BIOCHEMICAL POLYMORPHISM STUDIES IN BREEDS OF WOOL-SHEEP, HAIR-SHEEP AND THEIR HYBRIDS IN MALAYSIA

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Summary

A biochemical genetic study on blood enzyme/protein systems in some breeds/crosses of sheep in Malaysia was carried out using horizontal starch gel electrophoresis. Blood samples were collected from 435 sheep, representing 8 breeds/crosses. These included 5 wool sheep breeds (Thai Longtail, wiltshire, Suffolk, Dorsimal and cMBLx), 1 hair sheep breed (Barbados Blackbelly) and 2 hybrids between wool sheep and hair sheep (Cameroon × Thai Longtail and Bali Bali × Malin). Twenty loci systems were examined. Of these, ten (HBβ, ALB, TF, XP, CAT, DIA1, EsA, GPI, ME and NP) exhibited genetic variation whereas the other ten (AAT, CA, DIA2, αGLO, αGLU, LDH, MDH, PEP[leu-gly-gly], 6PGD and SOD) were monomorphic. The allelic frequencies which were obtained in 10 polymorphic markers are assessed and compared with the results obtained by previous workers. The estimations of inbreeding coefficient, intrabreed variation and breed relationships have been critically discussed and are used to reveal some important recommendations.

(**Key Words** : Sheep, Biochemical Polymorphism, Inbreeding, Genetic Distances, Malaysia)

Introduction

To increase the amount and to improve the quality of sheep products in Malaysia, several foreign breeds of wool sheep and hair sheep have been introduced over the past few years to upgrade the indigenous Malin sheep and for other crossbreeding purposes. Examples of these breeds are, Suffolk, Wiltshire, Dorset Horn, Merino-Border Leicester, Thai Longtail, Cameroon, Bali-Bali and Barbados Blackbelly. By using some of these breeds, several synthetic breeds are being developed, for example Dorsimal (Dorset × Malin), Bali-Bali × Malin and Cameroon × Thai Longtail.

Little is known of the genetic similarities and differences between the above breeds/crosses, with respect to the polypeptide composition of a given protein. Even though some of these breeds had been introduced into Malaysia some time ago, information of their stability and homogeneity at genetic level is scarce. Furthermore there is no documented genetic information available on the Thai Longtail, which over the past 3 years has been the major breed of sheep introduced into the country, or on some of the other popular synthetic breeds formulated in Malaysia.

Biochemical polymorphisms are increasingly being used to study the genetic variability within and between populations and to estimate genetic divergence in sheep. In genetic research of populations, genetically determined variants of protein and enzyme are widely used as markers of corresponding structural genes. The biochemical markers used do not depend on environmental factors and are stable throughout ontogenesis and have a simple type of inheritance. The data obtained on frequencies of genes and genotypes make it possible to compare the gene stocks of different animal groups and to study genetic variability under different conditions of selection.

The present study is initiated in an attempt to generate some genetic data that can be used to reveal some important suggestions on some of the breeds of wool sheep, hair sheep and their hybrids available in Malaysia. The principle of biochemical polymorphism and the technique of electrophoresis is utilised for this purpose.

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Materials and Methods

Animals

The experimental stock comprised 5 breeds of wool sheep, 1 breed of hair sheep and 2 hybrid types (table 1). Sampling was carried out on healthy adult males and females. The samples for the family studies were obtained from the flocks of Thai Longtail and Cameroon × Thai Longtail crosses.

The description of the breeds/crosses except Thai Longtail, Dorsimal, Cameroon × Thai Longtail and Bali Bali × Malin have been given by McDougall (1979) and Mason (1980):

Thai Longtail (TLT) is a medium sized sheep with a white or dark brown or mixed (patches of white brown and black) coarse wool. The head is characterized by a slightly convex profile, medium long and drooping ears and polled. It is believed to have originated from Myanmar and Northern Thailand and the success of breeding programmes involving this breed prompted the government of Malaysia to import large number of this animals from Thailand. It is farmed for meat production. At present, the research farm of University of Malaya maintains a nucleus herd of 250 heads this breed.

