CSIRO

Finewool Newsletter

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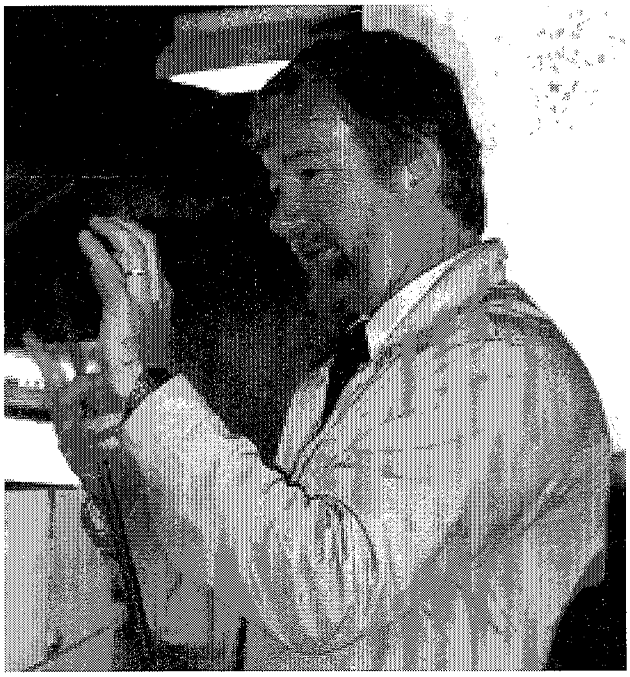
CSIRO

WOOLMARK

In this Issue:

Editorial



Well here it is Spring, and those in the Northern fine wool growing areas now have only a mild grimace on their face in contrast to the large frown they had prior to the welcome rains of early September.

Relative to the value of 12 months ago, the price of fine and superfine wools is not particularly flash. However, the important fact for fine and superfine ram breeders (and buyers) to remember is that while ever they produce animals that grow the same weight of good quality wool, but which slowly gets finer, they (and then clients) can only be better off.

Our challenge as researchers in this Project is to :

(i) give breeders the necessary information and techniques to allow them and their clients to decide what should be their breeding goals for the next 10 years.

(ii) continue to acquire the necessary knowledge that allows breeders to make genetic changes in their breeding goals at a faster rate, while ensuring that no adverse changes occur in other traits they consider important.

(iii) give breeders and their clients advice about different breeding strategies and technologies that has been based on sound scientific investigation and not on opinion.

(iv) ensure that breeders have knowledge about the genetic relationship between raw wool traits and processing performance, so that they can ensure their selection programs are producing positive outcomes for their customers.

It is an exciting time to be associated with the Fine Wool Project. The progeny born in 1991 (the first year in which all 11 bloodlines were represented) have had their four year old shearing; the 1992 drop their three year old shearing, and so on.

Slowly but surely we are acquiring the unique information that will enable us to advise breeders, with the confidence based on sound scientific experimentation, about almost any question relating to the breeding of fine and superfine sheep. Some of those questions and interim answers are presented in this edition of the Newsletter. It would greatly assist the group running the scientific side of the Fine Wool Project if readers of this Newsletter were to write back to us with questions of their own.

We will attempt to answer the questions posed, and where we think they are of interest to the wider audience we will reprint these questions and answers in future editions of the Newsletter. To some of the questions we will have no answers and in these cases this discovery may help us define and refine our ongoing research program.

Ian Purvis
Breeding for Wool Quality & Production
CSIRO, Armidale

Condobolin Fine Wool Project

Kathy Coelli
NSW Agriculture
Orange

1. The Project

The Fine Wool Project, initiated by the CSIRO Division of Animal Production, contains representatives from 9 fine wool bloodlines and 2 medium wool bloodlines from the northern and southern tablelands of NSW, Victoria and Tasmania. The project was established to examine all those characteristics of fine wool which contribute to its market value. In order to assess the performance of fine wool bloodlines in a traditionally medium wool environment, the wether portion of the Fine Wool Project flocks have been transported to Condobolin, a district with a long-term average of 23 microns from Merino wools. Wethers born in Armidale are transferred to Condobolin at 12 months of age, kept for 4 years and run with a local bloodline (Plevna) for comparison. The 1991 drop of wethers have been transferred and shorn twice in August 1993 and 1994. The 1992 drop were not transferred due to health reasons. The 1993 drop have been transported to Condobolin and their first shearing will occur in August 1995 along with the third shearing of the 1991 drop.

The aims of the Condobolin wether portion trial are to compare bloodline p2roductivity, economic profitability and processing performance of the fine wools between Condobolin and Armidale. Measurements taken on the wethers each year include the following:

1. production measures (fleece weight, fibre diameter and body weight)
2. wool quality measures (length, strength, colour, style, diameter and length distribution)
3. fleece and body visual traits, and
4. processing performance.

2. Project Results - 1993/94 shearings

2.1 Production traits

The relative performance of the bloodlines between the 1993 and 1994 shearings for greasy fleece weight and mean fibre diameter were almost identical, except for the local Plevna line. At the 1993 shearing, the Plevna bloodline was 80% above the mean of the Fine Wool Flocks for greasy fleece weight. This was because fine wool wethers transported from drought-affected Armidale were undernourished. Results from the 1994 shearing show the Plevna bloodline only 45% above the mean of the Fine Wool Flocks. There was a strong relationship between fleece weight and fibre diameter (Figure 1), but there is scope among the fine wool lines for increasing fleece weight.

2.2 Subjective (additional) quality traits

The wool quality characters of style, tenderness and colour were visually assessed at shearing. On average, style was about midway between best and good topmakers. There was some variation between bloodlines in style (Figure 2), but this variation was not related to the diameter of the bloodlines. The fine wool bloodlines were more likely to be assessed as tender (up to 50% of all fleeces) (Figure 3) but less likely to incur a colour (Figure 4) discount. For the medium wool bloodlines, the majority of fleeces attracted a colour discount. Objective and visual measures of dust penetration (Figure 5) showed greater levels of dust in fine wool bloodlines, but the relationship was weaker than that with tenderness and colour.

2.3 Economic consequences

A gross margin per dry sheep equivalent (DSE) was calculated for each bloodline using market values based on the first 3 quarters of the current wool selling season (July 1994 to April 1995). The calculation was done as follows:

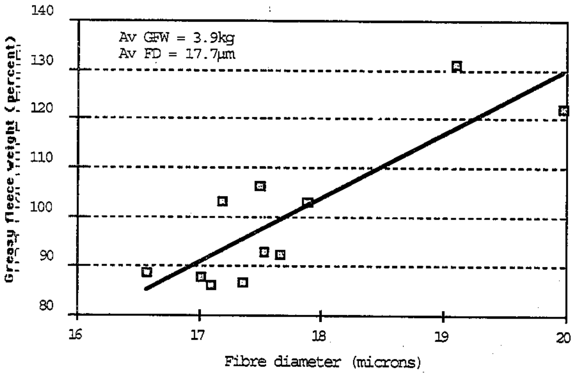


Figure 1. Condobolin 1993/94 shearing results -colour

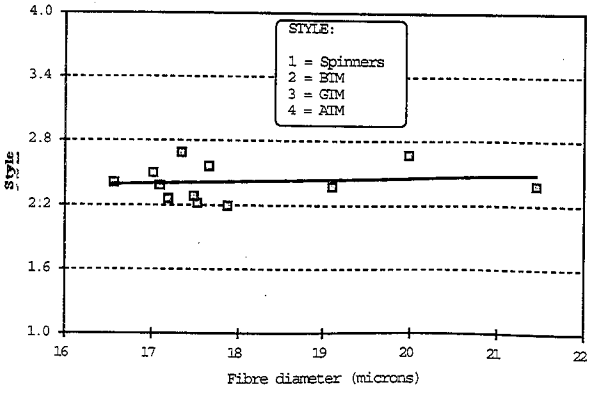


Figure 2. Condobolin 1993/94 Shearing results - style

Price per kilogram for each bloodline was estimated using the average fibre diameter, adjusted for style, staple length, colour and tenderness. Price was corrected to a whole fleece value by allowing 75% of the fleece weight for fleece wool and 25% for skirtings, locks and bellies. **Price per wether** for each bloodline was calculated from the clean fleece weight and corrected price, less levies, selling charges and variable costs. **Gross margin per DSE** was calculated using average body weights and assuming 1 DSE to be a 45kg wether.

