CHAPTER 2

LITERATURE REVIEW

LITERATURE REVIEW

2.1. GOATS

The total world population of domestic goat is about 653.84 million heads in 1995 as compared to 602.04 million heads in 1993 (Table 1). The goats are well distributed in seven regions as follows (FAO, 1996) : **Asia, Africa, North and Central America, Europe, Oceania, former USSR and South America .**

About 90% of the world's goats are raised in Asia and Africa. Therefore, it can be understood that the goats are regarded as important livestock in developing countries in Asia and Africa. (Horst and Hussain, 1991).

In Southeast Asia, goats are primarily kept for meat and milk and have a particular significance for subsistence farmers and for landless households. They often make effective use of land and vegetation that is unfit for cropping and generally do so more efficiently than sheep and cattle. Hence, research on goats can have considerable equity as well as productivity implications in developing countries (Mukherjee, 1992).

2.1.1 ORIGIN, ANCESTRY AND DOMESTICATION

Goats, as probably the first domestic species, form an important and integral part of symbiotic relationship of livestock with man, particularly of small holder agricultural situations, all over the world. The contributions of goats to the well being of humanity must be expected to assume a major role, guaranteeing human nutrition. It is believed that the domestication of goats took place first among the ruminants prior to the taming of sheep, cattle and pigs (Zeuner, 1963). They have occupied a place of honor in their

Table 1. Goat population of the world (FAO, 1996)

Region	Number of goats (1000 heads)			
	1979-1981	**1993**	**1994**	**1995**
Africa	138228	177345	184784	191620
North & Central America	13365	15717	14875	14925
South America	18538	23244	23933	24796
Asia	268188	361678	375548	398615
Europe	11770	15960	16210	15989
Former USSR	5811	7226	7128	6930
Oceania	415	872	956	961
World Total	**456315**	**602042**	**623434**	**653836**

long association with man over millennia, being the earliest animal domesticated (Herre and Rohrs, 1973) and next oldest to the dog (Zeuner, 1963).

Taxonomically, goats belong to the genus, *Capra*, and can be divided into three groups (Herre and Rohrs, 1973):

(a) ***C.a. aegagrus*** (Bezoar or Pasang)

(b) ***C.a. falconeri*** (Markhol)

(c) ***C.a. Ibex*** (Ibex)

These groups, especially the Markhol and Ibex, have been regarded as consisting of several geographically isolated sub-species. All groups are represented in the Near or Middle East, whereas the monophyletic root of the domestic goats is being traced to the first type (C. aegagrus or hircus). Domestication of goats is believed to have occurred in the mountainous region of Western Asia in the 7th to 9th millennium BC (Devendra and Burns, 1983). But at present goats are distributed in almost all countries, both developed and developing.

From Western Asia, where the domestication of goats occurred, two main routes of dispersion of goats to the east are postulated. One is the route from Iran and Afghanistan through Turkistan to Mongolia or to north China. This route had been used by pastoralists since ancient times and later established as the "silk road". The other route is to the Indian subcontinent through the Khyber Pass to Southeast Asia. This route is also an old one, since the Indo-Aryan people are known to have entered the subcontinent from the north through this way in the middle of the 2nd millennium BC. It is considered that Mongolia, China and India received domestic goats from the west through the nomadic and semi-nomadic pastoralists of western and central Asia who used these two main routes (Devendra and Nozawa, 1976). There is an evidence of a trade connection between India and south-eastern Asia since the 6th century BC

(Chakravarti, 1961). Along this maritime route Burma, Thailand, Malaysia and Indonesia would have received goats from India in the early Christian era at the latest, although Yamane (1943) considers that the goats entered Indonesia after the Moslem invasion (in the 14th century) on the basis of the fact that the Buddhist relics at Borobudor (built in the 9th century) have not shown any images of goats. It is also possible that the continental regions of Southeast Asia have received goats directly from South China.

The lineage and migration routes of the Asian indigenous goats from the area of domestication are shown diagramatically in Figure 1. It is stressed that these routes are based on present knowledge and confirmation remains to be made.

The domestic goat, *Capra hircus*, could be descendent of *C. aegagrus* of Persia and Asia Minor, *C. falconeri* of the Himalayas and *C. prisca* of the Mediterranean area (Mackenzie, 1974).

2.1.2. INDIGENEOUS GOAT BREED OF SOUTHEAST ASIA.

The domestic goats (*Capra hircus*) more commonly known as the katjang goats are the indigenous goats of Southeast Asia (Plate 1). These goats are well adapted and widely distributed all over this region; occurring in Malaysia, Indonesia, Thailand, the Philippines, Taiwan, Vietnam, Laos, Kampuchea and south-west islands of Japan. Phenotypically these goats resemble the native goats of Bangladesh, Mynmar and Eastern India (Epstein, 1971; Peters, 1979; Devendra, 1980 and Devendra & Burns, 1983).

Fig. 1. Postulated dispersion route of domestic goats from domestication area (shaded area) to East and South East Asia (Devendra and Nozawa, 1976).

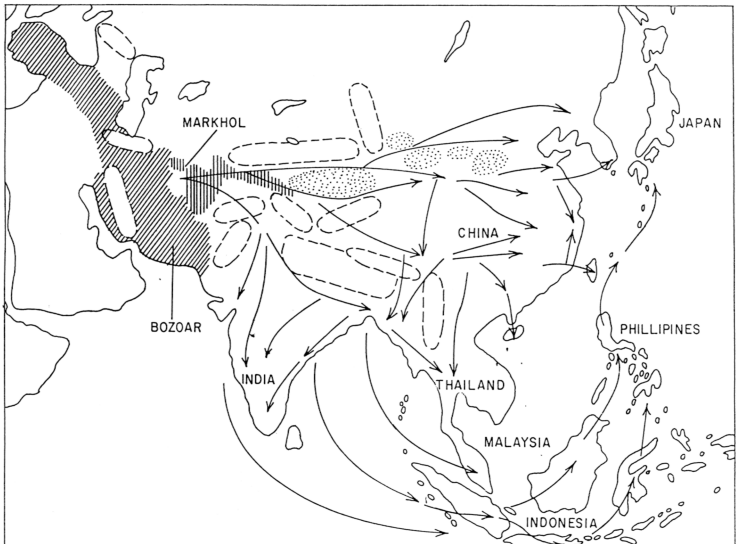
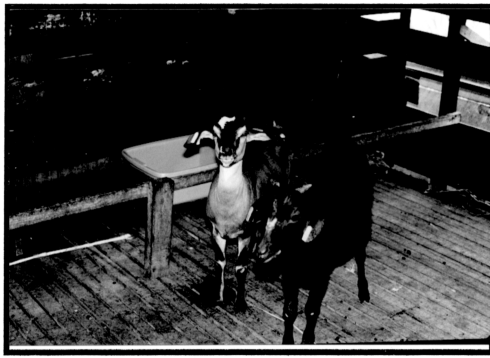


Plate 1. Indigenous Goat of Southeast Asia, the "Katjang Goats".



The indigenous goats have been described as a small and compact type of goat and renowned for its prolificacy and fecundity traits (Devendra and Burns, 1983). The katjang goat is also described as a hardy and nimble animal (Devendra and Burns, 1983). This breed is adapted to a wide range of management conditions and feeding regimes. It is usually black with patches of white in the middle of the body or underside of the belly. Several reports have indicated that color variation exists in this breed ranging from black to white with predominant color variation of either black and white or black and brown making up about 60-70% of the populations (Nishida *et al.*, 1975; Devendra and Burns, 1983).

Katjang goats have a thin coat with coarse hair which usually sticks to the skin. In the males, the hair covering tends to be more dense and usually typified by a mane which stands upright and can occasionally be bushy on the dorsal side of the body from the level of the neck to the tail. The skin is thin and has an approximate thickness of about 1.0 cm. It is relatively elastic and has a short but bright covering of hair (Devendra and Burns, 1983).

The head is triangular in shape and tapers forwards towards the lips. The muzzle is small and nostrils are well expended. Beards are common in males but not in females. Tassles and wattles may be present in both sexes but at a very low frequency. The horns are well developed in both sexes and sweep backwards and upwards. They are distinctly flat and scimitar shaped, thick at the base and curved to a point at the tip. The size of these horns vary from one individual to another, from being short and blunt in some goats, too long and neat pointed in others (Devendra, 1970; Devendra and Burns, 1983).

The ears of Katjang goat are generally erect and points diagonally forward. Less commonly the ears drop sideways, but are unlike the distinct lop ears in the Jamnapari and Anglo-Nubian breeds (Devendra, 1970; Devendra and Burns, 1983).

A mature male is about 25 kg in weight and a mature female weight is about 20 kg (Devendra and Burns, 1983). Their wither height of 60-65 cm for males and 56 cm for females make them fall into the category of small breeds. Birth was reported to range from 1.3 to 1.5 and lower values of dressing percentage, between 37.8% and 39.7% (Vidyadaran *et al.*, 1984) have been reported.

The meat of the katjang goats is of good quality. Although the udder is well-developed, milk yield is very low. Studies conducted at the University of Malaya's goat farm have shown that the katjang does can yield as high as 500 g of milk per day with good management practice (Metz, Mukherjee and Horst, 1985).

Apart from their main functions, the katjang goats are reared as multipurpose economical animals among the subsistence farmers producing quality skin and hide, hair, manure, horns, hooves and blood for serum and bone meal. All of these have significant commercial value (Horst and Hussain, 1991).

2.2. CONSERVATION AND UTILIZATION OF ANIMAL GENETIC RESOURCES

Genetic diversity within each species includes genetic variation within and between the populations. The loss of genetic diversity means the loss of breeds and strains, hence the prevention of further loss of genetic diversity has become a major concern among the scientists and policy makers. These include the total description and characterization of breeds, the development of data banks and the identification of certain populations as important genetic resources and their conservation (Sililuck,1995).

