

POPULATION GENETICS

Population genetics deals with the multiple traits that are controlled by many genes that are reflected phenotypically in production factors. It deals with what is being actually produced.

Population genetics moves on from mendelian genetics. It accepts that pedigree based breeding programmes are too difficult to predict because of the many complications and unknowns in animal genetics and the lack of certainty that can arise from that.

Population genetics starts with the study of variation and asks the question of what is causing this variation in a group of animals. The breeder deals with this variation by selection.

Population genetics requires collecting large amounts of data to find out about variations. That is then used to make breeding plans by focussing on the factors of significance rather than ancestors.

POPULATION DISTRIBUTION

The variation in a population will be distributed through it. In a normal population of sufficiently large enough size the typical distribution of any one variation when plotted on a graph shows a distinctive bell shaped curve with the majority of the animals in the middle of the population, and the positive and negative extremes at the edges.

To have meaningful results from analyzing the distribution of population requires sufficient numbers to get a true sample and recognition of the effects of age, sex, feed and other environmental factors on the performance of the particular factor.

The USA Leachman Cattle Company is a good example of the type of numbers required. The company had 10,000 recorded beef cows and a 500,000 cow pool feeding the central recorded herd to produce the Stabilizer Composite beef breed.

In measuring the phenotypic value or productive worth of an animal, the mean of the population is one of the three factors together with genotypic value and environment that will be reflected in the deviations from the mean.

Several genes influence one factor. Huge numbers of potential genotypes are needed for multi gene traits in a population with normal distribution. You need big numbers to make meaningful genetic gain and to create selection pressure.



VARIATION

Plotting one factor for a large group of goats on a graph to produce the characteristic bell shaped curve has the mean of the group at the highest point of the curve. We use

standardised methods to measure the variation so that we can describe both the group and the individual goats in it.

It is important when plotting variation that the data must be comparable. For example, for same age, sex and other environmental factors.

It is obvious that you need a reasonable number of animals to make enough points on a graph to be able to draw a realistic curve.

It is equally obvious that some factors can be measured and plotted more easily than others.

Some variation data is discrete or stopped such as number of kids born, and some variation data is continuous such as growth rate.

Variation from the mean may be good or bad. For example, lower or greater growth rates compared to the mean. But in addition, commercial farmers may be trying to reduce variation to standardise management. However seedstock breeders will be trying to use the variation and may be deliberately trying to increase it because mating unlike animals will produce a few at each extreme of the distribution of the variation, and highlight the really superior ones.

The effect of variables can cumulate but there may be:

1. Random genetic drift that needs flock in numbers of more than 1000 to counteract.
2. Some environments have a greater influence on some genotypes than others.
3. Responses skewed towards one aspect of a factor.
4. There will always be unexplained causes of variation in animal performance.

There can be phenotypic variations that are not genetic variations. For example a black bodied Angus mated with a red bodied Hereford will produce black bodied progeny because black dominated red coat colour, but a white face because the Hereford white face dominates the black Angus face. However interbreeding crossbreds from the F1 cross will produce a solid red beast, a solid black beast, a black beast with a white face and a red beast with a white face (Hereford). So at the F2 cross, although the animals look completely different phenotypically, they are genetically the same as the F1 cross.

Variation in the population is needed to be able to select the best and cull the worst, and measures of that variation are needed to be able to identify them.

Crossbreeding produces variation, and genetic variation is the real material of population genetics.

MATHEMATICS

Population genetics is all about mathematics.

Phenotypic value =
the population mean + the genotypic value + the environment.

The rate of genetic gain is a function of the selection pressure (the proportion used as parents in the next generation), the accuracy of genetic evaluation and the ability to rank animals genetically, and genetic interval.

EBV = h^2 (heritability) x (the difference between individuals and the group average).

When selecting for multitraits the percentage effect of each trait that will be introduced will be:

1 = 100%, 2 = 71%, 3 = 58%, 4 = 50%, 10 = 32%

A group of animals will breed back to the average of the population they came from UNLESS the breeder keeps identifying the genetically superior animals.

To identify genetically superior animals needs numbers. 200-300 does to show a difference in kidding percentage because of the discrete variation and 20-30 to show a difference in liveweight gain because of a continuous variation.

Gain per year =
$$\frac{h^2 \times \text{selection differential}}{\text{Generation interval}}$$

Gain per generation = $h^2 \times \text{selection differential}$

If any one of the three factors in the formula is small, the others need to be significantly larger to counteract that.

The law of diminishing returns applies to breeding progress which reaches a plateau. The only way to break above the plateau is from outcrossing.

The repeatability of performance factors is important despite environmental differences. Repeatability is the number of times that the factor will produce the same results.

Genotypic correlation requires a lot of good data that is difficult to obtain.

Rate of genetic gain per unit of time reflects the accuracy of selection as well as selection intensity.

Genetic gain =
$$\frac{\text{how good a selection (accuracy)} \times \text{how much selection (intensity)}}{\text{how often selection is made}}$$

Accuracy of selection depends on heritability of a factor, a uniform environment, adjustment for known environmental effects, contemporary groups, and the number of records available.

