Genetic Changes

Introduction

✓The main use of Estimated Breeding Values

to choose the parents of the next generation

to optimize the matings of the selected parents

to monitor the success of selections

on changing genetic average

EBVs of 20 dairy goats from one herd for lactation protein yields

EBVs using animal model with repeated records

Animal	Year of Birth	Protein EBV	Year of Production 91	92	93	94	95	96	97	98	99
1	90	+10	x								
2	90	-1	x	x							
3	91	+3	x	x							
4	91	+6	x	x	x						
5	91	-4	x								
6	91	+4		x	x	x	x				
7	92	+7		x	x	x					
8	92	-5			x						
9	92	+4			x	x	x	x	x		
10	93	+8				x	x				
11	93	+2				x	x	x			
12	93	+3					x	x	x	x	
13	94	-6					x	x			
14	94	+7						x	x	x	x
15	94	-8						x			
16	95	+5							x	x	x
17	95	0								x	x
18	96	+2								x	x
19	97	+1									x
20	97	+11									x

By Year of Birth

One trend, average EBV by year of birth

This measure the trend in female goats born and retained in the herd for producing milk

Female goats not retained likely sold to other producers or culled

Average EBVs of producing goats by year of birth

Year of Birth	Number	Average EBV
90	2	4.50
91	4	2.25
92	3	2.00
93	3	4.33
94	3	-2.33
95	2	2.50
96	1	2.00
97	2	6.00

Trend

Trends within a herd are very erratic because the number of new female goats coming into a herd as replacements per year is small

Thus, the average of EBVs have a very large standard error

Over a long period of time, a general trend

Combining results across all goat herds in country give a much better picture of the trend in the entire goat population

The standard error of those averages would be very small because they would be based on hundreds or thousands of animals

By Year of Production

The average EBV of female in each year of production would estimate the genetic average of live, active animals in each year

This reflect the management policies of owners and economic influences of the time

Economics may force owners to cull more stringently

Average EBVs by Year of Production

Year of Kidding	Number	Average EBV
91	5	2.80
92	5	3.80
93	5	3.20
94	5	5.00
95	6	2.50
96	6	0.33
97	4	4.75
98	5	3.40
99	6	4.33

The averages are slightly higher than previous table

This means that the better female goats are kept to produce longer in the herd, and poor EBV goats are culled

Trends in Males

The males in most species are more intensely selected than females

In dairy cattle, ~ 75% of female calves used as replacements, only ~ 400 bull calves chosen to be sires of next generation

The average EBVs of bull calves is a useful statistic for measuring the change in male side

The average EBVs of males is much higher than the average of female replacements

This average take some years to be noticed

Another trend is the average EBV of males used to breed females in a given year

Some males are more popular than others because of their EBVs for many traits, and are chosen more frequently by producers

Pathways of Selection

four basic pathways of selection in animal breeding:

- Sires of males pathway (SM)
  - The most stringent selection category
  - The best 5% of all male animals
  - Less than 0.1% of all male animals born
- Sires of females pathway (SF)
  - Males chosen for breeding to females

- Dams of males pathway (DM)
  - Females chosen to obtain males for breeding
- Dams of females pathway (DF)
  - Females chosen for breeding purposes to produce future female replacements

Trends based on year of birth more useful than trends based on year of production

Trends for each pathway of selection

The sire pathways are generally more accurately estimated - more progeny than females

More females per year of birth than males in these pathways, and the stability of the female trends is better

Remember: trends are a reflection of past selection and breeding decisions, and give an indication of how quickly the breeding goals are being achieve

Biased Trends

Incorrect Heritability

Trends assume that the correct parameters of the model to estimate the EBVs

If heritability in MME is too high, then range of EBVs becomes greater=> estimates of average EBVs to be biased upwards => more genetic change than exists

Biased Trends

Incorrect Heritability

if the heritability used in the MME is too low, then trends in average EBVs could be biased downwards

