University of New England

Genetic Evaluation, BLUP

Lecture 11

Introduction to Breeding and Genetics

GENE 251/351

School of Environment and Rural Science (Genetics)

Estimation of Breeding Values in livestock in Australia

- Genetic evaluation systems

  Beef: BREEDPLAN via breed societies

  Sheep: Sheep Genetics: Lambplan, MerinoSelect

  Dairy: ADHIS

  – Breeder submits phenotypes and pedigree

  – Genetic evaluation system returns EBVs
    - plus other information e.g. selection indexes, accuracies, inbreeding coefficients

  – Calculating of EBVs is generally via BLUP method

Extract from LAMBPLAN report

Terminals - Top 150

Analysis Date Friday, 15 June 2001

LAMBPLAN

Sires

ID	Stud of breeding	Wwt	Pwwt	Ywt	Pfat	Pemd	Carcase +	Progeny	Inbreeding & Accuracies Coeff	Weight	Carcase	Sire	Sire of Dam
161972-1999-990196	HILLCROFT FARMS	5.46	14.95	14.94	-1.19	1.62	226.64	38	0.133	83	70	1619721998980093	1630001993930134
162368-1998-980211	KURRALEA	6.60	12.39	12.69	-0.89	2.50	215.20	1148		97	96	1623681994940260	8600401992920175
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What is a BLUP EBV?

