CHAPTER 6

SUMMARY
AND
CONCLUSION

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A total of 600 blood samples from native goats were collected from three geographically separated areas in each of Malaysia and Indonesia, from two areas in each of Thailand and Sri Lanka and from one locality each in the Philippines and Australia.

Out of the 40 loci examined, **polymorphisms** were found in 8 erythrocyte systems: Carbonic anhydrase, Haemoglobin, Malic enzyme, Malate dehydrogenase, Nucleoside phosphorylase, **NADH**-Diaphorase 1 zone 1, **NADH**-Diaphorase 1 zone 2 and X-protein; and in 4 plasma systems: Albumin, Amylase, Alkaline phosphatase and Transferrin. The remaining twenty-eight systems were **monomorphic**. Family studies were also carried out to detect the pattern of inheritance for all these variable loci. It was revealed that Alb, Ca, Hb, Me, Mdh, Dia 1-1, Dia 1-2, Tf and Xp loci were autosomal and their alleles are codominantly inherited. Ap, Amy and Np alleles were found to show dominance and recessive inheritance.

The native goats of Southeast Asia show very extensive polymorphism for coat colour and therefore appear quite diverse phenotypically. However, this diversity seems to exist in all local populations, so there are no apparent phenotypic differences among the populations, and no specific strains or breeds are recognised.

The allele frequencies for the polymorphic loci showed differences among populations, but the same allele in each locus was the most common in almost all populations except for amylase [Amy^L was most common in eleven populations, but had a slightly lower frequency in the Sabah (0.480) and New South Wales (0.442) populations]; for alkaline phosphatase [Ap^O was most common in eleven populations, but had a slightly lower frequency in the Hat Yai (0.474) and Weerawilla (0.486)

populations]; for haemoglobin, [Hb^A was most common in nine populations, but Hb^B frequency was much higher in the Hambantota (0.850), Weerawilla (0.722), Thambuthegama (0.887) and New South Wales (0.769) populations], for malic enzyme, [Me^{100} was most common in all populations but showed lower frequency in the New South Wales (0.442) populations]; malate dehydrogenase, [Mdh^{100} was most common in all populations except for the Hambantota population where it was present at a lower frequency (0.450)]; for nucleoside phosphorylase, [Np^L was most common in all populations , except that it occurs at a lower frequency in the Sarawak (0.472), Bogor (0.470), Medan (0.450) and Thambuthegama (0.435) populations]; for NADH-Dia 1 zone 2, [Dia-2^{100} was most common in twelve populations, but was present at a significantly lower frequency in the New South Wales (0.279) populations]; for transferrin, [Tf^A was most common in eleven populations, but had a slightly lower frequency in the MARDI/IPSR (0.445) and Hat Yai (0.487) populations]; and finally for X-protein [Xp^2 was most common in all populations but was present at a significantly lower frequency in the New South Wales population (0.192)].

Among the populations, Musuan (+0.303) and Bogor (+0.311) showed an excess of heterozygotes for the locus Albumin. For the locus transferrin, Sabah (+0.187) and Musuan (+0.167) showed an excess of heterozygotes. The overall results of the native goat populations are qualitatively similar both in the overall observed deficiency of heterozygotes and the significant population differentiation.. These may also be indication of genetic drift in populations with small effective heterozygote deficiencies in some populations, which may have resulted from Wahlund effect, if all the animals sampled were not from a single random mating population.

Methods for studying genetic distances among goat populations have been established in this study. Essentially, this is the most extensive biochemical genetic

study on goats, both in terms of number of animals analysed and in the numbers of biochemical markers typed. By investigating the extent of genetic variation among goat populations using cellulose acetate and starch gel electrophoresis methods, the genetic distances were obtained.

The observed genetic distances values among populations (0.001 - 0.043) are within the range of those observed among defined breeds of livestock. The goat populations were classified into one big cluster of nine populations belonging to Southeast Asian region and two other clusters, each involving two populations. Genetic variation among populations may have resulted differential selection (natural or artificial), different degrees of inbreeding or from genetic drift, while gene flow would tend to reduce variations.

The average degree of genetic differentiation of subpopulations (F_{ST} - 0.163) clearly indicates substantial genetic differences among these goat populations. This is due probably to these populations having been largely isolated from one another, and that they have differentiated genetically due to genetic drift. From the genetic distance matrix and the dendrogram, no significant correlation between the geographic distances and genetic distances could be found.

The high level of within-population inbreeding (F_{IS} = 0.402, whether due to deliberate inbreeding or small effective population size, might be expected to accentuate genetic drift and lead to increase population differentiation. As compared to F_{IS}, the F_{ST} is relatively small, indicating that there had been sufficient gene flow among these populations to counter this differentiation.

In conclusion, the native goat populations have diverged due to genetic drift or differential selection so that there are genetically different strains, which are likely to differ in quantitative traits important to production, such as growth rate and milk yield.

With the available information from this study, genotype evaluation experiments of genetically similar animals comparatively under different environmental conditions and management, can be practiced in future. Also grouping of the various populations into genetic sets and sub-sets could be made from which a representative set may be selected for further evaluation in future work..

This research pertaining to the estimation of genetic variability among populations and genetic distance among them contribute to the fundamental knowledge on biodiversity in goats, and the knowledge gained through it may be extended to other classes of livestock.

Scientists, politicians and farmers around the world today acknowledges that '**Biodiversity**' *is* fundamentally important to the survival of our planet, the earth. As technology has found ways to manipulate genes and adjust nature, it has also posed a major threat to genetic diversity. With ever increasing competition in commercial farming systems and ever progressing modern techniques, farmers can now play 'god' with animals and as a result many animal varieties are slowly disappearing. This seems to be happening to the native goats of Southeast Asia. Local breeds of livestock are genetic resources which should be protected as part of the world heritage of biodiversity (WCMC, 1992).

There is now serious concern about the depletion of genetic resources in the field of livestock. Most of the breeds of domestic animals that are known to have existed at the turn of the century are either extinct or are in danger of extinction. In addition, the current trends of crossbreeding with exotic breeds, or by changing strains to adapt to different market needs can be result in the indigeneous breed/s being extinct in future . With modern techniques such as artificial insemination and embryo transfer, the damage can be done very quickly. The decrease in the world goat population between 1990-

1992 should be taken seriously to these effect. Therefore conservation criteria for the indigenous breeds need to be formulated. The diversity and unity measured through the study of electrophoretic variations may help in the formation of conservation criteria and also the choice of breeds/strains for conservation.

There are hundreds of native breeds of goats, cattle, sheep, pigs and many others which have been documented. No one really seems to know how many types of goats there are, nor how they differ from each other, genetically, in evolutionary terms. As a strategy to ensure the survival of animal resources, FAO is embarking on a massive inventory of native breeds and strains (WCMC, 1992).

The widespread or indiscriminate use of goats in crossbreeding is likely to result in the loss of potentially useful localised strain, in some instances before their characteristics can be documented. unless specific measures are implemented to conserve these strains. One technique which is currently available but not extensively used in livestock management yet is the conservation of genetic information "on ice", the gene bank. Since it is neither logistically nor economically feasible to conserve all populations, it is necessary to have the most worthy of conservation. Identification of these strains could be on the basis of known characteristics and genetic distances.

It is hoped that the present study involving Southeast Asian goat populations will be considered useful when a global data base on genetic variability of goats is presented in future.