Merino central test sire evaluation: medium wool (1989-1993) and fine wool (1990-1993).

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Merino Central Test Sire Evaluation: Medium Wool (1989 - 1993) and Fine Wool (1990 - 1993)

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Summary

Medium wool Merino Central Test Sire Evaluation (CTSE) has been conducted since 1987 in the NSW Riverina. Additional medium wool sites have since been initiated in NSW (Macquarie), Western Australia and South Australia. This report covers the presently available data from the Riverina (1989 - 1993), Macquarie (1990 - 1992) and Western Australia (1993) evaluations linked across years and sites by the use of common sires. South Australia will be linked to this group when their first evaluation (1995 drop) is available.

Fine wool Merino CTSE was initiated in the New England in 1990 and Victoria in 1992. This report includes all the available New England drops (1990 -1993), however no Victorian results are available at present.

CTSE has been developed to allow breeders to increase genetic progress by improved across flock selection of sires. A wide range of both measured and visually assessed traits are recorded to allow breeders with a wide range of objectives to benefit. The information allows participating breeders to benchmark their home tested sires performance to elite sires from throughout Australia.

The CTSE program provides the only objective comparisons of the genetic merit of rams from different studs which is independently conducted and publicly available to the industry.

The CTSE programs are primarily funded by participating breeders with the assistance of State and Australian Associations of Stud Merino Breeders, The University of New South Wales, NSW Agriculture, The Federation of Performance Breeders and Western Australia Department of Agriculture.

Keywords: Merino, sire evaluation, medium wool, fine wool.

Introduction

At present, Merino Central Test Sire Evaluation (CTSE) is conducted on medium wool sheep in the Riverina and Macquarie districts of NSW and more recently in Western Australia (Yardstick) and South Australia (Rosebank). Fine wool CTSE is being conducted in the New England district in NSW as well as Hamilton and Geelong in Victoria.

Common rams have been used across years and sites within the medium and fine wool sites to allow these sites to be compared. At present there are not satisfactory linkages between medium and fine wool sites to allow the two groups to be combined.

This paper is the annual update of the published medium wool results (Cottle et al. 1994a) with the addition of 1992 drop data from Riverina and Macquarie, as well as 1993 drop data from Riverina and Yardstick. This paper also updates the fine wool results (Cottle et al. 1994b). The Macquarie 1993 drop was not available for inclusion in the analysis due to a major loss of weaner progeny and the subsequent decision to terminate the evaluation of that drop.

Methods

At each Central Test site, the sires being evaluated were inseminated to an equal selection of about 60 commercial flock ewes representative of the strain of rams on test. Between 10 and 16 sires were evaluated at each site per year. All progeny at the site were managed equally and assessed for the traits considered important in the wool industry. All Central Test sites were located on independent properties and managed by local Committees with a majority of participating breeders. Technical representatives who carry out data analysis and presentation were involved to assist the committee where necessary. Each CTSE site has produced a report on the 1st (10 to 16 months of age) and/or 2nd (16 to 24 months of age) evaluations as they become available, with the exception of Hamilton Victoria (1992 drop) where there was no public release of the first evaluation pending second evaluation results being available. The sites provide their records to allow the combined analysis presented in this paper to be carried out.

While each site is independent, co-operation between all sites has ensured uniformity in the traits assessed and the method of assessment. This has been important in relation to visual assessment where the protocol had not been clearly defined previously (Casey 1992).

The major traits (as determined by the breeder representatives from all CTSE sites) have been analysed for this across site presentation. It is planned that fleece rot resistance, as defined by subjective scores, will be included in future years.

Presentation of results

The results are presented as

(i) Estimated Progeny Values (EPV) for greasy and clean fleece weight percentage, mean fibre diameter deviation and body weight percentage for both first and second evaluation. Where only one evaluation age was carried out, EPV's for that age are presented.

(ii) Percentages for sheep classer Top grade and Cull grade as a deviation from the average for both first and second evaluation. Conformation and Wool Quality traits are graded from high to low performance as, superior, good, average, poor and inferior.

EPV were derived using the BVest software (Gilmour 1993b), which is a multi-trait animal model BLUP program. Where first and second EPV's are combined into a single value for graphic presentation, equal weighting was given to both values. The calculation of EPV's accounted for the effects of type of birth (single, twin etc.), sex of lambs (male, female), and management group where appropriate.

Performance for classer assessed traits were analysed by least squares regression methods using REG (Gilmour 1993a). The model fitted to the classer grade, conformation and wool quality variables included classer (2 separate classers used), age at assessment, group and sire. The values reported are least squares sire group means in the case of classers grade and for Conformation and Wool Quality on 5% (+ , -) and 1% (+ +, - -) levels of significance above and below the mean.

Reliability of the EPV

The reliability of the EPV estimates for a sire is determined by the amount of information available on the sire through his progeny. Reliability increases with the number of progeny and the heritability of the trait. The EPV estimate includes reliability such that rams with low progeny numbers have their EPV moved (regressed) towards the average. The effect of numbers of progeny and heritability on accuracy and prediction error is described by James (1994).

Sires with less than 20 progeny (first or second evaluation) or 15 progeny (first and second evaluation) are not identified in the results as the accuracy (described as 'low') of their EPV are considered below the standard required by this public evaluation system. The EPV of sires with between 20 and 55 progeny (medium accuracy) may slightly increase or decrease with the addition of more information, while the EPV of sires with greater than 55 progeny (high accuracy) are unlikely to change. Figure 5 graphs the accuracy grades described above relative to the correlation between the 'true' and estimated progeny values.

EPV are presented relative to a fixed baseline which has the effect of maintaining over years a relatively stable EPV deviation for sires which are only assessed in one drop. The base line has been arbitrarily chosen as the average of the sires in the Hay, Deniliquin and Dubbo CTSE 1989 - 1991 for medium wools and New England 1990 - 1992 for fine wools. It is intended that these bases will be maintained.

Results

The results allow Merino sires evaluated at CTSE sites across Australia since 1989 to be accurately compared. CTSE performance can be used as,

(i) a benchmark by which the breeder or user of a sire can measure the industry status of a sire, and
(ii) an assessment of the genetic qualities of semen available for purchase for stud and flock improvement.

The use of Central Test sires in a well designed home test sire evaluation program will provide the links required to directly compare home tested sires with those from Central Test sires.

Merino Central Test Sire Evaluation results are not designed to define the 'best' sire as this very much depends on the breeding objective of each breeder. The results, however, have been presented in a format which may assist breeders to identify sires which may be suitable for their breeding objective.

Trait leaders are highlighted to assist breeders to identify high performing sires for a particular trait. All the qualities of a trait leader are however likely to be important to a breeder, therefore, the performance for other traits, apart from the trait in which the ram excelled, should be considered.

Fig. 1 (medium wool) and 3 (fine wool) graph CFW/FD and Fig. 2 (medium wool) and 4 (fine wool) graph Tops/Culls as a summary of performance for measured and visual assessment. The labels in the top left and bottom right on these graphs indicate the general way to read the performance described.

