



White Suffolk Conference 2011

LAMBPLAN Update

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LAMBPLAN Project Officer**

Agenda



- Changes in the last 12 months
- Genetic Progress/Trends
- Upcoming changes
- Web/Software developments
- Pilot Project/INF Outcomes
- Future direction for White Suffolks??

Terminal Analysis Update July 2010



- Updated analysis parameters
- Reset base
- Sire x flock year model
- Reproduction model
- Service sire filter
- ET lambs
- Trends
- Impact on Indexes
- Timing of future changes

Updated Parameters



- Heritabilities and correlations of traits have been updated in the LAMBPLAN Terminal analysis
- The range of breeding values within a trait is expected to decrease
 - Due to lower heritability (not performance)
- Correlations between old and new breeding values remains high

Terminal LAMBPLAN Parameters



Terminal LAMBPLAN genetic parameters for key traits. Heritabilities are on the diagonal; indicative genetic correlations are shown below the diagonal.

BWT	0.10										
WWT	+++	0.15									
MWWT			0.06								
PWT	++	+++		0.20							
AWT	++	+++		+++	0.35						
PFAT	-	-		-	-	0.25					
PEMD	-	-			-	++	0.30				
YGFW		+		+	+	-		0.29			
PWEC				+		-	-		0.20		
PSC		++		+++	++					0.30	
NLW	+	+		+	++			-		++	0.04
	BWT	WWT	MWWT	PWT	AWT	PFAT	PEMD	YGFW	PWEC	PSC	NLW

- / + = 0.1 to 0.24 = low, - - / + + = 0.25 to 0.49 = moderate, - - - / + + + >0.50 = high

Matching ASBVs to markets



Lamb carcass weight	Ewe type	Generic ASBV Specifications			
		BWT (kg)	PWT (kg)	PFAT (mm)	PEMD (mm)
18 - 22kg (Trade)	XB ewes	<0.5	>8	-1.0 to -0.5	1 to 3
	Merino Ewes	<0.4	>8	-0.5 to +0.5	1 to 3
24kg + (Export)	XB ewes	<0.5	>10	- 1.5 to -0.5	0.5 to 3.5
	Merino ewes	<0.4	>10	-1.0 to 0	0.5 to 3.5

Note that these are general suggestions and should be adjusted based on experience and in consultation with your ram breeder

Changes to Indexes



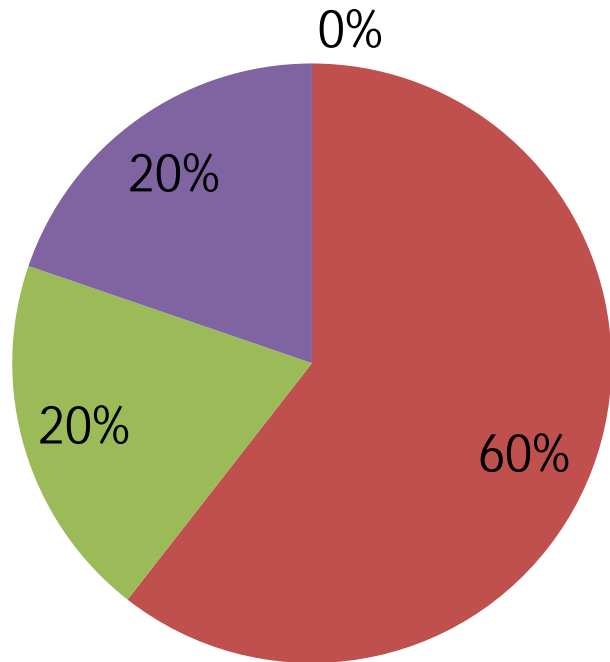
- Changes to the parameters resulted in less variation in ASBVs
- In turn led to less variation in Indexes
- The changes to parameters had a flow on effect to the response expected from indexes, especially Carcase +
- Carcase + weightings will be updated this year!

