Genomic evaluation system for Australian sheep
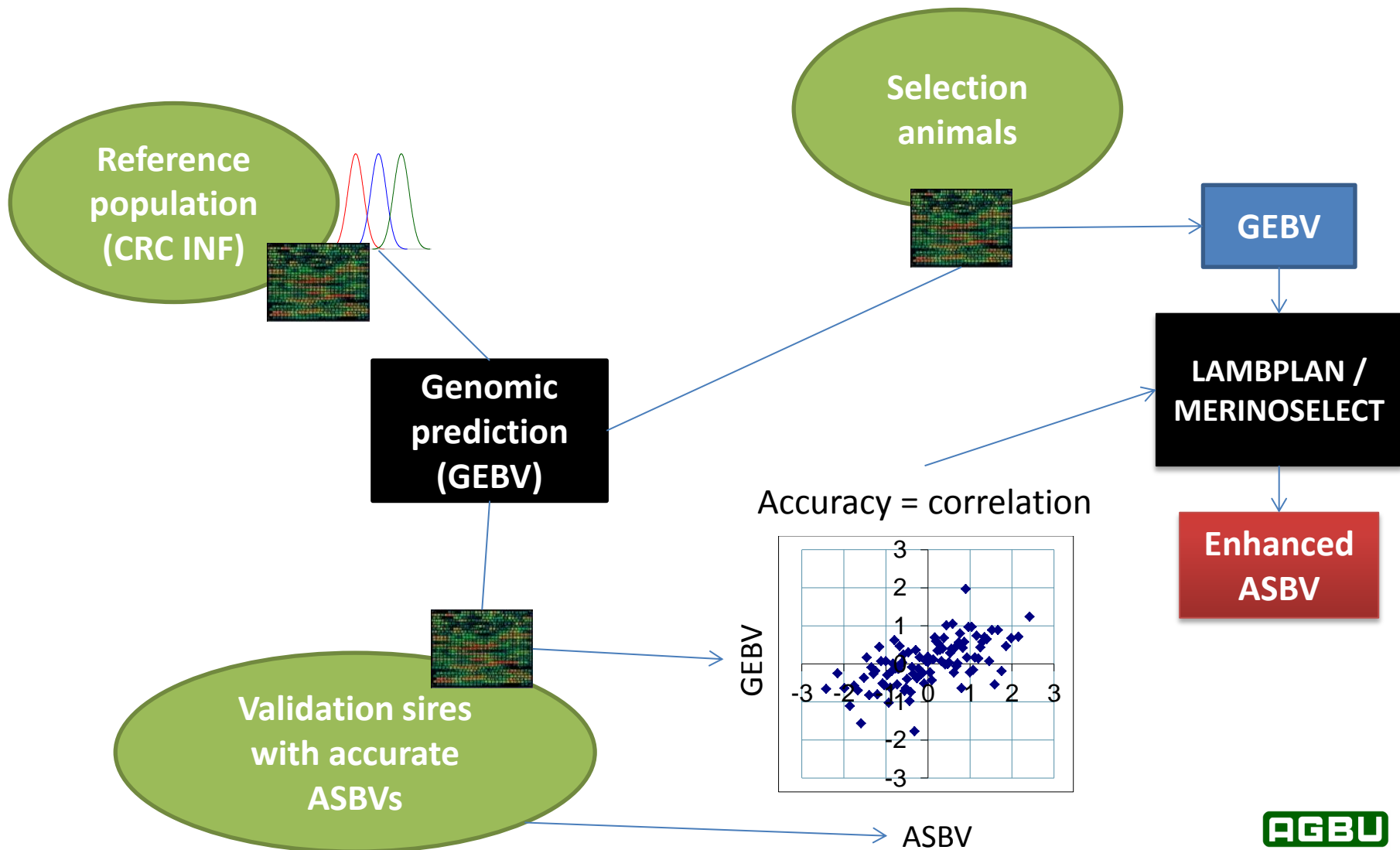
Andrew Swan

AGBU, UNE, Armidale

Outline

- A quick recap on the current genomic evaluation system

- RBV performance and genomic accuracy update

- Ongoing R&D

Making genomic predictions

Recap on the current system

- Merinos: 32 traits, 6(+) indexes, Poll/Horn test
- Border Leicesters: 18 traits, 5 indexes
- Terminal sires: 13 traits, 3 indexes

- Methods of calculation:
  - "Blending" for traits with ASBVs
  - "Single step" for carcass and eating quality traits (7 traits)