The solution is to use the best possible estimates of heritability

An experiment to test unbiasedness is to split the data into two sets:

- data up to time t
- data from time t+1 to the present

Biased Trends

Incorrect Heritability

Using a value for heritability, estimate the EBV for all animals using the first data set only. Then combine the two data sets and re-estimate the breeding values

The regression of the predicted EBVs from the first data set on the EBVs from the combined data set should be 1 if the correct heritability has been used

Biased Trends

Wrong Model

Suppose a trait is significantly affected by the age of the animal, but the age effect was omitted from the animal model

Estimation of EBVs could be biased by the age effects

Older animals might appear to be better genetically than young animals

Biased Trends

Wrong Model

Estimated genetic trends might be negative or close to zero

=> reason to continuously update the model for genetic evaluation, to make sure that all necessary factors are in the model

The models should take into account phenotypic time trends

Predicting Genetic Change

A breeding strategy describes the process (how and when) by which males and females are selected for the next generation of matings

The prediction of a future progeny of sire X and dam Z is simply the average of the EBVs of the sire and dam;

EBVprogeny = 0.5 (EBVsire + EBVdam)

The accuracy of prediction depends on the accuracy of the EBVs of the sire and dam

The mates for every mating are not known in advance for the next year or even the next 5 or 10 years

Fortunately, there is a general equation to predict future genetic change

Formula

$$\frac{\Delta \mathrm{G}}{\mathrm{year}} = \frac{r_{TI}\ i\ \sigma_a}{L}$$

ΔG is genetic change in a trait,

r_{TI} is the accuracy of selection (or reliability of the EBV),

i is the selection intensity,

σ_a is the additive genetic standard deviation of the trait, and

L is the generation interval in years.

Accuracy of Selection

The reliability of the EBVs is critical to genetic change

If EBVs are not very accurate then errors will be made in selecting animals for matings

This will decrease the amount of genetic change

Reliability of EBVs depends upon:
- Heritability of the trait,
- The statistical linear model, and
- The quality and quantity of data

- Selection accuracy
  - Range is 0 to 1
    - 0 is no information, 1 is full information
  - Relates to heritability
    - low heritability → less accuracy
  - Can be improved
    - use of repeated measures
    - information from correlated traits
    - information from relatives, especially progeny testing
- More information → more accuracy → more response

Response to selection II

Selection Intensity

Selection intensity, or selection differential is the difference in the mean of animals that have been selected versus the mean of all animals standardized to a variance of one

The assumption is that truncation selection is applied to a normally distributed trait

Selection Differentials, i

For .001 to .099 selected

	.000	.001	.002	.003	.004	.005	.006	.007	.008	.009
.00		3.400	3.200	3.033	2.975	2.900	2.850	2.800	2.738	2.706
.01	2.660	2.636	2.600	2.569	2.550	2.527	2.500	2.582	2.456	2.442
.02	2.420	2.400	2.386	2.370	2.363	2.336	2.323	2.311	2.293	2.283
.03	2.270	2.258	2.241	2.230	2.221	2.209	2.200	2.186	2.174	2.164
.04	2.153	2.146	2.136	2.126	2.116	2.107	2.098	2.087	2.079	2.071
.05	2.064	2.057	2.048	2.040	2.031	2.022	2.016	2.009	2.000	1.990
.06	1.985	1.977	1.971	1.965	1.958	1.951	1.944	1.937	1.931	1.925
.07	1.919	1.911	1.906	1.900	1.893	1.888	1.882	1.875	1.871	1.863
.08	1.858	1.852	1.846	1.841	1.837	1.834	1.826	1.820	1.815	1.810
.09	1.806	1.799	1.793	1.788	1.784	1.780	1.775	1.770	1.765	1.760