Change in Carcasse Plus

(emphasis %)

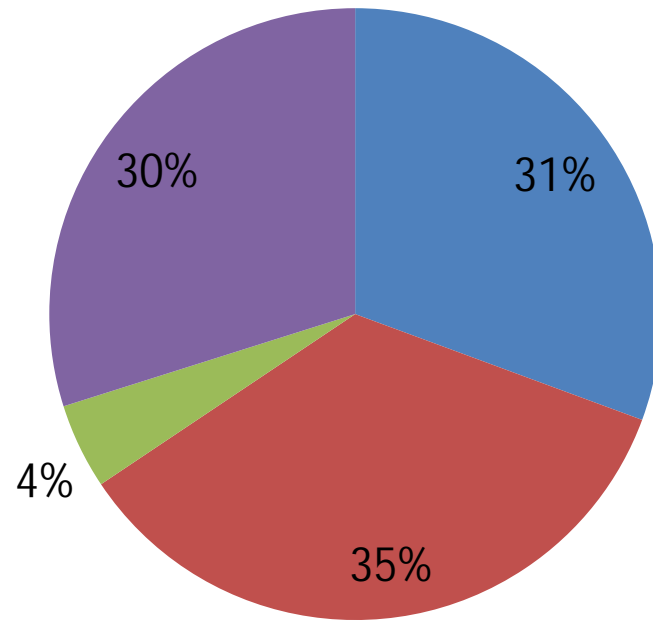
Original C+

■ WWT ■ PWT ■ PFAT ■ PEMD

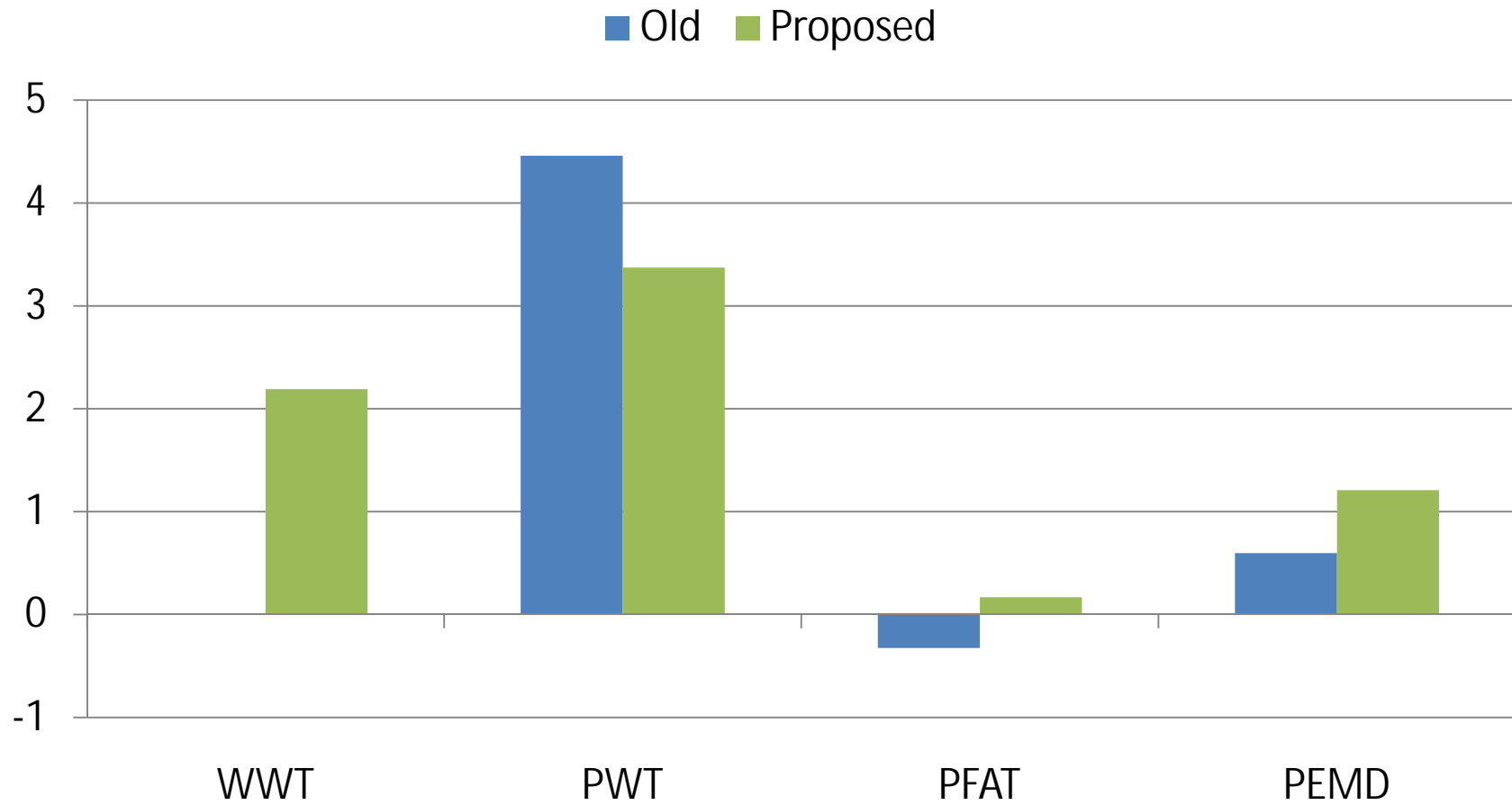


