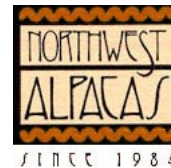




## **Genetic Improvement In The Alpaca Industry**

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By Chris Tuckwell



**Genetic Improvement In The Alpaca Industry**

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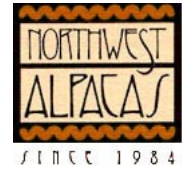
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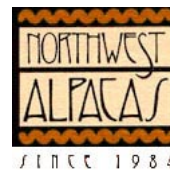
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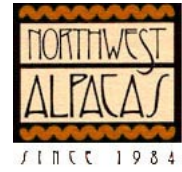
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*A paper for the Alpaca Owners and Breeders Association 1997 Annual Conference, June 11-15, 1997, Pueblo, Colorado.*

I am not a geneticist. This paper is prepared to give readers a very simple understanding of genetic improvement plans, the need to consider such plans for their stock and the factors that may influence the effectiveness and efficiencies of breeding programs.

Those who recognize the value of individual and industry breeding programs and intend to develop and implement a controlled breeding plan should seek the assistance of a geneticist. Although breeding programs for individual properties are important, genetic gains can be more significant and occur more rapidly if they are developed and used across and industry rather than limited to a particular property.

I have referred heavily to information prepared experienced geneticists and in particular work of Dr Raúl Ponzoni, the Principal Geneticist for the South Australian Research and Development Institute, Primary Industries, South Australia. Along with other responsibilities, Dr Ponzoni is the geneticist working with an integrated alpaca research project, 'Productivity and marketing improvement of the Alpaca fibre industry in Australia'.



## Genetic Improvement In The Alpaca Industry

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### INTRODUCTION

Knowledge of genetic resources gives breeders an understanding of the variation within the available genetic pool and of the opportunity to genetically improve the animal's performance.

Breeders attempt to quantify their genetic resources by measuring the performance of animals and their relatives.

The most objective way of comparing individual animals genetic ability is with Estimated Breeding Values (EBV's) that provide information on each animal relative to all the others in the group.

At present the United States and Australian Alpaca industries are based on small populations that are widely dispersed throughout each country. Most Alpacas are maintained in herds of less than fifty head and there is a large within-herd variability in quantity, quality and colour of fibre produced. There is obviously scope for genetic improvement in the production characters of the United States and Australian Alpaca by applying methods of animal breeding based on sound genetic principles.

In consideration of commercial profitability, selecting it for a high fleece weight, fibre diameter, yield and perhaps body weight seems desirable. This can only be achieved through the use by objective measurement, recording and analysis of animal performance (commercially important traits) and use of this information to select genetically superior animals for use in well designed genetic improvement programmes.

This discussion will consider animal breeding programs where selection is based on characters that are economically important in commercial production and where the animal breeding programme is designed to lead to genetic improvement of commercial production.

### UNDERSTANDING TERMINOLOGY

All genetic improvement programs aim to increase the profitability of animal production. Some programs aim to produce animals that have particular aesthetic traits (appearance of companion dogs). Other aim to develop aspects of natural behavior (speed of racehorses) and some aim to increase the efficiency of production of commercial commodities (wool and meat).

Whatever characteristic(s) a breeder aims to influence, design and implementation of genetic improvement programs requires an understanding of basic genetics and the meaning of terminologies used.

### **Cells, Genes and Chromosomes**

Bodies of all higher organisms are composed of cells, each of which contains heredity units called genes.

Genes are located along strips of deoxyribonucleic acid (DNA) called chromosomes that occur in pairs. Each gene is paired with a gene on same site on the other chromosome of the pair.

Genes are the basic units of heredity that maintain their individual identity between generations.

Alpacas have 37 pairs of chromosomes, half of which (37) are donated to the offspring by the sire and half by the dam.

### **Sex Linked Genes**

Sex linked genes simply means that the gene for a character being considered lies in one of the sex or X chromosomes so the character only appears with a particular sex.

### **Traits**

A trait is a distinguishing feature or character of an individual.

### **Quantitative Traits**

Quantitative traits are those influenced by many genes that cannot be identified. They are easily influenced by the environment and exhibit what is called continuous variation. This means their measurement is undertaken over a continuous scale with no clear boundary between good and bad. Their description and analysis is undertaken on a population basis rather than an individual basis.

### **Qualitative Traits**

These are traits influenced by only a few genes that are individually identifiable. They are not easily influenced by the environment and produce discreet, measurable classes of phenotype. They are described and analyzed in terms of individuals.

### **Genotype**

An individual's genotype refers to its genetic make up.

### **Phenotype**

The word phenotype refers to the appearance or measurable characteristics of an individual.

An individual's phenotype is a result of the genetic make up (genotype) of the individual and the environment to which it is exposed.

### **Homozygous**

An individual is said to be homozygous if the two genes it carries for a particular trait are the same. This means that the gene contributed to an offspring for a particular trait will always be the same.

### **Heterozygous**

An individual is said to be heterozygous if the two genes it carries for a particular trait are different. This means that either one of two genes for a particular trait may be contributed to an offspring. A breeder can never know which gene will be contributed to an offspring as the contribution is entirely random for each contribution.

### **Heterosis**

Is a description for hybrid vigour or increased level of performance of an offspring compared with the average of the parents.

Heterosis is a useful effect in commercial herds breeding to maximise commercial products.

The selection and use of individuals exhibiting heterosis usually results in limited genetic gain because gene combinations break up during segregation in testes and ovaries before mating.

### **Hybrid**

A hybrid is an offspring of parents that are genetically pure for particular characteristics. By definition hybrids are heterozygous animals. The first hybrid generation is usually described as the first filial

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generation or F1.

### Heritability

Heritability refers to the degree to which an individual of a superior phenotype (performance) will transmit that advantage to its offspring. A high heritability suggests that selection for that trait is likely to be effective.

### Genetic Distribution of a Population

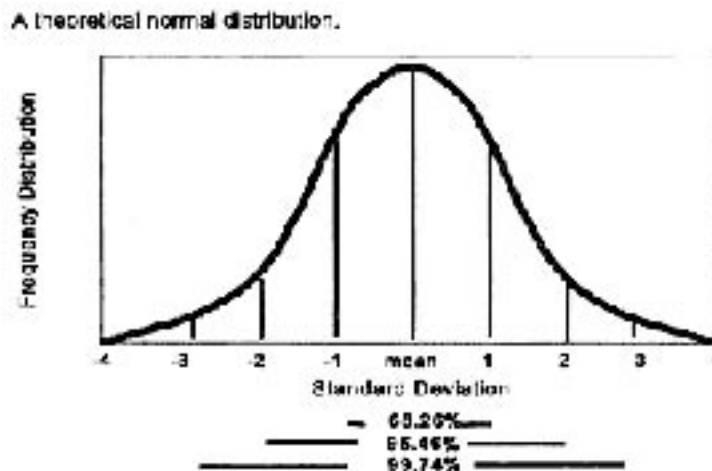
Most of the traits that are economically important are influenced by many genes and by many environmental factors (quantitative traits). In other words they exhibit continuous variation.

As quantitative traits are measured across populations rather than on an individual basis, measurement usually requires the collection of a large volume of data. The data then must be analysed statistically.

In its simplest form, this analysis consists of the measurement to decide the mean value for a trait and a measure of the variation around that mean.

Most biological measurements are considered normally distributed.

Figure 1



### Genetic Mean

Can be described as the central tendency of a population. It represents the arithmetic average value of a trait for a population.

### Standard Variation

The standard variation is a measure of the variation about a mean. In a normally distributed population, about two thirds of the population (68%) lie within one standard deviation of the mean, and about 95% lie within two standard deviations from the mean.

If, for a normally distributed population, reliable estimates of the mean and standard deviation are available, the expected proportion of the population that falls within a designated area of the graph can be determined.

Generally the smaller the standard deviation the less variation about the mean.

### **Variance**

Is a measure of the dispersion or variation of individual measurements about the population mean. Variation can be a result of both genetic and environmental influences. The variations result from the action of genes and gene combinations in response to prevailing environmental conditions.

It is important to remember that only the genetic variability can be transmitted to an individual from its parents, while variations due to the genetic interactions with the environment are not.

