UNIVERSITI PUTRA MALAYSIA

GENETIC CHARACTERISATIONS OF FOUR GOAT BREEDS IN MALAYSIA ASSESSED USING MICROSATELLITES

AMIE MARINI ABU BAKAR

FBSB 2014 33

GENETIC CHARACTERISATIONS OF FOUR GOAT BREEDS IN MALAYSIA ASSESSED USING MICROSATELLITES

By

AMIE MARINI ABU BAKAR

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Master of Science

October 2014

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

GENETIC CHARACTERISATIONS OF FOUR GOAT BREEDS IN MALAYSIA ASSESSED USING MICROSATELLITES

By

AMIE MARINI ABU BAKAR

October 2014

Chairman: Professor Tan Soon Guan, PhD

Faculty : Biotechnology and Biomolecular Sciences

The genetic characterisation of goat breeds in Malaysia as a genetic resource is essential for genetic improvement as well as a conservation strategy. The goat breeds in Malaysia comprise small-framed animals made up of the original Katjang goat with the addition of larger framed exotic goats such as Jamnapari and Boer. The local indigenous Katjang goat has a reasonably high degree of tolerance to the local environment. On the other hand, the Boer, Jamnapari and Savanna which are introduced breeds are well adapted in Malaysia.

However, little information is available on the goat breeds' genetic characteristics or genetic variabilities. Basically, information about the genetic background of a breed and its populations is required for proper breeding. Data based on adequate genetic studies for goat characterisation and their similarities are still lacking. The goat populations have to be genetically characterised because genetic information is considered as the primary and essential starting point of any goat husbandry project. Knowledge of the genetic variability of a species is a core element for the conservation and exploitation of animal diversity for breeding purposes. Thus, this study was conducted to evaluate the genetic variabilities of the goat breeds in Malaysia, namely Katjang the indigenous goat and the exotic Jamnapari, Boer and Savanna breeds, by using microsatellite markers for proper breeding, selection and conservation purposes.

Blood samples were randomly sampled from Katjang, n=37, Jamnapari, n=34, Boer, n=40 and Savanna, n=40. Thirty microsatellite primer pairs suggested by FAO/ISAG and seven microsatellite loci from other studies were used for the genetic diversity studies in the goats. The microsatellite markers were optimised using pooled DNA at different polymerase chain reaction (PCR) conditions followed by screening individuals for polymorphisms. The polymorphic microsatellite loci were used for the genetic diversity studies.

Thirty out of the 37 microsatellite loci were polymorphic in all four goat breeds, while six loci were monomorphic and one locus failed to amplify for the Boer goat breed suggesting that it was monomorphic for the null allele. The mean number of observed alleles ranged from 5.43 to 5.90. Meanwhile the observed heterozygosity values (Ho) were lower than the expected heterozygosities for the goat breeds studied. The Jamnapari and Boer goat breeds had the highest Ho (0.43), followed by the Savanna (0.42) and the Katjang showed the lowest Ho (0.36).

Genotypic linkage disequilibrium was observed between several loci but there was no consistency across the breeds. The overall mean inbreeding coefficient (F_{IS}) of 0.43 indicated the occurrence of inbreeding in all the four breeds studied. The mean F_{IT} and F_{ST} values of 0.46 and 0.06, respectively measured the degree of differentiation within and among breeds. The F_{ST} value indicated a lack of genetic differentiation among the goat breeds. The Nei's genetic identities among the four goat breeds ranged from 80% - 87%. The highest genetic distance value was observed between the Katjang and the Savanna goat breeds (0.2171) while the Boer and the Savanna goat breeds were found to be the most similar with a genetic distance value of 0.1325.

Based on this study it can be concluded that there are some genetic variations in the four goat breeds in Malaysia, although the Katjang has a slightly lower genetic diversity. However, further screening of the goat breeds, utilising more breeds and larger sample sizes are needed to ascertain more accurately the variability of the goat breeds in Malaysia. Microsatellite marker typing using the capillary technique and other more sensitive marker systems like SNP should also be considered. In addition, consideration should be given to genome mapping, using the latest high throughput genotyping platforms to obtain the best genomics solutions and applications.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

PENILAIAN PENCIRIAN GENETIK EMPAT BAKA KAMBING DI MALAYSIA MENGGUNAKAN MIKROSATELIT

Oleh

AMIE MARINI ABU BAKAR

Oktober 2014

Pengerusi: Profesor Tan Soon Guan, PhD

Institut : Bioteknologi

Pencirian genetik baka kambing di Malaysia sebagai sumber genetik adalah penting untuk pembaikan genetik serta strategi pemuliharaan. Baka kambing di Malaysia terdiri daripada haiwan berangka kecil iaitu kambing asli Katjang dengan tambahan kambing eksotik berangka lebih besar seperti Jamnapari dan Boer. Kambing Katjang tempatan mempunyai darjah toleransi yang tinggi terhadap persekitaran tempatan. Sebaliknya, Boer, Jamnapari dan Savanna adalah baka yang diperkenalkan dari luar dan telah menyesuaikan diri dengan baik di Malaysia.

Walau bagaimanapun, terdapat kurang maklumat tentang pencirian genetik baka ataupun variasi genetik kambing. Pada dasarnya, maklumat tentang latar belakang baka dan genetik populasi adalah perlu untuk program pembiakbakaan yang sesuai. Pangkalan data yang mengandungi pencirian dan persamaan terhadap kajian genetik kambing masih lagi sedikit. Pencirian genetik populasi kambing perlu dikaji kerana maklumat genetik ini dianggap sebagai titik permulaan dan penting dalam projek penternakan kambing. Maklumat variasi genetik pada sesuatu spesis merupakan elemen utama untuk pemuliharaan dan mengeksploitasi kepelbagaian genetik bagi tujuan pembiakbakaan. Oleh itu, kajian ini dijalankan untuk menilai variasi genetik baka kambing di Malaysia, iaitu kambing asli Katjang dan baka eksotik Jamnapari, Boer dan Savanna, dengan menggunakan penanda mikrosatelit untuk kegunaan pembiakbakaan, pemilihan dan pemuliharaan yang sewajarnya.

Sampel darah diambil secara rawak daripada Katjang, n=37, Jamnapari, n=34, Boer, n=40 dan Savanna, n=40. Tiga puluh pasangan primer mikrosatelit yang dicadangkan oleh FAO/ISAG dan tujuh lokus mikrosatelit yang dilaporkan daripada kajian lain telah digunakan untuk kajian kepelbagaian genetik pada kambing. Penanda mikrosatelit dioptimasikan menggunakan gabungan DNA pada keadaan PCR yang berbeza diikuti oleh pemeriksaan polimorfik terhadap individu. Lokus mikrosatelit yang polimorfik digunakan untuk kajian kepelbagaian genetik.