The gross margins for each bloodline (Figure 6 - below) show the influence of fibre diameter on gross margin and are a direct result of the fibre diameter premiums received during the 1994/95 wool selling season. However, there was wide variation within the fine and medium wools in profitability, indicating the scope for choosing specific bloodlines to maximise benefits from differences in fibre diameter and fleece weight.

The actual prices received for the Condobolin wool when sold in October of 1994 were 1711 for the fine wool and 994 for the medium wool in cents per kilogram clean.

3. Survey of Local Producers

A survey was undertaken to collect the opinions and perceptions held by local wool producers regarding the Fine Wool Project at Condobolin. The survey highlighted a relatively widespread perception among growers of the need to produce finer wool in the Condobolin district. It has also shown that producers were concerned about the prospects of lower wool cuts and greater dust penetration in finer genotypes, as well as the long-term viability of premiums for finer wool. An information day and viewing of the wethers was held in March 1995 once the results of the survey were collected. As a result it has been suggested by local producers that wethers from an additional three local bloodlines be run with future drops of fine wool wethers. Additionally, local producers would like to see the project run for a further five years, and possibly a small flock of fine wool breeding ewes be run at the Condobolin Research Station.

4. Implications

While this project is not promoting specific bloodlines as a basis for commercial production, the results show that extremely fine genotypes (17-18 micron) will produce fibre economically that performs adequately for processors. The opportunities, then, for using genotypes of intermediate diameter (20 - 22 micron) in the Condobolin district are greater than many commercial producers may have considered.

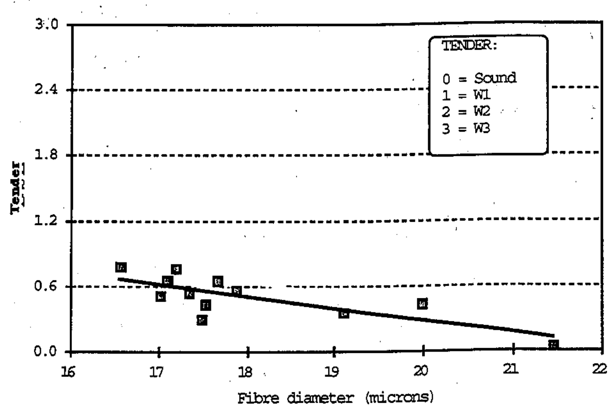


Figure 3. Condobolin 1993/94 Shearing results - tenderness

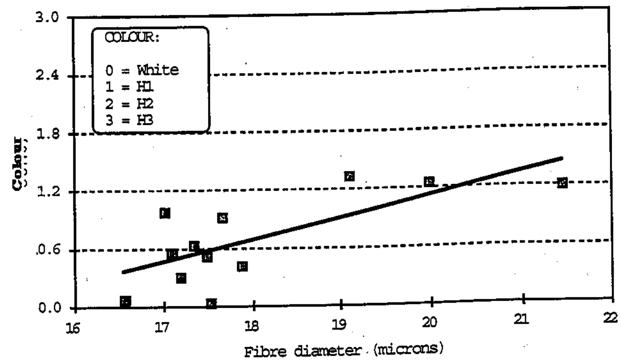


Figure 4. Condobolin 1993/94 Shearing results - colour

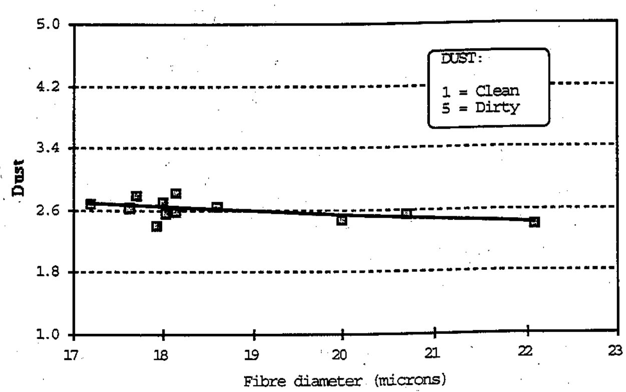


Figure 5. Condobolin 1994 Shearing results - dust

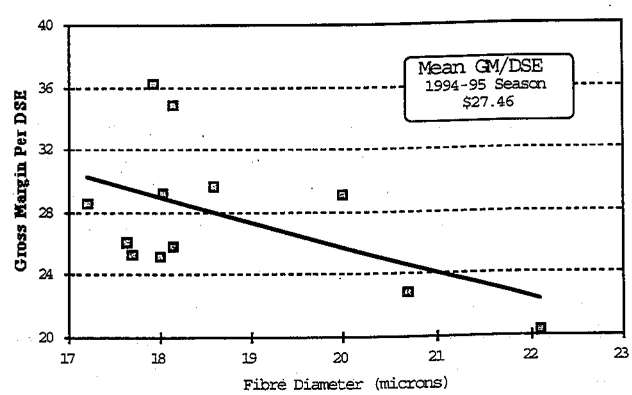


Figure 6. Condobolin 1994 Shearing results - gross margins

RMF and Liz Fulloon at the Longford Fine Wool Field Day

LONGFORD REPORT

R. M. Farrell

As with most producers in Fine and Superfine areas, Longford Field Station has continued to suffer from the effects of drought. We received good summer rainfall, but with an extremely dry Autumn which meant supplementary feeding, and like most places, we had a record dry spell during July-August. However, the September rains have been double the average, so our hopes for a good season are "springing with Spring".

Our Annual Classing Day at Longford reinforced most peoples' thoughts about holding Field Days in shearing sheds in winter; that is, this should not be repeated! However, despite the very trying conditions for staff and contributors, a most successful day was held and the seminar on the Friday was favourably received.

Listed in the table (right) are the scanning results for our ewes that were mated in May this year. As you can see we have an acceptable fertility for a single sire mating, but an incredibly low percentage of twins, and this may well be a reflection of the poor Autumn.

PLEASE NOTE: In some copies of my last report to you, the weaning rates for the 1994 drop were quoted incorrectly. The correct average weaning weight was 18.5 kg.

Fine Wool Flock at Armidale Scanned around day 50-60

Line	Single Bearers	Twin Bearers	Dry Ewes
01	163	12	14
02	185	7	16
03	153	12	31
04	145	10	45
05	171	16	23
06	130	21	47
07	176	2	19
08	169	3	19
09	145	7	45
10	149	11	28
11	180	2	19
Total	**1766**	**103**	**306**

Summary:
Conception rate: 85%
Twinning rate: 5.5%

Possible Merino Bloodline Differences in Resistance to Footrot

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Of the many diseases which are caused by bacteria, footrot and fleece rot are the most relevant to sheep producers. Other bacterial diseases we should be concerned with include: Clostridial infections (those covered by the 5 in 1 vaccines), brucellosis, dermatophilosis, pizzle rot, cheesy gland and Johne's disease.

Why footrot?

It is no news to most sheep farmers that footrot can be a devastating disease. Over the last 50 years intense research has given us considerable understanding of how the disease develops, the organisms involved, effective treatments and, more importantly, how to control it.

It is now a well recognised fact that some forms of the disease can be effectively eradicated from individual flocks/properties. However, successful eradication of all forms of footrot associated with virulent strains of the main organism, *Dichelobacter nodosus* previously known as *Bacteroides nodosus* (used to be *Fusiformis nodosus* 30 years ago), has not been demonstrated on a regional or state-wide basis. To make things even more complicated, there is now good evidence that the eradication of less virulent strains, the intermediate and benign strains of *D. nodosus,* will be even more difficult.

