

Genetic diversity and estimation of genetic
parameters for economically important
traits in Zambian cattle

by

Ellison Musimuko
(*BAgricSc, DipAgricSc*)

A Thesis Submitted for the Degree of Master of Philosophy at the
University of Adelaide, School of Animal and Veterinary Sciences

February 2014

Contents

Abbreviation	ix
Dedication.....	xi
Abstract.....	xii
Declaration.....	xiv
Acknowledgements.....	xv
Chapter 1.....	- 1 -
1.0 General introduction and Literature Review	- 1 -
1.1 Human population growth and livestock demand trends.....	- 1 -
1.2 Land as a major factor of cattle production system	- 6 -
1.3 Economic and non-economic value of cattle.....	- 7 -
1.3.1 Value of cattle traction as a trait	- 8 -
1.3.2 Value in supplying plant nutrients in agriculture systems	- 9 -
1.3.3 Value in investments, savings and supply of high quality dietary foods	- 9 -
1.3.4 Non-economic value of cattle in traditional cultures	- 10 -
1.4 Cattle distribution and production systems in Zambia	- 11 -
1.4.1 Cattle distribution.....	- 11 -
1.4.2 Cattle production systems in Zambia.....	- 12 -
1.5. Cattle breeds in Zambia	- 13 -
1.5.1 Angoni.....	- 14 -

1.5.2 Barotse.....	- 16 -
1.5.3 Tonga.....	- 16 -
1.5.4 Boran.....	- 17 -
1.5.5 Brahman	- 18 -
1.6 Origin and spread of cattle in Africa	- 18 -
1.6.1 Historical cattle disasters in Africa	- 20 -
1.6.2 Description of Zebu Cattle	- 21 -
1.7 Designing breeding objectives for Zambian cattle farmers	- 23 -
1.8 Use of Molecular Markers in Genomic Studies.....	- 26 -
1.8.1 Allozymes and Restriction Fragment Length Polymorphisms	- 26 -
1.8.2 Single-Nucleotide Polymorphisms.....	- 27 -
1.8.3 Microsatellite Markers	- 28 -
1.8.4 Application of Microsatellites in Genomic Studies in Africa.....	- 30 -
1.8.5 Major Causes of Gene Erosion in Cattle.....	- 32 -
1.9 Estimation of genetic parameters for production traits.....	- 34 -
1.10 Research Project Aims and Objectives	- 36 -
Chapter 2.....	- 39 -
2.0 Understanding Diverse Preferences for Cattle Attributes.	- 39 -
2.1 Introduction.....	- 39 -
2.2 Materials and Methods.....	- 41 -

2.2.1 Study Areas	- 41 -
2.2.2 Collection of Data	- 42 -
2.2.3 Interview Transcription and Data Coding.....	- 45 -
2.3 Data Analysis.....	- 47 -
2.4 Results and Discussion	- 47 -
2.4.1 Capturing information.....	- 47 -
2.4.2 General Management of Cattle	- 48 -
2.4.3 Breeding Practices.....	- 53 -
2.4.4 Disease and Parasite Management	- 56 -
2.4.5 Value of Indigenous Cattle in Zambia	- 58 -
2.4.6 Preference of Cattle Traits	- 60 -
2.4.7 Overall Preferred Traits.....	- 62 -
2.5 Conclusion	- 69 -
Chapter 3.....	- 70 -
3.0 Measuring Genetic Diversity: Population Differentiation and Structure	- 70 -
3.1 Introduction.....	- 70 -
3.1.2 Genetic Diversity	- 72 -
3.1.3 Population Differentiation.....	- 73 -
3.2 Materials and Methodology	- 75 -
3.2.1 Blood Sample Collection	- 75 -

3.2.2 DNA Extraction and Genotyping.....	- 76 -
3.2.3 DNA Microsatellite Markers.....	- 76 -
3.3 Data analyses	- 77 -
3.3.1 Genetic diversity analysis	- 77 -
3.3.2 Population differentiation.....	- 77 -
3.3.3 Population relatedness and structure.....	- 78 -
3.4 Results.....	- 79 -
3.4.1 Genetic diversity analysis	- 79 -
3.4.2 Genetic diversity within populations	84
Table 3.1: F- Statistics and Shannon migration estimates for three Zambian indigenous cattle breeds.	86
3.4.3 Population structure	88
3.5 Discussion.....	96
3.5.1 Genetic diversity	96
3.5.2 Genetic differentiation	99
3.6 Conclusion.....	103
Chapter 4.0.....	104
4.0 Measuring genetic parameters for growth traits	104
4.1 Introduction.....	104
4.2 Materials and Methods.....	108