Tiga puluh daripada 37 lokus mikrosatelit adalah polimorfik dalam kesemua empat baka kambing, manakala enam lokus adalah monomorfik dan satu lokus gagal diamplikasi untuk baka kambing Boer yang mencadangkan bahawa ia adalah monomorfik untuk alel tidak hadir. Purata bilangan alel yang dicerap berjulat daripada 5.43 kepada 5.90. Manakala nilai heterozigositi yang dicerap (Ho) adalah lebih rendah berbanding heterozigositi yang dijangka pada baka kambing yang dikaji. Baka kambing Jamnapari dan Boer mempunyai Ho yang tinggi (0.43), diikuti dengan Savanna (0.42) dan Katjang menunjukkan Ho yang terendah (0.36).

Ketakseimbangan rangkaian genotip dijumpai antara beberapa lokus tetapi ianya tidak konsisten pada seluruh baka. Keseluruhan purata pekali pembiakbakaan dalam (F_{IS}) adalah 0.43 menunjukkan kewujudan pembiakan dalam pada semua empat baka yang dikaji. Nilai purata F_{IT} dan F_{ST} adalah 0.46 dan 0.06, masing-masing diukur pada tahap perbezaan di dalam dan di antara baka. Nilai F_{ST} menunjukkan kekurangan perbezaan genetik di antara baka kambing. Kesamaan genetik Nei antara empat baka kambing berjulat di antara 80% - 87%. Nilai jarak genetik yang tinggi diperolehi di antara baka kambing Katjang dan Savanna (0.2171) manakala baka kambing Boer dan Savanna dijumpai mempunyai kesamaan berdasarkan nilai jarak genetik iaitu 0.1325.

Berdasarkan kajian ini ia dapat disimpulkan bahawa terdapat variasi genetik dalam empat baka kambing di Malaysia, walaupun Katjang mempunyai kepelbagaian genetik yang lebih rendah sedikit. Walaubagaimanapun, saringan lanjutan terhadap baka kambing dengan menggunakan lebih banyak baka dan bilangan haiwan yang lebih banyak diperlukan untuk menentukan dengan lebih tepat variabiliti baka kambing di Malaysia. Penanda mikrosatelit menggunakan teknik kapilari dan sistem penanda genetik yang lebih sensitif seperti SNP juga perlu dipertimbangkan. Disamping itu, pertimbangan harus diberikan kepada pemetaan genom, menggunakan hasilan tinggi yang terkini terhadap platform genotip untuk mendapatkan penyelesaian genomik dan aplikasi yang terbaik.

ACKNOWLEDGEMENTS

In the name of Allah, the most gracious, the most merciful. Alhamdulillah, I thank Allah the Almighty for giving me the health and patience to complete this project and thesis.

I would like to express my sincere and deepest appreciation to my supervisor Prof. Dr. Tan Soon Guan for his guidance, encouragement, patience and constructive suggestions throughout the period of the study. I would like to thank my co-supervisors, Prof. Dr. Jothi Malar Panandam and Dr. Johari Jiken Abdullah for all their support and discussions. I am also thankful to Dr. Engku Azahan for his help and indispensable advices.

My sincere thanks and appreciation to my friends and colleagues, Adibah, Azlina Azma, Wan Somarny, Roziatul Erin, Dr. Ainu Husna and Aslinda, for their help and support, and for sharing their knowledge. Not forgetting Mohamad Hifzan and Zawawi Ismail, for their help during blood collection.

I am grateful and thankful to my parents, parent in-laws and all family members, for all the love, support and understanding. To my love and caring husband, Ahmad Rizal Muhammad and my daughters, Qistina Auni and Adriana Amni, thank you for making my life so complete.

Special thanks go to the Malaysian Agricultural Research and Development Institute for providing me the fellowship for my Masters of Science programme.

Last but not least, I would like to acknowledge everyone who had help me in one way or another during the course of my study and conducting this project.

I certify that an Examination Committee has met on 21 October 2014 to conduct the final examination of Amie Marini Abu Bakar on her Master of Science thesis entitled "Genetic Characterisations of Four Goat Breeds in Malaysia Assessed Using Microsatellites" in accordance with Universiti Pertanian Malaysia (Higher Degree) Act 1980 and Universiti Pertanian Malaysia (Higher Degree) Regulations 1981. The Committee recommends that the student be awarded the Masters of Science.

Members of the Examination Committee were as follows:

Noorjahan Banu binti Mohamed Alitheen, PhD
Associate Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Chairman)

Patimah binti Ismail, PhD
Professor
Faculty of Medicine and Health Sciences
Universiti Putra Malaysia
(Internal Examinar)

Yuzine b Esa, PhD
Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Internal Examiner)

Badrul Munir Md Zain, PhD
Associate Professor
Faculty Sains dan Teknologi
Universiti Kebangsaan Malaysia
(External Examiner)

_____
ZULKARNAIN ZAINAL, PhD
Professor and Deputy Dean
School of Graduate Studies
Universiti Putra Malaysia

Date: 26 February 2015

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

Tan Soon Guan, PhD
Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Chairman)

Jothi Malar Panandam, PhD
Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Johari Jiken Abdullah, PhD
Lembaga Kemajuan Tanah Persekutuan (FELDA)
(Member)

_____
BUJANG KIM HUAT, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

Declaration by Graduate Student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-Chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials asstated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

Signature: _____ Date: _____

Name and Matric No.: Amie Marini binti Abu Bakar (GS23577)

Declaration by Members of Supervisory Committee

This is to confirm that:

- the research conducted and the writing of this thesis was under our supervision;
- supervision responsibilities as stated in the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) are adhered to.

Signature: _____	Signature: _____
Name of Chairman of Supervisory Committee: _____	Name of Member of Supervisory Committee: _____
Signature: _____	Signature: _____
Name of Member of Supervisory Committee: _____	Name of Member of Supervisory Committee: _____

TABLE OF CONTENTS

		Page
ABSTRACT		i
ABSTRAK		iii
ACKNOWLEDGEMENTS		v
APPROVAL		vi
DECLARATION		viii
LIST OF TABLES		xii
LIST OF FIGURES		xiv
LIST OF APPENDICES		xvi
LIST OF ABBREVIATIONS		xvii
CHAPTER		
1	**INTRODUCTION**	1
	1.1 Problem statement	3
	1.2 Objective	3
	1.3 Research hypothesis	3
2	**LITERATURE REVIEW**	4
	2.1 Goat origin	4
	2.2 Goat categories	4
	2.3 Definition of population, breed, hybrid and species	4
	2.4 Goat breeds in Malaysia	5
	2.4.1 Katjang goat	5
	2.4.2 Jamnapari goat	6
	2.4.3 Boer goat	7
	2.4.4 Savanna goat	8
	2.5 Importance of genetic characterisation and genetic variation	9
	2.6 Potential molecular marker	10
	2.7 Microsatellites	11
	2.8 Polymorphism studies in goats using microsatellite markers	13
3	**MATERIALS AND METHODS**	15
	3.1 The experimental material	15
	3.1.1 Sampling of representative goat breeds	15
	3.1.2 Collection of blood samples	16
	3.2 Preparation of genomic DNA	17
	3.2.1 Genomic DNA isolation	17
	3.2.2 Genomic DNA quantification	17
	3.2.3 Genomic DNA quality	18