In addition, it is also known that for benign strains, eradication or control is not an economically sensible decision. The disease associated with benign strains just does not warrant expensive control programmes. It is thus highly likely, given the best outcome for the State wide control/eradication programmes, we will be left with non-virulent footrot, including the intermediate strains some of which will continue to impose significant production losses.

One long-term option to control these forms of footrot, is to graze sheep that are relatively more resistant, so the disease has no impact on the profitability of the farm.

There is now decent evidence that not all sheep are equally susceptible to footrot. Industry knowledge of the relative resistance of the Romney Marsh, and some strains of Corriedales, has been documented by our trans-Tasman competitor, New Zealand. However, this information is of little use to committed Merino breeders.

Completion of a recent project at Sydney University's Centre for Sheep Research and Extension has shown that there is a moderate degree of genetic control over resistance to footrot within flocks of Merino sheep. The heritability, or the extent by which genes contribute to the differences we observe, is in the order of 25 to 30% for resistance to footrot. Although this puts it in the same order as resistance to some other important production diseases such as internal parasites, we do not have any easy selection strategies unless we directly challenge sheep with footrot.

One aspect that has not been well documented is the possibility of using resistant strains or bloodlines which might already exist in the sheep industry. The Fine-Wool Project presents us with a unique opportunity to investigate some aspects of bloodline differences in resistance to footrot.

How do we measure resistance?

At present the only way to screen individual, families or flocks for resistance is to expose sheep to footrot. Because footrot is a relatively complex disease, we need to keep all factors which can confuse the picture to a minimum. For that reason we have developed a semi-controlled challenge system for footrot. Infection of normal, dry healthy feet to *D. nodosus*, will **NOT** lead to footrot.

For sheep to develop footrot, it is first necessary to predispose them by exposing them to wet pasture. Secondly a source of infection is needed. This is usually provided by sheep which are already infected with footrot. During the transmission, or spread phase, pasture conditions need to be wet and not too cold. Once sheep become infected, the signs of footrot are not readily obvious for another 10-14 days.

Under our challenge system, we keep sheep on irrigated pasture for three weeks, and introduce donor (previously infected) sheep after the first week. All sheep are inspected for signs of footrot, and kept on pasture (non-irrigated) for another 6 weeks. During this period the disease is allowed to fully express itself (so we can tell which sheep are resistant or not) and we inspect the sheep twice more.

At this stage we expect over 70% of sheep to have footrot and over 50% will have severe footrot. At the third inspection, all sheep are vaccinated with a vaccine which is specifically targeted against the challenge strain. This has a marked effect in that, at the end of a 6 week vaccination program (2 vaccinations, 3 weeks apart), the cure rate of the vaccines leaves us with less than 5% of sheep infected. Quite often, the rate of infection is down to 1%! (This shows the power of a targeted recombinant DNA footrot vaccine!) To make sure that all sheep respond to the vaccine and none break down with footrot again, we monitor them for another 15 weeks.

The last few sheep are normally treated with antibiotics to cure them from footrot. We take blood samples each time sheep are inspected for antibody levels. The samples taken after vaccination tell us how well the sheep have responded to the vaccine.

Relevance to the Fine-Wool project

A sample of the 1992 drop Fine wool wethers born at Armidale, were transported to Camden for screening. In total 385 sheep were exposed to the treatment described above, and inspected for footrot on 2 occasions before challenge, and 6 occasions after challenge.

The degree of footrot is recorded by inspecting each foot and scoring the severity of footrot. In addition an overall score is given to the sheep which can range between 0 (no footrot) and 5 (severe footrot in at least 3 feet). The average severity of the footrot for the 11 flocks in the Fine wool project is shown in Figure 1. This figure shows the severity of footrot before and after vaccination. A number of important results are evident.

Firstly considerable differences were seen between the 11 flocks. The largest differences were evident before vaccination,

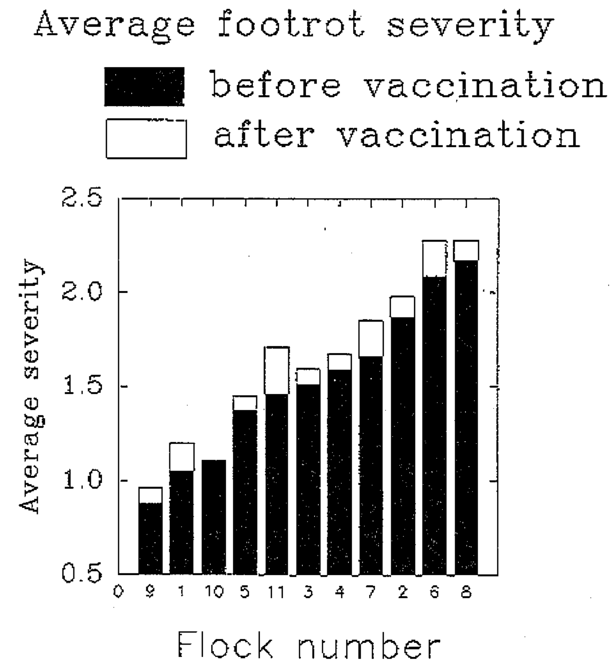


Figure 1. Severity of Footrot

when most of the footrot was seen. Also after vaccination some differences between flocks were still evident. One flock had no footrot after vaccination. The differences between flocks become more obvious when they are ranked on basis of their footrot.

If we take sheep which have any sign of footrot - see Figure 2, the most resistant flock had just over 45% of sheep affected, whereas the most susceptible had over 95% of sheep affected (Figure 2a).

When we consider only sheep which have severe footrot, where it has progressed under the sole and the hard horn of the hoof, the most resistant 2 flocks had less than 40% of sheep affected,

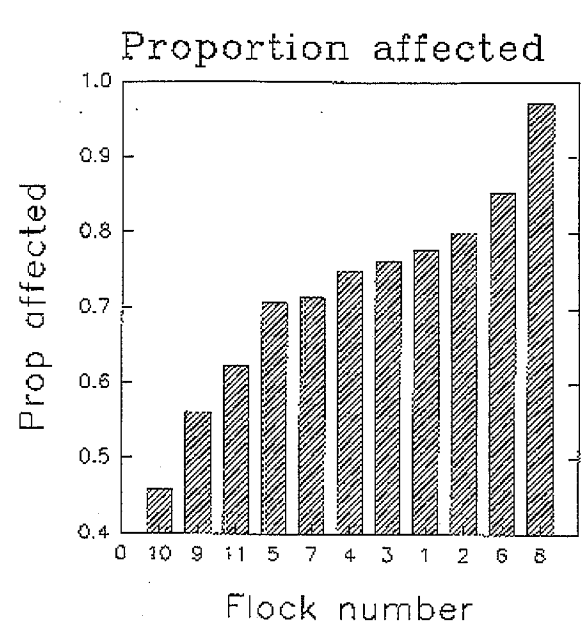


Figure 2a. Proportion affected by Footrot

and the most susceptible showed almost 80% of sheep with severe footrot (Figure 2b).