We can use contemporary group means and variance in place of mathematical adjustments. We express individuals in relation to group means as a ratio of 100.

SELECTION DIFFERENTIAL / SIGNIFICANT DIFFERENCE / SELECTION INTENSITY

Selection differential measures how much better or worse an animal is compared to the mean of the group that it comes from. Selection differential is a measure of how much pressure can be put on a production character which is important, because the more pressure the more progress.

There are standardised selection differentials depending on the size of the flock. For example with 100 animals,

| | |
|-----------------------------|-----------|
| if 1% is selected | SD = 2.51 |
| if 10 animals are selected | SD = 1.73 |
| if 90 animals are selected | SD = 0.19 |
| if 100 animals are selected | SD = 0 |

Comparing a flock of 10 animals with a flock of 100 animals, in a flock of 10 animals:

where one animal is selected (10%) SD = 1.54

but in a flock of 100 where 1 animal is selected SD = 2.51.

In a flock of 100 animals where 10%, i.e. 10 animals, are selected SD = 1.73 is still greater than SD for 10%, i.e. 1 animal, of a flock of 10.

Significant difference/selection differential is the difference between an individual and the group that they came from.

Selection Differential is defined as the average of the parents for the next generation compared with the average of the population that they came from, i.e. the superiority of parents over their previous generation.

The selection differential of each parent and the pressure that can be applied is important as it adds half the genetics to the progeny. However this needs a reasonably high culling rate of females as well as males. To achieve a high culling rate of females needs high fertility and low mortality to generate sufficient numbers to cull as well as to account for normal losses and productive culling.

It is much more difficult to show a significant difference in kidding percentage because of the discrete steps of 1, 2, 3 than in growth rate.

HERITABILITY

Heritability (h^2) is the amount of superiority that on average is passed on to offspring.

Heritability is a ratio not an absolute value. It does not show how much of a specific character will be in the next generation, but it is a % or on a scale of 0 to 1.

Because heritability is a ratio and can be measured in a number of different ways, different studies will produce somewhat different figures. You need to know which goats were studied, who did the studies, how good the figures were, the environment under which the studies were done. There are various goat heritability studies done around the world with a wide variety of goats in a wide variety of environments that do not necessarily relate to meat goats in the United States, or in New Zealand for that matter.

Sometimes heritability is confused with repeatability which tells how a goat will do the same thing again in its lifetime. Heritability tells how it will pass a factor onto the next generation.

With high heritability, an individual's own records can be adequate to project satisfactory progress without the need for other data.

Highly heritable traits can be improved by selection with no negative inbreeding risks.

The higher the heritability the more genetic variation there is amongst animals.

High heritability produces more influence due to genetics. Low heritability produces more influence due to the environment.

Heritability has been defined in various ways. It is the degree of offspring performance that reflects the parents' performance.

Traits associated with survival and reproduction are not highly heritable and can decline markedly from inbreeding.

STANDARD DEVIATION

Standard deviation describes the shape of the distribution curve of the variation or how the particular group of goats is distributed or how many goats have one factor that has been recorded compared with the normal distribution.

Standard deviation is the square root of the variance in the distribution of a population. Variance is the average squared deviation from the mean. Each population graph will have a specific SD units related to the mean itself.

Statistical laws state that in large number of animals with a normal distribution:

1. About 50% of the group will be within 1 SD unit on either side of the mean
2. $\frac{2}{3}$ of the group will be within 2 SD units on either side of the mean.
3. 1 in 5000 will be more than 3.5 SD units above or below the mean ($\pm 175\%$).
4. 1 in 10,000 will be more than 4 SD units above or below the mean ($\pm 200\%$).
5. The average of the group above the mean will be 0.8 SD units more than the mean.
6. SD is not a good measure of a skewed distribution.

Coefficient of Variation (COV) shows the size of the standard deviation in relation to the mean value so that the factors can be compared with each other. SD comes from a specific population but we can compare populations and the SD of each by using the COV.

$$\text{COV} = \frac{\text{Standard Deviation}}{\text{mean} \times 100\%}$$

GENERATION INTERVAL

Generation Interval (GI) is the average age of the parents when the progeny are born (some traits take some years to measure).

GI can be important because of the consequence of delaying breeding until parents are old enough to be able to express the factor of interest. For example, bucks need to be old enough to mate, and a factor such as lifetime performance can take many years to be reflected.

HYBRID VIGOUR

It can be difficult to predict HV even although it is likely that closer related breeds will have less and distantly related should have more. But Elk and Red Deer have little HV.

HV must be measured in the crosses to be able to predict it and that needs crossbreds and reciprocal crossbreds, and the purebreds of the same age farmed in the same environment.

However it is possible to estimate HV by comparing first crosses (F1) with subsequent interbred offspring because the F2 generation will have half of the HV of the F1 generation.

But there can also be an additive effect of genes that is not dominant. You need gene frequency and difference and dominance for HV.

The amount of hybrid vigour is not known for many traits or breed combinations.