- Blending:
  - Combines ASBV and GEBV from separate analyses into RBV
  - No RBV without an ASBV

Accuracy of RBV
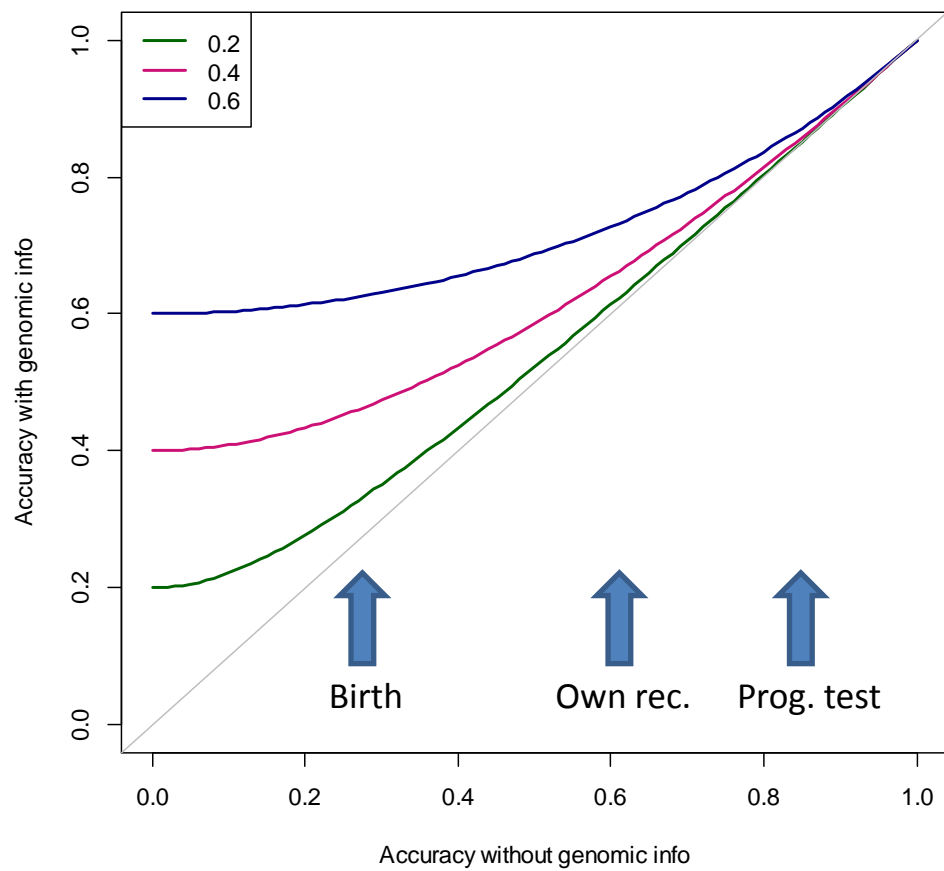
Genotyped animal counts (27-Aug-13)

	Reference	IN sires	Val. Sires	Pilot 1	Pilot 2	Pilot 3
Reference	16,684					
IN sires	1	377				
Val. Sires	0	338	1,561			
Pilot 1	0	56	234	312		
Pilot 2	0	0	154	0	787	
Pilot 3	0	0	0	0	1	2,484
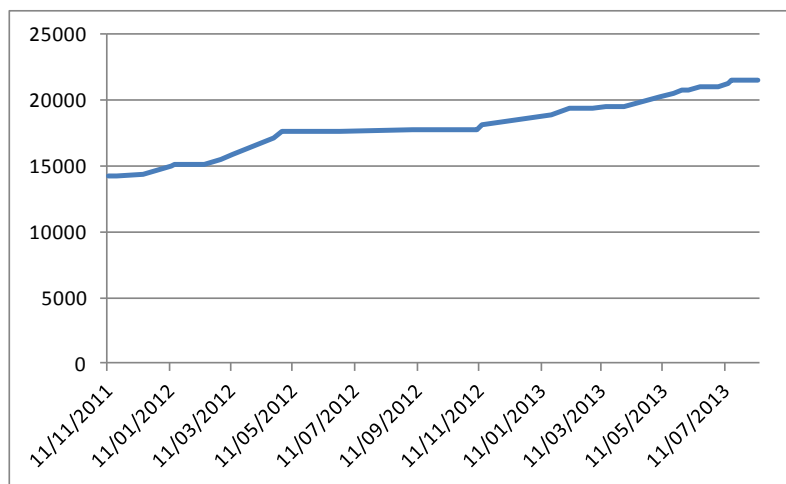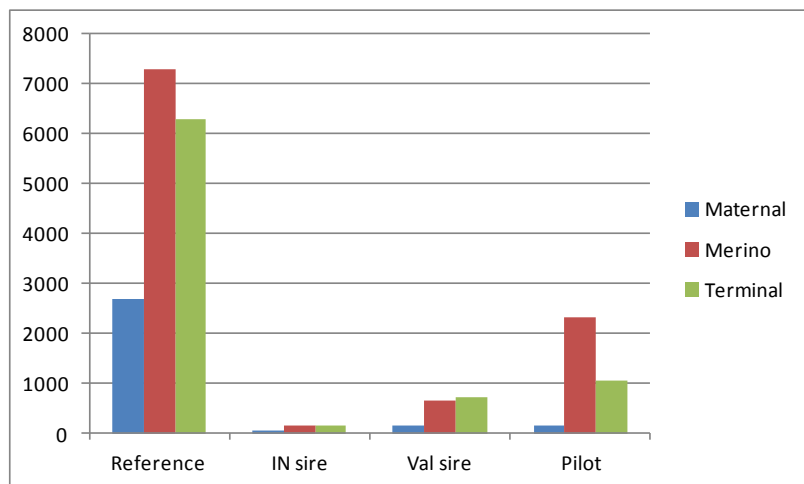
Evaluating the accuracy of genomic selection