Proposed C+

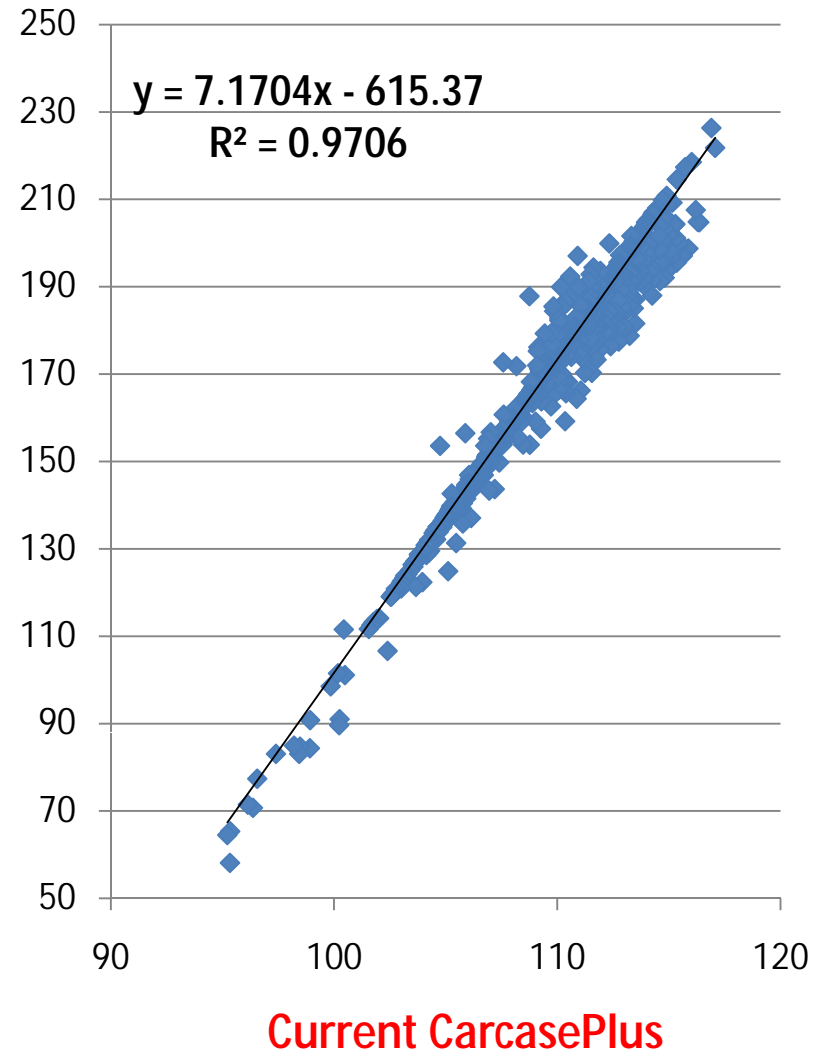
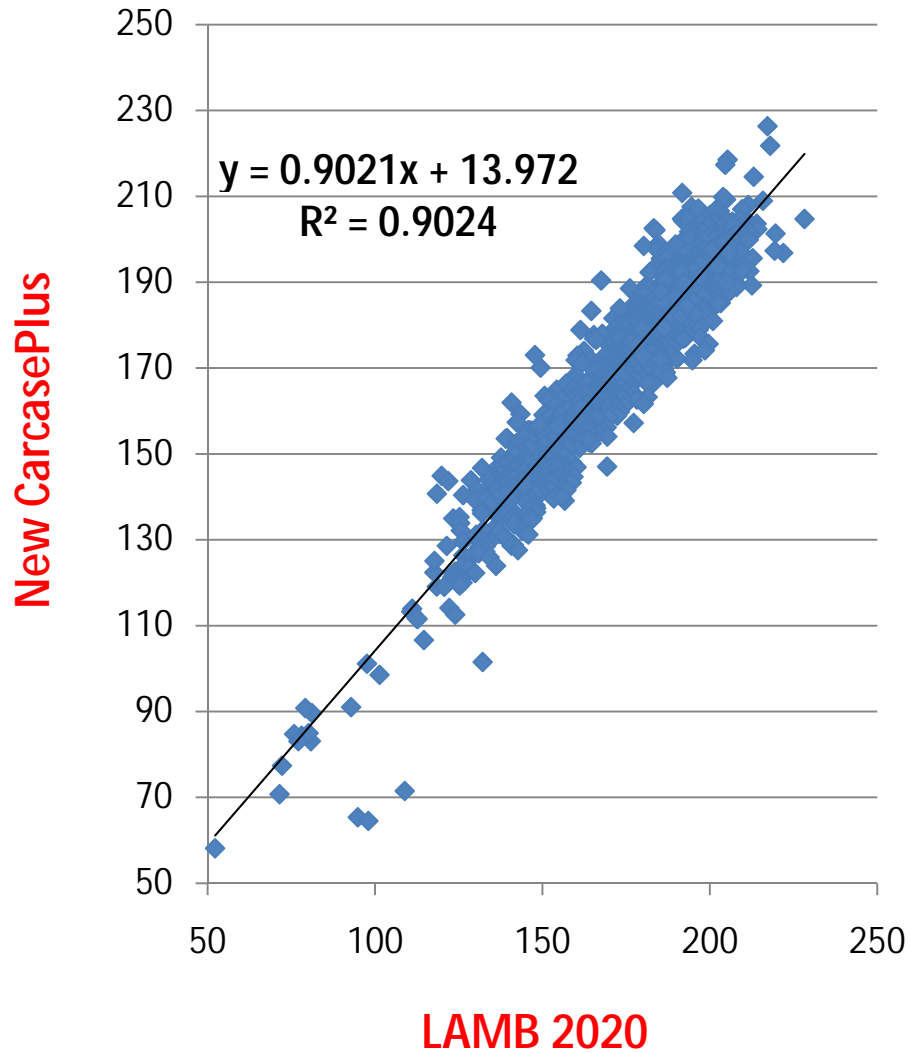
■ WWT ■ PWT ■ PFAT ■ PEMD