3.3 Genotyping using microsatellite markers 18
3.3.1 Microsatellite primers 18
3.3.2 PCR amplification of microsatellite loci 23
3.4 Gel electrophoresis 23
3.5 Screening and scoring of microsatellite loci 24
3.6 Statistical Analysis 24

4 **RESULTS** 29
4.1 Screening and optimisation of microsatellite markers 29
4.2 Allele size range, number and allele frequency 46
4.3 Genetic variation 57
4.4 Level of heterozygosity 57
4.5 Hardy-Weinberg Equilibrium (HWE) 59
4.6 Linkage disequilibrium 59
4.7 Inbreeding 59
4.8 Genetic differentiation 59
4.9 Genetic distance 68
4.10 Genetic structures 69

5 **DISCUSSION** 70
5.1 Screening and optimisation of microsatellite markers 70
5.2 Genetic variation of goat breeds 71
5.3 Level of heterozygosity 72
5.4 Hardy-Weinberg Equilibrium (HWE) and linkage disequilibrium 73
5.5 Inbreeding and breed differentiation 74
5.6 Genetic relationship of goat breeds in Malaysia 75

6 **SUMMARY AND CONCLUSION** 76

REFERENCES/BIBLIOGRAPHY 78
APPENDICES 88
BIODATA OF STUDENT 94
LIST OF PUBLICATIONS 95

LIST OF TABLES

Table		Page
2.1	Categories of microsatellites based on repeat types	11
2.2	Perfect, imperfect, interrupted and compound microsatellite repeats	11
3.1	Goat breeds and sample size of each breed	15
3.2	Microsatellite loci as recommended by FAO used in the genetic for diversity study of the goat breeds	19
3.3	Microsatellite loci from reported studies on goats used in the genetic diversity study of the goat breed	22
3.4	PCR protocol used in the study	23
4.1	Comparison of allele size ranges observed for polymorphic microsatellite loci in four goat breeds	47
4.2	Observed and effective number of alleles for each goat breed	49
4.3	Allele sizes and allele frequencies for polymorphic microsatellite loci recommended by FAO in four goat breeds	50
4.4	Allele sizes and allele frequencies for polymorphic microsatellite loci selected from other studies in four goat breeds	56
4.5	Genetic variation in four goat breeds in Malaysia	57
4.6	Observed (Ho) and expected (He) heterozygosity values obtained for each locus and breed	58
4.7	Exact tests of Hardy-Weinberg Equilibrium for the polymorphic loci in four goat breeds	60
4.8	Linkage disequilibrium in Katjang goat breed	61
4.9	Linkage disequilibrium in Jamnapari goat breed	62
4.10	Linkage disequilibrium in Boer goat breed	63
4.11	Linkage disequilibrium in Savanna goat breed	65
4.12	F_{IS} values for microsatellite loci among goat breeds	66

4.13	F-statistics values averaged over microsatellite loci in all goat breeds	67
4.14	Pairwise genetic distances and identities (Nei 1978) measured based on 30 microsatellite markers in four goat breeds	68

LIST OF FIGURES

Figure		Page
2.1	Katjang goat	6
2.2	Jamnapari goat	7
2.3	Boer goat	8
2.4	Savanna goat	9
3.1	Sampling locations of goat breeds	16
4.1	Example of polymorphic banding patterns observed for locus CSRD247	30
4.2	Example of polymorphic banding patterns observed for locus DRBP1	30
4.3	Example of polymorphic banding patterns observed for locus ETH10	31
4.4	Example of polymorphic banding patterns observed for locus ILSTS005	31
4.5	Example of polymorphic banding patterns observed for locus ILSTS011	32
4.6	Example of polymorphic banding patterns observed for locus ILSTS029	32
4.7	Example of polymorphic banding patterns observed for locus ILSTS087	33
4.8	Example of polymorphic banding patterns observed for locus INRA063	33
4.9	Example of polymorphic banding patterns observed for locus INRABERN172	34
4.10	Example of polymorphic banding patterns observed for locus INRABERN185	34
4.11	Example of polymorphic banding patterns observed for locus MAF065	35
4.12	Example of polymorphic banding patterns observed for locus MAF70	35
4.13	Example of polymorphic banding patterns observed for locus MAF209	36
4.14	Example of polymorphic banding patterns observed for locus McM527	36
4.15	Example of polymorphic banding patterns observed for locus OarAE54	37
4.16	Example of polymorphic banding patterns observed for locus OarFCB20	37

4.17	Example of polymorphic banding patterns observed for locus OarFCB48	38
4.18	Example of polymorphic banding patterns observed for locus P19(DYA)	38
4.19	Example of polymorphic banding patterns observed for locus SPS113	39
4.20	Example of polymorphic banding patterns observed for locus SRCRSP5	39
4.21	Example of polymorphic banding patterns observed for locus SRCRSP7	40
4.22	Example of polymorphic banding patterns observed for locus SRCRSP8	40
4.23	Example of polymorphic banding patterns observed for locus SRCRSP9	41
4.24	Example of polymorphic banding patterns observed for locus SRCRSP15	41
4.25	Example of polymorphic banding patterns observed for locus TCRVB6	42
4.26	Example of polymorphic banding patterns observed for locus TGLA53	42
4.27	Example of polymorphic banding patterns observed for locus BM1225	43
4.28	Example of polymorphic banding patterns observed for locus BM1329	43
4.29	Example of polymorphic banding patterns observed for locus OarHH35	44
4.30	Example of polymorphic banding patterns observed for locus TGLA122	44
4.31	Comparison of banding patterns between PAGE gel (a) and MetaPhor® agarosel gel (b) for the bands produced by primer pair TCRVB6	60
4.32	UPGMA dendogram based on Nei's unbiased distance values (1978) among four goat breeds	68
4.33	Population structure analysis of a sample of 151 individuals from four goat breeds	69

LIST OF APPENDICES

Appendix		Page
B1	Method to prepare Tris-Acetate EDTA (TAE) Buffer 50x in 1 litre water	88
B2	Method to prepare Tris-Borate EDTA (TBE) Buffer 10x in 1 litre water	89
C1	Polymorphism status for the microsatellite loci recommended by FAO among the goat breeds	90
C2	Polymorphism status for microsatellite loci selected from other studies among goat breeds	92
C3	Example of monomorphic banding patterns observed for locus SRCRSP3	93