It is generally considered the most useful measure of variability of populations and is calculated simply the squared standard deviation.

If the variation of a trait within a population is small, there is little chance of genetic improvement. The converse is also true.

### **Coefficient of Variation**

The coefficient of variation describes the standard variation as a percentage of the mean. This measurement is used to help geneticists assess differences between populations.

Generally the variation of traits which have measurements that are large (bodyweight) is greater than the variation in traits that have small measurements (fibre diameter).

It should be considered as a population measurement rather than an individual measurement.

### **Correlations**

Animal breeders are often interested in whether a particular trait in an individual is associated with another trait.

A correlation coefficient measures the degree of association between two traits. The coefficient ranges from -1.0 to +1.0. A value of +1.0 shows that for each unit increase in one variable there is a unit increase in the correlated trait. Conversely a value of -1.0 suggests that for each unit increase in one variable there is a unit decrease in the correlated trait.

### **Genetic Correlation**

A genetic correlation estimates the extent to which selection for one character on the parent will cause a change in another character in the offspring. As an example, if a significant positive genetic correlation exists between greasy fleece weight and fibre diameter, there is an implication that as parents are selected for greasy fleece weight so fibre diameter may increase in its offspring. It is worthwhile to note that the genetic correlation between greasy fleece weight and fibre diameter in Australian Merinos is not strong (+0.13 to 0.19). Holding fibre diameter relatively constant is possible while selecting for fleece weight.

### **Phenotype Correlation**

A phenotype correlation estimates the degree of association between two characters on the same animal. For example if data indicates that a significant and positive phenotypic correlations exist between greasy fleece weight, clean fleece weight, fibre diameter and staple length there is an implication that if a selected animal has a fleece weight higher than the average of the herd, then the selected animal is one with higher than average fibre diameter and staple length. This selection can, of course, only be considered from animals in the same group managed in the same environment. A high negative

correlation has the obvious reverse implications.

### Generation Interval

The generation interval varies between species. It is generally defined as the average age of the parents when their first offspring are born and the number of years they stay in the flock as breeders.

If a small number of replacements are selected each year the average of breeding animals will increase and so the generation interval will increase. Conversely if a large number of replacements are selected each year the average age of the flock will decrease and so the generation interval will decrease.

### Selection Influences

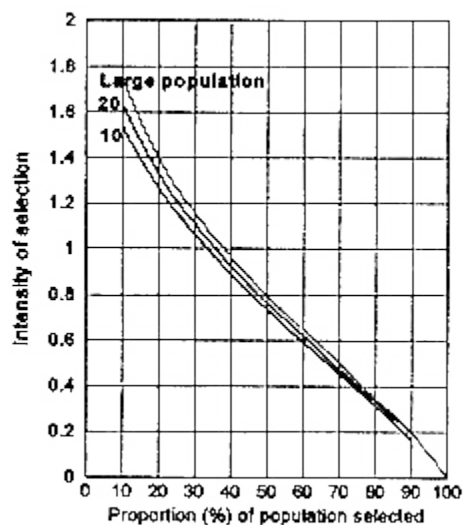
#### Selection Intensity

The selection intensity is a standard way of expressing the superiority of selected parents over the group from which they came.

The intensity of selection depends on the proportion of the population included in the selected group and can be determined from tables provided the distribution of phenotypic values is 'normal'.

As the percentage of a population selected as replacement breeders increase, the selection intensity decreases and so does the opportunity for genetic gain within the population. Figure 2 compares selection intensity for populations of 10, 20 and an infinitely large sample.

Figure 2 - The variation in selection Intensity with different population bases (adapted from Falconer 1981)



### **Selection Accuracy**

Accuracy of selection for a particular character is determined by the correlation between selection criteria and the selection objective. When selection is based on an individual's own performance selection accuracy equals the same as the square root of heritability (Ponzoni 1991).

The accuracy of selection is influenced by the heritability of the trait under consideration. For traits with high heritability (above 30%) an individual's performance provides a good estimate of its breeding value. When heritability is low (below 15%) performance of related individuals can be used to increase accuracy (Ponzoni 1991).

### **Repeatability**

Repeatability is closely allied to heritability and is useful for traits that are expressed several times during an animal's life time.

Repeatability can be considered as an estimate of future performance based on past performance.

Generally if repeatability is low it is important to take more than one indicative measurement of a character to improve accuracy of selection. If repeatability is high it probably follows that heritability is high so fewer measurements are necessary for acceptable accuracy.

### **Selection Differential**

The selection differential is the difference between the average measurement of a group of selected parents and the average of the whole population from which they were chosen.

### **Selection Response**

The selection response is the estimated annual change in the population mean produced by selection.

Breeding programmes are usually designed to maximise the selection response for a given trait. However, the relationship between intensity of selection and the proportion of the population selected is influenced by total population size.

The animal selection response can be calculated with the following formula (male response per generation + female response per generation) divided by (male generation interval + female generation interval) (Ponzoni 1991).

### **Estimated Breeding Values (EBV's)**

As discussed, the value of an animal as a parent cannot be measured from an animal. An animal's breeding value is estimated from records of performance of the animal or its relatives.

An EBV is the estimated value of an animal as a parent for a particular trait. It refers to the estimated breeding value of an animal compared with others in a particular discrete group.

Determination of an animal's EBV relies on measurement of the animal's performance and visual assessment. EBV's are used to estimate the amount of genetic gain that will be made from using one individual relative to others in the group.

EBV's are calculated using measurements of the animal's superiority within its group and includes a genetic scaling factor. A genetic scaling factor is an indication of the fraction of the measured superiority or inferiority of the parent itself (predictors) which will be passed on to the progeny (Maxwell and Brien

1988).

Information used to determine the genetic scaling factor includes the heritability of traits, genetic correlations between the traits selected and phenotypic correlations between the traits.

### **Inbreeding**

Inbreeding can be described as the mating, or breeding between relatives. It is also called line breeding and can be used to increase the homozygosity of a population or at least a selected trait for a population.

The rate of inbreeding is directly influenced by the size of the population from which replacements are selected.

### **Inbreeding depression**

Inbreeding depression can be simply described as the reduction in performance that results from increasing levels of inbreeding. Heterosis is of course the opposite effect and results from out crossing two 'pure lines'.

Ponzoni (1991) notes that as the selection intensity increases the effective population size usually decreases. He also indicates that if sires are introduced from an unrelated genetic source the annual rate of inbreeding will be zero.

### **Effective population size**

According to Ponzoni (1991) if the effective population size is known the calculation of the inbreeding rate is very simple.

### **Genetic Drift**

Genetic drift or random drift refers to changes in gene frequency, that occur due to chance, in populations of a limited number of parents.

The chance of changes in gene frequencies increases as the effective population decreases. In fact genes can easily become fixed or lost through chance, allowing for unplanned (often undesirable) phenotypic changes.

In breeding problems are often manifested as genetic drift especially as populations become increasingly homozygous.

Research shows that the smaller the populations, the greater change due to chance or the greater the variability in response to selection.

### **Coefficient of variation of response to selection (CVR)**

Geneticists often attempt to determine how large a population should be for genetic improvement by calculating the Coefficient of variation of response to selection (CVR).

**INDUSTRY BREEDING STRUCTURES**

If we accept that the commercial alpaca industry will primarily be a fibre-based industry it will most easily be compared with the Australian wool sheep industry.

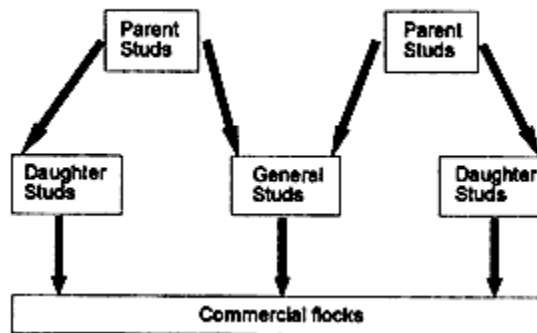
It is reasonable therefore to consider alternative structures used to distribute genetic gains throughout the industry population.

In the wool industry, like other well established livestock industries, the industry relies on breeding programmes undertaken in a small fraction of the population.

