

## **ABSTRACT**

Farm animal genetic resources are not only a source of food and animal protein, but also play a multi-functional role providing other commodities and services. The vast array of breeds and species found across the world is the outcome of the effects of the environment over thousands of years and human activities. Over the last decades, however, this diversity has become threatened. Indigenous and local breeds, which are often more adapted to the local environmental conditions and management systems, require low maintenance and are less prone to diseases, have been either replaced by imported high yielding breeds or have their gene pool introgressed with genes from these breeds. The exotic breeds, which have been subjected to high intensity selective breeding, tend to have narrowed genetic base. Genetic diversity is crucial for animals to adapt to changing environmental conditions and to survive in the face of disease outbreaks. It is also the resource for improvement of livestock productivity to meet current and future demands. The loss of genetic diversity among animal genetic resources has caused global concern as it affects food security, trade and livelihood of farmers. With the need to arrest further genetic erosion, the Global Plan of Action for Animal Genetic Resources was developed by the Food and Agriculture Organisation of the United Nations (FAO). The first of the four strategic priorities areas focuses on characterisation, inventory and monitoring of trends and associated risks.

The animal genetic resources of Malaysia comprise of the indigenous breeds, the local breeds, locally developed synthetic and composite breeds, traditional populations, commercial breeds and lines, and the introduced breeds. The indigenous and local breeds have been neglected in favour of imported breeds or have been indiscriminately crossed with other breeds resulting in non-

descript crosses. Except for the recently developed synthetic breeds, many synthetic breeds developed in the past can no longer be found or suffer from admixture with genes from other breeds. We are rapidly losing our animal genetic resources. In addition to this the genetic diversity within the existing populations is fast eroding as a result of mismanagement of breeding activities and failure to keep proper records. Conservation and sustainable utilisation and development of animal genetic resources is only possible through genetic characterisation to identify unique qualities and to detect threats of inbreeding and hybridisation.

Genetic characterisation is the evaluation of variation at the chromosomal or DNA level. It requires the assessment of genetic variability within and among populations, lines, breeds and species using molecular markers and specific genes. It may be used to explain population dynamics and migration patterns, and to identify inbreeding and admixture within livestock populations. It provides valuable information required for developing breeding strategies and genetic conservation strategies. Association analysis using DNA markers and candidate genes may pave the path for use of marker-assisted selection (MAS) through early and accurate identification of animals with high breeding values and unique qualities.

There are limited scientific studies evaluating the production and reproductive performances and genetic variability of local animal genetic resources. It is pertinent that the genetic structure of local animal genetic resources be evaluated and regularly monitored. Only then can our indigenous breeds, the locally developed synthetic breeds and non-descript crosses, and the introduced breeds be sustainably developed to further enhance the local livestock industry and ensure food security in the future.

## **INTRODUCTION**

The vast variety of animal genetic resources (AnGR) for food and agriculture found on this earth is the result of the combined effects of nature over thousands of years and human activities especially since domestication. However, over the recent decades, many of the indigenous and local breeds in the developed countries and in some developing countries have been either replaced by or crossed with specialised high yielding breeds resulting in genetic erosion. This loss of genetic diversity has caused global concern as it affects food security, trade and livelihood of farmers. With the need for consolidated interventions, the Global Plan of Action for Animal Genetic Resources was developed by the Food and Agriculture Organisation of the United Nations (FAO) with four strategic priority areas (FAO, 2007a). In this inaugural lecture I hope to highlight the importance of genetic diversity in animal genetic resources, some of the animal genetic resources in our country, and the need to characterise these. I would also like to share some of the works and findings of the research in this area in which I have been involved.

## **ANIMAL GENETIC RESOURCES AND GENETIC DIVERSITY**

Animal genetic resources as defined by FAO refers to all farm animals that are of some value for agricultural purpose at present time or have potential values for the future, be it economic value or of some other form (FAO, 1998; Schei & Tvedt, 2010). This definition of animal genetic resources includes domesticated farm animals as well as their wild relatives; and excludes household animals kept as pets, as well as non-domesticated animals found in the wild or in captivity. Although the essential role of farm animals is as a source of food and animal protein, they play a multi-

functional role. They also provide other commodities such as wool, hide, skin, antler velvet, etc., and some species, such as the buffalo, bullock, camel and donkey, are used as draught animals, especially in the developing countries (Akila & Chander; 2010; Mburu *et al.*, 2012). Farm animals also serve a cultural role in some parts of the world; they are given as gifts (Arriaga-Jordan *et al.*, 2005), are important components in religious and cultural ceremonies, and are used in sports and entertainment. To small scale farmers they are a form of savings and serve as a safety net in times of financial need (Kondombo *et al.*, 2005).

In 2010, the Commission on Genetic Resources for Food and Agriculture reported a global total of 8,054 breeds, of which 7,001 were local breeds and 1,053 were transboundary breeds (CGRFA, 2010). This diversity of breeds is the outcome of the varying climatic conditions across the world, from temperate to tropical and from arid to humid. Animals in a particular region are subjected to the environmental conditions thereof and develop adaptive attributes for the local conditions, sometimes these being unique qualities. In addition, when animals are kept in large populations and the farming practices adopt culling of poor performing animals rather than selection of a few individuals of high merit, a large gene pool is maintained and this allows indirect selection for resistance or resilience to local diseases and endo- and ectoparasites. This diversity is further enhanced by the influence of man. A particular species may be kept for different purposes in different parts of the world, even in different parts of a country. During selective breeding the traits of interest may be different, thus creating the different breeds of the same species. In some case, a particular breed or population is subjected to selection for traditionally important traits rather than economically important traits. For example, a docile temperament is often a selection criterion for meat, dairy

and draught cattle. However, aggressiveness and ferocity were considered important selection traits in Iberian fighting bulls (Silva *et al.*, 2006). The above factors are not only the cause of the large number of breeds, but also contribute to the vast variations among breeds and populations, creating gene pools of animal genetic resources.

Over recent decades, in the developed countries and some developing countries the livestock industry has undergone rapid changes, with a small number of specialised high yielding breeds dominating some sectors of the industry. These breeds have been developed for improved production efficiency and certain desired qualities through high intensity selection and use of breeding methods and biotechnology. This in turn has narrowed their genetic base and made them more vulnerable to environment stresses and susceptible to diseases, thus requiring high quality feed, expensive management facilities and greater health care. In addition, the intensification of production systems, loss of grazing and agricultural land, natural calamities, disease outbreaks, inappropriate breeding practices, changing cultural practices and urbanisation have further accelerated the genetic erosion.

Genetic diversity is crucial for species and breeds to adapt to changing environmental conditions, which includes climate change. It increases the chances of breeds or populations to survive in the face of disease outbreaks or harsh environmental challenges (FAO, 2007a). The world population is increasing rapidly; it has exceeded 7 billion and is anticipated to increase at a rate of 1.2% per annum in the next decade and to reach 7.7 billion by the year 2020 and near 10 billion by 2050 (UNDESA, 2011; USCB, 2012). Genetic diversity provides the genetic resources for animal breeders to design selection and breeding programmes to further improve livestock productivity and develop new genotypes to ensure food security.

The rapidly dwindling animal genetic diversity will jeopardise the ability of the industry to respond to market demands, socio-economic changes and changes in consumer preferences. There is a global concern about the loss of livestock genetic diversity, and the urgent need to prevent further genetic erosion cannot be ignored.

Animal genetic resources have to be properly managed so that they may be sustainably utilised. This is a challenge requiring strategic interventions. The Global Plan of Action for Animal Genetic Resources was developed by FAO to facilitate this. The Strategic Priorities for Action contain four Strategic Priority Areas (FAO, 2007a):

- Strategic Priority Area 1: Characterisation, Inventory and Monitoring of Trends and Associated Risks
- Strategic Priority Area 2: Sustainable Use and Development
- Strategic Priority Area 3: Conservation
- Strategic Priority Area 4: Policies, Institutions and Capacity-building

Knowledge and understanding of the distribution, characteristics, performance and genetic diversity of a country's animal genetic resources are essential for their effective management and sustainable utilisation and development.

## **ANIMAL GENETIC RESOURCES OF MALAYSIA**

The animal genetic resources of Malaysia comprise of the both the mammalian species (cattle, buffalo, goat, sheep, horses, pigs and rabbits) and the avian species (chicken, ducks, geese, turkey and ostrich). These species comprise of the indigenous breeds, the local breeds, locally developed synthetic and composite breeds, traditional populations, commercial breeds and lines, and the introduced breeds. The indigenous or native breeds are the breeds

believed to be autochthonous to a country or region. The Katjang goat and the Kedah Kelantan (KK) cattle are indigenous breeds of Malaysia. However, as with indigenous breeds in many parts of the world, these have been neglected in favour of imported breeds. The Katjang and the Kedah Kelantan have also been popularly used as the maternal breed and crossbred with imported exotic breeds (Panandam *et al.*, 1990, 1991, 1992; Johari *et al.*, 1994). Synthetic breeds, such as the Jermasia goat (Figure 1) (Panandam & Mukherjee, 1987; Mukherjee, 1991) and the Brakmas and Cherokee beef cattle (Johari & Jasmi, 2009) have been developed through planned crossbreeding programmes. The Katjang and the Kedah Kelantan have also been indiscriminately crossed with other breeds resulting in non-descript crosses which show high phenotypic and genetic variations (Figure 2). The local breeds, on the other hand, are those breeds that are not indigenous to the country, but have been brought in long ago either as purebreds or crossbreds, and have as a result of natural and/or artificial selection and local breeding practices become localised or adapted to the local environmental conditions and production systems. The Local Indian Dairy (LID) cattle, Malin sheep and the local South China Pig are local breeds which were once common in Malaysia, but now may be considered extinct or near extinct. The Brahman and Jersey breeds imported from Australia, the Nellore from Brazil, the Yellow Cattle from China and the Bali cattle from Indonesia are all introduced cattle breeds which are popular among medium-scale farmers. The recently introduced goat breeds are the Boer goats from Australia and South Africa, the Saanen, Anglo-Nubian, Jamnapari and the Shami. Although a number of hair and wool sheep breeds were imported into the country in the past, and even used in crossbreeding programmes, majority of these breeds can no longer be found. The Dorper is a recently introduced sheep breed. The swine and

poultry industry are dominated by commercial breeds and lines. The indigenous village chicken, which originates from the Red Jungle fowl, are kept mainly in small numbers and are not subjected to selection. These traditional populations have vast gene pools and exhibit variable body conformations and physical characteristics. These traditional populations have vast gene pools and exhibit variable body conformations and physical characteristics.