4.2.1 Study site.....	108
4.2.2 Cattle management.....	109
4.2.3 Data collection and analysis.....	111
4.3 Results.....	116
4.3.1 Distribution of births.....	116
4.3.2 Weaning Weight.....	116
4.3.4 Estimates of covariance components and genetic parameters	119
4.4 Discussion.....	122
4.4.1 Genetic parameters for weaning weight in zebu cattle	122
4.4.2 Non genetic parameters.....	124
4.5 Conclusion	126
Chapter 5.....	127
5.0 Summary.....	127
References.....	134
Appendix 2.1: Adapted and modified SADC Questionnaire.....	157
Appendix 2.3: In-depth interview Questionnaire	166
Appendix 2.2: Participant Information Sheet	168
Appendix 3.2: Microsatellites for Bovine Breed Identification	171
Appendix 4.1 Herd Book Society of Zambia Standard Code for cattle registration since 1966	174
Appendix 4.2: The average and standard errors of weaning weight (Kg).....	175

Tables

Table 2. 1: Number of questionnaires distributed in the study sites	44 -
Table 2. 2: Chi-square values for difference in preference for cattle traits.....	63 -
Table 2. 3: Raw correlations between cattle preference traits.....	63 -
Table 2. 4: Parametric tests and least squares means for cattle preference traits	64 -
Table 3. 1: Frequency.....	83
Table 3. 2: F- Statistics and Shannon migration estimates for three Zambian indigenous cattle breeds.....	86
Table 3. 3: Shannon analysis of breeds pairwise for all loci.	87
Table 3. 4: Shannon statistical analysis of molecular variance in Zambian indigenous cattle breeds using co-dominant microsatellite genotype data.....	88
Table 3.5: Pairwise estimates of genetic distance and identity.	89
Table 4.1: Genetic parameter estimates for beef cattle weaning weights in cattle.....	106
Table 4.2: Herd structure of data for Zambian zebu cattle (<i>Bos indicus</i>) from Lilaya Farm	112
Table 4.3: Description of models fitted.....	115
Table 4.4: Statistical analysis of variance for zebu cattle from Liyayi farm.....	117
Table 4.5: Estimated genetic parameters for weaning weight in zebu cattle (<i>Bos indicus</i>).	121

Figures

Figure 1 1: World projected data of milk and meat consumption.....	- 2 -
Figure 1 2: Trends of import and exports of beef in Zambia	- 6 -
Figure 1 3: Use of cattle as source of traction	- 8 -

Figure 1 4: Cattle density and distribution in Zambia.....	- 11 -
Figure 1 5: Distribution of Angoni cattle in central Africa	- 14 -
Figure 1 6: Zambian main cattle breeds (<i>Bos taurus indicus</i>).....	- 15 -
Figure 1 7: Original and migration routes of cattle in Africa.....	- 21 -
Figure 1 8: Status of world mammalian breeds.....	- 32 -
Figure 2.1 Map of study sites in Zambia where small-scale farmers were interviewed conducted.....	- 42 -
Figure 2.2: Some participants in the study from Namwala and Chipata. 2.2a= large farmer (P01/04) in Namwala district of Zambia and 2.2b= A group of emerging and medium cattle farmers in Chipata.	- 46 -
Figure 2.3: Female medium cattle (P02/02) farmer feeding her cattle.....	- 53 -
Figure 2.4: Emerging farmer spraying a bull to control ticks	- 57 -
Figure 2.5: Sign of Zambeef Plc (Private Limited Company)	- 66 -
Figure 2.6: Cattle dipping facility in Chipata donated by World vision Zambia	- 67 -
Figure 4.1: Location of Liyayi Farm	109
Figure 4.2: A herd of bulls from Lilayi Farm in Zambia.	110
Figure 4.3: Distribution of birth records from 1995 to 2009 on the Lilayi farm in Zambia.	116
Figure 4.4: Annual variation in weaning weight for Angoni and Boran calves born 1995 to 2009	118