The industry breeding structure is tiered and relies on the principal that the flow of genetics is always down away from the elite stud to the commercial growers. In Australia it is generally accepted that about 90% of merino flock ram requirements are met by registered ram breeders involved in the structure described.

Figure 3. Breeding structure of traditional industries

**Breeding structure of traditional industries**



In a commercial industry the suppliers of the elite genetics receive stock prices significantly higher than that paid for by commercial stock. This relates to costs incurred in establishing and controlling a genetic improvement programme and the fact that only a relatively few animals are sold annually.

**Traditional studs**

Traditional stud breeding systems are often called closed nucleus systems and are characterised by tiered breeding structures topped by elite breeding herds (figure 3). As discussed elite flocks specialise in supplying breeding stock to commercial breeders. The most common names for these flocks are studs.

Studs often control genetic gain made by the industry by imposing a high selection intensity over a large population bred each year.

In sheep ram breeding flocks as few as 1 or 2% of rams are needed as replacements in the stud flock. This very high selection intensity means the rate of genetic improvement in the population is maintained.

In this traditional structure the studs usually remain closed to outside introductions. There is usually some limited (often secretive) very carefully controlled movement between the parent studs and movement down towards commercial hands. There is never movement in the opposite direction.

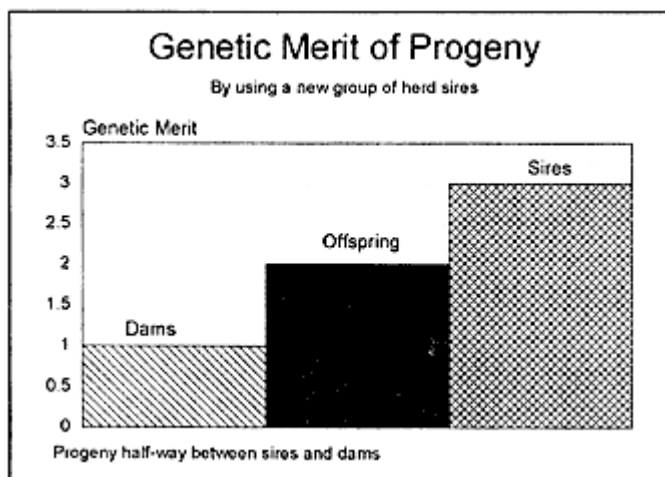
Culling of females in commercial flocks has no impact on the breeding program in studs. Only selection of sires and females in the stud's sire breeding flock can influence the stud's genetic improvement program.

This means the commercial (sire buyers) flocks is entirely dependent on improvements made in the stud (sire breeding) flock for long term genetic gain.

In commercial flocks, new sires which are genetically superior to those purchased previously are introduced each year. The offspring produced by the new sires are genetically half way between the new sires purchased and the females on the property and so are a little better than the previous year's offspring.

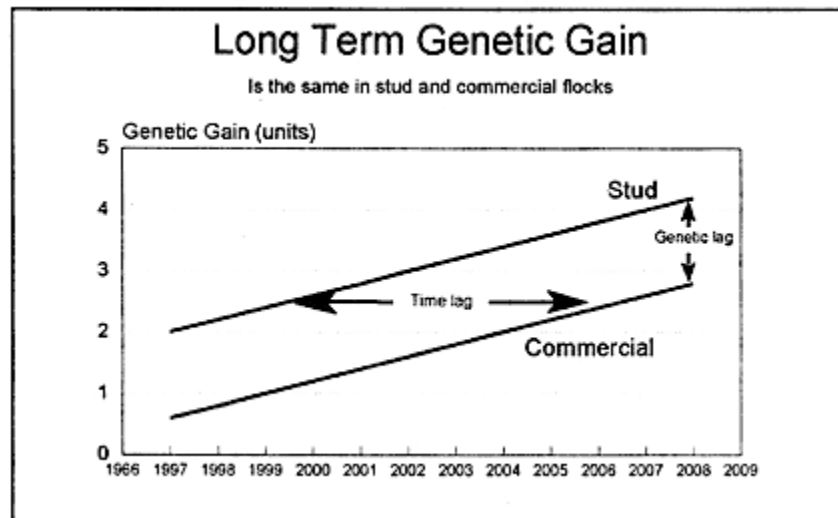
Imagine commercial flock females are all mated to one group of new flock sires. The genetic merit of the offspring will be half way between that of the sires and the females, as shown. Unless the offspring are backcrossed to the same sires repeatedly, the commercial flock will never get to a situation where it gets all the genes of those sires, and will always "lag behind" in genetic merit.

Figure 4. Genetic merit of progeny



With regular purchase of flock sires from the same stud, the commercial flock makes genetic gains at the same rate as the stud, although it lags behind in terms of absolute genetic merit. Furthermore, the genetic progression (direction and speed) of the commercial flock is the same as that of the stud, regardless of the individual sires used from the stud.

Figure 5 Genetic lag between stud and commercial flock



Provided the stud never allows the commercial flock to access its elite stock, the commercial flock can never catch up to the genetic merit of the stud.

However, the magnitude of the lag can be reduced in a commercial flock by:

- (i) reducing the generation interval (the time from birth until the production of first offspring);
- (ii) using sires of above average genetic merit;
- (iii) purchasing females from the stud herd to the commercial herd.

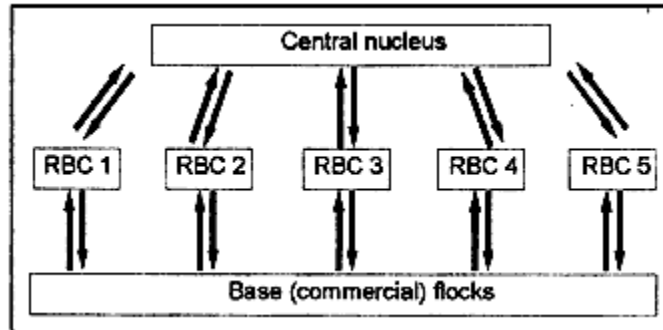
### Open nucleus

In contrast to more traditional structures, females can be taken into higher levels from lower levels.

Although selection of females in the top tier and also the lower tiers influences the programme at the top tier, the selection of sires remains the main way of making genetic improvement.

Figure 6. Breeding structure of a 3-tier nucleus breeding scheme.