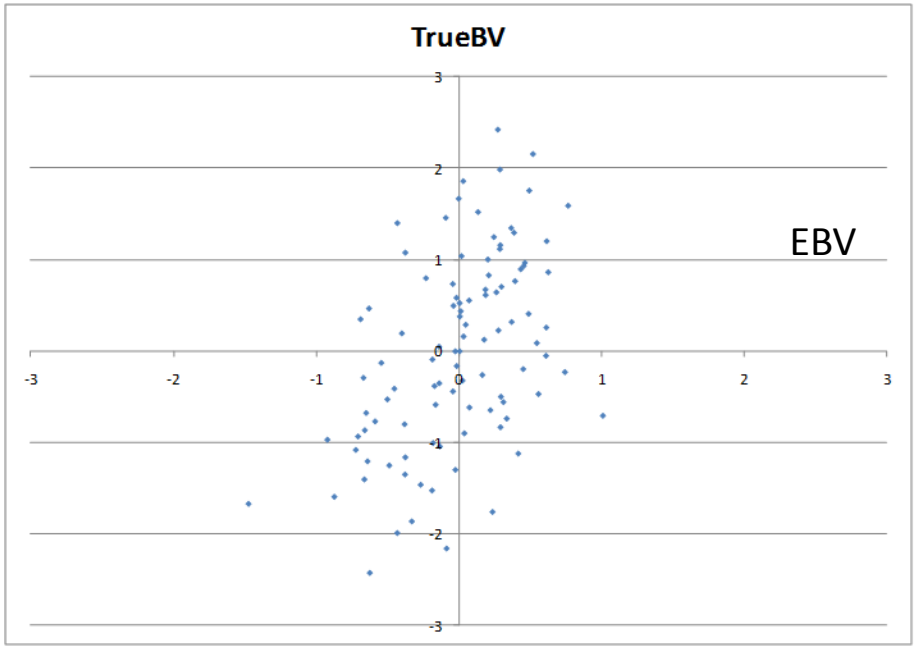
- Best Linear Unbiased Prediction

- Uses a statistical model (linear mixed model) such that

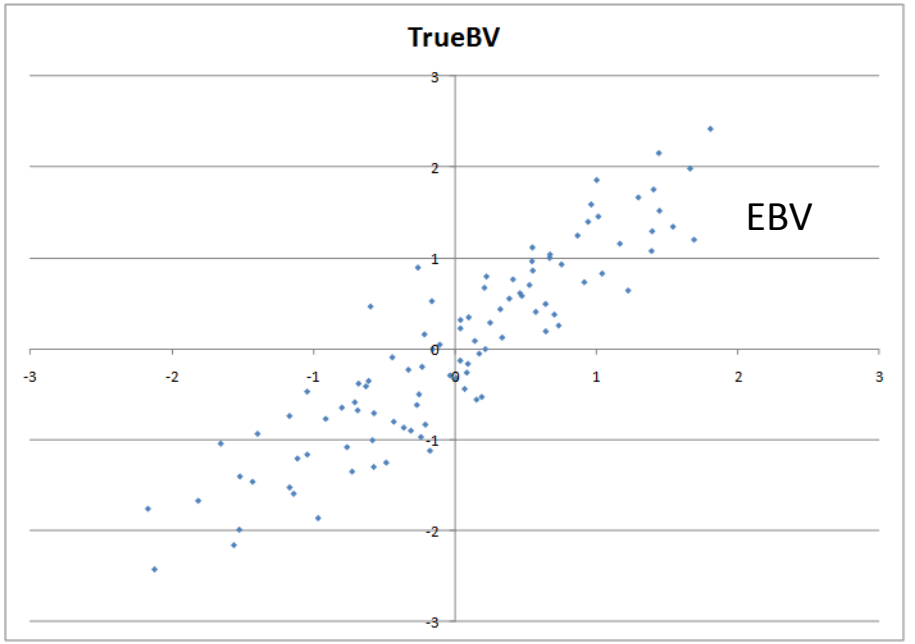
  - Information of all relatives is used — Best
  - Fixed effects are accounted for — Unbiased

  - The method accounts for selection over time
  - Non-random mating of sires and dams