In Malaysia, we have lost the local breeds. We are now at risk of not only losing whatever is left of our indigenous breeds but may also lose the synthetic breeds developed locally with investment of time, money and human expertise. These may not become extinct, but due to improper breeding practices as a result of lack of knowledge in animal breeding principles and poor record keeping, and due indiscriminate crossing, the gene pools of these animal genetic resources may suffer from the effects of inbreeding and admixture (Panandam, 2007). The unique traits and genes of these breeds will soon be lost. Conservation of local animal genetic resources is only possible through genetic characterisation, and sustainable utilisation and management.



**Figure 1** The Jermasia doe



**Figure 2** The non-descript Kedah Kelantan crosses

## **GENETIC CHARACTERISATION OF ANIMAL GENETIC RESOURCES**

Characterisation is a procedure which helps to identify the variations among breeds and populations as well as among individuals. Breeds may be characterised with respect to morphological traits, production and reproductive performances, geographic distributions and genetic makeup. Genetic characterisation is the evaluation of variation due to chromosomal number and structure or differences in genotypes at specific loci or differences in the DNA sequences at specific regions of the genome (de Vicente *et al.*, 2006). Genotypic differences may be detected by biochemical methods based on differences in protein product sizes (Lee *et al.*, 1995), or by molecular methods based on differences in allele sizes amplified using polymerase chain reaction (PCR) (Rajinder *et al.*, 2004; Cherenet *et al.*, 2004; Aziz *et al.*, 2011), or on differences in

the DNA sequences (Cheng *et al.*, 2004). Genetic characterisation allows the assessment of genetic variability within and among populations, lines, breeds and species (Bhassu *et al.*, 2004; Ramin *et al.*, 2008; Kashiani *et al.*, 2012). It also serves as a useful tool to evaluate population dynamics, identify inbreeding, the level of admixture within populations, and migration patterns of livestock species, and to monitor changes in populations over time as a result of human activities (Li *et al.*, 2007; Wilkinson *et al.*, 2011). It provides valuable information required for developing breeding strategies for improvement of breeds and populations as well as for planning genetic conservation activities (Hanotte *et al.*, 2005; Hanotte & Jianlin, 2006). This is especially important in livestock breeds which are subjected to assisted reproductive techniques and high selection intensity, and for herds kept as small populations with no documented pedigree information.

Genetic improvement of livestock involves selection of genetically superior breeding individuals. Conventional selection programmes require pedigree information and large families, and are time consuming. Improvement of sex limited traits, such as milk production traits, requires evaluation of a large number of siblings or progeny testing. Evaluation of terminal traits, such as meat quality traits, requires slaughter of animals. Marker-assisted selection incorporates DNA markers associated with specific traits or alleles at candidate genes for these traits into the selection criteria for genetic improvement of breeds (Guimarães *et al.*, 2007). DNA markers are DNA fragments of specific sizes identified by use of specific primer pairs and PCR. They may also be specific DNA sequences detected by cloning and sequencing of PCR amplified DNA fragments. Using marker-assisted selection (MAS), animals with high breeding values (to be used as parents of next generation) and highly productive animals (to be retained as producers in

herd) may be identified early and more accurately. In addition, since this approach is genotype-based selection, small family sizes would provide accurate information to evaluate the genetic merit of individual animals for sex-limited and terminal traits.

There are limited scientific studies evaluating the production and reproductive performances and genetic variability of local animal genetic resources. It is essential that the genetic structure of local animal genetic resources be evaluated and regularly monitored, so that inbreeding and effects of bottleneck and small populations as well as genetic hybridisations and admixtures may be identified early and attended to. The genetic data will also enable evaluation of the association between the genetic markers and performance traits which is a prerequisite for incorporating DNA markers into selection programmes. The following sections briefly describe some of the works conducted in characterisation of the local animal genetic resources.

## **GENETIC CHARACTERISATION OF THE BOER GOAT AND BOER CROSSES**

The Boer goat, which is distinguished by its short white haired bodies, distinctive red head and neck, and long, pendulous ears (Figure 3), has been reported to exhibit excellent body conformation, fast growth rate and high fertility rate, and to be a hardy animal with good adaptation to vast climatic conditions and farming systems (Greyling, 2000; Malan, 2000). The Boer originates from South Africa, but has over the past decade become popular for goat meat production across the American continent, Australia and Asia (FAO, 2007b).

In the effort to improve the goat industry in Malaysia, purebred Boer goats and Boer crosses (Figure 4) have been imported from

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Australia and South Africa, and many Boer goat farms have been established. A comprehensive knowledge of their performance under local farming conditions and the existing genetic variability in these imported breed types are required so that appropriate breeding programmes may be designed. In addition, there is a lack of genetic comparison of the Boer goats from the two regions.



**Figure 3** The Boer goat from South African



**Figure 4** The Australian Boer cross

### **Performance of the Boer Goat and the Boer Cross**

Traits of economic importance in meat goats are those related to growth and reproductive performance. The performance of the purebred Boer goat under intensive management system was evaluated, and the mean birth weight, weaning weight (at 3 months) and body weight at six months of age are displayed in Table 1 (Javanmard, 2011). Table 2 presents the means for body conformation traits of at weaning; body conformation traits are useful in assessing growth rate and carcass characteristics in farm animals. The mean litter size of the Boer does was 1.64.

The mean birth weight of the Boer goat was similar to that reported by Rashid *et al.* (2005) for Boer goat from South Africa and by Zhang *et al.* (2009) for Boer goat in China. However, the mean weaning weight was lower. Growth traits are multifactorial in nature, influenced by both multiple genes and environmental

factors. The observed difference may be due to differences in the genetic makeup, feed provided, management practices and effects of other environmental factors in the herds. Boer goats reared under intensive conditions have been reported to have ADG of 227 g/day (Van Niekerk *et al.*, 1996). A possible reason for the lower ADG observed in the present study could be that the optimal nutrition requirement of the Boer kids to display their growth potential was not met.

The mean birth weight, weaning weight (at 3 months) and 6-month body weight for the Boer cross under semi-intensive system are displayed in Table 3 (Tay, 2012). Table 4 presents the means for body conformation traits at weaning. The mean litter size was 1.62, with a twinning percentage of 54.32%. No significant differences were observed between the kids of the two sexes for weight at all ages. However, single born kids were significantly ( $P < 0.05$ ) heavier than twin born kids. The Boer cross kids appeared to be smaller than the Boer kids reported above. However, this would not be fair comparison as they were at different locations and under different management systems.

The quality of fresh and thawed frozen semen of the Boer goat and Boer crosses was evaluated by Nikbin (2012), and the characteristics are shown in Table 5. The values were in the normal ranges reported for goats (Sundararaman & Edwin, 2008; Anakkul *et al.*, 2011). As expected, storage for six months in liquid nitrogen caused a decrease in semen quality traits. This may be attributed to the physical and chemical stresses on the sperms caused by the freezing and thawing processes (Stradaioli *et al.*, 2007). General and progressive motility of sperms in fresh semen showed significant ( $P < 0.05$ ) correlation with most of the quality traits of fresh and thawed frozen semen, confirming these traits to be good indicators of semen quality for both fresh and frozen semen (Rijsselaere *et al.*, 2012).

There are limited scientific publications on the growth and reproductive performance of the Boer goat and Boer cross, especially in Malaysia. Since production traits are generally multifactorial in nature, identification of the influencing factors and understanding of genetic mechanism affecting the variations in these traits are vital to the implementation of optimal breeding and selection programs. In addition, the Boer goat and Boer crosses have to be compared in the same locations and in a number of locations as well as both under intensive and semi-intensive management systems to get a better picture of their performance in Malaysia.

**Table 1** LSmeans of birth weight and 3-month and 6-month body weights for Boer goats under intensive management system

	<b>Birth Weight (kg)</b>	<b>3-month Weight (kg)</b>	<b>6-month Weight (kg)</b>
<b>Sex</b>			
Female	3.87 ± 0.20 <sup>a</sup>	10.96 ± 0.82 <sup>a</sup>	19.99 ± 1.03 <sup>a</sup>
Male	4.97 ± 0.10 <sup>b</sup>	12.50 ± 0.81 <sup>b</sup>	22.34 ± 1.05 <sup>b</sup>
<b>Litter type</b>			
Single	3.19 ± 0.20 <sup>a</sup>	11.28 ± 0.77 <sup>a</sup>	20.97 ± 0.86 <sup>a</sup>
Twin	2.94 ± 0.20 <sup>ab</sup>	10.73 ± 0.77 <sup>ab</sup>	20.88 ± 0.86 <sup>ab</sup>
Triplets	2.58 ± 0.31 <sup>b</sup>	10.12 ± 0.85 <sup>b</sup>	18.10 ± 2.50 <sup>b</sup>
<b>Parity</b>			
First	3.01 ± 0.08 <sup>a</sup>	11.71 ± 0.36 <sup>a</sup>	19.64 ± 0.64 <sup>a</sup>
Second	3.01 ± 0.09 <sup>a</sup>	11.18 ± 0.38 <sup>a</sup>	20.69 ± 0.68 <sup>b</sup>
Third	4.93 ± 0.10 <sup>b</sup>	13.44 ± 0.42 <sup>b</sup>	20.75 ± 0.70 <sup>b</sup>

Means for a particular trait (column) in a subgroup that do not share any superscripts are significantly ( $P < 0.05$ ) different.