Table 1 (medium wool) and Table 2 (fine wool) present the following information;

The site:	The header on the tables describes the group, sites and years of drop in the results. Results are relative to all sires mated, including unlisted sires.
Graph code:	Allows a sire to be located on the graphs of CFW/FD and Tops/Culls (Figs. 1, 2, 3 and 4). Sires outside the limits of the graph have their location identified by an arrow.

Sire Code:	Allows the site and year a sire was first mated in CTSE to be identified by; Site (first digit): 1 = Hay, 2 = Deniliquin, 3 = Dubbo, 4 = New England, 5 = Yardstick (WA). Year (second digit): 9 = 1989, 0 = 1990, etc., Sire Number (last 2 digits): 01 = sire 1 for that site/year, etc. Some sires have been evaluated in more then one site and/or year. These are commonly sires with more than 55 progeny.
Sire Identity:	Sire Breeding Identity provides the stud who bred the sire and the sires identity number or name, eg. Boonoke (stud name) 9.1847 (number). Note that in some cases sires are not owned or entered by the breeder. Sires are listed in alphabetical order based on 'Sire Breeding Identity'.
Prog. No.:	Progeny number is the number of progeny from that sire from all sites and years in the analysis of measured traits.
Accuracy:	The general level of accuracy of a sires performance is described as either High, Medium or Low and follows the number of progeny in the tables. The analysis builds in a measure of accuracy into the performance records. Sires with a lower number of progeny being adjusted further toward the average. All procedures of management, recording, analysis and presentation are carried out so as to maximise accuracy of results.
Measured Assessment:	Estimated Progeny Values (EPV) are the units which describe the measured performance. EPV are expressed as deviations (dev) from the average of the base. EPV describe the expected performance of a sire's progeny relative to other sires in the evaluation. For example, a sire with a value of '+3.0' for GFW would be expected to have progeny that were 10% heavier for GFW, than a sire with a value of '-7.0' **Traits described**: GFW: Greasy Fleece Weight, CFW: Clean Fleece Weight, FD: Fibre Diameter, BWT: Body Weight. FD is described as microns, while all other traits are in percentage terms, ie. where the average is equal to 100 and 105% is a deviation of 5% (+ 5.0).

	1st and 2nd: The majority of Central Test sites evaluate progeny twice; first = 10 to 16 months evaluation, second = 16 to 24 months evaluation. When only one evaluation is carried out, only breeding values for that age are listed; for example, Yardstick has one evaluation at 18 months of age (2nd).
Visual Assessment:	**Top % & Culls %**: Classers grade all progeny as either 'Tops', 'Flocks' or 'Culls' based on their visual assessment of all traits. The two values for 'Tops %' and 'Culls %' express the values as deviations from the average of all sires. For example, a sire with '+12 % Tops', has 12% <u>more</u> top grade progeny than the average sire. A sire with '- 5% culls' has 5% less cull grade progeny.
	Conformation and **Quali**ty: The combined 1st and 2nd evaluation performance for conformation traits and wool quality traits, according to whether a sire has significantly above or below average performance on these trait groups. Above average: + + = superior, + = good; Below average: - = poor, - - = inferior. No score is average.
Unlisted Sires:	Sires with less than 20 progeny (1st or 2nd evaluation) and 15 progeny (1st and 2nd evaluation) are not listed as their results are considered below a minimum standard for accuracy.
	Some sites allow breeders to withhold the identity of a sire they have entered and in these cases the sire's performance is not published in these results.
Trait Leaders:	The top 10% of sires for the traits GFW, CFW, FD, BWT, Tops% and Culls% (based on combined 1st and 2nd test) are shown with a black background.

Index Performance

Table 3 and 4 presents index values for the top 10 sires in rank order on four indices which cover the range in fleece weight and fibre diameter breeding objectives commonly being used by industry (Atkins and Casey 1994). The indexes used are 2.5% micron premium (MP), 5% MP, 10% MP and 15% MP and are based on the Relative Economic Values (REV) proposed by Ponzoni (1993). The 2.5% MP option is equivalent to an objective that would increase fleece weight and maintain fibre diameter at its current level. The 15% MP value is intermediate between the 10% and 20% options presented by Ponzoni (1993). A 20% MP index would largely rank sires on FD as identified by the FD trait leaders.

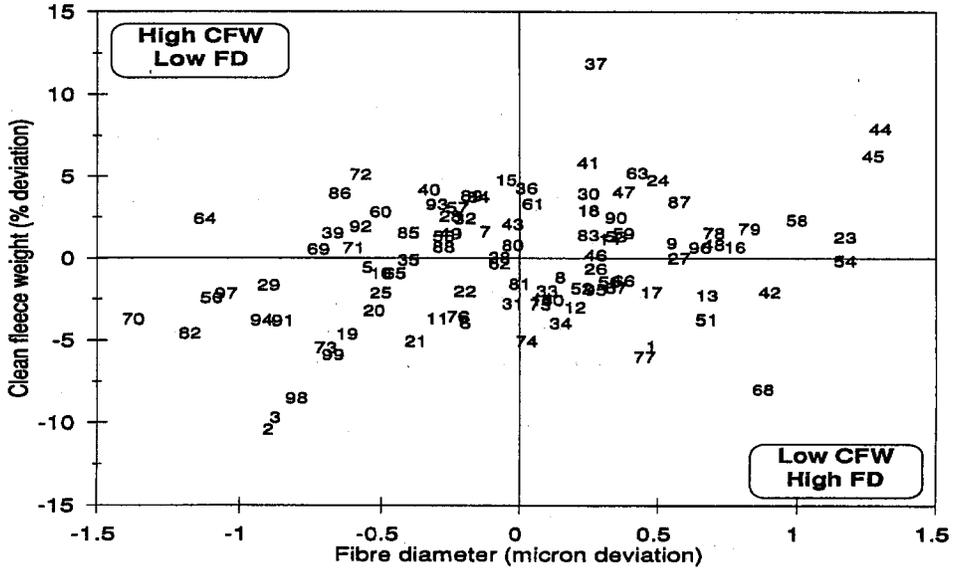**Fig. 1 Medium wool Sire Evaluation (1989-93) - Fleece wt / Fibre diameter EPV's**