Accuracy of EBV = correlation with True BV



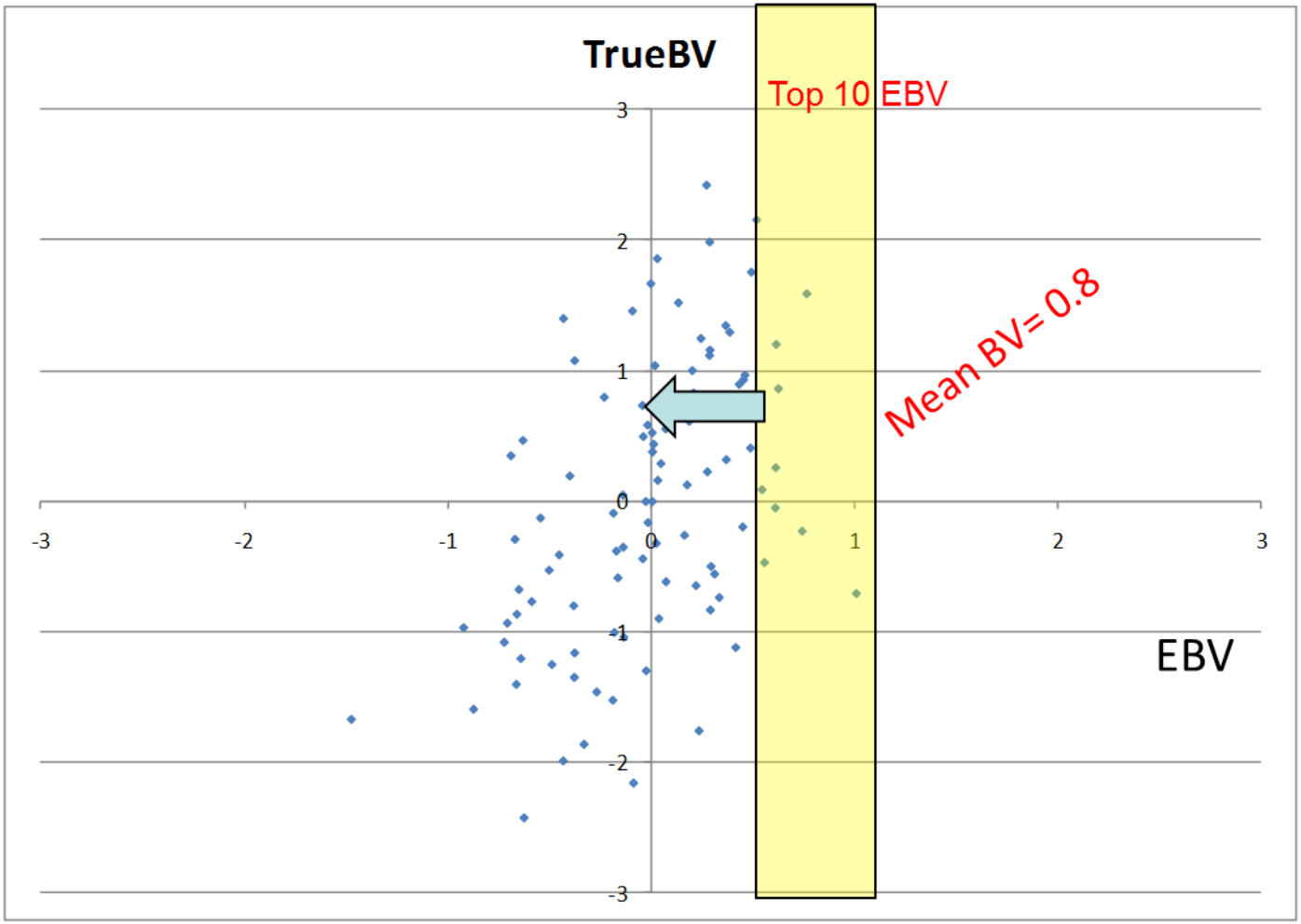
Accuracy = 45%



Accuracy = 90%

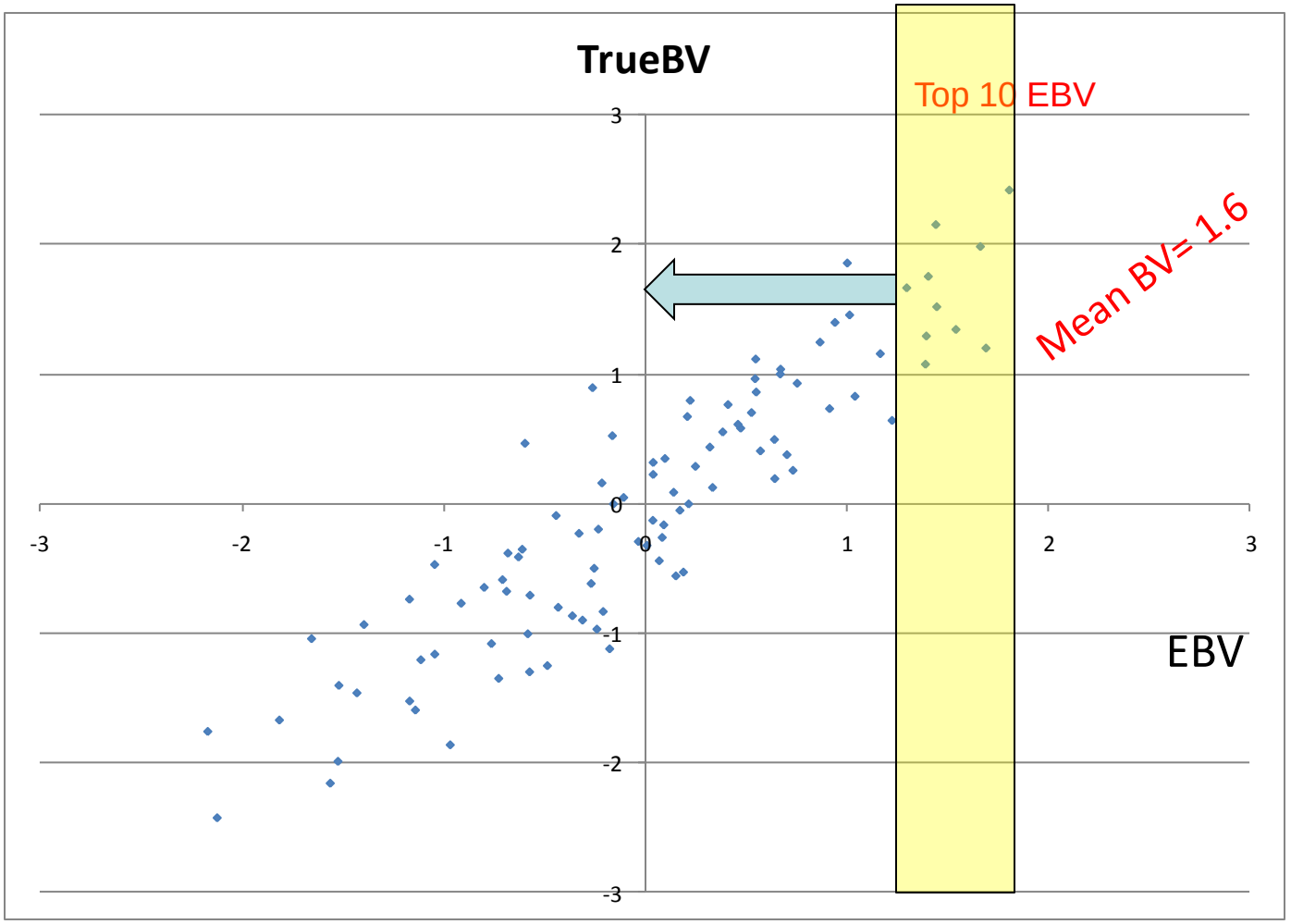
Select on EBV: accuracy related to response