**Table 2** LSmeans of body conformation traits at weaning for Boer goats under intensive management

	<b>Body Length (cm)</b>	<b>Height at Withers (cm)</b>	<b>Heart Girth (cm)</b>	<b>Chest Depth (cm)</b>
<b>Sex</b>				
Female	41.83 ± 1.73 <sup>b</sup>	44.03 ± 1.59 <sup>a</sup>	43.34 ± 1.85 <sup>a</sup>	18.8 ± 0.69 <sup>a</sup>
Male	44.01 ± 1.71 <sup>a</sup>	46.73 ± 1.56 <sup>b</sup>	48.04 ± 1.88 <sup>b</sup>	20.47 ± 0.70 <sup>b</sup>
<b>Litter type</b>				
Single	45.43 ± 1.64 <sup>a</sup>	46.53 ± 1.50 <sup>a</sup>	52.25 ± 1.70 <sup>a</sup>	21.65 ± 1.50 <sup>a</sup>
Twin	41.9 ± 1.64 <sup>ab</sup>	43.99 ± 1.50 <sup>a</sup>	47.51 ± 1.78 <sup>b</sup>	20.39 ± 0.66 <sup>a</sup>
Triplets	39.73 ± 1.50 <sup>ab</sup>	42.00 ± 1.39 <sup>a</sup>	45.08 ± 1.65 <sup>b</sup>	19.58 ± 0.61 <sup>a</sup>
<b>Parity</b>				
First	32.51 ± 5.91 <sup>a</sup>	42.30 ± 5.42 <sup>a</sup>	46.56 ± 6.40 <sup>a</sup>	19.06 ± 2.40 <sup>a</sup>
Second	43.80 ± 1.03 <sup>ab</sup>	44.19 ± 0.94 <sup>a</sup>	47.41 ± 1.11 <sup>a</sup>	20.54 ± 0.41 <sup>b</sup>
Third	45.57 ± 1.00 <sup>b</sup>	45.33 ± 0.91 <sup>a</sup>	49.12 ± 1.08 <sup>a</sup>	21.39 ± 0.40 <sup>b</sup>

Values in parentheses indicate sample size. Means for a particular trait (column) in a subgroup that do not share any superscripts are significantly ( $P < 0.05$ ) different.

**Table 3** LSmeans of birth weight and 3-month and 6-month body weights for Boer cross under semi-intensive management system

	<b>Birth Weight (kg)</b>	<b>3-month Weight (kg)</b>	<b>6-month Weight (kg)</b>
<b>Sex</b>			
Female	2.79 ± 0.06 <sup>a</sup>	11.32 ± 0.84 <sup>a</sup>	14.86 ± 0.85 <sup>a</sup>
Male	2.82 ± 0.06 <sup>a</sup>	12.20 ± 1.01 <sup>a</sup>	16.45 ± 0.95 <sup>a</sup>
<b>Litter type</b>			
Single	2.91 ± 0.07 <sup>a</sup>	12.13 ± 1.00 <sup>a</sup>	17.51 ± 0.82 <sup>a</sup>
Twin	2.71 ± 0.058 <sup>b</sup>	11.39 ± 0.89 <sup>a</sup>	13.81 ± 1.02 <sup>b</sup>

Means for a particular trait (column) in a subgroup (litter type or sex) that do not share any superscripts are significantly ( $P < 0.05$ ) different.

**Table 4** LSmeans of body conformation traits at weaning for Boer cross under semi-intensive management system

	<b>Body Length (cm)</b>	<b>Height at Wither (cm)</b>	<b>Heart Girth (cm)</b>	<b>Back Girth (cm)</b>
<b>Sex</b>				
Female	43.51 ± 1.91 <sup>a</sup>	42.33 ± 1.38 <sup>a</sup>	48.70 ± 1.20 <sup>a</sup>	50.43 ± 2.98 <sup>a</sup>
Male	43.10 ± 3.19 <sup>a</sup>	45.64 ± 2.30 <sup>a</sup>	51.95 ± 2.01 <sup>a</sup>	55.17 ± 4.98 <sup>a</sup>
<b>Litter type</b>				
Single	45.01 ± 4.10 <sup>a</sup>	46.91 ± 2.96 <sup>a</sup>	54.01 ± 2.58 <sup>a</sup>	55.96 ± 6.40 <sup>a</sup>
Twin	41.60 ± 2.14 <sup>b</sup>	41.06 ± 1.55 <sup>b</sup>	46.64 ± 1.35 <sup>b</sup>	49.63 ± 3.35 <sup>b</sup>

Means for a particular trait (column) in a subgroup (litter type or sex) that do not share any superscripts are significantly ( $P < 0.05$ ) different.

**Table 5** LSmeans ( $\pm$ SE) of semen quality traits for Boer goat and Boer cross

	Vol (ml)	SCON ( $\times 10^6$ )	Libido	MOT (%)	PROG (%)	LIVE1 (%)	Log ASR1 (%)	Live6 (%)	Log ASR6 (%)	ACI (%)
<b>Boer</b>	0.73 <sup>a</sup> (0.05)	6294.00 <sup>a</sup> (470.54)	4.25 <sup>a</sup> (0.11)	75.22 <sup>a</sup> (2.41)	45.57 <sup>a</sup> (2.44)	84.71 <sup>a</sup> (1.91)	0.59 <sup>a</sup> (0.03)	70.09 <sup>a</sup> (1.72)	0.78 <sup>a</sup> (0.02)	69.09 <sup>a</sup> (1.54)
<b>Boer Cross</b>	0.43 <sup>b</sup> (0.05)	7878.84 <sup>b</sup> (543.23)	4.30 <sup>a</sup> (0.12)	72.70 <sup>a</sup> (2.80)	74.07 <sup>b</sup> (2.85)	87.57 <sup>a</sup> (2.16)	0.53 <sup>a</sup> (0.03)	57.81 <sup>a</sup> (1.85)	0.79 <sup>a</sup> (0.02)	54.70 <sup>b</sup> (1.71)
<b>2-year</b>	0.47 <sup>a</sup> (0.05)	6462.94 <sup>a</sup> (542.58)	4.21 <sup>a</sup> (0.11)	75.66 <sup>a</sup> (2.80)	64.29 <sup>a</sup> (2.60)	88.92 <sup>a</sup> (2.15)	0.48 <sup>a</sup> (0.03)	66.39 <sup>a</sup> (1.87)	0.73 <sup>a</sup> (0.02)	63.96 <sup>a</sup> (1.64)
<b>3-year</b>	0.69 <sup>b</sup> (0.04)	7709.90 <sup>a</sup> (467.05)	4.34 <sup>a</sup> (0.10)	72.26 <sup>a</sup> (2.41)	55.34 <sup>b</sup> (2.31)	83.36 <sup>b</sup> (1.73)	0.64 <sup>b</sup> (0.02)	61.51 <sup>b</sup> (1.56)	0.84 <sup>b</sup> (0.02)	59.83 <sup>b</sup> (1.39)

VOL: volume of semen, SCON: sperm concentration, MOT: sperm motility, PROG: progressive motility, LIVE1: live sperm rate in fresh semen, LIVE6: live sperm rate in post-thaw semen after 6 months freezing, ASR1: abnormal sperm rate in fresh semen, Log ASR6: abnormal sperm rate in post-thaw semen after 6 months freezing, ACI: acrosome integrity in post-thaw semen after 6 months freezing.

## **Microsatellites Analysis of the Boer Goats and Crosses**

Microsatellites are simple tandem repeats of motifs of two to five nucleotides in the eukaryotic genomes. The alleles display length variation and are inherited in a Mendelian fashion (Khasa *et al.*, 2000). Microsatellite are amplified by PCR using specific primer pairs, and the alleles are detected using standard electrophoresis techniques. Microsatellites are widely used for population genetics studies (Tapio *et al.*, 2010) and sometimes for association analysis (Coltman *et al.*, 2001).

A study was conducted to evaluate the genetic characteristics of the South African and Australian Boer goats and the Australian Boer crosses in the country (Hamidah *et al.*, 2008, 2009a, 2009b, 2010; Hamidah, 2012). The 30 microsatellite loci recommended by FAO (2004) for genetic diversity studies in goats and 20 additional loci reported as polymorphic in population studies of goat were used for this purpose. Metaphor gel electrophoresis detected only 31 loci as polymorphic. The loci showed low levels of allelic variations in all three types of Boer goat populations, with two to four alleles per locus. The polymorphic loci showed the same alleles in the three populations. The monomorphic microsatellites loci were reported to be polymorphic in other goat breeds (Kotze *et al.*, 2004; Martinez *et al.*, 2004; Karthickeyan *et al.*, 2006). The effective numbers of alleles were only slightly lower than the observed numbers of alleles; and majority of the loci showed absence of rare alleles. The mean observed heterozygosity, which is a good indicator of the genetic variability within a breed or population, was moderate (0.45 - 0.52). Similar observed heterozygosity value was reported for the Boer goats in South Africa by Visser *et al.* (2004) despite using capillary electrophoresis to identify the alleles. The three Boer goat types also indicated presence of recent bottleneck. Bottleneck occurs when a population experiences reduction in size, thus inflating frequencies

of common alleles and causing loss of rare alleles (Luikart *et al.*, 1998). The low allelic richness in the Boer goat breed types is probably due to the breeding strategy and intensively selection for production traits adopted during the development of the Boer breed (Visser *et al.*, 2000). Despite the low genetic variability, no inbreeding was detected in all populations, inbreeding coefficient ( $F_{IS}$ ) was 0.02. Wright's fixation index ( $F_{ST}$ ) indicated the absence of genetic differentiation or structuring among the three Boer breed types. The microsatellite screening failed to detect any diagnostic markers for the South African and Australian purebred Boer goats or the Australian crossbred Boer goats. The high genetic similarity of purebred Boer from South Africa and Australia indicated that the founder populations in Australia had established a representative sample of the original gene pool and this has been maintained although the populations were reared in different countries and far apart. There could be some differences in the genetic sequences but microsatellite analysis cannot detect these. In the early stage of their production, the Boer crosses, which were generated by crossing with the Australian Feral goats, were probably genetically different. However, continuous controlled breeding with selected Boer bucks and selection may have caused indirect selection against the genes of the feral goats. Majority of the Boer crosses were also phenotypically similar to the purebred Boer goats.

Future breeding strategies for the Boer goat and Boer crosses should also be to increase the genetic variability of the herds. Though these populations do not face an immediate risk, the declined in genetic diversity should be of concern to animal breeders. Loss of genetic diversity may reduce the potential of small populations to respond to selection and would increase inbreeding, which may in turn reduce population performance and viability (Luikart *et al.*, 1998; Kathiravan *et al.*, 2008). Genetic monitoring coupled with

controlled breeding practices is recommended to maintain genetic variability and fitness, and to improve the production potential of the Boer goat.

### **Candidate Gene Polymorphism and Association Analysis in Boer Goat**

Candidate gene for a particular trait is the gene with a high probability to influence the trait. Polymorphisms at candidate genes, particularly in the exons and promoter regions, may be responsible for phenotypic variations observed for the traits (Vignala *et al.*, 2002). Candidate genes are selected based on known biological or physiological functions of the gene in relation to the trait (Zhu & Zhao, 2007).