Fig. 2 Medium wool Sire Evaluation (1989-93) - Classers tops / Culls grade
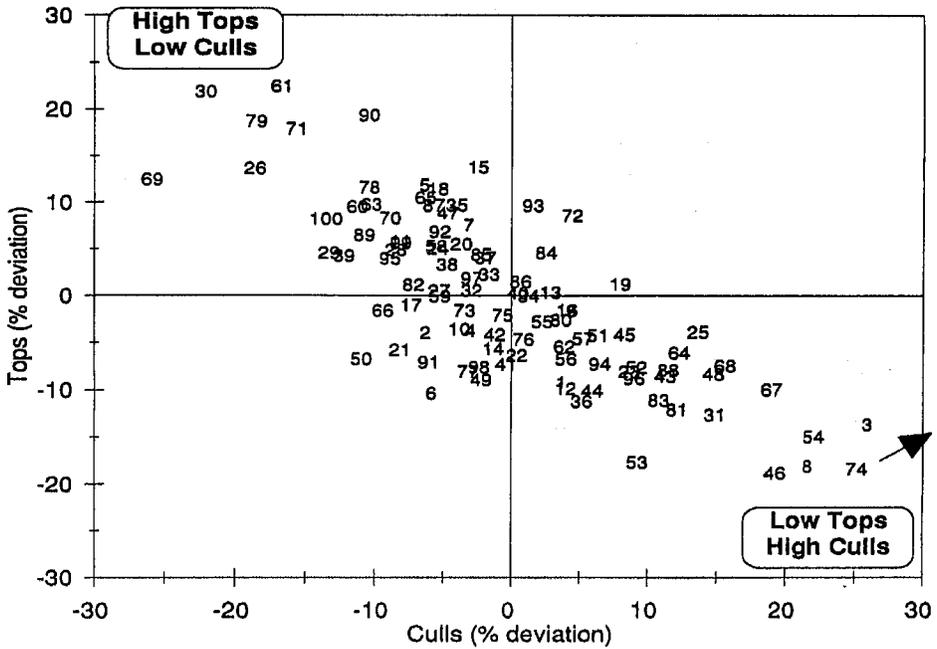
37

Allan E. Casey, K.D. Atkins, K.A. Coelli and D.J. Cottle — Merino central test sire evaluation: medium wool (1989-1993) and   37

Table 1 Medium wool: Hay(1989-91), Deniliquin(1989-93), Macquarie(1990-92), and Yardstick WA (1993)

Graph Code	Sire Code	Sire Breeding	Prog. No.- Accuracy	GFW % (dev) 1st	2nd	CFW % (dev) 1st	2nd	FD (dev) 1st	2nd	BWT % (dev) 1st	2nd	Tops % (dev) 1st	2nd	Culls % (dev) 1st	2nd	Conf.	Qual.
1	1904	AMS 4268	38 - M	-3.4	-6.3	-4.4	-6.3	0.6	0.3	9.4	8.7						·
2	1905	AMS 5414	42 - M	-5.3	-6.7	-9.4	-11.4	-0.8	-1.0	1.3	1.0						
3	1906	AMS GT 118	33 - M	-6.1	-13.2	-6.4	-13.0	-0.6	-1.1	1.4	2.8		-14		+26		·
4	1103	Avenel Oscar	27 - M	-0.5	-1.9	-1.9	-3.3	0.3	-0.1	-1.7	-2.6	-5	-2	+4	-10		
5	5310	Billandri 91.192	23 - M		-1.4		-0.7	-0.6	-0.6	-0.6	-0.6	+12	-10	-6	-6		
6	5303	Booloading 373	46 - M	0.6	-1.7		-4.7		-0.2		2.9	-5					· +
7	2306	Boonoke 9.1847	28 - M	0.6		2.0		-0.1		3.1		+8		-3	-6		
8	1001	Boonoke B2.807	21 - M	-1.7	-3.8	-0.6	-1.7	0.1	0.2	-0.1	-0.1	-15	-21	+17	+26		: +
9	2906	Boonoke B7.1273	24 - M	0.8	1.2	0.4	1.5	0.5	0.6	-3.5	-1.3	+8	-10	-3	+5		:
10	2002	Bungulla 4.178	29 - M	-2.0	-3.4	-1.6	-1.6	-0.3	-0.7	-3.6	-3.0	-1	-6	+8	-15		
11	3207	Burrungundy 4.87	25 - M	-3.8	-5.3	-3.1	-4.2	-0.3	-0.3	1.3	2.6	+1	+11	+6	-21	·	++
12	5307	Collinsville 244.721	47 - M	-4.7	-4.7	-3.5	-3.5	0.2	0.2	-4.5	-4.5	-10	-10	-5	+1		:
13	3201	Coonong 0.1	31 - M	-3.3	-3.5	-2.3	-2.2	0.6	0.7	5.1	4.4	0	+1	+7	-1		: :
14	2309	Coonong 26	20 - M	1.6		1.2		0.3		-0.1		-6		-1			
15	1909	Coonong 6.28	33 - M	5.4	8.6	3.1	6.5	-0.1	-0.0	1.8	1.4	+11	+14	-2	-2		
16	3103	Coonong 8.20	43 - M	1.3	1.9	0.3	1.1	0.8	0.8	1.5	0.9	-10	+7	-3	+11		:
17	3008	Coonong 8.33	54 - M	-3.8	-1.9	-3.4	-0.7	0.3	0.7	-1.4	0.6	-5	+3	-8	-6	+	:
18	1106	Coonong 8.82	17 - M	4.5	3.9	2.8	3.0	0.4	0.1	3.3	1.8	+22	+1	-7	-3		
19	3202	Cranbrook "Brian"	35 - M	-0.2	-4.8	-1.6	-7.6	-0.4	-0.8	-3.1	-2.5	+3	0	+4	+20		
20	2001	Cranmore Park 6.5	47 - M	1.2	-0.8	-1.6	-4.8	-0.5	-0.5	-0.3	0.2	+15	+22	-2	-5	·	
21	2201	Cranmore Park 7.1	39 - M	-3.4	-5.1	-4.4	-5.7	-0.4	-0.3	5.3	3.3	-5	-7	-11	-5	+	+
22	5309	Cranmore Park 9.2	36 - M	-2.8		-2.8	-2.5	-0.2	-0.2		4.5	-6	-6				
23	1913	Darajohn Red	69 - H	-2.6	2.9	-1.2	3.8	1.2	1.1	-3.2	-2.8	-10	-8	+7	+9		: ·
24	1908	Dunedin Park Regent	24 - M	2.6	4.4	4.0	5.6	0.3	0.7	-2.0	-0.7	-9	+5	-5	-5		++
25	2003	East Roseville Ross	26 - M	-1.8	-0.4	-2.1	-2.1	-0.6	-0.4	2.0	0.6	+11	+1	+12	+15		++
26	3204	GRASS 0.39	39 - M	0.2	1.7	-1.8	0.6	0.2	0.3	2.0	3.8	+1	+16		-29		:
27	2004	GRASS Sirius 6.1	83 - H	3.1	3.9	-0.2	0.2	0.6	0.5	1.4	1.5	+1	0	+4	-2	+	
28	1105	Goojgumbla 7.1	20 - M	3.3	1.7	3.4	1.7	-0.3	-0.2	-1.7	0.7	+11	-2	-7	-6		:
29	2209	Goojgumbla 8.125	27 - M	0.0	1.6	-1.8	-1.4	-0.4	-0.8	0.0	0.9	+2	+7	-14	-2		
30	2910	Goojgumbla True Blue	30 - M	1.8	5.6	2.5	5.4	0.1	0.4	4.5	6.8	+15	+22	-10	-17		:
31	1002	Goojgumbla True Blue Son	42 - M	-1.2	-2.6	-1.5	-4.0	-0.1	0.0	-0.6	-1.9	-10	-15	+11	+19		·
32	3007	Haddon Rig 6.17	54 - M	5.1	4.0	3.6	1.2	-0.3	-0.1	-0.2	-0.0	0	+1	-5	0	·	· +
33	3003	Haddon Rig 7.10	59 - M	-2.8	-3.7	-1.8	-2.1	0.0	0.2	0.5	0.7	+7	-2	-9	+6		·
34	3107	Haddon Rig 7.280	33 - M	-5.5	-5.3	-4.2	-3.7	0.1	0.2	1.7	1.6	-6	+6	-1	+4		

Table 1 (cont.)

