SHEEP CROSSBREEDING IN NEW ZEALAND — DATA AVAILABILITY AND INFORMATION GAPS

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SUMMARY
Data structure in a New Zealand sheep crossbreeding database is described and analysed. Most of the data were for pure and first cross genotypes, mainly in wool and growth traits and in the more productive farm classes. Little information is currently available for many crossbred genotypes. Some published data lack descriptions of the animals' ages or time of year of measurements and, in some cases, it is not possible to calculate standard errors of trait least squares means. Reports of breed trial results should include this type of information to assist any subsequent predictions of crossbreeding outcomes.
Keywords: crossbreeding, DSS, trait means.

INTRODUCTION
The use of crossbreeding has been increasing in the New Zealand sheep industry as farmers strive to increase returns. It has proved difficult to provide good extension advice for crossbreeding in specific environments (Price 1998). A sheep crossbreeding decision support system (DSS) is being developed at WRONZ and Lincoln University to assist farmers identify the most profitable crosses to use in their own environment. A functional database containing collated data from published literature, farm trials and field data supplied by farmers is needed for the DSS. This paper describes the data collected to date and some of the problems found in calculating breed trait means.

MATERIALS AND METHODS
The current available pure breeds (lines) and crossbred genotypes were of most interest in this project. These purebred genotypes included Romney (Rom), Perendale (Per), Coopworth (Coop), Merino (Mer), Super fine Merino (SFMer), Corriedale (Corr), Border Leicester (Bord), Poll Dorset (PD), Texel (Tex), Finnish Landrace (Finn), East Friesian (EF), Suffolk and Oxford Down (Oxford). The first breed named in the notation of crossbreds is the sire breed.

Data were collated for 42 traits in six categories and were aligned with the traits defined in the NZ Sheep Improvement Limited (SIL) database as much as possible. The main traits were: carcass: carcass weight (CarcassWt), eye muscle area (EMA), fat depth at GR; growth: birth weight (BWT), weaning weight (WWT), live weight at 6, 8, 12 months old (LW6, LW8, LW12, respectively); hogget wool brightness, bulk, yellowness (COLM), curvature (Curv), fibre diameter (FDIAM12), fibre diameter variation (FDCV), fleece weight (FW12), staple length (StLgth), yield; ewe wool: denoted by prefix E; reproduction: number of lambs born per ewe joined (NLB), number of lambs weaned per ewe joined (NLW), litter size (LitSize); reproductive traits for hogget ewes were denoted

as HNLB, HNLW and HlitSize; disease: faecal egg count before/after 1 March (FEC1/FEC2), nematode count before/after 1 March (NEM1/ NEM2), pinhole/ribbyness score (1-5) for lambskins (Pinhole/Ribby), and foot rot.

Literature and field data. Least squares means, standard error (SE) and number of observations for the traits and genotypes mentioned above were obtained from literature published from 1978 onwards. The age of the animals and time of year measurements were recorded wherever possible. Data were also obtained from breeding schemes and individual farmers. Direct and maternal heterosis estimates were also collated.

Each dataset was assigned an appropriate farm class following the definitions adopted from the Meat and Wool Economic Service of New Zealand (1- South Island High Country, 2- South Island Hill Country, 3- North Island Hard Hill Country, 4- North Island Hill Country, 5- North Island Intensive Finishing Farms, 6- South Island Finishing-Breeding Farms, 7- South Island Intensive Finishing Farms, 8- South Island Mixed Finishing Farms, 9-national/unknown). These data were entered into the database and used to produce generalised breed-trait means using the statistical model below.