Abbreviations

AFLP	Amplified Fragment Length Polymorphism
AI	Artificial Insemination
AMOVA	Analysis of Molecular Variance
AnGR	Animal Genetic Resources for Food and Agriculture
BLUP	Best Linear Unbiased Prediction
bp	base pair
CBPP	Contagious Bovine Pleuro pneumonia
CGIAR	Consultative Group on International Agricultural Research
DAD-IS	Domestic Animal Diversity Information System
DAGRIS	Domestic Animal Genetic Resources Information System
DNA	Deoxyribonucleic Acid
DS	Nei's Standard Genetic Distance
EAAP	European Association for Animal Production (http://www.eaap.org)
EBV	Estimated Breeding Value
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization of the United Nations Statistical
FMD	Foot-and-Mouth Disease
Ho	Observed Homozygosity
IAEA	International Atomic Energy Agency
IICA	Inter-American Institute for Cooperation on Agriculture
ILRI	International Livestock Research Institute (http://www.ilri.org)
ISAG	International Society of Animal Genetics (http://www.isag.org.uk)
LD	Linkage Disequilibrium
LU	Livestock Units
MACO	Ministry of Agriculture and Cooperative
mtDNA	Mitochondrial Deoxyribonucleic Acid

Ne	Effective Population Size
NIAH	National Institute of Animal Husbandry
PCR	Polymerase Chain Reaction
REML	Restricted Maximum Likelihood
RFLP	Restriction Fragment Length Polymorphism
SADC	Southern African Development Community
SNP	Single Nucleotide Polymorphism

Dedication

This thesis work is dedicated to my family and friends. A special feeling of appreciation goes to my loving wife, Rosemary Mhango Msimuko, for her tireless encouragement and pushy towards my successfully completion of this process. My children Phaskani, Fiskani and Luskani Taonga who continued performing well at school and you are exceptional. My warm and tender gratitude goes to my mother for her spiritual support throughout my entire program.

Further dedication goes to my special friends who have supported me throughout the process, especially Wido Nugroho for helping with technology skills in GIS. Finally the team in the picture below, I say, you are special.



The University of Adelaide Intercollegiate Meat Judging Team 2013: At far back are Nick van den Berg and Logan Dennis; (middle row) David Wooley, Kat Vallance, Julia Huser, Bonnie Chapman, Tracey Fischer (coach) and Reece Mason; (front) Megan Jaeschke, Emily Buddle, Cathy Dodd (coach), Ellison Musimuko and Sam Walkom (head coach).

Source: Sam Walkom

Abstract

Current genetic erosion of indigenous breeds is common. Globally, this has become a major concern. In Zambia, genetic improvement programs rely upon traditional selection and breed substitution, and do not utilise local animal genetic resources. The aim of this work was to provide information for genetic improvement strategies, including the preferred traits of cattle breeders, estimating genetic diversity and genetic parameters, to improve and conserve local well-adapted indigenous cattle.

This study used quantitative survey data, collected between September 2012 and December 2012. Both parametric and non-parametric tests were conducted to test if there were significant differences in preferences for traits between three regions of Zambia, namely Namwala, Chipata and Lundazi. The tests revealed that there were no significance differences for the traits preferred between the regions. However, large-scale farmers preferred larger sized animals and emerging small-scale cattle farmers preferred fertility traits.

Genetic data from 274 alleles generated using 32 microsatellite markers from 72 individuals representing three indigenous Zambian cattle breeds (Angoni, Tonga and Barotse) was used to assess genetic diversity and population structure. Although, Zambian indigenous cattle breeds did not exhibit a high and unique breed's purity, cattle exhibited a higher level of genetic diversity within breeds than between breeds. Despite the evidence of a close gene flow between the three populations, inbreeding was largely insignificant going by the Bayesian cluster at $K=2$. It may be further evidence of existing divergent and multi-loci genetic admixtures between and within breeds. If accurate, the uniqueness of the population

clustering offers valuable information on the gene pool available for selection within breeds for utilisation, genetic improvement and conservation. However, Tonga and Barotse breeds appeared to exhibit lower genetic diversity than Angoni.

