USING GENETIC MARKERS IN COMPARING THE BIODIVERSITY AMONG SOME EGYPTIAN AND EUROPEAN RABBIT BREEDS

By

AHMED MOSTAFA EMAM BADAWY

B.Sc. Agric. Sci. (Animal Production), Fac. Agric., Cairo Univ., Egypt, 2003
M.Sc. Agric. Sci. (Poultry Production), Fac. Agric., Cairo Univ., Egypt, 2010

THESIS

Submitted in Partial Fulfillment of the Requirements for the Degree of

DOCTOR OF PHILOSOPHY

In

Agricultural Sciences

(Poultry Production)

Department of Animal Production
Faculty of Agriculture
Cairo University
EGYPT

2018

SUPERVISION SHEET

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Title of Thesis: Using Genetic Markers in comparing biodiversity among some Egyptian and European rabbit breeds.
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Approval: 11 /1/ 2018

ABSTRACT

This thesis includes three studies to characterize, evaluate and invisitgate originality of local rabbit genetic resources in Egypt by using genetic markers. In the 1st study, 19 microsatellite loci were used to identify the genetic diversity for 3 Egyptian and one Spanish local rabbit breeds. Egyptian breeds were Egyptian Red Baladi (ERB), Egyptian Black Baladi (EBB) and Egyptian Gabali Sinai (EGS), while Spanish rabbits belong to a local domestic variety (Spanish Common rabbit, SCR) used in backyard raising. The previous breeds were compared with European Wild rabbits (EWR). This study indicated that lower genetic diversity exists in ERB, EBB and SCR than EGS and EWR. Results also suggested that ERB and EBB belong to one breed. The phylogenetic analysis confirmed that there is separation between domestic rabbit breeds and wild rabbit or recently domesticated in this study.

The objective of the 2nd study was to identify the genetic diversity of different populations of native Middle-Egypt rabbit (NMER) in North Upper Egypt province by using microsatellite polymorphism. Nineteen microsatellite loci were used in the study and an area of 231 km was surveyed, as native rabbits covered 14 points belonging to four Northern Upper Egypt governorates (South Giza, Fayoum, Beni Suef and Menya). Among NMER populations, Menya population gave the highest diversity. In contrast, South Giza population showed the lowest. Analysis results showed 2 main NMER rabbit groups: the Northern group (South Giza and Fayoum) and the Southern group (Beni Suef and Minya). This study provides an overview of genetic diversity of NMER populations in the Northern Upper Egypt province for to designate priorities for conservation of NMER.

The goal of 3rd study was to invistigate the maternal origin of 132 individuals belonging to rabbit breeds from Egypt and Spain, by using 450 base pairs (bp) of mitochonderial DNA (mtDNA) cytochrome b (cyt b) gene sequencing. A total of 353 mutations, 290 polymorphic sites, 14 haplotypes (A: N), 0.06126 haplotype diversity and 1.900 for Tajima's D were defined in this study ($P<0.05$). Haplotype A mostly occurred in 35.7% of Egyptian rabbits and 16.7% of EWR, while haplotype B occurred in 66.7% of Spanish rabbits and 33.3% of the EGS breed. The number of 46 published sequences for domestic and wild *Oryctolagus cuniculus* were used to investigate the origin and relation among tested rabbit breeds in this study. The most common haplotype (A) was combined with 43.5% of published sequences, while haplotype B was combined with only 4.3%. All haplotypes in this study were located in the same linkage (B) and distributed in 2 clusters. Analysis of mtDNA confirmed the limitation of genetic diversity for ERB, EBB and SCR, and that ERB and EBB belong to one breed. Further, this study proves for the first time that Egyptian breeds and Spanishbreed were originated from European rabbits.

Key Words: Genetic diversity, microsattelites, Egyptian rabbits, Spanish common rabbit, European wild rabbit, mtDNA, Origin, Native Middle-Egypt rabbit.