LIST OF ABBREVIATIONS

AFLP	-	amplified fragment length polymorphism
bp	-	base pair
° C	-	degree celsius
cm	-	centimetre
df	-	degree of freedom
ddH_2O	-	double distilled water
DNA	-	deoxyribonucleic acid
dNTP	-	deoxyribonucleotide triphosphates
DVS	-	Department of Veterinary Services
EDTA	-	ethylenediaminetetraacetic acid
FAO	-	Food and Agriculture Organization
F_{IS}	-	inbreeding coefficient
F_{IT}	-	deficiency or excess of average heterozygotes in a group of population
F_{ST}	-	degree of gene differentiation among populations
g	-	gram
He	-	expected heterozygosity value
Ho	-	observed heterozygosity value
HWE	-	Hardy-Weinberg equilibrium
ISAG	-	International Society for Animal Genetics
kg	-	kilogram
LD	-	linkage disequilibrium
MARDI	-	Malaysian Agricultural Research and Development Institute
mg	-	miligram
$MgCl_2$	-	magnesium chloride
ml	-	millilitre
mM	-	milimolar
mm	-	millimetre
µl	-	microlitre
µg	-	microgram
µM	-	micromolar
MoDAD project	-	The Global Program for the Management of Farm Animal Genetic Resources Project
Ne	-	effective number of alleles
Na	-	observed number of alleles
ng	-	nanogram
nm	-	nanometre
PAGE	-	polyacrylamide gel electrophoresis
PCR	-	polymerase chain reaction
RAPD	-	random amplification of polymorphic DNA
RFLP	-	restriction fragment length polymorphism
s	-	second
SNP	-	single nucleotide polymorphism
SSR	-	simple sequence repeats
STR	-	short tandem repeat
TAE	-	tris-acetate EDTA

TBE	-	tris-borate EDTA
U	-	Unit
UPGMA	-	unweighted pair group method with arithmetic mean
UV	-	ultraviolet
V	-	Volt
VNTR	-	variable number tandem repeat
1X	-	one time concentration
x g	-	relative centrifocal force

CHAPTER 1

INTRODUCTION

The goat population in Malaysia has increased over the years since 2000. In Peninsular Malaysia, the total goat in 1999 was 190,539, then it increased to 373,319 in 2007 and 413,359 in 2011. Meanwhile, the total goat in Malaysia, including East Malaysia (Sabah and Sarawak) was about 458,646 (DVS, 2010, 2011). However, increasing the number of goats are still not be able to supply enough chevon for the Malaysian consumers. The demand for chevon and mutton has steadily increased. The self-sufficiency rate for goat meat and mutton in 2011 was estimated at only 11.28% (DVS, 2011). The chevon and mutton industry in Malaysia needs to be further increased in order to reach the targeted self-sufficiency rate of 35% by 2015. The demand of chevon was met through importation of meat and live animals from Australia and New Zealand which has increased annually.

At present, there are about 4500 farmers and entrepreneurs rearing goats and sheep in Malaysia (Wan Zahari *et al*., 2008). Most of the goats and sheep are raised by small farmers (75%) and the rest pursued by commercial farmers (20%) and integration projects (5%). The Department of Veterinary Services (DVS) has a number of farms, in particular to carry out breeding of goats and sheep. Encouragement from the government to increase the population through the importation of goat and sheep breeds that are highly productive were the main strategies for developing the nation's goat industry. This effort expanded to private sector involvement in commercial breeding.

In commercial farming, high quality breeds must be available at the right time and in sufficient quantities. Therefore, there is great interest in goat farming in Malaysia. Improving the quality of livestock breeds and increasing animal productivity to maximise profit also is an important strategy in the development of the goat industry. The advances in biotechnology have been implemented to improve livestock production through breeding and selection. Reducing importation of live goats and chevon is necessary to improve the goat production in Malaysia. The characterisation of the breeds is important for improving the genetic performance and to decrease inbreeding.

One of the key drawbacks of the goat industry in Malaysia is the lack of proper breeding and selection. Basically, information about the genetic backgrounds of breeds and populations is required for proper breeding. Database on genetic studies on goat characterisation and comparison of breeds is lacking. The goat breeds and populations have to be genetically characterised because is considered as a primary and essential starting point of any goat genetic improvement project. The genetic characterisation of goat breeds in Malaysia as a genetic resource is essential for genetic improvement as well as a conservation strategy.

The goat breeds in Malaysia comprise of small-framed animals made up of the indigenous Katjang goat with the addition of larger framed exotic goats such as Jamnapari and Boer. The Katjang goat has acquired a reasonably high degree of tolerance to the local environment. The Boer, Jamnapari and Savanna which are introduced breeds have become well adapted in Malaysia. Nowadays, pure breed of the indigenous Katjang goat is difficult to find (Department of Veterinary Services, 2006). Most of the Katjang goat was crossbred with introduced breeds, particularly with Jamnapari goat. Currently, these introduced breeds are popular among farmers as high meat producers. They are been imported and bred in Malaysia to fulfill the industry's demand. However, disorganised and uncontrolled crossbreeding activities among farmers have contributed to inbreeding and admixture (Panandam, 2007). At the same time, the indigenous Katjang goats were been neglected and overlooked in breeding effort. Hence, special priority must be given to plan and execute strategic breeding programme, and to conserve the different goat breeds.

Thus, breed characterisation is the first step in developing programmes for sustainable utilisation and conservation. Breed or genetic characterisation can be carried out using molecular techniques. Numerous studies have been initiated to characterise goat breeds using molecular techniques. Microsatellite markers can be used to characterise animal species, breeds as well as for establishing genetic relationships among or within species (Kim *et al*., 2004; Sunnucks *et al*., 2001). Establishment of genetic relationships among the goat breeds will help in genetic improvement and conservation of the goat breeds in Malaysia.

1.1 Problem Statement

There are very limited documentations and published reports on genetic variations of the goat breeds in Malaysia particularly in the indigenous Katjang goats. The Jamnapari goats that have been brought in long ago, to be used for natural and/or artificial selection and local breeding practices are well adapted to the local environmental condition and production system. However, due to improper breeding practice, lack of knowledge in animal breeding principles and poor record keeping contributed to the loss of local breeds. Thus, it is essential to assess the genetic characteristics and variability of the goat breeds in Malaysia which include local and introduced breeds. Conservation of local animal genetic resources is only possible through genetic characterisation, sustainable utilisation and management. Furthermore, introduced breeds such as Boer and Savanna goats well adapted to the hot tropical climate in Malaysia should be evaluated and monitored for proper breeding utilisation.

1.2 Objective

The general objective of this study was to determine the genetic variability of goat breeds in Malaysia using microsatellite markers.
The specific objectives were:

1. To evaluate the genetic polymorphism of goat breeds in Malaysia
2. To establish the genetic distance and relationships between the indigenous Katjang goats and the introduced exotic goat breeds.

1.3 Research Hypothesis

The local Katjang goats originated from Malaysia and Indonesia. However, pure local Katjang goats are difficult to find since most of them have been crossed with introduced breeds. Meanwhile Jamnapari goats which originated from India were brought to and bred in Malaysia a long time ago. Genetically, Katjang and Jamnapari goats should differ in their genetic makeups, but may share similarities as the results would be influenced by their histories. On the other hand, Boer and Savanna goats which originated from South Africa and Australia, respectively, were recently introduced and developed in Malaysia. Therefore, Boer and Savanna goats should differ in their genetic structures. The genetic distance might reveal the Katjang and Jamnapari to be from the same cluster because of admixture with each other. Meanwhile, the Boer and Savanna could be in a similar group because of same origin.