Change in trait response



Difference between indexes



Genetic Trends



Software and SG web site



- Pedigree Wizard currently being upgraded
- New website features:
 - Semen Catalogue
 - Sale Catalogues
 - Pen Cards
 - Mating Predictor

Sale

es



Sale Details

Sale Type*

Title*

Description

Sale Location*

Postcode*

Contact name*

Contact phone number(s)*

Contact email address

Website

Sale dates from* to

(example dates: 25/10/2010 12am, 25/10, 25th October)

Remove listing on date*

Show on Sheep Genetics website*

Use this option to temporarily remove your Sale from the website, or to defer listing in the site until you are ready. Your Sale can only be displayed in the website after you have added animals to it.

Images

Optionally import images to display with your Sale description. You can import logos, photos, and other images. Please do not use images with a transparent background as they will not display correctly.

Sale Animals

Import the Excel file containing the list of animals for your Sale (or you can import the animals later). The file must be in a specific format. Download a [copy of the file to use](#)

Excel animals file to import:

Mating Predictor



Mating Predictor

Sheep Genetics » LAMBPLAN » IERMINAL » Mating Predictor



Mating predictor

Sire ids (comma-separated list, max 50)

239899-2009-090201, 239899-2009-090202

Dam ids (comma-separated list, max 50)

239899-2009-090203, 239899-2009-090204

Or, upload file of dam ids

(File must contain one id per line, maximum of 50 ids)

Mating Predictor



Sheep_Genetics > LAMBPLAN > TERMINAL > Mating Predictor

Home

Mating predictor

Sire ids (comma-separated list, max 50)

Dam ids (comma-separated list, max 50)

Or, upload file of dam ids

(File must contain one id per line, maximum of 50 ids)

