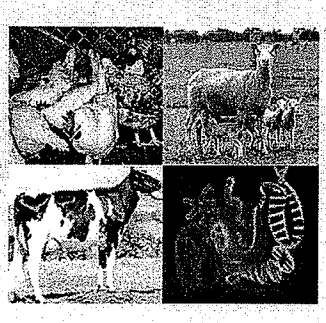
Properties of BLUP EBVs



Karen Marshall

UNE

IAEA, Korea, April, 2006

Genetic evaluation systems

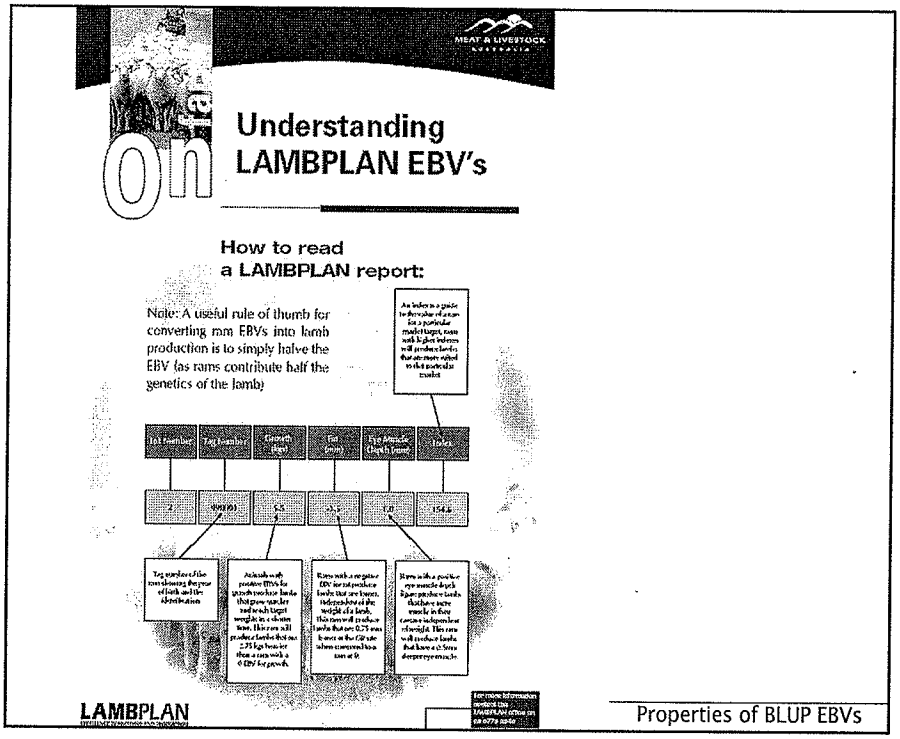
- Breeder submits phenotypes and pedigree
- Genetic evaluation system returns BLUP EBVs
  - plus other useful information e.g. selection indexes, accuracies, inbreeding coefficients
- Can be
  - Within herds
  - Across herds, within breeds
  - Across herds, across breeds (best)

