

GENETIC EVALUATION OF SOME SHEEP BREEDS

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Introduction

General improvement of genetic resources using selection and crossbreeding depends on genetic variability. In recent years, Malaysia has imported many new sheep breeds and a large number of deer from various sources (Rajion et al. 1993). Little is known of the genetic background of these animals. This project was initiated to evaluate the genetic variability within and between some breeds of sheep and some deer populations in the country using biochemical and molecular polymorphism techniques.

Materials and Methods

Six sheep breeds, namely the Bali Bali (BB), Barbados Blackbelly (BBb), Dorset-Malin cross (DM), Malin (M), Santa Ines (SI) and St. Croix (SC), and 2 populations of the rusa deer (*Cervus timorensis*) of different origins (from New Caledonia and Mauritius) were analysed for molecular and biochemical polymorphism. Blood samples from 30 animals from each population were analysed for molecular markers using the random amplified polymorphic DNA (RAPD) technique. Eight 10-mer oligonucleotide primers of arbitrary sequence were used to generate the RAPD data for 4 of the sheep breeds and two 12-mer primers were used for the deer.

Samples from 50 animals per population were analysed for biochemical markers using cellulose acetate electrophoresis (CAE). Nine markers were analysed for three of the sheep breeds and eight for the deer populations.

Results and Discussion

RAPD analysis of the sheep breeds generated 7 - 11 bands per primer and a total of 65 markers. One of the primers detected no polymorphism (OPD-09) while percent polymorphism for the others ranged between 36.36 - 100 %. The biochemical study showed haemoglobin, nucleoside phosphorylase and glucose phosphate isomerase to be polymorphic. Percent polymorphism for BB, SI and SC were 33.33, 22.22 and 11.11 %, respectively. RAPD analysis of the two deer populations also generated 7 - 11 bands per primer. Percent polymorphism for primer 06B was 83.3 % while that for primer 52A was 66.66 %. The biochemical study showed haemoglobin, malate dehydrogenase and malic enzyme to be polymorphic. Percent polymorphism was 37.5 % for the two populations.

Conclusions

As expected the molecular study was able to detect higher variation than the biochemical study. Work on analysing the remaining sheep breeds and deer populations are continuing. More biochemical markers are also being investigated.

References

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