Boer does imported from Australia were evaluated for genes identified as candidate genes for growth and meat quality in beef cattle (Javanmard *et al.*, 2008; 2009, 2010; Javanmard, 2012). The Boer goat showed slightly higher frequencies for the allele A (0.54) at the calpastatin *CAST/XmnI* locus and allele A (0.55) at the leptin *LEP1/ClaI* locus. Association analysis has shown that cattle with AA genotype at *CAST/XmnI* have more tender meat (Fortest, 2007). Shin and Chung (2007) showed allele A at *LEP1/ClaI* to be the favorable allele for growth and meat quality traits in Korean cattle. The Boer goat showed high frequency of allele A (0.85) at *LEP2/Sau3AI* (Liefers *et al.*, 2002). Zwierzchowski *et al.* (2001) reported that the Poland Black-and-White bulls of AA genotype consumed more feed and had higher carcass weight compared to the other two genotypes. For the *LEP3/Kpn2I* locus, the frequency of the T allele was higher than the C allele (0.65 vs. 0.35) in the Boer goat. Buchanan *et al.* (2002) reported favorable association of the C allele with lean carcass.

The Australian Boer goat and Boer cross were also screened for polymorphism at candidate genes for semen quality and meat quality traits, and where alleles were of sufficient frequencies, association analyses were carried out (Nikbin et al., 2011, 2012; Nikbin, 2012). PCR amplification, single strand conformation polymorphism (SSCP) detection and subsequent sequencing revealed three SNPs in the *FSHB3* (follicle stimulating hormone exon 3) locus, *FSHB3-1* (200A>G), *FSHB3-2* (226T>C) and *FSHB3-3* (237A>G). A single SNP in exon 2 of the *LHB* (luteinizing hormone) gene (207T >C), and one SNP with insertion of a thymine in position 29 of intron 2 of the *NPY* (neuropeptide Y) gene were also observed. All these loci showed predominance of a single allele in the Boer goat (0.96 – 1.00) and the Boer cross (0.94 – 1.00).

The *HSP70* (heat shock protein 70) gene revealed two novel SNPs, *HSP70-1* (73A>C) and *HSP70-2* (190C>G). Both SNPs were silent mutations and did not affect the amino acid sequence in the expressed protein. The C allele at *HSP70-1* and the C allele at *HSP70-2* were the predominant alleles in both the Boer goat (0.70 and 0.59, respectively) and the Boer cross (0.68 and 0.82, respectively). The AA genotype of *HSP70-1* was significantly ( $P<0.05$ ) associated with higher libido and sperm velocity traits, and with lower motility in the post-thaw semen. The AC genotype had higher sperm concentration compared to AA (by 58%) and CC genotypes (by 26%). The CG genotype of the *HSP70-2* had significantly ( $P<0.05$ ) reduced sperm concentration, general motility, progressive motility, and live sperms (by 29, 14, 4 and 7%, respectively) compared to the GG genotype. *HSP70*, as a molecular chaperon, protects proteins from stress related degradation (Parsell & Lindquist, 1993; Neuer *et al.*, 2000). Since spermatogenesis is a thermosensitive process (Bitto *et al.*, 2008), the *HSP70* protects sperm proteins of goats in tropical areas and,

therefore, may influence the semen quality. The GG genotype of this locus was also associated with lower drip loss, cooking loss and Chroma value. Higher water holding capacity and higher Chroma value are characteristics of higher meat quality. Post-mortem pH drop may cause denaturation in muscle protein structure, and consequently, affect water holding capacity and colour of meat (Hwang *et al.*, 2003). The discovered SNPs were synonymous, and yet significant association with semen quality and meat quality traits were observed. It has been found that 'silent' polymorphism in certain genes may change substrate selectivity although the protein sequence was unchanged (Faustino & Cooper, 2003; Nissim-Rafinia & Kerem, 2002). The varied effects of the different genotypes of *HSP70* loci could be related to the level of expression or translation of this gene.

Amplification of part of exon 2, intron 2 and exon 3 of the *HSP27* (Heat shock protein 27) gene detected two SNPs, one in intron 2, *HSP27b-1* (119:C>T), causing a change in amino acid from proline to leucine, and another in exon 3, *HSP27b-2* (132:C>G), which did not cause change in the amino acid sequence. The frequency of the allele T in the *HSP27b-1* locus was very low. At *HSP27b-2*, allele G was of higher frequency (0.77). Association analysis showed that the CC genotype at this locus was significantly ( $P<0.05$ ) associated with higher pH and lower toughness of meat. The candidate gene *HSP27b-2* is expressed in muscle, and may facilitate proteolysis of muscle fibre during post-mortem aging. The role of *HSP27* in preventing actin aggregation and, therefore, facilitating post-mortem action of proteases (Morzel *et al.*, 2008) probably influences meat tenderness.

The studies showed that the Boer goat and Boer cross have high frequencies of the alleles reported to be favourable for growth and meat quality. Analysis of growth and meat quality traits and test of

the association with alleles/genotypes at the candidate genes has to be carried out using larger number of animals and more populations to confirm the influence of these alleles. Only once their effects have been validated may the alleles at these loci be considered for use in selection programmes.

## **GENETIC CHARACTERISATION OF THE MAFRIWAL DAIRY CATTLE**

The Mafriwal dairy cattle (Figure 5) is a synthetic composite breed produced by the Department of Veterinary Services Malaysia (DVS) by crossing the Sahiwal x Friesian crosses imported from Australian with purebred Friesian. The project aimed to develop a tropicalised synthetic breed with high proportion of Friesian genes but adapted to the hot and humid local environment (Sivarajasingam *et al.*, 1983; Panandam & Raymond, 2005). It was hoped that the Mafriwal with Friesian genetic background would exhibit higher productivity and thereby boost the local dairy industry. This breed has also some infusion of genes from the Brazilian Gir breed. The Mafriwal breed have 50-75% Friesian genes.



**Figure 5** The Mafriwal dairy cow

### **Production Performance of Mafriwal**

Four Mafriwal breed groups, namely M50, M56, M63 and M75 with 50%, 56%, 63% and 75% Friesian genes, respectively, at the dairy farm of Institut Haiwan, Kluang, DVS were evaluated based on retrospective data (Kalaiselvi, 2004). The results showed no significant ( $P>0.05$ ) differences among the breed groups for lactation total milk yield (LTM), projected 305 days milk yield (P305M), days to peak milk (DPM), lactation length (LL), mean daily milk yield (DM) and dry period (DP). The least square means for milk production traits by breed group are given in Table 6. The non-significant difference among breed groups could be due to variation within the breed groups being higher than between the groups, which is confirmed by the high standard errors for the traits. However, earlier literatures have reported significant

( $P < 0.01$ ) differences in milk yield among the breed groups (Sivarajasingham & Kumar, 1989), and that the M63 significantly ( $P < 0.01$ ) outperformed the other breed groups in milk production (Raymond & Hawari, 1996). The earlier studies were carried out when the Mafriwal dairy cattle was still under development and there was segregation of genes in the population. Due to selection practices over the years, the breed groups probably have become more similar in performance. Breeding design at the start of the crossbreeding project was to develop a locally adapted Friesian-like breed. However, later, based on the observed performance, DVS decided to develop a synthetic breed with Friesian genes ranging from 56 - 70%, and selection and mating was based on performance without regards to breed group or gene composition. Furthermore, the present study only considered the Mafriwal cows with Friesian and Sahiwal genes; those with genes from other breeds such as the Gir or with unknown parental breed were excluded.

As for reproductive traits, the effect of breed group was not significant ( $P > 0.05$ ) for calving to first heat (CFH), calving to conception (CCo) and calving interval (CI). The least square mean values of reproduction traits for the four breed groups are shown in Table 7. Breed group had a significant ( $P < 0.05$ ) effect on calf birth weight (CBW); CBW was significantly ( $P < 0.01$ ) lower in M50 compared to M56 and M63.

**Table 6** Least square means ( $\pm$ SE) for milk production traits in the Mafrwal traits by breed group

Milk Production Traits	Breed Group			
	M50	M56	M63	M75
<b>LTM (kg)</b>	1309.12 $\pm$ 7 2.66 (587)	1269.77 $\pm$ 127.91 (146)	1467.42 $\pm$ 114.79 (186)	1209.68 $\pm$ 269.31 (67)
<b>P305M (kg)</b>	1921.99 $\pm$ 60.56 (422)	1874.89 $\pm$ 102.85 (111)	2140.50 $\pm$ 93.73 (143)	Non-est
<b>DPM (days)</b>	8.18 $\pm$ 0.26 (611)	8.18 $\pm$ 0.47 (150)	9.20 $\pm$ 0.42 (189)	7.32 $\pm$ 1.01 (69)
<b>LL (days)</b>	219.89 $\pm$ 8.26 (456)	226.37 $\pm$ 24.44 (105)	236.26 $\pm$ 13.38 (141)	197.99 $\pm$ 27.44 (49)
<b>DM (kg)</b>	5.87 $\pm$ 0.21 (545)	5.19 $\pm$ 0.58 (116)	6.55 $\pm$ 0.31 (144)	6.25 $\pm$ 0.65 (49)
<b>DP (days)</b>	217.52 $\pm$ 15.09 (282)	Non-est	258.29 $\pm$ 29.85 (54)	Non-est

For a particular trait (row), the means did not differ significantly ( $P > 0.05$ ) among the breed groups. Values in the parentheses show sample sizes, Non-est: values were non-estimatable due to small sample size. M50, M56, M63 and M75 are Mafrwal breed groups with 50%, 56%, 63% and 75% Friesian genes, respectively. LTM - lactation total milk yield, P305M - projected 305 days milk yield, DPM - days to peak milk, LL - lactation length, DM - mean daily milk yield, DP - dry period

**Table 7** Least square means ( $\pm$ SE) for reproduction traits in the Mafrilwal by breed group

Reproduction Traits	Breed Groups			
	M50	M56	M63	M75
<b>CI (days)</b>	432.76 $\pm$ 9.67 (164)	413.54 $\pm$ 16.83 (64)	430.88 $\pm$ 15.36 (126)	465.91 $\pm$ 22.36 (38)
<b>CFH (days)</b>	61.72 $\pm$ 2.92 (246)	53.00 $\pm$ 4.78 (117)	56.47 $\pm$ 4.47 (228)	58.48 $\pm$ 5.82 (93)
<b>CCo (days)</b>	142.37 $\pm$ 7.65 (209)	138.32 $\pm$ 12.73 (91)	136.57 $\pm$ 11.93 (172)	175.89 $\pm$ 16.21 (61)

For a particular trait (row), the means did not differ significantly ( $P > 0.05$ ) among the breed groups. Values in the parentheses show sample size. CFH - calving to first heat, CCo - calving to conception, CI - calving interval

## Microsatellite Analysis of the Mafriwal

The genetic variability of the Mafriwal was assessed using a random sample of 40 animals and 52 microsatellite loci (Kalaiselvi *et al.*, 2003; Kalaiselvi, 2004; Selvi *et al.*, 2004). The screening revealed 50 polymorphic loci; loci TGLA 53 and TGLA116 were monomorphic. The observed number of alleles per locus ranged from 4 to 8; the effective number of alleles ranged from 2.89 to 7.28. The allele frequencies ranged from 0.02 to 0.52. Significant ( $p < 0.05$ ) deviations from Hardy-Weinberg equilibrium (HWE) were observed for all polymorphic loci, and Wright's fixation index showed only eight loci to be 50% heterozygote deficit. Based on the results it may be concluded that the Mafriwal dairy cattle showed high genetic variability despite the small herd size and the use of artificial insemination and, to a small extent, embryo transfer in its development. This may be partly attributed to the fact that Mafriwal was developed by crossbreeding of *Bos indicus* and *B. taurus* breeds. In addition, although the initial plan was to develop a synthetic breed by grading-up, which increases homozygosity, the breed was stabilised with varying proportion of Friesian genes.