Dorsimal (DMx) is a medium sized sheep which was produced by crossing the polled Dorset with local Malin breed. The coarse wool with variation to finer fleece tend to be white in colour. The head is characterized by slightly convex profile, medium long and horizontal ears and the ram is either horned or polled but the ewe is always hornless. At present, it is mainly found in Rubber Research Institute of Malaysia (RRIM) and the plantations of Kumpulan Guthrie Berhad.

Cameroon × Thai Longtail (CMLTx) is a medium sized hybrid sheep of Cameroon (hair sheep) and Thai Longtail (wool sheep) that is being produced at the University of Malaya. It is partly hairy with kemp wool outercoat. Fine curly under wool is usually found in lambs. Body tends to be brown with black belly. The head is characterized by a slightly convex profile with medium long and horizontal ears. Ram can be horned or polled but ewe is polled.

Bali Bali × Malin (BMx) is a large sized hybrid sheep of Bali Bali (hair sheep) and Malin (wool sheep) that is being produced at MARDI. The fleece type is similar to the Cameroon × Thai Longtail hybrid. The head is characterized by sub-convex profile, medium long drooping ears and the ram is usually horned.

TABLE 1. BREED/CROSSES, THEIR ABBREVIATION, FLEECE TYPE, LOCALITY AND SAMPLE SIZE OF SHEEP SAMPLED

Breed/Crosses	Abbreviation	Fleece type	Locality	Sample size
Thai Longtail	TLT	Wool	IPT Farm, UM, Kuala Lumpur	98
Wiltshire	WS	Wool	IPT Farm, UM, Kuala Lumpur	45
Suffolk	SF	Wool	DVS Research Farm, Ijok	40
Dorsimal	DMx	Wool	RRIM, Sg. Buloh	45
Merino-border Leicester	cMBLx	Wool	DVS Research Farm, Ijok	52
Barbados Blackbelly	BB	Hair	MARDI, Kluang	54
Cameroon × Thai Longtail	CMLTx	Wool or hair	IPT Farm, UM, Kuala Lumpur	55
Bali Bali × Malin	BMx	Wool or hair	MARDI, Kluang	46
Total				435

UM - University of Malays.
IPT - Institute of Advanced Studies.
DVS - Department of Veterinary Services.

Electropharesis

Blood samples were collected into heparinized Venoject tubes by puncturing of the vena jugularis using Venoject needles. Plasma and erythrocyte lysates were stored at −70℃ until they were used.

Electrophoresis polymorphisms were analysed in plasma and in haemolysate samples by horizontal starch gel electrophoresis for twenty loci: haemoglobin-β (HB β), albumin (ALB), slow-α-globulin (αGLO), transferrin (TF), X-protein (XP), acid-α-glucosidase (αGLU), arylesterase (EsA), aspartate aminotransferase (AAT), carbonic anhydrase (CA), catalase (CAT), NADH diaphorase 1 (DIA1), NADH diaphorase 2 (DIA2), glucosephosphate isomerase (GPI), lactate dehydrogenase (LDH), malate dehydrogenase (MDH), malic enzyme (ME), nucleoside phosphorylase (NP), peptidase [leu-gly-

gly] (PEP), 6-phosphogluconate dehydrogenase (6PGD) and superoxide dismutase (SOD). The following electrophoretic procedure with slight modifications was used: HBβ (Evans et al., 1956), ALB (Tucker, 1968), TF and αGLO (Kristjanson, 1963), XP, EsA and CA (Tucker et al., 1967), αGLU, PEP, 6PGD and SOD (Harris and Hopkinson, 1976), AAT (Macaranas et al., 1993), CAT, LDH and MDH (Manwell and Baker, 1977), DIA1 and DIA2 (Cepica and Stratil, 1978), GPI (Manwell et al., 1985), ME (Yaman and Tucker, 1981) and NP (Tucker and Young, 1976).

Data analysis

Gene frequencies for polymorphic traits were calculated by direct gene counting method for the codominant systems (HBβ, ALB, TF, CAT, DIA1, GPI and ME) and by the square root method for complete dominant systems (XP, EsA and NP). The existence of the Hardy-Weinberg equilibrium was checked at the codominant loci by the X^2-test.