Extract from LAMBPLAN report

Terminals - Top 150 Sires — Analysis Date Friday, 15 June 2001 — LAMBPLAN

ID	Sbol of breeding	Wwt	Pwwt	Ywt	Pfat	Pemd	Carcase +	Progeny	Inbreeding & Accuracies Coef	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
162204-1999-990453	BETHELREI	8.52	13.38	15.87	-1.18	1.11	211.75	224		93	89	8601221993930205	1619721995950289
161972-1998-980093	HILLCROFT FARMS	5.15	14.40	16.00	-1.08	0.25	207.51	12		80	74	1630001993930134	1603361992920349
161972-1998-980527	HILLCROFT FARMS	8.46	13.45	10.97	-1.65	-0.47	204.10	25		85	76	1619721996960091	1630001993930134
860122-1993-930205	OHIO	6.95	11.94	13.72	-1.60	0.49	203.76	1522		98	97	8601221992920200	8601221987870073
161143-1999-990204	DERRYNOCK	8.39	12.10	12.19	-0.49	2.19	203.60	38		82	76	1623681998980211	1640001993930411
160060-1996-960004	ANNA VILLA	8.56	14.90	16.18	-0.49	0.24	200.47	151		93	87	1632801992920016	1623541990900584
161143-1999-990201	DERRYNOCK	5.43	11.83	11.14	-1.19	0.83	199.83	38		83	77	1623681998980211	1613151995950042
230034-1997-970504	BURWOOD	4.98	11.01	8.82	-2.27	-0.55	198.62	380	0.003	96	92	2300091994940171	2300341994940314
163677-2000-000140	FELIX	6.69	13.56	13.36	-0.59	0.61	197.58	56		70	63	1619721995950289	1600341994940020
160060-1997-970115	ANNA VILLA	6.30	14.47	11.69	-0.42	0.24	196.90	118		90	83	1600601996960004	1600601992920057
162204-1999-990394	BETHELREI	7.42	12.97	14.27	-1.03	0.14	196.85	24		82	74	8601221993930205	1622041996960579
161143-1999-990864	DERRYNOCK	5.10	11.20	10.10	-0.72	1.60	196.01	18		80	74	1623681998980211	1640001994940317
161972-1996-960020	HILLCROFT FARMS	5.32	12.96	10.66	-0.80	0.36	195.20	83		88	75	1630001993930134	
160185-1996-960001	JOLIMA	6.19	10.29	10.42	-1.56	0.63	194.57	101		90	83	1630001993930134	1613151991910870
161235-1997-970830	POLLAMBI	7.10	10.69	10.35	-0.88	1.50	194.54	34		87	79	1700991993930002	1612351991910691
163677-1999-990307	FELIX	7.09	12.52	11.59	-1.29	-0.47	192.45	54		83	74	8601221993930205	1636771994940008
162368-1999-990290	KURRALEA	5.53	10.84	10.58	-0.62	1.59	192.11	66		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	WARRURN	5.41	10.97	10.93	-1.71	0.37	190.26	14		73	65	1604621994940012	1640001993930411

Properties of BLUP EBVs



Properties of BLUP EBVs

Media Releases View Archived Media Releases

16 August 2004

MLA's LAMBPLAN database records one million sheep

Milly, a White Suffolk lamb is the one millionth animal to have been objectively measured and recorded on Meat and Livestock Australia's LAMBPLAN terminal sire database.

MLA LAMBPLAN manager Dr Alex Ball said this was a great achievement for the national genetic evaluation program LAMBPLAN and the genetic improvement of the Australian prime lamb industry.

"Recording the one millionth sheep in the LAMBPLAN terminal sire database reinforces the integrity of the system and what it has to offer," Dr Ball said.

"Since 1989, when LAMBPLAN first started operating, the Australian prime lamb industry has seen some phenomenal improvements in live weight growth, increased eye muscle area and decreases in fat.

"In fact genetic improvements have seen post weaning weights of 6-8 month lambs increase by 5.8 kilograms, fat decrease by 0.4mm and eye muscle area improve by 0.3mm."

For the average lamb producer this means an extra $5.80 per lamb produced in carcase value alone.

insight

Australian Sheep Genetics Database

at a glance...

mla

another innovation

Currently within the industry there are three main national genetic databases:

- Merino Benchmark database
- Merino Genetic Services database
- Central Test Sire Evaluation database (AMSEA)

There are also other smaller datasets sitting with CSIRO Select, Advanced Breeding Services and with private operators.

- The ASGD will combine the three national Merino databases as well as the other smaller industry databases.
- The ASGD will produce one consistent, high quality set of breeding information in the form of quality assured Australian Sheep Breeding Values (ASBVs).

BREEDPLAN INTERNATIONAL

BREEDPLAN is a modern genetic evaluation system for beef cattle breeders. It is based in Australia, with clients worldwide. BREEDPLAN offers bull breeders the potential to accelerate genetic progress in their herds, and to provide objective information on stock they sell to commercial breeders.

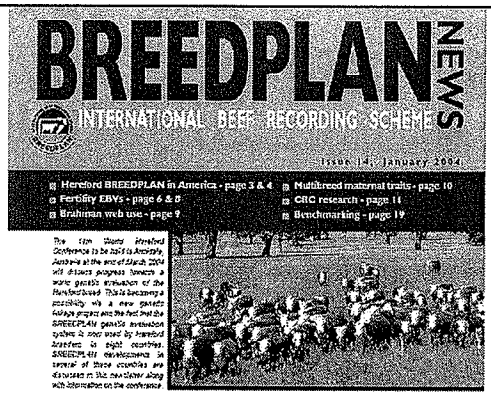
BREEDPLAN calculates Estimated Breeding Values (EBVs)* for a range of traits including:

Weight	Fertility	Carcase
Birth weight	Scrotal Size	Carcase weight
200-day milk	Days to Calving	Eye Muscle area
200, 400 and 600-day weight	Gestation length	Fat thickness
Mature cow weight	Calving ease	Meat Yield %
		Marbling

*(Note: EPDs are calculated for North American clients)

Included in the calculation of EBVs are the animal's own performance, the performance of known relatives, the heritability of each trait and the relationship between the different traits ie. a world class genetic evaluation model, combining all traits in one analysis.

