and Np not included as genotype frequencies were estimated assuming Hardy-Weinberg equilibrium.

(Contd.)

Table 24. Summary of results of Coefficients for heterozygotes deficiencies in each loci for each goats population

Locus / Locality	Alb	Hb	Ca	Me	Mdh	Dia-1	Dia-2	Tf	Xp
CHENGMAI	21	5	6	10	10	3	7	23	8
	(18.939)	(8.191)	(13.576)	(24.475)	(20.364)	(11.424)	(11.253)	(24.778)	(27.919)
	(0.109)	(-0.390)	(-0.558)	(-0.591)	(-0.509)	(-0.737)	(-0.509)	(-0.072)	(-0.713)
HAT YAI	24	2	4	8	11	0	12	22	5
	(18.701)	(1.974)	(7.273)	(16.351)	(19.701)	(10.286)	(14.918)	(19.740)	(17.883)
	(0.283)	(0.013)	(-0.450)	(-0.511)	(-0.442)	(-1.000)	(-0.196)	(0.114)	(-0.720)
HAMBANTOTA	7	7	3	1	7				3
	(4.789)	(5.947)	(2.684)	(7.000)	(5.211)	HOMO	HOMO	HOMO	(6.158)
	(0.462)	(0.177)	(0.118)	(-0.857)	(0.343)				(-0.513)
WEERAWILLA	7	4	8	3	11	HOMO	10	HOMO	2
	(6.425)	(3.887)	(14.648)	(20.493)	(18.127)		(12.174)		(20.225)
	(0.090)	(0.029)	(-0.454)	(-0.854)	(-0.393)		(-0.179)		(-0.901)
THAMBUTHEGAMA	3	0	7	9	0		4	3	7
	(2.902)	(3.803)	(6.311)	(16.672)	(5.508)	HOMO	(15.738)	(2.902)	(17.951)
	(0.034)	(-1.000)	(0.109)	(-0.460)	(-1.000)		(-0.746)	(0.034)	(-0.610)
NEW SOUTH WALES	11	2	14	6	2		11	12	12
	(9.932)	(1.978)	(18.641)	(29.485)	(29.485)	HOMO	(21.117)	(16.311)	(16.311)
	(0.108)	(0.011)	(-0.249)	(-0.797)	(-0.797)		(-0.479)	(-0.264)	(-0.264)

UPPER ROW = OBSERVED HETEROZYGOTES

MIDDLE ROW = EXPECTED HETEROZYGOTES

LOWER ROW = LEVEL OF HETEROZYGOTES DEFICIENCIES OR EXCESS. SIGNIFICANT OBSERVED DEFICIENCIES OF HETEROZYGOTES (-) AND SIGNIFICANT OBSERVED EXCESS OR HETEROZYGOTES (+).

HOMO = LOCUS HOMOZYGOTES

Amy, Ap and Np not included as genotype frequencies were estimated assuming Hardy-Weinberg equilibrium.

4.6. CONTINGENCY CHI-SQUARE TEST

A contingency chi-square was carried out to investigate whether there are significant difference between the observed and expected frequencies of alleles in different locations within a country. All test was carried out on a 5 percent and 1 percent levels of significances. No analysis was performed for localities in the Philippines and Australia as only one population in each of these two countries was observed.

4.6.1. Albumin

Contingency chi-square test for allelic distribution among localities within a country for albumin is shown in Table 25. Significant differences were observed for Sri Lankan goats population ($P<0.001$) and the Thai goat population ($P<0.01$). No significant difference was observed for Indonesian goat populations ($P= 0.80$-0.90)

4.6.2. Amylase

Contingency chi-square test for allelic distribution among the localities within a country for amylase is shown in Table 25. As seen from the table, it could be said the probability level for differences between observed and expected frequencies for each country lies within a particular range, as for example, Malaysia ($P = 0.10 - 0.20$), Thailand ($P = 0.75 - 0.80$), Indonesia ($P = 0.25 - 0.30$) and for Sri Lanka ($P = 0.50 - 0.70$).

4.6.3. Alkaline phosphatase

Contingency chi-square test for allelic distribution among localities within country for alkaline phosphatase is also shown in Table 25. There was no significant difference observed for Thai goat population ($P = 0.30 - 0.50$) and Sri Lankan

goat population (P = 0.50 - 0.70). Less significant difference was observed for the Malaysian goat population where the probability level is between 0.01 - 0.02. Significant difference was observed for the Indonesian goat population ($P < 0.01$).

4.6.4. Carbonic anhydrase

Contingency chi-square test for allelic distribution among localities within a country is shown in Table 25. It could be observed that there is a high significant difference ($P < 0.001$) for the Indonesian and Sri Lankan goat populations. Less significant difference was observed for the Malaysian (P = 0.02 - 0.05) and Thai (P = 0.05 - 0.07) goat populations.

