GENETIC PROFILE AND CLASSIFICATION OF THE LOCALLY DEVELOPED GELLAPPER MUTTON SHEEP IN NAMIBIA BASED ON MICROSATELLITE MARKERS

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ABSTRACT

A Gellapper breed was developed at the Gellap-Ost Research Station by crossbreeding Damara and Dorper sheep up to the desired sixth generation. The Gellapper mutton sheep possesses unique genetic and phenotypic characteristics that are well-suited to its existence in the harsh environment of southern Namibia, without treatments and extra feed. It has a unique colour pattern that shields it from predators. This report covers the genetic distinctiveness of the locally developed Gellapper mutton sheep, against the parent breeds (Damara and Dorper). Genetic diversity for the Gellapper population yielded values of Hz = 0,4290 for this population compared to values of Hz = 0,5816–0,6960 in other Meatmaster populations and Hz = 0,5413–0,6538 in the parent breeds. The DNA analysis indicated that the Gellapper has a low number of alleles A = 4,2 which is much lower than the A = 5,8–7,2 calculated for the parent breeds because the flock was closed and therefore all animals are closely related. Meatmaster rams had been introduced in the Gellapper flock in order to reduce inbreeding depression.

INTRODUCTION

The Namibian environment is characterized by diverse ecosystems ranging from deserts, to low and high grasslands and savannas. Thus the Gellapper was developed to thrive and produce under these harsh environmental conditions in Namibia giving it its unique characteristics. This mutton sheep is a boon to the communal farmers who possess no or very few resources for the maintenance of their flock during the dry years.

Locally developed sheep breeds are therefore an important asset for the communal farmers because of the unique combinations of adaptive traits that developed so effectively to respond to the pressures of the harsh environment (Buduram, 2004). Such adaptive traits include tolerance to various diseases, changes in feed quality, extreme climatic conditions and the ability to survive and reproduce for long periods (Hammond, 2000). The first opportunity for the application of the Meatmaster DNA database presented itself early during 2009 when F.W. Peters (Meatmaster Breeder's Association of South Africa) was requested by the Division of Livestock Research of the Ministry of Agriculture, Water and Forestry to look at the phenotypic characteristics of the Gellapper mutton sheep in relation to the RSA Meatmaster sheep breed and compare and interpret the DNA data of Gellapper sheep, to that of the RSA Meatmaster, Dorper and Damara Sheep (as parent breeds) and to advise on the way forward.

The aim of this study was (1) to determine whether the Gellapper forms a recognizable genetic group; (2) to describe the pattern and scale of genetic divergence between the Gellapper, Meatmaster and its parent breeds (Dorper and Damara); and (3) to describe within-population diversity in Gellapper flock and Meatmaster populations.

MATERIALS AND METHODS

Genotypes of 10 unrelated males and 30 unrelated females from the Gellapper flock (Gel) were sampled. Whole blood samples were taken from the jugular vein and collected into 7 ml Vacutainer tubes containing ethylenediaminitetraacetic acid (ETDA) as an anticoagulant. The samples were kept at 0 °C until DNA was extracted. DNA was extracted from the sheep blood samples with the Wizard Genomic DNA Purification Kit (Miller *et al.*, 1998).

Microsatellite markers were used for genetic characterization of the Gellapper sheep sampled. The following loci were used for the sheep genotyped: MCM527 (Hulme *et al.*, 1994), MAF65 (Buchanan *et al.*, 1991), OARFCB20 (Buchanan and Crawford, 1992), CSRD247 (Kemp *et al.*, 1993), ETH225 (Steffen & Eggen, 1993), INRA63 (Vaiman *et al.*, 1994) and TGLA53 (Crawford *et al.*, 1995). The Polymerase Chain Reaction (PCR) amplification was performed using a Perkin Elmer Gene Amp PCR System 9700 thermocycler. Amplified fragments were run on an ABI377 sequencer and finally analyzed using Genescan™ and Genotyper™ software (Applied Biosystems). Permission was obtained to make use of the existing DNA database of reference populations at the Agricultural Research Council (ARC, Irene) for the parent and other breeds. Preliminary statistical analyses of the Gellapper DNA data were performed at the University of the Free State in collaboration with Professor J.P. Grobler. To quantify levels of diversity within individual breeds and populations, observed heterozygosity (Ho), Nei's unbiased heterozygosity (Hz) (Nei, 1987) and average number of alleles per locus (A) were calculated using MSToolkit.