REFERENCES

Abdul Rashid Baba. 2008. Ciri-ciri kambing Boer. In *Penternakan Boer untuk Usahawan,* ed. Wan Zahari Mohamad, Mohd. Najib Mohd. Amin and Azizi Ahmad Azmin, pp 7-11. Kuala Lumpur: Program Penerbitan & Percetakan MARDI.

Adebambo, O., Williams, J.L., Blott, S. and Urquhart, B. 2003. Genetic relationship between Native Sheep breeds in Niferia on microsatellite DNA polymorphism. *Animal Genetic Resources Information* 34: 27-39.

Afroz, M.F., Faruque, M.O., Hussain, S.S., Han, J.L. and Paul, B. 2010. Genetic variation and relations in different goat populations of Bangladesh. *Bangladesh Journal of Animal Science* 39(1&2): 1-8.

Aggarwal, R.A.K., Dixit, S.P., Verma, N.K., Ahlawat, S.P.S., Kumar, Y., Kumar, S., Chander, R. and Singh, K.P. 2007. Population genetics analysis of Mehsana goat based on microsatellite markers. *Current Science* 92: 8:1133–1137.

Amie Marini Abu Bakar, Aslinda Kamal, Mohamad Hifzan Rosali, Muhammad Faisal Abu Bakar Shanmugavelu, S. and Musaddin Kamaruddin. 2011. *Identification of Growth Biomarker in Savanna and Kalahari Goats*. Proceedings of 6th MARDI Science and Technology, Kuala Lumpur, Dec. 5-7, 2011.

Allen, P. J., Amos, W., Pomeroy, P.P. and Twiss, S.D. 1995. Microsatellite variation in grey seals (*Halichoerus grypus*) shows evidence of genetic differentiation between two British breeding colonies. *Journal of Molecular Ecology* 4: 653-662.

Allendorf, F and Luikart, G. 2007. *Conservation and the Genetics of Populations.* Blackwell Publishing.

Aminafshar, M., Amirinia, C. and Torshizi, R.V. 2008. Genetic diversity in buffalo population of Guilan using microsatellite marker. *Animal and Veterinary Advances* 7(11):1499-1502.

Araujo, A.M., Guimaraes, S.E.F., Machado, T.M.M., Lopes, P.S., Pereira, C.S., Da Siva, F.L.R., Rodrigues, M.T., Columbiano, V.D.S. and Da Fonseca, C.G. 2006. Genetic diversity between herds of Alpine and Saanen dairy goats and the naturalized Brazilian Moxoto breed. *Genetics and Molecular Biology* 29: 67-74.

Asif, M., Mehboob-ur-Rahman, J.I. Mirza and Y. Zafar, 2008. High resolution metaphor agarose gel electrophoresis for genotyping with microsatellite markers. *Pakistan Journal of* Agricultural *Sciences* 45(1): 75-79.

Barker, J.S.F. *A Gglobal Protocol for Determining Genetic Distances among Domestic Livestock Breeds*. Proceedings of 5th World Congress Genetic Application of Livestock Production, Guelph, Canada, 1994.

Barker, J.S.F, Tan, S.G., Moore, S.S., Mukherjee, T.K., Matheson, J.-L. and Selvaraj, O.S. 2001. Genetic variation within and relationships among populations of Asian goats (*Capra hircus*). *Animal Breeding and Genetics* 118: 213-233.

Barendse, W., Amitage, S.M., Kosaarek, L.M., Shalom, A., Kirkpatrick, B.W., Ryan, A.M., Clayton, D., Li., L., Neibergs, H.L. and Zhang, N. 1992. A genetic linkage map of the bovine genome. *Nature Genetics* 6(3): 227-235.

Bowcock, A.M., Ruiz Linare, A., Tomfohrde, J., Minch, E., Kidd, J.R. and Cavalli-Sforza, L.L. 1994. High resolution of human evolutionary trees with polymorphic microsatellites. *Nature* 368: 455-457.

Bruford, M.W. and Wayne R.K. 1993. Microsatellites and their application to population genetic studies. *Current Opinion in Genetics & Development* 39: 939-943.

Buchanan, F.C., Adams, L.J., Litlejohn, R.P., Maddox, J.F. and Crawford, A.M. 1994. Determination of evolutionary relationships among sheep breeds using microsatellites. *Genomics* 22: 397-403.

Canon, J., Checa, M.L., C., Carleos, C., Vega-Pla, J.L., Vallejo, M. and Dunner, S. 2000. The genetic structure of Spanish Celtic horse breeds inferred from microsatellite data. *Animal Genetics* 31: 39-48.

Cañón, J., García, D., García-Atance, M.A., Obexer-Ruff, G., Lenstra, J.A., Ajmone-Marsan, P. and Dunner, S. 2006. The ECONOGENE Consortium Geographical partitioning of goat diversity in Europe and the Middle East. *Animal Genetic*s 37: 327–334.

Christiansen, F.B., Frydenberg, O., Gyldenholm, A.O. and Simonsen, V. 1974. Genetics of Zoarces populations VI. Further evidence based on age group samples of a heterozygote deficit in the EST III polymorphism. *Hereditas* 77: 225-236.

Cullis, C.A. 2002. The use of DNA polymorphisms in genetic mapping. *Biotechnology and Genetic Engineering Reviews* 24: 179-189.

Crawford, A.M., Dodds, K.G., Ede, A.J., Pierson, C.A., Montogomery, G.W., Garmonsway, H.G., Beattie, A.E., Davies, K., Maddox, J.F. and Kappes, S.W. 1995. An autosomal genetic linkage map of the sheep genome. *Genetics* 140: 703-724.

Davendra, C. 1975. Biological efficiency of milk production in dairy goats. *World Review of Animal Production* 11(1): 46-53.

Davendra, C. and Camoens, J.K. *Conservation and Utilization of The Indigenous Animal Genetic Resources*. Proceedings of Malaysian Applied Biology, Malaysia, 1979.

Davendra, C. and Nozawa, K. 1976. Goats in South East Asia – their status and production. *Journal of Animal Breeding and Genetics* 93: 101-120.

Di, R., Farhad Vahidi, S.M., Ma, Y.H., He, X.H., Zhao, Q.J., Han, J.L., Guan, W.J., Chu, M.X., Sun, W. and Pu, Y.P. 2010. Microsatellite analysis revealed genetic diversity and population structure among Chinese cashmere goats. *Animal Genetics* DOI: 10.1111/j.1365-2052.2010.02072.x

Dixit, S.P., Verma, N.K., Ahlawat, S.P.S., Aggarwal, R.A.K., Kumar, S., Chander, R. and Singh K.P. 2008. Molecular genetic characterization of Kutchi breed of goat. *Current Science* 95(7): 946-952.

DVS, 2006. Department of Veterinary Services. http://agrolink.moa.my/jph/dvs/statistics/quick/output0708e.pdf. Retrieved 27 February 2009.

