

Quantitative-genetic characterization of wool quality traits in German Merino

Natascha Zimmermann^{1,2}, Jörn Bennewitz², Wilhelm Pflanz¹ and Markus Schmid²

¹ Faculty of Agriculture Food and Nutrition, University of Applied Sciences Weihenstephan-Triesdorf, , 91746 Weidenbach Germany

² Institute of Animal Science, University of Hohenheim, 70599 Stuttgart, Germany

1. Introduction

To improve the objectivity, reliability, and reproducibility of the wool quality breeding value in German Merino sheep, an evaluation system for sheep wool fiber characteristics was developed. The aim of the study was to assess the suitability of these novel wool fiber traits for breeding by means of SNP-based quantitative-genetic analyzes in the German Merino nucleus population.

2. Material and Methods

Phenotypes:

Standardized wool samples were taken from 3,929 German Merino sheep (herdbook) during shearing at three measurement sites. These were located 15 to 20 cm laterally from the spine at the level of the shoulder blade (shoulder), the last rib (flank), and the sacrum (rump). Three wool quality parameters were measured for all samples using an OFDA2000 ("Optical-based Fibre Diameter Analyser"):

- **fiber diameter** in μm at the shoulder (**FDS**), flank (**FDF**) and rump (**FDR**)
- crimp of the wool fibers in °/ mm at the shoulder (CRS), flank (CRF) and rump (CRR)
- staple length in mm at the shoulder (SLS), flank (SLF) and rump (SLR)

Genotypes:

For 1,715 of these animals, genotype data were generated using the OvineSNP50 Genotyping BeadChip from Illumina.

Statistics:

After filtering, phenotypes of 1,650 female animals along with their genotype information at 63,154 SNPs were available for this study. The animals were assigned to four age classes (4, 5, 6, 7) according to performance testing (VDL, 2018; VDL and vit, 2016) and originated from eleven of the 30 breeding farms at which animals were sampled.

Descriptive statistics were generated from the raw data of the traits after plausibility check.

Variance components were estimated using univariate analyzes with the following mixed linear model:

$$y = Xb + Za + e$$

where:

y = vector of observations (Box-Cox transformed & z-standardized)

b = vector of fixed effects

a = vector of random additive-genetic effects of the animals

X = corresponding design matrix for the fixed effects

Z = corresponding design matrix for the random effects

e =vector of residuals

Animal effects were normally distributed with $a \sim N(0, G\sigma_a^2)$, where σ_a^2 is the additive-genetic variance and G is the genomic relationship matrix.

Fixed effects were tested using Wald statistics and included in the model if they were significant (p < 0.05).

Narrow sense heritabilities were calculated using standard notation and likelihood-ratio tests were conducted to test the significance of heritability.

Data processing: RStudio (Allaire 2012) & Analyzes: ASReml-R (Butler et al. 2020)

3. Results and Discussion

Descriptive Statistics:

Wool fineness, on average, aligns with the fiber diameter of $26-28~\mu m$ set in the breeding program (VDL 2021), but varies between 20 and 38 μm depending on the measurement point (Fig. 1). Differences between measurement points are evident across all observed wool quality parameters.

Significant non-genetic effects:

The fixed effects of the age class and farm were highly significant ($p \le 0.001$) for the traits of fiber diameter and staple length. For crimp, only the farm effect was significant ($p \le 0.001$).

Heritabilities:

Likelihood ratio tests revealed highly significant heritable variation for all traits (p<0.001). The estimated heritabilities of the traits (Tab. 1) showed moderate to high values. This implies considerable potential for selective breeding.

Multivariate analyzes are planned to generate a deeper understanding of their genomic background of the traits and their genetic correlations.