NB: RBC - Regional Breeding Centre

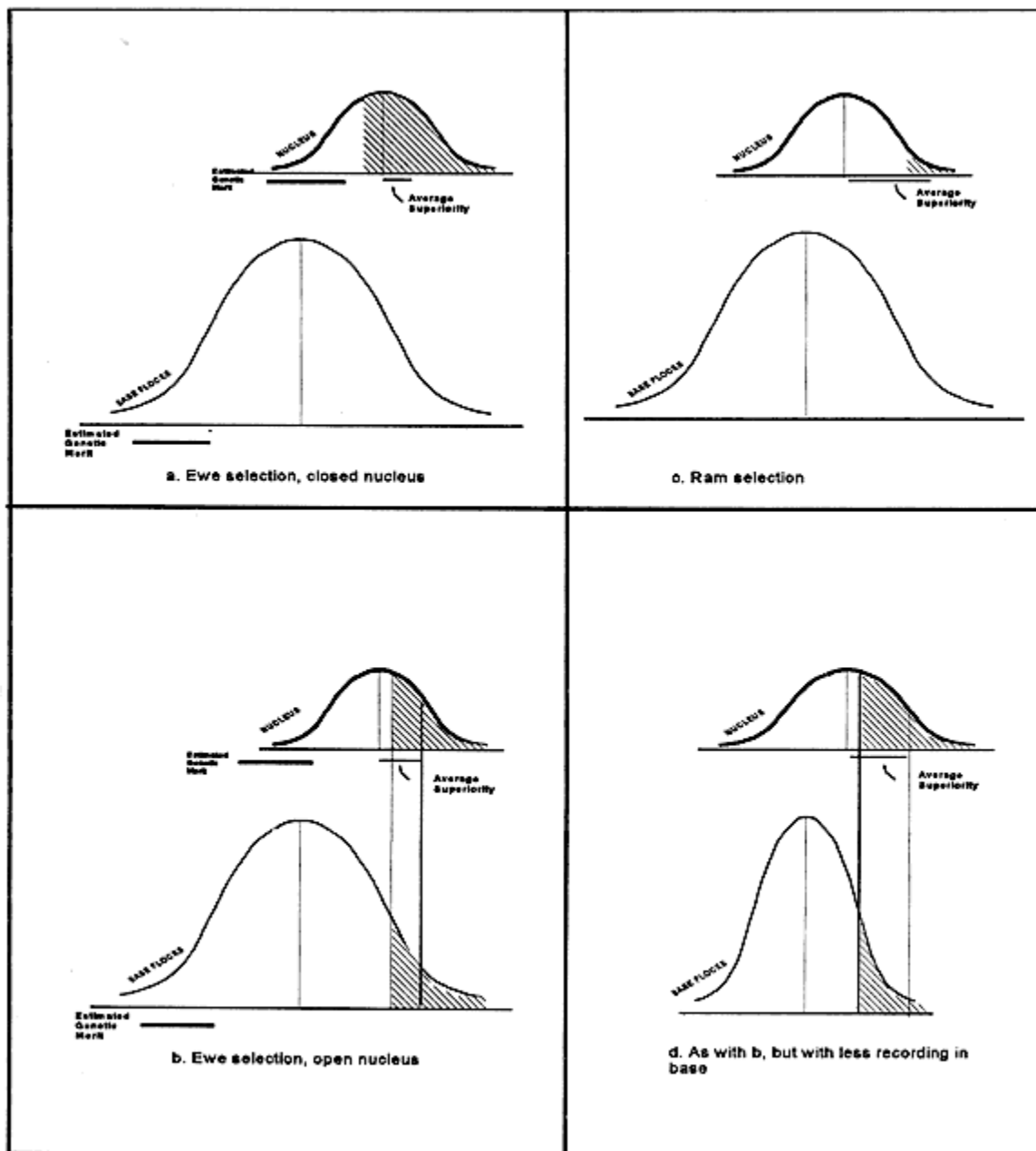


Because females can move upwards through the system, selection made in base flocks can affect the rate of genetic change of the whole scheme.

Selection with open and closed nucleus breeding system for sheep is described by Ponzoni (1991).

## Genetic Improvement In The Alpaca Industry

Figure 7: Selection with open and closed nucleus breeding system for sheep (Ponzoni 1991).



## Genetic Improvement In The Alpaca Industry

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In respect of figure 7, Ponzoni describes that section a shows the distribution of young females estimated genetic merit for the closed nucleus (stud) flock and base commercial flocks. He assumes that the number of young females required as replacements in the nucleus is about 60% of those available in the nucleus. As previously described no females go from the base to the nucleus. The average superiority of selected ewes is shown in Figure 7.

Ponzoni (1991) reports that section b represents an open nucleus system as ewe replacements are taken from both the nucleus and base flocks. He points out that although the average estimated genetic merit of females in the base flocks is lower than that average for the nucleus, the best females in the base are better than the worse females selected in section a. The average estimated genetic merit of selected females in section b is greater than the average of the selected females in section a, which should result in a greater response to selection.

Ponzoni describes that rams can usually be intensely selected. He says that genetic lag will usually be too great for base rams to have a greater estimated genetic merit than highly selected stud rams. Even if sire rams in the base flock had genetic merits that rivalled nucleus rams, Ponzoni says that it would be difficult to justify the cost and trouble of identifying them (performance recording). This is demonstrated in section c.

Ponzoni describes an advantage of having a closed nucleus system is that it can be managed with the aim of maximising genetic gain with less concern about commercial production. Also age structures can be reduced to minimise generation interval and detailed performance recording is often more economic (costs related to individual sale price).

The increase in intensity of selection on average estimated genetic merit in the closed nucleus is shown in section d.

Ponzoni also suggests that less accurate recording in the base flock results in a reduction in the variance of genetic merit which in turn reduces the scope for selection.

Ponzoni (1991) summarised results of comparative studies of closed nucleus breeding systems with open nucleus breeding systems. He reported that:

(i) Under favourable conditions the rate of genetic gain in an open nucleus could be about 10% to 15% above that in a closed nucleus;

(ii) The open nucleus system has a lower rate of inbreeding, which under practical situations would be approximately half that of a closed system. The effective number of animals is approximately doubled with the open system;

(iii) About 5% to 20% of the population should be in the nucleus, about 50% of replacement females for the nucleus should come from the base and all surplus nucleus females should be used as base dams.

### Group breeding schemes

Group breeding schemes are often a type of extended open nucleus breeding scheme where a number of breeders pool their genetic resources to form a nucleus flock. The nucleus flock then takes females from all breeders flocks and returns males back to them.

Group breeding schemes became very popular with sheep breeders in Australia and New Zealand in the

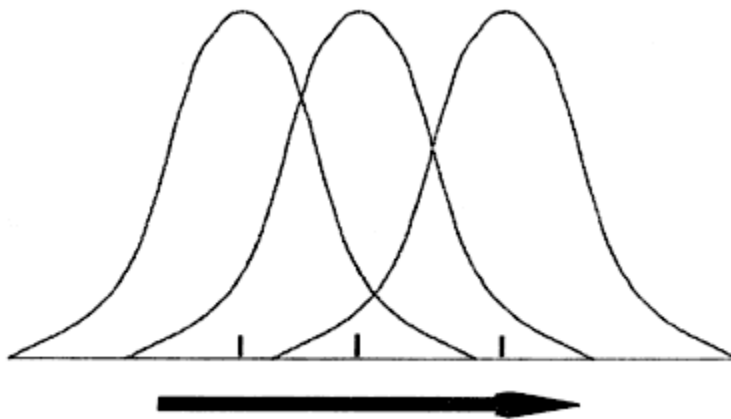
1960's and 1970's. Their population has declined in recent years for many reasons including changing breeding objectives of individual participants and the different breeding objectives required for the range of environments in which the members operated.

### AIMS OF A BREEDING PROGRAMME

Generally the aim of breeding programmes for most quantitative characters should be to improve the average economic performance of a flock by increasing the volume and/or the value of products produced.

This means there should be a continuous, gradual increase in the population average for each trait selected in successive generations.

Figure 8. A theoretically increasing genetic mean for a normally distributed character in a population.



### DESIGN OF BREEDING PROGRAMMES

Development of genetic improvement programs (Breeding Programs) should be undertaken with a clear goal of maximising profit from commercial production of marketable products.

Challenges to commercial producers are:

- (i) to know what, in what form and how much product the market wants now;
- (ii) to manage currently available gene pools to maximise profit from commercial production;
- (iii) To decide what future markets will demand (estimation of trends, changes in demand, new markets, etc.);
- (iv) to know how to efficiently identify the best genetics available in the population that will cost effectively produce products for future markets;
- (v) to know how to isolate and profitably use identified genetically superior animals.

The first step in designing a breeding program is to define the breeding objectives, i.e. what are the economically important production characteristics involved in alpaca breeding for fibre production. The first stop in designing a breeding programme is to define the breeding objectives, i.e. what are the economically important production characteristics involved in alpaca breeding for fibre production. Breeding objectives need to be continually reviewed.

Besides defining breeding objectives, the development of breeding programs requires information on genetic parameters (heritabilities, genetic correlations), phenotypic parameters (means, variances, repeatabilities, phenotypic correlations) and environmental effects (age of dam, type of birth/rearing).

Breeding programs can be described as well designed strategies for genetic improvement of a group or population of livestock. There are several steps that should be considered in designing a breeding programme. The first is to design the production system for the livestock species in consideration.

### **Step 1 - The Production System**

Designers need an adequate knowledge of life cycles, breeding intervals, fecundity, weaning age, feeding systems, product harvesting and all other biological and physical aspects to production.

Objective understanding of market requirements, including processing requirements is vital as any change in product quality must be aligned with the market requirements. Real costs, in relation to commercial value of products, of production must also be understood, is commercial production economically feasible.

It is important to remember that the commercial value of a product is solely determined by the next person in the product development chain. This information must be factual, not based on 'feelings' or 'general understanding'.