DVS, 2010. Perangkaan Ternakan 2009/2010. Kuala Lumpur: Jabatan Perkhidmatan Veterinar, Kementerian Pertanian & Industri Asas Tani, Malaysia.

DVS, 2011. Department of Veterinary Services. http://www.dvs.gov.my/web. Retrieved 31 May 2012.

Ellegren, H. 1992. Polymerase chain reaction (PCR) analysis of microsatellites – a new approach to studies of genetic relationship in birds. *The Auk* 109: 886-895.

Ellegren, H., Moore, S., Robinson, N., Byrne, K., Ward, W. and Sheldon, B.C. 1997. Microsatellite evolution – a reciprocal study of repeat lengths at homologous loci in cattle and sheep. *Molecular Biology and Evolution* 14: 854-860.

Falconer, D.S. and Mackay, T.F.C. 1996. *Introduction to Quantitative Genetic*. Fourth edition Pearson Education Limited.

FAO. 1982. FAO Animal Production and Health Paper: Sheep and Goat Breeds of India, Food and Agriculture Organisation of the United Nations, Rome. http://www.fao.org/dorcep/. Retrieved 1 Dec 2014.

FAO. 2004. Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans; Measurement of Domestic Animal Diversity (MoDAD): New Recommended Microsatellite Markers, Food and Agriculture Organisation of the United Nations, Rome. http://www.fao.org/dad-is/. Retrieved 1 March 2009.

Ferguson, A., Taggart, J.B., Prodohl, P.A., McMell, O., Thompson, C., Stone, C., McGinnity, P. and Hynes, R.A. 1995. The application of molecular markers to the study and conservation of fish populations with special reference to Salmon. *Journal of Fish Biology* 47: 103-126.

Fisher, R.A. 1935. The logic of inductive inference. *Journal of Royal Statistical Society* 98: 39-54.

Glaubitz, J.C. 2004. CONVERT: A user friendly program to reformat diploid genotypic data for commonly used population genetic software packages. *Molecular Ecology Notes* 4: 309-310.

Gottelli, D., Sillero-Zubiri, C., Applebaum, G.D., Roy, M.S., Girman, D.J., Garcia-Moreno, J., Ostranders, E.A. and Wayne, R.K. 1994. Molecular genetics of the most endangered canid: the Ethiopian wolf *Canis simensis*. *Molecular Ecology* 3: 301-312.

Gour, D.S., Ahlawat, S.P.S., Pandey, A.K., Sharma, R., Gupta, N., Gupta, S.C., Bisen, P.S. and Kumar, D. 2006. Analysis of genetic structure of Jamunapari goats by microsatellite markers. *Small Ruminant Research* 66: 140-149.

Gur-Arie, R., Cohen, C.J., Eitan, Y., Shelef, L., Hallerman, E.M. and Kashi, Y. 2000. Simple sequence repeats in *Escherichia coli*: abundance, distribution, composition and polymorphism. *Genome Research* 10: 62-71.

Hedrick, P.W. 1987. Gametic disequilibrium measures: proceed with caution. *Genetics* 117: 331-341.

Jandurova, O.M., Kott, T., Kottova, B. and Czernekova, V. 2004. Seven microsatellite markers useful for determining genetic variability in white and brown short-haired goat breeds. *Small Ruminant Research* 52: 271–274.

Jarne, P. and Lagoda, P.J.L. 1996. Microsatellites, from molecules to populations and back. *Trends in Ecology and Evolution* 11: 424-429.

Karima, F. M., Saleha, Y.M.A., Lamiaa, M.S., Sekena, H.A.El-Aziem and Amr, A.El-Hanafy. 2013. Genetic Diversity in Egyptian and Saudi goat breeds using microsatellite markers. *Journal of Applied Biosciences* 72: 5838-5845.

Kemp, S.J. Hishida, O., Wambugu, J., Rink, A., Longeri, M.L., Ma, R.Z., Da, J., Lewin, H.A., Barendse, W. and Teaale, A.J. 1995. A panel of polymorphic bovine, ovine and caprine microsatellite markers. *Animal Genetics* 26: 299-306.

Kim, K.S., Min, M.S., An, J.H. and Lee, H. 2004. Cross-species amplification of bovidae microsatellites and low diversity of the endangered Korean goral. *Heredity* 95(6): 521-525.

Kumar, S., Dixit, S.P., Sharmaa, R., Pandeya, A.K., Sirohia, G., Patelb, A.K., Aggarwala, R.A.K., Vermaa, N.K., Goura, D.S. and Ahlawata, S.P.S. 2005. Population structure, genetic variation and management of Marwari goats. *Small Ruminant Research* 59(1): 41-48.

Kumar, S., Dixit, S.P., Verma, N.K., Singh, D.K., Pande, A., Chander, R. and Singh, L.B. 2009. Genetic diversity analysis of the Gohilwari breed of Indian goat (*Capra hircus*) using microsatellite markers. *Journal of Animal Veterinary Science* 4(3): 49-57.

Hassen, H., Lababidi, S., Rischkowsky, B., Baum, M. and Tibbo, M. 2012. Molecular characterization of Ethiopan indigenous goat populations. *Tropical Animal Health Production* 44: 1239-1246.

Lewis, P.O. and Zaykin, D. 2002. Genetic data analysis: Computer Program for the Analysis of Allelic Data, Version 1.1 (d16c). Retrieved 20 May 2010 from http://lewis.eeb.uconn.edu/lewishome/software.html/.

Li, J.Y., Chen1, H., Lan, X.Y., Kong. X.J. and Min, L.J. 2008. Genetic diversity of five chinese goat breeds assessed by microsatellite markers. *Czech Journal of Animal Science* 53(8): 315-319.

Li, M.H., Zhao, S.H., Bian, C., Wang, H.S., Wei, H., Liu, B., Yu, M., Fan, B., Chen, L., Zhu, M., Li, S., Xiong, T. and Li, K. 2002. Genetic relationships among twelve Chinese indigenous goat populations based on microsatellite analysis. *Genetics Selection Evolution* 34: 729-744.

Litt, M. and Luty, J.A. 1989. A hypervariable microsatellite revealed by in vitro amplification of a dinucleotide repeat within the cardiac muscle actin gene. *American Journal of* Human *Genetics* 44: 397-401.

Lumsden, J.M., Lord, E.A. and Montogomery, G.W. 1995. Characterization and linkage mapping of ten sheep microsatellite markers derived from a sheep x hamster cell hybrid. *Animal Genetics* 27: 203-206.

Mac Hugh, D.E., Loftus, R.T., Cunningham, P. and Bradley, D.G. 1997. Microsatellite DNA variation and the evolution, domestication and phylogeography of Taurine Zebu cattle (*Bos taurus and Bos indicus*). *Genetics* 146: 1071-1086.

Mainguy, J., Llewellyn, A.S., Worley, K., Cote, S.D. and Coltman, D.W. 2005. Characterization of 29 polymorphic artiodactyl microsatellite markers for the mountain goat (*Oreamnos americanus*). *Molecular Ecology* 5: 809-811.