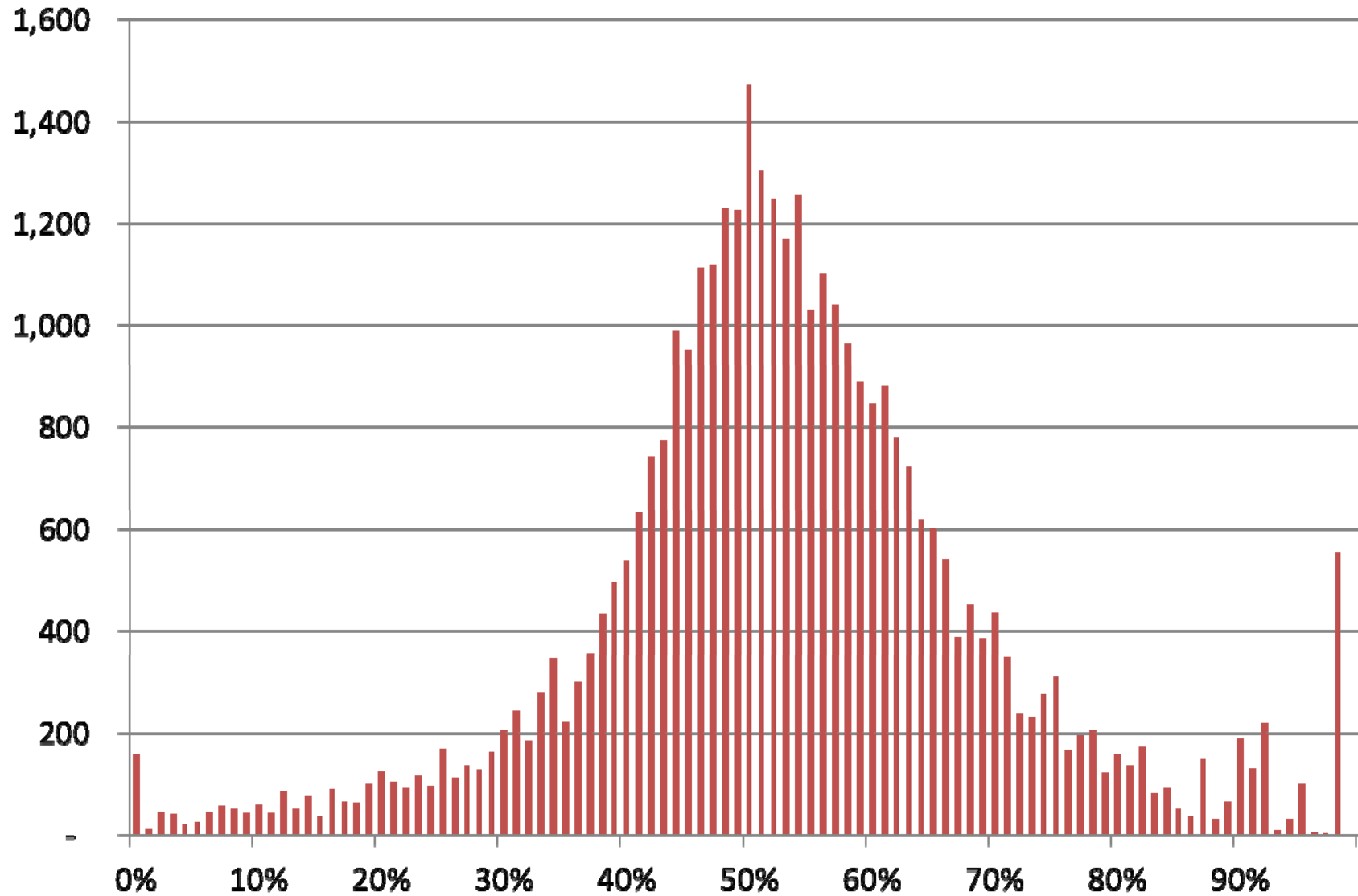
	BWT	WWT	PWT	YWT	HWT	AWT	PFAT	YFAT	HFAT	PEMD	YEMD	HEMD	WWEC	PWEC	YWEC	HWEC	PSC	YSC	LE_DIR	LE_DTR	NLB	NLW	GL_DIR	MWWT	C+	Trades	Lamb 2020	SRC
Sire 23999920090001 Sire 1	0.15 69%	7.9 71%	12.7 72%	12.9 73%	14.1 69%	15.9 67%	-0.7 72%	-1.0 69%	-1.4 65%	0.9 74%	0.7 71%	0.8 69%	-3 59%	3 64%	-2 56%	-1 56%	2.9 67%	2.2 70%	1% 56%	1% 57%	4% 49%	4% 50%	-0.9 74%	2.0 65%	190 60%	111 67%	109 67%	132 59%
x 23999920090003 Dam 3	0.07 48%	3.5 62%	6.9 63%	7.5 58%	7.4 54%	8.9 52%	-0.2 56%	-0.1 50%	-0.2 46%	2.1 56%	2.0 53%	1.9 50%	-	-	-	-	-	-	-	-	4% 29%	4% 29%	-	0.9 44%	153 56%	108 42%	107 42%	123 40%
Progeny predicted	0.11	5.7	9.7	10.1	10.8	12.4	-0.5	-0.5	-0.8	1.5	1.4	1.3	-	-	-	-	-	-	-	-	4%	4%	-	1.8	167	110	108	128
x 23999920090004 Dam 4	0.01 49%	4.2 61%	7.5 62%	8.2 56%	8.0 54%	9.7 51%	0.2 63%	0.3 56%	0.3 51%	2.3 66%	2.1 62%	2.0 56%	-	-	-	-	-	-	-	-	2% 20%	2% 20%	-	1.4 41%	153 56%	108 44%	108 44%	123 40%
Progeny predicted	0.08	6.0	10.1	10.5	11.0	12.8	-0.3	-0.4	-0.5	1.5	1.4	1.4	-	-	-	-	-	-	-	-	3%	3%	-	2.0	167	110	109	128
