Down Production on Cashmere Goats – Genetic Implications

A report for the Rural Industries Research and Development Corporation

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Foreword

This project aimed to seek an understanding of genetic factors, or a combination of such, associated with high phenotypic down production in cashmere goats.

Currently the low annual down production per head is a major constraint in productivity and financial return from this industry. An understanding of the basis of inherited down production would provide a catalyst for the economic development of the Cashmere gene pool in Australia.

While the down production average in Australia is similar to that of other countries, some very high production animals do exist in the Australian herd. Using a group of Cashmere animals selected for high down production, housed and fed a controlled ration, this project sets out to identify the range of fleece production patterns in the group and catalogue the genetic components influencing down growth.

An in-depth review of the literature suggests that for goats, this is the first attempt to map the basic components of down production under genetic influence. As such it provides a structure to link practical genetic manipulation, at the animal breeding level, with the fundamental Genomic Research in goats that is daily elucidating the building blocks of genetic control. The general principles in this report are equally applicable to the Mohair industry even though the emphasis on the fleece populations will be different. Given the very high level of Genomic similarity between the sheep and the goat it is likely that the findings of this paper could be applied to developing an understanding of the mechanics of wool production in sheep.

The information contained in this report will be of interest to both the practical breeder and the scientific community. For this reason it is presented in a popular readable format, with an underlying scientific discipline, that should satisfy both.

This project was funded from industry revenue, which is matched by funds provided by the Federal Government.

This report, a new addition to RIRDC’s diverse range of over 1000 research publications, forms part of our Rare Natural Animal Fibres R&D program, which aims to facilitate the development of new and established industries based on rare natural fibres.

Most of our publications are available for viewing, downloading or purchasing online through our website:

- purchases at www.rirdc.gov.au/eshop

Simon Hearn
Managing Director
Rural Industries Research and Development Corporation
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A very special note of thanks goes to Mrs. Gwenda Pearce who spent so many hours seeing to the needs and comforts of her animal charges. Without her this project would not have been possible.

- Jim Browne & Robert Pearce.
About the Authors

Jim Browne obtained a B.Agr.Sc. degree at the University of Melbourne in 1961 and an Honours Diploma in Agriculture from Dookie College Victoria in 1958. He was granted Graduate Membership of the Australian Institute of Physics for his contributions to research and development in High Vacuum physics. His interest in animal breeding and genetics began with the establishment of a fine merino sheep flock in 1967 and was further stimulated when he began selecting cashmere goats in 1979.

He has been involved in the Australian Cashmere Industry since its inception, in all aspects - from animal breeding to garment sale. He has been very involved with the development, calibration and application of objective fibre measurement for Cashmere; including the development of the IWTO International Standards for Cashmere Measurement.

Robert Pearce A.G.Inst.Tech (Chemistry, Textiles) and A.R.M.I.T. (Management), and was awarded for his research into determination of vegetable matter in wool.

Prior to establishing a speciality natural fibre processing operation, he was head of the Research and Development Department of a division of Felt and Textiles of Australia. More recently he established and ran a major 5 year private research project to establish the relationship between greasy wool parameters and resultant wool top fibre length.

Terminology

While it is acknowledged that micro metre (um) is the recommended standard scientific description for “one thousandth part of a millimetre”. The earlier term “Micron” (µ) is more widely used and understood within the Cashmere Industry. To make this paper more readable and understandable at industry level the term “Micron” has been adopted.

A data set is commonly referred to as data.
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Executive Summary

Project Title
Investigation into the Basis of Down Production in Cashmere Goats and its Improvement by Genetic Means.

Objectives
1. To establish an understanding of the fleece growth patterns of individual Cashmere animals with high annual down production.
2. To identify if possible, the genetic basis of some, or all, of the components that contribute to inherited down production in Cashmere goats.
3. To view these findings in the context of molecular genetics and available genomic data.
4. To identify and suggest areas with commercial implications for the Australian Goat Industry.

Background
Low annual cashmere down production (per head) is a major constraint to industry profitability. While the production average is similar to that of other countries, some very high production animals do exist in the Australian herd. The animals used in this project were selected from the Karakan herd in Victoria, Australia. This herd is one of the oldest ‘bred-on’ cashmere herds in Australia tracing its origins in part to the original CSIRO herd founded in 1972, (See Appendix B).

Analysis of data in the Karakan herd has identified a number of very high performing phenotypes (VHPP) for fleece production. Further analysis suggested that a number of individually inherited components contribute to overall performance.

This research project was made possible by the prior existence of a privately financed venture called Project KKN. Project KKN was originally established to develop the technology to produce Cashmere under housed conditions, similar to ‘Sharlea’ sheep (Reynolds 1969); and to select and multiply suitable animals for housed Cashmere production.

The opportunity to combine the selection of superior animals with a controlled environment led to the formulation of this project.

Research
A group of 120 females and 3 males that exhibited VHPP characteristics were selected and the females introduced into controlled environment conditions in Sept. 1997. These animals were made available for this project, which commenced in 1998 and ran for three years.

Given the limitations of the small number of animals involved and the short time frame, it was also considered necessary to draw heavily on the complementary knowledge available from a wide range of outside sources.

While the primary objectives of the project have been achieved, a full understanding of the bio-mechanisms involved provides a challenge for the future. The report suggests some possible future areas of exploration.

Outcomes
The Report has some elements of a specialist review and some elements of original work. The authors believe it to be the most complete work, yet published, on ‘Inherited Down Production’ in goats.
Some new techniques to examine the contributing components to fleece production in the subject animals were developed, and are described. One of these, the ‘Ofdagram’ is recommended for on farm use.

A range of inherited production characteristics, which appear to be discrete and repeatable between animals were identified. Of primary importance is the suggestion that an animal’s commercially saleable cashmere fleece is the product of contributions from a number of individual fibre populations. These overlay each other on the animal. The major populations are identified and a naming convention proposed. Fibre populations that cover the full-body have been called ‘Garbs’. The overlay regional populations have been called ‘Garblets’. The genetic and production implications of these findings are discussed.

It is demonstrated that commercial gains not only involve increasing down production, but also the manipulation of the guard hair coat to optimum levels. This improves returns to growers by reducing downstream fibre processing costs.

The key discovery of this report is that Fibre Growth Rate and Fibre Diameter are independently inherited. It is an undisputed and well known fact, that within an individual animal fleece, there is a strong relationship between down fibre length, the product of growth rate for a given time and given mean fibre diameter (mfd). This has led to the general industry assumption that, selecting for one, changes the other. This is not the case between animals and the production implications of this are considerable.

- For a given mfd and a given fibre density per unit skin area – ‘Growth Rate’ (down fibre produced/unit time) is the fundamental component of down production.
- For a given mfd - ‘Growth Rate’ is easily measured as ‘Change in Length’.
- There is demonstrated potential for selection - the measured growth rate in the best project animals was up to 3 times the growth rate of better feral animals.

Implications

The Cashmere goat

Measured fleece production figures for the Australian Cashmere Growers Association, National Fleece Competition, have been published annually for over 20 years. This database provides a striking illustration of production variation, even in selected goats, and the high levels of production achievable in superior individuals. This report demonstrates that, taken individually, the characters responsible for this ‘production variation’ can be manipulated with considerable effect.

The findings of this project are just a “beginning”, something parallel to exploring the world using a 17th Century map. However the age of biological discovery is upon us. The explosion of Genomic Research in the last few years has generated a mass of fundamental information on goat genes. Genomic studies deal with the very biochemistry of genes and the chemical mechanisms used to build observable genetic characteristics. This report breaks inherited down production into contributing components. This is a necessary first step in linking commercial gains with fundamental discovery.

Some of the techniques developed could be incorporated in on-farm breeding programs. The report provides some guidance to practical breeders choosing to make a start. Appendix A, for example, explains in detail, how to extract additional information from OFDA fleece test data that could be useful in assessing potential breeding sires.

The Mohair goat

The findings of this report also have some relevance to the Mohair goat. (The term Mohair goat is used throughout this report in preference to Angora goat. An Angora goat is a “breed”, a Mohair goat is a “type”. The distinction is important, and fundamental to understanding the approach taken in this study.) There is an emphasis on different fibre population elements, but the principles are inherently the same.
Also in sheep
The report draws attention to the great underlying similarities between fleece production in sheep and goats. A study of the genetic basis of fleece production in one - becomes a study of fleece production in the other – displaced in time. The Australian cashmere goat of today, represents a “genetic snapshot” of the “Australian sheep” of around 1805, before the creation of the modern Australian Merino. The relevance to the improvement of Merino Wool is covered in discussion.

