

New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website www.nzsap.org.nz

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

Share— copy and redistribute the material in any medium or format

Under the following terms:

Attribution — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

NonCommercial — You may not use the material for [commercial purposes](#).

NoDerivatives — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

BRIEF COMMUNICATION: Genetic parameters of stayability measures in a dairy goat herdM Wheeler^{a*}, BJ Foote^b and JF Foote^b^aAgResearch Ruakura, Private Bag 3123, Hamilton 3240, New Zealand; ^b859 Russell Road, RD 4, Hikurangi 0184, New Zealand

*Corresponding author. Email: mary.wheeler@agresearch.co.nz

Keywords: goats; Saanen; dairy; stayability; longevity**Introduction**

Doe longevity is an important factor in dairy goat farm productivity and sustainability, as the economic and environmental cost of raising replacement breeding animals per unit of milk production has less impact when spread over a longer period of return. Although stayability has been studied in sheep and cattle, there is little information regarding genetic parameters for longevity traits in New Zealand dairy goats.

The primary aim of this retrospective study was to obtain genetic parameters and breeding values for stayability in a New Zealand dairy goat herd. Several methods exist for measuring longevity, or stayability (McIntyre et al. 2012). Two main measures were used: age at final kidding, and survival from first kidding to each of several potential endpoints. Additionally, to determine whether producing triplets was causing does in this herd to “burn out” earlier, we examined the relationship between litter size and stayability. Litter size was defined in two ways: as number of kids born (NKB) and as triplets versus singles/twins (TripletYN).

Materials and methods

The longevity records in this study were from 4,910 Saanen does kidding from 1991 to 2011 inclusive, in a commercial dairy goat herd in Northland. Establishment, management and recording of this herd, as well as the genetic parameters of milk traits, reproductive traits and live weight, have been described by Morris et al. (1997, 2006, 2011). An index based on breeding values for kidding date and milk traits was used to select replacement does and future breeding bucks. Culling of adult does was primarily for commercial reasons, and culling rates were variable from year to year. Fates were not consistently recorded. Hence, unlike the study by McIntyre et al. (2012), no attempt was made in this analysis to distinguish between reasons for a doe exiting the herd, which may have been due to culling for commercial reasons such as poor health, conformation, reproduction status, or knowledge reasons based on recorded data and subsequent predictions of performance, or death.

Does failing to kid as yearlings were culled. In this herd, most does failing to get in-kid in subsequent years were also culled. Yearling kidding was taken as the starting point for longevity measurement. Only does who kidded at least once

were included in the data. The first longevity trait was age at final kidding, which was further defined as ‘actual’ or ‘projected’. The 4,088 does which either died or were culled during this twenty year period were assigned an ‘actual age at final kidding’. Using the method described by Brotherstone et al. (1997), does still alive in the herd, having kidded in 2011, were assigned a ‘projected age at final kidding’. The proportions of does in this herd that have historically survived from one age group to the next were used as a basis for the calculation. In this method, p_n is the probability of surviving to age $n+1$ of an animal which has survived to age n , and the expected lifespan of an animal which has survived to age n , is $n + p_n + p_n p_{n+1} + p_n p_{n+1} p_{n+2} + \dots$

Age at final kidding was analysed for the 4,088 does which had exited the herd. Projected age at final kidding, using the 4,088 actual and 822 calculated values, was analysed for all 4,910 does.

For the second group of analyses, six new traits were calculated. These binary traits were survival from first kidding to a series of end points: to the second kidding (Surv1-2), to the third (Surv1-3) and so on up to the seventh kidding (Surv1-7). If a doe was alive at a particular end point, she was scored as ‘1’, if dead she was scored as ‘0’, and if she was currently in the herd but had not yet attained this age, she was assigned a missing value.

Fixed effects and covariates were tested using least squares analyses (SAS 2004). For the longevity traits, sire, year of birth, birth rank, age of dam, and birth date were tested. Of these, only sire and year of birth were significant. Animal-model restricted maximum likelihood analyses were run using ASReml (Gilmour et al. 2009), with full pedigree data, to obtain genetic parameters and breeding values for these traits.

Number of kids born, especially triplet births, have only been consistently recorded in this herd from 2005 onwards. Hence, only kidding data from 2005 onwards was included, whilst still keeping all the longevity records. Litter sizes greater than three were coded as triplets. For the traits NKB and TripletYN, sire, year of birth, kidding year, age at kidding (1, 2, or 3+), age of dam and birth date were tested. Significant effects were sire, year of birth, kidding year and age at kidding. NKB and TripletYN were analysed using a repeatability model in ASReml, as single traits and in two-trait analyses with actual and projected age at final kidding. In the

Table 1 Estimates of heritability \pm standard error (in bold on the diagonal), genetic correlations \pm standard error (below the diagonal), and phenotypic correlations \pm standard error (above the diagonal) between age at final kidding, projected age at final kidding, number of kids born and triplets versus singles/twins.

Trait	Age at final kidding	Projected age at final kidding	Number of kids born	Triplets versus singles/twins
Age at final kidding	0.18 \pm 0.03	†	-0.03 \pm 0.02	0.01 \pm 0.02
Projected age at final kidding	†	0.13 \pm 0.03	-0.01 \pm 0.02	0.00 \pm 0.02
Number of kids born	-0.09 \pm 0.19	-0.04 \pm 0.18	0.09 \pm 0.02	†
Number of triplets versus singles/twins	0.09 \pm 0.20	-0.08 \pm 0.19	†	0.06 \pm 0.02

†ASREML analyses between these pairs of highly correlated traits did not run successfully

Table 2 Estimates of heritability \pm standard error (in bold on the diagonal), genetic correlations \pm standard error (below the diagonal), and phenotypic correlations \pm standard error (above the diagonal) between survival from 1 to 2 years of age (Surv1-2), 1 to 3 years of age (Surv1-3), 1 to 4 years of age (Surv1-4) and 1 to 5 years of age (Surv1-5).

