Basic Genetics of Cashmere Production

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Introduction

A brief scan of the literature will reveal that the peak period for cashmere production research was in the 1980s and 1990s and that the vast majority of this research was conducted in Australia and New Zealand (Bigham et al., 1993; Johnson, 1985; Kelly, 1988; Peterson and Gherardi, 1996; Restall and Pattie, 1990). Interest was high in the United States also and several conferences were dedicated to cashmere production. This author, as a young scientist, was a participant at a conference that was held in San Angelo, TX in 1992. While that conference paper is slightly dated, it still has many relevant concepts about breeding for cashmere production and has been included in this conference paper, which will concentrate on research that has happened since 1992. To easily distinguish between this conference paper and the 1992 conference paper, this conference paper will be formatted in Times Roman 12 pt font and the 1992 paper will be in Arial 10 pt font. Also, this conference paper will completely proceed the 1992 paper.

Heritability and Genetic Correlations

A notable omission in the 1992 conference paper was the reporting of heritabilities and genetic correlation for skin follicle densities (Pattie and Restall, 1989) and they are presented in Table 1. The heritabilities for skin follicle densities are low indicating that selection for increasing secondary follicle density would be a slow process. Whereas, the heritability for S/P ratio is moderate and would be more responsive to selection than would secondary follicle density. The genetic correlations between down weight and secondary density, between down yield and secondary density, between down yield and S/P ratio yield, between down length and primary density, between down length and secondary density, and between secondary density and S/P ratio are positive and significantly different than zero. An increase in one trait would result in an increase in the other trait.

In 1996 at the 6th annual conference of the Cashmere Producers of America conference, Australian researchers presented results of several generations of selection for important cashmere traits of down weight, down diameter, and liveweight (Pattie and Restall, 1996). The Australian researchers started with 680 breeding-age females and randomly divided them into four groups of 170 females each. One of the four groups was randomly chosen and 150 of the 170 females in that group were randomly chosen to be the Random Control line. The other three groups were randomly assigned to be either the Down Weight, Down Diameter, or Liveweight lines. Within each of these groups, the females were ranked according to that trait and the top 80 females formed the Plus line and the bottom 80 females formed the Minus line. Similarly, 30 of 330 males were randomly assigned to the Random Control line and the remaining males were randomly assigned into three groups (Down Weight, Down Diameter, or Liveweight) with 100 bucks each. However, for the males, only the top 6 were selected for the Plus line and the bottom 6 for the Minus line. For the Plus and Minus lines, selection

was made on the basis of first fleece record at nine months of age. All lines were closed at the beginning of the experiment and all replacement animals were chosen within each line, respectively. Figures 1 through 3 illustrate the response to selection. The down weight and down diameter groups showed diverging lines as the experiment progressed; however, the trend was not as clear with liveweight.

Genomics

In 1992, the full genomics revelation had yet to occur. Early work at the genomic level concentrated on microsatellites (Pepin et al., 1995; Ron et al., 1994), which are areas on the chromosomes where nucleotide base pairs repeat a sequence. These repetitions can range from a single base pair repeated numerous times or a sequence of nucleotide base pairs that repeat in the same order for several times. Microsatellites are also known as short tandem repeats (STRs) or simple sequence repeats (SSRs). In 2006, researchers in China used eleven microsatellite markers (Table 2) to study their association with body weight, cashmere (down) yield, and cashmere diameter in Liaoning goats (Jin et al., 2006). They reported that four of the eleven microsatellites had significant effects upon the traits that were studied. For LSCV13, the AA (212/212) and the BC (224/239) genotypes had significantly greater body weights than did AB (212/224), CD (239/246) and BB (224/224) genotypes. However, the AB (212/224) genotype had significantly cashmere yield than did the other genotypes. For CSSM11, the BB (168/168) genotype had significantly greater body weight than did the other seven genotypes, the AD (162/182) and BE (168/186) genotypes had greater cashmere yield than did the other six genotypes, and the AA (162/162) genotype had finer diameter than did the other seven genotypes. For IDVGA64, the DE (224/280) genotype had significantly greater body weight than did the other six genotypes, the BD (213/224) genotype had greater cashmere yield than did the other five genotypes, and the BC (213/215) and DE (224/280) genotypes had finer diameter than did the other five genotypes. For BMS2782, the BB (248/248) genotype had significantly greater body weight than did the other five genotypes, the BC (248/252) and DE (260/268) genotypes had greater cashmere yield than did the other four genotypes, and the CD (252/260) genotype had finer diameter than did the other five genotypes.

At the genomic level, attention has shifted from microsatellites to single nucleotide polymorphisms, usually abbreviated as SNP and pronounced snip (Matukumalli et al., 2009; Meuwissen et al., 2013; Yin and König, 2016). A consortium goat research institutions recently developed a 52K SNP chip for goat genomic research (Tosser-Klopp et al., 2014) and it has been used in many genome-wide association studies (Colli et al., 2018; Kumar et al., 2018; Mucha et al., 2017). Most recently, researchers in China have developed a 66K SNP chip for cashmere goats (Qiao et al., 2017). This 66K SNP chips has yet to be validated using production traits.

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Table 1. Heritabilities and genetic correlations involving skin follicles.

Trait		h^2
Primary density		.16
Secondary density		.17
S/P ratio		.29
	genetic correlations*	
bodyweight:	primary density	-.38
	secondary density	-.11
	S/P ratio yield	.19
fleece weight:	primary density	-.15
	secondary density	-.01
	S/P ratio yield	.05
down weight:	primary density	.19
	secondary density	.48*
	S/P ratio yield	.32
down yield:	primary density	.22
	secondary density	.53*
	S/P ratio yield	.35*
down diameter:	primary density	-.28
	secondary density	.08
	S/P ratio yield	.32
down length:	primary density	.48*
	secondary density	.55*
	S/P ratio yield	.11
primary density:	secondary density	.37
	S/P ratio yield	-.49
secondary density:	S/P ratio	.63*

*genetic correlations that are significantly (P<.05) different from zero.

