

## **FLOCK REFERENCING IN TASMANIA**

L.G. BUTLER<sup>1</sup>, G.M. HEAD<sup>1</sup> and B.C. RUSSELL<sup>2</sup>

<sup>1</sup>Department of Primary Industry, Fisheries and Energy  
P.O. Box 180  
Kings Meadows 7249

<sup>2</sup>Department of Wool and Animal Science  
University of New South Wales  
PO Box 1  
Kensington 2033

### **SUMMARY**

Flock referencing, which usually involves linked progeny tests of groups of rams, is promoted in Tasmania as a means by which commercial wool sheep breeders can, at reasonable cost, obtain performance comparisons between their flocks as well as estimating genetic progress achieved as a result of their breeding decisions. A total of six properties in Tasmania have participated to date, incorporating eight bloodlines referenced. The data from this limited sample of flocks indicate variable between flock levels of fleece weight, but remarkably uniform levels of live weight, yield and fibre diameter.

### **INTRODUCTION**

Flock referencing (Roberts et al. 1987a,b) is a method incorporating, in a relatively inexpensive manner, linked progeny tests in both stud and commercial flocks. In commercial flocks, this allows precise comparisons to be made between participating flocks across different locations and years. In particular, the system can be applied by commercial breeders to estimate the genetic progress achieved during the period between any two referencings. Further, it would be possible to estimate the relative genetic merit of the ram sources used by the commercial flocks. However, it is necessary to reference a sufficient number of commercial flocks based on each of the ram sources in order to provide a satisfactory sample of rams from those sources (Butler and Reid 1988). As a result, producers may then make a more informed assessment of the performance of their ram source, relative to that of other ram sources.

The Department of Primary Industry in Tasmania introduced flock referencing to the State to provide commercial breeders with a mechanism by which more informed assessments could be made of the efficiency of their breeding programs. This is seen as complementary to the use of information, such as performance records, supplied by the ram source (if they are kept and made available to the ram buyer). This paper presents the results of the flock referencing program conducted in Tasmania to date.

### **MATERIALS AND METHODS**

In 1987/88, commercial sheep breeders in Tasmania were invited to participate in a flock referencing scheme (Butler and Reid 1988). Flock referencing is essentially a progeny test of groups of rams. Each participant was required to divide a mob of 500 or more ewes into two random groups. Each of these mobs was then syndicate mated, either to the normal "home" rams or to a team of 10 "reference" (or link)

Table 1. Summary of information from flock referencing conducted in Tasmania. Bold figures in brackets are the amount by which the home flock exceeded the reference flock. Different superscripts within each flock comparison indicate statistically significant means ( $P < 0.01$ ). The number of fleece samples tested for yield and fibre diameter are given in the last column. Genotypic range is the range of differences in productivity between home and reference progeny

Location of home flock	Bloodline	No. of progeny	Body weight (kg)	Greasy fleece weight (kg)	Clean fleece weight (kg)	Fibre diameter ( $\mu\text{m}$ )	No. fleece samples tested
1.	Merino 1	157	34.9 <sup>a</sup> (-2.1)	4.66 <sup>a</sup> (-0.23)	3.65 <sup>a</sup> (-0.09)	22.3(+0.4)	50
	Reference	128	37.0 <sup>b</sup>	4.89 <sup>b</sup>	3.74	21.9	50
2.	Comeback 1	256	37.6(0.0)	4.40 <sup>ab</sup> (+0.06)	3.39 <sup>b</sup> (+0.01)	21.0 <sup>a</sup> (-0.02)	255
	Old Cobram	168	38.6(+1.0)	4.49 <sup>b</sup> (+0.15)	3.45 <sup>b</sup> (+0.07)	20.2 <sup>a</sup> (-0.79)	165
	Eloora	242	36.7(-0.9)	4.33 <sup>a</sup> (-0.01)	3.31 <sup>a</sup> (-0.07)	20.2 <sup>a</sup> (-0.77)	240
	Reference	113	37.6	4.34 <sup>a</sup>	3.38 <sup>a</sup>	21.0 <sup>b</sup>	107
3.	Egelabra	410			4.25 <sup>a</sup> (-0.36)		
	Reference	87			4.61 <sup>b</sup>		
4.	Corno	99	34.8(+1.5)	3.1 <sup>a</sup> (-0.3)		20.0(-0.1)	50
	Reference	120	33.3	3.4 <sup>b</sup>		20.1	49
5.	Comeback 2	174	30.9 <sup>a</sup> (-1.8)	4.05 <sup>a</sup> (-0.15)	3.19 <sup>a</sup> (-0.13)	23.2(+0.2)	50
	Reference	178	32.7 <sup>b</sup>	4.20 <sup>b</sup>	3.32 <sup>b</sup>	23.0	50
6.	Merino 2	259	29.5 <sup>a</sup> (-1.3)	3.18 <sup>a</sup> (-0.56)	2.39 <sup>a</sup> (-0.4)	18.2 <sup>a</sup> (-1.5)	259
	Reference	263	30.8 <sup>b</sup>	3.74 <sup>b</sup>	2.81 <sup>b</sup>	19.7 <sup>b</sup>	263
Genotypic range			3.6	0.71	0.47	1.9	
Phenotypic range			8.1	1.48	1.26	5.0	
Mean of home flock progeny			34.7	4.06	3.23	20.1	
Genotypic range as % of mean			10%	17%	15%	11%	
Phenotypic range as % of mean			23%	36%	39%	25%	