Other fleece bearing animals
The authors believe the same mechanisms and principles as discussed in this report, may apply to a wide range of fleece bearing animals, extending at least as far as the Family Camelidae.

From an Industry perspective, a framework now exists which may be useful in establishing future research priorities.
1. Introduction

1.1 Background

Objectives
1. To establish an understanding of the fleece growth patterns of individual Cashmere animals with high annual down production.
2. To determine, if possible, the genetic basis of some, or all of the components that contribute to inherited down production in Cashmere goats.
3. To view these findings in the context of molecular genetics and available genomic data.
4. To identify and suggest areas with commercial implications for the Australian Goat Industry.

History

THE PROJECT … Low annual cashmere down production per head is a major constraint to profitable Cashmere production. It is noted as a key R&D Issue to be addressed under Objective Four, RIRDC – Rare Natural Fibres R&D Plan 1998-2003. While the Australian production average is similar to that of other producing countries, some very high production animals do exist in the Australian Herd.

An objective analysis of the of annual classing data for the years 1994-1996 inclusive, in the “Karakan” cashmere herd in Victoria, identified a number of very high performing phenotypes (VHPP) for fleece production in both males and females. Further analysis of this VHPP group suggested a variety of fleece production patterns in high producing animals. Analysis of this data also suggested that a number of individually inherited components contribute to overall performance. Discussions with Dr. Jay Hetzel (then a CSIRO Animal Genetic Senior Principal Research Scientist) raised the possibility, that taken individually, contributory components to observed annual down production, may have a fairly simple form of genetic inheritance.

A survey of the historic data held in the Mitchell Library (Sydney, NSW) by Browne (unpublished) suggests that between 1805 and about 1860 the Australian sheep flock developed from a primitive, basically two-coated fleece to the single coated model of the modern merino. The parallel with the apparent emerging growth pattern in the Karakan Cashmere Herd is remarkable.

Background information on the development of the Karakan Herd is presented as Appendix B of this report. It explains observed changes in down production within the Herd in recent years. These changes may be recent phenotypic (and hopefully genetic) developments or the result of improved
observation; but what is certain is that specialist down producing animals, with production far in excess of the feral type, do exist and have been identified.
This research project was made possible by the availability of facilities created for Project KKN. Project KKN was a privately financed development project born of the realization that high producing cashmere phenotypes had considerable potential as an income earner but had specific husbandry requirements. It set out to:

- Develop the technology to produce Cashmere under housed conditions in a similar manner to Sharlea Sheep (Reynolds 1969).
- Select and multiply, under housed conditions, suitable animals for housed cashmere production.

The opportunity to combine, the selection of superior animals with a controlled environment and some lateral thinking on the consequences of production observations, led to the formulation of this research project.

**Industry Relevance**

**Industry Expansion is limited by ‘production per head’ …** The Cashmere Industry emerged as a new Australian Pastoral Industry of considerable potential in the early 1980’s.

Cashmere goats were seen as having a role in sustainable agriculture, as browsers of deep rooted species and ‘weed eaters’. Cashmere was a product with an acknowledged demand and restricted supply. Australia had the knowledge, technology and the infrastructure to spearhead the development of raw cashmere production. To take it from a primitive base and transform it into a modern fleece production industry.

The largest Cashmere Processor in the world at that time, Dawson International, UK. saw the potential. They claim to have spent over 5m Pounds (UK) trying to ‘kick start’ the industry in Australia and New Zealand. They spent a considerable proportion of their funds subsidising research projects in Australia and New Zealand. By the year 1987 Australia/NZ lead the world in all scientific and technological aspects of cashmere production. Some 1500 Australian Growers were producing cashmere. The Australian Cashmere Marketing Corporation Pool in that year was 55.8 tonnes of raw fleece (Cashmere and Cashgora). In 1986 Dawsons began a withdrawal from active participation in the Australian Industry on the realisation that down production would not meet their projected expectations. Dawsons together with the other major European processors moved their processing to the Peoples Republic of China, in response to Chinese export restrictions on raw cashmere. China became the dominant force in the marketing of finished cashmere products.

The 1990’s were years of wild price fluctuation in the prices of raw and finished cashmere. At one point raw cashmere was available at the lowest price for 60 years. The Australian industry underwent a period of severe rationalization. Only the dedicated breeders persevered and only the more productive animals were retained. The industry survived this trying period on the excellence of its organisational structure and the devotion of a band of volunteers. The installation of Australia’s first practical commercial dehairer in Geelong, Victoria, in 2000, provided the industry with new marketing options. Today world prices for dehaired cashmere are at near record levels.

Photo 1.1/2: Shearing the backline of a project doe. Note down fibre length of 160 mm.
Current production in Australia, for the year 2001 was 11.7 tonnes (hair-in) from 115 Growers (ACGA personal communication). Australia is now ideally situated to expand its cashmere production. It has the administrative structure, the marketing structure, the technical knowledge, the people and the animal base to prosper. Emerging pressures to establish sustainable agricultural pursuits favour controlled goat grazing. **At this time the basic restriction on sustained growth is economic and the economic restriction is ‘production per head’**.

**Project Benefits**
The project investigations deliver a dual dividend…

- There is considerable potential for an understanding of the basis of inherited down production, to contribute substantially to Cashmere viability when viewed against a background of the primitive, relatively unselected, Cashmere gene pool in Australia.

- They call attention to the unique opportunity that presents itself at this point in time to elucidate the mechanisms of the genetic development of the modern merino and to study the very basis of genetic molecular evolution.

**Past Studies**
At the outset it is important to define where the project animals fit in the Taxonomic Structure of the animal kingdom. There is considerable confusion in the literature. For example, Wildman (1954) in his landmark reference, The Microscopy of Animal Textile Fibres, refers to the Cashmere Goat as Capra hircus laniger, the Mohair Goat as Capra hircus aegagrus and the Common Goat as Capra aegagrus. One of the authors, of this report, Browne (unpublished), has made a study of fleece production on goats from around the world. From this study it is clear that the Cashmere goat, the Mohair goat and the Common goat, despite their widely diverse appearance are all the same species – they pass the ultimate test - readily interbreeding and producing fertile progeny. This was amply demonstrated by Bishop and Russel (1994) who describe the development of a new “Scottish Goat” from a very diverse base of British, Icelandic, Australian, and Siberian stock.

Wilson and Reeder (1993) published a major new taxonomic work, which redefines the relationship of many species and genera of mammals. Their approach, which has found general acceptance, classifies all goats, including the many different types found in Australia, as the one species Capra hircus. The veterinary index of SNOMED (Systematized Nomenclature of Medicine) lists the species Capra hircus as having no Subspecies and 105 accepted and classified child breeds. The genomic database GOATMAP maps the Genetic structure of Capra hircus.

*This report covers down production in the species Capra hircus. The project animals strictly belong to “The Australian Goat” a recognised child breed (strain) of the species. Reference is also made to other member breeds, the great majority of which produce some ‘Cashmere’. All the goats have a common genome with different minor variations that give them their ‘Breed’ features.*

**The inheritance of colour**
Any evaluation of the commercial benefits arising from an improved understanding of inherited down production would factor in fleece colour. Colour is a very important commercial consideration in setting the price paid for raw cashmere. However, no attempt was made to review or investigate the interaction of colour inheritance, with the other patterns of inheritance studied in this project.

The inheritance of fleece colour is fairly well documented and the basic mechanism common in a wide range of animals. It is likely goats (Cashmere & Mohair) and sheep share the same mechanism. Nicholas (1987) pp 345 provides an excellent review of the subject.
**Production Based Research**

A considerable volume of work relating to improving down production was published between 1980 and 1998. Much of this was published in Australia and New Zealand. A few papers came out of the Peoples Republic of China in the late 1980’s and the Macaulay Land Use Research Institute in Scotland, where Cashmere Breeders Ltd. are trying to develop superior cashmere animals. Between 1950 and 1990 a large volume of information was published in Russian in the USSR relating to improvements in the Don Goat and the Altai Mountain Goat. In total there are several hundred references involved.

**Australia and New Zealand**

Australian researchers and industry personnel led the field, some published a number of papers. The principal workers being: Browne, Bell, Clarke, Couchman, Gifford and Ponzoni, Ellis, Graham, Holst, Hopkins, Johnston, McDonald, McGregor, Mitchell, Norton, Patrick, Pattie and Restall, Rose, Schumann, Smith (Ian) and Tucker. Much of the early research & development work was funded by the Dawson International Plc., Australian Cashmere Research fund, under the Chairmanship of Mr. Fred Moylan.