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Reduced glutathione catalyse	Spanish goats	Absent	Tunon *et al.*, (1987b)
Malate dehydrogenase	Katjang goats	Present	Nishida *et al.*,(1975)
	Anglo-Nubian	Absent	Panandam (1981)
	Saanen	Absent	Panandam (1981)
	Ferals	Absent	Panandam (1981)
	Katjang goats	Absent	Panandam (1981)
	Spanish goats	Absent	Tunon *et al.*,(1987)
Malic enzyme	Sheep-goat hybrid	Present	Tucker *et al.*,(1989)
	Mediterranean breeds	Present	Stasio *et al.*,(1995)
αs1-Casein	Alpine goats	Present	Grosclaude *et al.*,(1987)
	European breed of goats	Present	Langley (1993)
	Somali Arab goats	Present	Stasio *et al.*,(1993)
	Italian &Mediterranean goats	Present	Ramunno *et al.*,(1994)
	Saanen & Alpine goats	Present	Bouniol *et al.*,(1994)

In a FAO Expert Consultation meeting in Rome (1989), scientists and policy makers got together and strongly recommended in live animal preservation. They indicated the urgency with which action is required, particularly in the identification of genetically distinguished populations of animals, their sizes and breeding practices, which may rapidly alter their composition (FAO,1989).

In 1994 , FAO sponsored a workshop on "Conservation of Indigeneous Genetic Resources" during the 5th World Congress on Genetics Applied to Livestock Production at the University of Guelph, Ontario, Canada, where various aspects of conservation as well as measures to educate public on conservation strategies were discussed. Also FAO's global programme for genetic distances analysis to provide objective information on genetic differentiation among breeds within each species (Barker,1994).

A number of authors including Epstein (1974), Archarya (1982), Devendra and Burns (1983), Mukherjee (1992) and Hall (1993) have drawn attention to the need for conservation programs for specific goat populations in developing countries. Many of the wide range of local breeds with unknown or unrealized potential are in danger of being lost as distinct entities, either because changed land-use patterns and social goals have made them apparently obsolete or because of cross-breeding and breed replacement in the pursuit of perceived short-term advantages. Some of these breeds may have special production or adaptation qualities (Quatermain, 1991).

While it may be impracticable to conserve all currently existing breeds, the emphasis is placed on conservation for optimum immediate or possible future utilization. Potentially useful genetic material should not be lost, as genetic variation is the basic material of the animal breeder for making selection decision (Barker, 1985).

2.2.1. Indiscriminate Crossbreeding

Indiscriminate crossbreeding may pose the greatest threat to animal production. It is becoming clear that some breeds in the developing countries are in immediate danger of loss through indiscriminate crossbreeding with exotic breeds, others are rare and in danger of extinction, while others are losing genes for high productivity because high performing animals are being withdrawn from breeding populations. High production of breeds in developed countries relative to that of native breeds in developing countries has led in the past unrealistic expectations of the potential for rapid improvement of productivity in the developing countries through importation (Barker, 1985).

2.2.2 Traditional Husbandry Systems

There is now increasing realization of the potential value of the native breeds, particularly in their adaptation to climatic and other stresses, and to traditional husbandry systems. In considering the value of native breeds, the focus on 'potential' needs to be stressed. In most cases, data are not available to identify the nature of specific adaptation, nor is the genetic basis known. Such specific adaptation for disease and parasite resistance, fertility and survival in stressful environment, may well depend, not on single loci, but on co-adapted gene complexes. In such cases, it is most imperative to identify and evaluate the breeds before they are effectively lost through crossbreeding, whether it be indiscriminate or planned. Once the integrity of any co-adapted gene complex is destroyed in the crossbred, it will be very difficult to recreate (FAO/UNEP report, 1981).

However, definition of this 'potential value' poses an immediate problem. The value of a particular breed may be that it carries a unique gene, for some specific trait or that it

is significantly superior to all other breeds for a quantitative character. These can be determined by evaluation, but this problem emphasizes the need, not only for evaluation but also for concurrent research to define in detail the traits to be considered (FAO/UNEP report, 1981; Barker, 1985).

The traditional husbandry system practiced by most small farmers in this region is very unlikely to change rapidly, hence, the most suitable and most productive breeds are required for these systems. Crossbreeding with exotic breeds may improve production over that of native breeds, some native breeds may be better than others, crosses among some native breeds may be better than the present breeds, but it is not known whether they are or not without appropriate evaluation. Proper documentation and evaluation of the local breeds will do much to raise their status and help to prevent their loss as distinct entities through indiscriminate cross-breeding (Quartermain, 1981).

2.2.3. Evaluation of the Animals

In Asia and Oceania, as elsewhere in the developing world, the primary issue in not conservation (or preservation), but evaluation and appropriate utilization of existing resources. Appropriate evaluation may be defined as the comparison under the same condition of contemporary animals from different breeds, strains or crosses with collection of objective data on them (Barker, 1980 & 1981; FAO/UNEP report, 1981; Quartermain, 1981. It is essential that the traits to be measured, the environment-management system used for evaluation, the breeds and crossbreds used and finally the experimental design employed must all be well defined before attempting to evaluate the resources.

In order to ensure that the evaluation is adequately done as well as being appropriate, one should also consider that the evaluation experiment be completed according to a defined experimental protocol.

If these specifications are accepted as a reasonable base for appropriate evaluation then each evaluation experiment will need to be large-scale, may include more than one environment and should include lifetime productivity so that viability (adaptive and disease resistance traits) and reproductive performance are fully evaluated.

Many of the "breeds" of the developing countries are very ill-defined, despite the fact that many references have been made on the breeds. It must be also considered that geographically separated populations may be different genetically to some extent as some of the different breeds. Hence, effort should be made to these different strains to be evaluated separately. Further crosses between different breeds and strains, both native and exotic should be considered for evaluation. Therefore, the major problem is that given the wealth of breeds, strains and geographically separated population to be considered, it obviously will not be possible to evaluate all of them with the limited technical and financial resources available (FAO, 1975; Barker, 1980 & 1981; FAO/UNEP, 1981, Quartermain, 1981 & 1991).

2.2.4. The Use of Gene Frequency

The major aspects of the phylogeny of plants and animals have been derived from morphological criteria studying both fossil and living organisms. Strictly, morphological affinity demonstrates similarity only and does not necessarily give the real genetic phylogeny. With the advent of immuno-genetics, however the genotypes of individual animals can be determined for a number of loci specifying the antigen structure of the

red blood cell membrane (i.e. blood groups). More recently, developments in biochemical genetics have allowed characterization of genotypes at loci specifying various proteins most usually enzymes, using the technique of electrophoresis. Therefore gene frequency data may be obtained for the populations under study, these may then be used to estimate genetic distances between each pair of populations and then these distances used to construct a phylogenetic tree. The techniques and analytical methods in the context of their application in evolutionary studies, are reviewed by Ferguson (1980).

If two populations are for geographic or reproductive reasons genetically isolated from each other (i.e. no gene flow between them) they will tend to accumulate different genes. The gene differences have been measured as a function of gene frequencies (Nei,1987). The reasons for this differentiation will be mutation, selection, and random genetic drift. Thus, if gene frequency data are available for only one or a few loci the estimated genetic distance and any phylogenetic tree will not be reliable. But, if a large number of loci is used, effects of genetic drift varying among loci or effects of selection (either natural or artificial) varying for different loci will be averaged out (Nei and Roychoudhury, 1974a; Nei, 1978). In addition the loci used should ideally be a random sample of the genome (Hubby and Lewontin, 1966; Leigh and Langley, 1979).

The best measure of genetic distance would be the number of nucleotide or codon differences per unit length of DNA i.e. differences in the genetic material itself rather than in the protein products of the genes (Nei and Tajima, 1981). While nucleotide sequencing is still very expensive and time-consuming, current advances in molecular genetics and associated technology are such that the information will be sought and will be made available. Indirect methods of nucleic acid analysis such as restriction endonucleases analysis or DNA hybridization are available but for the immediate future,

gene frequency data based on electrophoretic or immunological techniques will provide the most practical approach for phylogenetic studies (Barker, 1985).

2.2.5. Estimation of Genetic Relationship

The highest priority for evaluation will only be considered if there is sufficient amount of information available on each of the various breeds and strains. But even in the short term, this is just not good enough and it has been argued for some time (Barker, 1980) that the solution to this dilemma is to determine the genetic relationships among the breeds, strains and populations of each species of livestock so that they may be grouped into sets that are genetically similar and then to include in evaluation experiments one representative from each set.

Although this approach has not been used yet to determine candidate breeds, strains, etc for evaluation studies or for conservation, the methodology is well developed and in fact has been used in studies of relationships among livestock breeds. The methods derived from the studies in evolutionary genetics where interest has focused on the genetic differentiation of populations, races, subspecies, species and higher taxonomic categories, and on evolutionary relationships. These concepts are of prime importance viz. genetic distance and phylogeny (Ferguson, 1980).

2.2.5.1. GENETIC DISTANCE

Genetic distance is a measure, expressed as a single number, of the genetic difference between two populations determined as a function of difference between them in gene frequencies. This could also be interpreted as a measure of the magnitude of genomic difference between populations or species.

Theoretically, 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 population. Therefore, genetic distance is estimated by sampling a certain number of individuals from the population and examining a certain number of loci (Nei and Roychoudhury, 1974b; Nei, 1978).

Several measures of genetic distances based on gene frequency differences between populations have been proposed (e.g. Cavalli-Sforza and Edwards, 1967; Balakrishnan and Sanghvi, 1968; Hendrick, 1971; Rogers, 1972 and Nei, 1972). These measures are mathematically rather diverse, and for some, their biological interpretation is not clear (Nei, 1973). If the rate of gene substitution per year is constant, Nei's standard genetic distance is linearly related to the time after divergence of two populations. Further, the standard error of Nei's distance statistics can be estimated (Nei and Roychoudhury, 1974b). For these reasons, the Nei's genetic distance measures have been the most widely used in studies of evolutionary biology and populations classification. However, the correlation estimates among various populations have been found to be generally very high (Hedrick, 1975, Chakraborty and Tateno, 1976), particularly between local populations within a species (i.e. equivalent to livestock breeds or strains).