rams. The reference ram teams, very similar in average production, were provided by the University of New South Wales through its Falkiner Memorial Field Station at Deniliquin (Roberts et al. 1987a). These teams were selected from the ram drop of a randomly bred control flock in such a way that the average values of each selected team did not differ by more than 1% from the average fleece weight of the unselected drop. Data were analysed by a least squares analysis of variance procedure, based on the linear model  $Y_{ijk} = \mu + b_i + s_j + l_k + e_{ijk}$  where  $Y_{ijk}$  is the observation made on each animal,  $\mu$  is the mean,  $b_i$ ,  $s_j$  and  $l_k$  are the fixed effects of genotype, sex and location respectively, and  $e_{ijk}$  is the random residual effect specific to each observation.

## RESULTS

A total of six commercial breeders have participated to date and have referenced eight different bloodlines (Table 1). The phenotypic data and comparisons of the means of home flock ram progeny minus reference ram progeny are given in Table 1. Table 2 lists the genetic differences between genotypes (Egelabra was omitted due to paucity of data).

Table 2. Least squares means of four traits for seven bloodlines across six locations (number of records are given in Table 1)

Bloodline	Location	Body weight (kg)	Fleece weight (kg)		Fibre diameter ( $\mu$ m)
			greasy	clean	
Reference	1,2,4,5,6	32.1 <sup>11</sup>	4.03 <sup>a</sup>	3.29 <sup>acd</sup>	21.3 <sup>a</sup>
Merino1	1	30.0 <sup>bc</sup>	3.94 <sup>abd</sup>	3.20 <sup>a</sup>	21.7 <sup>a</sup>
Comeback1	2	32.1 <sup>11</sup>	4.08 <sup>ab</sup>	3.31 <sup>c</sup>	21.3 <sup>a</sup>
Old Cobram	2	32.9 <sup>ac</sup>	4.17 <sup>b</sup>	3.36 <sup>c</sup>	20.5 <sup>b</sup>
Eloora	2	30.7 <sup>b</sup>	4.02 <sup>a</sup>	3.23 <sup>d</sup>	20.5 <sup>b</sup>
Cormo	4	33.5 <sup>de</sup>	3.70 <sup>d</sup>	-	21.2 <sup>a</sup>
Comeback2	5	30.3 <sup>bc</sup>	4.14 <sup>ab</sup>	3.17 <sup>acd</sup>	21.5 <sup>a</sup>
Merino2	6	29.3 <sup>c</sup>	3.47 <sup>c</sup>	2.87 <sup>b</sup>	19.9 <sup>c</sup>
Mean		31.4	3.94	3.21	21.0
Genetic range as % of mean		13	18	15	9

<sup>1</sup>values with different superscripts are significantly different ( $P < 0.05$ )

## DISCUSSION

Due to the use of national reference ram teams in all locations, and adjustment for environmental effects, the differences observed in Table 2 are genetic in origin. Similarly, the difference in productivity between home flock and reference flock progeny (Table 1) is an estimate of the relative genetic differences between ram sources. The range of these differences indicate a remarkably uniform level of genetic productivity between the flocks in this small sample of Tasmanian flock genotypes. This is particularly so for yield, liveweight and fibre diameter, the range in genetic productivity being 2%, 10% and 11% respectively of the mean of the home flock values. The magnitude of the genetic differences between flocks in this work can be compared (Table 3) with between flock differences previously published. These figures compare with the phenotypic differences between home flocks (Table 1) which are considerably larger (2 to 2.5 times), indicating a substantial environmental effect.

Although there is only one flock using each bloodline, the small range of differences between flocks identified in this work is more remarkable given that the genotypes included both Merino and Comeback run in a variety of environments. However, there is the possible complication of heterotic effects influencing the results. In this respect, Comeback sheep in Tasmania generally have a very high proportion of Merino breeding in their background. Further Butler et al. (in preparation) have recorded some heterosis in growth, but little for wool traits, in Merino x Polwarth sheep in Tasmania. Genotype x environment interactions are also a potential bias to the results but cannot be determined in this work due to the lack of replication of the bloodline comparisons. However few such interactions of a significant magnitude have been published to date, suggesting that rankings would not be altered greatly.

Obviously the more bloodlines represented, the greater the value of the information generated. As more such comparisons are completed a library of information on a range of ram sources will be compiled. Using information such as this, commercial producers can evaluate, at a relatively low cost, whether the bloodline they are using is achieving the objectives they have set, and if not, which alternative bloodline may best serve their needs.

Table 3. Comparison of published values for between flock genetic differences in productivity (after Roberts et al. 1987b)

Character	% Difference Between Flocks		
	Tasmanian flock referencing	NSW Medium Peppin <sup>1</sup>	South African Merinos <sup>2</sup>
Liveweight	10	14	48
Greasy fleece weight	17	21	28
Yield	2	6	10
Clean fleece weight	15	24	29
Fibre diameter	11	7	17

<sup>1</sup>Atkins (1979)    <sup>2</sup>Poggenpoel and van de Merwe (1986)

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