Graph Code	Sire Code	Sire Breeding Identity	Prog. No.- Accuracy	GFW % (dev) 1st	GFW % (dev) 2nd	CFW % (dev) 1st	CFW % (dev) 2nd	FD (dev) 1st	FD (dev) 2nd	BWT % (dev) 1st	BWT % (dev) 2nd	Tops % (dev) 1st	Tops % (dev) 2nd	Cuts % (dev) 1st	Cuts % (dev) 2nd	Conf.	Qual.
35	3208	Haddon Rig 8.77	25 - M	0.5	-1.0	0.5	-0.7	-0.5	-0.3	-1.1	-0.1	+14	+6	-6	-1	-	+
36	5305	Haseley A1.65	20 - M		3.2		5.0		0.0	2.3	0.8		-11	+5	-5		
37	1709	Hazeldean 4.139	197 - H	7.9	9.9	10.6	13.2	0.2	0.3	1.3	-1.7	+4	+4	+5	+13	+	++
38	2909	Hazeldean 5.1312	21 - M	1.4	4.5	-0.9	1.0	-0.2	0.0	-1.8	-1.7	+4	+3	0	-5		
39	2005	Hazeldean 6.40	137 - H	2.4	0.8	2.3	0.8	-0.7	-0.7	-2.4	-2.7	+3	+4	+19	+11	‡‡	
40	2006	Hazeldean 7.64	24 - M	4.6	6.8	2.8	5.6	-0.1	-0.5	5.6	2.9	+4	+4	+4	+3	+	++
41	1003	Illawarra Y3	26 - M	5.3	6.7	5.6	6.1	0.3	0.2	-2.2	-3.4	+2	-16	-6	-9	+	+
42	5301	Karingal H472	32 - M		-3.0		-2.5	1.0	1.0	0.4	-2.7	+4	-16	-14	-10	-	
43	5312	Lewisdale 333	32 - M		-0.9		2.5	-0.0	-0.0	1.0	0.4			+11	+13	-	-
44	5308	Lewisdale 334	37 - M	9.7		9.1		1.4	1.4	11.6	11.9	-10	-10	+6	+6		+
45	5304	Lewisdale M111	32 - M	3.6		7.2				4.8	5.8	-4		+5	+9		
46	1004	Lone Pine 7.4	37 - M	-2.0	0.1	-0.6	1.0	0.3	0.3	0.1	-0.3	-18	-20	+18	+20	++	++
47	1910	Lowanna 7.1	38 - M	3.5	2.4	4.9	3.2	0.4	0.4	-0.3	-2.2	-1	-8	+7	+4		
48	1005	Lowanna Y454	35 - M	0.9	3.3	-0.2	1.9	0.7	0.7	-1.1	-1.2	-8	-9	+19	+11		+
49	1006	Meadow View 8.2	37 - M	1.8	1.3	1.2	1.8	-0.2	-0.3	1.2	-1.1	-7	-11	0	+4		
50	5311	Merino Tech 0187	29 - M		-2.4		-2.9		-1.2	0.8	0.8	-7	-7	-11	-11	‡‡	
51	3009	Mullengudgery 1308	34 - M	-4.0	-3.4	-4.2	-3.2	0.7	0.7	-1.3	-1.1	-2	-6	+7	+7		:
52	1813	N.R.F. 6.066	154 - H	-1.7	-2.6	-1.5	-2.2	0.3	0.1	3.2	3.0	-6	-9	+9	+10		:
53	1907	Old Ashrose 61	29 - M	1.2	-0.1	1.8	0.9	0.2	0.5	4.4	4.3	-18	-18	+9	+9		:
54	2008	Old Ashrose Angus	23 - M	-1.6	1.0	-1.3	1.0	1.0	1.3	1.0	1.9	-14	-16	+24	+21	-	-
55	2102	Old Ashrose M111	37 - H	1.5	-0.2	0.9	0.9	-0.3	-0.3	3.4	4.7	-4	-1	+5	+9	-	:
56	2101	Old Ashrose PCC 146	22 - M	2.7	-1.2	0.5	-3.4	0.5	0.2	6.5	4.3	-9	+4	+5	+13		
57	1008	Old Cobran Big Mac	24 - M	1.0	1.7	2.7	3.5	-0.4	-0.1	1.2	0.8	+8	-8	+6	+4	+	++
58	1903	Old Cobran Snowball	37 - M	0.6	1.3	2.4	2.3	0.8	1.2	-3.6	-3.2	-1	+5	+7	+5		
59	1911	One Oak 00.400	36 - M	1.3	0.8	1.3	1.8	0.3	0.4	0.7	0.1		0		-5		
60	2007	One Oak 009	26 - M	-0.0	1.8	1.4	4.3	-0.5	-0.5	0.7	0.5	+6	+14	+7	+7	+	++
61	1104	One Oak Atlas 438	19 - M	2.3	1.6	3.7	2.9	0.0	0.1	1.6	0.5	+24	+21	-27	-17		++
62	1007	One Oak G2	42 - M	-0.7	-0.6	-0.8	0.2	-0.1	-0.1	-1.7	-2.3	-9	-2	-7	-13		++
63	2206	One Oak Poll 3	48 - M	4.0	7.2	3.9	6.6	0.4	0.4	-1.3	-1.8	+8	+11	+6	+3		++
64	5306	Parakeelya 141	35 - M		5.8		2.8		-1.3	1.8	1.8			+24	+21	-	:
65	3006	Pemraw 6.123	115 - H	-1.4	-1.1	-0.9	-1.0	-0.3	-0.6	-1.2	-1.6	+9	+12	-6	-6	+	++
66	1902	Pooginook 4.2	35 - M	-2.9	-1.0	-2.2	-0.5	0.4	0.4	0.7	1.3	+9	-2	-6	-9	+	++
67	1009	Pooginook 8.11	45 - M	-1.7	-2.7	-1.2	-2.4	0.2	0.5	-1.1	-2.2	-10	-10	+19	+20	+	++
68	2205	Rambouillet	28 - M	-6.0	-8.9	-6.7	-9.2	0.8	0.9			-6	-9	+12	+20	+	:

Table 1 (cont.)

