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GENETIC VARIATION OF NATIVE GOATS OF SOUTHEAST ASIA, SRI LANKA AND AUSTRALIA

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Specially dedicated to

two dearest and wonderful people :

my late mother, Mrs Leelavathy Oyyan

and

my late aunt, Mrs.Mariyayee Ammal

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ABSTRACT

This research work undertaken is concerned with a systematic and complete analysis of the phylogenetic relationships existing between the native goats of Southeast Asia . Using gene frequency data on the polymorphic loci of blood proteins / enzymes detected by biochemical techniques such cellulose acetate electrophoresis for all loci except one using starch gel electrophoresis, estimates of genetic variability and genetic distance have been obtained in an attempt to identify the genetic relationships existing among the native goats in Malaysia, the Philippines, Indonesia, Thailand, Sri Lanka and Australia.

Forty blood genetic systems were analysed and 12 systems were found to be polymorphic i.e. Alb, Ap, Amy, Ca, Dia-1, Dia-2, Hb, Mdh, Me, Np, Tf and Xp. Allele frequencies showed differences among populations, but the same allele in each locus was the most common in almost all populations. Family studies revealed that Alb, Ca, Hb, Me, Mdh, Dia-1, Dia-2, Tf and Xp loci were autosomal and their alleles are co-dominantly inherited. Ap, Amy and Np alleles were found to show dominant - recessive inheritance. Excess of heterozygotes were observed in albumin for populations Musuan (+0.303) and Bogor (+0.311); and transferrin for populations Sabah (+0.187) and Musuan (+0.167).

The observed genetic distance 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. The average degree of genetic differentiation of subpopulation (F_{ST} = 0.163) clearly indicates substantial genetic differences among these goat populations and a high level of within-population inbreeding (F_{IS} = 0.402). As compared to F_{IS}, the F_{ST} is relatively small.

ABSTRAK

Kerja penyelidikan ini berkaitan dengan analisa hubungan filogenetik yang wujud antara kambing tempatan Asia Tenggara. Dengan mengunakan teknik biokimia, iaitu elektroforesis selulosa asetat untuk mengesan semua lokus polimorfik protin /enzim darah dan melainkan satu lokus yang dikesan oleh keadah elektroforesis gel kanji. Data frekuensi gen yang diperolehi memberikan anggaran variasi genetik dan jarak genetik yang bertujuan untuk menentukan hubungan genetik antara **Kambing** tempatan di Malaysia, Filipina, Indonesia, Negeri Thai, Sri Lanka dan Australia.

Empat **puluh** sistem genetik darah telah dianalisakan dan hanya 12 sistem, iaitu Alb, Ap, Amy, Ca, Dia-1, Dia-2, Hb, Mdh, Me, Np, Tf dan Xp didapati bersifat polimorfik. Frekuensi alel menunjukkan perbedzaan antara populasi tetapi alel yang sama dalam setiap lokus adalah paling kerap dalam kebanyakan populasi. Kajian famili mununjukkan lokus Alb, Ca, Hb, Me, Mdh, Dia-1, Dia-2, Tf dan Xp dikawal oleh autosom dan alel tersebut dapat diwariskan. Alel Ap, Amy dan Np menunjukkan pewarisan secara dominan dan resesif. **Bilangan heterozigot** yang tinggi telah diperhatikan dalam albumin pada populasi Musuan (+0.303) dan Bogor (+ 0.311). **dan dalam lokus transferin pula pada populasi Sabah (+0.187) serta Musuan (+0.167).**

Nilai jarak genetik **antara** populasi (0.001 - 0.043) berada dalam lenkungan nilai daripada baka haiwan ternakan yang telah dikaji. Populasi kambing tempatan ini boleh dikelaskan

kepada sekumpulan besar yang mengandungi 9 populasi Asia Tenggara dan 2 kumpulan yang setiapnya terdiri daripada 2 populasi. Purata perbedzaan genetik subpopulasi kambing (F_{ST} = 0.163) menunjukan perbedzaan genetik yang jelas antara populasi kambing tersebut dan kadar pembiakbiakan dalam yang tinggi. (F_{IS} = 0.402). Nilai F_{ST} didapati lebih rendah daripada nilai F_{IS}.