HV tends to be greater in traits of lower heritability, but these genes can have greater additive effect.

50/50 composite crossbred retains half hybrid vigour, i.e. mating 2 purebreds each time. 25/75% composite retains $\frac{3}{8}$ HV. 3 way cross of 3 purebreds retains $\frac{2}{3}$ HV.

HV comes from the interactions between alleles - the interactions between 2 alleles for one gene that reflect dominance. Interactions between 2 alleles of different genes can be epistasis.

BREEDING MANAGEMENT

1. Traits are observable and/or measurable.
2. You need to be able to measure to be able to make progress. To measure requires taking measurements and the physical difficulties of this can reduce both the number taken and their accuracy.
3. It is important to test both does and bucks but difficult to test does under commercial conditions and often large numbers are required.
4. There are problems in retaining bucks as entire long enough to measure and compare.
5. Management strategies for generating meaningful data are:
 1. To make the environment as uniform as possible (Kiko was subject to severe environmental situations at various periods so as to provide a negative limit on performance).
 2. Accurate field Measurement (Kiko had MAF independent measurement)
 3. Being able to make adjustments where possible for factors such as birthweight, sex, birthrank and dam age.
6. It is fundamental to select potential parents with the best breeding values. If this can be done then accuracy, selection intensity, generation interval are not as necessary to make maximum genetic sense. However this does not necessarily make maximum economic sense.
7. There are four methods of selection, being individual performance, pedigree, progeny test, sibling selection.

8. Progeny testing is most useful for weakly inherited factors OR for traits present in only one sex, e.g. milk, OR carcass data of the sire. Progeny test greatly increases generation interval and is costly.
9. Basic philosophy of Kiko breeding and any population genetically based breeding programme is mating best to best and not corrective mating.
10. Progress in one gene (e.g. kidding percentage) needs improvement with other associated factors such as survivability of kids, kid vigour in early life, milk production of the dam.
11. Population based breeding programmes will have an open nucleus structure to be able to introduce better animals if they are available.

COMPOSITES

The aim of composite breeding is economic performance, not hybrid vigour that it will reduce.

The market will dictate the qualities sought in a composite breed and not the breeders' choice. Composites can be stabilised or recreated each year.

There is more variation in production within breeds than between breeds. Composite breeding allows introduction of specific factors.

As the foundation purebreds of a composite breed are improving by selection, it might be more important to just crossbreed rather than try and stabilise the crossbreds as a composite. This decision requires a comparable evaluation of purebreds.

KIKO

It generally takes about 5 generations to become sufficiently homozygous at all loci controlling important traits. Kiko breed has been described as a composite in various USA publications. However it may be better defined as a synthetic breed where all genes are put in a pot and mixed up and the progeny selected for the traits desired by objective measurement and using an economic based valuation.

Kiko breeding did not set out to produce a composite breed but merely to produce an animal that met certain performance criteria. It may not even be able to be called a breed by strict definition.

Kiko breeding programme had emphasis on a maternal line reflected in growth rate of young stock, longevity of the dam, fertility/fecundity, and maternal factors. There are greater phenotypic benefits from HV in maternal lines.

Independent selection that was used in the Kiko development programme uses a minimum standard for each trait and requires some knowledge of heritabilities, overall economic importance and the numbers of animals available. Kiko was developed using such independent culling methods, i.e. if an animal failed in one trait it failed completely. It is important to note that the Kiko breed used only a few independent culling factors.

The breeding programme was forced to use independent selection levels because the information to generate a reliable selection index that uses economic values was not available.

It was perhaps fortunate for USA breeders that economic values were not used in NZ Kiko breeding decisions because economic values in the United States are not the same as in New Zealand

KIKONUI®

The Kikonui programme is an attempt to operate a group breeding scheme as an individual. It recognises the problem for commercial farmers of producing crossbred dams to mate to a purebred sire for a three breed progeny composite system, and that is overcome by the programme of keeping introducing new genes in the sires available to these farmers for them to use in their crossbred and base doe herds.

Kikonui® is based on P+P (productivity + profitability), and measured by efficiency of reproductive performance, survival to sale, kids weaned per doe liveweight, low wastage and meat per hectare.

It is an example of an individual group breeding scheme that used nine satellite herds in various locations and environments, management systems and sizes. The Project controls the breeding programme in the central herd, and the satellite farmers control the breeding in their own herds using mutually agreed bucks from the Project. The central herd provides one buck per 50 does to each satellite herd and there is an incentive for the central herd to provide the best bucks because it has first pick of 5 doe kids per buck back from the satellite flocks. There is an incentive for farmers to participate as they get very good bucks for the cost of 5 doe kids, and the effect of the buck is reflected in remaining progeny retained for their own herd replacements.

From 2015 the Project structure changed to one herd of mixed genes 400 does, many of which are Kikonui Xbreds, in one environment, with single sire mating of groups within that to develop specific attributes. This will allow greater monitoring and progress. However the open nucleus practice continues, as does the policy of breeding best to best. Selection emphasis continues on reproductive rate, farmability and overall performance under challenging conditions.