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Genetic evaluation of cashmere fiber traits in goats from the United States and New Zealand

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Introduction

Cashmere is a fine animal fiber produced by the secondary hair follicles of some goats (McGregor, 2014) and is valued for its softness, insulation, and lightweight properties. Although often classified as a luxury product, global cashmere demand has continued to grow, with the market projected to expand steadily over the coming decade (Fortune Business Insights). While China, Mongolia, and the Middle East dominate global production (van der Westhuysen, 2005), interest in cashmere production has increased in several non-traditional countries, including New Zealand and the United States. These emerging industries are characterized by relatively small cashmere goat populations, geographically dispersed flocks, and limited infrastructure for coordinated genetic improvement.

Cashmere goats originated in cold, high-altitude regions where natural selection favored the development of a fine insulating undercoat (Wu *et al*., 2023). In New Zealand, efforts to redevelop cashmere production from feral goat populations in the late twentieth century (Restall and Pattie, 1989) led to the establishment of structured breeding programs and coordinated industry improvement. In contrast, the U.S. cashmere population developed through a combination of imported genetics and selection within local goat populations (Cashmere Goat Association), and the industry remains comparatively underdeveloped. In the U.S., there are not any national genetic evaluation systems currently in place for cashmere goats, and thus genetic gain from selective breeding of economically important fiber traits is limited (Shumbusho *et al*., 2013). Given the shared ancestry of U.S. and New Zealand goats and ongoing gene flow between populations, collaborative analyses offer an opportunity to overcome limitations associated with small population size and limited data. The objective of this study was to combine data from U.S. and New Zealand cashmere goats to estimate the heritability and repeatability of cashmere fiber traits and to estimate the genetic correlations between fiber traits.

Materials & Methods

Three separate analyses of cashmere fiber traits were conducted based on goat origin: United States only (US), New Zealand only (NZ), and a combined US/NZ dataset. The combined analysis was enabled through international collaboration, data sharing, and gene flow between the two populations.

Study populations. The US dataset included 1,243 fiber records from 1,035 goats located on 32 farms across 17 states. The NZ dataset included 2,093 fiber records from 1,537 goats from a single farm. In total, the combined dataset consisted of 3,336 fiber records from 2,572 goats. Both males and females were represented, with most records collected from goats aged one to two years old. Producer participation and data sharing was voluntary. All animal management and sampling were conducted under standard production practices. All reported research meets the ethical guidelines and legal requirements of the study country and Institutional Animal Care and Use Committee approval was obtained where required.

Fiber sampling and trait measurement. Producers submitted fiber samples for analysis to either the Texas A&M Bill Sims Wool and Mohair Research Laboratory (San Angelo, TX, USA) or SGS Wool Testing Servies (Kilbirnie, New Zealand). In the US, a mid-side patch sample was clipped from each goat. In NZ, an individual goat's entire fleece was shorn and then subsampled using multiple random pinches. Samples in both the US and NZ were analyzed using an Optical Fibre Diameter Analyser 100.

Seven fiber traits were measured consistently across all three analyses: mean fiber diameter (MFD), standard deviation of diameter (SDD), coefficient of variation of diameter (CVD), curvature (CURV), standard deviation of curvature (SDCURV), spinning fineness (SpinF), and percentage of fibers with diameter ≤ 19 μm (Perc19). Guard hair thresholds differed slightly between laboratories (30 μm in the US and 35 μm in NZ); otherwise, trait definitions were consistent. Additional traits were only available and analyzed within individual populations. US-only traits included staple length (SL), greasy fleece weight (GFW), and coarse edge micron (CEM). NZ-only traits included down staple length (DSL), yield (YD), fleece weight (FW), down weight (DW), coarse edge (CE), and percentage of medullated fibers (MED).

Genotype and pedigree data. Hair samples were collected by producers and submitted for genotyping using the Goat GGP 70K BeadChip (Neogen Corp.). In total, there were 1,462 animals (1,036 US and 426 NZ) with genotypes available. After quality control, 1,372 animal genotypes were retained for the combined analysis. Quality control included removal of animals and single nucleotide polymorphisms (SNP) with low call rates (< 0.90) and SNP with minor allele frequency less than 0.05.

Pedigree records were provided by producers and varied in depth from one to five generations. The final pedigree for the combined analysis included 3,874 animals. Pedigree connectedness between populations was achieved through shared male germplasm, including several NZ sires used extensively within US flocks.