To measure the genetic parameters for growth, data for 266 Angoni and 606 Boran weaning weights for 15 years were used in linear mixed models to estimate variances and heritabilities. The change in the log-likelihood was used to test for improvements when comparing models. Fixed effects of sex, breed, and age were determined on weaning weight. Random effects included breed by animal and breed by dam. Separate breed variances were not significant and so the overall direct heritability and maternal heritability was moderate (20% and 19%, respectively) using the best model (6). Thus, these heritability estimates of direct and maternal effects on weaning weight indicate it should be possible to make good genetic progress for this trait.

Zambian indigenous cattle provide rich genetic resources, exhibiting moderately heritability, and therefore, have the potential to be improved by using appropriate planning and flexible breeding programs. This is important because the current trends show a substantial increase in demand for meat worldwide and if farmers in Zambia wish to develop an export market, beef production must be improved. However, Zambia will require separate breeding objectives and genetic parameter estimates for large-scale farmers and emerging small-scale farmers in order to exploit the wide range of diversity through genetic selection. This could be through focusing on different breed for each group.

Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

I give consent to this copy of my thesis, when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library Search and through web search engines, unless permission has been granted by the University of Adelaide to restrict access for period.

Ellison Musimuko

February 2014

Acknowledgements

This task was huge and required a team effort. Therefore, I am indebted to numerous people and organisations that contributed significant time and resources to enable me complete this research.

I would like to acknowledge and thank the providers of the Scholarship, Australia Awards Scholarships for Africa (AusAID), for the considerable financial support I received to undertake this study and the government of Zambia for granting me paid study leave.

In recognition of my principal supervisor Associate Professor Wayne Pitchford, thank you very for your guidance that is exceptional and ever valuable in imparting research knowledge and skills. Your dedication to work has indeed motivated me to take any future challenges without fear or favour. Out of your busy schedule, you always found time for me without that I would not have completed my work as scheduled. You are truly my living example across numerous domains of my life ranging from professional development, teaching to general outlook.

A significant appreciation goes to my co supervisor Associate Professor Cynthia DK Bottema (Animal Genetic Technologies, South Australia), for her swift and tremendous feedback on written and oral work that was provided during the course of my study. In particular many thanks for your assistance in addressing genotyping requirements and providing all necessary laboratory facilities for the DNA extraction. Your input really was tremendous special to me. Thank you ‘Cindy.’

To Dr Dana Thomsen, my social science advisor and editor, thank you for showing the strong commitment to this work for supporting and comments provided to chapter two of this

thesis. Your advice on the outline, structure, methods and results has been particularly valuable. Social science is too bulky and can easily wear someone out, but you quickly helped and your time provided important advice on how to integrate both social and the core science in my project. Above all for being my editor that which you highlighted spelt checks, citations and clarity of ambiguity. Many thanks to you.

Most sincerely, acknowledgement goes to Professor Emily Piper from The University of Queensland (Science Leader, Animal Genetics Laboratory Group) for providing the genotyping services for this work in Chapter 3. At a short notice, you and your group were able to provide the real services required at a reasonable cost. Thank you.

Rugang Tian, I am in awe of the laboratory skills you provided to me. Your patient and nature inspires me. I am grateful.

This project has drawn on numerous data sources and I am very grateful to have had access to such a wide array of data. In particular, thanks to Mr Alan Miller, Boran and Angoni breeder, for kindly allowing me access the animal performance records on his Lilayi farm. In addition, I appreciate the farm manager, Mrs Charity Monga for her guidance on the records formatting. Without her, the data would be meaningless.

To scientists within the Genetic Characterisation of Indigenous Cattle Breeds in Zambia Project, thank you very much for all your help in blood sample collection and other laboratory facilities provided. Special thanks to Mr Bwalya Katati for the entire help given to me while working in his laboratory in Zambia.

I would like to acknowledge the cattle farmers interviewed in this study. The success of this research depended on cattle farmers in Namwala, Chipata and Lundazi who willingly

accepted to be interviewed and respond to the questionnaires. I am indebted to all farmers and each interview was enjoyable.

To the research group, I say thanks for all the comments during my presentations and the research day organisers for awarding me with a second best poster in 2013.

Special thanks to Dr. Stephen Lee, Cathy Dodd and Dr. Sam Walkom for their contributions to data analysis and approach.

Finally, I acknowledge several individuals whom I may not include in the lists including from other universities I had contacted for assistance in data analysis and allowing me to use their bioinformatics tools.