Table 2. Microsatellite markers used by (Jin et al., 2006).

Microsatellite	Forward primer sequence (5′-3′)	Reverse primer sequence (3′-5′)
MAF064	AATAGACCATTCAGAGAAACGTTGAC	CTCATGGAATCAGACAAAAGGTAGG
LSCVl3	GAATCTTGGAGGTGACCAG	CCCCGAGCGCACATTTG
BM1312	CCATGTGCTGCAACTCTGAC	GGAATGTTACTGAACCTCTCCG
BM4307	ATAACACAAAAAGTGGAAAACACTC	ATTTTATCTCAGGTCCCTTTTTATC
INRA011	CGAGTTTCTTTCCTCGTGGTAGGC	GCTCGGCACATCTTCCTTAGCAAC
CSSMl1		
LSCV37	GACAACCAACAAGGACAACAAG	CAGGTGTATAGCCAAGTGATTC
IDVGA64		
LSCV24	CACAGAGAGGCAAACCCCTC	CTCAAGATAGTCCAGCCCAC
ILSTS082	TTCGTTCCTCATAGTGCTGG	AGAGGATTACACCAATCACC
BMS2782	TGTGCAGCAATAAGACCCAG	TGTAAGTGGGAGGGCAAGTC

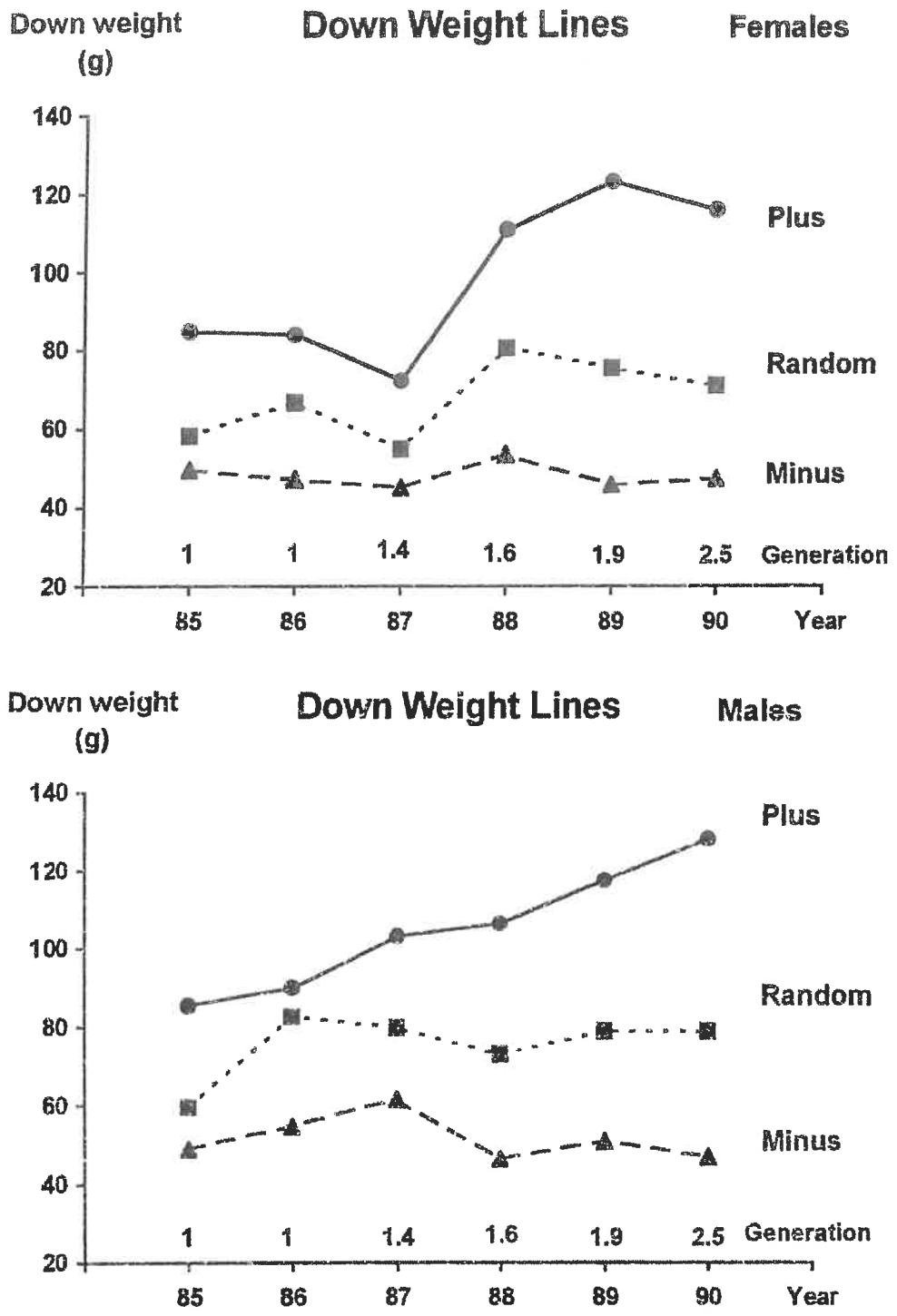

Figure 1. Down weights at 9 months - direct selection

(Pattie and Restall, 1996)

