CHAPTER I

INTRODUCTION

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The genetics of native goats (*Capra hircus*) of Southeast Asia, commonly known as " katjang goats " is essentially unknown and have been neglected from the point of view of research as well as developmental aspects. Although the native goat forms an integral part of small holders' farming system in Southeast Asia, their population size has been rapidly declining due to high extraction rate and improper or no breeding management strategy.

In Europe and even in some parts of Asia (China and India), well -defined breeds of goats are recognized, but native goats throughout Southeast Asia are morphologically similar. Some geographic populations of native goats, particularly in Indonesia , have been given local names, but distinct breeds generally are not recognized. In Malaysia, the native katjang breed is believed to be similar to Indonesian katjang and the native goats of Thailand and Philippines are also morphologically similar to katjang goats (Devendra and Burns,1983). Nevertheless, given the wide geographical range of goat populations, local populations may have been isolated to some extent, and thus may have differentiated genetically. If there were large genetic differences among these goat populations for production traits (growth, milk, etc), it would be advantageous to use the best population as a basis for genetic improvement program, and as a source of improved sires for use in other populations.

Experiments to obtain comparative performance data on all populations are just not feasible, but as a first and objective measure, the magnitude of genetic differentiation and genetic relationships among the populations can be estimated using biochemical markers.

It is clear that in many of the developing countries including Malaysia, the native goats are in immediate danger of extinction through indiscriminate cross-breeding with exotic breeds. For example , in the case of katjang goats in Malaysia, the population size has decreased from 480,000 in 1970 to 280,000 in 1995 (MSAP Newsletter,1996). This may pose the greatest threat, as the potentially useful genetic material of the native animals would be lost. Furthermore, goats with high genetic merit are often withdrawn from breeding programs due to pressure from marketing groups to fetch these animals for slaughter and subsequent sale of goat meat. This problem arises because of ignorance of many goat breeders in the value of conservation of goats with superior genetic merit.

Many recent breeding programs on goats are still giving priority to cross-breeding as strategy for improvement. Although crossbreeding programmes entail crossing between native and European breeds , yet it is possible to improve local populations through either inter-population or intra-population selection involving breeds of the region. Therefore, it is important to determine genetic variation between and within populations of native goats to evaluate the genetic distance between the potential strains and also to identify any reproductive barriers which might occur as a result of crossing the parental strains. The genetic distance data is especially likely to be a good guide to the formulation of cross-breeding programs since the greater genetic distance between parental strains is expected to result in the higher value of heterosis for productive and reproductive traits. Hence, to avoid the extinction of the native breed of goats, it is not only necessary to devise measures for conservation of the genetic resources, but also to determine the genetic variation present in the blood.

The application of genetics to improving goat productivity entails either :

1. *Utilisation of heterosis and complementary effect through cross-breeding followed by either, grading-up to the superior breed /strain, or development of a synthetic*

population through selection involving F_1, F_2, F_3 *and subsequent generations (Horst et al., 1984 .)*

2. *Utilisation of within breed / strain variations through selection .*

The second option above for genetic improvement of goat has been given scant consideration in Southeast Asia because it depends on there being genetic differences among goat populations of the region and there is absolutely no available datum.

The possible application of the available options depends upon knowing if there are genetic differences among populations, and if there are, identification of population(s), that are superior for the trait(s) of interest - milk, meat , etc.

It has been noted that the identification of superior population(s) depends on the appropriate evaluation of all populations, i.e. comparison under the same conditions, of contemporary animals from the different populations, with collection of objective data on them. In practice it is not possible to evaluate all the available populations because there are very large number of geographically separate populations of goats . Therefore, it will be necessary to determine the genetic relationships among the populations, so that they may be grouped into sets that are genetically similar, and only one representative population of each set is then included in evaluation studies. Such information will be also very beneficial as genotypes of individuals are ascertained and the genetic structure of each population studied . This could enable us to establish the levels of inbreeding and the amount of genetic variation present. (Barker ,1985).