The Australians had some five years start on New Zealand researchers who began to make major contributions in the mid 1980’s stimulated by Dawson “seed” funding and a massive upsurge of interest by New Zealand farmers in goat fibre production. Much of the New Zealand work was directed at nutritional aspects of goat management under high rainfall conditions, but Baker, Betteridge, Bigham, Devantier, Fitzgerald, McCall and Nicoll worked mainly on fibre histology and the genetics of fibre production.

One of the largest earliest and longest running projects, was mounted by Pattie & Restall, on the New South Wales Department of Agriculture herd, at Wollongbar. A considerable number of papers have been published on the results of their investigations. Unfortunately most of their excellent work was done on animals sampled randomly from a feral population, with low annual cashmere production figures (around 50g annual), in an environment that was not ideally suited to cashmere growth. Only McGregor and to a lesser extent Couchman and Schumann did significant work during the 1980’s with higher producing animals. During the decade of the 1990’s, those researchers who maintained their interest, worked with selected animals exhibiting annual production figures of the order of 200g. McGregor was the most prolific, addressing a variety of issues. The other principle contributors were Restall and Johnston.

Australian & NZ researchers elucidated much of the world’s present understanding of the Cashmere Down fibre and its production aspects. These general references, all of which have some relevance to the project in hand, are too numerous to cite individually.

**China**

The peoples Republic of China, and the Chinese Autonomous Region of Inner Mongolia, together produce around half the world’s production of quality cashmere. Despite this, very little information was available, in English, on animal performance or production-based research, until a visit to China in April/May 1987 by a group of Australian Breeders under the leadership of Terry Mitchell. The group which included one of the authors (Browne) returned with a large amount of information on the Chinese industry including data on the country’s elite nucleus sire herd based at Gai Country Cashmere Goat Farm near Gai Xian in Liaoning province. (See Snippet August 1987). Jiang Ying (1987) released further performance figures and statistics as a supplement to the proceedings of the 2nd International Cashmere Conference in New Zealand. Since then there have been more regular releases on information in a variety of publications and the Internet.

**Russia**

Russian research delved more deeply into the genetic aspects. Several papers were published on colour and pattern inheritance. The majority of projects involved cross breeding with the Don to produce an animal more closely related to the Australian Cashgora, than to the Australian Cashmere. Most papers were published in Russian, the only easy “English” access being through Abstracting services. The authors were only able to glean a limited understanding of Russian discoveries.
Genomic Research
In recent years there has been a massive increase in the collection and ordering of fundamental genetic information on humans and domestic animals. Every cell of an organism has a "Genome" - a set of chromosomes containing the heritable genetic material that directs its development. The genetic material of chromosomes is DNA. Each of the paired strands of the DNA molecule is a linear array of subunits called nucleotides. Genes are discrete stretches of nucleotides that carry the “template” information the cell uses to construct the biochemical molecules that build and regulate all life forms. These nucleotide templates control the building of the cells amino acids (of which there are 20) into polypeptides which combine in different ways to form proteins and the processes that control and manipulate them. Nicholas (1987) describes the process clearly and in great detail.

As an example and at our current level of understanding - the human genome is composed of about 3 billion chemical base pairs and contains approximately 30,000 genes. The genes take up only about 5 to 10 percent of the DNA; some of the remaining DNA, which does not code for proteins, may regulate whether or not proteins are made, but the function of most of it is unknown.

The main goal of a Genome Project is to map the location of all the genes on every chromosome and to determine the precise sequence of nucleotides of the entire genome. Two types of maps are constructed: genetic linkage maps and physical maps. A genetic linkage map provides the relative location of genes and other markers on the basis of how frequently genes are inherited together; the closer genes are to each other on a chromosome, the more likely they are to be inherited together. Physical maps locate genes in relation to the presence of known nucleotide sequences that act as markers along the length of a chromosome. A relatively detailed physical map is needed before sequencing can begin. Sequencing, in which the precise order of the nucleotide sequence is determined, is the most technically challenging part of the project.

A study of these Genome databases highlights the surprisingly high level of common genes with similar functions in widely disparate organisms. Information gathered on the DNA of the laboratory mouse (Mus musculus), the nematode worm Caenorhabditis elegans, the fruit fly (Drosophila melanogaster), the yeast Saccharomyces cerevisiae, and the bacterium Escherichia coli is being used to study their genomic counterparts found in human beings. This all leads to the belief that the species of the world evolved from a common molecular base by a series of molecular changes and combinations of their DNA. The historic classification of the biological kingdom into taxonomic groups has produced a “tree of life”. The current genomic studies are correcting and reinforcing this concept. The study of the pattern of molecular evolution presumes that like species have developed from a common base and that their path of evolution and the relative timing of any split can be determined by a study of their genome.

On this basis it is presumed that the goat and the sheep are closely related species and that both have evolved from the “bovid” (cattle) group. Goats and sheep have a very high proportion of their genomes in common. Any study of the breeds within each species will demonstrate that there are many sheep that look like goats and many goats that look like sheep. Goats and sheep are so closely related that hybrids of the two are known to exist. Nijman et al. (2002) gives a short review of the topic and describes a method of sequence analysis of satellite DNA, which allowed the verification and disapproval, respectively, of two cases of suspected goat-sheep hybridization.

It seems very likely indeed that the commercial improvement of the Cashmere goat will follow that of the Merino sheep.

It is important for the reader to learn to think about genetic topics at a genomic level. A study of genomic data for the Family Bovidae, which includes cattle, sheep and goats, illustrates this point. As explained sheep and goats are so closely related they will hybridize - yet sheep (Ovis aries) have 54 chromosomes while goats and cattle have 60. At a first glance sheep and goats would appear to be quite unrelated. Both have much the same DNA material, but it is arranged in quite a different way. It is the DNA nucleotide segments (genes) that are important, not the arrangement (chromosomes).
**Databases**

From the genetic point of view, the sum of all knowledge to date is indexed in two databases freely available on the Internet. …

**Online Mendelian Inheritance in Animals** (OMIA) is a database of gene and phene (familial trait or phenotype) [http://www.angis.su.oz.au/Databases/BIRX/omia/](http://www.angis.su.oz.au/Databases/BIRX/omia/) Editor F.W. Nicholas, Faculty of Veterinary Science, University of Sydney, NSW 2006, Australia.

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The Online Mendelian Inheritance in Animals (OMIA) is the online version of MIA (Mendelian Inheritance in Animals – database). OMIA currently contains bibliographic details for 7850 publications on 1111 traits across 32 species.


An integrated and comparative Genomic map of the goat. This map constitutes the most significant effort so far to gather and list all Genomic research related to goats and to compare the Goat Genome with that of other ruminants and with primates (man).

*At the time of publication there were no identified and mapped genes, relevant to the scope of this project, reported in the literature.*

**Transgenic Research**

Any consideration of genetic improvement in cashmere production needs to acknowledge the possibility of the introduction of production boosting components from outside sources. Transgenics is the science of splicing one species' genes onto the genome of another. Goats have already been involved in transgenic experiments to produce superior fibre, but in a quite unexpected way. Turner, J., (2000), In a Commercial Press Release on behalf of Nexia Biotechnologies, Quebec, Canada; reports the transgenic splicing of genes from the "Orb Weaver" spider, that spins the world's toughest natural material, into two Nigerian dwarf goats Webster and Pete. These sires have been used to produce does whose mammary glands are able to produce the complex proteins that make up spider silk. Their milk looks and tastes like the real thing, but once its proteins are filtered and purified into a fine white powder, they can be spun into tough thread. The Nigerian dwarf goat was the perfect candidate, as it begins breeding and lactating at just 13 weeks.

Attempts to create artificial spider's web have failed in the past because it is difficult to make the very long protein chains found in the natural version. The silk milk technique works because the way mammals produce milk proteins and spiders make silk proteins are broadly similar. These strands of silk, just 3 microns thick, are three times as tough as DuPont's bulletproof Kevlar. A woven cable as thick as your thumb can bear the weight of a jumbo jet. Once perfected, the silk will be used for featherweight ballistic vests, medical sutures and artificial ligaments.

Any transgenic manipulation first requires the precise identification and definition of the components to be manipulated and this is part of the scope of this report.