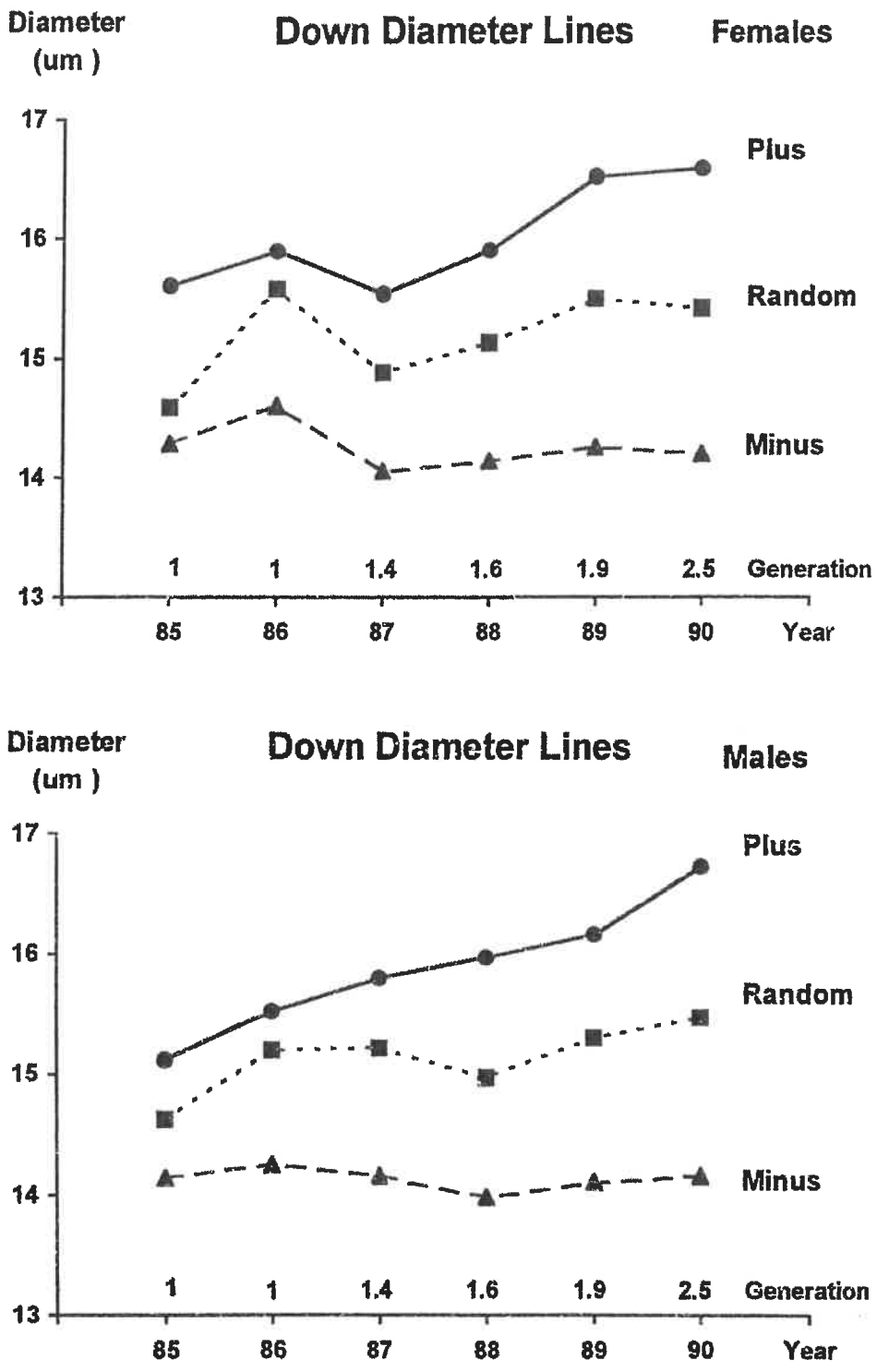

Figure 2. Down diameter at 9 months - direct selection

(Pattie and Restall, 1996)