Properties of BLUP EBVs


BREEDPLAN NEWS

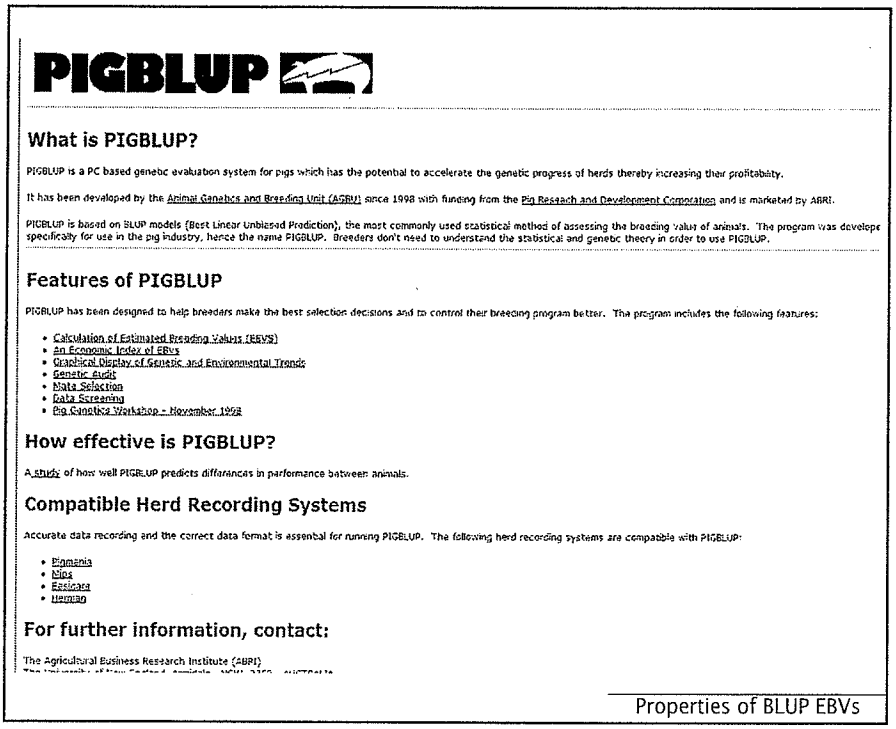
INTERNATIONAL BEEF RECORDING SCHEME

Issue 14: January 2004

- Hereford BREEDPLAN in America - page 3 & 4
- Fertility EBVs - page 6 & 8
- Brahman web use - page 9
- Multibreed maternal traits - page 10
- CRC research - page 11
- Benchmarking - page 19

Towards global Hereford genetic evaluation

Properties of BLUP EBVs



PIGBLUP

What is PIGBLUP?

PIGBLUP is a PC based genetic evaluation system for pigs which has the potential to accelerate the genetic progress of herds thereby increasing their profitability.

It has been developed by the Animal Genetics and Breeding Unit (AGBU) since 1998 with funding from the Pig Research and Development Corporation and is marketed by ABRI.

PIGBLUP is based on BLUP models (Best Linear Unbiased Prediction), the most commonly used statistical method of assessing the breeding value of animals. The program was developed specifically for use in the pig industry, hence the name PIGBLUP. Breeders don't need to understand the statistical and genetic theory in order to use PIGBLUP.

Features of PIGBLUP

PIGBLUP has been designed to help breeders make the best selection decisions and to control their breeding program better. The program includes the following features:

- Calculation of Estimated Breeding Values (EBVS)
- An Economic Index of EBVs
- Graphical Display of Genetic and Environmental Trends
- Genetic Audit
- Mate Selection
- Data Screening
- Pig Genetics Workshop - November 1998

How effective is PIGBLUP?

A study of how well PIGBLUP predicts differences in performance between animals.

Compatible Herd Recording Systems

Accurate data recording and the correct data format is essential for running PIGBLUP. The following herd recording systems are compatible with PIGBLUP:

- Pigmania
- Nips
- Easicare
- Herman

For further information, contact:

The Agricultural Business Research Institute (ABRI)

Properties of BLUP EBVs

Consider the features we want in an EBV

Case study:

A breeder selects a young ram that has a high EBV based on his own phenotype only. The ram has 30 progeny and his EBV drops.

Why?