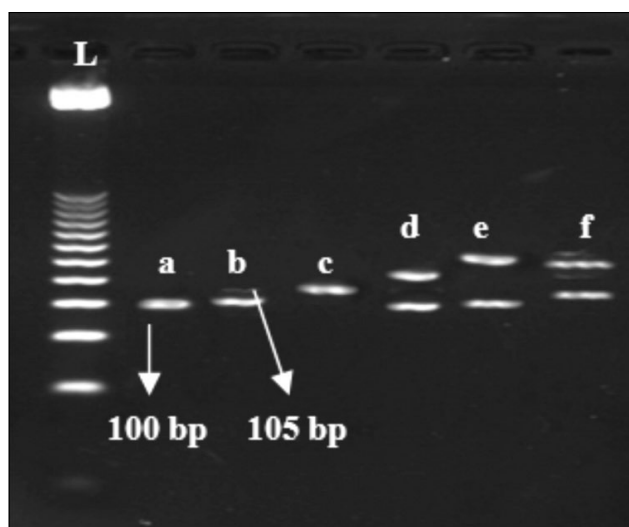
The Mafriwal was evaluated for association of genetic markers with milk production performance (Kalaiselvi, 2004; Kalaiselvi *et al.*, 2002). Retrospective performance data and DNA from all dairy cows available at Institut Haiwan Kluang, DVS during the study period was used. The high (HP) and low (LP) milk producers, identified based on their milk production traits (LTM, LL and DM), were screened for the 50 polymorphic microsatellite loci.

Majority of the loci did not show significant difference between the HP and LP cows in their allelic composition although some of the microsatellite loci had been suggested in earlier reports to be associated with QTL affecting milk production traits. The probable reason could be that the genes with substantial effects

on milk production traits were still segregating in the population. Although selection for milk production, fertility and adaptability were practiced during the development of Mafriwal, the intensity of selection may have been low as establishing a herd of sufficient size may have been a limiting factor. In addition, the two groups were defined based on their production and not generated using appropriate selection methods. Furthermore, the presence of many common alleles in the two producer groups clearly indicates the need for large sample sizes for association studies. Larger samples will show the predominant alleles in a particular group. Bulk segregation analysis would have been more appropriate if the herd was of larger size.

Alleles at three loci showed no significant association with average daily milk yield in the individual producer groups. However, when comparison was made using pooled data (LP, HP and the random sample, n=96) significant ( $P<0.05$ ) differences were observed for this trait in the presence of five alleles (Table 8). Allele *BM1290:142* was absent in the high producers. Analysis of pooled data showed animals without this allele had significantly ( $P<0.01$ ) higher average daily milk yield (Figure 6). Similarly, absence of the *BM143:105* and *BM1329:198* alleles resulted in higher average daily milk yield ( $P<0.05$ ).

This five microsatellite alleles may be potential markers for use in MAS. However, these have to be validated before they could be considered as informative markers for identifying high or low producing cows. This may be achieved by screening larger samples and future generations for these alleles and conducting association analysis using performance data and pedigree information.



**Figure 6** Alleles at locus BM143 detected using MetaPhor agarose gel electrophoresis. BM143:100 (a) and BM143:105 (b) appeared to be associated with average daily milk yield. L – 25 bp DNA size marker.

**Table 8** Comparison of average daily milk yield (kg/day) in presence and absence of selected microsatellite markers

Allele	Presence of Allele	Low Producers			High Producers			Pooled Data		
		LSmeans ± SE	Significance 0 vs 1	LSmeans ± SE	Significance 0 vs 1	LSmeans ± SE	Significance 0 vs 1	LSmeans ± SE	Significance 0 vs 1	
BM143:100	0	4.47 ± 2.47	ns	9.46 ± 1.07	ns	5.80 ± 3.12	*			
	1	4.18 ± 2.39		9.09 ± 1.83		7.78 ± 2.94				
BM143:105	0	4.57 ± 2.53	ns	9.84 ± 1.75	ns	7.22 ± 3.15	*			
	1	4.32 ± 2.42		10.83 ± 1.24		5.47 ± 3.11				
BM1290:135	0	4.46 ± 0.83	ns	9.21 ± 1.70	ns	6.40 ± 2.96	*			
	1	3.51 ± 0.83		9.10 ± 1.20		8.14 ± 3.95				
BM1290:142	0	4.71 ± 2.32	ns	9.19 ± 1.65	-	7.86 ± 3.00	**			
	1	1.58 ± 1.10		-		1.58 ± 1.10				
BM1329:198	0	4.16 ± 0.67	ns	9.69 ± 0.53	ns	7.19 ± 0.42	*			
	1	3.51 ± 0.95		7.65 ± 1.30		4.51 ± 1.05				

0 – absence of allele, 1 – presence of allele. Pooled data refers to high producers + low producers + random sample. \* significance at P<0.05, \*\* significance at P<0.01

## **GENETIC CHARACTERISATION OF THE KEDAH KELANTAN CATTLE AND THE KEDAH KELANTAN CROSSES**

The Kedah Kelantan (KK) is indigenous beef cattle in Malaysia (Devendra *et al.*, 1973). The KK cattle has a small and compact body with light to dark brown coat, a broad and short head, small pointed and drooping ears, small horns of variable shape, and a poorly developed dewlap (Figure 7). The female has small udders and teats. The hump is moderately developed in males and small in females. The means for reproductive, growth and carcass traits of the KK cattle are summarized by Sivarajasingam (1985) and Mohd Nasir *et al.* (2008). The KK is well adapted to the local environment, resistant to ticks and internal parasites, and has high fertility (Raymond & Ratnakumar, 1997). It is highly productive under good management (Payne & Hodges, 1997).



**Figure 7** The Kedah-Kelantan bull.

In order to improve the size and productivity of the KK, the breed has been crossbred with a number of imported, exotic breeds. Systematic crossbreeding of the KK with Brahman and Charolais by the Malaysian Agriculture Research and Development Institute (MARDI) has resulted in the development of two synthetic beef breeds, the Brakmas and the Charoke. The Brakmas (Figure 8), with approximately 50% Brahman and 50% KK genes, has white/grey coat colour, is bigger than KK, and has minimum health problems. This breed is suitable for beef production under oil palm plantations (Johari & Jasmi, 2009). The Charoke breed (Figure 9) has approximately 50% Charolais and 50% KK blood line. It has yellowish white coat, and is bigger than the KK, with higher birth, weaning and yearling weights. The Charoke shows better growth and reproduction on improved pastures and in feedlot compared to the KK cattle. In addition to these two breeds, indiscriminate crossbreeding of the KK has resulted in a number of non-descript composite breed types with various proportions of KK genes (Raymond & Ratnakumar, 1997).



**Figure 8** The Brakmas bull.



**Figure 9** The Charoke cow

### **Microsatellite Analysis of the Kedah Kelantan Cattle and KK Breed Types**

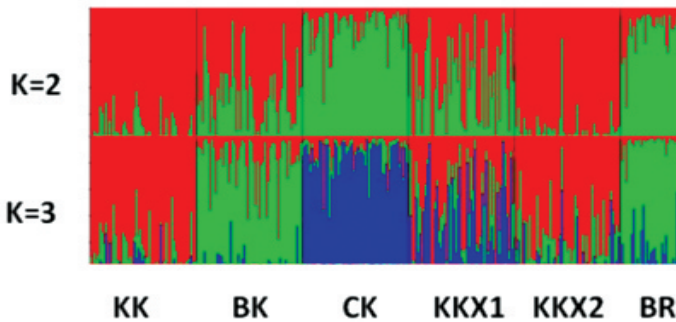
The genetic diversity within the Kedah Kelantan (KK), Brakmas, Cherokee and two non-descript KK crosses (KKX1 and KKX2) were screened for the 30 microsatellite loci recommended by the FAO/ISAG advisory group (FAO, 2004) for cattle genetic diversity (Abdelwahid *et al.*, 2008, 2009, 2011, 2012; Panandam *et al.*, 2010; Abdelwahid, 2012). The KK breed had the lowest mean number of alleles (8.2 vs. 8.5 – 9.3). This was as expected as crossbreeding would have incorporated the alleles of both the parental breeds into the crosses, increasing the number of alleles. The mean number of alleles of the KK and KK breed types were lower than that reported for four Chinese native cattle breeds (10.1 - 10.5) (Zhang *et al.*, 2007), but higher than those reported for six Spanish native cattle breeds (4.9 - 6.7) (Martín-Burriel *et al.*, 2007). The KK

breed exhibited moderate genetic variability with mean observed heterozygosity ( $H_o$ ) of 0.54. The Charoke had the highest  $H_o$  (0.65), and  $H_o$  ranged from 0.57 to 0.59 for the rest of the breed types. Mean observed heterozygosity is the best general measure of genetic variation (Allendorf & Luikart, 2007). High heterozygosity values could be attributed to long-term natural selection for heterozygous forms, or due to the mixed nature of the breeds, or due to gene flow between different populations. High level of inbreeding ( $F_{IS}$ ) was observed in the KK (0.212), KKK2 (0.232), and Brakmas (0.205). The inbreeding values observed in all breed types were higher than that reported for 27 native cattle breeds in China (0.007- 0.147) (Zhang *et al.*, 2007), and eight native Ankole populations in Uganda (-0.040 – 0.054) (Kugonza *et al.*, 2011).