*In summary:*  
*There has been ample discussion by Australian authors, and others, on the macro components affecting down quality and down quantity. A full review of these papers finds no reference to the concept “that taken individually, contributory components to observed annual down production may have a fairly simple form of genetic inheritance.”*  

*At the opposite end of the spectrum major advances have been made in recent times in the understanding and mapping of the molecular mechanisms that govern inheritance. There is little reference to the practical application of this information to the improvement of Down production. This report starts to build the bridge between these two pillars of knowledge.*
1.2 Project Design and Methodology

The Research Project was commenced on 1st July 1998 as planned. Some 9 months were spent on advance planning and preparation prior to the commencement of the Project.

Analysis of feeding, animal health and management information available in the literature and from personal communication enabled the development of an "Annual Cycle - Management Plan" for the housed animals on a 'best guess' basis. The Project is indebted in particular to Bruce McGregor (Agriculture Victoria) and Ted Scarlet (NSW Agriculture) for their help in this foundation phase.

Dr Jay Hetzel, who agreed to act as Genetic Consultant in the early stages of the project, visited the project at Clonbinane on July 2nd 1998. Some useful discussion developed on the mapping techniques under consideration. In subsequent correspondence Dr. Hetzel stated …

"In my opinion the data set to be collected will be unique and potentially very valuable in providing baseline data from which to develop genetic hypotheses."

A number of issues had to be dealt with to establish the stable environmental conditions required for the Project. This entailed the development of a number of innovative husbandry techniques. Social interaction between animals caused some major problems, as did several disease challenges. A major problem with "Fleece Eating " took nearly 18 months to understand and resolve.

Development of the feed ration was on-going. During the first year of the project, subjective assessment suggested that the commencement ration promoted fleece quality at the expense of quantity. Over the life of the project controlled changes were made to the ration with beneficial results.

Stage 1. - Collecting the Data (Year 1 & Year 2 with confirmation in Year 3.)

The project commenced with a group of 120 females and 3 males that exhibited VHPP characteristics. These had already been selected as part of Project KKN. The females were introduced into controlled environment conditions shortly before kidding in September 1997.

All animals commenced the project adjusted to a basic ration of 5.5 MJ per day. The ration was originally designed to strike the balance between fibre quality and fibre quantity. By the beginning of 1998 the animals were reasonably settled socially and showing visible signs of Cashmere growth.

In general terms, an animal grows and sheds its cashmere down on an annual basis. Growth starts in late spring and shedding begins in mid to late winter. The fleece is typically harvested by shearing at or about shedding time, or combing several times over the shedding period.

This report covers three such cycles …

- Spring 1997 to Spring 1998 – The 1998 cycle (includes data collected prior to the official commencement of the Project.)
- Spring 1998 to Spring 1999 – The 1999 cycle
- Spring 1999 to Spring 2000 – The 2000 cycle

The task was to sample, quantify, map and classify into types; components of the annual fleece production of the study group. The aim was to identify groups of animals that seem to have common characteristics associated with down production and develop a model for the contributing

<table>
<thead>
<tr>
<th>Sex</th>
<th>Age</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Doe</td>
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<td>15</td>
</tr>
<tr>
<td>Doe</td>
<td>2</td>
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<td>Doe</td>
<td>6+</td>
<td>30</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>120</td>
</tr>
</tbody>
</table>

Buck 1 2
Buck 6+ 1
Total 3

Table 1.2/1: Project animals as at September 1997.
components of down production. For example, continuous growth as opposed to seasonal growth, the “type” of Guardhair, the presence or absence of a “mane”, the “type” of down population. 

To follow the example “type of Guardhair” …. A few animals have virtually no Guardhair, some have a short “kemp-like” Guardhair, some have long coarse hair, some have long flexible hair, some have short flexible hair and some have a bit of everything! In addition there is a pattern component to Guardhair growth – it may, or may not, grow on different parts of the body.

A computerised data tracking system was produced to collect and analyse the large amount of data involved. Data collection was repeated in Year 2 and Year 3 to further develop the model and develop an estimate of data reliability.

Stage 2. Developing the Genetic Model (Year 2 & Year 3.)
Data collected from Stage 1 was used to develop a hypothesis as to the genetic basis of the observed phenotypic performance. An interesting but incomplete picture was sketched by the Data collected in 1998. Modifications were required to the 1999 data collection program. By the end of Year 2 sufficient information was available to begin to construct hypothetical models of the inheritance of some of the components involved.

As the project progressed some areas of interest were abandoned and others developed in an effort to elucidate some of the emerging patterns.

The goal of Stage 2 was to endeavour to dissect an individuals observed down production into contributing parts; then for each component, to suggest a model for genetic inheritance, a partial model, or a statement that no such model could be found.
1.3 Project Facilities and Animal Management

The Animal Shed
The animals were housed in a single shed with insulated roof and wood-batten floor. The shed was
divided into 8 pens of about 15 animals each and equipped with overhead fans for air circulation in
the summer.

Each pen was fitted with an automatic water supply and feed holes giving access to a central feeding
aisle. This system allowed for differing feed formulae and quantity to be supplied to each pen.
Required bucks were accommodated (in yearly groups) in two small adjacent electrified buck
paddocks, equipped with water supply, shelter, feeding, and restraining facilities; with convenient
and controlled shed access.

Other Facilities
Adjacent hay and straw shed.
Attached room - housing feed mixing, storage, recording, veterinary, and husbandry equipment.
Equipment for feed additive mixing and dispensing.
Digital LCD display feed and fleece weighing scales reading to 1g. with tare facility.
A numbered feed bucket for each pen.
Shearing area - Shearing, fleece collecting, and fleece weighing equipment.
Restraining facilities - both at shearing area and individually in each pen.
Fully equipped veterinary facilities.
All necessary animal husbandry and tagging equipment.
Large whiteboard for recording purposes.
Fresh running water and water disposal facilities.
Covered, sheltered, weaner pen adjacent to shed.
Adjacent exercise paddock with controlled shed access.
Computer Facilities for data recording and manipulation.
Feed Regime

The basic ration consisted of oats (augmented with appropriate additives) plus straw roughage fed at a level sufficient to maintain average body condition of Score3 (which was checked routinely at 3 monthly intervals and monthly for animals under particular observation). Pens consisted of groups of does with like ration needs. Late pregnancy rations were augmented to provide for kidding and lactating needs. Bucks were fed at similar levels with similar feed mix.

General Husbandry

All traditional husbandry matters were routinely attended to:

- Hoof trimming at 3 monthly intervals was found necessary.
- All animals were tagged (at birth in the case of kids). This tag consisted of a unique number together with a letter signifying year of birth. Additionally each animal’s dam was recorded on the tag. Original animals had a secondary tag identifying details of their history.
- Regular worm count monitoring was carried out on shedded animals. It was found unnecessary to continue worm treatment as these animals after an initial treatment registered zero count. Bucks were treated annually.
- All kids were vaccinated with Glanvac 3 at 6 weeks and 12 weeks, and all animals similarly vaccinated annually at shearing.
- Animals were monitored regularly for presence of body lice. None were detected at any stage and accordingly no treatment was undertaken.
- Body condition was routinely checked at 3 monthly intervals, (or more frequently if required).

The 'Fleece Eating' Problem

Significant unexpected data loss occurred during the first measurement cycle due to "Fleece Eating". The animals will not eat Guardhair but under stress eat the pure cashmere. Almost all animals in the program had long cashmere that extended well past the Guardhair in the second half of the growing season. If the cashmere is attached and growing the ‘plucking’ process causes pain and the victim responds to control the ‘plucking’. It seems that when the cashmere sheds at the end of the growing cycle there is no pain and there is no ‘victim resistance’. Large quantities of cashmere down 'disappeared' within a matter of days. It is estimated that serious fleece loss occurred during the first
measurement cycle in about 75% of the Project animals. Yield and Down Weight comparisons were useless and Mean Fibre Diameter comparisons limited, due to the need to select different sampling sites on different animals.

This setback had only limited impact on the research project, but it did prevent the establishment of a performance baseline for the project animals.

The problem was the subject of considerable investigation.

A number of factors were implicated and appropriate strategies implemented. The result of these actions was the virtual elimination of the 'fleece eating' problem, combined with excellent health of the animals. No animals were lost to ill health once this protocol was established, and no general health problems were encountered.
2. Setting the Scene

2.1 Project Limitations – Addressing the Limitations

Project Limitations
Looking at the Objectives in the light of available resources there are two obvious limitations …
- The Project only covers three full annual cycles.
- The population under examination is very small.