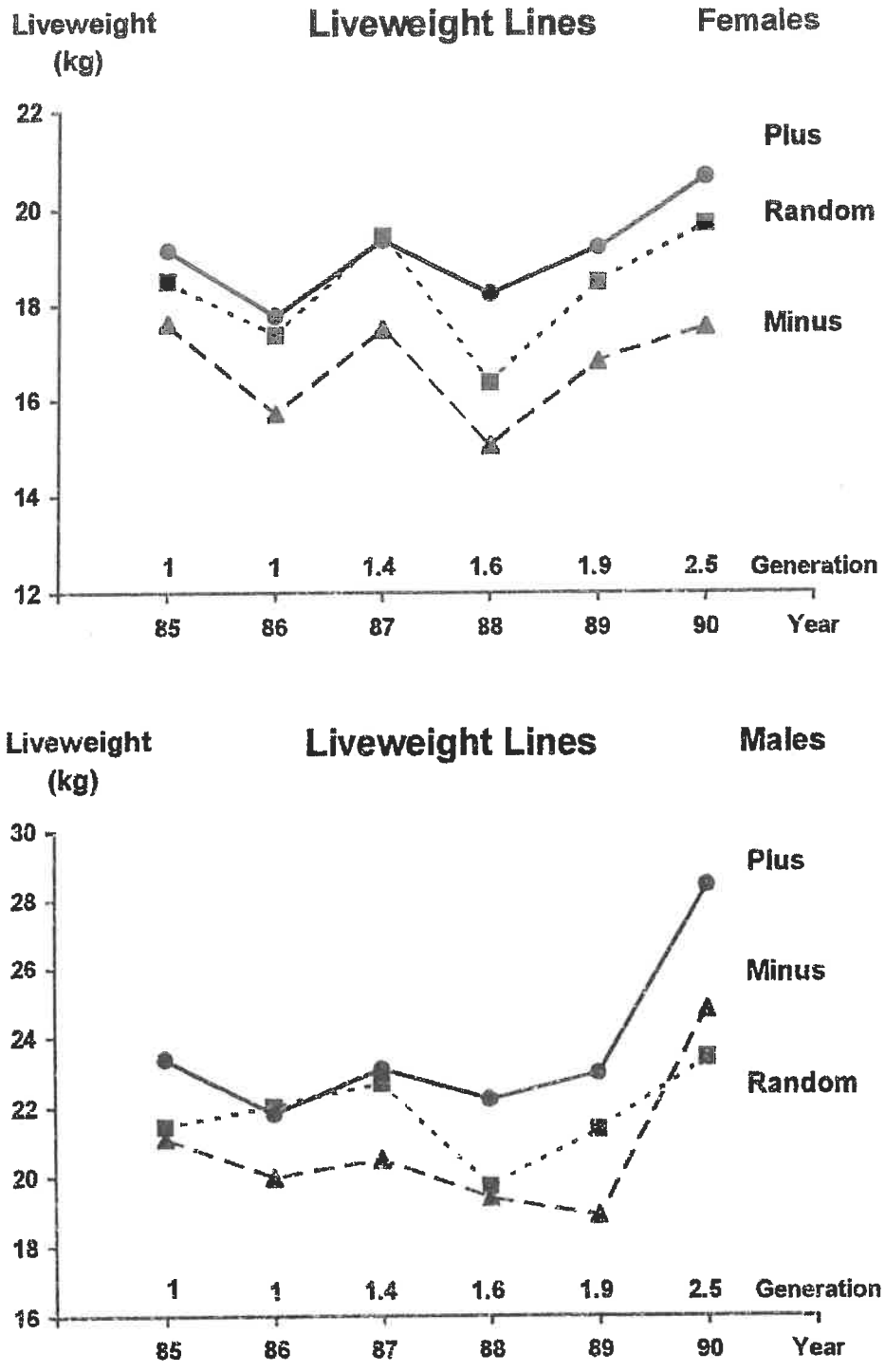

Figure 3. Liveweight at 9 months - direct selection

(Pattie and Restall, 1996)

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Breeding for Cashmere Production

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Introduction

One of a cashmere producer's primary concerns is to increase the productivity of his/her animals. Productivity may be measured in many different ways. It may be increased down weight or finer down diameter. If the producer is concerned about meat production, it may be heavier bodyweight or more kids weaned per doe. The success or failure of this quest to increase productivity is dictated by many different factors. Two factors that play a dominant role are heredity and the selection of sires and dams. Using the principles of heredity, the animal breeder has fashioned tools that aid in the selection of breeding stock. The objective of this paper is to illustrate these principles and tools with examples of emphasizing cashmere production.

Qualitative Versus Quantitative Traits

In the livestock industry, only a few of the economically important traits are controlled by a single gene or are influenced by a single gene. These qualitative or simply inherited traits include such items as the Booroola gene in sheep, the milk flow gene in dairy goats, the double-muscling gene in cattle, and the halothane sensitivity gene in swine. In most cases, the selection of individuals based on the presence or absence of the gene is simple and straight forward. Either the animal exhibits the trait, or it does not, there is no middle ground.

The vast majority of the economically important traits are controlled by a large number of genes resulting in a wide degree of expression or variability of the trait. These quantitative or polygenic traits include such items as fleece and fiber traits in goats and sheep; milk and fat production in dairy cattle and goats; egg production in poultry; and birth, weaning, yearling, and mature weights and average daily gain in all domestic species. The selection of individuals based on these traits is not as simple as with qualitative traits. The measurable or observable expression of these traits is affected not only by the genetic makeup of the individual but also by the environment in which the individual made the record. This can be represented in the following simple equation:

$$Phenotype = Genotype + Environment$$

$$(Observable) = (Nature) + (Nuture)$$

The genetic component is the factor of prime interest because it can be passed to offspring. The environmental component may be temporary and affect only one record, or it may be permanent and affect every record of an individual. The environmental component may be repeatable from one record to the next or from one locale to the next, or it may be non- repeatable and exist only at a given time for a given locale. However, from a single observation, the influence of heredity and environment cannot be separated.

The effects of heredity and environment can be illustrated by the following two examples. A slick Spanish doe is given the best of management care yet only produces a negligible amount of cashmere. In this case, no amount of managerial intervention (environment) will counteract the lack of genetic potential (heredity). In the second example, one cashmere animal with the genetic capability of producing 400 g of down is placed on an unimproved pasture in the humid sub-tropics, is never dewormed and produces 40 g of down.

A second cashmere animal with a genetic capacity of producing 200 g of down is placed on improved pasture in Colorado, dewormed as needed and produces 190 g of down. An evaluation of only the records would lead to the conclusion that the second animal is the superior animal, when, in fact, it is the genetically inferior animal. In this case, the environment has masked the genetic differences between these two animals.

For quantitative traits, if one were to plot the number of observations over the spectrum of the trait, one would notice that the plot or curve has the shape given in Figure 1. This is the well-known bell-shaped curve or the normal distribution as it is known to statisticians. Two parameters completely define the normal distribution. They are the mean (μ) and the variance (σ^2). The mean is the arithmetic average, and the variance is a measure of dispersion around the mean. A wider dispersion results in a greater variance. Another parameter that is often associated with the normal distribution is the standard deviation (σ), which is the square root of the variance. The variability of a trait is of great interest to animal breeders because through statistical methods; it can be partitioned into its two components: genetic and environmental variances.

Heritability and Genetic Correlations

For the last half-century, animal breeders have been tackling this problem of accurately estimating genetic and environmental variances. With accurate partitioning, selection decisions can be made on the basis of genetic merit alone. This labor has given birth to two parameters which are used constantly by animal breeders; heritability (h^2) and genetic correlations.

Heritability can be defined as the degree of variability that is associated with heredity. Heritability can be calculated as the ratio of genetic variance to phenotypic or total variance. In theory, variances are always positive, and h^2 is a part-whole ratio, thus h^2 ranges from 0 to 1. A h^2 of O indicates that heredity plays no role in the variability of that trait, and a h^2 of 1 indicates that heredity accounts for 100% of the variability. Estimates of h^2 for bodyweight and cashmere traits are presented in the upper ¼ of Table 1. Caution should be taken not to use h^2 as an absolute value. For example, down weight has a h^2 of .61. This does not mean that if an animal produces 300 g of down that 183 g is due to heredity and 117 g are due to the environment but that 61 % of the variability associated with down weight is due to heredity and 39% is due to the environment. An inspection of the estimates of h^2 in Table 1 reveals that h^2 estimates range from .22 for bodyweight to .90 for down yield. On average, bodyweight is the least heritable, and down diameter is the most heritable. However, based on these estimates, all traits would be considered moderately to highly heritable. Selection on any one of these traits should result in a steady and noticeable improvement in that trait. Caution should also be taken not to use h^2 as a universal constant. Heritability estimates are calculated for a given population in a given time period. Those estimates may or may not be applicable to other populations or at a later time period.