The standard genetic distance of Nei (1972) has been used extensively in studies of evolutionary genetics of natural populations, and in some livestock studies. The genetic distances among seven cattle breeds ranged from 0.007 to 0.180 (Gonzalez *et al.*, 1987). Van Zeveren *et al.*, (1990) estimated distances of 0.0693 - 0.1030 among four pig breeds of Europe, and Zanotti Casati *et al.*, (1990) of 0.0124 - 0.0599 among five Italian native sheep breeds. These values are generally within the range of 0.00 - 0.05

indicated by Nei (1987) for local races of variety of species from insects to man. These estimates have been further discussed in the fifth chapter of this thesis.

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2.2.5.2 PHYLOGENY

A **phylogeny** is an evolutionary history where the evolutionary relationships among taxa are usually presented diagrammatically as phylogenetic trees i.e. a two-dimensional pattern of nodes and branches where closely related taxa are placed on adjacent terminal branches and distantly related taxa may be separated by many nodes (Sneath and Sokal, 1973; Clifford and Stephenson, 1975).

For the construction of phylogenetic trees, again a variety of methods have been proposed (e.g. Sneath and Sokal 1973, Cavalli-Sforza and Piazz, 1975; Felsenstein 1981). When a tree is derived for a set of incompletely isolated populations (such as the livestock strains or breeds to which these methods are to be applied), it will represent the genetic relationship among the populations at the time the gene frequency survey is made. In this case, the tree produced is generally called a dendrogram. Once the matrix of genetic distance among all pairs of population has been produced , the simplest method to produce a dendrogram is the unweighted pair group with arithmetic mean (UPGMA), (Sneath and Sokal, 1973).

2.2.6. Prospects for Evaluation

In identifying candidate breeds for evaluation, it would be desirable to have genotype data for a large sample of variable loci so that reliable genetic distance estimates will be made (Levin, 1975; Nevo, 1978; Nei, 1987). A reasonably large number of loci (say 20-30) might be readily assayed i.e. blood groups and electrophoretic techniques are already

defined, but some proportion of these almost certainly will be monomorphic in the population studied. That is, all populations will be homozygous for the same allele at certain loci and these loci will not help differentiate the populations. However, it must be recognized that the method does not end with the first sample of individuals tested from each population nor with the initial sample of loci that are assayed. Additional samples from the same population or data on additional loci can be added to the gene frequency data base at any time to update or expand the analysis (Robertson, 1966; Barker, 1981).

While the method is proposed to attack a specific problem and to provide specific information, additional information of value also will flow directly from the data obtained. Because genotypes of individuals are ascertained, the genetic structure of each population studied can be defined in terms of level of inbreeding and amount of genetic variation present (Barker, 1981).

At this time very little is known about the mechanism maintaining genetic variation at polymorphic enzyme loci. At some of the loci, variation is probably actively maintained by heterozygote superiority i.e. higher fitness of heterozygotes in terms of survival on reproduction (Schall and Levin, 1976; Singh and Zourous, 1978; Nei, 1987). In such cases, a controlled crossbreeding programme to deliberately create heterozygotes would contribute to improving just those characters that are difficult to improve by selective breeding (Robertson, 1966). Ford (1940) described the preservation of genetic variability (polymorphism) through selection and further demonstrated "balanced polymorphism" with *Drosphila* for the presence of different allele genes as well as for the presence of different allelic chromosome arrangements.

It has been noted that when overdominance occurs or when the heterozygote has superior reproductive fitness to both homozygotes, it permits the establishment of an

equilibrium through which both alleles may remain indefinitely within the population provided the selection coefficients remain constant (Strickberger,1985).

Finally, the estimated genetic distances among populations could be useful in predicting the expected heterosis in crosses between particular pairs of populations (Goddard and Ahmed, 1982) which would be of value in formulating breeding policies. The results from this approach will also help to rationalize research programs to minimize inefficient use of scarce resources in breed evaluation and will facilitate choice of the most suitable and productive breeds for the traditional husbandry systems of the small farmers.

2.3. ELECTROPHORESIS

Improvements in the techniques for separation of proteins have made possible the detection of a great number of genetic protein variants in man and farm animals. Electrophoresis is one of the most powerful analytical techniques in biochemical research. Its scope of application has been broadened tremendously in recent years by the availability of pure support media. It has been very useful in providing a means of estimating gene frequency for polymorphic biochemical markers which could be used to define breeds and strains of organisms as well as their relationships with one another. Unfortunately, not much data showing electrophoretic variations is available for Southeast Asian goats.

The electrophoretic techniques are based on the ability of charge particles to migrate in an electrical field, and the different rates of migration observed due to differences in the net charge. Different structures of protein carry different net electrical charges and as a result respond differently to an electric field. Single proteins move

through the gel matrice at the same rate but mixtures of protein separate into a series of bands in the gel column (Smithies, 1955).

In electrophoretic separation of proteins, the net charge on the protein molecule is determined by the dissociation of ionic groups and binding of buffer ions. It is designed to separate protein fractions in a form which resembles the condition in which they exist *in vivo* (Bodman, 1960).

Although the ability of a protein molecule to migrate and its rate of migration are primarily determined by its net charge, these can be varied within quite wide limits. For example, by changing the pH of the electrophoretic medium it is possible for a given protein to travel towards either electrode according to the levels of acidity or alkalinity.

In an alkaline solution [e.g. pH 8.6] most protein molecules are negatively charged and travel toward the anode. Of the major serum proteins, albumin possesses the greatest charge and hence has the greatest mobility, while gamma-globulin is virtually uncharged at this pH, and in the absence of other influences remains near the point of origin. At pH 7.0 alpha-globulin is positively charged and thus migrates towards the cathode, whereas albumin still bears a net negative charge and moves in the opposite direction, that is towards the anode (Wilkinson, 1970)

Other factors which can modify the effect of net charge in separating protein molecules during electrophoresis are the nature of the buffer solution used, that is, its viscosity, ionic strength and chemical components, which may exert different effects on different proteins, and the buffer ions may react with uncharged groups to form charged complexes, e.g. borate ions combined with sugar molecules, and the size and shapes of protein molecules because the gel matrice act like a molecular sieve.

The currently popular media for electrophoresis are starch, acrylamide, cellulose acetate and agarose. It is important to realize that no single support medium is routinely

superior to any other for allozyme electrophoresis; each has its own particular advantages and disadvantages. The final choice will depend upon the resources available to the researcher and also upon the type of research work envisaged. The suitability of the main procedures for determining particular biochemical polymorphisms is briefly described.

2.3.1. Starch Gel Electrophoresis [STAGE]

Smithies (1955) introduced partially hydrolysed starch gel for the electrophoretic separation of protein mixtures. Its wide application during the past 35 years is due to the various advantages of the medium. Electrophoretic separation is not only based on charge differences but also on differences in the molecular sizes of the proteins. This is due to the ability of the medium to act as molecular sieve (Bleomendel, 1967).

Absorption of proteins is reduced to minimum with supporting medium, and it provides the best resolution of protein mixtures compared with other supporting media. In addition, this procedure has been shown to be sensitive enough to discriminate between two homologous proteins differing in a single net charge due to a single amino acid difference in their primary structures. This has been explicitly demonstrated in studies on human haemoglobin (Huisman *et al.*, 1968).

The methodology involved in the application of this high resolution technique is also relatively simple and only very small quantities of crude proteins are required for analysis. In addition, the versatility of these techniques in comparative protein studies has been greatly enhanced by the staining procedures for the detection of a variety of enzymes and non-enzymic proteins after completion of electrophoresis (Hunter and

Markert, 1957; Shaw and Prasad, 1970). Over and above these scientific advantages, this technique is economically more practicable.

Horizontal starch gel electrophoresis is the most commonly used procedure. Watanabe *et al.* (1965) and Watanabe and Suzuki (1966) used vertical starch gel electrophoresis which was carried out using discontinuous buffer system.

Nguyen and Bunch (1980) and Barbancho *et al.* (1984) identified biochemical polymorphisms in goat red blood cells, serum and plasma using horizontal starch gel electrophoresis according to the method described by Smithies (1955).

2.3.2. Cellulose Acetate Electrophoresis [CAE]

Cellulose acetate electrophoresis was introduced by Kohn in 1957. This technique is used routinely for the separation of plasma proteins, glyco and lipoproteins, hemoglobin, enzymes and other proteins.

Here a supporting medium of cellulose acetate membrane strips is used. This method has several advantages such as reduction in protein absorption. The membrane strips are chemically homogeneous and can be readily rendered transparent so that stained protein bands can be determined by scanning and adequate separation of bands for analytical purposes can usually be achieved within one to two hours.

As a support medium for electrophoresis, cellulose acetate strips possesses a number of advantages over polyacrylamide or starch gel [STAGE] in the following areas (Meera Khan, 1973; Harris and Hopkinson, 1976; Gordon, 1980 and Richardson *et al*, 1986):

1. **Amount of stain required**: Conventional stains for STAGE involve volumes of 20-100ml. The cellulose acetate strips require only 2-3 ml of stains. The subsequent

cost saving can be considerable, especially for enzyme stains containing a very expensive ingredient.