The low number of alleles observed in the KK and KK breed types could be attributed to inbreeding. This in turn would be the effect of small herd sizes, assortative mating and lack of pedigree data (Allendorf & Luikart, 2007). The KK, Brakmas and Cherokee populations investigated were considered nucleus herds, therefore, the low genetic variability should be a concern. The nucleus herd size, the nucleus structure, the age structure of the nucleus, selection criteria and selection accuracy for the bulls and replacement cows, and the completeness of performance and pedigree records are vital factors to consider when establishing and managing nucleus herds (Phillips, 2001).

The level of genetic differentiation among the KK and KK breed types was low (mean  $F_{ST} = 5.4\%$ ). This could be attributed to the fact that the most of the KK crossbred types were developed or originated from crosses with KK as the maternal line; thus they share many common alleles. The degree of between breed differentiations indicated high gene flow between the KK, KKK1 and KKK2 (13.39 - 16.84%). Brakmas and Charoke showed low

inter-breed gene flow (5.04%), which could be explained by the physical separation of the two breed populations, and the breeding and selection programs practised in the respective farms. The results of the structure analysis showed that the populations were split into three clusters: KK and KKK2 in the first cluster, Brakmas and Brahman (used as an outgroup) in the second cluster, and Charoke in the third cluster. KKK1 was distributed in all three inferred clusters (Figure 10).



**Figure 10** Clustering assignments of 312 animals representing the six cattle breed types. KK – Kedah Kelantan, BK – Brakmas, CK – Cherokee, KKK1 & KKK2 – non descriptive KK crosses, BR – Brahman (outgroup), K - number of clusters.

The KK and KK breed types were screened for Zebu and taurine diagnostic alleles (MacHugh *et al.*, 1997; Loftus *et al.*, 1999; Ibeagha *et al.*, 2004) to determine the level of zebu-taurine admixture. All breeds had higher proportions of the zebu alleles. The proportion of Indian zebu genes in the KK and the KK breed types (18.4 – 25.8%) was higher than the African zebu genes (2.5 - 7.4%) and the European taurine genes (1.6 – 4.7%). This is supported by the history of the zebu animals in Southeast Asia; they originate from the zebu cattle from India introduced through the

human migrations and ancient sea trading routes (Payne & Hodges, 1997). Charoke had the highest proportion of African and European taurine diagnostic alleles (7.4% and 4.7%, respectively). This was as expected as Charoke was a Charolais (*B. taurus*) cross.

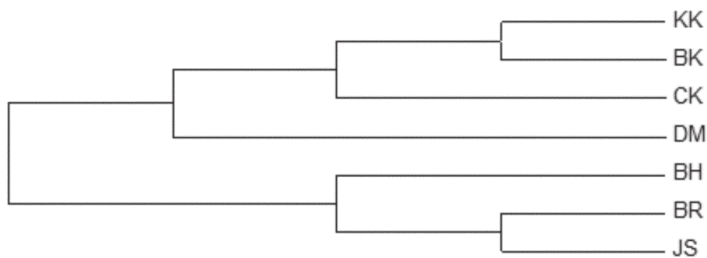
## **Mitochondrial DNA Analysis of Cattle Breeds in Malaysia**

The *B. indicus* cattle are found in the tropical countries. The *B. taurus* cattle while indigenous to Europe are also found in Africa and Asia. The cattle breeds in Malaysia comprise of the indigenous *B. indicus* Kedah Kelantan (KK), and the imported *B. taurus* breeds, as well as the synthetic breeds and composite population derived from crosses between these two species of cattle.

The KK, Brahman, Brakmas, Brangus, Charoke, Droughtmaster and the *B. taurus* Jersey breeds were screened for 16 RFLP mitochondrial DNA (mtDNA) loci (Yow et al., 2009, 2010; Panandam et al., 2010; Yow, 2011). The overall percentage of polymorphism was 50%; eight loci were polymorphic. For the polymorphic loci, the KK was monomorphic for the *B. indicus* alleles at the loci *D-loop/DdeI* (435, 301, 228 bp), *Cytb/MspI* (812, 334, 83 bp), *Cytb/MspR9I* (663, 417, 149 bp) and *ND5/TasI* (278, 135, 115 bp). KK was also monomorphic for the B allele (755, 755 bp) at the locus *ND5/HindIII*. The Brakmas and Charoke showed very high frequencies of these alleles ( $\geq 0.90$ ). This is as expected since these two breeds were developed using the KK as the maternal line. The Brangus was monomorphic for the *B. taurus* allele B at the *Cytb/MspR9I* (1080, 149 bp) and *ND5/TasI* (278, 250 bp) loci; Jersey had frequencies of 0.8 for both these alleles. The *D-loop/BstXI* locus had two alleles, A (510 and 454 bp) and B (964 bp), but the B allele was observed only in two samples of Droughtmaster. Mitochondrial DNA is maternally inherited. The presence of both

alleles at the polymorphic loci in the Jersey and Droughtmaster implies the use of both *B. taurus* and *B. indicus* maternal lines in their development

Nei's genetic distance estimates clearly showed that KK was closer to the Brakmas and Charoke. On the other hand, KK and Brangus had the furthest relationship. Jersey had the closest relationship with Brangus. The dendrogram based on genetic distance showed two clusters for the seven cattle breeds (Figure 11). One consisted of KK, Brakmas, Charoke and Droughtmaster, while the other grouped Brahman, Brangus and Jersey. The similarity between Brangus and Jersey is due to Brangus having the *B. taurus* Angus as its maternal line and Jersey being a *B. taurus* breed. Brahman not being grouped with the *B. indicus* KK was also reported by Johari and Marini (2007) based on the study using microsatellite markers. This is expected noting that the Australian Brahman, which is generally found in Malaysia, was developed from the founder populations imported from United States of America (USA) and Brazil (ABBA, 2012). These in turn originate from the Indian cattle breeds imported into USA in the early 1900s and developed with some infusion of British-bred cattle (Sanders, 1980).



**Figure 11** Dendrogram based on mtDNA data using neighbor-joining method showing the relationship between the 7 cattle breeds . KK - Kedah Kelantan, BK - Brakmas, CK - Charoke, BH - Brahman, DM - Droughtmaster, BR - Brangus, JS - Jersey

## **Candidate Gene Polymorphism in the Kedah Kelantan, Brakmas and Cherokee**

The Kedah Kelantan (KK), Brakmas and Cherokee breeds were screened for 16 candidate gene loci for growth and meat quality traits (Panandam *et al.*, 2010). The loci showed 50% polymorphism. The predominant alleles were generally the same for the three breeds, except for two loci. The Brakmas and Cherokee shared higher frequencies of the same allele for the calpain-2 (0.73 and 0.87, respectively) and calpastatin promoter (0.65 and 0.91, respectively) loci compared to the KK (0.24 and 0.13, respectively). The similarity between the Brakmas and the Cherokee may be attributed to the breeds being synthetically developed by crossbreeding with the Brahman and Cherolais, respectively. These latter breeds are improved beef breeds and, therefore, their allelic composition at candidate genes for growth and meat quality would have been influenced by the selection practices. These genes would have in turn been passed on to the Brakmas and Cherokee. The KK has not been subjected to such intense selection for beef production.

## **GENETIC CHARACTERISATION OF THE DEER SPECIES IN MALAYSIA**

In Malaysia deer are non-conventional species farmed as economic enterprises for meat, velvet and eco-tourism (Vidyadaran *et al.*, 1993). The establishment of artificial populations in enclosures, generally in small population sizes, has been a contributory factor to loss in genetic variation. Over the last four decades, deer of various species and subspecies have been imported from countries such as Australia, Thailand, Mauritius and New Zealand and a number of deer farms have been established. The three popular species which are still farmed in large numbers are *Cervus timorensis* (rusa or timor

deer), *C. unicolor* (sambar) and *C. nippon* (sika). *C. timorensis* is native to the islands of Indonesia, and the subspecies vary between the islands. *C. unicolor* is the largest of the tropical deer species , with a natural distribution stretching from India through South East Asia to the Philippines (Semiadi *et al.*, 1996) (Figure 12). *C. nippon* is native to Japan and is widely distributed in Eastern Asia (Figure 13). It is vital that a detailed study to evaluate and document the genetic makeup of the deer species and populations in Malaysia be conducted before the gene pool is indiscriminately reduced by inappropriate breeding practices or altered by inter-species breeding. A study was conducted to investigate the genetic variability within and between the *C. timorensis*, *C. unicolor* and *C. nippon* in Malaysia, using cytogenetic, biochemical and molecular techniques.



**Figure 12** The sambar deer (*Cervus unicolor*)



**Figure 13** The sika deer (*Cervus nippon*)

### **Karyotypes of *C. timorensis*, *C. unicolor* and *C. nippon***

Karyotype is the paired array of chromosomes arranged accordingly to length and position of centromere, showing the total chromosome complement of a typical cell. The karyotype differs among species with respect to the diploid chromosome number ( $2n$ ), and chromosome sizes and structures. These characteristics allow its use in species identification and study of evolution. The karyotype is also used to detect numerical and structural aberrations of chromosome (Sumner, 1990). Banded karyotypes facilitates the identification of homologous chromosomal pairs, alterations in structure of the chromosomes and homology between chromosomes of closely related species.

The family Cervidae displays extreme chromosomal diversification, with diploid numbers ( $2n$ ) ranging from 68 to 70, and the fundamental number (FN) ranging from 70 to 74. Fontana and Rubini (1990) proposed that chromosome fission events increased the karyotype from an ancestral diploid number

of about 20 chromosomes to 70 and 74. Wang and Du (1983), on the other hand, believed that the chromosome number in Cervinae actually evolved through a decrease in chromosome number by Robertsonian fusions. In addition to variations in chromosome numbers among the Cervidae, variation in chromosome numbers of individual species has also been reported. The chromosome number (2n) of *C. nippon* has been reported to range from 64 to 68 (Hsu & Beneirschke, 1977), and that of *C. unicolor* from 56 to 68 (White, 1973).