Genetic correlation is a measure of the degree of association between two traits that is due to heredity. Like h^2, a genetic correlation is a part-whole ratio, but unlike h^2, a genetic correlation can be negative; thus, a genetic correlation ranges from -1 to 1. A genetic correlation of -1 indicates that for every unit increase in one trait, there is a corresponding one-unit decrease in the other trait. A genetic correlation of 1 indicates that for every unit increase in one trait, there is a corresponding one-unit increase in the other trait.[1] A genetic correlation of zero indicates that for every unit increase in one trait, there is no corresponding change in the other trait whatsoever. Favorable or unfavorable relationships do not depend on the sign of the correlation but upon the selection objectives. For example, from Table 1, a negative (unfavorable) relationship exists between body weight and down weight. That is as bodyweight increases, down weight decreases. A positive (unfavorable) relationship also exists between down weight and diameter. That is, as down weight increases, down diameter, also increases.

The estimates of h^2 and genetic correlations under the heading Aust. #1 in Table 1 were confirmed in a five-year selection experiment (Pattie and Restall, 1991). Animals were selected for a high vs. low line for body weight, a high vs. low line for down weight, a high vs. low line for down diameter, and a control line was randomly mated. Realized heritability and realized genetic correlations were calculated from the actual

net gain or loss in the selected trait and from the corresponding changes in other traits. These realized parameters were in agreement with the estimated parameters.

Heritability and genetic correlations aid the animal breeder to predict the rate of improvement that can be made in a trait due to selection and the consequences of selection on other traits.

Selection and Consequence

Depending on the number of traits, selection can take on several forms. The simplest form of selection is called truncation selection and is practiced on one trait. The word truncate means to shorten by cutting off a part or to cut short. A conscious decision is made that all animals that are to be kept for breeding purposes must meet some minimum level, also called the point of truncation (Figure 1). The arithmetic difference between the mean of the population before selection and the mean of the selected individuals is called the selection differential or reach. The selection differential can be expressed in terms of the number of animals kept for breeding and the variability of the trait:

$$selection\ differntial\ (S) = \overline{X}_{selected} - \overline{X}_{population} = i \times \sigma_P$$

Where *i* is called the intensity of selection, and σ_p is the phenotypic standard deviation. The intensity of selection is inversely related to the percentage of the animals selected (Figure 2).

As the percentage of animals kept for breeding increases, the intensity of selection decreases. For sheep and goats, approximately 45-55% of the females and 2-5% of the males must be kept for breeding just to maintain herd size. This translates to a selection intensity of around .8 for females and 2.05 for males. Since half of the genes comes from the female and the other half from the male, the preceding example would yield a combined intensity of selection of approximately 1.43. The response or change in the selected trait is the greatest under truncation selection and is given by the following formula:

$$Response\ (R) = h^2 \times S = i \times h^2 \times \sigma_P = i \times h^2 \times \sigma_a$$

Where i is as previously defined, h is the square root of h^2, also called the accuracy of selection, σ_a. is the genetic standard deviation, and R is measured in improvement per generation.

One of the major problems with truncation selection is that it ignores all other traits that might be of economic importance. Genes that affect one trait may also affect a second or third trait, and this influence may not be in a desired direction.

Two traits that are easily measured on the ranch are fleece weight and body weight. The measurements of down traits are usually expensive because of the sophisticated equipment required. Two scenarios involving truncation selection are envisioned: the first for a strictly cashmere operation using fleece weight as the selection objective; the second for a combination meat/cashmere operation using bodyweight as the selection objective. This latter scenario seems to be an economically viable option for a cashmere enterprise in Texas and in some other states (Lupton and Shelton, 1990; Shelton and Lupton, 1990; Teh, 1990). Direct and correlated responses for selection on fleece weight and on bodyweight are presented in Table 2. These calculations were based on heritabilities and genetic correlations under Aust. 1 in Table 1 and that 50% of females and 5% of males are kept for breeding purposes.

For direct selection on fleece weight, the increase in fleece weight would also result in an increase in body weight, down weight, down diameter and down length but in a decrease in down yield (Table 2). The changes in down diameter and yield are in an undesirable direction. For direct selection on body weight, the increase in body weight would also result in an increase in fleece weight but in a decrease in down weight, down diameter, down length and yield. The changes in down weight, down length, and yield are in an undesirable direction.

Tandem selection is a form of selection where truncation selection is practiced on a single trait until some

desired level is achieved, and then truncation selection begins on a second trait. The major disadvantage with tandem selection is that if the h^2 of the second trait is high and the genetic correlation between the first and second trait is unfavorable, then the genetic variability in the second trait may become extremely small by the time the first trait has reached its desired level. An example of this would be to concentrate solely on fleece weight for several generations and then to commence selection on down diameter.

Another form of selection is independent culling levels. This technique uses truncation selection on two or more traits consecutively. Independent culling levels are convenient to use when several traits cannot be measured in the same time frame. An example of this would be to practice truncation selection on birth weight, then on weaning weight and then finally on yearling weight. Caution must be used in this approach because the overall selection objective would be to select for a larger frame size at all points of the individual's life. This would possibly induce a higher incidence of dystocia due to overly large kids. A more appealing approach might be to measure birth weight and to select on moderate weights. Then weaning weights would be measured, and individuals selected on pre-weaning average daily gain (ADG). This would be repeated on yearling weight and selection on post-weaning ADG.

The last form of selection is index selection. Index selection is the most efficient form of selection in terms of desired responses for all traits in the index. The index is the most difficult to construct. It requires the teamwork of an animal breeder and an agricultural economist. The animal breeder provides estimates of h^2 and genetic correlations. The agricultural economist provides relative economic values for the traits in the index. Agreeing upon which traits to include in the index is never an easy task for these two specialists.