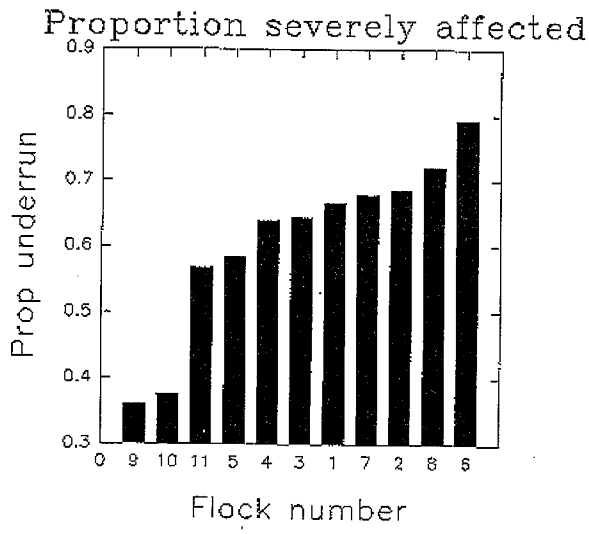


Figure 2b. Proportion severely affected by Footrot

Another interesting finding was an apparent relationship between body weights of the flocks and the severity of footrot which developed after challenge. Body weights were taken of all sheep on all inspections, but in this case only body weight before challenge is shown in Figure 3. When the average body weight of the 11 flocks is plotted against the average severity of footrot of the flocks over all inspections, a trend was clearly visible.

As the average body weight of the flocks increased, so did their susceptibility to footrot. It is only possible to speculate on the nature of this relationship, but it may have something to do with the pre-disposition of sheep on the wet ground. Heavier sheep may become more pre-disposed during the first three weeks of challenge.

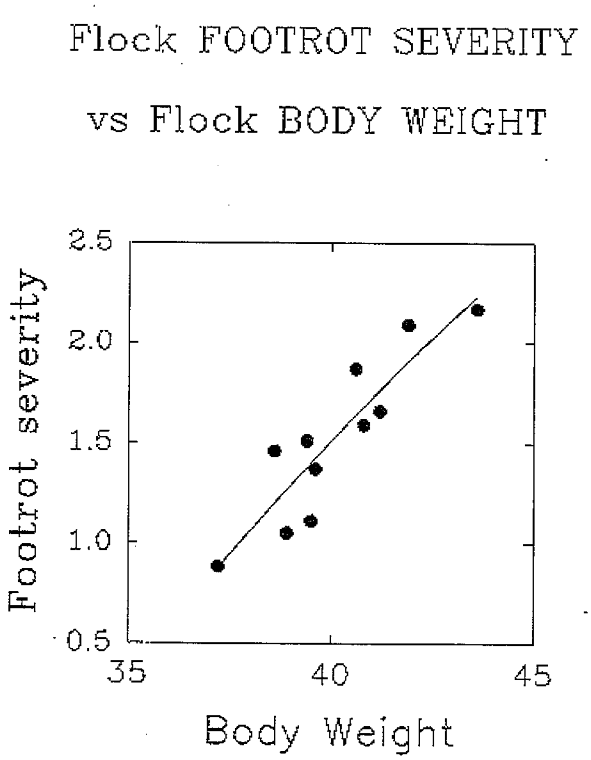
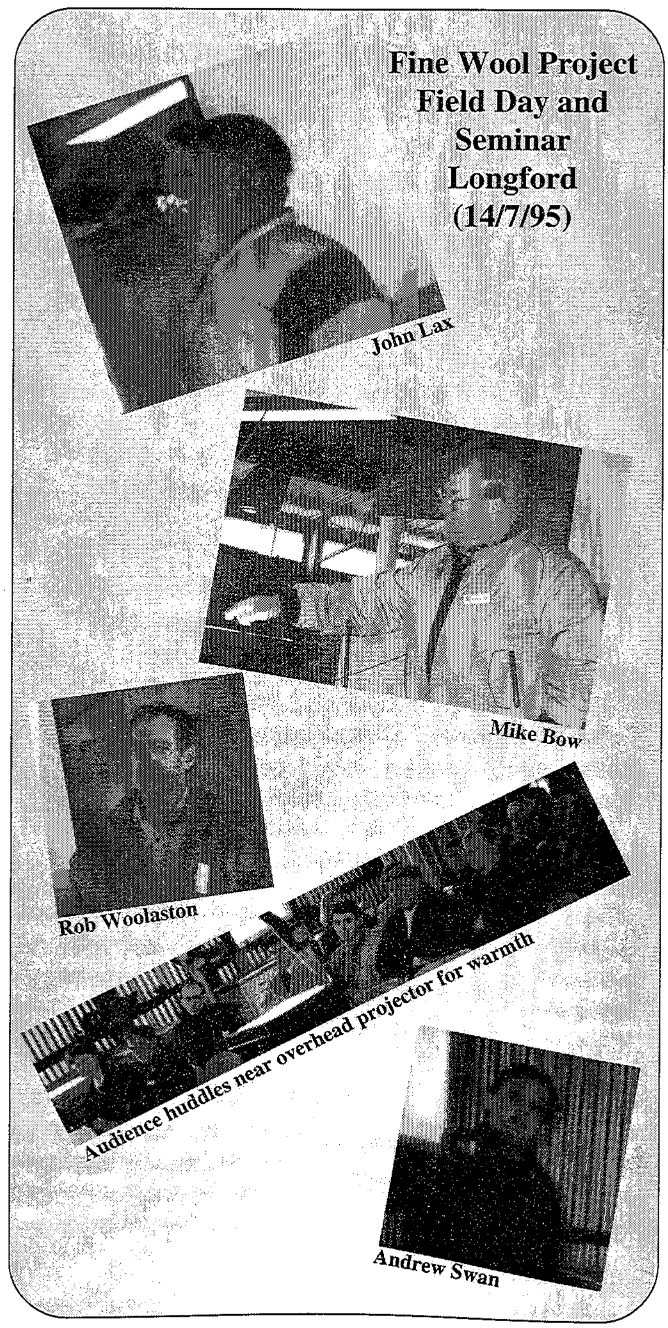


Figure 3. Severity of Footrot vs. Liveweight

Where to from here?

The data presented here are quite exciting in that it is the first time that a range of bloodlines from one breed have been exposed to severe footrot under semi-controlled conditions. The results suggest that under challenge with a virulent strain of *D. nodosus*, some bloodlines may be more resistant than others. This is perhaps surprising in that it is unlikely that studs would have actively selected for increased resistance to footrot.

Alternatively, some bloodlines may have become more susceptible to footrot as an unintentional consequence of selection for other traits (may be body weight?). Although we expect Merino bloodlines to be different for a range of production traits, we cannot always assume that this is the case for disease resistance, as has been observed in the case of resistance to internal parasites. This preliminary investigation suggests that the unexpected differences reported here should be explored further to increase our knowledge and hence options to deal with footrot.



How do fine wool sheep selected on follicle traits measure up against those selected on production traits?

Ian Purvis
Wool Quality & Production
CSIRO, Armidale

If we select replacement sires and ewes in our breeding flocks on the basis of fleece weight and fibre diameter what changes can we expect in the follicle populations in the skin of the next generations? Conversely, if we had the capacity to select replacement animals on follicle characteristics, what would be the changes we could expect over 10 years in the productivity and fleece value of these animals?

An important feature of the Fine Wool Project is that it provides answers to such questions, using data collected from animals that represent the important fine and superfine bloodlines in this part of the national Merino population. We acquire this information by collecting skin samples from the midside area just prior to shearing, and then processing the samples using histological and image analysis techniques to give us a measure of

- i) the density of follicles (primary + secondary) per square millimetre of skin - that is how closely packed together are the follicles (and hence the wool fibres);
- ii) the number of primary follicles per unit area; and
- iii) the number of secondary follicles per primary follicle.

[Note: Primary follicles are the first ones initiated in the skin of the unborn lamb and they are distinguished by having a sweat gland and a small muscle attached to them. The density of these primary follicles is not very variable between animals, nor between strains of Merinos, nor even between breeds. It is the number of secondary follicles (these begin initiation around day 90 of gestation) that shows considerable difference between animals and between the strains of Merino. Hence, it is common to report the ratio of secondary to primary (S/P) follicle number.]

To date, our laboratory at Prospect has completed the processing of the samples from two of the drops born at our Longford Field Station west of Armidale - namely the 900 or so animals born in 1990 and 1991 that survived to be sampled and shorn as hoggets in 1991 and 1992.