Statistical methods. Data were analysed using $1/SE_i^2$ as weight for the ith mean to provide weighted least squares means for each breed and trait, adjusted over all farm classes. Some traits, for example weaning weight, were adjusted to a common age using age as a covariate. GR was adjusted to a common carcass weight in a similar manner. The generalised linear model (Genstat 5 version 4.1) used was: *y=**m**+ breed + farm class + covariate (where applicable) + error.*

RESULTS AND DISCUSSION
Data for a total of 82 genotypes (pure breeds and crosses) were obtained from 51 published NZ papers and 17 field datasets. Most data were in farm classes 5 (28%), 6 (20%) and 7 (27%), covering better farming land. Most information was available for wool traits (54% of the total 1217 records), carcass traits (19%) and growth traits (18%). Twelve percent of records were of carcass weight data produced in the 1970's when there was no premium for carcass quality traits, such as GR and EMA. Fifty percent and 37% of all the data in the database were for purebred and first cross genotypes respectively (Table 1). Breed least squares means (and SE) are presented in Tables 2 and 3 for the

Table 1. Number of records in the database (number of genotypes in brackets)

TraitName	Purebred (14)	First cross (38)	Back cross and F2 (17)	Further crosses (13)	Trait subtotal
Hogget wool	258	186	83	29	556
Ewe wool	104	29	17	1	151
Growth	103	89	21	18	231
Carcass	125	119	0	0	244
Reproduction	45	40	0	0	85
Disease	15	14	10	0	39

Table 2. Generalised means and SE of hogget wool traits for the most common crossbreeds (adjusted to 240 days of growth; the first breed named is the sire breed)

Breed	Brightness (Y)	Bulk (cm^3/g)	COLM (Y-Z)	FDIAM12 (μm)	FW12 (kg)	StLgth (cm)	Yield (%)
EFCorr	62.6 ± 6.3	25.6 ± 2.2	4.0 ± 3.8	32.8 ± 2.2	4.13 ± 0.66		82.6 ± 5.6
TexCorr	65.4 ± 9.8	25.0 ± 5.5	3.5 ± 4.7				82.7 ± 8.0
Tex(TexCorr)	64.7 ± 7.8	28.0 ± 3.3	2.7 ± 3.3				78.0 ± 6.5
Tex(Tex(TexCorr))	63.4 ± 8.3	28.7 ± 4.2	3.2 ± 4.1				79.5 ± 6.9
TexRom	64.1 ± 2.3	27.1 ± 1.0	3.0 ± 1.2	32.2 ± 1.0	3.20 ± 0.34	8.7 ± 3.7	75.0 ± 1.3
Tex(TexRom)	59.6 ± 12.4	28.4 ± 2.1	0.5 ± 7.7	32.6 ± 2.7	2.45 ± 0.66	8.3 ± 5.6	75.2 ± 4.2
(TexRom)Rom		25.4 ± 1.2	2.9 ± 1.4	32.1 ± 1.5	3.19 ± 0.74		72.5 ± 1.8
(PDRom)(TexRom)		31.5 ± 2.1	2.4 ± 3.7	32.0 ± 3.3	2.96 ± 0.74		72.6 ± 4.1
TexRomF2		29.0 ± 2.1	3.1 ± 3.7	32.1 ± 3.3	3.05 ± 0.74		70.5 ± 2.9
BordRom		20.6 ± 0.8	3.1 ± 0.9	36.4 ± 1.0	3.71 ± 0.17		79.1 ± 2.1
CoopRom		21.5 ± 0.8	3.1 ± 0.9	35.5 ± 1.0	3.72 ± 0.17	14.0 ± 2.4	77.2 ± 2.1
FinnRom	72.2 ± 12.7	24.4 ± 5.7	2.1 ± 8.2	28.8 ± 1.1	2.34 ± 0.44	13.7 ± 6.9	77.4 ± 2.5
EFRom		23.0 ± 5.7		32.3 ± 1.9	2.35 ± 3.58	7.6 ± 8.9	86.6 ± 16.6
TexCoop	60.3 ± 4.7	26.6 ± 1.8	0.8 ± 2.9	35.3 ± 1.2	3.00 ± 0.35	9.0 ± 4.0	78.8 ± 2.0
MerRom		26.3 ± 4.0	3.5 ± 5.8	23.6 ± 1.3	3.89 ± 2.53	10.1 ± 3.1	77.3 ± 11.8
(EFCorr)Corr	62.2 ± 7.7	25.5 ± 2.8	3.4 ± 6.1	29.7 ± 1.5	3.41 ± 0.92		81.7 ± 6.4
RomPer	53.3 ± 2.7		4.9 ± 1.1	32.6 ± 0.7	2.63 ± 0.25		73.5 ± 1.3
PDMer		32.5 ± 2.6	2.3 ± 5.7	25.3 ± 2.2	1.46 ± 1.04	8.8 ± 4.0	69.9 ± 7.6
BordMer		27.0 ± 2.6	2.3 ± 5.7	27.2 ± 2.2	2.26 ± 1.04	12.8 ± 4.0	75.0 ± 7.6
TexMer		31.2 ± 2.6	2.9 ± 5.7	26.0 ± 2.2	1.76 ± 1.04	10.7 ± 4.0	73.3 ± 7.8