- Pilot project performance:
  - weaning RBVs of young animals shown to be more accurate than weaning ASBVs

- Validation sire accuracies:
  - comparing GEBVs of validation sires with their true breeding values

- Demonstrating increased rates of genetic gain:
  - final proof but doesn't exist…

Pilot project performance

- Compare ASBV and RBV at weaning with "final" ASBV
  - (ASBV$_W$ *versus* ASBV$_F$ and RBV$_W$ *versus* ASBV$_F$)

- Comparisons presented for two sets of animals:

  - All pilot project (2&3) animals who have changed accuracy substantially (proxy for trait measurement)

  - Pilot project animals who have become sires

Problem: ASBV$_F$ needs to be highly accurate → True Breeding Value (TBV)

Expected correlation with "final" ASBV
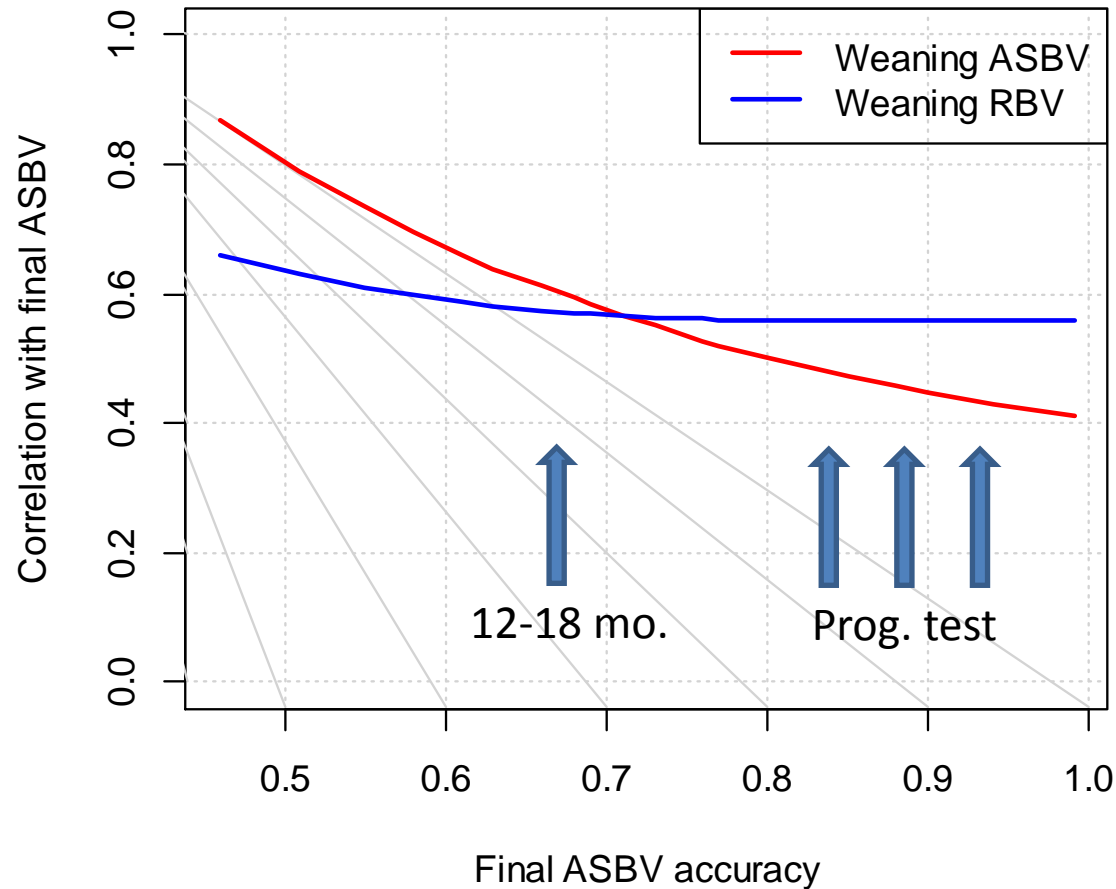
Weaning ASBV may look better until accuracy of final ASBV approaches TBV