The study of protein polymorphisms has contributed to understanding genetic variation and changes at the phenotypic and molecular levels that have occurred under the influence of domestication (Buic and Tucker,1983; Ordas and Primitivo,1986). Protein characters, however appear not to have been shaped directly and deliberately during the process of domestication and artificial selection because most of them are neutral and nearly neutral with respect to selection. However possibilities exist for correlated response in changes of frequencies of certain genes due to direct selection for productive traits although no such results have been documented in the past in goats.

The use of cellulose acetate and starch gel electrophoresis in this study has been most useful. It provides a means of estimating gene frequencies for polymorphic biochemical markers which could be used to identify breeds and strains of organisms as well as their relationships to one another. The loci analysed most likely will have no (or little) effect on production traits of interest; the point to determine if populations are genetically different for what is hoped will represent a random sample of the genome..

Much research has been carried out worldwide into blood biochemical polymorphisms in order to study the genetic relationships between population of various species of farm animals, especially the domestic sheep, *Ovis aries* (Watanabe,1971; Tucker and Young,1976; Nguyen and Bunch 1980) and cattle (Kidd *et al*.,1980; Namikawa,1981; Singh and Bhat *et al*.,1981). However, very little work has been done with goats. The only extensive work was done by Tunon *et al*., (1989) Barbancho *et al*., (1984) on the Spanish breeds , Fesus *et al*., (1983) on the Hungarian breeds while Nozawa *et al*.,(1978 a,b); Katsumata *et al*.,(1981a,b & 1982) and Bhat (1986) studied few breeds from Asia. In the early nineties Kumar and Balaine (1990) reviewed blood groups and biochemical polymorphisms in goat blood. However, these data are limited in that only a small number of local populations from the same region was considered, samples sizes often were small and number of polymorphic loci per population was only 2-7. Caution is necessary therefore in comparing these studies with others.

The Australian Centre for International Agriculture Research (ACIAR) funded a research programme undertaken jointly by the University of Malaya, the Universiti Pertanian Malaysia and the University of New England, Armidale, Australia, in a project entitled "Genetic identification of strains and genotypes of swamp buffaloes and goats of Southeast Asia". The present study is a major part of this project where investigation is carried out to determine the genetic differences among the goat populations in Malaysia, the Philippines, Indonesia, Thailand, Sri Lanka and Australia. Samples from the Sri Lankan goat populations were carefully and randomly collected which only include animals morphologically similar to katjang goats and not the Sri Lankan dwarf type goats.. The Australian feral goats were included in the study for a comparative analysis.

The objectives of this investigation are as follows:

- *To develop the use of cellulose acetate electrophoretic technique in the study of isozymes in goats,*
- *To determine whether the forty enzyme / protein loci examined are monomorphic or polymorphic,*
- *To analyse the pattern of inheritance of biochemical markers in pedigreed samples,*
- *To estimate gene frequencies for different biochemical markers in various populations of Southeast Asia, Sri Lanka and Australia,*
- *To estimate the level of heterozygosity of population,*
- *To use these data to estimate genetic similarity (genetic distances) among the populations,*
- *To derive a dendogram of phylogenetic relationship from these genetic distances, and to group these animals into sets that are genetically similar.*

This research work constitute one of the very few attempts at a systematic and complete analysis of the phylogenetic relationships existing among the Southeast Asian, Sri Lanka and Australian native goat populations with the help of forty biochemical markers, and a fairly substantial population size. The results from this study should be able to assist in rationalising research programs, to minimise inefficient use of scarce resources in breed evaluation , and to facilitate choice of the most suitable and productive strains. In addition, the estimated relationships should be useful in predicting expected heterosis in crosses between populations. A complete description of the genetic differences between any of the two populations is not possible but the measure of genetic distance provides the best available objective description of this variation.