Graph Code	Sire Code	Sire Breeding Identity	Prog. No- Accuracy	GFW % (dev) 1st	2nd	CFW % (dev) 1st	2nd	FD (dev) 1st	2nd	BWT % (dev) 1st	2nd	Tops % (dev) 1st	2nd	Culls % (dev) 1st	2nd	Cont.	Qual.
69	3205	Roseville Park 0.938	48 - M	-0.2	-2.0	0.9	0.2	-0.6	-0.8	-1.3	-1.7	+8	+17	-20	-31	++	++
70	2104	Roseville Park 0133	77 - H	-2.5	-2.6	-3.4	-4.0	-1.1	-1.6	-4.3	-4.3	0	+17	-6	-12	++	++
71	2108	Roseville Park 1232	48 - M	1.7	0.2	0.9	0.3	-0.6	-0.6	-0.3	1.1	+4	+32	-15	-16		++
72	3104	Roseville Park 3253	58 - M	4.8	5.9	4.2	6.1	-0.6	-0.6	-3.2	-4.4	+4	+14	+3	+7		
73	3110	Roseville Park 7470	25 - M	-0.2	-5.1	-3.2	-7.7	-0.6	-0.8	1.3	-0.5	-12	+8	0	-7		
74	3002	Roseville Park 912	46 - M	-3.8	-4.2	-4.7	-5.4	-0.6	0.2	-3.4	-3.6	-20	-12	+33	+27		
75	1101	Somerset M302	19 - M	-2.9	-0.4	-3.2	-2.4	0.1	0.1	0.4	1.9	-7	+3	+2	-3		
76	2912	Strathcluan W305	140 - H	-1.3	4.1	-2.3	-4.9	-0.0	-0.4	1.2	2.0	+3	+3	0	+2	,	
77	5302	Sunny Valley 7	33 - M	3.1	-1.1	1.5	-7.1		0.5		0.1	-5	-8	+8	-3		+
78	3101	Sunset 555	54 - M	3.1	2.9	1.6		0.6	0.8	1.4	2.2	+4	+20	-11	-9	+	++
79	3206	Sunset 9.14	35 - M	5.0	1.7	3.4	0.2	0.8	0.9	-0.7	-2.4	+28	+9	-21	-16	++	++
80	2203	The Grange 03014	15 - M	4.7	3.8	1.1	0.5	-0.1	0.1	1.5	-0.1	+4	-9	+1	+7		
81	2204	The Grange 05253	33 - M	-0.1	-2.2	-0.4	-2.7	-0.1	0.1	-0.8	-2.7	-10	-14	+11	+13		
82	2202	The Grange 82325	20 - M	-2.4	-6.7	-2.6	-6.5	-1.1	-1.3	-3.0	-4.8	-1	+3	+8	-17		:
83	2106	The Grange G2	16 - M	0.4	0.2	1.7	1.1	0.1	0.4	-2.5	-3.1	-14	-8	+6	+16		
84	2107	The Grange GR80068	22 - M	0.4	3.5	2.5	5.1	-0.2	-0.1	-3.6	-4.1	0	+9	+4	+1		++
85	2105	The Grange GR80100	29 - M	-1.3	-0.1	1.0	2.1	-0.6	-0.2	-5.3	-4.1	+1	+8	-6	+2		++
86	2911	Uardry Windermere	28 - M	1.7	4.1	2.6	5.4	-0.6	-0.7	-3.1	-2.2	+1	+2	+1	+1		++
87	1102	Wanganella pep5.1121	34 - M	1.7	4.1	2.3	4.7	0.3	0.8	-5.1	-2.1	-1	+20	+3	-14		:
88	2904	Wanganella pep6.377	53 - M	-0.3	-0.8	0.5	0.9	-0.3	-0.2	-0.0	0.9	-5	-10	+5	+19		
89	2901	Wanganella pep6.596	192 - H	2.7	-2.3	5.3	2.4	-0.2	-0.1	-1.8	-3.9	+8	+5	-14	-7	+	++
90	2902	Wanganella pep7.1272	20 - M	1.2	2.5	1.6	3.4	0.5	0.2	1.1	0.6	+4	-9	+1	+7		
91	2903	Wanganella pep7.1356	50 - M	-5.1	-8.8	-2.2	-5.4	-0.7	-1.0	-0.8	0.9	-10	-14	+11	+13		
92	2207	Wanganella pep8.332	32 - M	-2.4	-0.5	0.3	3.6	-0.5	-0.7	0.0	-1.8	-1	+3	+8	-8	:	+
93	2208	Wanganella pep9.3316	36 - M	1.7	1.0	3.5	3.1	-0.3	-0.3	-2.5	-2.8	+16	+4	+6	+16		
94	2210	Willandra 6.3	55 - M	-2.1	-3.9	-2.9	-4.6	-0.9	-1.0	0.1	0.3	+4	-10	+11	+2	,	
95	1912	Willandra Wes	52 - M	-3.9	-1.4	-2.8	-1.0	0.0	0.5	-0.9	0.7	-12	+4	-9	+4		:
96	1010	Willurah 6.1	41 - M	1.2	-1.2	1.7	-0.3	0.6	0.7	5.9	4.4	+4	-14	+8	+11		+
97	2103	Woolaroo 052	29 - M	-0.7	-2.8	-1.1	-3.2	-0.9	-1.2	0.8	1.8	-11	0	+3	-2		+
98	2010	Woolaroo Blue 203	32 - M	-6.4	-4.7	-8.6	-8.4	-0.7	-0.9	-3.6	-2.0	+4	+4	+8	-12	:	:
99	2011	Woolaroo Blue 237	40 - M	-4.2	-6.1	-4.7	-7.1	-0.6	-0.7	2.1	2.7	-5	+16	-7	-9	,	++
100	3209	Wyuna 6.10	31 - M	-3.3	-4.9	-1.7	-3.4	0.3	-0.1	1.5	1.3	+9	+7	-14	-13	++	++