Merino wool traits: all pilot animals

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
ygfw	962	38	58	67	0.70	0.65
ycfw	922	37	57	63	0.71	0.65
yfd	1117	43	66	78	0.79	0.75
ydcv	1008	36	49	67	0.53	0.46
yss	853	28	45	55	0.50	0.42
ysl	811	32	58	62	0.79	0.80

Merino wool traits: pilot sires

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
ygfw	30	49	72	71	0.76	0.79
ycfw	30	47	72	68	0.77	0.83
yfd	30	53	78	77	0.88	0.86
ydcv	30	48	60	69	0.50	0.38
yss	30	40	51	57	0.73	0.65
ysl	30	47	65	66	0.79	0.86

Merino weight and scanning: all pilot animals

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
wwt	140	43	54	70	0.58	0.61
pwt	258	46	62	69	0.71	0.62
ywt	451	47	64	68	0.76	0.68
pemd	723	34	46	62	0.67	0.60
pcf	637	26	41	54	0.73	0.62
yemd	742	34	44	62	0.73	0.71
ycf	645	27	37	54	0.76	0.73

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Merino weight and scanning: pilot sires

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
wwt	30	65	68	84	0.72	0.76
pwt	30	61	69	82	0.73	0.78
ywt	30	59	72	79	0.75	0.77
pemd	30	44	58	66	0.69	0.62
pcf	30	39	54	60	0.71	0.43
yemd	30	45	54	66	0.75	0.76
ycf	30	40	44	59	0.78	0.76

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Maternal breed traits: all pilot animals

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
bwt	21	61	66	79	0.89	0.89
wwt	20	66	70	84	0.87	0.88
pwt	59	62	68	74	0.82	0.78
awt	61	56	63	67	0.84	0.68
pemd	72	50	54	69	0.66	0.55
pcf	72	52	55	71	0.68	0.46

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Maternal breed traits: pilot sires

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
bwt	16	61	66	83	0.86	0.85
wwt	16	67	71	88	0.87	0.86
pwt	16	65	70	87	0.87	0.88
awt	16	57	64	76	0.90	0.91
pemd	16	54	57	83	0.53	0.42
pcf	16	56	58	85	0.50	0.47

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Terminal breed traits: all pilot animals

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
bwt	99	61	61	80	0.67	0.46
wwt	94	63	65	79	0.72	0.59
pwt	105	61	65	78	0.68	0.54
pemd	191	58	64	75	0.89	0.78
pcf	177	56	60	73	0.76	0.66
pwec	129	12	37	63	0.37	0.58

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Terminal breed traits: pilot sires

Trait	N	Accuracy			Correlation with $ASBV_F$	
		$ASBV_W$	RBV_W	$ASBV_F$	$ASBV_W$	RBV_W
bwt	108	61	62	77	0.75	0.66
wwt	108	65	67	79	0.73	0.68
pwt	108	65	68	79	0.77	0.77
pemd	108	66	70	80	0.89	0.84
pcf	108	64	67	79	0.81	0.70
pwec	108	20	41	37	0.72	0.62

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Bottom line for pilot project results

- Average (RBV correlation – ASBV correlation) → want this to be positive!