2. **Amount of sample required**: The other support media commonly requires 10-50 microlitres per sample per enzyme run. whereas cellulose acetate requires only 0.5-2 microlitres.
3. **Preparation time**: Gels made from starch, acrylamide or agarose have to be made up just prior to use . Cellulose acetate gels, however, come ready to use.
4. **Run time**: Cellulose acetate gels need only run for 1-2 hours and acrylamide and starch gels usually runs longer - sometimes overnight.
5. **Staining time**: Isoenzymes are stained much more quickly on cellulose acetate gels, since the stains ingredients 'surround' the isoenzymes rather than having to diffuse into the gel.
6. **Run voltages**: Lower voltages are required for cellulose acetate electrophoresis than for some of the other support media.

2.4. BIOCHEMICAL POLYMORPHISM STUDIES IN GOATS

Biochemical genetics plays a vital role in the studies of phylogeny of goats. The similarities and differences between goat species or between populations or sub-populations within species in the polypeptide composition of given proteins will probably provide invaluable clues to the inter-specific and intra-specific relationships.

Considerable research has been carried out worldwide into biochemical polymorphisms in order to study the genetic relationships between population of various species of farm animals, especially cattle and sheep (Tucker *et al.*,1967; Wilson *et al.*,1970; Tucker,1971; Kidd ,1974; Tucker,1975; Abe *et al.*, 1977, Ordas and San

Primitivo, 1986). However, very little work has been done in goats, especially with the indigenous goat breed of Southeast Asia, apart from few studies on Indonesian goats (Katsumata *et al.*, 1981b), Thailand native goats (Watanabe and Suzuki, 1973), and the Malaysian goats (Nishida *et al.*, 1975; Shotake et al.,1976 and Hasima, 1986). A summary of reports on genetic markers in goats by various workers is shown in Table 2.

2.4.1 Early studies on polymorphic markers

While doing this review on early studies, a chronological year by year development of electrophoretic identification of various systems has been presented. An attempt was made to present the review separately for different systems in this section but this was done while presenting results and discussion in the following chapters. A comparison of the results on gene/genotype frequencies was not made here because of differences in sample size, methodology and breed/strains used in various studies. However an attempt to make some comparisons between these reports and the results of the present study will be made in the discussion section of the thesis.

Biochemical Polymorphisms Work Between 1965-1974:

The ß-globulins of the native Japanese goats, Swiss and Hungarian Saanen, German coloured and Italian Alpine goats were identified as transferrin and were classified into three phenotypes by Watanabe *et al.*, (1965a). The following year, they investigated the mode of inheritance of serum transferrin types and the gene frequencies in several breeds. It was then suggested that these transferrin types were controlled by 2 allelomorphs Tf^{I} and Tf^{II}, giving three genotypes Tf I/Tf I, Tf I/TfII and Tf II/Tf II.

The 2 alleles are codominant. The gene frequencies were 0.915 for Tf^{I} and 0.085 for Tf^{II}.

Serum albumin of goats from 1628 heads of Japanese Saanen, Japanese native goats (Tokara goat), native goats and their hybrids in Rhukyu Island, Saanen goats in Switzerland, German colored goats. Alpine goats in Italy, Saanen goats in Hungary, native goats and their hybrids and Angora goats and their hybrids in Formosa were classified into three types Alb AA, Alb BB and Alb AB by different mobility's. The albumin phenotypes were controlled by two autosomal alleles (Watanabe and Suzuki, 1967).

Studies carried out on protein polymorphism in goat population of South Italy (Salerno *et al.*, 1968) revealed three phenotypes for transferrin, Tf AA, Tf AB and Tf BB which is controlled by two codominant alleles, Tf^{A} and Tf^{B} with allele frequency of 0.835 and 0.165 respectively. In the case of albumin, three phenotypes were observed, Alb FF, Alb FS and Alb SS, also controlled by two codominant alleles: Alb^{F} and Alb^{S} with frequencies 0.34 and 0.65 respectively.

Watanabe and Suzuki (1973), encountered three additional phenotypes while working with transferrin (Tf AC, Tf BC and Tf CC) and redesignated the alleles as Tf^{A} and ^{TfB}, and postulated a new allele, Tf^{C} in serum transferrin. The serum transferrin in goats was then controlled by 3 codominant alleles, Tf^{A}, Tf^{B} and Tf^{C}. The gene frequencies of Tf^{C} was low in native goats in Korea (0.072), Philippines (0.019) and Thailand (0.006). The gene frequencies of Tf^{A} and Tf^{B} are 0.723 and 0.205 for Korea, 0.763 and 0.219 for the Philippines, and 0.317 and 0.677 for Thailand respectively.

Biochemical Polymorphisms Work Between 1975-1984:

Limited studies with very small numbers of animals (range: 2-23) have been made on genetic polymorphisms in Malaysian goats. Nishida *et al.*, (1975) while working with Malaysian Katjang goats, Jamnapari and crossbreds, screened for 13 loci, namely, albumin (Alb), plasma slow α-2-macroglobulin, hemoglobin (Hb), esterase-D (Est-D), adenylate kinase (AK), 6-Phosphogluconate dehydrogenase (6PGD), NADH-Diaphorase (DIA), Glucose phosphate isomerase (GPI), Lactatre dehydrogenase-B (LDH-B), Malate dehydrogenase (MDH), tetrozolium oxidase (SOD), Transferrin (Tf) and phosphohexose isomerase (PHI). Ten loci were completely monomorphic for the alleles common to the Japanese goats. Only three loci showed variations, namely malate dehydrogenase, esterase and transferrin.

The malate dehydrogenae and esterase loci were observed to have variants, each of which appeared to be present in only one Sarawak goat. The appearance of those variants, however, may be due to the denaturation of the blood samples. The genetic polymorphisms of the transferrin locus is indicated by high frequency of Tf^{B} alleles for the Katjang goat populations of Peninsular Malaysia (0.57). However, the frequencies of Tf^{A} was much higher in the East Malaysian Katjang Goats (0.78) but lower in the Jamnapari breed (0.05) and the crossbred (0.44) (Nishida *et al.*, 1975).

The activity of PGM_3 (phosphoglucomutase-3) was investigated by Pretorius *et al.*, (1976), in 150 'Boerbok' goats and 132 Angora goats by horizontal starch gel electrophoresis. No polymorphism was reported in the 'Boerbok' goats but in the Angora goats three phenotypes have been recognized : PGM_3 FF, PGM_3 FS and PGM_3 SS and it is controlled by two common alleles : PGM_3^{F} and PGM_3^{S} at an

autosomal locus. The frequencies observed for PGM_3^F and PGM_3^S alleles were 0.618 and 0.382 respectively.

A study conducted by Baruah and Bhat (1980) on Indian breeds of goats, the Barbari, Jamnapari and Black Bengal showed the presence of two alleles for transferrin, Tf^A and Tf^B with frequencies of 0.44, 0.27, 0.37 for Tf^A and 0.56, 0.73 and 0.63 for Tf^B respectively.

Two X-protein phenotypes were observed, one consisting of a major and 2 minor band, designated X +ve, following the nomenclature of Tucker and Clarke (1980), and the other in which all three bands are absent, designated X-null. The latter is now accepted as equivalent to X negative, and the major or single intensely staining band is taken as the X-positive phenotype (Tucker *et al.*, 1980).

Panandam (1981) studied the blood protein markers of 5 breeds of goats in Malaysia, that is, 12 Anglo-Nubians, 11 British Alpines, 18 Saanens, 19 Ferals and 25 Katjang breeds. They did not exhibit any variant phenotype for 4 erythrocyte enzymes (malate dehydrogenase, lactate dehydrogenase, alkaline phosphatase and 6-phosphogluconate dehydrogenase) and plasma protein, transferrin. Absence of any variation in these loci may due to the small sample size. Only haemoglobin marker showed any variant, with 2 forms, Hb AA and Hb AB. The Hb BB phenotype was not observed in any of the goat samples analysed. All the breeds had both phenotypes, except for the Anglo-Nubian, which exhibited only the Hb AA phenotype.

Katsumata *et al.*, (1981a), studied 7 populations of Saanen breed reared in Japan. They estimated genetic variabilities in the goat population by using gene frequencies obtained from the starch gel electrophoretic examination of 27 genetic loci controlling the structure of 25 kinds of enzymatic and non-enzymatic blood proteins. Genetic polymorphisms were observed at 11 loci, namely, haemoglobin, transferrin, plasma non-

specific esterase, alkaline phosphatase, prealbumin-3, amylase, cell esterase-D, phosphohexose isomerase, cell estrase-1, adenylate kinase and peptidase-B.

Katsumata *et al.*, (1981b) also studied 28 loci for Etawa and katjang goats in Indonesia. Only 4 loci displayed polymorphisms namely transferrin, esterase-D, prealbumin-3, and alkaline phosphate. Three phenotypes (Tf A, Tf AB and Tf B) were observed for transferrin with two codominant alleles Tf^A and Tf^B, three phenotypes for prealbumin-3 (PA-3 1, PA-3 2) with two codominant alleles $PA\text{-}3^1$ and $PA\text{-}3^2$, two phenotypes each for alkaline phosphatase (Ap F and Ap O) and esterase (Es-1 and Es-2).

The following year, Katsumata *et al.*, (1982), carried out investigations on blood protein polymorphism at 32 genetic loci starch gel electrophoresis on 6 populations of Korean native goats. Genetic polymorphisms were observed at general esterase, alkaline phosphatase , prealbumin-3, cell esterase-D, lactate dehydrogenase A and peptidase B.

Blood samples of 398 Saanen goats and 500 kids of these goats were analysed by starch gel electrophoresis by Sartore *et al.*, (1982). They reported, 3 Hb types [Hb A, Hb AB and Hb B], while 2 other types, representatives of fetal-Hb (A and F) were found in adults and were in Hardy-Weinberg equilibrium. Data from various mating types confirmed that the Hb phenotypes were controlled by 2 codominant autosomal alleles Hb^A and Hb^B.