Sire 23888820090002 Sire 2	0.21 51%	6.6 63%	11.2 65%	12.1 60%	11.9 57%	14.0 54%	-0.3 66%	-0.1 59%	-0.2 54%	1.5 69%	1.4 64%	1.4 60%	-	-	-	-	-	-	-	-	9% 32%	9% 32%	-	1.6 46%	171 61%	111 46%	109 46%	133 43%
x 23999920090003 Dam 3	0.07 48%	3.5 62%	6.8 63%	7.5 58%	7.4 54%	8.8 52%	-0.2 56%	-0.1 50%	-0.2 46%	2.1 56%	2.0 53%	1.9 50%	-	-	-	-	-	-	-	-	4% 29%	4% 29%	-	0.9 44%	153 56%	108 42%	107 42%	123 40%
Progeny predicted	0.14	5.0	9.0	9.8	9.7	11.4	-0.2	-0.1	-0.2	1.8	1.7	1.6	-	-	-	-	-	-	-	-	7%	7%	-	1.3	162	110	108	128
x 23999920090004 Dam 4	0.01 49%	4.2 61%	7.5 62%	8.2 56%	8.0 54%	9.7 51%	0.2 63%	0.3 56%	0.3 51%	2.3 66%	2.1 62%	2.0 56%	-	-	-	-	-	-	-	-	2% 20%	2% 20%	-	1.4 41%	153 56%	108 44%	108 44%	123 40%
Progeny predicted	0.11	5.4	9.3	10.2	9.9	11.8	0.0	0.1	0.1	1.9	1.8	1.7	-	-	-	-	-	-	-	-	6%	6%	-	1.5	162	110	109	128
Breed averages	0.24	6.0	9.4	10.0	10.6	11.9	-0.6	-0.7	0.0	0.7	0.6	0.4	-1	-1	-1	-1	2.6	2.2	-1%	-3%	2%	2%	-0.1	1.8	160	107	107	123