4.6.5. Haemoglobin

Contingency chi-square test for allelic distribution among localities within a country for haemoglobin is also shown in Table 25. No significant difference was observed for the Malaysian goat population (P = 0.5 - 0.1) and Thai goats population (P = 0.25 - 0.30). Less significant difference was observed in Sri Lankan goat population (P = 0.025 - 0.05). Significant difference was observed in the Indonesian goat population for this locus ($P < 0.01$).

4.6.6. Malic enzyme

Contingency chi-square test for allelic distribution among localities within a country for Malic enzyme is shown in Table 25. Significance differences were observed for the Malaysian ($P < 0.05$) and Sri Lankan ($P < 0.001$) goats populations. Both the Thailand and Indonesian goat populations were found to be not significant with probability levels (P = 0.50 - 0.70) and (P = 0.10 - 0.20) respectively.

4.6.7. Malate dehydrogenase

Contingency chi-square test for allelic distribution among localities within a country for Malate dehydrogenase is also shown in Table 25. High significant difference was observed for the Thai goat population ($P < 0.01$) and the Sri Lankan goats population ($P < 0.001$). Both the Malaysian and Indonesian goat populations were not found significant with the probability levels lying between ($P = 0.10 - 0.20$) and ($P = 0.05 - 0.10$) respectively.

4.6.8. Nucleoside phosphorylase

Contingency chi-square test for the allele distribution among the localities within a country is shown in Table 25. No significant difference was observed for both the Thai ($P = 0.30 - 0.50$) and Sri Lankan ($P > 0.50$) goat populations. It was found to be less significant in the Malaysian and Indonesian goat populations with the probability levels between 0.025 - 0.05.

4.6.9. NADH-Diaphorase 1 zone 1

Contingency chi-square test for the allelic distribution among the localities within a country for the locus was only performed for Malaysia and Thailand. All localities in Indonesia and Sri Lanka are known to be homozygotes for the locus. No significant difference was observed in the Thai goat population ($P > 0.50$) but the Malaysian goat populations ($P > 0.01$) showed significant differences (Table 25).

4.6.10. NADH-Diaphorase 1 zone 2

Contingency chi-square test for the allelic distributions among the localities within a country indicates highly significant differences among Malaysian, Thailand and Sri Lankan goat populations with the probability level $P < 0.001$ and significant difference for Indonesian goat populations ($P < 0.01$) (Table 25).

4.6.11. Transferrin

Contingency chi-square test for the allelic distribution among the localities within a country is shown in Table 25. No significant difference was observed for Thailand ($P = 0.05 - 0.01$), Indonesia ($P = 0.10 - 0.20$) and Sri Lankan ($P = 0.05 - 0.10$) goat populations. There is a highly significant difference observed for the Malaysian goat population ($P < 0.001$).

4.6.12. X-Protein

Contingency chi-square test for the allelic distribution at various localities within a country is shown in Table 25. There are significant differences for the goat populations of Malaysia ($P < 0.005$), Thailand ($P < 0.001$) and Indonesia ($P < 0.005$). Less significant difference was observed in the Sri Lankan goat population ($P = 0.01 - 0.02$).

4.6.13. Contingency chi-square analysis at all loci, for all populations.

Pooled chi-square analysis for distributions of alleles for the 12 polymorphic loci is shown in Table 26. The chi-square values are very high (2432.816) corresponding to a probability of less than 0.001 except for Amylase locus ($P = 0.025 - 0.05$). Hence, it could be concluded that the distributions of all the alleles for the 12 polymorphic loci are not independent of the populations.

Table 25. Summary of results of Contingency Chi-square Test for loci within respective country