For each breed/cross, the average inbreeding was evaluated by computing the estimate of the inbreeding coefficient, F, as proposed by Kidd et al. (1980). The coefficient is calculated at each codominant locus as the proportionate deviations of heterozygosity from the Hardy-Weinberg equilibrium, and the overall loci of these values are combined as one estimate. However, due to low level of polymorphism in ALB and GPI, the inbreeding coefficient was estimated by using HBβ, TF, CAT, DIA1 and ME data individually.

Genetic variability within breeds/crosses was measured as the unbiased estimate of mean heterozygosity (Nei, 1978).

Genetic distance between breeds/crosses per locus was estimated from the gene frequencies by means of the Nei's (1972) standard genetic distance. It was chosen out of many distance measures to enable possible comparisons with previous studies on sheep relationships by Ordas and San Primitivo (1986), Tsunoda et al. (1990) and Zanotti et al. (1990) who used the same distance measure.

Based on the genetic distance, the breeds/crosses were clustered according to the unweighed pair group method with arithmetic averaging (Sneath and Sokal, 1973). The final result is presented as a dendrogram.

Results and Discussion

Allele frequencies

AAT, αGLO, PEP (leu-gly-gly) and 6PGD which have never been investigated in sheep were found to be monomorphic in all the breeds/crosses. Monomorphism observed in αGLU, DIA2, LDH, MDH and SOD loci were in accordance with the report by Manwell and Baker (1977). CA which was observed to be polymorphic by Tucker et al. (1967), Buis and Tucker (1983) and Nugyen et al. (1992) was monomorphic for all the breeds/crosses in this study.

The gene frequencies obtained at each polymorphic locus are presented in table 2. Since the comparison between the plasma and haemolysate in this study and international standard references has not been carried out, the allelic variation described are presumably the same as those reported previously. ALB and GPI systems which were polymorphic in breeds where pedigree data were not available were interpreted by using the method of Manwell et al. (1985) and Tucker (1968) respectively.

All of the breeds/crosses were either fixed for the $HB\beta^B$ allele or with $HB\beta^B$ frequencies considerably higher than those of $HB\beta^A$. Similar results have been obtained by Bunch and Foote (1976) and Zanotti et al. (1988). However, in contrast, Buis and Tucker (1983) found that in some Dutch breeds (Friesian, Schoonebeker, Drente and Kempen), $HB\beta^A$ was the more common allele compared to $HB\beta^B$. Nguyen et al. (1992) also made the same observation in France Rambouillet breed. It is interesting to note that all the Asian sheep breeds studied so far showed that the frequnecy of $HB\beta^B$ is higher than $HB\beta^A$ (John and John, 1977; Wang et al., 1988; Tsunoda et al., 1990; Kumar et al., 1991). Thai Longtail, the only Asian breed studied, also showed similar result.

The ALB^D, ALB^V and ALB^T which were observed in Russian Romanov breed (Fesus, 1974), Czechoslovakian Sumava breed (Stratil and Glasnak, 1974) and Indian Mecheri sheep (Krishnamurthy et al., 1974) respectively were not found in this investigation. However, ALB^F and ALB^W alleles which were found in English Finnish Landrace breed by Tucker (1968) were observed at a very low frequency in Thai Longtail breed (0.020) and Barbados Blackbelly breed (0.048). Wiltshire and Suffolk being the European breeds showed the highest frequencies of TF^C allele (0.500 and 0.424 respectively) whereas hybrid sheep which involved local Malin sheep (Dorsimal and Bali Bali × Malin) gave highest frequency for TF^D (0.489, 0.660). The relatively high TF^E frequency (0.518) observed in Cameroon × Thai Longtail crosses may be contributed by Thai Longtail which has very high TF^E frequency (0.709).

XP^- was predominant for all the breeds/crosses in this study. In contrast, previous studies by other workers showed that XP^+ was predominant in American Suffolk, Targhee, Rambouillet and Merino breed (Tucker et al., 1967), Spanish Churra breed (Ordas and San Primitivo,

