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Small Ruminant Research 57 (2005) 175–186
Small Ruminant Research
www.elsevier.com/locate/smallrumres

Estimates of genetic parameters and genetic change for reproduction, weight, and wool characteristics of Rambouillet sheep☆

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Received 7 January 2004; received in revised form 15 June 2004; accepted 12 July 2004

Abstract

Records were for Rambouillet sheep from data collected from 1950 to 1998 at the U.S. Sheep Experiment Station, Dubois, Idaho, USA. Number of observations were 44,211 for litter size at birth and litter size at weaning, 35,604 for birth weight, 34,114 for weaning weight, 39,820 for fleece weight, 39,821 for fleece grade, and 3574 for staple length. Genetic parameters from both single- and two-trait analyses for prolificacy, weight, and wool traits were estimated using REML with animal models. Direct heritability estimates from single-trait analyses were 0.09 for litter size at birth, 0.06 for litter size at weaning, 0.27 for birth weight, 0.20 for weaning weight, 0.51 for fleece weight, 0.16 for fleece grade, and 0.58 for staple length. Estimates of direct genetic correlation between litter sizes at birth and weaning was 0.76 and between birth and weaning weights was 0.60. Estimates of genetic correlation between fleece weight and staple length was positive (0.45), but negative between fleece weight and fleece grade (−0.47) and between staple length and fleece grade (−0.52). Estimates of genetic correlations were near zero between birth weight and litter size at weaning, small and positive between birth weight and litter size at birth, and moderate and positive between weaning weight and litter size traits. Fleece weight, fleece grade, and staple length were slightly but negatively correlated with both litter size traits. Estimates of correlations between weight traits and fleece weight were positive and low to moderate. Estimates of correlations between weight traits and fleece grade were negative and small, while estimates between weight traits and staple length were positive and small. Breeding values from both single- and seven-trait analyses calculated using the parameters estimated from the single- and two-trait analyses were compared across years of birth with respect to genetic trends. Estimated breeding values averaged by year of birth from both the single- and seven-trait analyses for the prolificacy and weight traits increased over time, while those for fleece weight decreased and those for the other wool traits were unchanged. Estimated changes in breeding values over time did not differ substantially for the single- and seven-trait analyses, except for

☆ Published as paper no. 14469, Journal Ser., Nebraska Agric. Res. Div., Univ. of Nebraska, Lincoln 68583-0908.

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0921-4488/$ – see front matter
doi:10.1016/j.smallrumres.2004.07.003

traits highly correlated with another trait that was responding to selection (i.e., litter size at birth, which was highly correlated to both litter size at weaning and weaning weight).

Keywords: Genetic correlation; Heritability; Litter size; Prolificacy; Weaning weight

1. Introduction

Few long-term selection studies have been conducted with dual-purpose Western range sheep in the U.S. Lasslo et al. (1985) reported genetic improvement in Targhee sheep selected for weaning weight over 20 years, in a range environment. Burfening et al. (1993) found that 18 years of selection based on a reproductive index of lifetime number of lambs born resulted in a favorable response in Rambouillet range ewes. Ercanbrack and Knight (1998) showed that selection solely for litter weight of lamb weaned substantially increased lamb production with only minor penalties in wool production for four breeds of range sheep selected for a 12-year period. Although Sakul et al. (1999) reported only slight improvement in litter size and 120-day weight over a 30-year period for Targhee sheep in a range environment, the authors concluded that the response represented a potentially significant economic advantage. Analyses of Columbia and Targhee sheep selected concurrently with the Rambouillet sheep summarized in this paper indicated that both Columbia and Targhee sheep respond favorably to selection for weaning performance (Hanford et al., 2002, 2003).

The objective of this study was to document genetic trends in production traits of the Rambouillet breed at the United States Sheep Experiment Station (USSES), Dubois, Idaho, USA, over a 49-year period (1950–1998), where selection has been based on weaning performance under range conditions. The traits analyzed included prolificacy, weight, and wool traits. Another objective was to compare genetic trends for each trait estimated from either a single-trait analysis or from a seven-trait analysis.

2. Materials and methods

2.1. Animals and management

The Rambouillet breed, although originally developed in France as a wool breed, after importation in the mid 1800s (Dickson and Lush, 1933), was developed into a dual-purpose breed in the U.S. (Hultz and Hill, 1931). The Rambouillet was the foundation of most Western U.S. range flocks (Wentworth, 1948). The Rambouillet breed has been maintained and included in a variety of selection projects at the USSES (Ercanbrack and Knight, 1981, 1998) and is one of the foundation breeds used in development of the Columbia, Targhee and Polypay breeds (Terrill, 1947; Wentworth, 1948; Hulet et al., 1984). This population of Rambouillet sheep represents the longest time span (49 years) and the largest number of animals (approximately 44,000 lamb records) currently available for determining genetic parameters for the Rambouillet breed. Currently, few estimates of genetic parameters for the Rambouillet breed are available. Bromley et al. (2000) estimated genetic parameters using data collected from 1977 to 1996 from this population.

For 49 years (1950–1998), the Rambouillet breed at USSES was subjected to different selection criteria, all generally related to increasing weaning weight. Early in the period studied, selection favored wool and growth traits (approximately 1950–1969), followed by selection for individual lamb weaning weight and litter size (1969–1976), for weaning weight of the lamb or total litter weight weaned of the ewe (1976–1992) and finally for wool or total litter weight weaned (1992–1998). For many of these years, a random bred control line was also maintained. Lines were re-randomized when new selection criteria were imposed. Rams in control lines that were superior for the selection traits were often used in the appropriate selection lines. The effects of specific selection objectives could not be accounted for because of the re-randomization of breeding animals over the years of this study. The genetic trend in this flock, however, may represent general, but changing, selection emphases of the American sheep industry over this time period.

The number of records per trait, as well as unadjusted means and standard deviations, are presented in Table 1. Ercanbrack and Knight (1998) and Hanford