Country \ Locus	Alb	Amy	Ap	Ca	Hb	Me	Mdh	Np	Dia-1	Dia-2	Tf	Xp
MALAYSIA	10.351 (2) 0.0056	4.225 (2) 0.1209	9.019 (2) 0.1100	7.563 (2) 0.0227	8.023 (4) 0.0907	15.727 (4) 0.0033	3.363 (2) 0.1861	6.917 (2) 0.0314	16.226 (2) 0.0003	33.696 (4) 0.0000	25.582 (6) 0.0003	15.069 (4) 0.0046
INDONESIA	0.332 (2) 0.8469	2.412 (2) 0.2993	11.292 (2) 0.0035	34.597 (2) 0.0000	11.155 (2) 0.0037	6.741 (4) 0.1502	5.265 (2) 0.0719	6.283 (2) 0.432	HOMO	12.715 (2) 0.0017	8.636 (6) 0.1951	16.858 (4) 0.0020
THAILAND	3.719 (1) 0.0537	0.092 (1) 0.7613	1.004 (1) 0.7613	3.776 (2) 0.0520	1.239 (1) 0.2656	0.950 (2) 0.6219	7.141 (1) 0.0075	0.864 (1) 0.3525	0.206 (1) 0.6496	13.114 (2) 0.0014	4.815 (2) 0.0900	31.975 (2) 0.0000
SRI LANKA	14.467 (2) 0.0007	1.108 (2) 0.5746	0.878 (2) 0.6445	28.560 (4) 0.0000	6.067 (2) 0.0481	25.113 (4) 0.0000	25.184 (2) 0.0000	1.000 (2) 0.6665	HOMO	54.800 (6) 0.0000	4.638 (2) 0.0983	12.806 (4) 0.0123

UPPER ROW = CHI SQUARE VALUES

MIDDLE ROW = DEGREES OF FREEDOM (No of population - 1) (No of alleles)

LOWER ROW = PROBABITLIY LEVEL

HOMO = LOCUS-HOMOZYGOTES

Table 26. Summary of results of Contingency Chi-Square Test Over all loci in thirteen populations

Locus	No of alleles	Chi-square	Degrees of freedom	Probability level
Alb	2	64.195	12	P < 0.001
Amy	2	21.868	12	P = 0.02-0.05
Ap	2	45.137	12	P < 0.001
Ca	3	285.738	24	P < 0.001
Hb	3	613.894	24	P < 0.001
Me	4	224.960	36	P < 0.001
Mdh	2	57.919	12	P < 0.001
Np	2	36.979	12	P < 0.001
Dia-1	3	211.404	24	P < 0.001
Dia-2	4	452.279	36	P < 0.001
Tf	4	166.867	36	P < 0.001
Xp	3	251.578	24	P < 0.001
Total		2432.816		P < 0.001

Degrees of Freedom = (M - 1) (N - 1)

M = No of populations

N = No of alleles

4.7. Estimation of Fixation Indices

F-Statistics are useful for the understanding of the breeding structure of population and the patterns of selection associated with polymorphic alleles. F-statistics estimated using the method of Nei (1977) show the substantial inbreeding within populations (F_{IS}) for Ca, Mdh, Dia-1, Dia-2 and Xp loci. However, the highest average within population inbreeding coefficient is shown by Me, with large significant deficiencies of heterozygotes in all the 13 goat populations that were polymorphic for the locus (Table 27).

One locus, Hb (0.476) makes the highest contribution to among-population differentiation (F_{ST}) and four loci, Ca (0.177), Dia-1 (0.133), Dia-2 (0.198) and Tf (0.143) making lesser contribution to the among-population differentiation (Table 27). Over all loci, the mean F_{ST} (0.163) indicates significant genetic differentiation among the populations.

In the computation of these values, F_{IT} is quite large (0.499), and this is largely due to F_{IS} (=0.402) rather than to F_{ST} (=0.163). The fixation indices for individual loci, particularly F_{IS} and F_{IT} vary considerably. A chi-square test shows that the F_{IS} for the loci is again significantly different from zero.

Hierarchical F_{ST} estimates (Wright, 1978) were computed to assess genetic differentiation among localities within countries, and among countries (Table 28). The estimates of 0.062 for among localities within countries and 0.096 for among countries show that all differentiation is among localities, and that there is no structuring of localities among countries except for two cases i.e. Ujung Pandang - Bogor and

Table 27. Summary of F-Statistical at all loci

Locus	F_{IS}	F_{IT}	F_{ST}
Aib	0.000	0.000	0.065
Ca	0.495	0.584	0.177
Hb	0.226	0.594	0.476
Me	0.684	0.713	0.092
Mdh	0.495	0.532	0.072
Dia-1	0.590	0.645	0.133
Dia-2	0.497	0.597	0.198
Tf	0.000	0.119	0.143
Xp	0.648	0.679	0.090
Mean	**0.402**	0.499	0.163

Table 28. Hierarchical F_{ST} estimates (Wright, 1978) combined across all loci

COMPARISON	F_{ST}
Among localities within country	0.062
Among countries	0.096

Weerawilla - Hambantota. Populations in the same country are just as likely to be genetically different as are populations from different countries.

4.8. GENETIC DISTANCE

The genetic distance between two populations is defined in terms of population allele frequencies for all loci in the genome. In practice, however, it is virtually impossible to examine all genes for all loci in the populations. Therefore, we must estimate the genetic distance by sampling a certain number of individuals from the population and examining a certain number of loci.