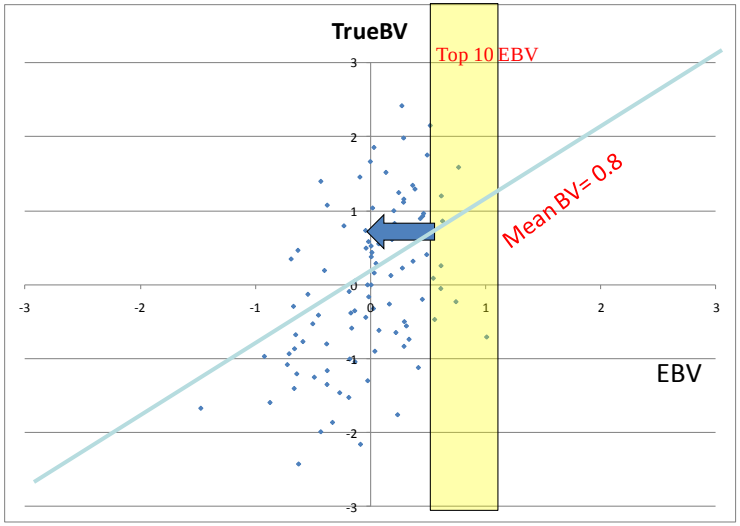
Accuracy = 45%



Double accuracy gives double selection response!

Accuracy = 90%





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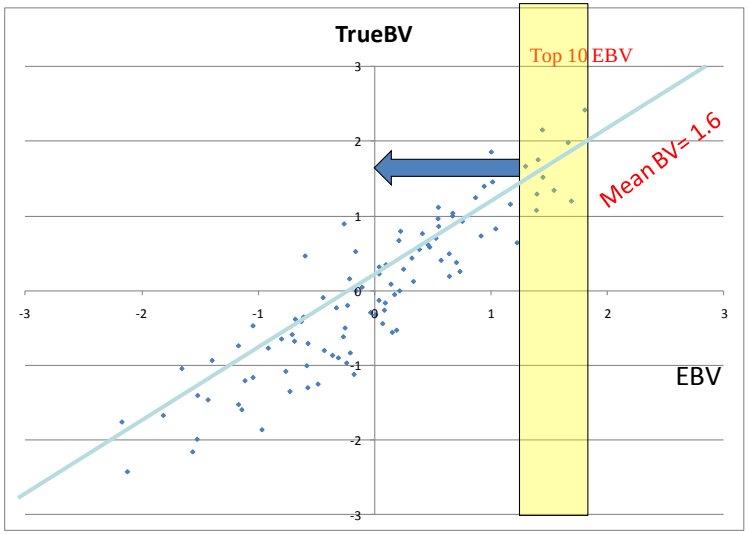