Statistical analyses. All traits available in that dataset were analyzed separately within the three analyses: US, NZ, or combined. Variance components were estimated using single-step genomic best linear unbiased predication (ssGBLUP) using the BLUPF90 software suite (Misztal *et al.*, 2014). Heritability was estimated using univariate animal models fitted to the first available record per animal using the general animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e} \quad (1)$$

where **y** is a vector of phenotypic observations, **b** is a vector of fixed effects, **u** is a vector of direct additive genetic effects, and **e** is a vector of residuals. Matrix **X** and **Z** relate observations to fixed and random effects, respectively. Fixed effects tested for model inclusion were animal sex, animal age at fiber collection, and contemporary group. Contemporary group was defined as fiber testing year for the NZ analysis and farm by testing year for the US and combined analyses. Additive genetic effects were assumed to follow $\mathbf{u} \sim N(0, \mathbf{H}\sigma_u^2)$, where **H** is the combined pedigree and genomic relationship matrix.

Genetic correlations between traits were estimated using bivariate animal models fitted to first records only. Repeatability was estimated using all available records per animal with the following repeated records model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wp} + \mathbf{e} \quad (2)$$

where **p** is a vector of permanent environmental effects, **W** is the corresponding incidence matrix, and other elements were previously defined in Eq.1.

Results & Discussion

Variance component estimates from the US and NZ analyses were generally similar to those from the combined analysis; therefore, results presented focus on the combined analysis (Table 1) which benefited from increased sample size.

Table 1. Heritability (diagonal), phenotypic correlations ± standard error (upper triangle), and genetic correlations ± standard error (lower triangle) for cashmere fiber traits[1] in the combined analysis.

	MFD	**SDD**	**CVD**	**Curv**	**SDCurv**	**SpinF**	**Perc19**
MFD, µm	**0.46 ± 0.04**	0.38 ± 0.03	-0.28 ± 0.03	-0.68 ± 0.03	-0.35 ± 0.03	0.93 ± 0.01	-0.71 ± 0.02
SDD, µm	0.39 ± 0.10	**0.26 ± 0.04**	0.77 ± 0.02	-0.30 ± 0.03	0.15 ± 0.03	0.62 ± 0.03	-0.40 ± 0.03
CVD, %	-0.41 ± 0.10	0.69 ± 0.07	**0.26 ± 0.04**	0.15 ± 0.03	0.40 ± 0.03	0.00 ± 0.03	0.06 ± 0.03
Curv, °/mm	-0.70 ± 0.05	-0.33 ± 0.12	0.19 ± 0.12	**0.33 ± 0.04**	0.44 ± 0.03	-0.65 ± 0.03	0.50 ± 0.03
SDCurv, °/mm	-0.60 ± 0.08	-0.08 ± 0.14	0.37 ± 0.12	0.81 ± 0.05	**0.24 ± 0.04**	-0.24 ± 0.03	0.29 ± 0.03
SpinF, µm	0.98 ± 0.01	0.59 ± 0.08	-0.20 ± 0.12	-0.68 ± 0.06	-0.54 ± 0.09	**0.40 ± 0.04**	-0.71 ± 0.02
Perc19, %	-0.73 ± 0.06	-0.66 ± 0.10	-0.27 ± 0.13	0.61 ± 0.09	0.45 ± 0.11	-0.85 ± 0.05	**0.29 ± 0.04**

[1] MFD (mean fiber diameter); SDD (standard deviation of diameter); CVD (coefficient of variation of diameter); Curv (curvature); SDCurv (standard deviation of curvature); SpinF (spinning fineness); and Perc19 (percentage of fibers with diameter ≤ 19 µm).

Heritability and repeatability. MFD had a high heritability and repeatability (0.62 ± 0.02), consistent with other studies (Pattie and Restall, 1989). Mean fiber diameter is one of the most economically relevant traits in cashmere production and these results reinforce MFD as a trait with high genetic selection potential. Measures of diameter variation, including SDD and CVD, had lower heritability than MFD but still relatively high repeatability estimates (0.50 ± 0.03). A similar heritability estimate for SDD was reported for goats in Scotland (Bishop and Allain, 2000). Curvature has been identified as an important determinant of resistance to compression, an objective measure of fiber softness (McGregor, 2003). Curvature and SDCURV were moderately heritable and highly repeatable (0.67 ± 0.02 and 0.55 ± 0.03, respectively), supporting their potential utility in selection programs. Although SpinF was highly heritable and repeatable (0.61 ± 0.02), SpinF is mathematically derived from MFD and CVD. Therefore, breeding programs may achieve greater genetic progress from direct selection on its component traits rather than SpinF. Selection for Perc19 may provide more targeted control over the fiber diameter distribution, but MFD's higher heritability and repeatability may make it more effective for improving overall fiber fineness. The moderate to high repeatability of fiber traits indicates that an animal's initial fiber record is a good predictor of subsequent performance, suggesting that less frequent fiber testing strategies could be explored in the design of future genetic evaluation programs.