Investigations were further carried out in order to characterize certain breeds of goats (Katsumata *et al.*, 1983) using the data on biochemical polymorphisms of haemoglobin , serum transferrin, red cell carbonic anhydrase, ceruloplasmin and arylesterase on 224 Hungarian native female goats and 21 imported male goats comprising of German Improved Fawns, Saanens, Nubians and Slovakian white breeds.

Table 2. Some of the investigations carried out on genetic markers in goats

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Plasma Albumin	Native Norwegian goats	Absent	Efremov & Braend (1965)
	German Colored	Present	Watanabe & Suzuki (1967)
	Hungarian Saanen	Present	Watanabe & Suzuki (1967)
	Italian Alpine goats	Present	Watanabe & Suzuki (1967)
	Swiss Alpine goats	Present	Watanabe & Suzuki (1967)
	Tokara & its hybrids	Present	Watanabe & Suzuki (1967)
	Tokara	Present	Watanabe & Suzuki (1967)
	Angora & its hybrids	Present	Watanabe & Suzuki (1967)
	Lucania (Southern Italy)	Present	Salerno *et al.*, (1968)
	Boer	Present	Osterhoff & Ward-Cox (1972)
	Indigenous (South Africa)	Present	Osterhoff & Ward-Cox (1972)
	Angora, aborters	Present	Osterhoff & Ward-Cox (1972)
	Angora, non-aborters	Present	Osterhoff & Ward-Cox (1972)
	Toggenburg	Present	Tjankov (1970)
	Indigenous (Bulgaria)	Present	Tjankov (1970)
	Saanen	Present	Tucker & Clarke (1980)
	Hungarian Native goats	Absent	Fesus *et al.*, (1983)
	Granadina (Spanish)	Present	Barbancho *et al.*, (1984)
	Murciana	Present	Barbancho *et al.*, (1984)
	Malaguena	Present	Barbancho *et al.*, (1984)
	Serrana	Present	Barbancho *et al.*, (1984)
	South African Angora goats	Present	Osterhoff *et al.*, (1987)
	Spanish goats	Present	Tunon *et al.*, (1987b)
	Katjang	Present	Hasima *et al.*, (1986)
	Norwegian goats	Absent	Braend *et al.*, (1987b)
	Spanish goats	Present	Stasio *et al.*, (1988)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)
	French goats	Absent	Pepin & Nguyen (1994)
	Angora X Zhougwei goats	Absent	Han *et al.*, (1996)
	Cashmere goats (China)	Absent	Ma Ning *et al.*, (1996)

(Contd. Table 2.) Some of the investigations carried out on genetic markers in goats

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Plasma Amylase	Braune & Weisse Deutsche Edelziege	Present	Meyer (1967)
	Angora	Present	Fechter & Pretorius (1970)
	Boer	Present	Osterhoff & Ward-Cox (1972)
	Indigenous (South Africa)	Present	Osterhoff & Ward-Cox (1972)
	Angora, aborters	Present	Osterhoff & Ward-Cox (1972)
	Angora-non-aborters	Present	Osterhoff & Ward-Cox (1972)
	Toggenburg	Present	Tjankov (1972)
	Japanese Saanen	Absent	Ishimoto (1972)
	Indigenous (Bulgaria)	Present	Tjankov (1972)
	Appenzeller	Present	Kunz (1974)
	Verzasca	Present	Kunz (1974)
	Walliser Schewarzhals	Present	Kunz (1974)
	Hungarian Native goats	Present	Fesus *et al.*, (1983)
	Pashmina goats	Absent	Bhat (1987a)
	Spanish native goats	Present	Stasio-L *et al.,*(1988)
	Czechoslavakian goats	Present	Trakovicka (1991)
	Cashmere goats (China)	Present	Ma Ning *et al.*, (1996)
	Angora x Zhongwei	Present	Han *et al.*, (1996)
Haptoglobin	Japanese Saanen	Absent	Ishimoto (1972)
Nucleoside phosphorylase	Saanen	Absent	Tucker & Clarke (1980)
	Saanen & its hybrids	Present	Tucker & Clarke (1980)
	South African local	Present	Tucker & Clarke (1980)
	Boer	Present	Tucker & Clarke (1980)
	Spanish goats	Absent	Tunon *et al.*, (1987b)
	Italian breeds	Present	Rizzi *et al.*, (1987)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)

(Contd. Table 2.) Some of the investigations carried out on genetic markers in goats

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Cell lactate dehydrogenase	Katjang goats	Absent	Nishida *et al.*, (1975)
	Saanen	Absent	Tucker & Clarke (1980)
	Grey goats (China)	Present	Zhang *et al.*, (1995)
Cell NADH diaphorase	Saanen	Absent	Ishimoto (1972)
	Saanen	Absent	Tucker & Clarke (1980)
	Hungarian Native goats	Present	Fesus *et al.*, (1983)
	Spanish goats	Present	Tunon *et al.*, (1987a)
	Okinawa meat goats	Absent	Nozawa *et al.*, (1987b)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)
Esterase-D	Etawa goats	Present	Katsumata *et al.*, (1981b)
	Katjang goats	Present	Katsumata et al., (1981b)
	Korean Native goats	Present	Katsumata et al., (1982)
Plasma alkaline phosphotase	Japanese Saanen	Present	Watanabe (1971)
	Tokara	Present	Watanabe (1971)
	Korean Native goats	Present	Watanabe (1971)
	Angora	Present	Watanabe (1971)
	Swiss Saanen	Present	Watanabe (1971)
	German coloured	Present	Watanabe(1971)
	Italian Alpine goats	Present	Watanabe (1971)
	Hungarian Saanen	Present	Watanabe (1971)
	Etawa goats	Present	Katsumata *et al.*, (1981b)
	Katjang goats	Present	Katsumata *et al.*, (1981b)
	Russian mohair goats	Present	Kazanovkii *et al.*, (1984)
	Pashmina goats	Present	Bhat *et al.*, (1987b)
	Spanish goats	Present	Tunon *et al.*, (1987b)
	Cashmere goats (China)	Present	Ma Ning et al.,(1996)

(Contd. Table 2.) Some of the investigations carried out on genetic markers in goats

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Plasma ceruloplasmin	Pashmina goats	Absent	Bhat (1987a)
	Spanish goats	Absent	Tunon *et al.*, (1987b)
	Czechoslavakian goats	Present	Trakovicka (1991)
Plasma Transferrin	Etawa goats	Present	Katsumata *et al.*, (1981b)
	Sri Lankan goats	Present	Shotake *et al.*, (1986)
	South African Saanen	Present	Osterhoff *et al.*, (1987)
	Pashmina goats	Present	Bhat (1987a)
	Spanish goats	Present	Tunon *et al.*, (1987b)
	Angora goats (Turkey)	Present	Erkoc *et al.*, (1987)
	Malabari goats & crossbreds	Present	Shamsuddin *et al.*, (1988)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)
	Ibex (Italy & Switzerland)	Present	Randi *et al.*, (1990)
	Alpine goats	Present	Randi *et al.*,(1990)
	Alpine-Angora	Present	Wang *et al.*., (1991)
	Anglo-Nubian	Present	Wang *et al.*, (1991)
	Saanen	Present	Wang *et al.*,(1991)
	Spanish goats	Present	Wang *et al.*,(1991)
	Australian Angora	Present	Vankan & Bell (1992)
	Cashmere goats	Present	Vankan & Bell. (1992)
	Dairy breed (Australian)	Present	Vankan & Bell (1992)
	French breeds	Present	Pepin & Nguyen (1994)
	Angora X Zhongwei goats	Present	Han *et al.*, (1996)
	Cashmere goats (China)	Present	Ma Ning *et al.*, (1996)

(Contd. Table 2.) Some of the investigations carried out on genetic markers in goat.

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Haemoglobin			
	Japanese Saanen	Present	Katsumata *et al.*,(1981a)
	Hungarian Native goats	Present	Katsumata *et al.*,(1983)
	South African goats	Present	Tucker *et al.*,(1983)
	Russian Mohair goats	Present	Kazanovski *et al.*, (1984)
	Saanen	Present	Sartore *et al.*, (1982)
	Jamnapari & Sirohi goats	Present	Bhat., (1986)
	South African Native goats	Present	Osterhoff *et al.*, (1987)
	South African Native Boer	Present	Osterhoff *et al.*, (1987)
	Norwegian goats	Present	Braend *et al.*, (1987a,b)
	Ganjana & Black Bengal goats	Present	Panda *et al.*, (1987)
	Pashmina goats	Absent	Bhat *et al.*, (1987a)
	Katjang goats	Present	Hasima (1986)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)
	Alpine	Present	Wang *et al.*, (1991)
	Angora	Present	Wang *et al.*,(1991)
	Anglo-Nubian	Present	Wang *et al.*,(1991)
	Spanish goats	Present	Wang *et al.*, (1991)
	French breed of goats	Present	Pepin & Nguyen (1994)
	Angora x Zhingwei goats	Present	Han *et al.*, (1996)
	Cashmere goats (China)	Absent	Ma Ning *et al.*, (1996)
	West African Dwarf goats	Present	Ologun & Imumorin (1996)
X-Protein	Spanish goats	Present	Tunon *et al.*, (1987a)
	Spanish goats	Present	Tunon *et al.*,(1987b)
	Norwegian goats	Present	Braend *et al.*, (1987)
	Katjang goats	Present	Hasima *et al.*,(1988)
	Sheep-goat hybrid	Present	Tucker *et al.*,(1989)
	French breed of goats	Present	Pepin & Nguyen (1994)
Carbonic anhydrase	Spanish goats	Present	Barbancho *et al.*,(1984)
	Spanish goats	Present	Tunon *et al.*, (1987b)
	Italian breed of goats	Absent	Rizzi *et al.*,(1987)
	South African Angora	Absent	Osterhoff *et al.*,(1987)
	Saanen	Absent	Osterhiff *et al.*,(1987)
	Boer	Absent	Osterhoff *et al.*,(1987)
	South African Native goats	Absent	Osterhoff *et al.*,(1987)
	Sheep-goat hybrid	Present	Tucker *et al.*, (1989)
	French breed of goats	Absent	Pepin & Nguyen (1994)

MARKER	GOAT BREEDS	POLYMORPHISM	REFERENCES
Reduced glutathione catalyse	Spanish goats	Absent	Tunon *et al.*, (1987b)
Malate dehydrogenase	Katjang goats	Present	Nishida *et al.*,(1975)
	Anglo-Nubian	Absent	Panandam (1981)
	Saanen	Absent	Panandam (1981)
	Ferals	Absent	Panandam (1981)
	Katjang goats	Absent	Panandam (1981)
	Spanish goats	Absent	Tunon *et al.*,(1987)
Malic enzyme	Sheep-goat hybrid	Present	Tucker *et al.*,(1989)
	Mediterranean breeds	Present	Stasio *et al.*,(1995)
αs1-Casein	Alpine goats	Present	Grosclaude *et al.*,(1987)
	European breed of goats	Present	Langley (1993)
	Somali Arab goats	Present	Stasio *et al.*,(1993)
	Italian &Mediterranean goats	Present	Ramunno *et al.*,(1994)
	Saanen & Alpine goats	Present	Bouniol *et al.*,(1994)

All males were homozygous for Hb AA, , Tf AA and Amy AA types. Polymorphism was observed only in haemoglobin, transferrin and amylase for female goats.