Although this number of animals is insufficient for the calculation of meaningful estimates of heritability and genetic correlations (which are needed to predict the long term results of different selection programs), the data are sufficient to examine the effect of phenotypic associations between traits.

For example we could choose the top 5% of animals on the basis of their hogget mean fibre diameter (MFD) alone, and then examine how this subset of animals differs from the original unselected group in this characteristic and others of interest. The associated differences in other traits will be a function of how tightly the traits are correlated, or co-vary. We can illustrate how two traits are correlated by constructing a graph where the values of the two traits are plotted against each other for all animals.

On the next page, are pictured some of the relationships between production traits and traits of the skin. The words ***phenotypic relationship*** are used to signify that the association between the two traits is due to the combined effects of genetic and non-genetic causes. Some relationships are reasonably strong - for example, between MFD and Density - whilst others are very weak - for example, between clean fleece weight (CFW) and Density.

The vertical and horizontal lines on the graphs are the 5% cut-off points for the two traits.

The relationship between MFD and Density suggests that if we choose animals from this population that are below average in MFD, the selected animals will tend to have skins containing follicle populations that are more dense than average. By contrast, the sheep with denser follicle populations have a wide range of fleece weights - that is, there is no relationship between the two traits.

Well, what does all this mean to a breeder of fine wool Merino sheep?

Most breeders have breeding goals that focus on improving per head returns. For this discussion, if we restrict ourselves to the wool enterprise, then improvement of **fleece value per head** is a logical focus, and the traits that make an overwhelming contribution to variation in this, are clean fleece weight and mean fibre diameter. We can construct an ***index*** (a way of combining the individual bits of information into a single number) that reflects the genetic merit of any animal for CFW and MFD and the relative economic value of changing the traits by a single unit. So this simple index could be calculated as

I% = 100 + [Relative value of a 1 μm change in MFD x genetic merit of the animal for hogget MFD]

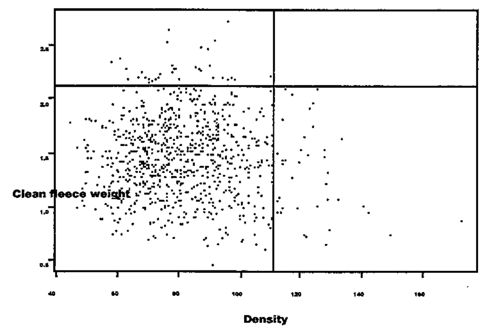
+ [Relative value of a 1 kg change in CFW x genetic merit of the animal for CFW]

The price information that should go into this index calculation is that which is relevant to the wool typically produced from this flock.

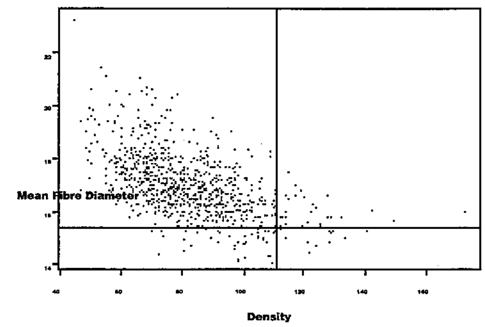
Breeders could select animals on the basis of any of the skin traits, CFW, MFD or on the Index. By knowing the relationship between the traits we can calculate the effect on any trait of selecting on the basis of any other trait (or combination of traits).

In Table 1 the results of selecting the best 5% of animals (ignoring sex) is presented. For example, the best 5% of animals in this population for S/P ratio (that is, the animals with the highest ratio of secondary follicles per primary follicle) will have a S/P ratio of 35:1 compared to the average of 22:1. Because of the relationship between S/P ratio and the other traits, the selected animals will have a density of 107 follicles per square mm of skin (compared to the average of 82); a

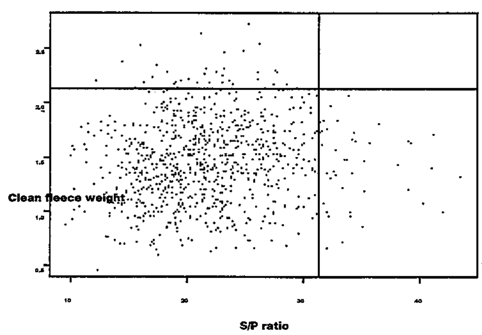
Fine Wool Flocks - Phenotypic relationship between CFW and Density



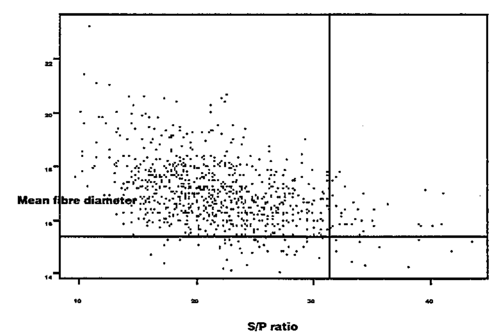
Fine Wool Flocks - Phenotypic relationship between MFW and Density



Fine Wool Flocks - Phenotypic relationship between CFW and S/P ratio



Fine Wool Flocks - Phenotypic relationship between MFW and S/P ratio



fleece weight of 1.5 kg clean (right on average); a MFD of 16.1 µm (1µm finer than the average), and a 10% index value of 107 (average = 100).

Similarly, if the top 5% of animals were chosen on the basis of any of the other traits, the corresponding effect of that selection for any of the other traits is presented in Table 1.

Table 1. The current generation effect of selecting the top 5% of animals on wool or skin traits and an index of fleece weight and fibre diameter

	Trait Mean Value				
	S/P ratio	Density	CFW	MFD	10% Index
***Select top 5% on*:**					
S/P Ratio	**35**	107	1.5	16.1	107
Density	30	**123**	1.4	15.9	109
CFW	22	82	**2.3**	18.4	103
MFD	27	103	1.2	**15.1**	117
10% Index	26	98	1.7	15.6	**123**
Overall Mean	22	82	1.5	17.1	100

In practical terms the information in this table shows that if we had skin measurements available on all animals and we chose sheep with the densest follicle populations we would have chosen animals with higher than average S/P ratio, slightly lower than average CFW, much lower MFD and animals 9% above the average on this Index. By contrast, selection on the basis of mean fibre diameter, will choose animals well above average in Density, S/P ratio and Index score, below average in CFW and the selection criterion, MFD.

Selection on the 10% Index results in the choice of animals that are close to the lowest in MFD, but above average in CFW, Density, and S/P ratio.

While these results are relevant only to the current generation (ie., they do not predict what will happen to the progeny of the chosen animals) the information that will come out of the Fine Wool Project flocks over the next two years will allow us to accurately predict the long term consequences of a range of selection programs. These could include almost any production trait, visually assessed conformation and wool quality trait, skin and follicle trait, and the important measures of processing performance.

Measuring the genetic differences between animals for wool traits

Andrew Swan
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CSIRO, Armidale

There are a number of objective measurements of wool traits available to ram breeders, which are potentially useful for breeding purposes. Some examples, that are measured in the Fine Wool flock, include: Greasy Fleece Weight (GFW), Yield (YLD), Clean Fleece Weight (CFW), Mean Fibre Diameter (MFD), Standard Deviation of Diameter (SD), C.V. of diameter (CV), Staple Length (SL), and Staple Strength (SS). Obviously there are a range of other traits important in fine-wool breeding, most notably style, but these are not dealt with here.

Before such traits can be used effectively in breeding programs several questions must be answered:

1. Is there an economic benefit from selecting on a trait?

That is, does selection on a certain trait either increase returns or reduce the costs of wool growing? Table 1 below shows the relative effects of each of these traits on profitability, along with the relative costs of measurement. The two most important traits are clean fleece weight and fibre diameter, as they have the largest effect on net returns.