Fig. 3 Finewool Sire Evaluation (1990-93) - Fleece wt / Fibre diam EPV'S
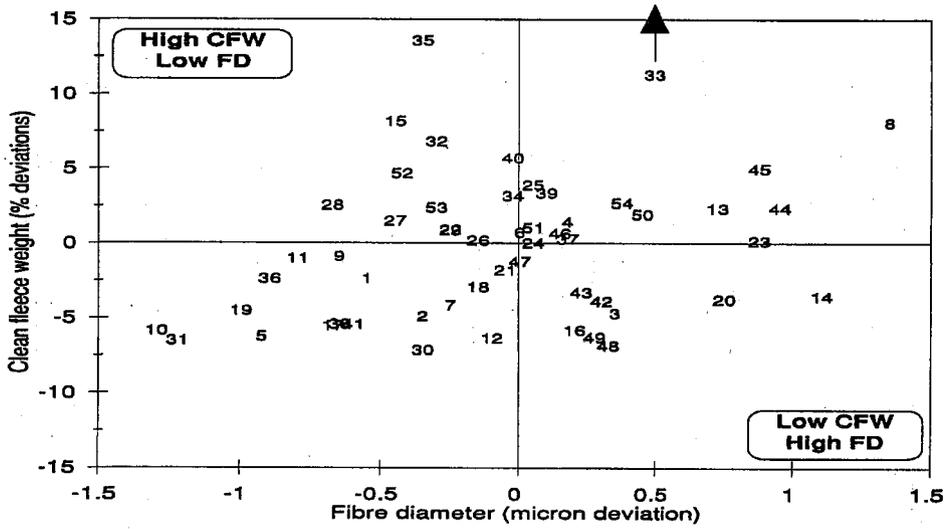
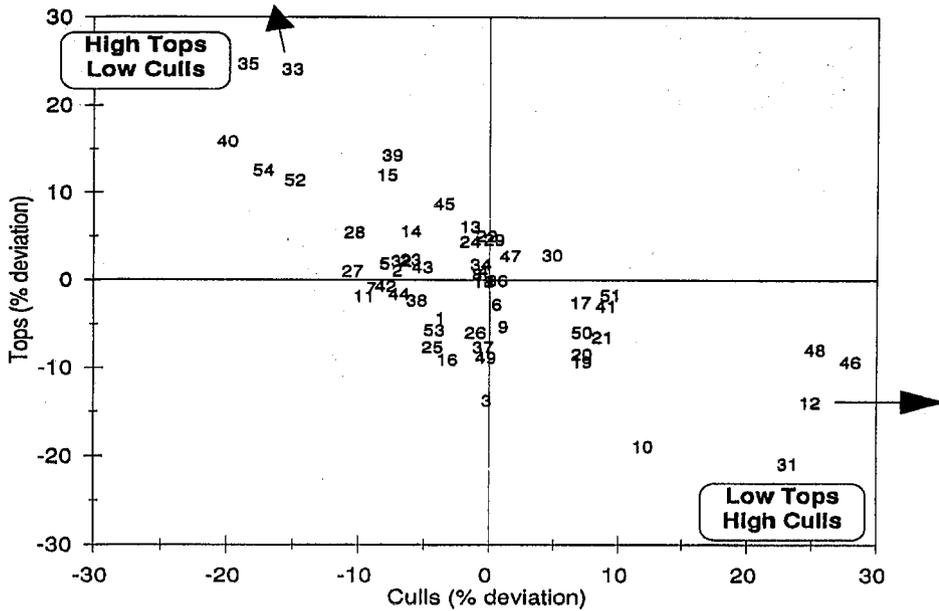**Fig. 4 Fine wool Sire Evaluation (1990-93) - Classer tops / Culls grade**

Allan E. Casey, K.D. Atkins, K.A. Coelli and D.J. Cottle

Table 2 Fine wool New England(1990-93)

Graph Code	Code Code	Sire Breeding Identity	Prog. No.- Accuracy	GFW % 1st	2nd	CFW % 1st	2nd	FD (um) 1st	2nd	BWT % 1st	2nd	Tops % (dev) 1st	2nd	Culls % (dev) 1st	2nd	Conf.	Qual.
1	4308	Alfoxton 0192	29 - M	-2.8		-2.3		-0.5		2.7		-4		-4		-	
2	4204	Auchen Dhu Blue 205	37 - M	-6.5	-7.9	-4.2	-5.5	-0.3	-0.4	-2.6	-3.0	+4	-2	-9	-5		++
3	4114	Auchen Dhu Orange 112	31 - M	-2.4	-4.9	-2.8	-6.5	0.4	0.4	-0.9	-1.4	-14	-14	-3	+3		
4	4003	Auchen Dhu Red 13	52 - M	2.2	0.4	2.6	0.3	0.1	0.3	2.7	2.5	+6	-4	-2	+1		
5	4115	Bullamalita Super Johnny	24 - M	-5.2	-5.9	-5.6	-6.8	-0.7	-1.1	-1.7	-1.0	-6	+10	+3	-18		++
6	4303	CSIRO 0289L 8484	29 - M	-0.7		0.8		0.0		1.4		-3		+1		-	
7	4302	CSIRO 91A 0619	35 - M	-3.0		-4.1		-0.2		4.7		-1		-9			
8	4014	East Roseville 2299	24 - M	6.3	7.8	7.1	9.2	1.1	1.7	-3.3	-2.6	+1	+1	-1	0		- -
9	4314	East Roseville 3178	38 - M	0.6		-0.8		-0.6		3.5		-5		+1			
10	4111	Europambela Blue 308	31 - M	-4.4	-6.4	-4.4	-7.2	-1.2	-1.4	-1.2	-0.9	-19	-19	+9	+15	-	-
11	4306	Europambela Blue 742	41 - M	1.4		-1.0		-0.8		0.6		-2		-9			
12	4214	Europambela Blue 980	35 - M	-5.3	-4.1	-6.5	-6.2	-0.1	-0.1	-3.3	-1.5	-11	-18	+31	+38	- -	- -
13	4212	Gianna 19 RM	22 - M	1.0	3.6	1.2	3.5	0.7	0.8	-1.8	-0.4	+10	+2	+5	-7		
14	4007	Grathlyn Super Blue	46 - M	-1.3	-3.3	-2.0	-5.1	1.3	0.9	0.1	-0.9	+5	+6	-9	-3	+	++
15	4207	Hazeldean 7.1048	28 - M	11.1	10.5	8.9	7.5	-0.4	-0.4	4.2	2.2	+22	+2	-11	-4	++	-
16	4108	Lorelmo 108	25 - M	-4.0	-5.2	-4.8	-6.8	0.2	0.2	0.4	0.7	-18	0	+4	-10		++
17	4206	Lorelmo E31.1709	17 - M	-7.0	-7.9	-5.2	-5.7	-0.5	-0.8	-0.1	0.3	+4	-9	+7	+7	-	
18	4012	Lorelmo J4	27 - M	-1.9	-3.1	-1.9	-3.9	-0.2	-0.1	-0.9	0.5	+2	-3	+2	-2		++
19	4208	Lorelmo S4.1523	36 - M	-5.6	-9.7	-3.1	-5.8	-0.9	-1.1	-0.6	-2.1	-4	-14	+7	+8	- -	+
20	4209	Merrignee Brilliant 1	30 - M	-2.7	-5.2	-2.7	-4.8	0.6	0.9	-3.1	-4.6	-5	-12	-4	+19	- -	
21	4312	Merrignee Brill. Ex. 170	34 - M	-3.2		-1.8		-0.0		-0.1		-6		+9		- -	
22	4113	Merrignee P2	26 - M	-0.4	1.5	-0.4	2.3	-0.3	-0.2	-0.2	-0.5	-4	+14	+4	-4		++
23	4010	Miramoona 698	30 - M	0.8	0.4	0.6	-0.2	0.8	1.0	2.7	2.5	+7	-2	-6	-6		-
24	4008	Miramoona 703	26 - M	-1.6	1.7	-2.1	2.2	0.1	0.0	3.4	3.2	+5	+4	-3	+1	+	
25	4106	Miramoona 812	25 - M	3.1	3.3	3.7	4.2	0.1	0.1	0.7	0.1	-12	-3	-8	-1		-
26	4201	Mirani 108.7	27 - M	0.7	0.2	-0.2	0.6	-0.1	-0.2	-0.9	-1.4	-4	-8	-4	+2		
27	4304	Mirani 174.9	41 - M	0.9		1.5		-0.4		-1.5		+1		-10			

Merino Central Test Sire Evaluation

Table 2 (cont.)