RESULTS

Table 1. Gellapper sheep DNA profile data

Sample	OarFCB20		MCM527		CSRD247		Inra63		MAF65		ETH225		Tgla53	
1	96	102	170	186	224		186		128	132	144		159	
2	94	96	168	186	224		186		128	132	144		157	
3			166	168	224		186		128	130	144		149	159
4	90	90	166		224	228	174	186	128	130	144		147	157
5	90	90	166	170	224	228	186		128		144		159	
6	94	102	168		224		186		128	130	144		147	
7	90	94	168		224		174	204	130	132	144		147	159
8	96	96	170		224		186		128	132	144		159	
9	90	96	168	170	224		186		130		144		159	
10	90	96	166	170	224		174	186	132		144		137	147
11	94		170		224		186		130	132	144	148	159	
12	90	96	166	170	224		186		128	130	144	148	147	157
13	90	102	166	186	224		174		128	130	144		159	
14	90	96	166	186	224		174	186	128		144		161	
15	90	94	170		224		174	186	128	130	144		159	
16	90	94	166		224		174		128		144		147	159
17	94	102	166		224		174	186	128		144			
18	90	94	168		224		174	186	128		144			
19	96	102	166	170	224	228	186	204	128	132	144			
20	90	94	186	186	224		174		128	132	144		159	
21	94	102	166	170	224		174	186	128		144		157	159
22	96		170		224		186		132		144		147	159
23	94		166	170	224		186		128	130	144		147	
24	90				224		186		128	130	144		137	143
25	90	94	170		224		174	174	128	132	144			
26	94		166		224		186		128	130	144		159	
27	90	96	170		224		186		128	132	144		147	159
28	96	102	166		224		174	186	128		144		159	
29	96		166	168	224		186		128	132	144		159	
30	96	102	166	168	224		174	186	128	130	144		159	
31	90	96	170		224		174	186	128	132	144		157	159
32	90	94	166		224		174	186	128	130	144		157	161
33	94		166	170	224	228	174	186	128	132	144		159	161
34	90	102	166	168	224		186		130		144		147	157
35	96		166		224		178	186	128		138	144	147	159
36	90	102	166		224		174	186	128		144		151	161
37	96	102	170		224		174	186	128		138	144	161	
38	96	102	166	170	224		174	186	128	130	144		147	161
39	90	96	166		224		186		128		144		157	159
40	94		170		224		174		128	130	144		151	157
41	94		166	168	224		186		130	132	144		157	

Table 2. Genetic diversity of 12 sheep populations

Population	Sample size	Loci typed	Unbiased Hz	Unbiased Hz SD	Obs Hz	Obs Hz SD	No Alleles	No Alleles SD
SAM	35	5	0,6962	0,0420	0,5810	0,0374	6,60	2,30
Dam	34	5	0,6538	0,0754	0,6606	0,0368	7,20	2,05
Dor	34	5	0,5413	0,1288	0,3824	0,0373	5,80	2,39
VaR	32	5	0,6762	0,0570	0,5555	0,0403	6,00	1,87
IFr	40	5	0,7324	0,0440	0,5450	0,0352	6,60	1,82
RoR	35	5	0,4522	0,1347	0,4241	0,0377	3,80	1,64
Mme	55	5	0,6818	0,0784	0,6073	0,0294	8,00	1,22
Mve	40	5	0,5816	0,0944	0,5000	0,0354	6,80	2,17
Mho	40	5	0,6601	0,0845	0,5550	0,0351	8,20	2,05
MPr	40	5	0,6960	0,0683	0,5850	0,0348	8,60	1,95
NaA	34	5	0,6138	0,1018	0,4801	0,0387	6,00	2,55
Gel	41	5	0,4290	0,1439	0,3645	0,0340	4,20	2,28