### **Step 2 - The Breeding Objective**

In designing a breeding objective or objectives, knowledge of the economically important production characters of the species is essential. For alpaca these are likely to be fibre and eventually meat aspects while with Llama they may be hardiness, ability to carry heavy loads and temperament.

Information is required on genetic parameters (heritabilities, genetic correlations), phenotypic parameters (means, variance, repeatabilities, phenotypic correlations) and environmental effects (age of dam, type of birth/rearing).

A defined breeding objective should describe the aim or goal of the breeding program.

### **Step 3 - Selection Criteria**

Selection criteria are those criteria that can be measured and used to estimate an individual's genetic merit.

The selection criteria must be based on characters which can be objectively measured. That means every person who measures the character using the same measuring equipment and technique will produce

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the same result. If selection is based on subjective measurement (fee, touch, handle, etc.) not all assessors will produce the same result.

Sometimes there are very experienced assessors who can estimate subjectively assess characters and arrive at the same conclusions as somebody who objectively measures these characters. However these skills are only learned after extensive experience and over many years. Objective assessment can be quickly taught.

The characters that are objectively measured may not always be the same as the traits considered in the breeding objective.

Each trait selected in the breeding objective must have an economic value.

It is generally accepted that animals should only be compared when they are the same age, same sex and have been managed in the same environment (feed, climate, management skills, stocking density, etc.). Adjustment factors may allow meaningful comparison between animals of different age, sex and production status and environmental effects. These factors are usually developed over long periods of recording.

### **Step 4 - Animal Evaluation**

An evaluation system should be an integral part of a breeding program. An evaluation system is often called a performance recording system, and is the only objective way of measuring achievement and objectively assessing differences between individuals.

Characters must be able to be objectively measured. Some can be measured on the individual directly (birth weight, growth rate, fleece weight, fibre diameter), some can only be measured on relatives (carcase weight, maternal merit of sires) and some can only be assessed after the animal has died (longevity, lifetime fertility).

### **Step 5 - Select Animals and Design Mating Programs**

In this step the manager of the breeding programme decides first which animals must be culled and those which must be included in a breeding programme. The breeding programme manager must decide which animals must be joined to which and which animals in the breeding programme must be replaced.

These decisions are affected by the intensity of selection required and the accuracy of the selection process.

Along with the generation interval, these factors control the rate of genetic change achieved by the breeding programme. The generation interval can be minimised and therefore the rate of genetic change, maximised by breeding programs that use animals as soon as practical after their selection.

### **Step 6 - Continuous Amendment**

There are many factors that can influence a breeding program.

Influencing factors include not only changes to economic and marketing situations but also to technological advances in reproduction and measurement technology.

There is also a need to forecast likely changes in the market if changes in consumer demand patterns mean that breeding programs need to focus in a different direction.

For example it is generally accepted within the Australian wool industry that to genetically change the average fibre diameter of a flock by 1.0 micron will take about 10 years. This assumes average management, replacement and husbandry techniques.

An important assumption used in genetic theory of animal breeding programme development is that an infinite population is available. Small populations can affect expected responses to breeding programmes because of uncontrollable chance outcomes.

### SELECTION FOR MORE THAN ONE CHARACTER

It is unusual for selection programs to only consider one trait. There are several ways of selecting for more than one trait at the same time.

Ponzoni (1991) considers that they are all variations of three basic systems, they include:

- Tandem Selection

- Independent Culling Levels

- Selection Index

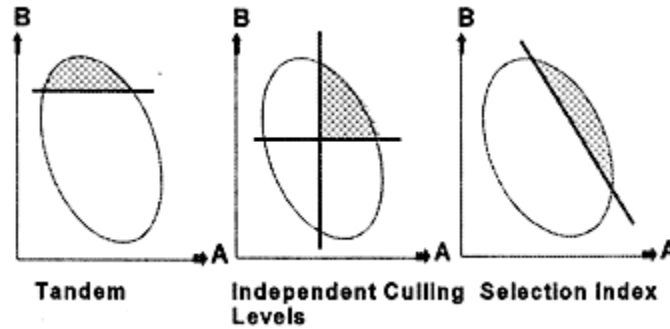
Ponzoni (1991) describes Tandem selection as “. . . selecting for one character in one year in one generation, but the selected character may change from one year to the next or from one generation to the next.”

He describes Independent Culling Levels as a situation where “. . . a minimum standard is established for each character. An individual must be above a minimum standard for all characters if it is to be accepted. The standards should be in such a way that the number of accepted individuals equals the number of necessary replacements. With many characters this system becomes very complicated.”

He describes the Selection Index approach as involving “. . . recording all characters in all individuals and then calculating a weighted sum of all the values, thus obtaining an index value for each individual. The individuals with the highest index values are selected as replacements.”

According to Ponzoni (1991), figure 9 “Illustrates the selection process when tandem, independent calling levels and selection index are used. The points inside the eclipse represent the range of variation in the true characters. High values of A are in this case often associated with low values of B, and vice versa. The shaded area represents that part of the population that is selected. With the tandem system selection is for character B”.

Figure 9: Different selection methods with two characters (Ponzoni 1991)

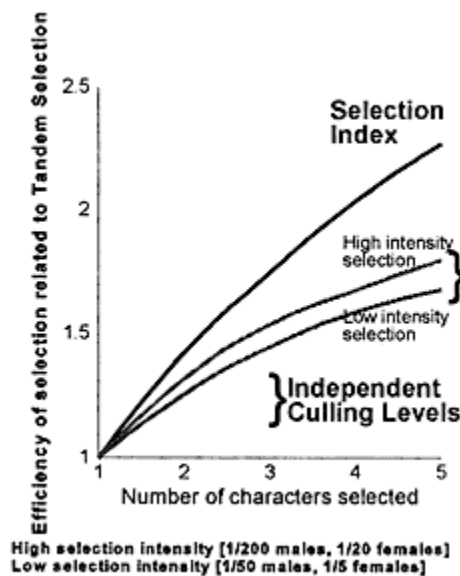


Ponzoni (1991) goes on to describe that the most effective scheme is based on the standard deviation, the heritability and the economic value for each trait involved and the related phenotypic and genetic correlations.

Each system will suffer if any of this data is not available.

Ponzoni (1991) reports that graph 10 assumes the most economically effective scheme is used in each system. Selection in the tandem system is for the trait resulting in the greatest unit economic gain. With independent culling levels those culled result in the greatest economic gain and optimum coefficients are used in the selection index.

Figure 10. Relative Efficiency of Selecting Systems (Ponzoni 1991)



METHODS OF SELECTION

Selection refers to the method of choosing the parents of future generations. The two main techniques

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for selecting individuals are family selection and mass selection. Family selection involves using records on relatives of the individuals under selection. Examples of family selection are pedigree selection and progeny-test.

Mass selection is the simplest form of selection of individuals and involves selecting the animal on its own performance relative to other animals of the same sex and age, and affected by a similar environment.

Performance can be defined as either:

- (i) a visual appraisal of one or more characteristics of the animal (e.g. conformation, structural soundness - feet, jaws, etc.).
- (ii) one measured characteristic (e.g. fleece weight).
- (iii) a combination of measured characteristics (e.g. fleece weight, fibre diameter, bodyweight).
- (iv) a combination of visual and measured characteristics.

Selection of individual animals within a herd has a twofold effect on production:

- (i) production in the current herd will be increased by those selected superior animals exhibiting a large proportion of their superiority for the remainder of their productive lifetime.
- (ii) production in future generations will increase by the selected superior animals passing on, to their offspring, a high proportion of their superiority.

### DETERMINATION OF ECONOMICALLY IMPORTANT TRAITS

Traits are economically important because of their influence on income or expenses.

The economic value of traits used as selection criteria can simply be expressed as the average net profit for all levels of the trait less the net value change (can be positive or negative) from increasing the trait by one unit.

Profit is defined as income less expenses including fixed costs.

However it is important not to have an excessive number of traits included in a selection programme and the traits included must relate to economic preference of the animal.

According to Ponzoni (1991) the size of the economic value depends on the units in which each trait is expressed and the values do not give any indication about the genetic variation that exists within a population. He reports that the limitations described can be overcome by multiplying the economic value of a trait by genetic standard deviation for the trait.

