



# EBVs and sire ranking: The impact of pedigree integrity on selection in South African Angora goats

C Garritsen, C Visser<sup>#</sup> and E Van Marle-Köster  
 carina.visser@up.ac.za



Table 1 Estimated Breeding Values (EBV) and sire ranking for on-farm recorded pedigree and DNA-verified pedigree for weaning weight for 21 Angora goat sires

Weaning weight EBV		Sire ranking	
On-farm pedigree	DNA-verified pedigree	On-farm pedigree	DNA-verified pedigree
-0.80	1.72	21	1
0.66	0.33	5	15
1.63	1.45	2	3
0.29	1.67	9	2
-0.24	0.87	18	9
0.13	0.43	13	14
-0.77	1.35	20	4
-0.38	0.86	19	10
0.79	-1.19	4	21
2.00	0.15	1	18
-0.22	0.92	17	6
0.52	0.30	8	16
0.62	-0.10	7	19
-0.08	1.09	15	5
0.94	0.51	3	13
0.16	-0.71	12	20
0.63	0.18	6	17
-0.16	0.72	16	12
0.18	0.90	10	7
0.17	0.81	11	11
0.10	0.88	14	8

## Introduction

Genetic progress, with special focus on mohair traits is of utmost importance to South African Angora breeders to maintain their position as leader in the world mohair production. Genetic evaluations and predictions take pedigree soundness for granted in all livestock production systems. Negative effects of pedigree inaccuracies on genetic progress have been documented in dairy and beef cattle, sheep and goats. Furthermore, South African Angora goat breeders make use of group mating and overmating in addition to single sire mating and AI, providing ample opportunity for errors in paternity records. In the current study, pedigree records of a South African Angora goat breeder were verified using a panel of 12 microsatellite markers. The effect of the errors in the recorded pedigree on possible genetic progress was determined by examining the difference in EBV estimation and sire ranking between the two pedigrees for economically important mohair traits.



## Conclusion

The PE of the marker panel was lower than what was expected, probably as a result of the Angora goat population in the current study belonging solely to one breeder as many of the sires were related.

The error in on-farm pedigree recording was lower than what was typically reported in previous studies – a result of this particular breeder making use of AI. However, the 3.1% error in the pedigree records resulted in substantial inaccuracies observed in EBV estimation and ranking of the breeding sires. The study demonstrates the importance of pedigree soundness for accurate selection and the valuable role played by DNA marker-based parentage verification in genetic progress for South African Angora goats.



## Aim

The aim of the study was to determine the effect of inaccuracies in pedigree records on Estimated Breeding Value (EBV) estimation of breeding sires and sire ranking.

## Materials and Methods

381 Angora goats were selected from a number of herds belonging to one breeder. The population consisted of eight half-sib families, 16 putative sires and 40 unallocated offspring. Genotyping was performed using a panel of 12 microsatellite markers (INRA 63, BM 1818, CSRD 247, MCM 527, BM 1258, OarFCB 48, BM7160, SRCRSP8, BM1329, HSC, SRCRSP5, INRABERN192) Parentage was assigned using Cervus™ 3.0. EBVs for the breeding sires were calculated using ASREML software for fleece traits (fleece weight and fibre diameter at second shearing) and body weights (birth weight, weaning weight, eight month weight, yearling weight and 16 month weight). The 21 sires were ranked for each trait using the Spearman rank correlation method.

## Results

Panel: Probability of Exclusion = 0.996; Polymorphic Information Content = 0.700.  
 3.1% error in on-farm recorded pedigrees (11 out of 357 offspring)  
 40 Previously unallocated offspring (11%) allocated to new sires.  
 Pedigree error had a significant effect on the estimation of EBVs of the sires and their re-ranking. Greatest effect observed in weaning weight, where lowest-ranked sire based on on-farm pedigree was re-ranked to top sire in DNA-verified pedigree (Table 1).