TABLE 2. GENE FREQUENCIES OF PROTEIN POLYMORPHISMS FOR EACH LOCUS AND BREEDS/CROSSES

Locus symbol	Alleles	Breeds/crosses							
		TLT	WS	SF	DMx	cMBLx	BB	CMLTx	BMx
HBβ	A	0.046	0.316	0.061	0.267	0.269	0.065	0.009	0.140
	B	0.954	0.684	0.939	0.733	0.731	0.935	0.991	0.860
ALB	S	0.980	1.000	1.000	1.000	1.000	0.952	1.000	1.000
	W	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	F	0.000	0.000	0.000	0.000	0.000	0.048	0.000	0.000
XP	+	0.413	0.184	0.227	0.167	0.154	0.177	0.427	0.220
	−	0.587	0.816	0.773	0.833	0.846	0.823	0.573	0.780
TF	A	0.083	0.184	0.076	0.089	0.269	0.065	0.373	0.220
	B	0.015	0.053	0.030	0.022	0.067	0.113	0.009	0.020
	C	0.173	0.500	0.424	0.189	0.356	0.387	0.100	0.100
	D	0.020	0.026	0.030	0.489	0.240	0.226	0.000	0.660
	E	0.709	0.079	0.167	0.144	0.038	0.048	0.518	0.000
	F	0.000	0.158	0.273	0.067	0.029	0.161	0.000	0.000
CAT	F	0.587	0.605	0.067	0.778	0.442	0.355	0.442	0.440
	S	0.413	0.395	0.323	0.222	0.558	0.645	0.558	0.560
DIA1	F	0.536	0.895	0.788	0.578	0.663	0.565	0.464	0.620
	S	0.464	0.105	0.212	0.422	0.337	0.435	0.536	0.380
EsA	A	0.148	0.184	0.167	0.056	0.163	0.145	0.118	0.180
	a	0.852	0.816	0.833	0.944	0.837	0.855	0.882	0.820
GPI	F	0.000	0.000	0.106	0.067	0.000	0.000	0.000	0.100
	S	1.000	1.000	0.894	0.933	1.000	1.000	1.000	0.900
ME	F	0.566	0.868	0.894	0.800	0.856	0.790	0.691	0.820
	S	0.434	0.132	0.106	0.200	0.144	0.210	0.309	0.180
NP	H	0.077	1.000	0.227	0.556	0.635	0.355	0.236	0.200
	I	0.923	0.000	0.773	0.444	0.365	0.645	0.764	0.800

1986) and Italian Sarda breed (Zanotti et al., 1990). For CAT locus, as reported by Manwell and Baker (1977), two alleles namely CAT^F and CAT^S have been observed. Tsunoda et al. (1990), however found 3 alleles namely CAT^A, CAT^B and CAT^C in some Bangladeshi sheep. Since direct comparison have not been done, it still remains to be determined whether or not the present study and the report of Tsunoda et al. (1990) involve the same variants.

Most of the breeds studied by other workers showed that the frequency of DIA^F was higher than DIA^S (Ordas and San Primitivo, 1986; Tsunoda et al., 1990) except for Czechoslovakian improved Sumava breed (Cepica and Stratil, 1978) and Dutch Mergelland breed (Buis and Tucker, 1983). In this study, DIA^S was the more common allele in Cameroon × Thai Longtail crosses (0.536). The two European breeds (Wiltshire and Suffolk) tended to be predominant with DIA^F. EsA^a and ME^F were respectively more comomon that EsA^A and ME^S in all the breeds/crosses studied. Simlar results have been obtained by Yaman and Tucker (1981) and Tsunoda et al. (1990). GPI^F allele appeared only in Suffolk, Dorsimal and Bali Bali × Malin. The NP^H occurred with high frequency in majority of the breeds studied in other countries (Ordas and San Primitivo, 1986; Zanotti et al., 1990; Reljic and Jovanovic, 1990). However, in this finding, only 3 (Wiltshire, Dorsimal and cMBLx) out of the 8 examined breed/crosses showed NP^H frequency higher than NP^I. NP^H was fixed in Wiltshire, wheraas NP^I was almost fixed in Thai Longtail (0.923). Thus NP locus gave a distinct difference between these two breeds.

Hardy-Weinberg equilibrium

The loci suitable for this analysis are: HBβ, ALB, TF, CAT, DIA1. GPI and ME. Majortiy of X^2 values were found to be nonsignificant. There are, however, significant differences between observed proportions and Hardy-Weinberg expectation for the TF locus in Thai Longtail ($p < 0.001$), Wiltshire ($p < 0.001$) and Dorsimal ($p < 0.001$), the DIA1 locus in Thai Longtail ($p < 0.05$) and GPI locus in Dorsimal ($p < 0.05$). Since only 5 of the 45 comparisons were significant, it may be suggested that there are no biological phenomena or sampling error biases with a nett effect for sufficient differences between observed and expected proportions.