Australian researchers have proposed a two-stage selection index for cashmere goats (Pattie and Restall, 1992). The objective of a two-stage index is to use a simplified first-stage index to screen the entire population. Then a more complicated second-stage index is used to screen the top-ranking animals of the first stage. This strategy allows for inexpensive screening of a large number of animals. The index for the first stage is:

$$I_1 = w_1 \times bodyweight + w_2 \times down\ length$$

The Australian researchers suggest that only the top 25% of the bucks from the first stage should become candidates for the second stage. The index for the second stage is:

$$I_2 = w_1 \times bodyweight + w_2 \times down\ length + w_3 \times down\ weight + w_4 \times down\ diameter$$

w_1, w_2, w_3, and w_4 are index weights; body weight is measured in kilograms, fiber length in millimeters, down weight in grams, and fiber diameter in microns. All measurements are expressed as deviations from the mean. This is the animal's individual measurement minus the mean measurement for the group at a particular sampling period. For the first stage and second stage, index weights are in Table 3. Notice that the index weights for bodyweight and down length change even though they are elements of both stages (Table 3). Down length is another trait that is measurable on the ranch and the relationship between down weight and down length is strong and desirable (McDonald, 1988; Table 1). The Australian researchers have also calculated index weights when the selection objective is to reduce down diameter by .25 µm or by .40 µm (Table 3). These index weights are provided for selection on the bucks only. Notice the large changes in the index weights.

Other Australian researchers have also developed selection schemes and indexes for cashmere (Ponzoni and Gifford, 1990). These researchers derived index weights using a profit equation and discounting techniques. This equation includes several traits that affect income and expenses for both cashmere and meat production. They chose down weight (yDW), down diameter (yDD) and bodyweight (yBW) measured on the young goat and number of kids weaned (dNKW) in their selection index. The index weights they derived were 105 for yDW, -1310 for yDD, 642 for yBW and 104 for dNKW. The number of kids weaned (dNKW) is important because it accounts for the variability in down traits and body weight due to single, twin, or triplet births. Down traits in the young goat, especially yDD, are highly correlated with down traits in the adult animal. The genetic correlation for down diameter at one year-of-age with a down diameter at

two years-of-age is .92 (Pattie and Restall, 1992). Thus measurements for down traits can be taken only once on the young goat and not repeated later on the adult animal. Including down length for the young goat in the selection, index contributed virtually nothing to the efficiency of the index, profit-wise (Ponzoni and Gifford, 1990). The Australian researchers also noted that the efficiency of the index was reduced o ly slightly when yBW and dNKW were deleted from the index. They cautioned about deleting dNKW because it adjusted down traits and bodyweight for the type of birth. If dNKW is deleted, then single births are given precedent over twins and triplets. When production costs are ignored in the selection process, the economic worth of the traits in the index is overestimated. Therefore, the index suffers a loss of inefficiency. Ironically, the Australians did not include the cost of determining down diameter in their profit equation. They also encountered a major obstacle in this study. Heritability and genetic correlation estimates for some biological traits in the index were not available. The profit equation depends upon these parameters and the index. Therefore, guesses of these parameters had to be made.

Index calculation can best be illustrated by the following hypothetical example, using the two-stage Australian index.

For the first stage, buck A weighed 55.5 kg and had an average cashmere fiber length of 83 mm; buck B weighed 49.8 kg and had an average cashmere fiber length of 80 mm, and buck C weighed 44.0 kg and had an average cashmere fiber length of 39 mm. Average measurements 49.8 kg body weight and 67 mm cashmere fiber length. Index scores for the first stage for individual bucks are:

$$I_1 \, for \, A = .101 \times (55.5 - 49.8) + .322 \times (83 - 67) = 5.7$$

$$I_1 \, for \, B = 4.2$$

$$I_1 \, for \, C = -9.6$$

For illustration purposes, index scores for the second stage will be calculated for all three bucks. For the second stage, buck A had a fleece weight of .97 kg with 66% yield and an average cashmere fiber diameter of 17.7 µm; buck B had a fleece weight of .61 kg with 38% yield and an average cashmere fiber diameter of 15.5 µm, and buck C had a fleece weight of .80 kg with 9% yield and an average cashmere fiber diameter of 15.2 µm. Average measurements were .79 kg fleece weight with 38% yield and 16.0 µm cashmere fiber diameter. Calculations for individual bucks are:

$$I_2 \, for \, A = .36 \times (55.5 - 49.7) + .333 \times (83 - 67) + .145 \times (970 \times .66 - 790 \times .38) - 9.45 \times (17.7 - 16) = 40.6$$

$$I_2 \, for \, B = -0.9$$

$$I_2 \, for \, C = -36.9$$

The Australians have studied the non-genetic factor of age on fiber traits. As age increases, so does down weight and diameter (Pattie and Restall, 1992). They have also studied the effect of changing fiber traits, mainly fleece weight, on reproduction. They noticed that as fleece weight increased, the reproductive rate stayed the same, but the incidence of multiple births decreased. They also noted that as body weight increased, so did reproductive rates.

Caution must be used before employing either of the Australian selection indexes in the American context. As was mentioned earlier, the estimates of h^2 and genetic correlations may or may not be relevant for the cashmere goat population in the United States. A second factor is the applicability of the index weights. It is true that Australia and the United States share the same cashmere buying market; however, the profit equation associated with the cashmere enterprise of each country may differ drastically. The efficiency of the selection index is very dependent on the heritabilities and index weights involved (Smith, 1983). Texas A&M University has started a meat and cashmere goat performance test at San Angelo. However, index scores for bucks were not calculated (TAES, 1991). There was no single index that could be developed or

agreed upon. Growth rate is not included in the Australian two-stage index. The growth rate would be an important economic factor in a cashmere enterprise in Texas and in many other states.