Graph Code	Code Code	Sire Breeding Identity	Prog. No.-Accuracy	GFW % 1st	GFW % 2nd	CFW % 1st	CFW % 2nd	FD (um) 1st	FD (um) 2nd	BWT % 1st	BWT % 2nd	Tops % (dev) 1st	Tops % (dev) 2nd	Culls % (dev) 1st	Culls % (dev) 2nd	Conf.	Qual.
28	4001	Mirani 214.5	117 - H	2.5	2.9	2.4	2.8	-0.6	-0.7	-2.2	-2.8	+7	+4	-8	-13		++
29	4107	Mirani 220.7	28 - M	0.6	0.5	0.9	0.9	-0.3	-0.1	0.6	-1.3	-1	+10	+4	-3		
30	4009	Mirani 95.2	27 - M	-5.8	-6.1	-6.7	-7.5	-0.2	-0.4	1.0	-0.4	+5	+1	+5	+6		
31	4110	Moutere (NZ) Silky	29 - M	-6.9	-5.1	-7.5	-5.5	-1.0	-1.4	-1.6	-1.5	-22	-20	+25	+22	- -	- -
32	4205	Nerstane 27	35 - M	7.6	3.7	8.5	5.2	-0.4	-0.2	3.0	1.9	+4	0	-13	0		
33	4109	Nerstane 225	63 - H	15.5	15.1	17.6	18.3	0.4	0.7	3.7	2.7	+38	+25	-20	-14	++	++
34	4213	Nerstane 473	21 - M	2.5	4.3	2.1	4.3	-0.1	0.1	-2.5	0.2	+6	-2	-4	+3		
35	4015	Nerstane 697	53 - M	10.8	15.2	10.6	16.6	-0.5	-0.2	-0.0	-2.2	+23	+26	-21	-15	++	+
36	4310	One Oak 00/B55	27 - M	-2.5		-2.3		-0.9		-0.2		0		+1			
37	4116	One Oak 0032	36 - M	-1.5	1.6	-1.7	2.3	0.0	0.4	-5.2	-4.3	-13	-2	+4	-4		
38	4005	Petali 556	30 - M	-4.7	-4.9	-5.1	-5.7	-0.5	-0.7	-2.3	-1.7	-6	+1	-4	-7		+
39	4013	Roseville Park 69	22 - M	2.3	3.1	2.8	3.9	-0.0	0.3	0.7	1.5	+14	+15	-15	+1	++	
40	4006	Ruby Hills 225	22 - M	4.7	4.6	5.6	5.9	0.0	-0.0	2.1	0.2	+18	+14	-15	-24		++
41	4307	Ruby Hills 6548	41 - M	-6.8		-5.4		-0.6		-4.1		-3		+9		- -	
42	4104	Ruby Hills 6602	35 - M	-4.0	-2.2	-4.7	-3.0	0.4	0.3	-0.3	1.9	-8	+7	+1	-16		
43	4210	Ruby Hills 82149	31 - M	-6.1	-4.9	-4.2	-2.3	0.2	0.3	1.8	2.1	+1	+2	-8	-1		
44	4309	Saumaraz 0.427	41 - M	1.9		2.4		1.0		3.1		-2		-7		+	- -
45	4203	Saumerez 8.1182	33 - M	4.1	7.1	3.9	6.1	1.1	0.7	0.7	0.8	+11	+7	-10	+3	++	- -
46	4311	Shalimar Park 919	33 - M	-1.6		0.7		0.2		-7.0		-9		+28		- -	
47	4004	Sierra Park Urq 64	21 - M	-0.7	-1.3	-0.7	-1.7	0.1	-0.1	0.7	1.6	+11	-5	-1	+4		+
48	4211	Winton 515/6339	31 - M	-3.8	-4.7	-5.7	-7.9	0.3	0.4	-1.4	0.7	-3	-13	+23	+28	-	- -
49	4112	Winton Trump	23 - M	-4.4	-5.6	-5.2	-7.3	0.3	0.3	-0.9	-0.4	-20	+2	+8	-8		
50	4202	Woolaroo 237	29 - M	3.1	6.1	1.2	2.7	0.4	0.5	2.2	2.5	+3	-15	+6	+9	+	- -
51	2010	Woolaroo Blue 203	28 - M	1.3	0.5	1.5	0.6	0.1	0.1	2.3	0.7	+2	-5	+10	+10		-
52	4103	Yalgoo 644	30 - M	3.8	3.6	4.7	4.8	-0.3	-0.5	4.7	5.5	+8	+15	-12	-17	++	+
53	4301	Yalgoo 924	40 - M	2.0		2.4		-0.3		1.5		-6		-4			
54	4002	Yalgoo 942	24 - M	2.1	2.6	2.4	3.0	0.4	0.4	1.1	0.6	+22	+4	-18	-16	+	

Table 3 Medium wool CTSE sires ranked (top 10) on 2.5%, 5%, 10% and 15% Micron Premium index values

Index: 2.5% Micron Premium		Index: 5% Micron Premium	
Sire Identity	Value	Sire Identity	Value
Hazeldean 4.139	147.3	Hazeldean 4.139	143.8
Lewisdale 334	134.9	Parakeelya 141	131.7
Lewisdale 9.77	130.3	Hazeldean 7.64	126.7
Goolgumbla True Blue	128.4	Goolgumbla True Blue	125.2
Hazeldean 7.64	122.9	Uardry Windermere	122.3
Coonong 6.28	121.8	Coonong 6.28	122.2
Haseley A1.65	121.2	Haseley A1.65	120.8
Parakeelya 141	118.1	Roseville Park 3253	120.6
Old Ashrose M111	116.2	One Oak 009	120.6
Dunedin Park Regent	115.5	Old Ashrose M111	119.4
Index: 10% Micron Premium		**Index: 15% Micron Premium**	
Parakeelya 141	152.0	Parakeelya 141	172.3
Hazeldean 4.139	138.6	Woolaroo 052	151.2
Uardry Windermere	134.0	Merino Tech 0187	150.4
Hazeldean 7.64	132.4	Roseville Park 0133	149.2
Woolaroo 052	132.3	Uardry Windermere	145.0
Roseville Park 3253	130.9	Goolgumbla 8.125	143.0
Merino Tech 0187	130.5	Roseville Park 3253	141.1
One Oak 009	129.5	One Oak 009	138.4
Goolgumbla 8.125	126.8	Hazeldean 7.64	138.1
Roseville Park 1232	125.6	Roseville Park 0.938	136.8

Table 4 Fine Wool CTSE sires ranked (top 10) on 2.5%, 5%, 10% and 15% Micron Premium index values