Inbreeding (F)

For the complete dominant systems, it is not possible to determine the observed heterozygosity. Therefore, only the codominant systems allowed a comparison of expected and observed heterozygosity. However, low level of polymorphism in ALB and GPI preclude their use. For each of the 8 breeds/crosses, the F was estimated based on HBβ, TF, CAT, DIA1 and ME individually (table 3). The inbreeding coefficient of the Wiltshire breed is exceedingly high (F = 0.239); in fact it is just slightly lower than that expected if all of the animals were progenies of full-sib mating (F = 0.250). Also, the F of the Dorsimal (0.132) is greater than expected for mating of half-sibs. An extremely high value of F based upon the differences between observed and expected heterozygosity can have three explanations. It could reflect actual inbreeding of individual animals in the sample. It could be due to Wahlund effect which occurred with subdivisions of a population or due to the problem in detection of heterozygotes or viability problem for heterozygotes. Since all the breeds sampled were from a single flock, Wahlund effect seems unlikely, but actual inbreeding from the mating of closely related animals probably exists. Inbreeding, or the mating of animals which are more closely related than average, increases the level of homozygosity in the population. When such mating occurs frequently, it has little effect in changing the overall gene frequencies but has important effect in increasing the frequency of homozygotes.

TABLE 3. ESTIMATION OF THE INBREEDING COEFFICIENT (F) AT THE SINGLE LOCUS AND AVERAGE

Breed/crosses	HBβ	TF	CAT	DIA1	ME	Average F
Thai Longtail	−0.043	0.006	−0.110	−0.204	0.029	−0.038
Wiltshire	0.051	0.323	0.249	−0.088	0.327	0.239
Suffolk	−0.048	−0.134	0.328	0.107	0.213	0.012
Dorsimal	0.213	0.206	−0.017	−0.081	0.039	0.132
Merino-border Leicester	−0.065	−0.086	0.151	0.019	−0.003	−0.036
Barbados Blackbelly	−0.052	0.032	0.307	−0.097	0.138	0.047
Cameroon × Thai Longtail	0.000	−0.300	0.072	−0.050	−0.012	−0.127
Bali Bali × Malin	−0.140	−0.008	0.045	0.085	0.071	0.005

In most mammalian species, an increase in the proportion of homozygous loci results in an average decrease in fitness because of the greater chance of a rare deleterious recessive trait being expressed. This has been confirmed in a study of inbreeding in sheep (Rae, 1982). Weaning weight, yearling weight, clean and greasy fleece weight all showed significant decrease with inbreeding. Assuming that the increased homozygosity at these polymorphic loci provides an accurate estimate of the inbreeding coefficient and hence of increased probabilities of homozygosity at all loci, the Wiltshire and Dorsimal were likely to show a large amount of inbreeding depression. On the other hand, the high F found in these two breeds also suggested that the breeding practices were not optimal.

Table 3. also showed that the inbreeding coefficients in Thai Longtail, cMBLx and Cameroon × Thai Longtail sheep are negative. This can be explained by the observed heterozygosity being higher than the expected one. The observed deviation may be ascribed to small sample size or may be due to Robertsonian effect of which the excess of heterozygotes arises simply from any difference in the gene frequency between reproducing males and females. The bias due to the Robertsonian effect is especially important in Thai Longtail and Cameroon × Thai Longtail crosses since the breeding practices of these two types of sheep involved small number of sires.

Intrabreed variation

The results of genetic variability within breeds/crosses measured using unbiased estimate of mean heterozygosity (Nei, 1978) are shown in table 4. As a whole, the average

heterozygosity (H) obtained ranged from 0.134 (Wiltshire) to 0.167 (cMBLx). Based on these results, it can be concluded that Wiltshire breed was the most homogeneous breed whereas cMBLx was the most heterogeneous breed. H value ranging from 0.070 to 0.217 for certain European breeds, Australian breeds and Bangladeshi sheep had been reported by Manwell and Baker (1977) and Tsunoda et al. (1990). However, the results of the present study are not exactly comparable with the above which were obtained by different methods of estimation based on different breeds or different numbers and kind of gene loci. A loss of genetic variability in certain breed can be due to the occurrence of deliberate inbreeding, a large amount of genetic drift or a large founder effect in their ancestry. For the examined Wiltshire breed, the low value of H may be caused mainly by the occurrence of deliberate inbreeding since inbreeding coefficient of this breed was extremely high (higher than F value of half-sib mating).