Improving Response to Selection

As was discussed earlier, response to selection is dependent upon the intensity of selection, the accuracy of selection, and the genetic standard deviation. An increase in any or all of these factors would result in an increased rate of response. The intensity of selection is constrained by the percentages of animals needed to maintain herd size. In most cases, genetic variance and covariances will decrease after several generations of effective selection, thus decreasing the genetic standard deviation. That leaves the accuracy of selection as the one factor that can be manipulated so that response can increase. Accuracy of selection can be improved by including records on the individual's ancestors (Figure 3), by including more records on the individual (Figure 4), or by including records on the offspring of the individual (Figure 5). In short, by including more information into the selection process, better selection decisions can make, thus increasing the response to selection. For example, the selection of 5 % of the top bucks based on one record of fleece weight would result in a 47.3 g increase. The inclusion of an additional record on fleece weight would result in an additional 11.5 g increase and the inclusion of fleece weights on 25 offspring would result in an additional 35.6 g increase.

There are costs associated with the inclusion of this additional information. One of these costs is time. It takes time for an individual to produce a second or third record, and it takes time for an individual to produce offspring and for those offspring to produce records. Remember, response is measured as change per generation and inclusion of additional information lengthens the generation interval. The exact combination of number of individual records and number of progeny records to achieve an optimal rate of improvement per year is not known. Further research in this area with the incorporation of economic inputs/outputs would greatly benefit the cashmere industry.

Marker-Assisted Selection

Another means for improving the accuracy of selection is through marker-assisted selection (MAS). Although MAS is not a new tool for the animal breeder, the discovery of restriction fragment length polymorphisms (RFLPs) has renewed considerable interest in this field (Kennedy et al., 1990). In essence, MAS is a marriage of qualitative and quantitative genetics. The objective of MAS is to use qualitative traits such as blood or milk proteins as an aid in pinpointing the physical presence of quantitative trait loci (QTL). These QTL's are the genes that affect a quantitative trait. This exploration is achieved via the enzymatic cleaving of chromosomes into multiple length fragments. These fragments are then labelled with a radio-active probe (marker) and separated using gel electrophoresis. Via statistical methods, the probes with their linked fragment are associated with the quantitative trait. After the linkage between one or a set of markers and the QTL is established, the animals are then screened for that marker or set of markers. Selection decisions are based on the absence or presence of the marker(s). MAS increases the accuracy of selection by providing a means of direct selection on the genotype. It also increases response by reducing the generation interval, because screening for the marker(s) can occur as early as birth or even before birth. One barrier to MAS is that a very large number of markers are required for success and few markers have been identified in the goat. There has been considerable progress in mapping bovine chromosomes or genome and in the subsequent identification of possible markers (Massey and Georges, 1992). Due to the syntenic nature of the mammalian genome, progress in mapping the caprine genome will not lag farbehind.

Conclusions

Heritability and genetic correlations are two tools that the animal breeder uses to chart a course for livestock improvement. The heritability of bodyweight and down traits are moderate to highly heritable and should respond well to selection. For the most part, the genetic correlations of bodyweight and down traits are in a desirable direction. The simplest form of selection is truncation selection; however; it ignores all other traits and ignores the possible undesirable changes in other traits. The most efficient form of selection is

selection index, but it is the most complicated to construct. Also, the reliability of the estimates of heritability, genetic correlations, and relative economic weights used in the construction of a selection index dictates the efficiency of the index and the rate of change for all traits in the index. One means of increasing response to selection is to increase the accuracy of selection. This can be accomplished through the incorporation of additional information into the selection scheme. Additional information can take on the form of pedigree information, additional information on the same trait and same animal or progeny information. This additional information costs in terms of lengthening the generation interval. A means of increasing accuracy of selection without increasing the generation, interval is marker-assisted selection. In fact, marker-assisted selection could decrease the generation interval. Marker-assisted selection provides for direct selection on the genotype; however, this technology is not yet advanced beyond the laboratory.

There are several gaps in the cashmere industry that need to be filled before a national selection scheme can be implemented. Firstly, estimates of heritabilities and genetic correlations for all traits that affect the profitability of a cashmere or cashmere/meat enterprise need to be calculated for the US cashmere population. Secondly, an economic evaluation of the cashmere industry needs to be undertaken with the help of an agricultural economist. With these first two needs fulfilled, the construction of a selection index can begin. Finally, close cooperation with molecular geneticists is needed to identify possible markers that are associated with cashmere down traits.

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Table 1. Heritabilities and genetic correlations for cashmere production traits.

Trait		Australia[a] 1	Australia[a] 2	Australia[a] 3	NZ[a]	China[b]
		heritabilities				
bodyweight		.29	.26	-	.22	.35
fleece weight		.29	.42	.45	.25	-
down weight		.61	.36	.38	.45	.42
down yield		.90	.23	.30	.52	-
down diameter		.47	.70	.68	.83	.45
down length		.70	-	-	-	.39
		genetic correlations				
bodyweight:	fleece weight	.17	.17	-	.09	-
	down weight	-.18	-.13	-	-.17	-.12
	down yield	-.24	-.39	-	-.20	-
	down diameter	-.06	-.16	-	-.14	-
	down length	-.31	-	-	-	-
fleece weight:	down weight	.34	.83	.83	.43	-
	down yield	-.13	.39	.37	-.21	-
	down diameter	.14	.12	.48	.23	-
	down length	.05	-	-	-	-
down weight:	down yield	.84	.85	.80	.74	-
	down diameter	.62	.04	.77	.51	-.12
	down length	.88	-	-	-	.59
down yield:	down diameter	.57	.04	.77	.51	-
	down length	.78	-	-	-	-
down diameter:	down length	.52	-	-	-	-

[a]as cited in Pattie and Restall, 1992.
[b]Lixian and Junquian, 1992.

Table 2. Correlated responses to direct selection[a].