Breed	All animals	Sires
Merino	-0.04	0.00
Maternals	-0.09	-0.02
Terminals	-0.08	-0.07

- Correlations mostly fit with expectations
- RBV correlations improving as progeny test information increases
- Less so for Terminals, but high initial ASBV acc and lower GEBV acc

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Accuracies from validation sires

- Best information currently available on effectiveness of genomic selection

- Calculated as correlation between sire GEBV and ASBV:
  – GEBV is genomic prediction based on information nucleus data
  – ASBV is independent of information nucleus data with accuracy approaching 100%
  – Correlations from this method used during pilot 2

- Alternative REML analysis:
  – Estimate genetic correlation between GEBV and target trait phenotypes
  – Can remove genetic group effects (flocks, strains, breeds)
  – Less reliant on having high accuracy ASBVs (can use pilot animal data as well as validation sires)
  – Correlations from this method used during pilot 3

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Merino wool trait accuracies: yearling

Trait	Sires	Pilot 2	Pilot 3	REML
ygfw	329	0.65	0.40	0.37
ycfw	223	0.66	0.40	0.34
yfd	329	0.72	0.50	0.52
ydcv	330	0.44	0.30	0.32
yss	249	0.35	0.35	0.32
ysl	227	0.55	0.50	0.42

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Merino wool trait accuracies: adult

Trait	Sires	Pilot 2	Pilot 3	REML
agfw	138	0.65	0.40	0.50
acfw	80	0.58	0.40	0.56
afd	135	0.71	0.50	0.49
adcv	135	0.35	0.30	0.39
ass	111	0.34	0.35	0.68
asl	72	0.61	0.50	0.53

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Merino body weight

Trait	Sires	Pilot 2	Pilot 3	REML
bwt	249	0.37	0.35	0.54
wwt	400	0.34	0.35	0.19
pwt	297	0.49	0.50	0.48
ywt	334	0.58	0.50	0.58
hwt	290	0.59	0.50	0.55
awt	97	0.60	0.50	0.47

Merino muscle, fat, wec, breech wrinkle

Trait	Sires	Pilot 2	Pilot 3	REML
pemd	155	0.45	0.25	0.33
pcf	155	0.42	0.25	0.27
yemd	221	0.37	0.25	0.26
ycf	218	0.22	0.25	0.22
pwec	224	0.25	0.30	0.26
ebwr	184	0.33	0.30	0.37
lbwr	36	0.43	0.25	0.20

Maternal breeds

Trait	Sires	Pilot 2	Pilot 3	REML
bwt	110	0.41	0.40	0.41
wwt	99	0.40	0.40	0.47
pwt	92	0.42	0.40	0.62
ywt	79	0.51	0.50	0.33
hwt	51	0.32	0.30	0.22
awt	32	0.42	0.40	0.45
pemd	80	0.26	0.25	0.34
pcf	80	0.25	0.25	0.34
pwec	100	0.06	0.00	0.10

Terminal breeds

Trait	Sires	Pilot 2	Pilot 3	REML
bwt	426	0.15	0.15	0.19
wwt	406	0.26	0.25	0.23
pwt	390	0.35	0.35	0.23
pemd	357	0.40	0.40	0.41
pcf	357	0.30	0.30	0.37
pwec	238	0.31	0.30	0.32

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Genomic accuracy summary

Trait group	Merino	Maternal	Terminal
Wool	0.30 to 0.50		
Weight / scanning	0.25 to 0.50	0.25 to 0.50	0.15 to 0.40
Worm egg count	0.30	< 0.10	0.25

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Ongoing R&D

- Development of single step software:

  - Computation for genotype processing advancing rapidly

  - Working models available, and have been implemented for carcass traits

  - Still to be incorporated in main OVIS evaluation

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Next generation of ASBVs: "Single Step"

- One analysis combining:
  - Performance records
  - Pedigree
  - Heritabilities and genetic correlations
  - Genomic information

  All animals in SG, genotyped or not

- Benefits:
  - Increased size of reference population (all animals genotyped and recorded)
  - Genomic information extended to un-genotyped relatives
  - Automatically line up animals to ASBV scale (still subject to linkage)

Increased size of reference with Single Step

Breed	Trait	Current reference	Pilot animals	Validation sires	Validation sire progeny
Merino	yfd	4,800	500	400	52,000
Merino	pemd	9,600	500	140	6,800
Terminals	pemd	9,600	500	500	72,000

- If you have animals measured and genotyped you are your own reference

- All animals benefit whether they are genotyped or not

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Summary

- Pilot project results:
  - Weaning RBVs performing as expected for Merinos and Maternals
  - Disappointing for Terminals (but high accuracy weaning ASBV relative to GEBV)
  - Need more pilot animals to be progeny tested

- Accuracies from validation sires:
  - Data building up
  - Current analyses confirm previous results

- Single step analyses under development