Table 1: Relative economic importance and cost of measurement for wool traits

Trait	Economic importance	Cost of measurement
GFW	++	+
YLD	+	++
CFW	++++	++
FD	++++	++
SD	++	++
CV	++	++
SL	++	+++
SS	++	+++

2. Do animals differ genetically for these traits?

In other words, do superior animals pass on the benefits to their offspring?

3. How does selection on one trait effect others?

For example, does selection on fleece weight increase mean fibre diameter, and by how much?

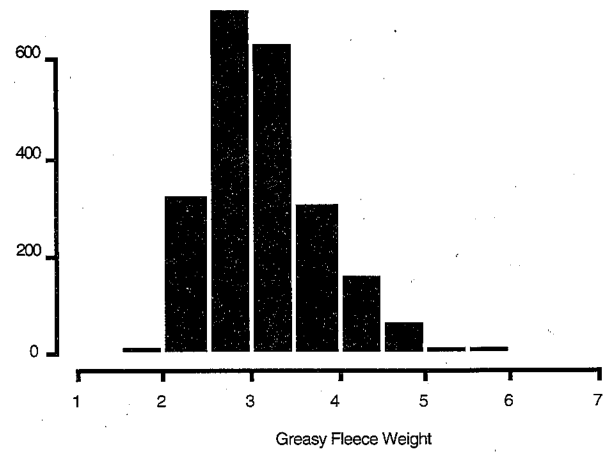
4. Are measurements made at early ages good indicators of lifetime performance?

Since wool is harvested throughout the life of the sheep, it is important to confirm that selections made early-on (for example when animals are hoggets or 4-tooths) correlate well with later production.

The Fine Wool Project was established partly to provide answers to questions 2, 3, and 4. This article provides some information on these issues, although at this stage of the project it is difficult to give precise answers, especially for lifetime performance. To set the scene, we will explore the concepts of variability and association.

What is variation?

Figure 1. Variation in greasy fleeceweight



Whenever measurements are made on a group of animals, a range of values is observed. For example, the figure above is a "histogram" of the 4-tooth greasy fleece weights in the Fine Wool flock. The "x" axis shows that values for this trait ranged from 1.5kg to 6kg, while the "y" axis shows the number of animals with fleece weights in each 0.5kg. class. For example, around 600 animals had fleece weights between 3kg and 3.5kg.

This figure depicts the "variation" that has been observed in the flock for this trait. What causes these differences? There are a number of factors, some which can be identified, and others which cannot. Identifiable factors include the effects of different years of birth, running groups of animals in different paddocks, differences between males and females, and singles and twins. Importantly, animals also differ in their genetic make-up ie., genetic variability.

Genetic variability in the Fine Wool flock can be further broken down into two sources:

Between-bloodline genetic variation.

Bloodlines may differ for several reasons: they have been founded on animals from different sources, they originate from different environments, they are subject to different selection histories, and simply because of random chance.

Within-bloodline genetic variation.

Animals within a bloodline may also differ substantially in their genetic make-up. Most traits are influenced by a number of genes, of which there are often a number of different types, or "alleles". Obviously there are many different combinations which can arise from these, leading to genetic variability.

These sources of variation are useful in different ways. Between-bloodline variation may represent an opportunity for a wool grower to choose a different bloodline from which to buy rams. Within-bloodline variation may be used to choose individual rams from an existing flock. Within-bloodline is the more important for two reasons.

- Firstly, it is not always clear which bloodline is "best" since there are a range of traits to be considered, and different bloodlines excel in different traits, although those with favourable combinations of fleece weight - fibre diameter are a logical starting point
- Secondly, benefits from "selecting" a new bloodline occur only once, while selection of animals within-bloodline can occur across generations, with the benefits accumulating.

Many people strive to achieve uniformity in their flocks using strategies such as "corrective mating". However, even this will result in a large amount of genetic variation in the progeny by virtue of the large number of genes affecting different traits. In most situations, it is better to accept the variability which exists, and use it to your advantage by selecting the animals that will push mean performance in the right direction.

What is association? (or correlation)

When we speak of "association", we are referring to the way two traits are related, or how values of one trait change with those of the other. Two concepts are important here.

- Firstly, we can think of *positive* and *negative* associations. With positive associations, the values of the two traits *increase* together. With negative associations, as the values of the first trait *increase*, those of the second trait *decrease*.
- Secondly, we can think of the *strength* of the association. For example, there is a *strong* positive association between greasy and clean fleece weight: animals with high greasy fleece weights almost always have high clean fleece weights.

On the other hand, there is a *weak* positive association between fleece weight and fibre diameter: there is some tendency for animals with high fleece weights to have high fibre diameters, but this is not always the case. It is not particularly difficult to select animals with favourable fleece weight - fibre diameter combinations.

How do we measure variation and association?

The trick of the geneticist is to take a data-set and to separate the different sources of variation using statistical techniques. Having done this, there are various ways to present the results:

1. *Between-bloodline variation:*

- Firstly, we can measure this variation as a percentage of the total. So we could make statements like "20% of the variation we see in hogget greasy fleece weight is attributable to differences between bloodlines".
- Secondly, we can present the mean for each bloodline, or alternatively deviations (differences) from an overall mean.

2. *Within-bloodline variation:*

- We can also express within-bloodline variation as a percentage of the total. We could say something like "35% of the total variation within a bloodline for greasy fleece weight is genetic". You often hear this percentage referred to as *heritability*. One way to explain heritability is that it is the percentage of the superiority of the parents which is transmitted to their progeny. So for a trait with a heritability of 35%, if the selected parents were on average 1 unit above the mean of their drop, we would expect that their progeny would be on average 0.35 units above the mean of their parents' drop.
- We can examine the genetic worth of individual animals by calculating Estimated Breeding Values, or Progeny Values. These figures can then be used to select the best animals. Firstly however, we must know what the heritabilities are, and also what the associations between traits are.

3. *Within-bloodline association:*

- Associations between traits are generally investigated at the within-bloodline level. The measure of association is the *correlation*. Simply put, this is a number ranging from -1 to +1. Negative values indicate *negative associations*, while positive values indicate *positive associations*. Also, the closer the correlation gets to +1 (or -1), the *stronger* the association, while a correlation of 0 indicates the traits are not associated at all.

Having given some detail on the type of information which the Fine Wool Project can provide, we will now go on to some of the results to-date.

Results from hogget measurements (10 months)

1. *Between-bloodline results*

Table 2 shows bloodline deviations for hogget traits, along with the overall means for each bloodline. Rather than number the bloodlines from 1 to 11, bloodlines have been allocated to obvious groups based on the combination of performance in clean fleece weight and mean fibre diameter. There are three groups shown in the left-hand column of the table. Group 1 contains the finest bloodlines, and may be thought of as a "superfine" group. Group 2 contains two bloodlines which are only slightly broader, but still within the range of the superfine group. They also have higher fleece weights than the superfine group, and can be referred to as the "fine-wool" group. Group 3 contains the two medium wool bloodlines ie., the "medium-wool" group.

Bloodlines within the superfine and fine-wool groups fall within a 0.6 micron range (from -0.6 to 0.0). Relative to the mean of 16.7 microns, this represents only a small amount of between-bloodline variation. This contrasts with a 0.4 kg range for clean fleece weight, which relative to the mean of 1.6kg indicates there is more between-bloodline variation in clean fleece weight. The results indicate that for these two traits, there are differences between bloodlines for fleece weight - fibre diameter combination, indicating that there will also be differences in profitability between bloodlines.

For other traits several observations can be made, most of which follow our expectations:

- trends for greasy fleece weight are similar to those for clean fleece weight, as expected.