Nei's distance measures (1978) have been used for this analysis since the sampling theory of other distance measures is not well developed. The matrix of genetic distance/genetic similarity among all loci between each pair of population is given in Table 29. The dendrogram derived from these distances is in Figure 17.

From the dendrogram, it is observed that the goat populations were classified into a big cluster of nine populations and two each of two populations. As expected from the results of the hierarchical F_{ST} analysis. there is no obvious within-country clustering, except for Bogor-Ujung Pandang and Hambantota-Weerawilla.

The genetic distance coefficients in the 13 goat populations ranged from 0.001 (Sabah-Chengmai) to 0.043 (MARDI/IPSR - New South Wales) goat populations. Hence, in general the genetic similarity between the goat populations was quite high (>0.990) except for the Sri Lankan and the Australian Feral goats whose similarity with other goat populations ranges between 0.958 (MARDI/IPSR-New South Wales) to 0.985 (Sabah-Weerawilla) as shown in Table 29.

Table 30 displays average genetic identity values of comparisons of populations in locations within and between countries. The lowest value belongs to comparison between populations of Indonesia and Australia i.e. 0.960. The highest value (0.996) was found when average genetic identity between its locations was estimated. Similar value was also obtained when between locations of Thailand-Malaysia and Thailand Philippines were compared.

It could also be observed from the dendrogram that Southeast Asian goats belong to one big cluster and the Sri Lankan with the Australian goats in another group of clusters. Furthermore there is considerable genetic distance between Australian and Sri Lankan goats.

Table 29. Matrix of Nei's Genetic Distance/Identity (1978) for each of population.

	Population	1	2	3	4	5	6	7	8	9	10	11	12	13
1	MARDI / IPSR	*****	.995	.995	.991	.993	.995	.993	.997	.993	.965	.976	.966	.958
2	SABAH	.005	*****	.998	.994	.994	.998	.996	.999	.996	.975	.985	.976	.968
3	SARAWAK	.005	.002	*****	.993	.992	.996	.997	.997	.996	.963	.976	.969	.966
4	BOGOR	.009	.006	.007	*****	.997	.995	.992	.994	.990	.969	.975	.968	.959
5	UJUNG PANDANG	.007	.006	.008	.003	*****	.996	.995	.995	.989	.980	.980	.970	.962
6	MEDAN	.005	.002	.004	.005	.004	*****	.995	.998	.992	.974	.984	.975	.960
7	MUSUAN	.007	.004	.003	.008	.005	.005	*****	.998	.994	.973	.979	.972	.966
8	CHENGMAI	.003	.001	.003	.006	.005	.002	.002	*****	.996	.977	.984	.977	.969
9	HAT YAI	.007	.004	.004	.010	.011	.008	.006	.004	*****	.969	.979	.963	.961
10	HAMBANTOTA	.036	.025	.037	.031	.020	.026	.028	.024	.031	*****	.994	.983	.973
11	WERAWILLA	.024	0.15	.024	.025	.020	.017	.021	.016	.022	.006	*****	.989	.976
12	THAMBUTHEGAMA	.035	.025	.031	.033	.030	.026	.028	.023	.038	.017	.011	*****	.989
13	NEW SOUTH WALES	.043	.032	.035	.042	.039	.041	.035	.032	.040	.028	.024	.011	*****

Below diagonal: Nei (1978) unbiased genetic distance

Above diagonal: Nei (1978) unbiased genetic identity

Table 30. Average Genetic Identity values and between populations

COUNTRY	Number of Populations	MALAYSIA	INDONESIA	PHILIPPINES	THAILAND	SRI LANKA	AUSTRALIA
1 MALAYSIA	3	0.996 (0.995-0.998)					
2 INDONESIA	3	0.994 (0.991-0.998)	0.996 (0.995-0.997)				
3 PHILIPPINES	1	0.995 (0.993-0.997)	0.994 (0.992-0.995)	******** (N.C)			
4 THAILAND	2	0.996 (0.993-0.985)	0.993 (0.983-0.998)	0.996 (0.994-0.998)	0.996 (0.996-0.996)		
5 SRI LANKA	3	0.972 (0.963-0.985)	0.975 (0.968-0.984)	0.975 (0.972-0.979)	0.975 (0.963-0.984)	0.989 (0.983-0.994)	
6 AUSTRALIA	1	0.964 (0.958-0.968)	0.960 (0.959-0.962)	0.966 (0.966-0.966)	0.965 (0.961-0.969)	0.979 (0.973 - 0.989)	******** (N.C)

***** = No Comparisons
(N.C)

Figure 17. Dendrogram of genetic relationship (Nei's Genetic Distance, 1978) among thirteen goat populations.