The gene frequencies of Hungarian Native were for haemoglobin, Hb^{A} = 0.954 and Hb^{B} = 0.046, for transferrin, Tf^{A} = 0.588 and Tf^{B} = 0.412 and for amylase , Amy^{A} = 0.996 and Amy^{B} = 0.004. On the basis of their results, these workers concluded that the examined biochemical traits cannot be used efficiently in parentage control and in correlation studies. There was no apparent association between haemoglobin and transferrin types of the females and their reproductive performances.

Tucker *et al.*, (1983) carried out a joint study in a search for new phenotypes markers in the blood of different goat herds in South Africa and England. Haemoglobin (Hb) phenotypes were investigated using isoelectric focusing (IEF). Anemic Hb type A, AB and B goats, all produced a Hb with an identical electrophoretic pattern. Hb A predominated in all the goat populations tested. All goats tested had an identical carbonic anhydrase (CA) type. Two phenotypes were observed for X-protein, the X-negative and the X-positive. The positive phenotype was predominant in all goat populations tested. At least two phenotypes were observed in the goat populations for nucleoside phosphorylase, the common one showing a broad zone of NP activity (type 1) and less common variant (type 2) which lacked the more cathodal region of type 1.

Kazanovskii *et al.*, (1984) while working with Soviet Mohair goats identified five Tf alleles, 2 alleles for Hb, 2 alleles for carbonic anhydrase, 2 alleles for arylesterase and 3 for alkaline phosphatase. They observed a very high frequency for allele Tf^{D} (0.462) and for alkaline phosphatase allele Ap^{B} (0.738). Alleles with low frequencies were Tf^{A} (0.008) and alkaline phosphatase Ap^{C} (0.03).

Barbancho *et al.*, (1984) demonstrated biochemical variation of 4 genetic markers (Hb, Al, Tf and X-protein) in the blood of 4 Spanish goat breeds using gel electrophoresis. Only 2 haemoglobin types (Hb A and Hb B) were found. Most of the world's breeds are either fixed for Hb^A allele (Efremov and Braend 1965, Kunz 1974, Crottaz 1975) or have Hb A frequency considerably higher than that of Hb B (Osterhoff and Ward-Cox 1972, Crottaz 1975, Milovan and Granciu 1978, Fesus *et al.*, 1983). The frequencies of the Hb^A allele in the Spanish breeds studied are higher than for most of the other breeds studied so far. Three transferrin alleles were found namely, Tf^A, Tf^B, and Tf^C. Three albumin phenotypes have been described: Alb FF, Alb FS and Alb SS.

Biochemical Polymorphisms Work Between 1985-1996:

Bhat (1986) examined blood samples from 592 Jamnapari and 30 Sirohi goats by starch gel electrophoresis. Gene frequencies in the Jamnaparis for Hb^A and Hb^B were 0.99 and 0.01 respectively. Gene frequencies for Tf^A, Tf^B and Tf^C were 0.146, 0.845 and 0.008 respectively in Jamnapari. This was the first report of a 3rd Tf allele in an Indian goat breed. No variation was found for haemoglobin and transferrin in the Sirohi goats. Gene frequencies for Amy^1 and Amy^2 were 0.97 and 0.03 respectively in the Jamnapari, and 0.98 and 0.02 in Sirohis. Cerulopasmin, arylesterase and erythrocyte potassium were monomorphic in these two breeds.

The native Sri Lankan goats were phenotypically similar to the small meat type in Southeast Asia. Shotake. *et al.*, (1986) described that of the 33 blood proteins loci examined electrophoretically, Sri Lankan goats were characterized by relatively high frequency of the Tf^B allele compared with other Southeast Asian goats. A new Tf

variant, Tf^A was found in the Galle goat population in Sri Lanka. Three phenotypes (PA-3 1-1, PA-3 2-1 and PA-3 2-2) were observed for prealbumin-3 with two codominant alleles $PA\text{-}3^1$ and $PA\text{-}3^2$. The PA-3 2 allele frequency were much higher ranging from 0.650-0.861.

Three phenotypes were also observed for ß-haemoglobin (Hb 1-1, Hb 1-3 and Hb 3-3) with only animals showing variant Hb 1-3 and two individuals showing variant Hb 3-3. Two phenotypes each were observed for alkaline phosphatase (Ap O and Ap F) amylase (Amy 1-1 and Amy 1-3), esterase-D (EsD 1-1 and EsD 1-2) and malate dehydrogenase (Mdh 1-1 and Mdh 1-2) (Shotake *et al.*, 1986).

In contrast, Ugrar *et al.*, (1986) reported the electrophoretic work on 48 plasma samples from Angora goats of Turkey, the most frequent Tf allele in their study was Tf^A. Their results revealed 54.17% Tf AA, 31.25% Tf BB and 14.58% Tf AB types.

Osterhoff *et al., (*1987) undertook an investigation in search of genetic markers, i.e. haemoglobin, transferrin, albumin, acid phosphatase, phospho-glucomutase, 6-phosphogluconate dehydrogenase, carbonic anhydrase and X-protein in the most important goat breeds in South Africa-Angora, Saanen, Boer and native goats. Polymorphisms were detected in albumin, transferrin and haemoglobin. Following genes frequencies were observed for Hb in Boer (Hb^A : 0.998, Hb^B : 0.002), Native (Hb^A : 0.950, $Hb\,B$: 0.050), Saanen (Hb^A : 0.740, Hb^B : 0.260)and Angora (Hb^A : 1.00, Hb^B : 0.000). Alb in Boer (Alb^A : 0.00, Alb^B : 1.00), Native (Alb^A : 0.00, Alb^B : 1.00) Saanen (Alb^A : 0.00, $^{Alb\ B}$: 1.00) and Angora (Alb^A : 0.02, Alb^B : 0.98). For transferrin in Boer (Tf^A : 0.58, $^{Tf\ B}$: 0.42), Native (Tf^A : 0.79, Tf^B : 0.21), Saanen (Tf^A : 0.61, Tf^B : 0.39) and Angora (Tf^A : 0.79, Tf^B : 0.21). In the enzyme systems phosphohexose-isomerase , 6-phosphogluconate dehydrogenase, phosphoglucomutase, carbonic anhydrase and acid phosphatase no polymorphism was observed.

The genetic variability was studied for 27 genetic loci in the meat goats in Okinawa Islands of Japan (Nozawa *et al.*, 1978b). Of the 27 genetic loci examined 18 loci that is, α-Haemoglobin, haptoglobin, plasma slow-σ 2 macroglobin, ceruloplasmin, prealbumin-1, prealbumin-2, 6-phosphogluconate dehydrogenase, phosphohexose isomerase, malate dehydrogenase, NADH-diaphorase, acid phosphatase, tetrazolium oxidase, lactate dehydrogenase-A, lactate dehydrogenase-B, esterase-1, esterase-2, adenylate kinase and catalase were observed to lack any variation. Polymorphisms were only observed at 8 loci i.e. ß-hemoglobin, albumin, transferrin, plasma non-specific esterase, plasma alkaline phosphatase, plasma leucine aminopeptidase, amylase and esterase-D.

Rizzi *et al.*, (1987) examined electrophoretically blood samples from Chamois coloured goats on 2 farms in Italy. They reported that only the albumin, haemoglobin, nucleoside phosphorylase and X-protein loci were polymorphic. There was no variation observed in transferin, esterase and carbonic anhydrase loci.

Bhat (1987a) further examined the biochemical polymorphism of blood serum proteins and enzymes in Pashmina goats of India. In his studies of 206 Cheghu goats, the frequencies of the Tf^A, Tf^B and Tf^C alleles were 0.79, 0.19 and 0.02 respectively, as compared to the gene frequencies obtained for 52 Changthang goats 0.66, 0.30 and 0.04 respectively. All goats showed 2 albumins bands. There was no variation observed for haemoglobin, amylase or ceruloplasmin.

In another study by Bhat *et al.*, (1987b) in Pashmina goats of India with 200 Cheghu and 48 Changthang goats, the gene frequencies for alkaline phosphatase were Ap^F (0.09) and Ap^O (0.91) for the Cheghu goats and Ap^F (0.20) and Ap^O (0.80) for the Changthang goats. There was no significant differences observed between the two breeds in blood potassium or sodium concentration, and neither of these were significantly affected by sex.