DEDICATION

I dedicate this work to whom my heart felt thanks; to my parents and sisters for all the support they lovely offered along the period of my postgraduate studies.

ACKNOWLEDGEMENT

Thanks to ALLAH.

The author heartily wishes to express his deepest thanks and gratitude to ***Dr. Nagwa A. Ahmed****, professor of Poultry Physiology, Faculty of Agriculture, Cairo University, for close supervision, encouragement, follow up of the work and great help in writing and preparation of the thesis.*

Deep thanks are due to ***Dr. Gamal Mohamed Kamel,*** *Associate professor of Poultry Physiology, Animal Production Department, Faculty of Agriculture, Cairo University, for his kind supervision, great help in writing and fruitful advice during the study.*

My deepest thanks to ***Dr. Abou Bakr Ahmed Azoz****, Head Research of Animal Husbandry, Rabbit Department, Animal Production Research Institute (APRI), Agricultural Research Center (ARC) for his close supervision and suggesting the design of the research work.*

Sincere thanks and great appreciation to Prof. ***Nuno Ferrand****, dean of CIBIO Research Center in Biodiversity and Genetic Resources, university of Porto, for his providing facilities and valuable help throughout this study. Also, the author wishes*

to thank ***Sandra Afonso****, (Research Technical) and* ***Susana Lopes,*** *(Senior Researcher) at CIBIO, for the in technical support.*

Grateful appreciation is also extended to Prof. Dr. ***Pedro González Redondo****, Associate professor of Animal Production at the University of Seville and Dr.* ***Luis Ródenas****, researcher at the Polytechnic University of Valencia, Spain for their great assistance in collecting rabbits samples in Spain.*

LIST OF ABBREVIATIONS AND INITIALS

GR	Genetic Resources
AnGR	Animal Genetic Resources
FAGR	Farm Animal Genetic Resources
DAD-IS	Global Databank for Farm Animal Genetic Resource
EGS	Egyptian Gabali Sinai
APRI	Animal Production Research Institute
FG	Flemish Giant
GB	Giant Baladi
ERB	Egyptian Red Baladi
EBB	Egyptian Black Baladi
EWB	Egyptian White Baladi
Line M	Line Moshtohor
NG	New Giza
V-line B	V-Line Black
V-line R	V-Line Red
EWR	European Wild Rabbits
CIP	Central of Iberian Peninsula
SWIP	South -West Iberian Peninsula
NEIP	North -East Iberian Peninsula
SCR	Spanish Common Rabbit
NZW	New Zealand White
Blub	Best Linear Unbiased Prediction
DNA	Deoxyribose Nucleic Acid
PCR	Polymorphism Chain Reaction
NCBI	National Center For Biotechnology Information
EMPL	European Molecular Biology Laboratory
LG	Linkage Group
BAC	Bacterial Artificial Chromosome
mtDNA	Mitochondria Dna
Cytb	Cytochrome B
O.C	*Oryctolagus Cuniculus*
bp	Base Pare
TBE	Tris Borate EDTA
CTM	Center of Molecular Analysis
NMER	Native Middle Egyptian Rabbit
NA	Number of Alleles
MNA	Mean Number of Alleles
F_{IS}	Intra Breed Structure
H*o*	Observed Heterozygosity

H*e*	Expected Heterozygosity
FCA	Factorial Correspondence Analysis
NJ	Neighbor Joining Tree
PVT	Privet Alleles
PIC	Polymorphism Information Content
HWE	Hardy- Weinberg Equilibrium
K	Number of Clusters
MCMC	Markov Chain Monte Carlo
F_{ST}	Fixation Index Structure
F_{IT}	Individual Within The Total Population
S	Polymorphism Information Content
h	Haplotype
Hd	Haplotype Diversity
π	Nucleotide Diversity
$\boldsymbol{\eta}$	Total Number of Mutation
TD	Tajima's D
UPGMA	Unweighted Pair Group Method Arithmetic