### PRODUCTION CHARACTERS OF IMPORTANCE

Alpacas primarily produce fibre (wool) with meat and skins likely to be important only in the long term future. Breeders should be concerned with the alpacas' ability to produce fibre in sufficient quantity and

of an acceptable quality in a given environment at minimum cost. Therefore many production characters will be of interest, but it must be remembered that the fewer the characters in a selection programme, the more rapid the progress that may be made in each.

For alpaca fibre production, the economically important production characters are likely to include:

- body size (only as large as is necessary to maximise fleece production economically).
- greasy fleece weight (as high as possible).
- fibre diameter (fibre of a lower diameter is likely to command a higher price per kg in the long term).
- fleeces of single uniform colour (reduces skirting and clip preparation needs and, large volumes of single colour fibre are more attractive to processors).

However, before deciding which characters should or should not be subjected to selection, it is necessary to determine whether the character can be objectively measured, whether it is heritable and what phenotypic and genetic correlations exist between the characters.

Various researchers (Fernández-Baca 1991) suggest that the characters of prime importance for alpaca selection are live weight at first shearing and weight of the fleece removed at the first shearing.

Experience with the Australian merino wool industry suggests that a commercial alpaca industry, income traits likely to be economically important are those listed in Table 1 (this estimate does not consider sale of cull animals for slaughter).

Table 1. Traits likely to important in commercial alpaca breeding

<b>Product/Character</b>	<b>Measurable Trait</b>
Clean Fleece weight	Greasy Fleece weight
Average fibre diameter	Fibre diameter
Live weight	Live weight at various ages

**Alpaca Selection Considerations**

Although commercially managed alpacas should primarily be seen as fibre producers, non fibre aspects of production should also be considered when selecting animals for breeding.

As previously discussed they include reproduction performance, physical defects and temperament.

Commercial production of alpaca fibre is, or will be undertaken for profit. With this in mind selection and management of breeding stock should be undertaken with a view to maximising profit from individuals or even more correctly from flocks.

As previously discussed in this paper producers must be aware of both what buyers want, and more positively what they are prepared to pay premium prices for. With this knowledge producers can

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determine cost-effective production strategies to maximise profit.

Most sheep and alpaca wool economic data shows that when considered only from a fibre diameter perspective, fine fibre returns more per kg than course fibre. It is also generally true that sheep and alpaca with coarse fleece produce a greater weight of clean fleece than do animals with fine fleeces.

A trade off exists for commercial producers which means often it is more profitable to produce more fleeces of an average (middle range) fibre diameter than a little very fine fibre or a lot of very coarse fleece.

This is of course dependent on the price differential between very fine fleece and very coarse fleece and the associated production differential.

Index selection of breeding animals that relies on knowledge of trait heritability, relative economic value, correlation between traits etc will assist selection to maximize profit.

Other characters that may be considered as selection criteria include factors including fleece type (suri/huacaya), testicle size, face cover, leg fleece cover, etc.

### MEASUREMENT OF CHARACTERS

The objective measurement of those production characters mentioned above provides information that can be used in direct selection for productivity. All of those characters can be measured, some are relatively simple and cheap to measure (e.g. body weight and greasy fleece weight) while others are time-consuming and expensive (e.g. fibre diameter).

Greasy fleece weight can be easily measured with a spring balance and weighing pan, but to measure fibre diameter, and clean scoured yield requires some special equipment, such as a projection microscope or air flow testers.

It is important to remember that a test giving a mean fibre diameter of, say, 30 microns does not mean that the animal will always produce 30 micron fibre. Older animals produce coarser fibre than younger animals and nutrition influences fibre diameter.

### Effects on Fibre Production and Quality

Assessment of animals for use in a breeding programme must consider a range of factors that influence an animal's phenotype.

Animals that have identical genetic merit can have divergent phenotypes. As discussed earlier an animal's phenotype is predominantly (at least 60%) determined by its environment.

Environmental influences that affect an animal's phenotype include: age, sex, production status, nutritional status, health status, management strategies to which it is exposed, climate, birth type, age of dam, etc.

There are obvious dangers in selecting animals purely on their phenotypic appearance.

## Genetic Improvement In The Alpaca Industry

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Without detailed information about the animal's environment and the performance of its peers estimation of genetic merit is very difficult.

Even limited data can be misleading. Davis 1997 describes the following example: Fibre diameter of a reference sire's offspring in one flock may average 23 microns while in another flock managed at high nutritional status his offspring may average 28 microns. A sire used in the first flock whose progeny average 25 microns is inferior (2 microns coarser) to the reference sire. However a sire from the second flock whose progeny average 25 microns would be superior (3 microns finer) to the reference sire.

Age, production status (pregnant, lactating, growing) and health status also affects an animal's fibre diameter.

Animals that are '2 years old' can often vary from 18 months to 30 months and the possible effect on average fibre diameter is important.

In summary, the phenotype (appearance or performance) of each animal is the result of the genetic make up of the animal's genotype and the environment in which it is run (Phenotype = Genotype + Environment).

Therefore valid comparisons can only be made between animals of the same type (sex, age), in the same production status (pregnancy, lactation, growth), run under the same conditions (same property) and at the same time (e.g. same shearing dates).

### HERITABILITY OF CHARACTERS

Heritability refers to the degree to which an animal of a superior phenotype (performance) will transmit to its offspring that advantage. For example, if the heritability of body weight at tuis age is 50 per cent and the parents each have a selection differential of 10 kg, then on average, they would transmit 50 per cent (or 5 kg) of their advantage to their offspring. The remainder of their advantage may not have resulted from their genotype, but rather from having been reared in a favourable environment. This part of their advantage cannot be handed on to the next generation.

It must be remembered that the machos and hembra contribute equally to the genotype of their offspring and therefore when estimating the improvement in the offspring, gains expected from each parent must be averaged [selection differential of the sire x heritability x  $\frac{1}{2}$  + selection differential of the dam x heritability x  $\frac{1}{2}$ ]. In the example above, the total gain expected in the next generation would be,  $10 \times 50/100 \times \frac{1}{2} + 10 \times 50/100 \times \frac{1}{2}$  or 5 kg in bodyweight at tuis age.

There are few estimates of heritability for production characters of Alpacas and therefore we have to rely on the limited available information, which it self is limited and of a preliminary nature.

However, the following heritability values have been estimated by research workers in Peru. The characters can be classified as having high (greater than 0.30), medium (0.15 to 0.30) or low (less than 0.15) heritability.

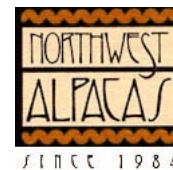


Table 2. Alpaca heritability estimates Huacaya alpaca  
(adapted from Fernández-Baca 1991)

Character	Age	Heritability Estimates
Body Weight	at Birth	0.34; 0.53
	at Weaning	0.39
	at First Shearing	0.55; 0.69
Fleece Weight	at First Shearing	0.21; 0.22; 0.35
Survival to Weaning		0.10

The heritability of a character gives an indication whether selection for that character will be effective. The fleece characters outlined above have moderate to high heritability estimates, suggesting that gains in these characters can be made relatively quickly.

The heritability of fibre diameter in Merino sheep is high at 0.5 (A Ram Breeders Guide to Wool Plan 1988). Although less is known about the heritability of fibre diameter in alpaca, it is reasonable to assume that the heritability in alpaca is high as it is in sheep.

#### ASSOCIATION BETWEEN CHARACTERS

##### Phenotypic correlation

A phenotypic correlation estimates the degree of association between two characters on the same animal. The following phenotypic correlations have been estimated by researchers in Peru.

Table 3. Phenotypic correlation estimates for Huacaya alpaca  
(Fernández-Baca 1991)

Characteristics			Age	Machos	Hembras
Body Weight	with	Fleece Weight	Juveniles (< 4 years)	0.40	0.58
	With	Fleece Weight	Adults (> 4 years)	0.45	0.32
	With	Survival		0.26	0.26
Fleece Weight	with	Staple Length	Juveniles (< 4 years)	0.30	
	With	Staple Length	Adults (> 4 years)	0.32	0.20
Fibre Diameter	with	Fibre Length	Adults (3 years)		0.27
	With	Yield	Adults (3 years)		0.42
	With	% Grease	Adults (3 years)		-0.28
Fibre Length	with	Yield	Adults (3 years)		0.40
	With	% Grease	Adults (3 years)		0.18

### Genotypic correlation

Few genetic correlation have been reported for traits in alpaca. Fernández-Baca (1991) reports only correlations between live weight and fleece weight at the first shearing and between birth weight and survival to weaning. The average correlations reported are summarised in table 4.

