

OPEN ACCESS

EDITED AND REVIEWED BY Martino Cassandro, University of Padua, Italy

RECEIVED 26 July 2024 ACCEPTED 28 August 2024 PUBLISHED 05 September 2024

CITATION

Becker GM, Woods JL, Schauer CS, Stewart WC and Murdoch BM (2024) Corrigendum: Genetic association of wool quality characteristics in United States Rambouillet sheep. *Front. Genet.* 15:1471185. doi: 10.3389/fgene.2024.1471185

COPYRIGHT

© 2024 Becker, Woods, Schauer, Stewart and Murdoch. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Corrigendum: Genetic association of wool quality characteristics in United States Rambouillet sheep

Gabrielle M. Becker¹, Julia L. Woods¹, Christopher S. Schauer², Whit C. Stewart³ and Brenda M. Murdoch¹*

¹Department of Animal, Veterinary and Food Sciences, University of Idaho, Moscow, ID, United States, ²Hettinger Research Extension Center, North Dakota State University, Hettinger, ND, United States, ³Department of Animal Science, University of Wyoming, Laramie, WY, United States

KEYWORDS

60S ribosomal protein L17-like, ABCC8, central performance ram test, GWAS, sheep production

A Corrigendum on

Genetic association of wool quality characteristics in United States Rambouillet sheep

by Becker GM, Woods JL, Schauer CS, Stewart WC and Murdoch BM (2023). Front. Genet. 13: 1081175. doi: 10.3389/fgene.2022.1081175

In the published article, there were errors in **Results**, **Discussion**, Table 5 and Figure 6. The details of these errors are given below:

A correction has been made to **3 Results**, *3.4 Genomic context of significant markers*, paragraph 1. This sentence previously stated:

"Four SOX family TFBS were predicted at rs404487383 and a YY2 and MZF1 TFBS were predicted at rs402689377. There were no TFBS with score difference of 3/-3 or greater predicted at SNP OAR19_14805437.1."

The corrected sentence appears below:

"Four SOX family TFBS and a TCF7 TFBS were predicted at rs404487383. Three TFBS with a score difference of $\pm 3/-3$ or greater were predicted at both rs402689377 and SNP OAR19_14805437.1."

A correction has been made to **4 Discussion**, paragraph 4. This sentence previously stated:

"Two potential TFBS were predicted with matrix score changes between SNP alternate and reference alleles at s29455.1, a marker associated with skin wrinkle scores. The TF MZF1 has been shown to diminish the expression of the gene PADI1 in human keratinocyte cells (**Dong et al., 2008**). These *in silico* analyses suggest functional ramifications of variant alleles associated with wool quality characteristics."

The corrected sentence appears below:

"These data suggest potential functional ramifications of variant alleles associated with wool quality characteristics."

There was an error in [Table 5] as published. [The alternate allele used in the query sequence of rs404487383 and OAR19_14805437.1 were incorrect, and the query sequence of rs402689377 was given for the non-coding strand. The

Becker et al. 10.3389/fgene.2024.1471185

TABLE 5 Predicted TFBS for SNPs located within genes. Query sequences were analyzed with the major allele as "wild type" and the minor allele as "variant" sequence. The score depicts the difference of wild type versus variant predictiosns.

Marker ID	Predicted TFBS	Score	Query
rs404487383	SOX10	-0.90	TCTTT[T/C] GTTGC
	SOX2	-0.50	
	SOX2	-0.49	
	SOX17	-0.45	
	TCF7	-0.32	
rs402689377	ETS2	-0.56	CTTTC[C/T] GGCTC
	TFCP2	-0.32	
	RUNX2	0.55	
OAR19_14805437.1	MEIS1	0.33	AGTGA[T/C] TCTGG
	MEIS2	0.41	
	NR2F2	0.58	

corrections of these errors result in the following changes: for rs404487383, the SOX10 score is corrected from -0.91 to -0.90, the SOX17 score is corrected from -0.39 to -0.45, and the transcription factor TCF7 is included with a score of -0.32; for rs402689377, the transcription factors YY2 and MZF1 are removed and ETS2

(score -0.56), TFCP2 (score -0.32), and RUNX2 (score 0.55) are included; and for OAR19_14805437.1, the transcription factors MEIS1 (score 0.33), MEIS2 (score 0.41), and NR2F2 (score 0.58) are included.]. The corrected [Table 5] and its caption **[Predicted TFBS for SNPs located within genes. Query sequences were analyzed with the major allele as "wild type" and the minor allele as "variant" sequence. The score depicts the difference of wild type versus variant predictions.] appear below.

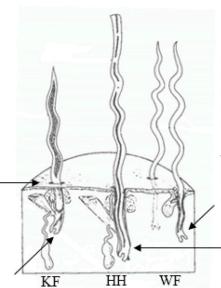
There was an error in [Figure 6] as published. [The transcription factor MZF1 was incorrectly referenced in this figure]. The corrected [Figure 6] and its caption **[Genes with biological functions relevant to follicular growth. Significant SNPs identified in GWAS are located within or near genes with known biological roles relevant to skin and follicular growth, including ULK4 (Luo and Yang, 2022), U6 spliceosomal RNA (Hilcenko et al., 2013), 60S ribosomal protein L17-like (Yang et al., 2016), ribosomal protein S19 (Kuramoto et al., 2005), ABCC8 (Shorter et al., 2008) and WT1 (Wagner et al., 2008). The significant SNPs within 60S ribosomal protein L17-like and ABCC8 had predicted TFBS score differences between reference and alternate alleles. The figure illustrates the three types of fibers which comprise sheep's wool, adapted from Bradford and Fitzhugh (1983). KF, kemp fiber; HH, heterotype hair; WF, wool fiber.] appear below.

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

<u>ULK4</u> shown to inhibit apoptosis through PI3K (Luo and Yang 2022)

U6 spliceosomal RNA Implicated in poikiloderma skin disease (Hilcenko et al., 2013)

60S ribosomal protein L17-like Highly expressed in velvet skin undergoing follicle formation (Yang et al., 2016); predicted SOX family TFBS



Uncharacterized gene similar to <u>ribosomal protein S19</u> associated with sparse and wavy hair disorder in rats (Kuramoto et al., 2005)

<u>ABCC8</u> Codes SUR1, ATPsensitive potassium channel in hair follicles (Shorter et al., 2008)

WT1-positive fibroblasts in follicular papilla and perifollicular sheath of normal human skin (Wagner et al., 2008)

FIGURE 6

Genes with biological functions relevant to follicular growth. Significant SNPs identified in GWAS are located within or near genes with known biological roles relevant to skin and follicular growth, including ULK4 (Luo and Yang, 2022), U6 spliceosomal RNA (Hilcenko et al., 2013), 60S ribosomal protein L17-like (Yang et al., 2016), ribosomal protein S19 (Kuramoto et al., 2005), ABCC8 (Shorter et al., 2008) and WT1 (Wagner et al., 2008). The figure illustrates the three types of fibers which comprise sheep's wool, adapted from Bradford and Fitzhugh (1983). KF, kemp fiber; HH, heterotype hair; WF, wool fiber.

Becker et al. 10.3389/fgene.2024.1471185

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated

organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.