most common breeds and crosses. The cells in the tables were left blank where no data were available.

The generalised means and the collated heterosis estimates will be used to estimate crossbreeding parameters (Wolf *et al*. 1995) in the DSS. The estimation of these parameters was not covered in this paper. Only 32 estimates of direct heterosis and no estimates of maternal heterosis were available in the NZ literature surveyed, while 100 international literature estimates of direct heterosis and 54 of maternal heterosis were found and used.

Genetic improvement and changes in farm management with time make older data less relevant for predicting present day performance. It is possible for data from earlier studies to be given lower weightings but this was not done in the current analyses mainly because of the difficulty in defining an appropriate weighting system for such diverse breeds and traits. However, this issue will be dealt with in future developments of the DSS. In many cases the age or date on which data were recorded was not given making it difficult to correct for these factors. The data in some papers were of no use because it was not possible to calculate mean standard errors.

Table 3. Generalised means and SE of other traits for the most common pure and cross breeds (the first breed named is the sire breed)

BreedName	CarcassWt[1] (kg)	EMA[2] (cm^2)	GR[2] (mm)	BWT (kg)	WWT[3] (kg)	LW12[4] (kg)	LitSize (lamb)	NLW (lamb)
Romney	15.9±0.7	11.8±0.3	9.6±0.8	4.2±0.1	21.0±0.8	40.7±1.5	1.40±0.27	1.15±0.02
Finn					26.1±10.3	44.6±11.5	1.96±0.61	
Coop	18.5±0.5		10.8±0.8	4.8±0.2	19.6±0.9		2.04±0.29	1.53±0.09
Merino	14.1±1.5	14.7±0.3	9.1±1.3		20.9±5.7	41.2±7.6	1.20±0.61	0.92±0.08
TexRom	19.1±1.8	12.6±0.6	10.2±1.6	5.1±0.2	24.9±1.6	51.5±3.8	0.96±0.61	
BordRom	16.7±1.9	11.7±1.2	8.5±3.5	4.5±0.1	21.6±1.3	47.0±2.8	1.56±0.29	1.40±0.04
CoopRom	17.6±1.2		14.3±2.3	4.2±0.1	20.4±1.0	44.5±2.8	1.56±0.29	1.31±0.04
OxfordRom	17.9±3.2	12.0±0.6	10.5±2.6		23.4±10.3	59.2±11.5	1.16±0.61	
SuffolkRom	18.0±1.4	12.3±0.7	11.0±1.6		22.2±10.3	57.8±11.5	1.16±0.61	
MerRom	14.3±1.3	11.9±0.3			23.4±3.0	48.2±8.2		1.19±0.10
EFCoop				5.5±0.8	25.4±5.8		2.80±0.34	2.15±0.09

[1] Adjusted to 300 days of growth period [2] Adjusted to 19.5 kg hot carcass weight
[3] Adjusted to 90 days age [4] Adjusted to 360 days of growth period

The aim of the crossbreeding DSS is to estimate crossbreeding effects using existing information and then predict unknown crossbred performance (Wolf *et al*. 1995). A simple dominance model is normally sufficient (Kinghorn 1997) and has been used by us. In the database, 14 purebred genotypes are available which require 91 first cross genotypes to obtain biased estimates of direct heterosis, when no reciprocal first crosses are available (Nitter 1978). The existing data cover only 40% of this requirement, so there is a deficiency of F_1 data. There is also a general dearth of information on second and further crosses, thus it has been difficult to estimate maternal heterosis. The deficiency of data in some farm classes means predictions may be inaccurate if there are significant genotype by environment interactions.

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