Table 4. Genetic correlation estimates for Huacaya alpaca (from Fernández-Baca 1991)

Characteristics			Age	Correlation
Body Weight	with	Fleece Weight	Juveniles (1 year)	-0.26
Birth weight	with	Survival to weaning	Birth	0.18

**Repeatability estimates**

Repeatability is a concept closely aligned with heritability. When considered an individual’s performance is the basis of selection is equals the square root of the heritability. Where a trait is measured several times during a life time repeatability is useful is determining that portion of the variation of a trait that is due to non environmental influences.

Table 5. Repeatability estimates for Huacaya alpaca (adapted from Fernández-Baca 1991)

Charasteristic	Repeatability
Birth weight	0.33 to 0.33
Weaning weight	0.31 to 0.36
Weight of fleece at first shearing	0.6

COMMERCIAL FIBRE ASSESSMENT

**Breeder Requirements**

Relate to maximising profit from live animal sales. The characters which are important in a breeding-based industry may not be important in a commercial industry.

For example while fleece face cover may be important to the visual appeal of an animal and therefore important in a breeder sale-based industry, it may not be correlated with commercially important traits. Therefore, selection for commercial fibre production may not consider face cover.

**Processing**

Understanding commercial product buyer requirements and the premium price they are prepared to pay for it is the most important economic aspect of commercial production.

In both sheep wool and alpaca fibre, the price paid for coarse fleeces is less per kg than the price paid for fine fleeces.

However it is also true that animals that produce fleeces of a finer average micron usually produce less total fleece weight than animals that have an average fibre diameter that is coarse.

In a commercial fibre production programme there is an economic trade off between fibre diameter and fleece weight and the most economic fleece production requires consideration of both factors at the same time (these factors have a genetic association).

### **Fleece characters**

#### **Fineness and Handle**

Handle is said to be directly related to micron and the feel of the fibre and also considers the degree of softness in the fibre.

#### **Uniformity of Micron**

Relates to the evenness of fineness/softness throughout the fleece.

#### **Sheen/Lustre**

This relates to light reflection of the alpaca fibre. It takes into account breed type.

#### **Uniformity of Colour**

The evenness and uniformity of colour throughout the fleece.

#### **Character/Style**

This relates to the wave/crimp and crinkle within the staple with consideration of the breed type.

#### **Length**

Length must be uniform throughout the entire fleece and be related to a 12 month growing season. Excessive length incurs discounts as do fleeces that are short.

#### **Impurities**

Vegetable matter, staining and tip damage cause fleece discounts. Tender fleeces are also discounted.

#### **Medulation**

Contamination with broad, continuously medullated fibres causes discounts.

#### **Clean Fleece Weight**

The percentage of scourable impurities within the fleece. Yields average approximately 90% for alpaca.

#### **Crimp**

Crimp is the natural wave structure of alpaca and sheep fibre. Crimp measurement, the number of crimps per inch, was the traditional way of classing the fineness of Australian Sheep fleece. This measurement was used in the absence of a more objective method of measurement.

Although there is a relationship between the crimp and the fineness (fibre diameter) of a fleece the relationship is not exact. Today fibre diameter can be measured very accurately with a range of specialised equipment.

However a visual assessment of the fleece crimp is a rough guide to the likely fibre diameter of the fleece.

Some consider that fibre must have well defined crimp to maximise commercial value.

The only people that can answer that question are processors and a question must be put appropriately. It may be that crimp is a necessary processing factor in its own right. It may be that crimp and fibre diameter are related and inseparable (correlated characters) so crimp is a requirement by default. It may be that fibre of the right length, fibre diameter, does not need crimp to be valuable.

### FLEECE COMPETITIONS

Fleece competitions can be exiting and promote a manager's ability to produce a desirable fleece. Without detail described above it should not be used as an indicator of the genetic merit of an animal.

### SHOW COMPETITIONS

Show competitions have a place in commercial fibre producing industries. I think though, they more reflect a manager's ability to prepare an animal for visual appeal in the show ring. The heritability of the phenotype buyers are presented within the show ring needs much more objective and detailed assessment.

### SIRE REFERENCING

Sire referencing is a technique that allows objective comparisons of males that have been born and reared in different flocks or herds.

According to Brien et al (1992) the basis of sire referencing is to use progeny testing in one of two alternate systems.

#### **Central tests**

This system involves the management and progeny testing of males on a central test site. Males compared can be derived from any property genetic, environmental or management background.

Ideally mating is undertaken using artificial insemination (AI) to avoid any problems of natural mating.

The distinct advantages central test sire referencing are that management can ensure correct mating and objective measurement is undertaken to ensure a meaningful test and all males are managed and tested in the same environment and production data on progeny is collected at the same time of the year.

Its disadvantages relate to high costs and the number of males that can be tested is limited by the stock carrying capacity of the property.

#### **On-Farm Sire Referencing**

On farm sire referencing can be undertaken in two ways, either independent of central tests or linked to central tests.

##### (i) Independent of central tests

A group of breeders nominate two or more reference sires which must be progeny tested in several or all participating herds. Ideally the sires are mated through AI to allow concurrent matings in all flocks. There must be enough overlap in the reference sires to allow all flocks to be linked.

Because the costs are less, the advantages of on farm referencing include that each breeder can test a greater number of males and there is (theoretically) no limit to the number of properties that can participate. If management and recording was maintained at a high level there are opportunities for

greater genetic progress than with central tests only.

Disadvantages include:

- ensuring testing is undertaken correctly and honestly
- different management programs may influence collection times
- some breeders may not wish to use sires bred outside the herd
- some breeders see the use of two sires per property as costly (females needed, testing costs, etc)

(ii) Linked to central tests

This method relies on reference sires being tested together on a central test site and then undertaking on-farm sire referencing by using one or more of the sires from the central test group.

Brien et al (1992) suggests that if a group of breeders chooses to use this system, it may be desirable to test the sires at the central sites that represent the extremes of environments found among the participating breeders.

This method allows breeders with closed herds the ability to avoid use of outside males on their own property.

Users of sire referencing information must remember that it is misleading to assume that an elite sire from a sire referencing program must have its origins in an elite herd. Only small numbers of sires from each property are used in central testing programs and variability of genetic merit within a source will mask variability between sources.

EXAMPLE CALCULATIONS

**Generation interval**

If we assume a population of breeding females has a mortality rate of 2%, first produce their first offspring at 2 years of age and stay in the breeding herd for 10 years, the flock structure would be as shown in Table 6.

Table 6. Flock structure (female breeders) for two alternate fictitious flocks

Age (years)	Proportion in each age group	Number of breeding females in the flock	
		400 females	40 females
2	0.1203	48.1	4.8
3	0.1179	47.2	4.7
4	0.1155	46.2	4.6
5	0.1132	45.3	4.5
6	0.1110	44.4	4.4
7	0.1087	43.5	4.3
8	0.1066	42.6	4.3
9	0.1044	41.8	4.1
10	0.1023	40.9	4.0

If the herd uses a male:female mating ratio of 10 males per 100 females, a flock of 400 breeders needs 40 males and a flock of 40 breeders needs 4 males. Males are used in fictitious this flock for 3 years so the structure of the male flock is:

Table 7. Flock structure (male breeders) for two alternate fictitious flocks

Age (years)	Number of Males Required	
	400 female breeders	40 female breeders
2	13.6	1.4
3	13.3	1.3
4	13.1	1.3

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Also assume in our fictitious flock reproduction performance of breeding females is 80%. That is 80% of the females will wean an offspring in any year. Also assume that 50% of progeny are males and 50% are females. This means the 400 breeding female herd will produce on average 160 male and 160 female offspring. The 40 female herd will produce 16 male and 16 female offspring.