Addressing the Limitations
The Objectives, as set, are very broad. The very nature of this project is exploratory. In view of the limitations stated - a suitable investigatory technique would be one of observation and deduction. In principle this project has proceeded along these lines.

For most fleece characters under consideration it was necessary to ‘observe – deduce – conclude’; then revisit the issue and look again in the light of the conclusions. In this way it was possible to “drill down” through the various layers of observation, to get to the nub of the matter. The dictionary definition of the word “nub - The choicest, or most essential, or most vital part of some idea or experience”, describes the goal exactly.

The traditional methods of data collection, quantitative analysis, and statistically tested comparisons were used, where possible, to support or disprove deduced conclusions.

To address the obvious limitations stated, the Project has drawn heavily on outside information. This information was typically used to - widen the base of an observation, support a deduction, or aid a conclusion. Some of the items investigated would not have been obvious from the Project dataset. They were brought into focus by knowledge gained in other areas, at other times.

The principal sources of outside information were:
- Literature – both published and unpublished. The authors have in their possession a considerable amount of information that is unpublished or has only seen very limited publication. Information from these sources is explained more fully in the text.
- Personal Unpublished Material – mostly data and photographs from earlier projects. This is noted where used.
- Personal Observation – The authors’ prior personal observations and experiences were often taken into an account when making a judgement. The process was to compare and contrast the project findings with currently accepted lore; then seek the reasons for any differences, - or - draw judgemental strength from any confirmations.

*It is acknowledged that the findings of this Project have been arrived at in a subjective manner – the authors could see no other way of achieving their objectives. Results unless otherwise stated are presented on a ‘Best Guess’ basis. ‘Estimates of Certainty’ are given. These factors should not, however, make the findings any less valuable.*
2.2 What Do We Know About Cashmere Production?

Commercially, Cashmere Down is the primary interest and increasing Down production the primary goal. This report however looks at Fleece Production as a whole. Cashmere Down is just one of the components of the total fleece. It is just as important to understand the genetic manipulation of Guardhair (which has commercial implications), as it is to understand the genetic influences that might increase Cashmere Down production.

Definitions

As a starting point it is necessary to define the terms Cashmere and Guardhair.

CASHMERE - is the fine, non-medullated undercoat of a Cashmere producing goat. The words DOWN and CASHMERE are often used interchangeably.

GUARDHAIR – is the coarse fibre forming the primary protective coat of a two (or more) coated goat. The fibres are usually quite stiff and commonly have a diameter greater than 30 microns. They are generally derived from primary follicles and are often medullated.

A raw cashmere fleece is made up of a number of contributing fibre populations. In general terms Growers perceive there are two – Down and Guardhair. It is commonly acknowledged that, in some less desirable fleeces, there is a third “intermediate fibre”.

This report will demonstrate that there are a number of contributing fibre populations that could turn up in a commercially acceptable cashmere fleece. Commercial acceptability is a function of the overall effect of the combination (is the product saleable?), which is as much a function of ‘quantity present’, as it is of type.

There have been a variety of papers published on the definition of cashmere and considerable argument as to the cut-off point for coarse fibre and what type of fibres should be included. For the purposes of this project Cashmere is considered to be any material that would meet the Cashmere specifications laid down by the Australian Cashmere Marketing Corporation Ltd.

The fleece as harvested is not all fibre

The harvested fleece commonly comprises ...

- **Fibre** – the major component – usually around 90% of a ‘clean’ Australian fleece.
- **Grease/Sweat** – typically averaging 3% but variable and increasing as selection progresses. [Couchman & McGregor (1983), Tucker et.al. (1990),]
- **Dirt and dust** – variable dependent on range conditions.
- **Contaminants** - such as seed, thistle, burr, blackberry, sticks, bark, straw and other vegetable matter.

All buyers purchase cashmere on a “clean down” basis. The price they pay for raw fleece is based on their estimate of its Yield. Yield in cashmere strictly means the usable clean down in a fleece expressed as a percentage of its raw fleece weight. In Australia, with its large range of phenotypes, where harvesting is by shearing and most fleece is fairly clean – increasing yield is primarily a function of breeding.

The project animals (being shed reared) were generally clean and free from dirt and dust contamination. There was some vegetable contamination from feed husk and straw. The project animals were all selected for high yield. As a group they would be at the high end of the world spectrum for yield ((Down/Clean Raw Fleece) %).

*From this point on, in this report – only the Fibre component of a fleece is considered. This component is assumed to be perfectly presented and free of all contamination.*
Most of the world's understanding of cashmere production has been elucidated in Australia in the last 25 years ...

**Skin Histology and the Annual Growth cycle**
McDonald (1985), (1987) describes the skin histology of the Cashmere Goat and the changes that take place from birth to maturity. He states that Hair fibres grow from the “primary” follicles of the skin, the Cashmere fibres growing from the “secondary” follicles. He mentions that, at birth, the primary follicles occur in groups of three with very few secondary follicles being in evidence. He quotes the S/P ratio as generally less than 1:1. Following birth there is a rapid development of secondary follicles and by 1 month of age the S/P ratio has risen to about 5:1. Harmsworth and Page-Sharp (1970) describe an exactly parallel development in sheep. McDonald also describes in detail the seasonal changes in fleece composition that take place with the annual growth and shedding of down fibre. He investigates the control processes that influence the annual growth cycle.

**Changes with age and predictability of adult production**
Restall (1998) examines, in detail, Coat Score at birth and Yield and Diameter as predictors of adult production. Yield and Diameter were measured on patch samples, from Neck, Midsise, and Hip at approximately 6, 12, 18, and 24 weeks of age. No parameter provided a useful predictor of cashmere down weight, but diameter measurement at 18 weeks was a useful predictor of adult cashmere diameter. Browne (unpublished) has found that diameter measurement, taken on a Midsise patch sample at 20 weeks of age, when considered in conjunction with the Coefficient of Variation of the Diameter measurement, provided an accurate predictor of the potential adult diameter of the fleece. The lower the COV, the less the increase in mean fibre diameter with age.

**The relationship of Down Weight to Fibre Diameter and Down Length**
It would seem obvious that both fibre diameter and down length are partial determinants of down weight. Bishop & Russell (1997) illustrate in detail how selection to reduce fibre diameter will have a disproportionate negative effect on down weight. Graham & Bell (1990) explain the relationship between down weight and fibre diameter and provide “expected performance” tables for 1, 2 and 3 year old bucks. These tables were compiled from a survey of 509 AWTA tested bucks from all parts of Australia. The Patrick Index (Snippet May 1989 p28) quantifies this relationship in the form of a regression curve, such that animals of different down diameter can be compared for relative phenotypic performance. Winter (1985) demonstrated the strong correlations between down weight and down length in unselected Australian Feral Does and their progeny of both sexes.

**Heritability and Genetic Correlations**

The majority of these estimates are in general agreement and show that Down-weight, Mean Fibre Diameter (at the Midsise), and Cashmere Length are all fairly highly heritable. These characters should respond to selection and the various authors suggest breeding plans and selection indices aimed at genetic gain.

**The estimates of Couchman & Wilkinson stand out as different.** Table: 2.2/1 lists the three Heritability data- sets compiled on Australian Goats.
Table 2.2/1 Heritability estimates for Australian Cashmere (with standard errors)

<table>
<thead>
<tr>
<th>Study</th>
<th>Total Flc Wt</th>
<th>Down Wt.</th>
<th>Down Diam.</th>
<th>Down Lngth.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Couchman &amp; Wilkinson (1988)</td>
<td>0.14 ±0.08</td>
<td>0.20 ±0.06</td>
<td>0.32 ±0.11</td>
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</tr>
<tr>
<td>Gifford et al (1989)</td>
<td>0.42 ±0.16</td>
<td>0.36 ±0.13</td>
<td>0.70 ±0.19</td>
<td></td>
</tr>
<tr>
<td>Pattie &amp; Restall (1989)</td>
<td>0.29 ±0.11</td>
<td>0.61 ±0.18</td>
<td>0.47 ±0.15</td>
<td>0.70 ±0.19</td>
</tr>
</tbody>
</table>

The estimates of Couchman & Wilkinson (1988) are around half the average of the other two estimations in all characters under consideration. The authors, themselves, suggested their figures were more closely aligned with Misarev et.al. (1969), who assessed the inheritance of undercoat production in the Russian Don Goat, than they were to the other two Australian studies. The estimates calculated by Couchman & Wilkinson were obtained from selected down bearing animals with some angora ancestry and an average annual production of 172.3g down.