Table 3. F_{ST} values for 8 sheep breeds compared to the Gellapper population

F_{ST} values with Meatmasters pooled:									
	SAM	Dam	Dor	VaR	IFr	RoR	MM	NaA	Gel
SAM	0								
Dam	0,19131	0							
Dor	0,2377	0,1051	0						
VaR	0,17889	0,06558	0,08629	0					
IFr	0,12009	0,17843	0,16604	0,1351	0				
RoR	0,25419	0,13215	0,18064	0,1464	0,2573	0			
MM	0,15436	0,02764	0,04287	0,0368	0,13888	0,0955	0		
NaA	0,18982	0,11999	0,20144	0,1329	0,1551	0,1856	0,1147	0	
Gel	0,32484	0,39072	0,44521	0,3893	0,34207	0,5226	0,3304	0,3902	0

SAM SA Mutton Merino
Dam Damara
Dor Dorper
VaR Van Rooy
IFr Ile De France
RoR Ronderib Afrikaner
MM Meatmaster
NaA Namakwa Afrikaner
Gel Gellapper
Mme Meatmaster (Meyerton)
Mve Meatmaster (Venterstad)
Mho Meatmaster (Hopetown)
MPr Meatmaster (Prieska)

DISCUSSION

It is important for the future recognition and management of the developing Meatmaster breed to establish whether genetic differences between populations of this breed, and parent breeds, indicate real genetic distinctiveness or simply reflect random genetic drift (Peters *et al.*, 2010).

Artificial selection may result in inbreeding depression and a reduction in fitness because relatively small populations are involved. The coefficients of genetic diversity used show that genetic diversity in individual Meatmaster populations is comparable to the higher end of the range of diversity values in the established parent breeds. However genetic diversity for the Gellapper population yielded values of Hz = 0,4290 for this population compared to values of Hz = 0,5816–0,6960 in other Meatmaster populations and Hz = 0,5413–0,6538 in the parent breeds (Table 2). The average heterozygosity in the Gellapper population of 0,4290 was very low compared to values of 0,620–0,728 calculated in sheep breeds by Quiroz *et al.* (2008). This indicated inbreeding depression in the Gellapper population.

The F_{ST} value of 0,3304 for the Gellapper population (Table 3) compared to the pooled value for Meatmasters indicated that the Gellapper was nearer to the Meatmaster breed than to its parent breeds for which F_{ST} values of 0,3907–0,4452 were registered.

The A value (number of alleles) in the Gellapper population was 4,2 (Table 2), which is much lower than the A = 5,8–7,2 calculated for the parent breeds and also consider-

ably lower than the A = 6,8–8,6 for Meatmaster populations. The low A value is particularly noteworthy since Spencer *et al.*, (2000) demonstrated that A may be the most accurate indicator of population bottlenecks. The high A value in the Meatmaster breed shows good retention of genetic diversity (Peters *et al.*, 2010) while the low A for the Gellapper indicates a population bottleneck.

CONCLUSION

Genetic diversity in the Gellapper sheep population was very low compared to diversity values in the parent breeds and other Meatmaster populations. F_{ST} values however indicated that the Gellappers were closer to the Meatmaster breed than to any of the parent breeds. The low A value recorded for the Gellapper population also indicated that a population bottleneck was already experienced. F.W. Peters consequently proposed that the Gellapper be incorporated as a distinct Meatmaster population as part of the new Meatmaster sheep breed and that Meatmaster genetics from the South African Meatmaster populations be introduced, whereby the genetic variation of the Gellapper flock could be increased and the Meatmaster breed further expanded.

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