The proportion selected as replacements each year can be determined by dividing the number of replacements needed each year by the population available. Therefore in this example the proportion of females annually selected as replacements from available progeny is 0.3006 for both the 400 female herd (40.1/160) and the 40 female herd (4.8/16). In this example the proportion of male progeny selected as breeder replacements annually is 0.085 for both flocks.

By definition, the **generation interval** is the average age in years when the offspring that replace them are born.

For the females in these examples it can be calculated as:

$$(2 \times 0.1203) + (3 \times 0.1179) + (4 \times 0.1155) + (5 \times 0.1132) + (6 \times 0.1110) + (7 \times 0.1087) + (8 \times 0.1066) + (9 \times 0.1044) + (10 \times .1023) = 5.865 \text{ years}$$

For the males in the example the generation is calculated as:

$$(2 \times 0.3400) + (3 \times 0.3325) + (4 \times 0.3275) = 2.988 \text{ years}$$

### Intensity of selection

From tables (Falconer 1991) is 1.159 for the 400 female flock and 1.075 for the 40 female flock. The selection intensity is approximately 1.687 for the rams selected for the female flock of 400 and 1.201 for the female flock of 40.

### Selection differential

For example, if in the fictitious flock described above there is no difference between male and females and the average first shearing fleece weight for a flock of alpaca is 2.0 kg and the selected group has an average first shearing fleece weight of 2.5 kg, then the selection differential is 0.5 kg.

### Selection response

For the larger female group in the example under consideration, the animal selection response (for first shearing fleece weight) is calculated as:

[(selection intensity for males + selection intensity for females) x heritability x standard deviation] divided by [male generation interval + female generation interval]

$$= [(1.687 + 1.159) \times (0.30) \times (0.5)] / [2.49 + 5.86] = 0.051 \text{ kg per year}$$

For the smaller female group the annual selection response is:

$$= [(1.201 + 1.075) \times (0.30) \times (0.5)] / [2.49 + 5.86] = 0.041 \text{ kg per year}$$

These calculations estimate that in our larger fictitious flock the annual rate of improvement in the first shearing fleece weight will be 0.051 kg.

Calculations for the smaller flock (40 breeders) estimate an annual improvement in the first shearing fleece weight of 0.041 kg per year. The heritability used is an estimate from Peruvian research.

The estimated rate of genetic increase from the larger flock is approximately 25% greater than for the smaller flock. The difference in expectation is largely due to the greater selection intensity in the larger flock.

However, this improvement is only likely if it were the only trait included in the breeding objective. The reality is that if other traits are included in the breeding objective the response to selection is likely to be less.

### Effective population size

Ponzoni (1991) provides the formula to calculate effective population size ( $N_e$ ) as:

$$N_e = [4sdL]/[s + d] \text{ where:}$$

$s$  = number of new sires incorporated into the flock each year

$d$  = number of new dams incorporated into the flock each year

$L$  = average of female and male generation lengths

In the two fictitious flocks used in this paper, the 400 female herd use 40 male annually and replaced 48 females and 20 males annually. The 40 female herd replaced 5 females and 2 males annually.

To calculate the generation interval for the two fictitious flocks used in this paper, we must first calculate the average generation interval.

$$\text{For each flock : } L = [5.865 + 2.988] / 2 = 4.4265$$

$$\text{For the 400 female flock: } N_e = [4 \times 13.6 \times 48 \times 4.4265] / [13.6 + 48] = 188$$

$$\text{For the 40 female flock: } N_e = [4 \times 1.4 \times 4.8 \times 4.4265] / [1.4 + 4.8] = 19$$

In the two fictitious flocks used in this paper, the 400 female herd use 40 male annually and replaced 48 females and 20 males annually. The 40 female herd replaced 5 females and 2 males annually.

### Annual rate of inbreeding

The annual rate of inbreeding for each flock calculated, according to Ponzoni's (1991) equation:

$$\text{Annual rate of inbreeding} = 1 / [2 \times N_e \times L].$$

So for the 400 female flock the annual rate of inbreeding is:

$$1 / [2 \times 188 \times 4.4265] = 0.06\%,$$

and for the 40 female flock the annual rate of inbreeding is:

$$1 / [1.4 \times 19 \times 4.4265] = 0.8\%$$

These simplified calculations show how the rate of inbreeding with populations increases markedly as effective population size decreases.

### Coefficient of variation in response to selection (CVR)

Ponzoni (1991) notes that an approximate estimate of CVR can be obtained from the formula:

$$\text{CVR} = [2 \times L]^{0.5} / [Q (N_e \times t)]^{0.5}$$

where:

L = average generation between males and females

Q = the average of the product of selection intensity (i) and the accuracy of selection (r) for females and males

$N_e$  = the effective population size

t = the number of years after which the selection program is to be evaluated

The average of the product of selection intensity (i) and the accuracy of selection (r) for females and males, Q is calculated (Ponzoni 1991) as:

$$Q = [i_F \times r_F + i_M \times r_M] / 2$$

where:

i = intensity of selection

r = accuracy of selection

F = females

M = males

Results obtained earlier for the two fictitious flocks are summarised in table 3. The table assumes that selection is made on the basis of fleece weight at first shearing and that the accuracy of selection of that trait is 0.55 (square root of heritability). The table also show the calculated Q values for this fictitious situation and assumes that the program will be evaluated after 5 years (t = 5).

Table 8. Calculation of Q values

Factor	400 female flock	40 female flock
L	4.4265	4.4265
$N_e$	188	19
i (males)	1.687	1.201
i (females)	1.159	1.075
r	0.55	0.55
Q	0.78265	0.6259
t	5	5

The selection response for first shearing live weight has already been calculated (see the section on selection response) and is 0.051 kg and 0.041 kg per year for the 400 female flock and 40 female flock respectively.

Using the detail above we can calculate the CVR. Table 4 demonstrates data used and CVR for each of the fictitious flocks considered.

Table 9. Calculation of CVR values

Factor	400 female flock	40 female flock
L	4.4265	4.4265
Q	0.78265	0.6259
$N_e$	188	19
t	5	5
CVR	12%	49%

In the selection section above a calculated annual response for the improvement in first shearing fleece weight was 0.051 kg per year (400 flock) and 0.041 (40 flock).

This means that in five years (the evaluation time nominated) the total response will be:

$$0.051 \times 5 = 0.255 \text{ kgs per head (400 flock).}$$

$$0.041 \times 5 = 0.205 \text{ kgs per head (40 flock)}$$

If the CVR for first shearing fleece weight is 12% (the 400 female flock), the standard deviation is:

$$0.255 \times 0.12 = 0.031 \text{ kgs}$$

If the CVR for first shearing fleece weight is 49% (the 40 female flock), the standard deviation is:

$$0.205 \times 0.49 = 0.100 \text{ kgs}$$

The likely variation from this small population is much greater than that expected for the larger population.

According to Ponzoni (1991) suggests that CVR values of 10 to 15% are considered low enough, but that lower values would add credibility to the program.

Ponzoni goes on to say that the formula for calculating CVR can be rearranged to estimate a population size required to obtain a credible CVR.

$$N_e = [2 \times L] / [(CVR \times Q)^2 \times t]$$

If it is assumed that the required CVR = 15% and  $t = 5$  as in above:

For the flock of 400 females:

$$N_e = [2 \times 4.4265] / [(0.15 \times 0.78265)^2 \times 5] = 208.3$$

and from above:

$$s = N_e / 4L = 208.3 / [4 \times 4.4265] \text{ _ } 12 \text{ new sires per year}$$

This suggests that in the flock with 400 females and considering other genetic parameters used, to achieve a CVR of 15%, 12 new sires would need to be used annually.

For the flock of 40 females:

$$N_e = [2 \times 4.4265] / [(0.15 \times 0.6259)^2 \times 5] = 200.9$$

and from above:

$$s = N_e / 4L = 200.9 / [4 \times 4.4265] \text{ _ } 23 \text{ new sires per year}$$

This suggests that in the flock with 40 females and considering other genetic parameters used, to achieve a CVR of 15%, 23 new sires would need to be used annually. This herd only uses 4 sires annually, so this results suggests that the risks from inbreeding in the herd is significant.

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