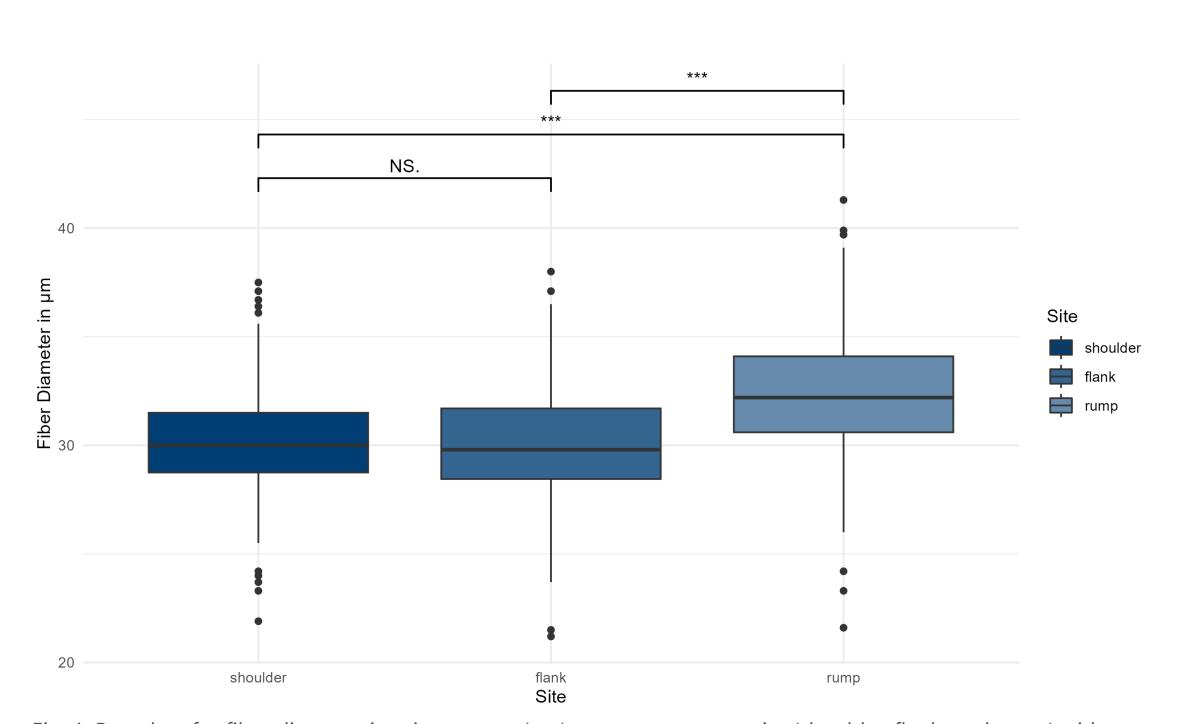


Fig. 1: Box plots for fiber diameter in micrometers (µm) per measurement site (shoulder, flank, and rump) with contrast significances for 1,650 female Merinoland sheep

Tab. 1: Heritabilities (h^2) with standard errors (SE) of fiber diameter at the shoulder (FDS), flank (FDF), and rump (FDR); crimp at the shoulder (CRS), flank (CRF), and rump (CRR); staple length at the shoulder (SLS), flank (SLF), and rump (SLR); p<0.001 for all parameters

Wool Quality Parameters		h ²	SE
Fiber diameter	shoulder	0.595	0.057
Fiber diameter	flank	0.534	0.060
Fiber diameter	rump	0.539	0.059
Crimp	shoulder	0.654	0.054
Crimp	flank	0.580	0.059
Crimp	rump	0.545	0.059
Staple length	shoulder	0.306	0.059
Staple length	flank	0.409	0.062
Staple length	rump	0.389	0.063

4. Reference

Allaire, J. J. (2012): RStudio: Integrated development environment for R. Boston, MA, 770(394), 165–171.; Butler, D. G., Cullis, B. R., Gilmour, A. R., & Gogel, B. J. (2020): ASReml-R Reference Manual Version 4.1 (4.1.0.130): VSN International Ltd. VDL & vit. (2016): Vertrag über die Erbringung von Zuchtwertschätzdienstleistungen bei Schafen zwischen VDL und vit, 2016.; VDL-Richtlinie zur Durchführung von Leistungsprüfungen, Kassel. VDL – Vereinigung Deutscher Landesschafzuchtverbände. (2021): Zuchtprogramm Merinolandschaf.





FUNDING