the more accuracy,
the more response

Accuracy of predicting a breeding value

Info used. h2 = 0.25	Accuracy of EBV
Sire + Dam	0.35
Prog Tested Sire + Dam	0.49
… ……. + Own Record	0.63
..... + DNA markers	0.71
..... . + 30 progeny	0.85
..... + 1000 progeny	0.99

Features of EBVs

High accuracy, for high response *'best'*

- *highest correlation between true and estimated breeding value*

Lack of any bias, for fair comparison *'unbiased'*

- *Comparisons between animals should not be affected by non-genetic effects*

Possible causes of bias from ‘fixed effects’

- Problem: Animals reared as different birth/rearing type
- Solution: Compare phenotypes with others of same type

- Problem: Animals producing in different herds
- Solution: Take phenotypic deviation from herd mean

- Problem: Animals are measured at different ages
- Solution: Correct phenotypes back to the appropriate age

Correcting for age differences

	Age (mo)	Weaning Weight Kg.
Alfy	11	280
Betty	13	295

Population mean
at 12 mo = 285kg

Correcting for age differences

	Age (mo)	Weaning Weight Kg.
Alfy	11	280
Betty	13	295

Population mean at 12 mo = 285kg

Correct phenotypes to a 'constant' age

If growth per month is 9 kg/mo) →

Corrected weights

A: 280 – 9.(11 - 12) = 289 kg → P = +4

B: 295 – 9.(13 - 12) = 286 kg → P = +1

Example of contemporary groups

Bull	YW	Herd Ave	P	EBV h^2=40%
Bert	330	300	+30	+12
Flossy	300	260	+40	+16

Note that this assumes that herds have the same *genetic* mean

Can not always take simple deviation from herd averages

	Herd A	Herd B
Progeny of Sire 1	320	
Progeny of Sire 2	300	
Progeny of Sire 3	-	310
Progeny of Sire 4	-	330

Can not always take simple deviation from herd averages

	Herd A	Herd B
Progeny of Sire 1	320	
Progeny of Sire 2	300	
Progeny of Sire 3	-	310
Progeny of Sire 4	-	330
Progeny of Sire 5	290	340

Link sire

A linear model is used to correct for unbalanced data

Possible causes of bias ‘fixed effect confounded with genetic effect’

- Problem: Animals producing in different herds, and the different herds have different genetic means (*no longer can take phenotypic deviation from herd mean)*

- Solution: Use reference sires as links between herds, and simultaneously evaluate herd and sire effects

A feature of BLUP

In most genetic evaluation programs:

- Linkage between flocks/herd is now substantial
- This allows across-flock and even across-breed analysis

Possible causes of bias
'unequal merit of mates'

- Problem: Some sires have better mates

Sire 1: +300	Dam 1: +200	Progeny: +250
Sire 2: +300	Dam 2: +300	Progeny: +300

Without information on the dams, sire 2 would 'look better' due to a higher progeny mean

- Solution: Account for mates by evaluating all animals jointly

A feature of BLUP

Possible causes of bias ‘selection bias’

– Problem: There is culling and selection

- worst sires have more progeny culled ‘culling bias’
- animals are from selected parents

Culling bias

ID	*Sire*	*Weaning Weight*	*Progeny mean*	*Yearling Weight*	*Progeny mean*
101	1	160		300	
102	1	140	140	280	280
103	1	120		260	
104	2	140		280	
105	2	120	120	260	270
106	2	100		no record as culled	

Sire 2 gets an unfair 'lift' in progeny mean of yearling weight, due to culling at weaning.