Low heritability estimates suggest environmental influences are playing a large part in the observed result – or – they suggest that more than one, independently inherited, genetic character, is involved in the measurement group – or – they suggest both.

For reasons explained in Section 3.3, the authors believe the estimates of Couchman & Wilkinson for down heritability values cover at least two overlying populations whereas those of the other two projects could reasonably be expected to represent a single down population at the points of measurement. The estimates calculated by Gifford et al (1989) were for selected down bearing animals heavily classed for traditional style. Those of Pattie & Restall (1989) were for a feral type with a clearly defined cashmere style of fleece and an average annual down production of 49.6g.

**Nutrition and health effect production**

Cashmere growth, guardhair growth and fibre diameter are all effected by nutritional intake. This has been amply demonstrated by McGregor (1988), (1989), (1990), (1992). The response to nutritional change would seem to be higher in higher producing goats. Johnson and Rowe (1984) and Ash and Norton (1984), both working with animals derived from a feral base, and having an annual down production of around 60g, could measure no response to nutritional changes. All McGregor’s work was done with goats selected for higher productivity – around 150 g down. It seems that nutritional issues will become more important as fibre production per head increases.

**Competition for nutrients**

In addition to overall nutritional effects, it is reasonable to expect there may be some competition between the various hair and down populations on an animal for available nutrients. The partitioning of available nutrients between cashmere and guardhair has been studied in detail by McGregor (1988). He found that supplementary feeding had the same pro-rata effect in increasing the cashmere production of both high and low producing goats. He also found (overlying the overall effect of nutrition on growth), energy-deprived goats which lost liveweight, diverted nutrients preferentially to cashmere growth, while goats fed ‘adlib’ partitioned nutrients towards hair growth. It is not clear, from this or any other study reviewed by the authors, if the growth or partitioning mechanism is under any form of variable genetic control.

It is also not clear if identification, and elimination (by selection), of unwanted fibre populations would lead to more nutrients being available for cashmere growth.

*It was understood at the start of the project that the fibre populations under investigation would be influenced by the level of health and feed intake of the project animals over their growth period. Considerable steps were taken to keep the animals in good health and to match their ration to their dietary requirements.*
In Summary - Cashmere down production is affected by environmental factors, but there are genetic components. The heritability of down diameter is high, as is the heritability of down length and down weight. Table 2.2/1 presents three sets of heritability estimates on three flocks of Australian goats. Investigation of the backgrounds of each of the three measured flocks, provides a clue to the discovery of the major premise of this report.

2.3 A hypothetical Concept

The dictionary defines …

Hypothesis - “A concept that is not yet verified, but that if true, would explain certain facts or phenomena.”

Concept – “An abstract or general idea inferred or derived from specific instances.”

More than a hypothesis – but not (as yet) a fully proven concept!
The complex interaction of the components of fleece production is best understood by examining the final proposition and then working back through the supporting details.

This investigation suggests it is useful to think of a goats fleece cover in terms of human clothing. When the Creator first dressed the Cashmere goat against the rigours of a harsh climate, he started with a nice warm neck-to-knee under garment of pure fine cashmere and a neck -to-knee ‘coverall’ of hair. To this he added optional dress – varying from goat to goat - an additional under-garment, and perhaps an additional hair garment, a waist coat, trousers, a bib, a neck scarf. In places, for extra protection, he added some hairy patches, and for some goats, a tough neck-to-knee overcoat of long hair. All these articles of clothing seem to be represented by a nearly equivalent fleece component. They are not worn as one substituting for the other, but as true articles of clothing - one overlaying the other. Some goats wear many items of clothing – others just a few. An ideal Cashmere goat would have just two, the primary neck-to-knee under garment of pure fine cashmere and the ‘coverall’ of hair. Such an animal (if it exists) would be rare.

The primary underclothing is generally made of cashmere. Secondary underclothing may be made of longer, stronger cashmere or straighter mohair like fibres.

The waist coat is typically any “non-hair” fibre. In the Authors experience the waist coat is never made of a finer material than the trousers.

The trousers are thought to be the exception to the rule. They are NOT an overlying fibre population, but an area free of overlays that allows full expression of the underlying populations.

Just like people – the goat wears extra clothing in winter and may remove some items (typically underclothing) in the summer.
2.4 The Concept of a “Fleece Production Units” (FPU)

It was assumed at the beginning of this project that observed phenotypic fleece production could be broken down into a number of contributing parts or “Fleece Production Units” (FPU). The phenotypic product of each of these parts was considered to be a function of the interaction of genetics and environment. It was assumed that ultimately continuing this dissection process to the extreme would result in a FPU where only genes at a single locus were involved and their influence could possibly be identified. It is acknowledged that this is a simplistic concept and that in many cases genes at more than one locus will effect the FPU. However within the limits of the available resources, the aim was to identify as many of these Fleece Production Units as possible and hopefully learn something of their genetic control.

Recording an FPU

The basic features of each FPU discussed are reported in a Local Summary table. These Local summaries are combined into a Master Summary table, presented and discussed under Outcomes. A Local Summary table was given the following format.

<table>
<thead>
<tr>
<th>RefNo</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
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<tr>
<td></td>
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</tr>
<tr>
<td>Comment (Sex Linked?)</td>
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<tr>
<td>Further Questions</td>
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</tr>
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</table>

**RefNo** – Reference Number. This sets the order in the Master table and provides a simple reference tag in discussion.

**FPU** – Fleece Production Unit. The name of the unitary component of Fleece Production under consideration (for the purposes of this report).

**Genetic Control** – A subjective estimate of the type of genetic control.

- NONE – No evidence of genetic control.
- SIMPLE – Control by genes at a single locus.
- MULTIPLE – Control by genes at more than one locus.

**Certainty** – A subjective estimate of “Confidence of assessment”.

The options considered: VERY HIGH, HIGH, MEDIUM, LOW.

**Environmental Modifiers** – The observed environmental factors that modify phenotype. Typically these would be Animal Age, Sex, Health, Nutritional Intake.

**Comment** – any notable features. If genetic control is thought to be Sex Linked, this would be noted here.

**Other References** – Specific references to other work taken into account in arriving at the subjective estimate of genetic control.

**Further Questions** - Draws attention to items needing further investigation.
3. The ‘Big Picture’ – Guardhair, Down and Macro Patterns

This report proposes that the observed ‘clean’ total fleece of a cashmere animal is made up of a number of independently inherited fibre populations. A full investigation of these fibre populations, their interactions, their inheritance and their quantitative operating mechanisms is an enormous task and not achievable within the scope of this project.

Sections 3, 4 and 5 of this report cover a limited investigation of some of the more prominent of these fibre population and their interaction. Where possible an attempt is made to speculate on their form of inheritance. The investigational tools used are discussed in detail and the large amount of data collected is presented on the CD.

Down and Guardhair

For the purpose of this paper it is convenient to divide these populations into two groups on the basis of their commercial application. The combined ‘hairy’ populations (usually coarse) have little commercial value and are commonly known as GUARDHAIR. The balance of the populations, are grouped together in this paper under the general term DOWN. The distinction between Down and Guardhair in commercial fabric production is based on the stiffness and structure of the fibre rather than diameter. Guardhair is stiff, usually medulated, has poor dye uptake and does not “bond” in spinning. Fine Guardhairs, known in the processing trade as ‘Shiners’ (around 30 microns in diameter) are difficult to remove in commercial dehairing. They are somewhat more flexible, and due to poor dye uptake, are very obvious in the final product. They should be avoided in any selection program. Down fibres are flexible, spin well and take up dye evenly.

Fibre diameter in all populations (both Down and Hair) has a range of values – these can be plotted for each population on a distribution curve similar to a ‘Cashmere Histogram’.

Classifying the Down Component as a Commercial Product

Commercially, the Down fibres are split into groups depending on the mean fibre diameter (MFD) of the sample (and to some extent its range) and the STYLE of the fibre. If the MFD is under 19 microns it falls within the Cashmere range. Over 22 microns it falls within the Mohair range – moving through ‘Kid’, ‘Young Goat’ to ‘Adult’ as the diameter increases. The ‘Middle Micron Range’, 19-22 microns may be blended either way or sold as ‘Cashgora’ depending on its style. The STYLE of the fibre is important in any fibre classification. Cashmere has a ‘lazy crinkle’, Mohair tends to be straight. Cashgora is an accepted mixture of both types. Plain straight fibre, irrespective of diameter, will not be accepted as Cashmere. Cashgora is expected to have some ‘cashmere like’ component. ‘Cashmere like’ fibre in Mohair is not perceived as a commercial problem.