Properties of BLUP EBVs

Consider the features we want in an EBV

Case study:

A breeder is performing assortative mating. He sells his sire with the highest EBV - this sire produces in another herd and his EBV drops.

Why?

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'

- true breeding values are distributed around predicted breeding values

BLUP and accuracy

BLUP maximises EBV accuracy by

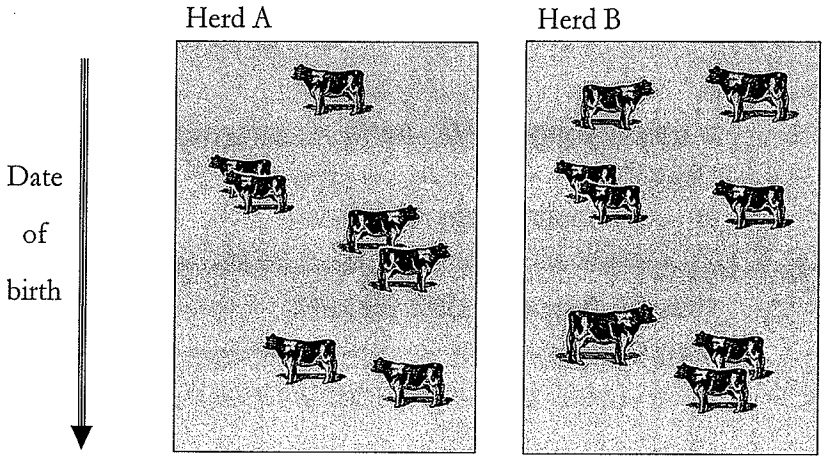
- calculating EBVs using all information sources
  - Information from relatives
  - Information from correlated traits
- using proper index weights
- just the same as a selection index
  (note BLP = selection index)

BLUP and lack of bias

BLUP ensures EBVs are unbiased

- unbiased EBVs are a matter of fair comparison
- *note selection index (BLP) + unbias = BLUP*

What 'fixed effects' would need to be accounted for so all animals have comparable EBVs?



Properties of BLUP EBVs

Possible causes of bias 'fixed effects'

Can account for some bias easily e.g.

- Problem: Some animals reared as singles, other as twins
- Solution: Correct phenotypes for effect of rearing type

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

- Problem: Animals are measured at different ages
- Solution: Correct phenotypic observations for age

Properties of BLUP EBVs

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

Properties of BLUP EBVs

Use of link sires

Progeny means

Flock	Sire 1	Sire 2	Sire 3	Sire 4	Sire 5
A	45	40			45
B			45	40	50

Sire 1 is superior in flock A, & sire 3 is superior in flock B.

But which sire is the best overall?

Properties of BLUP EBVs

Use of link sires

Progeny means

Flock	Sire 1	Sire 2	Sire 3	Sire 4	Sire 5
A	45	40			45
B			45	40	50

Assuming ewes are of equal merit in flock A and flock B, the sire 5 data indicates that flock B is performing in a better environment.

Thus sire 1 is genetically superior to sire 3, as sire 1 produces the same phenotype despite the worse environment.

In practice

- Linkage between herds / flocks within the major genetic evaluation systems (e.g. LAMBPLAN / BREEDPLAN) 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: +400	Progeny: +350

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

Properties of BLUP EBVs

In practice

- Genetic evaluation systems encourage recording of phenotypes on mates
- If no dam information is provided, the dam is presumed to be 'average'

Properties of BLUP EBVs

Possible causes of bias 'selection bias'

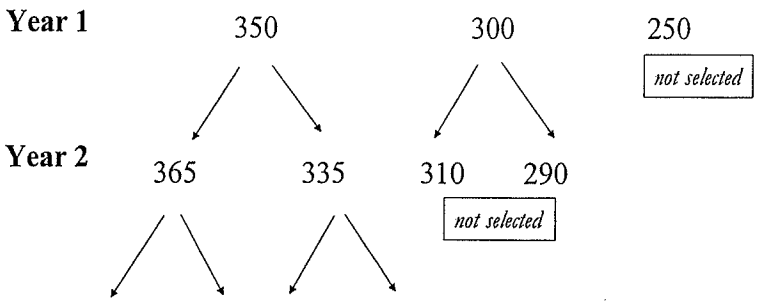
- Problem: There is culling and selection
  - worst sires have more progeny culled 'culling bias'
  - animals are from selected parents

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



Genetic mean changes as years go by due to selection

Animals born in recent years are expected to be genetically better than those born in past years