Six animals of *C. timorensis*, *C. unicolor* and *C. nippon*, three males and three females of each species, were karyotyped (Habiba, 2005). The conventional and banded karyotypes indicated that the three deer species differed in chromosome number and morphology (Table 9). The findings suggested that the Malaysian *C. unicolor* may be the same or closely related subspecies as that in China, as the diploid number was the same as the Chinese *C. unicolor dejeani*; and differed from the Philippines *C. unicolor mariannus* and the Indian *C. unicolor niger* (Wang & Du, 1991). The karyotype of *C. nippon* was in agreement with that reported by Bartos and Zirovnický (1981) for sika in Italy, but was different from that reported by Wang and Du (1982) for the Japanese sika. All three species had a large acrocentric X chromosome and a small acrocentric Y chromosome. Wang and Du (1983) and Ismail *et al.* (2001) had described the Y chromosome of *C. timorensis* as being submetacentric, but the present study showed Y chromosome in *C. timorensis* as acrocentric. Although the chromosome diploid number varied among the three deer species, the fundamental number (FN) remained the same, 70. The results bear evidence to the close relationship among the three species, and the closer relationship between *C. timorensis* and *C. unicolor* as compared to *C. timorensis* and *C. nippon*.

**Table 9** Number and morphological characteristics of the chromosomes of male and female *C. timorensis*, *C. unicolor* and *C. nippon*

Species	Sex	Number of Autosomes		Sex Chromosomes		FN	Number of chromosomes (2n)
		SM/M	AC	SM/M	AC		
<i>C. timorensis</i>	Male	10	48	0	2	70	60
	Female	10	48	0	2	70	60
<i>C. unicolor</i>	Male	8	52	0	2	70	62
	Female	8	52	0	2	70	62
<i>C. nippon</i>	Male	4	60	0	2	70	66
	Female	4	60	0	2	70	66

M- metacentric, SM- submetacentric, AC- acrocentric, FN - fundamental number

### **Biochemical Analysis of *C. timorensis*, *C. unicolor* and *C. nippon***

Biochemical polymorphisms, which provide biochemical profiles of individuals based on inherited variations of biomolecules, are useful in pedigree and parentage studies (Henkes *et al.*, 1994). Biochemical analysis of populations, breeds and species may be used to estimate genetic distances between the various groups (Barker *et al.*, 1990; Kumar *et al.*, 1991) and to study population evolution (Dratch & Pemberton, 1992) and dynamics (Selvaraj *et al.*, 1991). Unique protein forms may also serve as genetic markers for associated performance traits or disease resistance (Ignjatovic *et al.*, 1995).

The three deer species, *C. timorensis*, *C. unicolor* and *C. nippon*, were analysed for eight red blood cell proteins/enzymes and seven plasma proteins/enzymes (Habiba, 2005; Habiba *et al.*, 2005). All three deer species were polymorphic for hemoglobin (HB), but there was no significant ( $P>0.05$ ) difference in the genotype distributions. Frequency of allele HB<sup>A</sup> was 0.553 for *C. timorensis*, 0.426 for *C. nippon* and 0.389 for *C. unicolor*. Glucose-6-phosphate dehydrogenase (G6PD) was polymorphic. However, *C. timorensis* and *C. unicolor* were homozygous for the same allele, and *C. nippon* was homozygous for a different allele, further confirming the genetic similarity between the earlier two species.

### **RAPD Analysis of *C. timorensis*, *C. unicolor* and *C. nippon***

The randomly amplified polymorphic DNA (RAPD) technique for identifying genetic polymorphisms is based on the PCR amplification of genomic DNA templates using a short sequence, arbitrary oligonucleotide primers. This technique can rapidly detect

a large number of anonymous markers distributed over the entire genome, and does not require knowledge of the DNA sequence. RAPD may be used to generate fingerprints for relatedness (Geng *et al.*, 2002) and estimate inbreeding (Dinesh *et al.*, 1993), and for analysis of genetic variations (Bahy, 2003), pedigrees (Scott *et al.*, 1992) and population structures (Chapco *et al.*, 1992), as well as for construction of phylogeny (Landry *et al.*, 1993). It may also be used to developed specific DNA markers for identification of breeds (Yeo *et al.*, 2002) and fingerprints for identification of species (Huang *et al.*, 2003).

The genetic variations within and among *C. timorensis*, *C. unicolor* and *C. nippon* were examined using RAPD fingerprinting (Habiba, 2005; Habiba *et al.*, 2008). The 10 primers used amplified 164 reliable DNA markers with an overall percent polymorphism of 99.39%. The three species shared 59 polymorphic markers and one monomorphic marker. The genetic distance values from RAPD analysis suggested that the *C. timorensis* and *C. nippon* were genetically more similar than *C. timorensis* and *C. unicolor*. However, this observed close relationship is not reliable as it is probably due to the lesser number of RAPD markers generated for *C. unicolor* as a result of the small sample size used (n=9); sample sizes used for *C. timorensis* and *C. nippon* were 38 and 34, respectively.

*C. unicolor* had five exclusive monomorphic markers, 52A-14:150, 95A-14:220, 06B-14:350, 60B-11:320 and 67B-7:550. The five exclusive monomorphic markers may not yet be considered as unique identifiers for the species or population as only nine animals represented this species. *C. nippon* had one exclusive monomorphic marker, 105R-9:520, and *C. timorensis* had none. The RAPD marker 105R-9:520 has potential of being an unique identifier for *C. nippon*. However, its presence in other populations

of the species and absence in other populations of the other deer species in Malaysia must be established before it may be declared as a marker for species identification.

### **Microsatellite Analysis of *C. timorensis*, *C. unicolor* and *C. nippon***

There are no genetic maps for rusa and sika. The development of species-specific microsatellite primers could be a time-consuming and expensive process (Vial *et al.*, 2003). To overcome this disadvantage one strategy is to use microsatellite primers developed for closely related species (Postma *et al.*, 2001; Moghim *et al.*, 2012).

DNA samples from *C. timorensis* and *C. nippon* were screened using microsatellite primer pairs which had been successfully used in other species (Khaledi *et al.*, 2005, 2006a; Khaledi, 2008). Of the 11 reindeer microsatellite primer pairs (Roed & Midthjell, 1998) which also successfully amplified DNA samples from red deer, roe deer and fallow deer (Poetsch *et al.*, 2001), five showed successful amplification for rusa and eight for sika. Of the two white-tailed deer microsatellite primer pairs which had shown successful amplification in the Japanese sika population (Tamate *et al.*, 2000; Goodman *et al.*, 2001), only one showed successful amplification in the local population; it showed no amplification for rusa. Of the 15 bovine primer pairs screened, only five showed successful amplification in sika, although they had shown successful amplification in the Vietnamese sika deer and four had also been successful in the Japanese sika deer (Tamate *et al.*, 2000; Bonnet *et al.*, 2002). The findings confirm that the microsatellite flanking sequences are to some extent conserved across species, (Slate *et al.*, 1998) and primers may be used for cross-species amplification. However, it is not always successful; it may not work even in

subspecies. Currently the karyotypes of rusa and sika deer have not been aligned with those of other ruminants. Based on the common loci amplified in rusa, sika, and in the other cervidae as well as the bovidae species, it is possible to identify chromosome segment homologies for these species.

Rusa and sika may be distinguished morphologically and based on their karyotype (Habiba, 2005). However, the meat, animal parts and body fluids from different sources are sometimes not distinguishable based on visual parameters. The physically undistinguishable nature of meat and animal products often leads to illegal poaching and sale of meat from protected animals going undiscovered. Ability to distinguish meat and meat products from different sources, and body fluids is important to prevent fraudulence and the illegal killing of protected animals. DNA markers reliable for species identification

Rusa did not show any diagnostic RAPD marker, but sika had one diagnostic RAPD marker, 105R-9:520 (Habiba, 2005). Microsatellite analysis revealed two loci which may be used as diagnostic markers to distinguish the rusa (BM2113:126) and sika (NVHRT34:144) (Khaledi *et al.*, 2006b; Khaledi, 2008). However, as only one rusa and one sika population were investigated, before these two markers may be declared as diagnostic markers for distinguishing the two species, more rusa and sika populations must be screened. Furthermore, the allele sizes reported for locus BM2113 in *Bos taurus* are between 123-143 bp and that for *Ovis aries* are between 128-150 bp (Ihara *et al.*, 2004), and the European bison was monomorphic for this locus with an allele of 128 bp (Gralak *et al.*, 2004). Therefore, the marker BM2113:126 is not suitable for distinguishing the rusa from the cattle, sheep and bison.

The analysis of allele frequencies for bottleneck effects, under the assumption of mutation-drift equilibrium, exhibited

recent bottleneck in the sika deer population (Khaledi *et al.*, 2007; Khaledi, 2008). Since the sika population investigated originated from a small number of animals imported from Taiwan and is only the second generation of the initial population, this was probably due to founder bottleneck effect. The results of this study suggest that in time the gene diversity of the established sika population in Malaysia may be reduced if not properly managed. Rare alleles detected at the microsatellite loci investigated and at other loci, risk being lost forever from this population.

### **rRNA Sequence Variation Within and Between the Deer Species**

The partial sequence of the 12S rRNA gene of four deer species, namely the sambar deer (*C. unicolor*), sika deer (*C. nippon*), rusa deer (*C. timorensis*) and the barking deer (*Muntiacus muntjac*) were compared (Mohd Izwan, 2009). Although there was very high sequence similarity within the species, there were some variations detected in the conserved 12s rRNA gene sequence, especially among the *M. muntjac*. The variations were generally due to base substitutions. Comparison between the deer species showed that *C. nippon* and *C. unicolor* had the highest similarity, while *M. muntjac* differed the most from the other species (Table 10). The screened region of the 12s rRNA gene showed a number of base substitutions in *M. muntjac* which were not displayed in the other species. In addition there was a single base deletion at position 16 and a deletion of 14 bases at positions 292 – 305 (Figure 14). This higher difference compared to the other three deer species is as expected since *M. muntjac* belongs to a different genus, while the other three deers are from the *Cervus* genus. The 12S rRNA gene is popularly used to differentiate species.