Trait	direct selection on: fleece weight	bodyweight
fleece weight	33.0[b] g	5.5 g
bodyweight	.25 kg	1.4[b] kg
down weight	7.2 g	-3.3 g
down diameter	.07 µm	-.03 µm
down length	.55 mm	-3.2 mm
yield	-1.1%	-2.0%

[a]assuming 50% of females and 5% of males are kept for breeding purposes.
[b]response to direct selection.

Table 3. Weights for the two-stage selection index.

Objective	Selection index weights[a] (w) for traits: w_1	w_2	w_3	w_4
	Stage I			
general (female)	.151	.003		
general (male)	.101	.322		
.25 µm reduction (male)	.151	.005		
.40 µm reduction (male)	.156	-.032		
	Stage II (males only)			
general	.360	.333	.145	-9.450
.25 µm reduction	.766	.277	.672	-16.592
.40 µm reduction	.814	.271	.058	-17.430

[a]w_1: bodyweight; w_2: down length; w_3: down weight; w_4: down diameter.

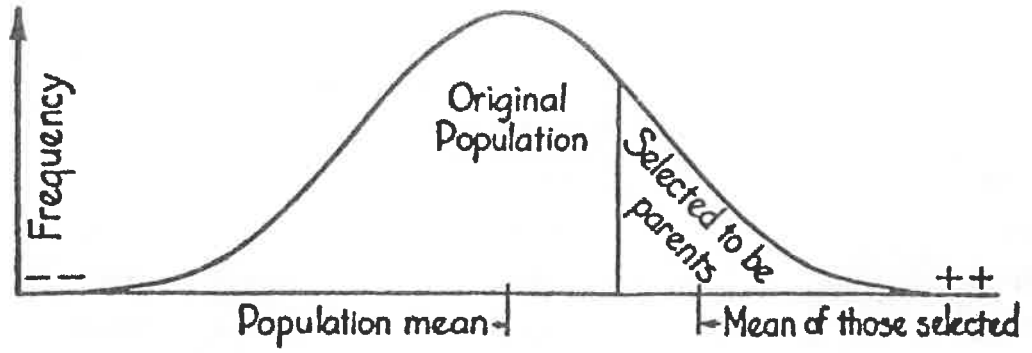

Figure 1. Truncation selection.

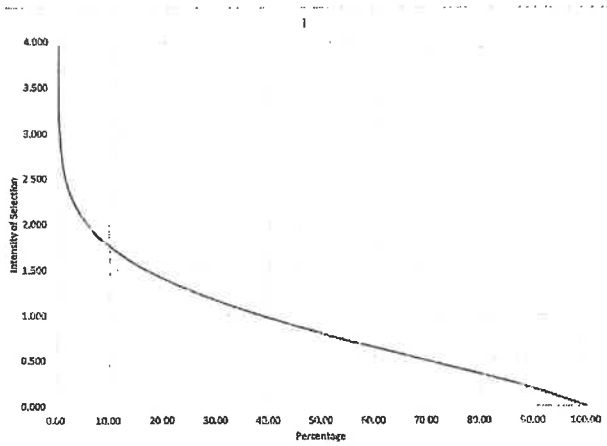

Figure 2. Relationship of intensity of selection and the percentage of animals kept for breeding purposes.

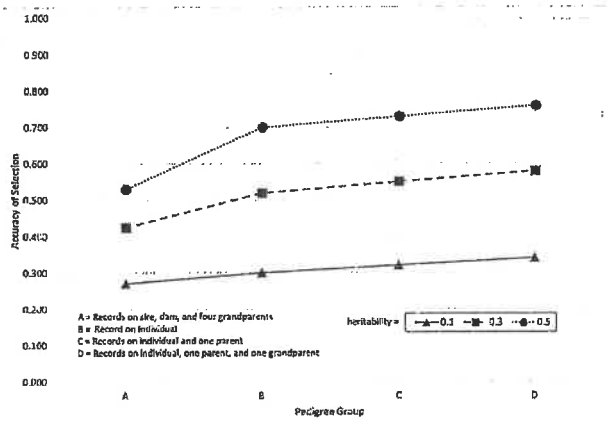

Figure 3. Relationship of accuracy of selection and pedigree groups.

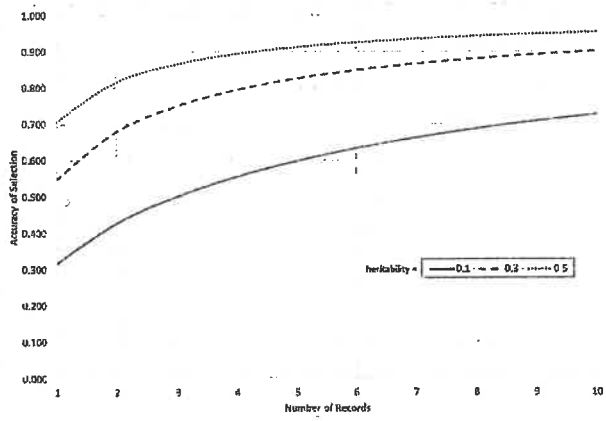

Figure 4. Relationship of accuracy of selection and the number of records available for an individual.

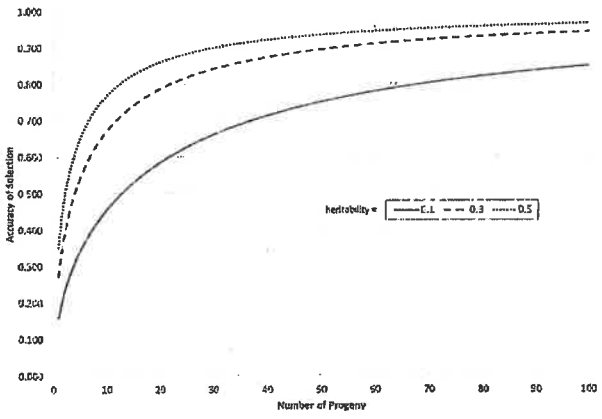

Figure 5. Relationship of accuracy of selection and the number of progeny records available for an individual.