If EBVs are calculated as a deviation from the year mean, this wouldn't be accounted for

Properties of BLUP EBVs

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

A feature of BLUP

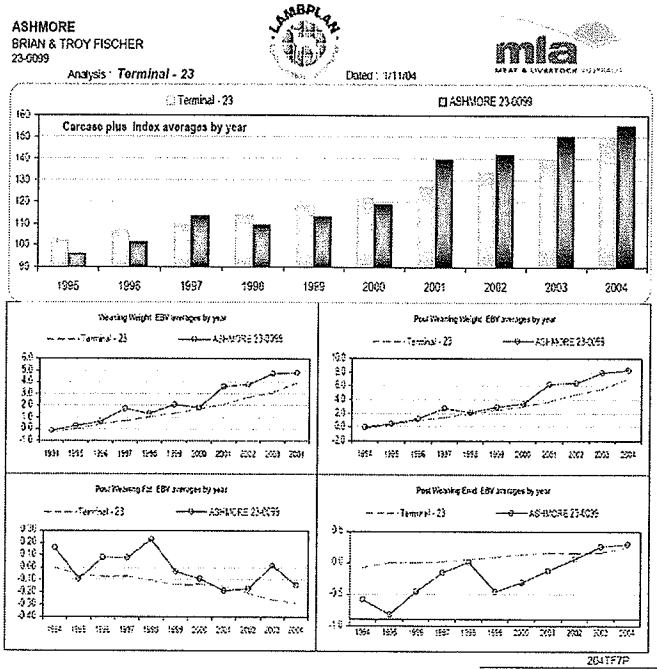
In practice

- Information on culled animals should be included in the evaluation
- Similar to links between herds, links between years are required

Genetic trends

As BLUP separates genetic and year effects

genetic trends can be observed by plotting BLUP EBVs over years



Properties of BLUP EBVs

In practice

- Genetic evaluation services often provide genetic trends to their clients
- Genetic trends are used as marketing tools

Possible causes of bias 'unbalanced designs'

- Problem: Some animals have more information than others
  - different number of sibs
  - different number of progeny
  - etc.
- Solution: Construct a 'customised' selection index for each animal

A feature of BLUP

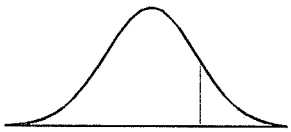
In practice

- Optimal weightings are placed on each information source
- Only the EBVs (rather than the index weights) are reported

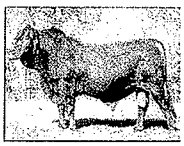
Another feature of BLUP

EBVs can be compared directly over age classes

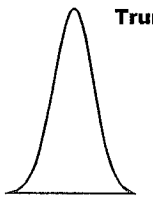
Selection on BLUP EBVs results in optimisation of the generation interval



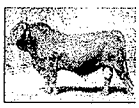
proven sires



Truncation Point



young sires



Another feature of BLUP

BLUP uses family information (and more so at lower heritabilities)

Selection on BLUP EBVs can thus results in higher F than selection on phenotypes alone

How BLUP works

A joint evaluation of all animals
- uses all additive genetic relationships
- uses data on all animals jointly

Works as a linear model
- corrects different effects for each other
- jointly estimates animal effects and fixed effects

Has selection index properties
- each EBV is the result of a customized index

BLUP summary

Optimal weights for all information sources
- *lots of different sets exist of optimal weighting factors, BLUP does it automatically*

Allows comparisons of EBV's of animals in different herd (possibly with different genetic means)
- *but links need to exist in the data!*

Accounts for culling and selection, non-random mating
- *but culled, non selected animals and mates need to be included in the analysis!*

Allows selection across age classes – optimises generation interval

Provides an estimate of genetic trend

In practice

Accuracy of BLUP EBVs depends on quality of the data (as well as the trait heritability)

- Accurate phenotypic measurements
- Correct pedigree
- Correct recording of fixed effects & assignment to 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

Questions

How easy would it be to cheat the system ?

Could an animal have different EBVs when evaluated under more than one evaluation systems ?

When is an animal's EBV likely to change within the one evaluation system ?

From a 'letter to the editor' submitted to *The Land* 1999. Indicates a lack of understanding by the breeder.

> "Dr Banks criticises [a particular genetic evaluation system] as he believes it is only regarding phenotype — the individual animal — while Lambplan can compare animals across flocks, regions, climates and feed buckets ...
>
> However, as a current user of Lambplan, we can say the question of feed history of our sheep is never asked for, nor recorded so environmental factors have no say."