Animals are from selected parents

Year 1

Mean = 300

350 300 250

Year 2

325 315 285

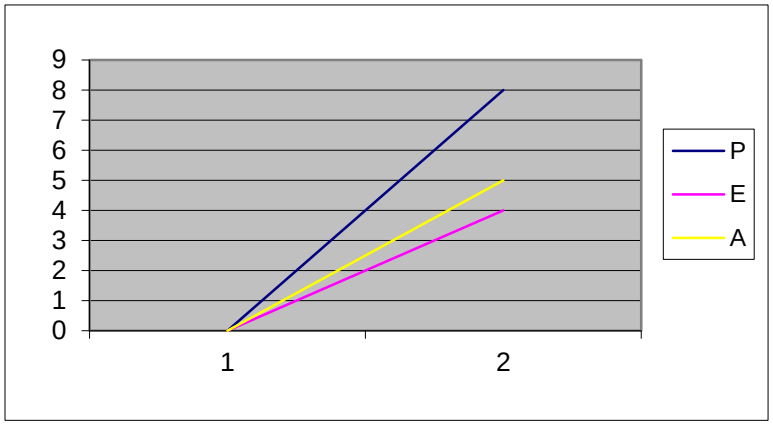
Mean = 308

Estimating genetic trend

	Ave EBV	Year Effect
Year 1		
Mean = 300	0	300
Year 2		
Mean = 308	5	304

	350	300	250
EBV:	14	-2	-13

	325	315	285
EBV:	10	8	-4



Possible causes of bias ‘selection bias’

- Problem: There is culling and selection
  - worst sires have more progeny culled ‘culling bias’
  - animals are from selected parents
- Solution: Do joint evaluation
  - account for culling bias by evaluating first and later traits jointly
  - account for selection by joint evaluation over years
  - Information about culled animals should be included in analysis