New Developments



- Weaning Scans will be introduced in March
 - 80% correlation with later scan ASBVs
 - Will have to use a minimum condition score as well as weight range as a guide
- Matings Module to be implemented asap
 - To allow recording of AI and Joining dates, Pregnancy Scan results, joining and lambing groups etc
- Online reports/Flock health check

Breed Composition (% 23)



Genetics Extension Review



- Sheep CRC
 - Genetics Training Project Plan
 - Independent industry review of the successes and failures of the current genetics extension
 - Detailed interviews with 90 industry members and internet surveys
 - Focus groups to test industry response to proposed plan

Management Groups

- Management groups identify animals that have equal opportunity to express their potential
- Breeder defined management groups
 - Birth weight – paddock effects
 - Weaning weight – paddock effects
 - Post weaning management group
 - Sickness
 - Orphan / fostered lambs
 - Show & sale teams
 - Time off feed

Single Sire Management Groups

SHEEP GENETICS



Progeny from a single sire that are run together **do not** allow Sheep Genetics to separate genetic and environmental effects on performance

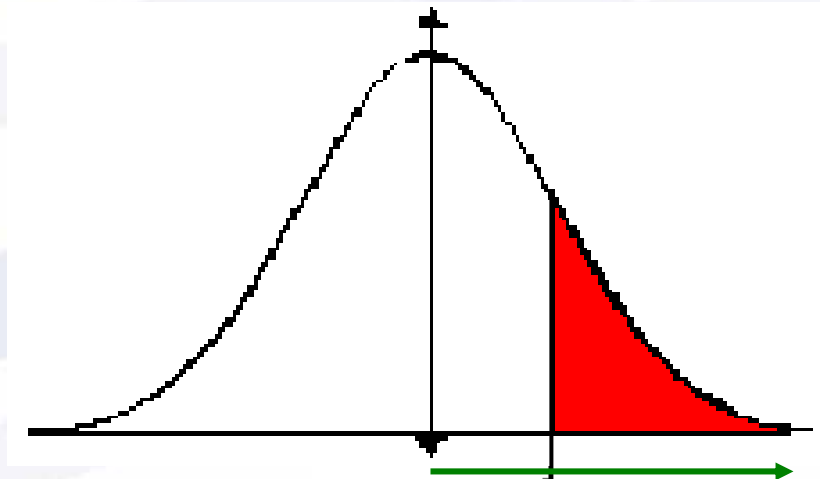
Single Sire Management Groups should be avoided

Data quality

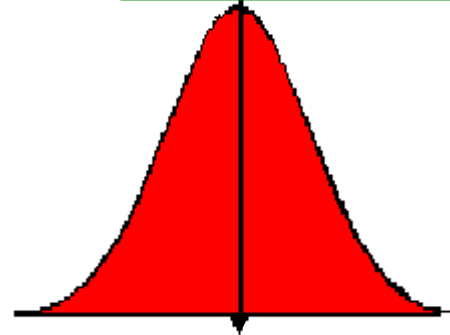
- **Accurate pedigree**
 - Sire (% of flock)
 - Dam
 - Date of birth (Bulk date vs week of birth)
(AI vs natural)
- **Whole flock recording**
 - Selective recording (excessive culling) may lead to severe biasing of ASBVs
- **Rams for maiden ewes**
 - OVIS adjusts for ewe age but it is recommended that rams used on maidens also be used over some mature ewes