Genetic correlations. Cashmere breeding programs generally emphasize selection on MFD given its strong influence on cashmere quality and economic value. Therefore, the genetic relationships between MFD and other fiber traits are of particular interest. Mean fiber diameter had a positive genetic correlation with SDD, indicating that selection for finer fiber

diameter would also reduce absolute diameter variation. In contrast, the genetic correlation between MFD and CVD was negative, as a consequence of the ratio-based definition of CVD and highlighting challenges associated with selection on ratio traits (McCaw *et al.*, 2025). Strong negative genetic correlations were found between MFD and both CURV and SDCURV, indicating that selection for finer fiber diameter is expected to increase fiber curvature and curvature variability. The role of curvature in commercial classification and pricing of cashmere is not yet well defined, and whether these genetic correlations are favorable may depend on individual breeding objectives. As expected, MFD was strongly genetically correlated with SpinF due to the inclusion of MFD in the calculation of SpinF (Butler and Dolling, 1992). A strong genetic correlation was observed between MFD and Perc19, consistent with finer fleeces containing a greater proportion of fiber meeting cashmere fineness thresholds (FTC, 1939). Selection on MFD is likely to induce correlated responses in other fiber traits, including potential unfavorable changes in CVD and SDCURV, which should be considered in breeding programs.

Conclusions

This study is an international genetic evaluation of cashmere fiber traits using combined U.S. and New Zealand datasets. Moderate to high heritability and repeatability were observed for most fiber traits, indicating that genetic selection can effectively improve fiber characteristics. Genetic correlations suggest that selection for finer fiber diameter will produce correlated responses in other traits, including potentially unfavorable increases in variability of fiber diameter and curvature. Overall, this study provides foundational information to support future international genetic evaluation efforts.

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References

Bishop S.C., and Allain D. (2000) Proc. 7th Int. Conf. Goats, Tours, France.

Butler K.L., and Dolling M. (1992) Aust. J. Agric. Res. 43(6):1441-1446. doi.org/10.1071/AR9921441

Cashmere Goat Association, Cashmere Goat FAQ. Available at: www.cashmeregoatassociation.org/post.php?pid=3, visited on: 23-01-2026.

Federal Trade Commission (FTC). (1939) Wool Products Labeling Act of 1939. Available at: www.ftc.gov/legal-library/browse/rules/wool-products-labeling-act-text, visited on 25-01-2026.

Fortune Business Insights, Cashmere Clothing Market Size, Share & Industry Analysis, by Product, by Demography, by Distribution Channel, and by Regional Forecast, 2025-2032. Available at: www.fortunebusinessinsights.com/cashmere-clothing-market-107398, visited on 23-01-2026.

McCaw Z.R., Dey R., Somineni H., *et al*. (2025) HGG Adv. 6(2):100406. doi.org/10.1016/j.xhgg.2025.100406

McGregor B.A. (2003) Aust. J. Exp. Agric. 43(10):1199-1209. doi.org/10.1071/EA01178

McGregor B.A. (2014) J. Text. Inst. 105(6):597-608. doi.org/10.1080/00405000.2013.828448

Misztal I., Tsuruta S., Lourenco D., *et al*. (2014) Manual for BLUPF90 family programs. Available at: https://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all.pdf, visited on 24-01-2026.

Pattie W.A., and B.J. Restall. (1989) Livest. Prod. Sci. 21(3):251-261. doi.org/10.1016/0301-6226(89)90054-7

Restall B.J., and Pattie W.A. (1989) Livest. Prod. Sci. 21(3):157-172. doi.org/10.1016/0301-6226(89)90046-8

Shumbusho F., Raoul J., Astruc J.M., *et al*. (2013) J. Anim. Sci. 91(8):3644–3657. doi.org/10.2527/jas.2012-6205

van der Westhuysen J. M. (2005). Small Rumin. Res. 60(1-2):215–218. doi.org/10.1016/j.smallrumres.2005.06.033

Wu C., Ma S., Zhao B., *et al*. (2023) BMC Genom. 24:428. doi.org/10.1186/s12864-023-09333-1