For .01 to .99 selected

	.00	.01	.02	.03	.04	.05	.06	.07	.08	.09
.10	1.755	1.709	1.667	1.628	1.590	1.554	1.521	1.488	1.458	1.428
.20	1.400	1.372	1.346	1.320	1.295	1.271	1.248	1.225	1.202	1.180
.30	1.159	1.138	1.118	1.097	1.078	1.058	1.039	1.021	1.002	.984
.40	.966	.948	.931	.913	.896	.880	.863	.846	.830	.814
.50	.798	.782	.766	.751	.735	.720	.704	.689	.674	.659
.60	.644	.629	.614	.599	.585	.570	.555	.540	.526	.511
.70	.497	.482	.468	.453	.438	.424	.409	.394	.380	.365
.80	.350	.335	.320	.305	.290	.274	.259	.243	.227	.211
.90	.195	.179	.162	.144	.127	.109	.090	.070	.049	.027

For example, suppose the genetic standard deviation,σ_a, is 1000 kg of milk and the mean BV of all current animals is = +500 kg

if the top 8.3% of the animals have been selected, the superiority of the mean of the selected animals, s compared to the entire population:

$$\begin{aligned}\mu_s &= \mu + (i)\sigma_a, \\ &= +500\text{kg} \ + \ (1.841)\ 1000\text{kg} \\ &= 2341\text{kg}\end{aligned}$$

If the top 41% were chosen then the mean:

$$\begin{aligned}\mu_s &= +500\text{kg} \ + \ (.948)\ 1000\text{kg} \\ &= 1448\text{kg}.\end{aligned}$$

Genetic Standard Deviation

There is little that can be done, in the short term at least, to increase the genetic standard deviation of a trait

The genetic variance must be estimated, but this is usually not a problem

Generation Intervals

Generation interval, average age of males or females when a future male or female replacement is born

The shortest generation interval (biologically) is the age of maturation plus the gestation length

This natural barrier can possibly be decreased through reproductive technology

Generation intervals are longer than the minimum possible because producers want to have reliable EBVs before making breeding decisions

Balance between reliability of EBV and generation interval

Decreasing the generation interval means choosing animals whose EBVs are usually much less reliable age at maturation and the gestation length of a species must be known to determine generation intervals

Some species have very long generation intervals , other species can have very short generation intervals

- Another example of calculating L

Age structure of animals selected for breeding					
Age (years)	2	3	4	5	Total
Male	7	5			12
Female	200	150	100	50	500

$$L_{male} = \frac{(7x2)+(5x3)}{7+5} = 2.4\,years$$

$$L_{female} = \frac{(200x2)+(150x3)+(100x4)+(50x5)}{200+150+100+50} = 3.0\,years$$

$$L_{average} = \frac{2.4+3.0}{2} = 2.7\,years$$

Response to selection I

- Balancing i and L: consider age structures

Age	2	3	4	5	6
Males	5	5			
Females	100	100	100	100	100

Higher i : replacing 5 / 250 males and 100 / 250 females
Higher L : Lm=2.5 years, Lf=4.0 years, L=3.25 years

Age	2	3	4	5	6
Males	10				
Females	125	125	125	125	

Lower i : replacing 10 / 250 males and 125/ 250 females
Lower L : Lm=2.0 years, Lf=3.5 years, L=2.75 years

Response to selection I

$$R_{year} = \frac{i_m + i_f}{L_m + L_f} \sigma_P h^2$$

- Thus high i → high L & low i → low L
  - this does not fit well with maximising i / L
- The *best compromise* between i and L is required

Response to selection I

Example of response calculation

- Sheep breeder has 180 ewe flock, selecting for FW
- Rams first selected at 2 years old, and mated for 2 years
- Ewes first selected at 2 years old, and mated for 4 years
- Each ram mated to 30 ewes, 90% lambing, 50:50 sex ratio
- No significant mortality in adults
- Trait heritability = 0.25, and σ_P=0.6kg
- What is R per year ?