TABLE 4. ESTIMATION OF MEAN HETEROZYGOSITY (UNBIASED ESTIMATE) AT POLYMORPHIC LOCI IN EACH BREED/CROSS

Breed/cross	HBβ	ALB	XP	TF	CAT	DIA1	EsA	GPI	ME	NP	Mean heterozygosity
Thai Longtail	0.088	0.040	0.487	0.462	0.487	0.500	0.253	0.000	0.494	0.142	0.140 ± 0.047
Wiltshire	0.444	0.000	0.309	0.700	0.491	0.193	0.309	0.000	0.235	0.000	0.134 ± 0.047
Suffolk	0.116	0.000	0.357	0.721	0.451	0.339	0.282	0.193	0.193	0.357	0.150 ± 0.046
Dorsimal	0.396	0.000	0.281	0.699	0.350	0.493	0.106	0.126	0.324	0.499	0.144 ± 0.050
Merino-border Leicester	0.397	0.000	0.263	0.743	0.498	0.451	0.276	0.000	0.249	0.468	0.167 ± 0.052
Barbados Blackbelly	0.123	0.094	0.297	0.766	0.465	0.500	0.252	0.000	0.337	0.465	0.165 ± 0.052
Cameroon × Thai Longtail	0.018	0.000	0.494	0.588	0.451	0.502	0.210	0.000	0.431	0.364	0.153 ± 0.050
Bail Bail × Malin	0.246	0.000	0.350	0.516	0.503	0.481	0.301	0.184	0.301	0.327	0.160 ± 0.044

Breed relationship

The genetic distance (D) between the 8 breeds/crosses are given in Table 5. Based on their genetic distance, they were clustered into one dendrogram (figure 1.). D value of the breed pairs fluctuated between 0.007 and 0.155. The highest coefficient of genetic distance was obtained between Wiltshire and Thai Longtail (0.155) and the lowest coefficient, between Cameroon × Thai Longtail and Thai Longtail (0.007). The topology of the dendrogram can be further used to differentiate 2 subclusters or groups: (1) Thai Longtaill and Cameroon × Thai Longtail, (2) cMBLx, Barbados Blackbelly, Dorsimal, Bali Bali × Malin and Suffolk. Wiltshire was totally separated from the above two subclusters.

TABLE 5. GENETIC DISTANCES AVERAGED OVER 20 LOCI BETWEEN 8 BREEDS/CROSSES OF SHEEP

Breeds/crosses	1	2	3	4	5	6	7	8
1. Thai Longtail	****							
2. Wiltshire	.155	****						
3. Suffolk	.028	.091	****					
4. Dorsimal	.043	.085	.023	****				
5. cMBLx	.051	.077	.022	.013	****			
6. Barbados Blackbelly	.031	.105	.014	.021	.011	****		
7. Cameroon x Thai Longtail	.007	.135	.024	.031	.036	.026	****	
8. Bali bali x Malin	.038	.116	.024	.019	.021	.013	.032	****

As indicated by Nei (1976), for local breeds comparison, the Nei's distances were in the range of 0.000 to 0.058. Similar results have been obtained by several workers. For examples, Ordas and San Primitivo (1986), when considering different flocks of dairy sheep in Spain (Churra, Lacha and Manchega) estimated the genetic distances between breed in the range of 0.0094 to 0.0599 (mean 0.0314) using the data of 8 genetic systems. Zanotti et al. (1990), by using the data of 11 loci, found a distance ranging from 0.0124 to 0.0599 (mean 0.0387)

between some of the local Italian native sheep (Sards, Comisana, Bergamasca, Gentilie di Puglia and Massese). The breed investigation in this study consisted of breeds from Asia (Thai Longtail), Australia (cMBLx), Europe (Wiltshire, Suffolk), Africa (Barbados Blackbelly) and some of the hybrids between the African and Asian breeds or hybrids between European breeds and local Malin breed. This is the reason why some of the Nei's distances obtained in this study were out of the range 0.000-0.058. Similarly, Tsunoda et al. (1990) by considering different flocks of Bangladeshi sheep and some European breeds (Suffolk, Cheviot, Corriedale, Finnish Landrace and Border Leicester) and by using the data of 19 loci, estimated the Nei's distances to be in the range of 0.0194-0.0885(mean 0.0502) with some of the values outside the range of 0.000-0.058.