Maletsanake, D., Nsoso, S.J. and Kgwatalala, P.M. 2013. Genetic variation from 12 microsatellite markers in an indigenous Tswana goat flock in South-eastern Bostwana. *Livestock Research for rural Development* 25(2): article 21

Mariante, A.S., Albuquerque, M.S.M., Egoito, A.A., McManus, C., Lopes, M.A. and Paiva, S.R. 2009. Present status of the conservation of livestock genetic resources in Brazil. *Livestock Sciences* 120: 204-212.

Martinez A.M., Carrera, M.P., Acosta, J.M., Rodriguez-Gallardo, P.P., Cabello, A., Camao, E. and Delgado, J.V. 2004. Genetic characterization of th Blanca Andaluza goat based on microsatellite markers. *Animal Science* 34: 17-19.

Meffe, G.K. and Carroll, C.R. 1994. Principles of conservation biology, 2nd ed, pp. Sunderland, Mass.: Sinauer Associates, 1994.

Missohou, A., Pout, M.R., Nenonene, A., Dayo, G.-K.., Ayssiwede, S.B., Talaki, E., Issa, Y. and Fané, A. 2011. Genetic diversity and differentiation in nine West African local goat breeds assessed via microsatellite polymorphism. *Small Ruminant Research* 99: 20-24.

Mohamad Hifzan, R. and Musaddin, K. 2013. Savanna: Kambing eksotik untuk penternakan komersial [bm]. In Agromedia, bil. 40 pp. 18-19. Kuala Lumpur: Pusat Perkhidmatan Teknikal, MARDI.

Moore, S.S., Sargeant, L.L., King, T.J., Mattick, J.S., Georges, M. and Hetzel, D.J.S. 1991. The conservation of dinucleotide microsatellites among mammalian genomes allows the use of heterologous PCR primer pairs in closely related species. *Genomics* 10: 654-660.

Morgante, M., Hanafer, M. and Powell, W. 2002. Microsatellites are preferentially associated with nonrepetitive DNA in plant genomes. *Nature Genetics* 30: 194-200.

Muema, E.K, Wakhungu, J.W., Hanotte, O. and Han, J. 2009. Genetic diversity and relationship of indigenous goat of Sub-Saharan Africa using microsatellite DNA markers. *Livestock Research for Rural Development* 21(2): article 28.

Mujibi, N.F. 2005. *Genetic Characterization of West Dwarf (WAD) Goats using Microsatellite Markers*. MSc thesis, Kenyatta University, Nairobi, Kenya.

Musaddin Kamaruddin, Abd. Rashid Baba and Azizan Abd. Rashid. 2007. Manual Teknologi Pengeluaran Kambing Pedaging di Malaysia [bm]. Kuala Lumpur: Program Penerbitan & Percetakan MARDI.

Nei, M. 1972. Genetic distance between populations. *The American Naturalist* 106(949): 283-292.

Nei, M. 1973. The theory and genetic distance. In Morton NE (ed.). In *Genetic Structure of Populations*. University Press of Hawaii, Honolulu, U.S.A.

Nei, M. 1978. Estimatation of heterozygosity and genetic distance from a small number of individuals. *Genetics* 89: 583-590.

Nei, M. 1987. *Molecular Evolutionary Genetics*. Columbia University Press, New York.

Nei, M. and Roychoudhury, A.K. 1974. Sampling variances of heterozygosity and genetic distance. *Genetics* 76: 379-390.

Nomura, K., Ishii, K., Dadi, H., Takahashi, Y., Minezawa, M., Cho, C.Y., Sutopo, M., Faruque, O., Nyamsamba, D. and Amano, T. 2012. Microsatellite DNA markers indicate three genetic lineages in East Asian indigenous goat populations. Animal Genetics DOI: 10.1111/j.1365-2052.2012.02334.x

Nsoso, S.J., Machete, J.B., Molatole, M., Ndebele, R.T., Lebani, N.N., Chabo, R.G., Kalake, A.M., Jacyna, L., Segadimo, B.W. and Mine, O.M. 2001. The impact of traditional management on a seasonal internal parasite burdens and productivity of indigenous Tswana goats in southern Bostwana. *Veterinary Research* 68: 101-104.

Nsengimana, J., and J.H. Barrett, 2008. Power, validity, bias and robustness of family-based association analysis methods in the presence of linkage for late onset diseases. *Annals of Human Genetics* 72(6): 793-800.

Nyoman Sulabda, I., Ni Nyoman, W.S., Ni Luh, G.S.H. and Ketut Puja, I. 2012. Genetic diversity of Gambrong goat based on DNA microsatellite markers. *Global Veterinaria* 9(1): 113-116.

Okumus, I., and Çiftci, Y. 2003. Fish population genetics and molecular markers: II-molecular markers and their applications in fisheries and aquaculture. *Turkish Journal of Fisheries and Aquatic Sciences* 3: 51-79.

O'Reilly, P. and Wright, J.M. 1995. The evolving technology of DNA fingerprinting and its application to fisheries and aquaculture. *Journal of Fish Biology* 47: 29-55.

Ochsenreither, S., Kuhls, K., Schaar, M., Presber, W. and Schonian, G. 2006. Multilocus microsatellite typing as a new tool for discrimination of *Leishmania infantum* MON-1 Strains. *Journal of Clinical Microbiology* 44: 495–503.

Panandam, J.M. 2007. *Animal Breeding – Where Are We*. Proceedings of the 7th National Congress on Genetics, Kota Bharu, 5-7 May 2007.

Panandam, J.M. 2012. *Genetic Characterisation of Animal Genetic Resources for Sustainable Utilisation and Development*. Universiti Putra Malaysia Press, Serdang, Selangor.

Patricy, A.S., Santos, S.C., Rondina, D. and Weller, M. 2010. Genetic variability of six indigenous goat breeds using major histocompatibility complex-associated microsatellite markers. *Veterinary Science* 12(2): 127-132

Peter C., Bruford, M., Perez, T., Dalamitra, S., Hewit, G. and Erhardt, G. 2007. Genetic diversity and subdivision of 57 European and Middle-Eastern sheep breeds. *Animal Genet*ics 38: 37-44.

Pieters, A. 2007. *Genetic Characteization of Commercial Goat Populations in South Africa*, MSc thesis, University of Pretoria, Pretoria.

Pieters, A., Marle-Köster, E.V., Visser, C. and Kotze, A. 2009. South African developed meat type goats: A forgotten animal genetic resource? *Animal Genetic Resources Information* 44: 33-43.

Pritchard, J.K., Stephens, M. and Donnelly, P. 2000. STRUCTURE: Inference of population structure using multilocus genotype data. *Genetics* 155: 945-959.

Ramamoorthi, J., Thilagam, K., Sivaselvam, S.N. and Karthickeyan, S.M.K. 2009. Genetic characterization of Barbari goats using microsatellite markers. *Veterinar Science* 10(1): 73-76.