Index: 2.5% Micron Premium		Index: 5% Micron Premium	
Sire Identity	Value	Sire Identity	Value
Nerstane 225	173.2	Nerstane 225	167.3
Nerstane 697	150.7	Nerstane 697	155.1
Hazeldean 7.1048	138.4	Hazeldean 7.1048	143.7
Yalgoo 644	131.1	Yalgoo 644	136.2
Nerstane 27	131.1	Nerstane 27	134.6
Ruby Hills 225	122.8	Ruby Hills 225	122.9
East Roseville 2299	121.4	Mirani 214.5	115.6
Saumarez 8.1182	117.5	Yalgoo 924	114.7
Roseville Park 69	115.8	Miramoona 812	114.6
Miramoona 812	115.3	Roseville Park 69	114.5
Index: 10% Micron Premium		**Index: 15% Micron Premium**	
Nerstane 697	161.8	Nerstane 697	168.5
Nerstane 225	158.5	Hazeldean 7.1048	159.8
Hazeldean 7.1048	151.7	Yalgoo 644	151.4
Yalgoo 644	143.8	Nerstane 225	149.6
Nerstane 27	139.9	Nerstane 27	145.2
Mirani 214.5	127.7	Europambela Blue 308	144.1
Ruby Hills 225	123.2	Mirani 214.5	139.8
East Roseville 3178	122.4	One Oak 00/B55	137.3
Europambela Blue 742	122.1	Europambela Blue 742	136.5
One Oak 00/B55	121.0	Moutere (NZ) Silky	136.1

Figure 5

Accuracy Grades (Low, Medium & High)

and

Correlation between: "True" (infinite number of progeny) and "Estimated" (number of progeny tested) Progeny Values
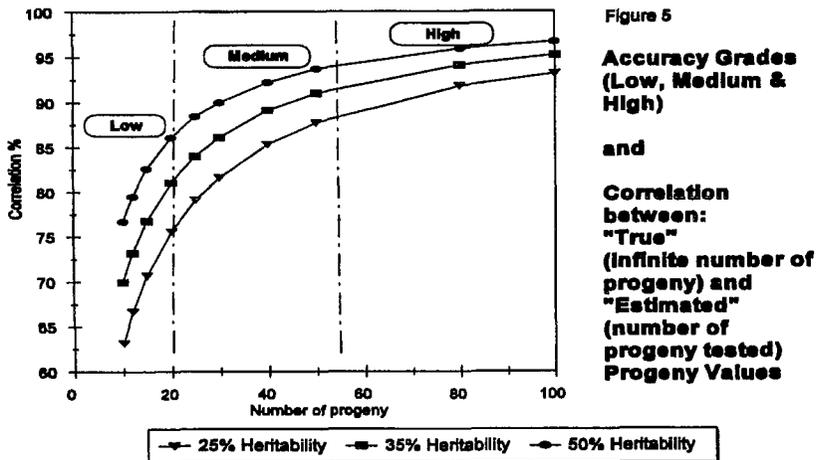
Discussion

The results reported provide the performance for the traits considered important by the majority of breeders. This therefore allows a breeder to identify sires which would have high performance for any particular breeding objective. Other traits not in this report and of importance to a breeders objective are likely to be reported in a sire's test site report. The high performing sires selected from this combined report can be considered for the additional traits using the site report. The drop a sire was evaluated in can be identified by the 'sire code'.

The genetic improvement which will flow from CTSE to the industry will be significant for two reasons. Firstly, CTSE can accurately identify superior sires from different sources. Secondly, many sires in CTSE have originated from flocks which were not recognised semen sources. This means that the Australian wool industry would not have identified these sires by chance through the systems available prior to CTSE being established.

The inability to combine medium and fine wool CTSE groups using internal links is an impediment to a significant and growing number of medium wool breeders with an objective to reduce fibre diameter. Both the necessary use of common sires and further development of analysis procedures are required to allow fine and medium CTSE groups to be accurately linked.

The recording of sire performance based on a combination of traits (index) will become increasingly important as the number of sires in the evaluation increases and breeders need a system to rationalise the amount of information considered. Breeders

need to be encouraged to develop their own breeding objective to allow them to use an index which accurately reflects their requirements (Atkins et al. 1994) and even more importantly to gain confidence in indices as a valuable system to assist their breeding program. Once breeders have a personalised index they should utilise the services available to calculate index performance for measured traits. Historical MP values which could be considered when developing a personalised breeding objective can be identified (Atkins et al. 1994 and Cottle 1995). Cottle (1995) suggested 10% and 20% indices were appropriate for general use by the medium and fine wool schemes respectively.

An index will remain limited in its ability to provide a measure of the value of sires while the traits being assessed visually in CTSE are not included in the index, as the great majority of breeders use a significant level of their selection emphasis on these traits (Atkins and Casey 1994). The lack of visually assessed traits in the index options may also signal to breeders a significant bias toward measured traits, which while not the case, could alienate some breeder who may otherwise benefit from the technology. There is a pressing need for both the heritability and correlations between traits to be estimated to allow these visual traits to be analysed as progeny values and allow them to be included in an overall index of merit.

Acknowledgment must be extended to the innovative breeders and service groups who have developed and maintained the Central Test Sire Evaluation sites at Hay and Deniliquin (Riverina), Walcha and Armidale (New England), Dubbo (Macquarie), Dale River (Yardstick), Hamilton and more recently Rosebank in South Australia and Geelong in Victoria. Through the forward thinking, hard work and financial backing of these groups, they have achieved a milestone in the development of the Australian Merino Industry. The Australian and State Associations of Stud Merino Breeders and the Federation of Performance Breeders have made a major contribution to the initiation and co-ordination of the Central Test Sire Evaluation program. RAMPOWER, the recently established national industry body formed to maximise the genetic improvement of Merinos, is also involved in promotion of CTSE.

While there is a need to ensure an increase in the number of rams being entered in CTSE is maintained, an even more pressing challenge is to ensure that breeders utilise the identified sires and the potential for industry gains is achieved at stud and then commercial flock level. An important component of this will be to ensure stud breeding programs are linked to CTSE so that breeders can identify the best sires to enter in CTSE, ensure they can make accurate selections from CTSE in the future, and they can pass on to other breeders a strong and definable endorsement of Central Test. When links to CTSE are established by the use of a sire evaluated in CTSE, it should be via a sire that is the most suitable for the breeder in question, because, although any sire with satisfactory numbers of progeny will provide a link, the value of the overall program will be very much judged on the suitability of the progeny for the breeder's particular objective.

The analysis procedures used for CTSE are now commonly use to link on-farm breeding programs. While a small number of innovative breeders have been obtaining linked CTSE/on-farm analysis for several years, more breeders need to utilise the improved accuracy of an analysis to compare on-farm and CTSE sires (Cottle 1995). These breeders will not only be using CTSE as a source from which sires can be identified but will also using CTSE as a path by which they can link to other on-farm breeding programs. This will allow them to significantly increase the number of sires whose breeding value can be accurately assessed and reduce the time lag in identifying rams which are first progeny tested at home before being entered in CTSE.

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