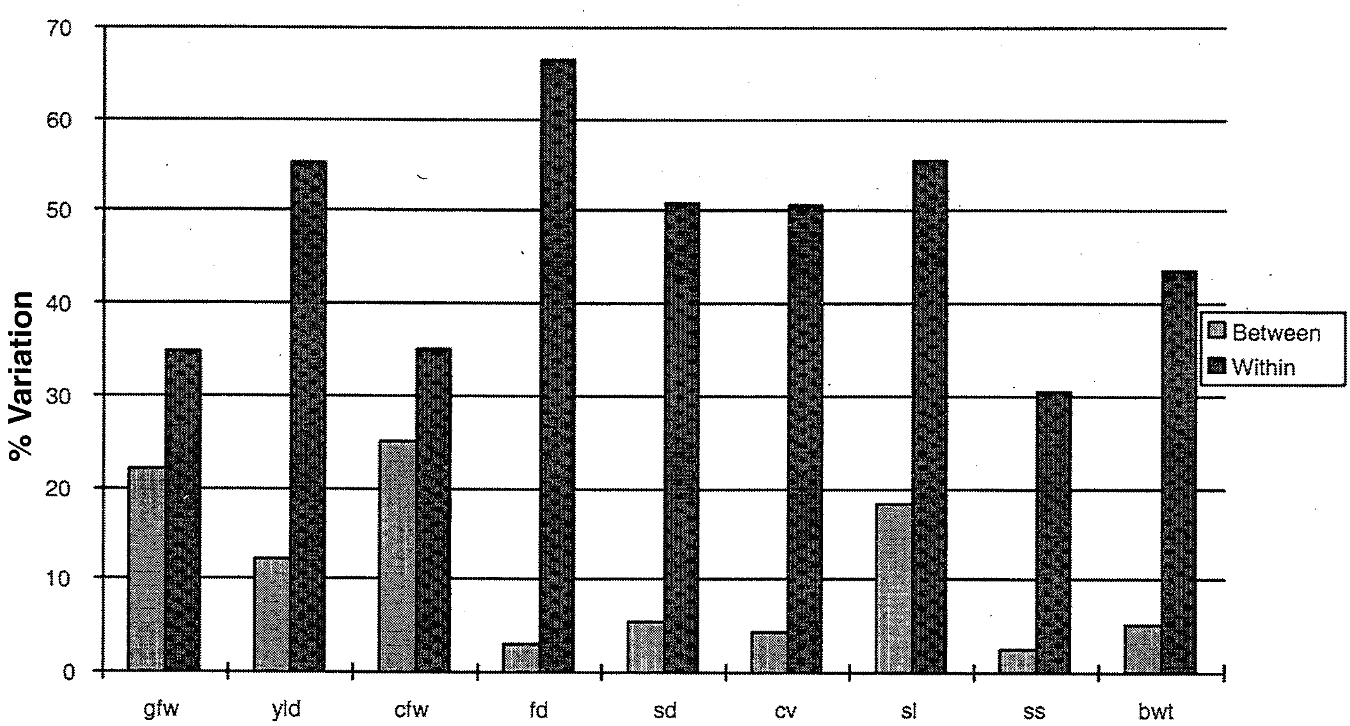
- there is a tendency for superfine bloodlines to be lower yielding than bloodlines in the other two groups.
- fibre diameter variability, as indicated by standard deviation and CV of fibre diameter, is lower in superfine bloodlines. That is the distributions are "tighter".
- superfine bloodlines have shorter staples.
- for staple strength, there are no obvious patterns between the three groups.

Table 1: Bloodline deviations for traits measured on hoggets (10 months)

Group	GFW	YLD	CFW	FD	SD	CV	SL	SS
1	-0.1	-2.1	-0.1	-0.6	-0.3	-0.9	-0.4	0.4
1	-0.1	1.2	0.0	-0.5	0.0	0.5	-0.4	1.3
1	-0.3	-0.6	-0.2	-0.5	-0.1	-0.3	-0.4	0.3
1	-0.3	-1.5	-0.3	-0.3	-0.2	-1.1	-0.3	-1.4
1	-0.3	1.5	-0.2	-0.3	-0.1	-0.3	-0.5	3.4
1	-0.3	-1.1	-0.2	-0.2	-0.1	-0.6	-0.6	-0.1
1	-0.2	-1.8	-0.2	0.0	-0.1	-0.8	-0.4	1.5
2	0.1	1.9	0.1	-0.3	0.0	0.4	0.2	-0.4
2	0.2	0.6	0.1	-0.1	0.0	-0.1	0.7	-2.3
3	0.7	2.0	0.5	1.0	0.4	1.4	1.3	0.4
3	0.5	-0.1	0.4	1.7	0.6	1.9	0.8	-3.0
Mean	**2.1**	**73**	**1.6**	**16.7**	**3.0**	**18**	**7.1**	**38**

2. *Within-bloodline results*

Figure 2 Genetic variation Between and Within Bloodlines for objectively measured hogget traits



[Note: Between bloodline variation calculated on a within-strain basis]

In Figure 2 the percentages of between- and within-bloodline genetic variation for each trait are shown. The consistent pattern is that for all traits, within-bloodline variation (heritability) is greater than between-bloodline variation. Heritabilities range from just over 30% for fleece weight to over 60% for fibre diameter. This indicates that there is considerable potential to improve fine-wool sheep for these traits.

For fleece weight, the levels of between-bloodline variation are quite high, and we observe the lowest heritabilities. The reverse is true for fibre diameter. This implies that if a breeder wishes to boost fleece weight, it may be quickest to look outside the flock (within the strain), whereas if a reduction in fibre diameter is required it may be quite efficient to identify the superior animals within the flock.

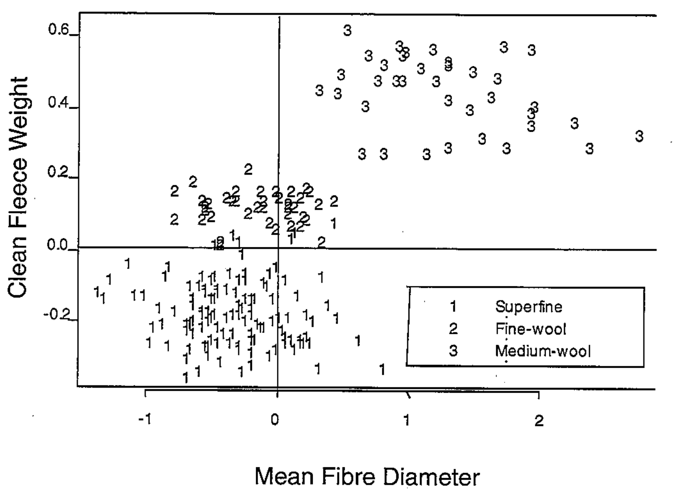
Associations between traits are more difficult to present: for the nine traits included in the above graph, there are 36 different genetic correlations! However some of the highlights are:

- the estimated genetic correlations between fleece weight and fibre diameter are approximately 0.2. This is an unfavourable association because it implies that as we increase fleece weight, fibre diameter tends to increase as well. However, because the association is not particularly strong (the correlation is closer to 0 than to +1), it implies that it is still possible to improve fleece weight and fibre diameter simultaneously.

Figure 3 shows the mean progeny values for each sire that has been used in the Fine Wool flock, identified according to the groups described above. These progeny values reflect the genetic value of the sires for these two traits. Although, on first glance it appears that the association between the traits is quite strong, each group of sires should be treated separately. Within individual groups, the associations are not strong, and there are sires with favourable fleece weight - fibre diameter combinations. However, overall the fine-wool sires are in the location that will reflect greater fleece values (depending, of course, on the premium for changes in MFD).

- the estimated genetic correlation between CV of fibre diameter and staple strength is around -0.6. That is if we place selection on pressure to reduce CV, staple strength is likely to improve. Therefore, CV of fibre diameter may be an alternative to measuring staple strength.