In the commercial world fibre prepared for spinning is the result of a blend. The components have been carefully selected to produce a desired end result consistent with a preset input cost. Material containing small amounts of “off-type” fibre may be used for economic reasons.

3.1 A Naming Convention

Garbs and Garblets

Of the fibre populations under consideration there seem to be two types – those covering the whole body (with, perhaps, the exception of the extremities) and those which are regional. The “whole-body” populations have been termed ‘garbs’. The regional populations termed ‘garblets’. It is proposed by this report, that all identifiable garbs or garblets, be named to facilitate their common identification and further investigation. The naming of regional populations is easy and in most cases is self descriptive.
Naming Garbs (‘full-body’ populations)
Naming ‘full-body’ populations in a readily understandable format is more difficult. It is proposed they should be named AAgarb to ZZgarb. AAgarb, being the ‘outer’ coat of coarse guardhair and ZZgarb being the finest ‘undercoat’ (cashmere) population. Hopefully there are less than 24 sets of loci controlling full-body populations in-between! The dual letters serve a purpose. Firstly they are more recognizable as defining something than a single letter. Secondly they may be useful in describing the allele combinations inherited from each parent that give rise to a variety of effects originating from the one locus. If necessary, numbers, superscripts or subscripts could be added to describe complex situations.

It is suggested that the ‘two capital letters’ be used when referring to a Garb in general terms and that the name be enclosed in square brackets when referring to it in specific terms, such as describing the relationship between alleles. Example: The AAgarb is thought to exist as both long-haired and short-haired phenotypes. The short-haired type [AAgarb] is thought to exert simple dominance over the long-haired type [aagarb]… etc.

Naming Garblets (‘regional populations’)
To extend this concept to garblets (‘regional populations’) it is proposed they be coded HHname (eg. HHbib) for Hair populations, DDname for Down populations and MName for down type populations that fall outside the cashmere range. Numbers, superscripts or subscripts can be added to describe complex situations. The term ‘garblet’ should be used as a collective term. It seems redundant to use it in addition to the identifying name. The square bracket naming rules would apply to Garblets as they do to Garbs.

It may well be that DDname and MName populations are one and the same – this is discussed in detail in Section 5.

Photo 3.1/1: Two of the project does.

On Z85 the ZZgarb is prominent having grown longer than the AAgarb. The [AAgarb] in this animal is the ‘short haired’ phenotype (see Section 3.2). Two regional hair Garblets (populations), the HHbritch and HHbelly are obvious and still long enough to protrude through the ZZgarb. The HHbritch was present in many, but not all of the project animals.
3.2 Guardhair Patterns

- **The AAgarb – Overall Coverage of Guardhair.**
- **HHgarblets – Hairy Segments.**
- **Exploring the Inheritance of Mane, Bib and Britch.**

Guardhair comes in a variety of forms. Long-and-stiff as on the mane of a goat. Short-stiff-and-chalky – similar to Kemp in sheep. Long and more flexible as in a Long Guardhair Goat – the long, fine, flexible hair can be very hard to remove in commercial dehairing – in sheep these long flexible hairs are known as Gare.

In addition some goats have a further overall covering of long hair – worn rather like an overcoat. In practice all these hair populations get mixed up and supply the apparently extensive array of guardhair variation.

**The AAgarb - Overall Coverage of Guardhair**

At this point in their development all Cashmere goats have an overall coat of guardhair. In some of the project animals the relative contribution of guardhair to the total fleece weight was less than 30% by weight. It was the authors perception, that with selection, guardhair could be reduces to such low levels as to render dehairing unnecessary. It remains to be seen if guard hair can be totally eliminated by selection, but small amounts of short guardhair could be removed, without dehairing, during the normal carding process.

The long haired goat with an overall coverage of long, usually flexible, hair - is a type. The hair usually grows to a length of about 100mm in a year. Records held by Browne (unpublished) suggest this ‘long haired’ type is fairly quickly and permanently eliminated from a herd by selection. This would suggest single locus control.

At least one of the companion alleles would appear to produce short hair, as typified by the draw diagram for the buck Z124. (Fig: 3.2/1). The short haired guardhair coat was the most common in the project animals. Intermediate forms of guardhair do exist. The question arises, are they all manifestations of a variety of alleles at the same locus – or – are the observed phenotypic combinations of additional populations (eg. AAgarb + BBgarb) – or – both. This would be one of the aspects worthwhile investigating as a future project. The basic data should be fairly easy and cheap to collect. The elucidation may provide some clues to the action of loci covering the down populations.

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>AAgarb: Overall guardhair long /short (and what else?)</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?) | Sex Linked – No

Other References

Further Questions | Intermediate forms of guardhair do exist. Are they all manifestations of a variety of alleles at the same locus – or – are the observed phenotypic combinations of additional populations?

**Long Haired Asian Goat**

The very long haired goats of Asia are a product of their management regime. They are not shorn annually, but usually clipped back to a length of 100mm or so before combing. At the end of the season their hair length will be up to 200mm. Shorn Australian goats never reach anywhere near this length.
An Example

The animals in this project included only one goat of the ‘Long Haired’ type (a doe Z001). She was mated to ‘Non-long-haired’ Bucks. None of the progeny born to her during the project had her long hair coat.

Figure 3.2/1 Test mating Doe Z001

Figure 3.2/1 presents the fibre draws for Z001, one of the bucks she was mated to, Z124, and the resulting progeny B023. The draw technique is described in Section 4.1. Essentially the components of a small sample of fleece are spread out, progressively sorted by length.

In Z001 the guardhair is longer than the down. The draw of Z124 would appear to show two down populations, one longer than the guardhair and one shorter. In this case the progeny seems to have ‘inherited’ (remember these observations are really phenotypic) a down, ranging from the long of the sire to the short of the dam, and a guardhair ranging from the long of the sire to the short of the dam. There was no sign of a second, distinct, Down 2 population, as displayed in the sire.
**HHgarblets – Hairy Segments**

The elimination of ‘Overall Long Guardhair’ reveals a number of other independently inherited areas of concentrated hair producing follicles.

Overlaying the overall Guardhair population (or populations) are a collection of “Hairy segments”, (Garblets) not all of which are present on every animal. The Mane was the most prominent on the project animals, with many animals exhibiting hairy ‘Britch’, ‘Backleg’, ‘Bib’, ‘Scarf’ and ‘Belly’. A review of photographs of a wide range of goats suggests there may be other hair segments behind the front leg. This garblet was not observed in the Project animals.

The HHbackleg, HHscarf, and HHbelly garblets were not able to be investigated in great detail. They were not identified as separate entities until quite late in the data collection phase. Sufficient records are available to demonstrate their clear-cut presence or absence, but not to produce any meaningful quantitative data.

Fig: 3.2/2 Hair Garblets – HHscarf, HHbib, HHbritch, HHbackleg.

It may be that the HHbackleg as shown is divided into an upper and lower segment. The “Backleg” FPU(2) is inherited separately to the Britch.

<table>
<thead>
<tr>
<th>RefNo</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>HHbackleg: Regional long guardhair/short (and what else?)</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?) Sex Linked – No
Other References
Further Questions Is this ON/OFF or are there a range of manifestations.

Fig: 3.2/3 Hair Garblets – HHbelly

The HHbelly may also possibly be split into two or more segments. There is a suggestion that the longer hair that occurs forward of the udder may be a separate garblet, possibly overlaying rather than replacing, in part, the main belly garblet.
Exploring the inheritance of the Mane – the HHBib – the HHBritch
For many animals, a significant contribution to the hair portion of their shorn fleece is made by hair 
from the Mane, the Bib and the Britch. There are good commercial reasons for attempting to reduce 
or eliminate these components from the fleece of the Cashmere goat. This section of the work has 
attempted to develop some understanding of the mode of inheritance and the relationship between 
these components.

Definitions and Assessment Techniques.
Initially Mane growth was considered to be a clearly defined, individual component of fleece growth. 
As the records developed it seemed that the mane was divided into two segments, a “Withers Mane” 
(coversing the withers, and running up the neck to a point between the ears – later to be called the 
Neck Mane) and the “Back Mane” (running from the rear of the withers to the tail).