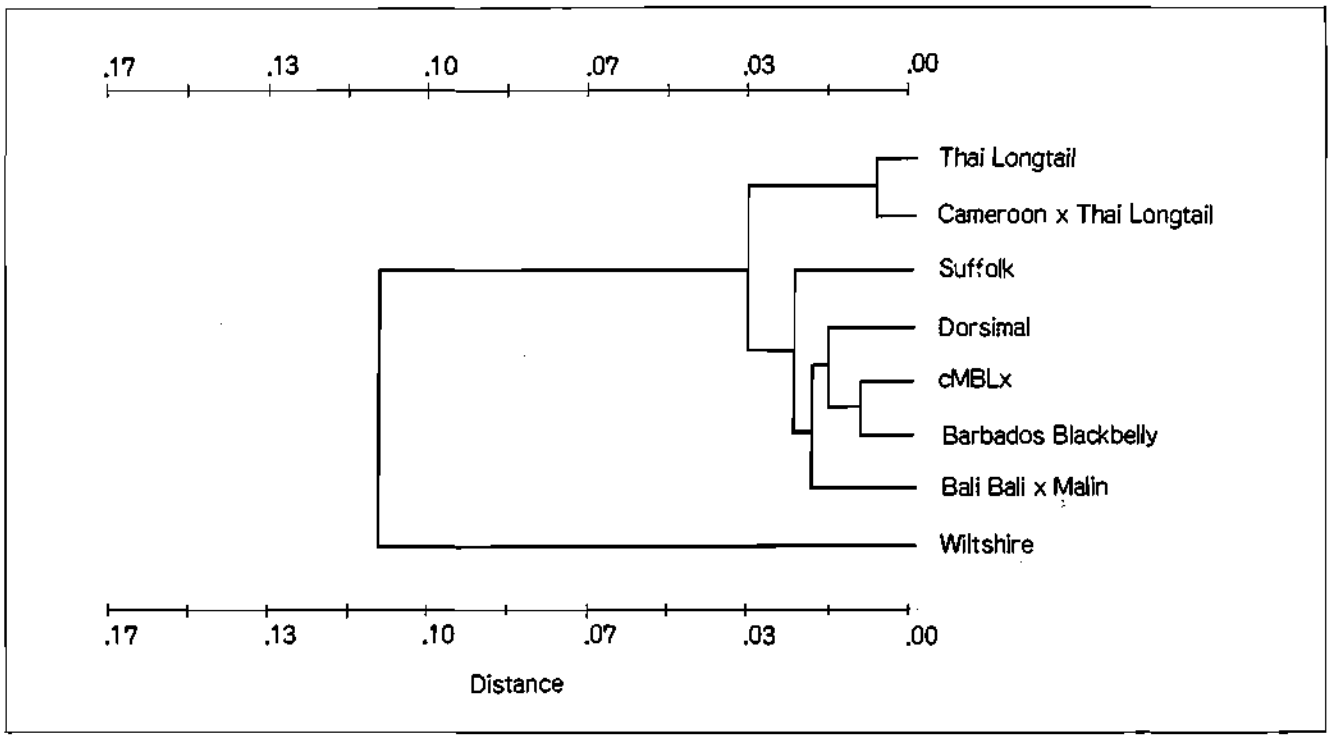

Figure 1. Dendrogram showing genetic distances between sheep breeds/crosses.

Based on the highest value of Nei's genetic distance (0.155) and the lower values of mean heterozygosity (Wiltshire = 0.134 ± 0.047, Thai Longtail = 0.140 ± 0.047), breeding programmes involving the crossing of Wiltshire and Thai Longtail is recommended, since crosses between breeds which are homogeneous but distinctly different in their relationship would produce more hybrid vigour (heterosis) in the crossbred progeny.

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