Figure 3 Progeny mean values for Mean Fibre Diameter and Clean Fleece Weight identified (1, 2, or 3) according to bloodline groupings



Results from 4-tooth measurements (21 months)

1. Between-bloodline variation Table 3 below shows the performance of the ewe portion of the flock based on their 4-tooth shearing at 22 months of age. It should be noted that because we need information on all surviving animals in order to accurately estimate heritabilities and genetic correlations, these figures represent the performance of the un-culled flock. That is, all animals contribute to these 4-tooth figures, irrespective of the hogget classing decisions of the stud classer.

Table 3 Bloodline deviations for traits measured on hoggets (22 months)

Group	GFW	YLD	CFW	FD	SD	CV	SL	SS
1	-0.4	-1.7	-0.4	**-0.8**	-0.3	-1.2	-0.5	0.5
1	-0.4	1.7	-0.3	**-0.7**	-0.2	-0.6	-0.4	2.3
1	0.0	1.1	0.0	**-0.7**	0.0	0.5	-0.3	1.7
1	-0.5	-1.5	-0.5	**-0.6**	-0.3	-1.3	-0.6	-1.8
1	-0.5	-3.8	-0.5	**-0.5**	-0.1	-0.2	-1.0	-2.6
1	-0.4	-0.9	-0.4	**-0.4**	-0.2	-0.6	-0.4	0.9
1	-0.3	-2.3	-0.3	**0.2**	-0.1	-0.9	-0.5	0.5
2	0.3	3.5	0.3	**-0.4**	0.0	0.6	0.3	-1.0
2	0.3	0.7	0.2	**0.1**	-0.1	-0.6	0.8	0.0
3	1.3	2.9	1.1	**1.5**	0.5	1.6	1.7	0.0
3	0.8	0.4	0.6	**2.4**	0.9	2.7	0.9	-0.6
Mean	**3.3**	**75**	**2.5**	**18.6**	**3.1**	**17**	**8**	**47**

Relative to the hogget figures (both sexes and 1990-1993 drops), the performance of the 4-tooth ewes (1990-1992 drops) show significant differences: (over)

I. Increases in greasy and clean fleece weight of 57% and 56%, respectively;

II. Increase in mean fibre diameter of 11% or 1.9μm over all bloodlines, with the superfine group increasing by 1.6μm to 18.0μm, the fine-wool group by 1.9μm to 18.4μm, and the mediums by 2.5μm to 20.6μm;

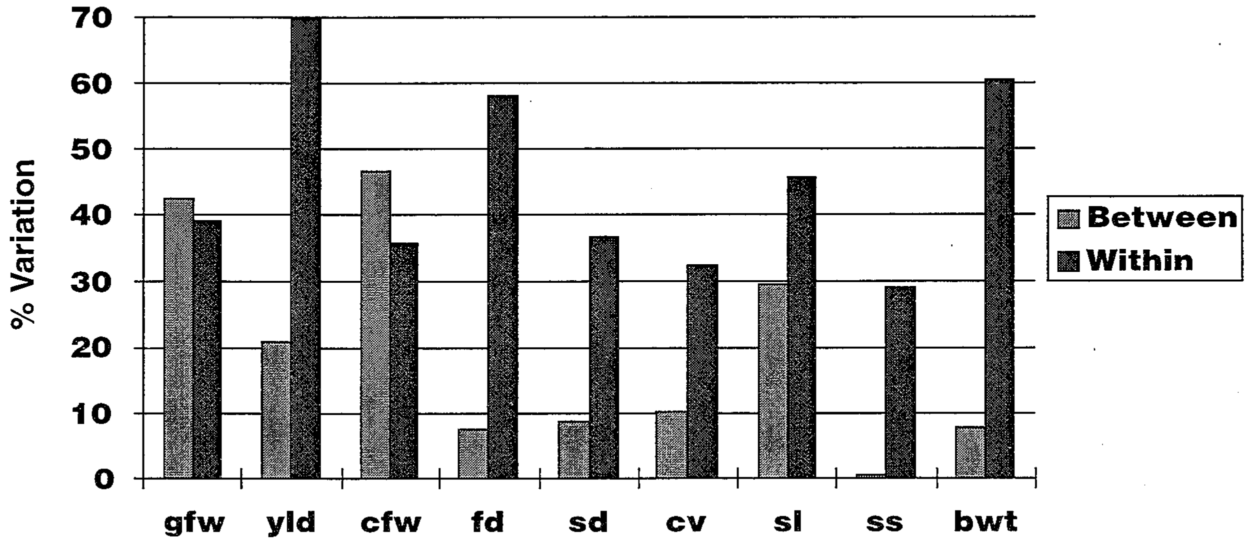
III. virtually no changes in SD and CV% of fibre diameter;

IV. moderate increase in staple strength (24%).

In summary, most of the differences between the bloodlines and "groups" at the hogget shearing are maintained but magnified at the 4-tooth shearing.

2. Within-bloodline variation

Figure 4. Genetic variation Between and Within Bloodlines for objectively measured traits at the 4-tooth shearing (22 months of age)



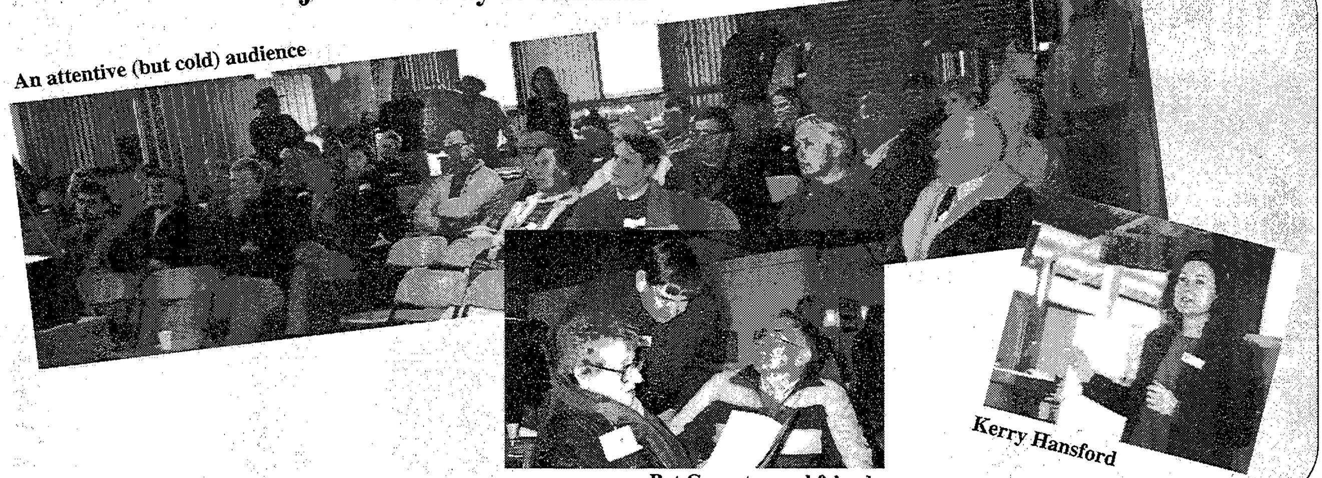
[Note: Between bloodline variation calculation on a within-strain basis]

Again, the general features of the hogget genetic story are maintained when ewes are shorn as 4-tooths. That is, the fleece weight measures show substantial genetic differences between bloodlines, but genetic variation in mean fibre diameter lies predominantly within bloodlines. However, several of the 4-tooth heritability estimates are higher than for the corresponding 2-tooth traits. This is particularly so for yield% and liveweight.

These 4-tooth figures are based only on 2 drops of ewes and a further two years of data are necessary before we will have the necessary precision in the figures to be confident about predictions. This applies especially to the genetic correlations between hogget traits and other adult traits.

In the next issue of the Newsletter we will present information on how to tie all these results together in the development of a breeding program.

The Fine Wool Project Field Day & Seminar



An attentive (but cold) audience

Pat Coventry and friends

Kerry Hansford