Ramljack, J., Mioc, B., Urkovic, M., Pavic, V., Ivankovic, A. and Medugorac, I. 2011. Genetic diversity measures of the Croatian spotted goat. *Acta Veterinaria* 61: 373-382.

Ramsay, K.A. and Donkin, E.F. *A Review of The Current Status of Goat Research and Development in South Africa,* Proceedings of the Regional Workshop on Goat Development in Southern Africa, Mangochi, Malawi, 31 July- 4 August 2000. University of Malawi.

Ramsey, K., Harris, L. and Kotze, A. 2000. Landrace breeds: South Africa's indigenous and locally developed farm animals. Eds. Ramsey, K., Harris, L. and Kotze, A., Farm Animal Conservation Trust, Petoria.

Riyadh, S.A., Muneeb, M.M, Mohamed, A. A.-S., Osama, M. B. and Mansour F. H., 2012. Genetic diversity of Ardi goat based on microsatellite analysis. *African Journal of Biotechnology* 11(11):16539-16545.

Rout, P.K., Thangraj, K., Mandal, A. and Roy, R. 2012. Genetic Variation and population structure in Jamunapari goats using microsatellites, mitochondrial and milk protein genes. *The Scientific World Journal* DOI: 10.1100/2012/618909.

Rout, P.K., Joshi, M.B., Mandal, A., Laloe, D., Singh, L. and Thangaraj, K. 2008. Mirosatellite-based phylogeny of Indian domestic goats. *Biomedical Central Genetic* 9(11): 1-11.

Sadeghi, R., Mahmoudi, B., Babyev, M.S., Ramsehknia, Y. and Daliri, M. 2009. Genetic analysis in Tali goats based on 13 microsatellite markers. *Biological Sciences* 4(6): 734-737.

Saitbekova, N., Gaillard, C., Obexer-Ruff, G. and Dolf, G. 1999. Genetic diversity in Swiss goat breeds based on micosatellite analysis. *Animal Genetics* 30: 36-41.

Schlötterer, C. and Harr, B. 2001. *Encyclopedia of Life Sciences: Microsatellite Instability*. Vienna: Nature Publishing Group.

Sechi, T., Usai, M.G., Miari, S., Mura, L., Casu, S. and Carta, A. 2007. Identifying native animals in crossbred populations: the case of the Sardinian goat population. *Animal Genetics* 38: 614-620.

Semagn, K., Bjørnstad, Å. and Ndjiondjop, M.N. 2006. An overview of molecular marker methods for plants. *African Journal of Biotechnology* 5(25): 2540-2568.

Serrano, M., Calvo, J.H., Matiniez, M., Marcos-Carcavilla, A., Cuevas, J., Gonzalez, C., Jurado, J.J. and Tejada, P.D. 2009. Microsatellite based genetic diversity and population structure of the endangered Spanish Guadarrama goat breed. *Genetics* DOI:10.1186/1471-2156-10-61

Steffen, P., Eggen, A., Stranzinger, G., Fries, R., Dietz, A.B. and Womack, J.E. 1993. Isolation and mapping of polymorphic microsatellites in cattle. *Animal Genetics* 24(2) 121-124.

Sunnucks, P. 2001. Efficient genetic markers for population biology. *Tree* 15: 199-203.

Takahashi, H., Nyamsamba,D., Mandakh, B., Zagdsuren,Yo., Amanno, T., Nomura, K., Yokohama, m., Ito, S. and Minezawa, M. 2008. Genetic structure of Mongolian goat populations using microsatellite loci analysis. *Asian-Australian Journal of Animal Sciences* 21(7): 947-953.

Tautz, D. 1989. Hypervariabflity of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Research* 17(16)**:** 6463-6471.

Tesfaye, A.T., Fidalis, M.N., Hoeven, E., Yadav, B.R., Hanotte, O. and Hanlin, H. *Genetic characterization of indigenous goat populations of Ethiopia using microsatellite DNA markers*. Proceedings of 29th International Conference of Animal Genetics, ISAG, Tokyo, Japan, 11-16 September 2004,

Thilagam, K., Ramammorthi, J., Sivaselvam, S.N. and Karthickeyan, S.M.K. 2006. Kanniadu goats of Tamildanu, India: genetic characterisation through microsatellite markers. *Livestock Research for Rural Development* 18(10): 149-150.

Tóth, G., Gáspári, Z. and Jurka, J. 2000. Microsatellites in different eukaryotic genomes: survey and analysis. *Genome Research* 107(7): 967-981.

Traoré, A., Álvarez, I., Tamboura, H.H., Fernández, I., Kaboré, A., Royo, L.J., Gutiérrez, J.P., Sangaré, M., Ouédraogo-Sanou, G., Taguyeni, A., Swadogo, L. and Goyache, F. 2009. Genetic characterisation of Burkino Faso goats using microsatellite polymorphism. *Livestock Science* 123(2): 322-328.

Verma, N.K., Dixit, S.P., Aggarwal, R.A.K., Chander, R., Kumar, S. and Ahlawat, S.P.S. 2007. Genetic analysis of the Sirohi breed of Indian goat (*Capra hircus*). *Korean Journal of Genetics* 29: 129-136.

Vicente, M.C., Guzman, F.A., Engels, J. and Ramantha Rao, V. 2005. *Genetic characterization and its use in decision making for the conservation of crop germplasm. The Role of Biotecnology*. Paper presented at the meeting of The Role Biotechnology, Italy, March 2005.

Visser, C., Hefer, C.A., Marle-Koster, E.V. and Kotze, A. 2004. Genetic variation of three commercial and three indigenous goat populations in South Africa. *South African Journal of Animal Science* 34 (Supplement 1): 24-27.

Wan Zahari, M. 2008. Industri penternakan ruminan di Malaysia masa kini [bm]. In *Penternakan Boer untuk usahawan*, ed. Wan Zahari Mohamad, Mohd. Najib Mohd. Amin and Azizi Ahmad Azmin, pp. 1-5. Kuala Lumpur: Program Penerbitan & Percetakan MARDI.

Weber, J.L. and May, P.E. 1989. Abundant class of human DNA polymorphisms which can be typed using the polymerase chain reaction. *The American Journal of* Human *Genetics* 44: 388-396.

Wilson, D.E. and DeeAnn, M.R. 2005. Mammal Species of the World: A Taxonomic and Geographic Reference, 3rd ed., pp 2142. Johns Hopkins University Press.

Weir, B.S. 1996. Intraspecific differentiation. In *Molecular Systematics*, 2nd ed. D.M., Hillis, C., Moritz, and B.K., Mable, pp. 385-406. Massachusetts: Sinauer Associates.

Wikipedia, the Free Encyclopedia 2009, http://en.wikipedia.org/wiki/Jamnapari goat. Retrieved 11 February 2009

Yeh, F.C., Boyle, T. and Yang, R. 1999. *POPGENE version 1.31*. Microsoft window-based Freeware for population genetic analysis (http://www. ualberta.ca/ ~fyeh/popgene_download.html).