A feature of BLUP

Genetic trends

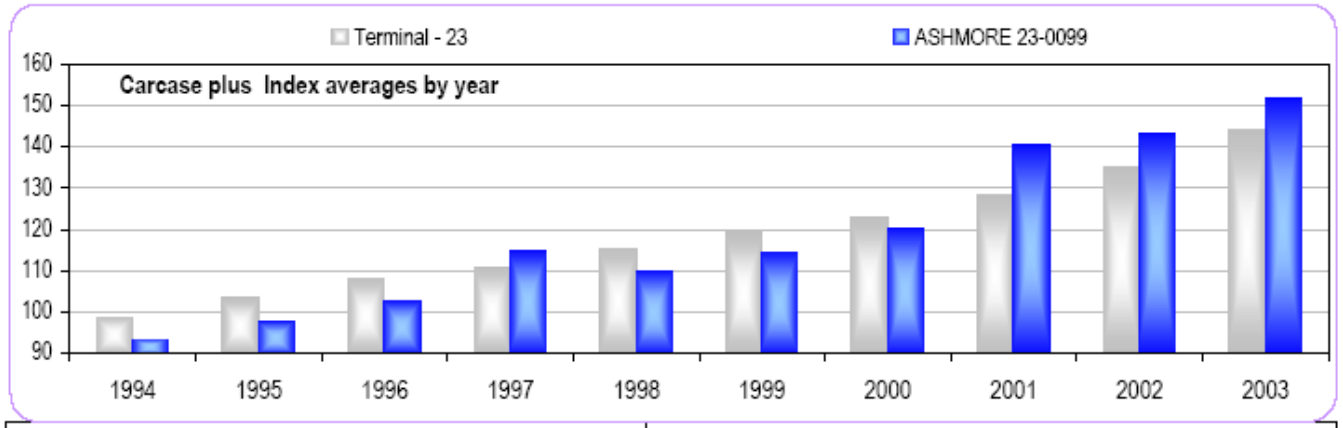
BLUP separates genetic and year effects

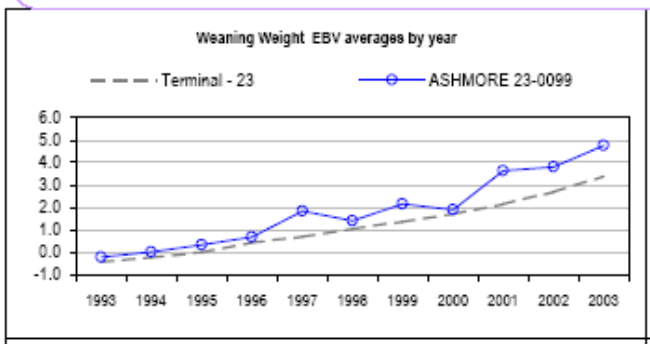
genetic trends can be observed by plotting BLUP EBVs over years