Trait	Surv1-2	Surv1-3	Surv1-4	Surv1-5
Surv1-2	0.04 \pm 0.02	0.63 \pm 0.01	0.44 \pm 0.01	0.29 \pm 0.01
Surv1-3	0.69 \pm 0.19	0.05 \pm 0.02	0.73 \pm 0.01	0.52 \pm 0.01
Surv1-4	0.69 \pm 0.22	†	0.05 \pm 0.02	0.74 \pm 0.01
Surv1-5	0.44 \pm 0.24	0.86 \pm 0.11	0.96 \pm 0.07	0.10 \pm 0.03

†Correlation approached 1.0 and was unable to be estimated.

two-trait analyses, fixed effects for each trait were the same as those used in the single-trait analyses.

Results and discussion

Mean age at final kidding was 3.44 years, whilst the mean of projected age at final kidding was 3.78 years. The standard deviations of these traits were 2.19 and 2.20 years, respectively.

Age at final kidding was moderately heritable (\pm standard error), at 0.18 ± 0.03 (Table 1). Heritability of projected age at final kidding was lower, at 0.13 ± 0.03 . This was likely due to the uncertainty surrounding prediction of lifespan.

From 2005 to 2011, when litter size was consistently recorded, there were 8,218 NKB results. Almost all yearling does gave birth to either singles or twins (86% singles, 13% twins), 53% of two-year-olds gave birth to twins (45% singles, 3% triplets) and older does were more prolific again (31% singles, 57% twins, 11% triplets). Heritability estimates for the litter size traits were low, but significant. Repeatability estimates were 0.15 ± 0.01 and 0.14 ± 0.01 for NKB and TripletYN, respectively.

The genetic and phenotypic correlations between stayability and litter size traits were non-

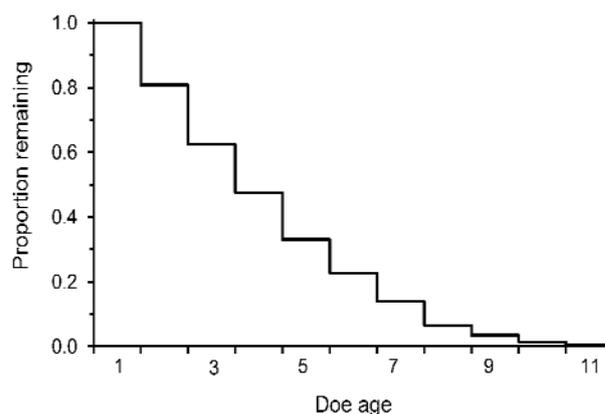
significant, and the sign of the correlations was not consistent. This would suggest that having triplets has no significant effect on a doe's stayability in this herd.

Table 2 shows the heritability estimates and genotypic and phenotypic correlations between survival from first kidding to endpoints of two, three, four and five years. Endpoints of six and seven years kidding were also analysed.

The three heritability estimates for survival to two, three or four years averaged 0.04 ± 0.02 , whilst those for survival to five, six or seven years averaged 0.10 ± 0.03 . Genetic and phenotypic correlations between these six traits were high, averaging 0.81 ± 0.14 and 0.49 ± 0.01 , respectively.

Figure 1 shows the proportion of does remaining after each kidding year. There is a fairly steep initial drop in numbers per cohort, of around 20% per year after the first, second and third kiddings. Only 23% of does remained in the herd for a sixth or subsequent kidding. Therefore, to get a good estimate of survival for individuals in this herd, the mean of the breeding values for Surv1-2, Surv1-3, Surv1-4 and Surv1-5 was calculated. Breeding values for the litter size traits were plotted against this mean, and again only a weak association was seen, albeit in the direction favouring higher litter size.

Figure 1 Proportion of does remaining in the herd ; each age



In conclusion, stayability measures in this herd had low to moderate heritability, and stayability measures to various endpoints were highly correlated. Using the available kidding data, there does not appear to be an unfavourable relationship between stayability and increased litter size. Future work should include an investigation of the relationships between stayability and other recorded traits in this herd, such as live weight and milk production traits, with a view to incorporating stayability into a revised selection index.

References

- Brotherstone S, Veerkamp RF, Hill WG 1997. Genetic parameters for a simple predictor of the lifespan of Holstein-Friesian dairy cattle and its relationship to production. *Animal Science* 65: 31–37.
- Gilmour AR, Gogel BJ, Cullis BR, Thompson R 2009. ASReml user guide release 3.0. VSN International, Hemel Hempstead, UK.
- McIntyre SB, Newman S-AN, Young EA, JC McEwan 2012. Genetic and phenotypic parameters for stayability in a New Zealand research flock. *Proceedings of the New Zealand Society of Animal Production* 72: 152–155.
- Morris CA, Wheeler M, Hosking BC, Watson TG, Hurford AP, Foote BJ, Foote JF 1997. Genetic parameters for milk yield and faecal nematode egg count in Saanen does. *New Zealand Journal of Agricultural Research* 40: 523–528.
- Morris CA, Wheeler M, Lanuzel M 2006. Genetic trend and parameter estimates for milk yield traits and kidding date in a Saanen goat herd in New Zealand. *New Zealand Journal of Agricultural Research* 49: 175–181.
- Morris CA, Wheeler M, Foote BJ 2011. Relationships between live weight and herd-test traits in a Saanen goat herd in New Zealand. *New Zealand Journal of Agricultural Research* 54: 315–320.
- SAS 2004. SAS/STAT 9.1 user's guide. SAS Institute Inc., Cary, North Carolina, USA.