Response to selection I

Answer

Age structure of animals selected for breeding					
Age(yrs)	2	3	4	5	Total
Male	3	3			6
Female	45	45	45	45	180

- 180 ewes, 90% lambing → 162 lambs total (81 of each sex)
- Need to select 3 out of 81 males each year
  - P=3/81=3.7%, which corresponds to an *i* of 2.18
- Similarly need to select 45 out of 81 females each year
  - P=45/81=55%, which corresponds to an *i* of 0.72
- L_{male}=2.5years, L_{female}=3.5years

$$R_{year} = \frac{i_{male} + i_{female}}{L_{male} + L_{female}} \sigma_p h^2$$

$$R_{year} = \frac{2.18 + 0.72}{2.5 + 3.5} x0.6x0.25 = 0.07kg$$

FW is expected to increase by 0.07kg per year

Response to selection I

Expansion of General Formula

The expanded formula is:

$$\frac{\Delta \mathrm{G}}{\mathrm{year}} = \frac{\Delta_{SM} + \Delta_{SF} + \Delta_{DM} + \Delta_{DF}}{L_{SM} + L_{SF} + L_{DM} + L_{DF}}$$

$$\Delta_{ij} = r_{TI-ij} i_{ij} \sigma_a$$

Each pathway has a different **reliability** of EBVs

Each pathway has a different **selection intensity**

Each pathway has a different **generation interval**

Example Predictions

Information related to dairy cattle selection programs for milk production

	Pathways of Selection SM	SF	DM	DF
r_{TI}	.95	.70	.50	.35
i	2.336	1.755	2.975	.424
L years	9	6	5	3
Δ_G	2219.2	1228.5	1487.5	148.4

genetic standard deviation is 1000 kg

Bulls are 9 to 11 years before replacement is born

Bulls are 6 years when daughters are born

Dams of males are also highly selected and have usually completed 3 lactations→ they are at least 5 years

Dams of other females, only need one lactation record or less

	Pathways of Selection SM	SF	DM	DF
L years	9	6	5	3

Reliabilities of EBVs:

Sires of females need only a minimally reliable EBV which is .70 or higher

Sires of males must be much higher

Dams of males, might have one daughter, reliability .50

Dams of females close to heritability (.30)

	Pathways of Selection			
	SM	SF	DM	DF
r_{TI}	.95	.70	.50	.35

Selection intensities:

Sires of males, the top 10 out of 400 bulls (2.5%)

Sires of females, the top 40 out of 400 bulls tested per year (10%)

Dams of males, the top 400 out of 100,000 (0.4%)

Only 25% of females are culled per year leaving 75% to produce future females

	Pathways of Selection			
	SM	SF	DM	DF
i	2.336	1.755	2.975	.424

Example Predictions

	Pathways of Selection			
	SM	SF	DM	DF
r_{TI}	.95	.70	.50	.35
i	2.336	1.755	2.975	.424
L years	9	6	5	3
Δ_G	2219.2	1228.5	1487.5	148.4

$$\begin{aligned}\frac{\Delta_G}{\text{yr}} &= \frac{2219.2 + 1228.5 + 1487.5 + 148.4}{9+6+5+3} \\ &= \frac{5083.6}{23} = 221.0\text{kg/yr}\end{aligned}$$

SM and DM, two largest contributors (about 73%)

Increasing Reliability

Molecular genetic technology

Change reliability of EBVs to 85% or better

Keeping SS pathway at 95%, and improving all others to 85%, contributions of each pathway:

SM 2219.2 kg **SF 1491.7 kg**
DM 2528.7 kg **DF 360.4 kg**

$$\Delta_G = 287 \text{ kg/yr}$$

This is 30% greater progress than the traditional selection program

Decreasing Generation Intervals

Molecular genetics, give 85% reliable EBV as soon as an animal is born

Dairy cattle are sexually mature at one year of age for bulls and 16 months for females

Suppose all generation intervals could be reduced to 2 years