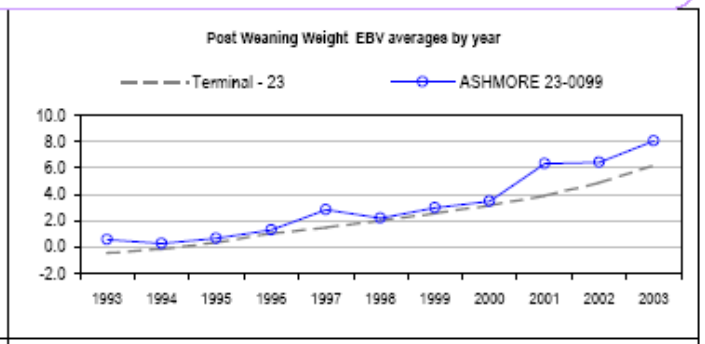
ASHMORE
BRIAN & TROY FISCHER
23-0099

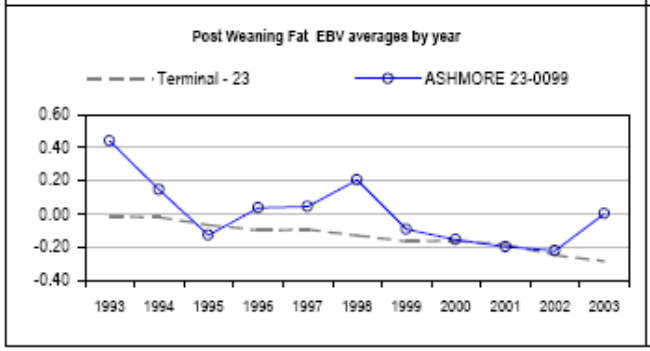
Analysis : ***Terminal - 23***

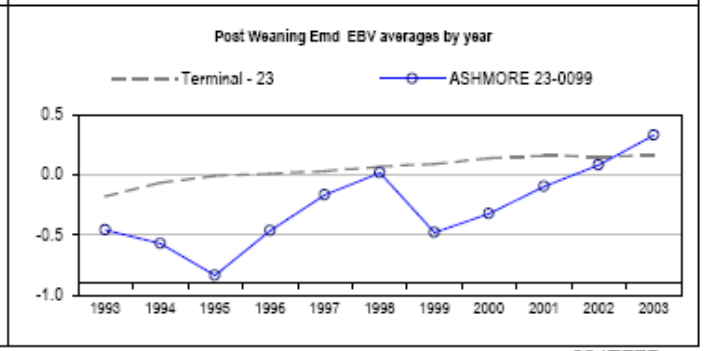
Dated : 1/11/03











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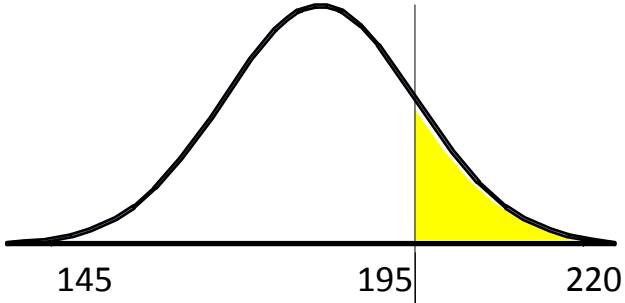
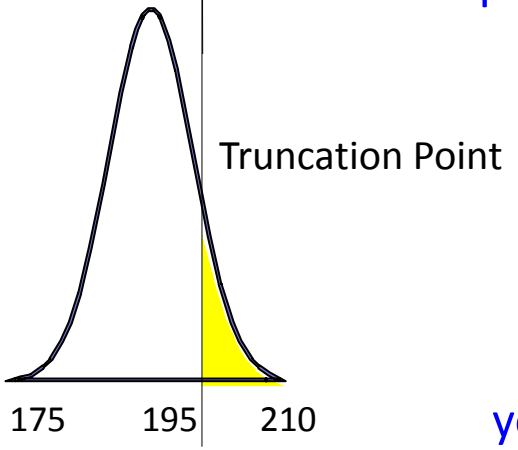
BLUP helps selecting between old and young bulls

- EBVs can be compared directly over age classes
- Selection on BLUP EBVs optimizes generation interval



proven sires



young sires

Example of BLUP selection (truncation)

Terminals - Top 150

Analysis Date Friday, 15 June 2001

LAMBPLAN

Sires

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Consider top 15 sires, truncation point = 195

Sires in top are from various age classes

Another feature of BLUP

- BLUP uses family information (and more so at lower heritabilities)
- Selection on BLUP EBVs can thus results in higher inbreeding than selection on phenotypes alone
- Best strategy: Balance merit and genetic diversity
  - Start selecting from top, but leave an animal out if sibs have been selected already

Example of BLUP selection

Terminals - Top 150

Analysis Date Friday, 15 June 2001

LAMBPLAN

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162368-1999-990290	KURRALEA	5.53	10.84	10.58	-0.62	1.59	192.11	68		69	62	1623681998980211	1630001993930160
860074-1995-950044	ADELONG	7.17	14.47	13.22	-0.80	-0.94	191.15	448		96	94	8600741993930189	
163000-1998-980575	RENE	7.59	12.01	13.06	-0.50	0.99	190.92	12		71	60	1623681994940260	8600371992920165
162368-1997-970443	KURRALEA	6.58	12.13	7.96	-1.00	0.08	190.69	178		88	83	1640001993930411	8600401992920175
160034-1999-991208	MOSSLEY	5.52	13.45	10.27	-0.53	0.04	190.41	17	0.003	78	70	1621001998980130	1600341994940171
161437-1999-990006	WARBURN	5.41	10.97	10.93	-1.21	0.37	190.26	14		73	65	1604621994940012	1640001993930411

These are sibs so might not select all of them as flock sire

Good methods need good data

- Accuracy of BLUP EBVs depends on amount and the quality of the data (as well as the trait heritability)
  - Accurate phenotypic measurements
  - Correct pedigree
  - Correct recording of fixed effects & contemporary groups
  - Appropriate data structure (e.g. information on mates, culls)
- Remember, if BLUP doesn't know a piece of information, it cannot account for it

BLUP summary

- Uses information on all relatives optimally
- Accounts for fixed effects such as herd, birth type, age
- Accounts for unequal usage of sires in different herds
- Can compare across herd or flocks but need links to exist
- Accounts for culling and selection, non-random mating
  - *but non selected animals and mates need to be included in analysis!*
- Allows selection across age classes
- Provides an estimate of genetic trend

Why is selection on BLUP EBVs better than selecting on an animals' phenotype?

Why is selection on BLUP EBVs better than selecting on an animals' phenotype?

- Phenotypic information has been corrected for fixed effects → BLUP EBV is unbiased
- Information from relatives has been included in BLUP EBV → BLUP EBV is more accurate
- BLUP EBV allows fair comparisons of animals from different age classes (accounted for genetic trend)