Submitting selected data

Average = 45kg



+ 6 kg



Average = 49kg

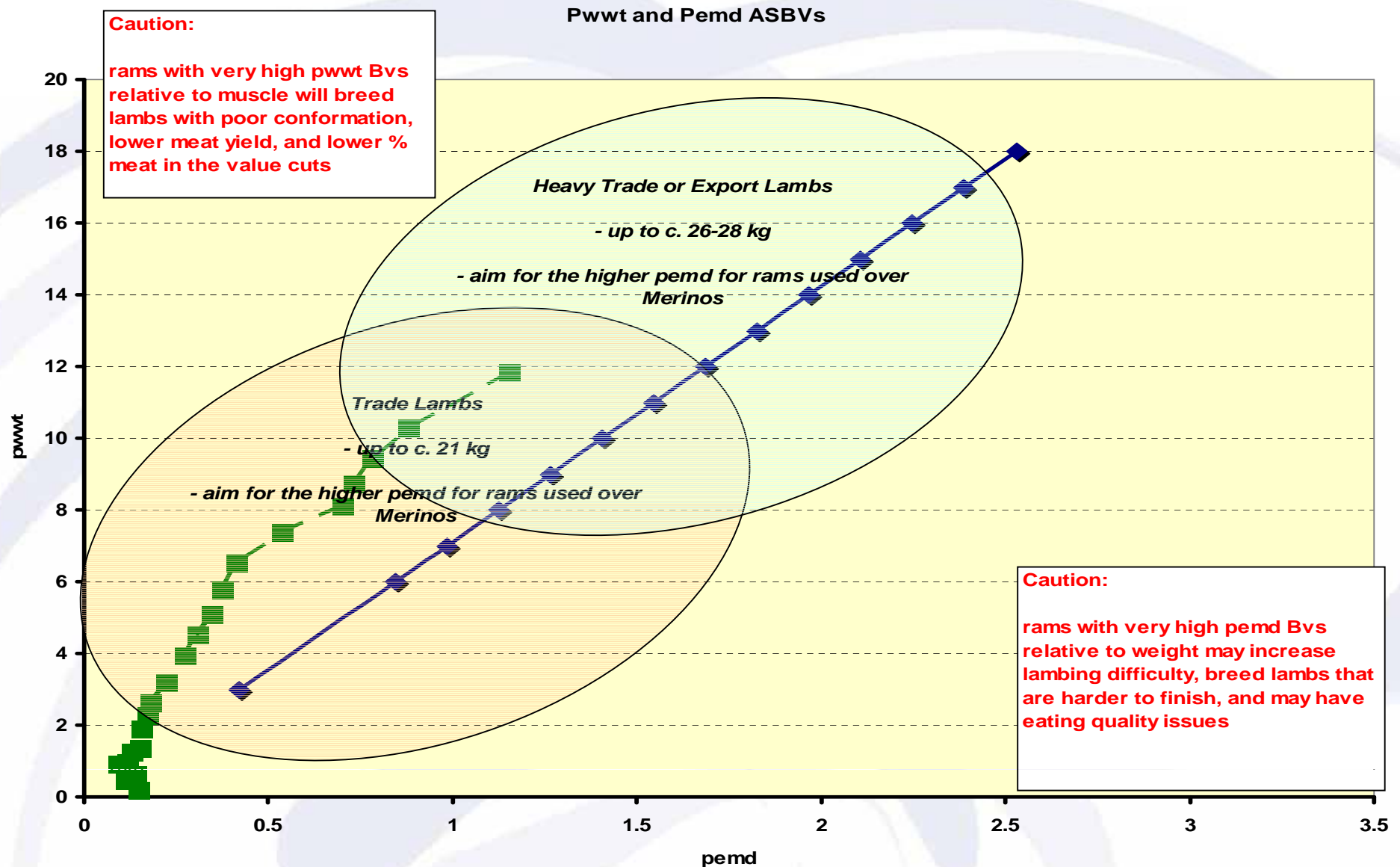
+ 2 kg

Future Direction for White Suffolks



- More attention needs to be paid to maintaining moderate BWT and LE
- Excellent gains have been made for growth
 - Needs to be balanced with greater gains to muscling

Balancing Growth and Muscle



Future Direction for White Suffolks



- More attention needs to be paid to maintaining moderate BWT and LE
- Excellent gains have been made for growth
 - Needs to be balanced with greater gains to muscling
- Continued attention to moderate fat depth

Pilot Project & INF



- Initial RBVs from the Pilot Project have been released for Terminals and Merinos
 - Standard weight and carcass traits
 - Some improvement in accuracy
- From March 2011 RBVs for new carcass traits will be released utilising DNA info and INF abattoir data
 - IMF, SF, LMY
 - DNA information will have a greater impact on the low heritability and hard to measure traits
- Intend to run another round of the Pilot Project in June
- The current mating of the INF flock is the last under the current project
 - To continue under a industry funded model