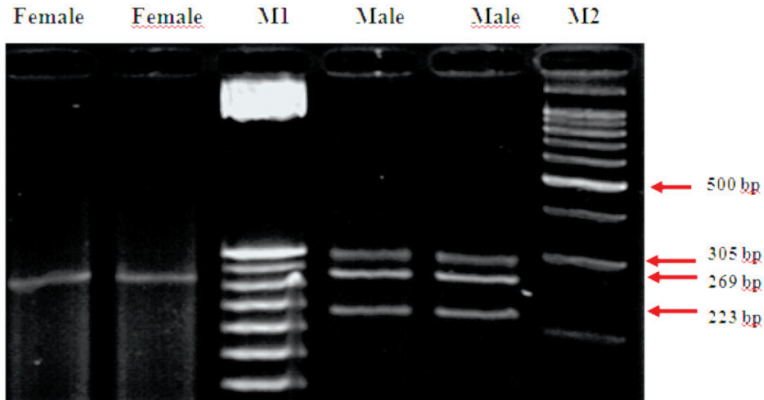


## Molecular Sex Determination in Rusa Deer

Molecular sexing has wide applications; it is used in forensics (Bidmos *et al.*, 2010), archaeology (Hay *et al.*, 2008), animal breeding (Millar *et al.*, 1996) and conservation (Lawrence *et al.*, 2008). It is especially useful in embryonic stages where anatomical sexing is not possible, or when only tissue samples are available. Mammals can be molecularly sexed by PCR amplification of Y chromosome region, or co-amplification of homologous regions of the X and Y chromosomes, which are discriminated by size polymorphism (Fredsted and Villesen, 2004; Delgado *et al.*, 2005). The SRY gene is used as Y-specific fragments for sex identification (Bryja and Konecny, 2003). The amelogenin and zinc finger protein (ZF) genes are used in co-amplification of the X and Y chromosomes (Pomp *et al.*, 1995; Ortega *et al.*, 2004; Pfeiffer and Brenig, 2005; Villesen and Fredsted, 2006). The coding regions of X and Y chromosomal amelogenin genes are approximately 87% identical; they differ quite significantly in size and sequence, and consequently can be used as markers for the two chromosomes. In most deer species, the male is identified by amplifying the SRY gene (Takahashi *et al.*, 1998; Pajare *et al.*, 2009). AMELX and AMELY have been used in sexing the European red deer (Pfeiffer and Brenig, 2005) and the sika deer (Yamauchi *et al.*, 2000).

Four primer pairs, AMEL2, AMGX/Y, AMGX/Y2 and SE47/48, were used to amplify the amelogenin gene regions in the rusa deer (Khaledi, 2008). The primer pairs AMEL2, AMGX/Y and AMGX/Y2 each amplified similar banding patterns for the males and females, confirming the presence of the amelogenin gene on the X and Y chromosomes in rusa and them being unsuitable for sex determining of rusa deer. The primer set SE47/48 generated one band of 269 bp for the females, but exhibited an additional two

bands (223 and 305 bp) for the males. The primer set SE47/48 is suitable for molecular sexing of rusa deer (Figure 15).



**Figure 15** Amelogenin banding patterns generated by primer set SE47/48 for rusa deer (*Cervus timorensis*). M1 and M2 are 25 bp and 100 bp DNA size markers, respectively.

## **SUSTAINABLE UTILISATION AND DEVELOPMENT OF ANIMAL GENETIC RESOURCES**

Our indigenous breeds and many of the locally developed synthetic breeds and non-descript crosses will soon be lost unless keeping them is profitable to the farmers. Characterisation of our animal genetic resources will not only identify unique traits and characteristics of the locally available breeds and populations, but will also provide the information necessary to decide on breeding strategies for their development and to identify the breed(s) suitable for specific production systems and conditions. Unique qualities and characteristics of animal genetic resources have to be identified so that values may be added to them (LPP, LIFE Network, IUCN–WISP and FAO, 2010).

In order to ensure food security and be able to meet the challenges to be faced by the livestock industry in the future, it is crucial that in addition to characterisation of animal genetic resources there is sustainable development of these resources. There should be continued improvement in their production performance, along with improvement in husbandry and production process, the quality of products and processing, and the marketing. Productivity of the animal genetic resources has to be continuously enhanced according to the environmental challenges, market demands and consumer preferences. In the case of the commercial exotic breeds, this is taken care of by animal breeders in the countries that developed these. However, the indigenous breeds and the locally developed synthetic breeds and breed types as well as the non-descript crosses and traditional populations too require continuous improvement, else they will become threaten or even lost. The performance and genetic structure of these genetic resources should be evaluated and monitored. Biotechnology tools may be used for these purposes as well as to increase the population size and enhance the genetic merit of the breeds and populations. Breeding strategies and programmes should be designed for individual breeds, based on the production systems, economic needs of the farmers and the current and future markets. It is pertinent that selection based on genetic merit and correct breeding strategies are adopted. This is only possible if proper data recording is practised at all levels of the livestock production system. Standard, user-friendly database management systems should be developed and customised for the different livestock sectors in the country to facilitate this (Panandam, 1991, 2001). Implementation of correct breeding practices requires training and technical support. Continued research is crucial for the development of livestock productivity and conserving animal genetic resources. Local education institutions have vital roles in

conducting research, capacity building and in the development of training resources based on the local livestock industry. Training is required in animal genetics, animal breeding, genetic variability assessment, and data recording and management (Malmfors *et al.*, 2002; Ojango *et al.*, 2010). Farmers associations and breed societies should be established to facilitate dissemination of information and organise training programmes for farmers, farm managers and others involved in the livestock industry.

## **CONCLUSION**

Local animal genetic resources are assets of a country. They represent the germplasm pool that is vital for further improvement of livestock productivity, enabling the livestock industry to meet current and future challenges and to ensure food security. The rapid erosion of animal genetic diversity should be our concern and measures to reduce further loss should be adopted. Local animal genetic resources have to be characterized; their performances and genetic diversity have to be evaluated and monitored. Capacity building and investment in human capital are necessary. The task of spearheading characterisation of local animal genetic resources for sustainable utilisation and development has to be government-driven and government-supported. However, success may only be achieved through the cooperation and concerted efforts of government agencies, livestock farmers, research organisations, education institutions and non-governmental organisations (NGOs).

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## **BIOGRAPHY**

**Jothi Malar Panandam** was born in 1957 in Kuala Lumpur. She started her primary education at Kampung Pandan Girls' School and later continued at Pudu English Primary School, both in Kuala Lumpur. She received her secondary education at Pudu English Secondary School and completed her Form Six at Cochrane Road School, Kuala Lumpur. She then obtained her bachelor degree in Genetics with Honours Class I from University of Malaya in 1981. She was awarded the Research Fellowship by University of Malaya to pursue her masters degree as well as her doctorate in Animal Breeding, which she attained in 1985 and 1991, respectively. She was offered the German Academic Exchange Service (DAAD) scholarship to pursue part of her doctorate training at the Technical University of Berlin, Germany.

Jothi Malar Panandam started her academic career as a lecturer in 1991 at the Institute of Advanced Studies, University of Malaya. In 1993, she moved to Universiti Pertanian Malaysia as a lecturer in the Department of Animal Science, Faculty of Veterinary Medicine and Animal Science. She was promoted to Associate Professor in 2004 and to Professor on 1 September 2010. At the department, she is the coordinator of the Genetics Laboratory, which she was responsible for establishing, and the Cell Culture Laboratory. She has served in various department and faculty committees. At the university level, she is a member of UPM COPPA Panel of Assessors and a member of the Advisory Committee for AgriBiogene Bank.

Jothi Malar Panandam has been actively involved in research. Her interest is in small ruminant breeding, population genetics, and application of molecular marker technologies in animal science. She has headed eight research projects in these areas, and has been a collaborator in many. She has in the past been involved in projects funded by German Foundation for International Development

(GTZ), Australian Center for International Agricultural Research (ACIAR), and European Commission (EC). From her research involvement, she has 150 publications, which includes journal articles, chapters in books, and publications in international and local reports and proceedings. She has also edited a book, a national report and a number of proceedings. She has supervised 17 and co-supervised 26 graduate students, and 28 undergraduate students.

Jothi Malar Panandam is well known as a lecturer and researcher in the field of Genetics and Animal Breeding, both locally and internationally. She has been invited as a lecturer and a facilitator for training courses and workshops on animal breeding, conservation of genetic resources, molecular marker technology, bioinformatics, research methods, scientific writing and presentation skills. She has served as examiner of MS and PhD theses from local and foreign universities. To her credit, she has served as the Chief Editor for Bulletin PGM of the Genetics Society of Malaysia, a member of the editorial committee for Malaysian Journal of Animal Science, and as reviewer to a number of local and international journals. She was invited as country representative to the Regional Planning Workshop of ILRI/SLU Project on Capacity Building, the Workshop on Capacity Building for Sustainable Use of Animal Genetic Resources in Developing Countries, and the John Vercoe Memorial Conference. She was also invited as one of the Malaysian representative on the Biotech Study Tour to United States of America, and as a visiting researcher to the International Livestock Research Institute (ILRI), Kenya. Her expertise has also been acknowledged by the invitations as plenary speaker, member of panel discussion, moderator at expert discussion, chairman of scientific sessions, and chairman of scientific subcommittee in a number of national and international conferences. At national level, she is currently a member of the Genetic Modification

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Advisory Committee (GMAC), Department of Biosafety Malaysia. She was a member of the Technical Sub-committee on Animal Genetic Resources, the Advisory Committee for the State of the World Animal Genetic Resources (SOW-AnGR) - Malaysia, the Working Committee for the Development of National Policy on Domestic Animal Biodiversity, and the Evaluation Panel for Science Fund R&D Projects for Biotechnology Cluster. She has also held responsible positions in the Genetics Society of Malaysia (convener for the Consultative Working Group on Animal Genetics, exco member, auditor and at present the honorary treasurer), the Malaysian Society for Animal Production (auditor), and the Malaysian Society of Applied Biology (auditor).

In community service, Jothi Malar Panandam has been actively involved in St Johns Ambulans Malaysia (SJAM). She holds the position of Principal Staff Officer (Training). She has been involved the development of the SJAM First Aid Syllabus and Training Guidelines, in First Aid training and training of the trainers and tutors, in organising national training seminars and workshops, and in providing First Aid service to the public. In recognition of her service, she was awarded the SJAM Pingat Jasa Gemilang in 2006 and the Pingat Bakti Perkasa in 2012.



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- I would like to thank the management and staff of Universiti Putra Malaysia, in general, and the Faculty of Agriculture, in particular, and my friends and colleagues thereof for your support and kind assistance.
- I am greatly indebted to my late father and to my mother for their love, inspirations and all they have done for me. I would also like to express my sincere gratitude to my family for their continuous support and encouragement; I cherish your love and the wonderful times we have shared.
- I am sure there are many, whom I have not addressed above, who have in one way or another contributed to my success. To all of you I say thank you.

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