

**Genetic and phenotypic characterization
of native fowl populations in South Africa**

by

Esté van Marle-Köster

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SUPERVISORY COMMITTEE

**Prof NH Casey : Department of Animal & Wildlife Sciences
University of Pretoria**

**Prof LH Nel : Department of Microbiology & Plant Pathology
University of Pretoria**

**Dr MAM Groenen : Department of Animal Breeding and Genetics
Wageningen Agricultural University
The Netherlands**



For

Heinrich Marle & Emma

“Mortui Vivos Docent”

Voorwoord

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Abstract

Native fowl populations in South Africa were characterized genetically and phenotypically. Four South African native populations, two dual-purpose breeds, and two populations from Mozambique and Botswana were included for genetic analysis. For phenotypic characterization, two commercial lines were also included as a benchmark. Twenty-three microsatellite markers were selected and tested to obtain genetic data for estimation of genetic variability and distance. Growth (weight gain) and egg production were included for phenotypic characterization. A relatively high (53% – 64%) genetic variation was found among the populations, which suggests conservation as a genetic resource for future use. The lowest genetic variation (53%) was found for the Koekoek and Australorp populations, which are the two populations that were subjected to formal selection, while the highest variation was observed in the Naked Neck population (64%). The New Hampshire has often been included in upgrading programs and this is evident from the close relationship with both the Lebowa-Venda and Naked Neck fowls. Phenotypic trials indicated significant differences among the populations included for growth, carcass and egg production traits. The Koekoek and New Hampshire populations had the best performance for egg production and growth (weight gain) in the study. Genetic and phenotypic differences indicate that the populations can be distinguished as different breeds or groups of fowl. The results of this study may contribute to selection for improved performance for household food production, as well as conservation of the populations as a genetic resource.

Samevatting

Inheemse pluimveepopulasies van Suid-Afrika is fenotipies en genotipies gekarakteriseer. Vier Suid-Afrikaanse inheemse populasies, twee dubbeldoel rasse en twee populasies van Mosambiek en Botswana is ingesluit vir genetiese analise. Vir fenotipe karakterisering is ook twee kommersiële lyne as 'n verwysing ingesluit. Drie-en-twintig mikrosatelliet merkers is geselekteer en in die populasies getoets om data vir beraming van genetiese variasie en afstand te verkry. Groei (massatoename) en eierproduksie is vir fenotipe karakterisering ingesluit 'n Relatiewe hoë (53% – 64%) genetiese variasie is tussen populasies aangetref, wat dui op bewaring van die populasies as genetiese bron vir toekomstige benutting. Die laagste genetiese variasie (53%) is gevind vir die Koekoek en Australorp populasies, die enigste twee populasies wat formele seleksie ondergaan het, terwyl die hoogste variasie in die Kaalnek populasie (64%) gevind is. Die New Hampshire is dikwels ingesluit in opgraderingsprogramme en dit word weerspieël in hulle nou verwantskap met beide die Lebowa-Venda- en Kaalnek hoenders. Betekenisvolle verskille in die groei-, karkas- en eierproduksie-eienskappe is gevind tussen die populasies met fenotipe proewe. Die Koekoek en die New Hampshire het die beste prestasie vir eierproduksie en groei (gewigstoename) gehad. Genetiese en fenotipe verskille dui aan dat die populasies as verskillende rasse of pluimveegroepe onderskei kan word. Die resultate kan 'n bydrae maak tot seleksie vir verhoogde produksie vir huishoudelike voedselsekuriteit, asook bewaring van die populasies as bron van genetiese materiaal.

List of Abbreviations

AFLP	amplified fragment length polymorphism
AU	Australorp
bp	basepairs
BS	Botswana
cDNA	complementary DNA
CRI	chicken repeat element
CSB	clone/sequence based markers
DAD-IS	Domestic Animal Diversity Information System
DFP	DNA fingerprint
D_m	Nei minimum genetic distance
dNTP	deoxynucleoside triphosphate
D_R	Roger's distance
D_s	Nei standard distance
EDTA	ethylenediamine tetracetic acid
FAO	Food and Agricultural Organization
FST	fixation index
H	heterozygosity
IAM	infinite alleel model
LV	Lebowa-Venda
kb	kilobase
KK	Koekoek
MAS	marker assisted selection
Mb	megabase
MHC	major histocompatibility complex
MS	Mozambique
NN	Naked Neck
NH	New Hampshire
NJ	Neighbour-joining tree
OV	Ovambo
PCR	polymerase chain reaction
PIC	Polymorphic information content
QTL	quatitative trait loci
RAPD	randomly amplified polymorphic DNA
RE	restriction enzyme
RFLP	restricted fragment length polymorphism
SMM	stepwise mutation model
SNP	single nucleotide polymorphism
STS	sequence tagged sites
UPGMA	unweighted pair wise group method with arithmetic mean
VNTR	variable number tandem repeats
ZM	Zimbabwe

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