Blood samples from 1370 goats of 14 Spanish breeds were analysed for 14 constituents by Tunon *et al.*, (1987b). Out of the fourteen blood genetic systems analysed eight were polymorphic : erythrocyte potassium, Haemoglobin, diaphorase, X-protein, alkaline phosphatase, amylase, transferrin and albumins. Reduced glutathione, catalase, malate dehydrogenase, carbonic anhydrase, nucleoside phosphorylase and ceruloplasmin were monomorphic.

Panda *et al.*, (1987) while examining 145 adult blood samples of Ganjam goats and 20 Bengal goats of India noted that all the goats were homozygous for Hb A. In the same year another group of researchers from Mohanpur, India led by Mandal *et al.*, using starch gel electrophoresis described polymorphism at the transferrin locus in 110 Black Bengal goats. They discovered that the population was not in Hardy-Weinberg equilibrium and there were 3 codominant alleles i.e. Tf A, Tf B and Tf C expressing 5 phenotypes which are Tf AA, Tf AB, Tf BB, Tf BC and Tf AC. Following this Mandal *et al.*,. (1987b) further reported that 92 Black Bengal goats studied showed polymorphism at the serum albumin locus with 2 codominant alleles and the population studied was in Hardy-Weinberg equilibrium.

A study on the genetic polymorphisms of blood proteins and enzymes in Soviet Mohair and Dagestan White goats in relation to breeding improvement was done by Ostapenko and Ol'khovskaya (1987). They identified 5 Tf alleles and 10 phenotypes in the Soviet Mohair with the most frequent type being Tf CD at 16.2%. In Dagestan White goats, which produce cashmere, there were 4 Tf alleles and six phenotypes with the most common type being Tf CC with a frequency of 30.9%. Allele Tf^{E} was absent in Soviet Mohairs and allele Tf^{D} was absent in Dagestan Whites. There were significant breed differences in allele frequencies. In both breeds, 2 arylesterase alleles, controlling 3 phenotypes, were identified. For alkaline phosphatase, there were 3 alleles

in Soviet Mohairs, controlling 5 phenotypes; in Dagestan Whites, 2 alleles controlled 3 phenotypes. Both breeds had a high frequency of allele Ap^B and phenotype Ap BB homozygotes. The Dagestan Whites had 3 alleles at the albumin locus while the Soviet Mohairs were monomorphic.

Braend *et al.*, (1987b) examined 150 Norwegian goats from 4 herds. They were typed for serum albumin and transferrin , and for erythrocyte carbonic anhydrase, alkaline phosphotase. X-protein and potassium concentration. Only the X-protein nucleoside phosphorylase showed variation. Isoelectric focussing [IEF] over pH range 6-8 showed that 145 samples were of Hb type AB. The type was resolved into further sub-types by separation over pH 6.9 - 7.5 in Immobiline polyacrylamide gels. 2- or 4-band patterns were present in 136 of the samples. A hypothesis based on 4 genetic variants of Hb A is proposed. Fourteen samples had a 3-, 5-, or 6-banded Hb pattern. It was assumed that these were heterozygotes for a variant of the gamma-gene.

Three NADH Diaphorase 1 phenotypes were observed in blood samples from 1368 goats of 14 Spanish breeds (Tunon *et al.*, 1987a). Two regions of diaphorase activity were observed on starch gel electrophoresis. Region 2 consisted of a single band activity in the most cathodal area and no variation was observed. In region 1, one or two bands appeared in a more anodal position than region 2. Three phenotypes were observed : Dia F, Dia FS and Dia S. They concluded that the polymorphism was controlled by 2 autosomal, codominant alleles : Dia^F and Dia^S. Gene frequencies of allele Dia^F was high for all breeds ranging from 0.822 to 1.00.

Haemoglobin samples from 260 Norwegian goats were electrophoresed using the Immobiline technique by Braend *et al.*, (1987b). They observed either 2- or 4- banded patterns. Using polyacrylamide gel electrophoresis on 52 samples in order to separate α- and ß-chains, 3 ß-chain phenotypes were detected, and segregation data from 106

families indicated that there were 4 ß-globulin alleles, viz. A2, A4, A6 and A8. In goats with 2-banded Hb patterns, the average ratio between anodal and cathodal bands was 74:26 ; 27 animals had reversed ratios. In 15 families where 1 parent had a reversed ratio, 8 offspring had the reversed ratio type, indicating a simple mode of inheritance of the reversed type. Reversed ratio animals all had the same α-chain phenotype, which was different to that of animals with the normal ratio. Nine goats had 3- and 5- banded patterns, which were assumed to be the result of heterozygosity at II α, and at II σ and ß-globulin genes respectively.

While conducting research work on the relationship of blood potassium, haemoglobin and transferrin and fibre sulphur proteins with mohair quality in Angora goats, Erkoc *et al.*, (1987) confirmed that there was no significant co-relations of the genetic markers with mohair staple quality, fibre diameter or the percentage of medullated fibres, and mohair quality was not affected by sulphur protein values. In their 830 blood samples collected from Angora goats in Turkey, they found that the most common Hb types were A, AB and B, in that order. Transferrin phenotype A was the most frequent followed by AB, B, BC and CC. Two potassium phenotypes, HK (high potassium) and LK (low potassium) were noted. The HK and LK character is genetically determined by a single locus with two alleles, HK being recessive.

Genetic polymorphism of X-protein in the red blood cell of Katjang goats was demonstrated by Hasima *et al.*, (1988) by starch gel electrophoresis. Two new phenotypes were observed, in addition to the 2 known phenotypes, suggesting that one new allele is involved. The available data were consistent with control of the X-protein phenotypes by 2 autosomal, codominant alleles, Xp^{1} and Xp^{2} and an autosomal, recessive allele, Xp^{O}. A new nomenclature for the X-protein was proposed.

Kumar and Yadav (1988) examined 74 goats of the Jhakrana, Kutshi [Gujarati], Marwari and Sirohi breeds of northwestern India, electrophoretically for transferrin polymorphisms. Six phenotypes and 3 alleles were detected. They observed that the frequency of Tf^{C} allele was higher in Jhakrana goats (0.219) than in Kutchi, Marwari or Sirohi goats (0.026, 0.026 and 0.075 respectively). Braend and Tucker (1988) attempted to study the haemoglobin types in Saanen goats by the use of Immobiline technique at pH ranges from 7.0 to 7.6 and 6.9 to 7.9, 16 Hb phenotypes were observed in 61 Saanen goats. It is hypothesised that there are 5 ß-globin genes (A4, A6, A8, E and D) and 2 closely linked α-globin loci ('alpha and "alpha), of which the "alpha has a variant allele, previously called "alpha X. Family data and observed and expected Hb frequencies were in agreement with the hypothesis.

Electrophoretic studies on transferrin polymorphism in Malabari goats and its exotic crossbreds were conducted by Shamsuddin *et al.*, (1988). Blood samples from 188 Malabar, Saanen X Malabar and Alpine X Malabar goats were typed electrophoretically and 4 phenotypes were observed. The most frequent in all breed types was Tf AB and phenotype AC was only observed in goats with Saanen or Alpine ancestry. The Tf^{B} allele was most common in Malabar goats, Tf^{A} was the most common in crossbred goats and Tf^{C} was found only in crossbreds. Goats with the Tf AA phenotype had a higher 1st - lactation yield and peak yield than other phenotypes for Malabar and Alpine X Malabar breed types, and higher birth weight and lower kidding interval for Saanen X Malabar crossbreds.

Biochemical polymorphism was reported in haemoglobin, X-protein, albumin, amylase, alphas1-casein and alphas2-casein loci in the French-Alpine goats by Stasio-L and Di-Stasio (1988).

Tucker and Baker (1989a) in their efforts to the understanding of blood and milk polymorphisms of goats and sheep listed the following polymorphic loci in goats: albumin (Al), Amylase (Amy), Casein Alpha S1 (CnalphaS1), Casein Alpha S2 (CnalphaS2), Catalase (Cat), Erythrocyte antigen J System (EAJ), Haemoglobin Alpha 1 (Hbalpha1), Haemoglobin Beta (Hbbeta), Haemoglobin Beta C (HbbataC), Haemopexin (Hbx), NADH Diaphorase (Dia), Potassium Transport (Ke), Transferrin (Tf) and X-Protein (Xp).

Tucker *et al.,* (1989b) conducted an electrophoretic studies on blood samples from a female sheep-goat hybrid and its back-cross male offspring for plasma albumin (ALB), transferrin (Tf), plasma esterase (ES), red cell carbonic anhydrase (CA), nucleoside phosphorylase (NP), NADH-diaphorase (NADH-DIA), X-Protein (XP), superoxide dismutase (SOD), malic enzyme (ME) and haemoglobin (Hb).The results from this study indicated that the red cell markers 'X'-protein, NADH-diaphorase 1 and 2, malic enzyme, superoxide dismutase and nucleoside phosphorylase in the hybrid had a phenotype that could not be attributed to either sheep or goat alone. Hybrid bands were clearly seen in the hybrid animals in the case of 'X'-protein and Dia-1 and also in superoxide dismutase.

In an attempt to study genetic variability and conservation , Randi *et al* ., (1990) typed 10 protein and enzyme loci in 20 ibex in Italy and Switzerland, 20 feral goats on Montecristo Island, 20 domestic (Alpine) goats and 1 ibex x domestic goat hybrid. They reported the heterozygosity level in the four populations as 0.024, 0.021, 0.009 and 0.023 respectively.

The distribution of variants at transferrin and haemoglobin among the Alpine, Angora, Anglo-Nubian, Saanen and Spanish goats was studied by Wang *et al.*, (1991). Two alleles, Tf A and Tf B were detected at the transferrin locus and their frequencies

differed ($P<0.05$) between Spanish and Alpine goats. The beta-globin variants Hb beta-A, Hb beta-D and Hb beta-E were detected using isoelectric focusing at pH ranges 5-8 and 6.7 - 7.7. Haemoglobin beta-D was not found in the Alpine and Angora breeds. Allelic frequencies at the haemoglobin-beta locus differed significantly ($P<0.05$) among the breeds.

Polymorphisms were reported in serum ceruloplasmin and amylase in 219 Czechoslovakian white polled goats by Trakovicka (1991). The gene frequencies for ceruloplasmin (Cp) A and B were 0.719 and 0.281 respectively and those of amylase (Amy) A and B genes were 0.84 and 0.156.

Two variants of transferrin B, designed B1 and B2 were detected using a thin-layer polyacrylamide gel electrophoresis at pH 7.9 including previously reported Tf variants which is Tf A, Tf B and Tf C (Vankan and Bell,1992). The study was conducted among the Australian and Angora, cashmere and dairy breeds showed that the Tf A allele was the most common with gene frequencies ranging from 0.652 to 0.977. Tf B1 and Tf B2 occurred in all the four breeds, while Tf C was observed only in Australian Angora and cashmere breeds, but at very low frequencies. Family studies involving 1816 matings among Tf variants A, B1, B2 and C showed that the genes controlling variants Tf A, Tf B1, Tf B2 and Tf C segregated in an autosomal codominant fashion. The genotypes were in Hardy-Weinberg equilibrium in all the breeds studied.

Four variants of lactate dehydrogenase isoenzyme bands were observed in the semen samples of grey goats of China (Zhang *et al.*,1995). Agarose-gel electrophoresis was used to identify the variants: LDH-1, LDH-3, LDH-4 and LDH-x. Isoenzyme LDH-x comprised almost 75% of the total content of lactate dehydrogenase.

Further studies on the erythrocyte malic enzyme in goats by Stasio *et al.*,. (1995) described the presence of another new variant. Blood samples from 534 goats of 4

Mediterranean breeds were analysed using starch gel electrophoresis and the three variants are ME-A, ME-B and ME-C. The segregation of the variants was consistent with three codominant alleles. The frequency of the new allele varied from 0.09 to 0.28 in the 4 breeds.

Ologun and Imumorni (1996) made a preliminary study on the effects of haemoglobin genotype on some performance traits in West African dwarf goats in Nigeria. In their investigation using cellulose acetate electrophoresis they reported that the frequencies of Hb alleles were Hb A (0.53) and Hb B (0.47) and genotypes were: Hb AA (0.30), Hb AB (0.46) and Hb BB (0.24). They also observed that the population is in Hardy-Weinberg equilibrium.

A recent study on the polymorphism of serum proteins and amylase in crossbreds of Angora X Zhongwei goats was carried out by Han *et al.*,1996. They used polyacrylamide electrophoresis and detected polymorphisms in transferrins, haemoglobin and amylase and no variation was observed at the albumin, post-albumins and slow alpha-2 globin loci.

Another group at Changchun Province in China (Ma Ning *et al.*,1996) while working with blood samples from 124 does of Liaoning cashmere goats, 48 Arbus does and 148 Erlangshan does of Inner Mongolian cashmere goats reported polymorphisms at the transferrin (Tf), amylase (Amy), alkaline phosphatase (AP) and esterase (Es) loci. No variations were observed at the haemoglobin (Hb) and albumin (Alb) loci for the three populations studied. The genotypes of the variants were distinguished by polyacrylamide gel electrophoresis. There were three Tf genotypes Tf AA, Tf AB and Tf AC in Liaoning goat and 4 Tf genotypes in the Mongolian goats: Tf AB, Tf AC, Tf BB and Tf BC. There were two AP genotypes : AP f and AP o controlled by Ap f and Ap o alleles, 3 Amy genotypes: Amy AA, Amy AB and Amy BB controlled by Amy A

and Amy B alleles and 3 Es genotypes: Es AA, ES AB and Es BB controlled by Es A and Es B alleles in the two breeds of goats.

2.4.2. Milk Protein Polymorphism

A study on Mendelian polymorphism underlying quantitative variations of goat α_{s1}-Casein was undertaken by Grosclaude *et al.*, (1987). This was done by using polyacrylamide-gel electrophoresis and rocket immunoelectrophoresis. They showed that locus α_{s1}-Casein is controlled by a minimum of six alleles, named A, B, C, B-, F and O (or null allele). In 213 Alpine goats from 49 flocks studied, they reported that the frequency for alpha-s1-CnA was 0.14, for alpha-s1-CnB was 0.05, for alpha-s1-CnC was 0.01, for alpha-s1-CnB- was 0.34, for alpha-s1-CnF was 0.41 and finally for alpha-s1-CnO (null) was 0.05. The frequencies in 159 Saanen goats from 52 flocks were 0.07, 0.06, 0, 0.41, 0.43 and 0.03 respectively. These studies confirmed that alpha-s1-Cu and alpha-s2-Cn are closely linked. Alleles A, B and C are associated with high content of α_{s1}-Casein, compared to allele F with low content and allele B- with an intermediate content (Brignon *et al.*, 1989). The polymorphism of α_{s2}-Casein is controlled by two alleles A and B. Recent data confirm that loci α_{s1}-Casein and α_{s2}-Casein are closely linked (Grosclaude *et al.*, 1987). A seventh allele named D was discovered by Mahè and Grosclaude (1989).

Much of the research work carried out between 1993 and 1996 has been focused towards the genetic polymorphism of goat milk caseins. Langley (1993) in his work described that alpha-s1-Casein has seven variants (A, B, C, D, E, F, G, O) and its polymorphism is of considerable importance in the determination of suitable milk for cheese making. It was noted that F variant of alpha-s1-casein is associated with strong

'goat' flavour in cheeses, while the A variant is associated with high milk yields and a firm smooth texture in cheeses. The other goat milk caseins exhibit similar polymorphisms: alpha-s2-casein has three variants (A, B and C), beta-casein also has 3 variants (A, B and O) and kappa-casein has two (A and B). The O variants of alpha-s1-casein and beta-caseins are associated with their absence in goat milk. The absence of beta-casein adversely affects the coagulation of goat milk and results in cheese with a very soft consistency (Augulo *et al.*,1994).

Stasio *et al.*, (1993) examined electrophoretically 138 Somali Arab goats' milk samples and revealed that the frequencies of alpha-s1-casein 1A, 1B, 1C, 1E, 1F and 1O alleles were 0.55, 0.22, 0.02, 0.06, 0.13 and 0.02 respectively. Results from these studies indicated that alpha-s1-casein locus in Somali Arab goats is similar to other breeds of Mediterranean origin.

2.4.3. Genetic Distance Estimates:

Tunon *et al.*, (1989) studied the genetic relationships among 14 native Spanish breeds of goats. The genetic distance separating the 14 Spanish goat breeds were calculated from gene frequency data for 14 polymorphic blood loci : reduced glutathione (GSH), red cell potassium (Ke), haemoglobin (Hb), diaphorase (Dia), catalase (Ct), malate dehydrogenase (MDH, carbonic anhydrase (CA), X-protein (Xp), nucleoside phosphorylase (Np), alkaline phosphate (Alp), amylase (Am), ceruloplasmin (Cp), transferrin (TF) and albumin (Al). A dendrogram was produced which demonstrated considerable genetic similarity among Negra Serrana, Zamorana, Guadarrama, Retinta, Blanca Andaluza [Andalusian White], Berciana and Pirenaica goats, and among Canaria [Canary Island], Murcian, Blanca Celtiberica [Castille Mountain], Verata, Palmera,

Malaga and Granada goats. The genetic distance ranged from 0.003 (Granadina-Malagnina) to 0.097 (Marciana-Retinta).

In a study undertaken by Pepin and Nguyen (1994) on 827 blood samples obtained from French Alpine (169 animals), French Saanen (195 animals), Guadeloupean Creole (155 animals), Guinean (147 animals) and West African Sahel (161 animals) goats reported polymorphisms at the transferrin, haemoglobin and X-protein. No variation was observed at albumin and carbonic anhydrase loci. Three variants of transferrin (Tf A, Tf B and Tf C) were observed .In the breeds studied the predominance of Hb A allele was observed (frequencies:0.73-0.99) while Hb D only occurred in each of the five breeds, but its allele frequency was only noticeable in Saanen (0.15) and west African Sahel (0.27). Genetic distances, calculated by four different methods, showed that the smallest distance was between two European breeds - Alpine and Saanen goats, both of which originated from Switzerland. Saanen and Guinean goats were separated from each other by the largest. On average, the estimated distance between European and African breeds was 2-4 times greater than that between local breeds. The Guadeloupean Creole appeared to be closer to African than to European breeds.

Few studies of genetic distance have been undertaken for breeds of goats in the Asian region. The studies carried out so far are in eight populations in Okinawa (Japan), the distance found were from 0.004 to 0.0025 (Nozawa *et al.*, 1987b); higher values were found in seven native Indonesian populations, ranging from 0.0011 to 0.0174 (Katsumata *et al.*, 1981b); seven population of Japanese Saanen goats showed genetic distances ranging between 0.004 and 0.0065 (Katsumata *et al.*, 1981a); and finally, values of 0.0011 to 0.0056 were found for six native populations in Korea (Katsumata *et al.*, 1982). Pepin and Nguyen (1994) in their study of protein polymorphisms among five goat breeds estimated the genetic distances using four methods. The genetic

distances between Alpine-Saanen was 0.034 and between Sahel-Saanen was 0.121 using methods by Cavalli-Sforza & Bodmer,1971; using methods of Gregorius,1984 the distances are 0.121 for Alpine-Saanen and 0.311 for Sahel-Saanen; using Balakrishnan & Sanghvi methods (1968), the distances are 0.202 for Alpine-Saanen and 0.697 for Sahel-Saanen; and using Nei 's (1972) method the distances are 0.016 for Alpine-Saanen and 0.153 for Sahel-Saanen. They concluded that the smallest distance estimated by the four different methods was observed among the two European breeds of Alpine and Saanen, both of which originated from Switzerland.