Fig: 3.2/1 Components of the Mane

The initial sets of observations classified 
observed mane as: 
• Mane present M+
• Mane absent M-
Subsequent observations classified 
observed mane as: 
• Withers Mane W+ or W-
• Back Mane K+ or K-

The study of over 1000 file photographs 
associated with the preparation of this 
report suggests that the Withers segment 
can be further subdivided into:
• Withers (an area about the size of 
a human hand situated at the base 
of the neck, where it joins the 
body).
• Neck (from the withers to the 
head).
These file photographs cover Cashmere 
type animals, from a wide range of 
backgrounds.

However all observations noted below were made on the basis of Withers and Neck considered as 
one.

Table: 3.2/1 1998–99 Presence/Absence of Mane in Adult Animals: 

<table>
<thead>
<tr>
<th></th>
<th>M+</th>
<th>M-</th>
<th>n</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A. Does</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aug. 98 (shearing)</td>
<td>87% (105)</td>
<td>13% (16)</td>
<td>121</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nov. 98</td>
<td>95% (62)</td>
<td>5% (3)</td>
<td>94 (No growth 29 animals)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Jan. 99</td>
<td>92% (59)</td>
<td>8% (5)</td>
<td>92 (No growth 28 animals)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>July 99 (shearing)</td>
<td>76% (70)</td>
<td>24% (22)</td>
<td>92</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>M+</th>
<th>M-</th>
<th>n</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>B. Bucks</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aug. 98 (shearing)</td>
<td>100%</td>
<td>0%</td>
<td>5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nov. 98</td>
<td>100%</td>
<td>0%</td>
<td>5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Jan. 99</td>
<td>100%</td>
<td>0%</td>
<td>5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>July 99 (shearing)</td>
<td>100%</td>
<td>0%</td>
<td>5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

These results were simplistic, but they did suggest that mane growth could be present or absent and 
therefore, possibly under genetic control. The comparison between summer and winter results 
suggested some animals changed their classification.
From August 1998 the overall Mane was further subdivided into the two growth segments:

- **K+** Back Mane present
- **K-** Back Mane absent
- **W+** Withers Mane present
- **W-** Withers Mane absent

In addition, the relationship between the mane and other prominent areas of hair was studied. Observations were taken regarding presence or absence of ‘Bib’ hair (the clothing equivalent of a large Bib on the front of the chest) and Britch hair:

- **Bb+** Bib hair present
- **Bb-** Bib hair absent
- **Bh+** Britch hair present
- **Bh-** Britch hair absent

All animals present were assessed (using this scoring system) in May 1999, before shearing in July 1999 and again in March 2000. The raw data from these observations is included in the Digital Appendix as “Mane assessment2.xls”. Not all this data is directly comparable from sample date to sample date. Young replacements were introduced and some cull animals eliminated.

### Changes in Hair Growth Segments Over Time

A close look at the full data set confirmed, as suggested earlier, that animals did seem to change their classification. The change was always from Negative to Positive (100% of cases). Logic suggested two possible scenarios – either or both of which may occur:

- The change was apparent only.
- The change was an actual physical change – the most likely cause being aging.

To eliminate the effect of age as far as possible a subset of the data was studied – those mature adult animals, which were available for assessment over the full period.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Does (32 animals)</th>
<th>Bucks (4 animals)</th>
</tr>
</thead>
<tbody>
<tr>
<td>W+</td>
<td>100% (32)</td>
<td>100% (4)</td>
</tr>
<tr>
<td>K-</td>
<td>13% (4)</td>
<td>nil</td>
</tr>
<tr>
<td>K- &gt;&gt;&gt; K+</td>
<td>47% (15)</td>
<td>75% (3)</td>
</tr>
<tr>
<td>K+</td>
<td>40% (13)</td>
<td>25% (1)</td>
</tr>
<tr>
<td>Bb-</td>
<td>44% (14)</td>
<td>25% (1)</td>
</tr>
<tr>
<td>Bb- &gt;&gt;&gt; Bb+</td>
<td>19% (6)</td>
<td>25% (1)</td>
</tr>
<tr>
<td>Bb+</td>
<td>38% (12)</td>
<td>50% (2)</td>
</tr>
<tr>
<td>Bh-</td>
<td>9% (3)</td>
<td>nil</td>
</tr>
<tr>
<td>Bh- &gt;&gt;&gt; Bh+</td>
<td>6% (2)</td>
<td>25% (1)</td>
</tr>
<tr>
<td>Bh+</td>
<td>85% (27)</td>
<td>75% (3)</td>
</tr>
</tbody>
</table>

Note: Because of the relatively fixed accommodation facilities, a number of adult does (approximately equal to the number of retained kid does), were necessarily disposed of each year. Cull animals were selected according to quality characteristics in order: colour / coverage / yield / size / fibre diameter / fleece style. This may have introduced an element of bias into Table 3.2/2. No attempt has been made to measure this bias.

Table 3.2/2 lists results from 32 does and 4 bucks for which 3 full observations had been carried out.

The display type K- >>> K+ is used to record the situation where an animal is initially observed to have the original feature, changing to the second feature at the next or subsequent observation. eg. 13% of Does are K-, while 87% (47% + 40%) of Does eventually turned out to be K+, although some did not appear to be at first. The number of observations on bucks, when taken alone, are too low to give meaningful data.
The apparent classification changes documented in Table: 3.2/2 are considerable and illustrate the principle that a less prominent mane can be buried in down growth and apparently disappear at the peak of the growing season. Other measurements plotting incremental down growth (described in Sect 4.3) illustrated that down growth and sometimes hair growth did not commence in some animals until January.

This suggests that March is a prime time to accurately classify animals for growth of Mane segments – late enough in the season to show reasonable growth, and early enough not to be buried.

Changes with animal age
There is a suggestion from the data that an animal may move from a negative to a positive classification for hair growth - as it matures into an adult. This occurs often in the animal kingdom – even in man. This hypothesis was investigated in detail.

Fig: 3.2/2 Plots the percentage of animals classified as K-, Bb-, Bh- in each age group, against a scale showing 1½Year, 2½Year and Adult (3½Years and older).

All animals were classified at the same point in time. All ages of Does were represented, but only 1 & 2 Year Bucks (no adults) were available.

The table attached to Fig:3.2/2 shows that a significant percentage of young animals are ON (+) and a detailed examination of adult does, by age, identified K-, Bb- and Bh- scores (in each case) amongst the oldest animals surveyed.
Traditional wisdom suggests that young animals become more “Hairy” as they age – this was also observed in Project animals. The judgement, at this time, is that this is only a change in hair prominence rather than an ON (+) / OFF (-) change. If ‘change with age’ took place in each characteristic considered young animals should have been all OFF and old animals should have been all ON – this was not the case. (Unless ‘change with age’ is a genetic variable, ie. exists in some and not in others?)

At first glance the charts seem to support the “change with age “ hypothesis – this would be an incorrect assumption. **What the charts do show, is the significant difference in performance between two datasets that have different derivations.** The 1½ Year animals, which were all the result of selective mating, and the 2½ Year and older animals, which were selected at random (for the characteristics under consideration) from a very large population.

**Clues to the genetics of Mane Growth - by segment.**

Taking all the above factors into consideration, the most suitable dataset for further investigation, was that taken in March 2000 for all available animals 1½ years and over (61 does and 15 bucks). Even at this late stage in the accepted growth season, there was no growth registered for 5 does leaving a total of 55 for consideration. The full dataset is listed in the attached Digital appendix as Mane assessment2.xls.

This data was examined in two segments based on the genetic background of the traits under consideration:
- 34 Does 2½ years and older - random selection and 4 Bucks 2½ years – random selection.
- 21 Does 1½ years –selectively bred and 12 Bucks 1½ years – selectively bred.

**Table: 3.2/3 March 2000 Hair Growth – by Segment - for Randomly Selected Animals:**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1½ Year Old Does: [n =34]</th>
<th>2½ Year Old Bucks: [n = 4]</th>
</tr>
</thead>
<tbody>
<tr>
<td>W+</td>
<td>100% (34)</td>
<td>100% (4)</td>
</tr>
<tr>
<td>K+</td>
<td>85% (29)</td>
<td>100% (4)</td>
</tr>
<tr>
<td>Bb+</td>
<td>53% (18)</td>
<td>75% (3)</td>
</tr>
<tr>
<td>Bh+</td>
<td>91% (31)</td>
<td>100% (4)</td>
</tr>
<tr>
<td>W-</td>
<td>nil</td>
<td>W-</td>
</tr>
<tr>
<td>K-</td>
<td>15% (5)</td>
<td>K-</td>
</tr>
<tr>
<td>Bb-</td>
<td>47% (16)</td>
<td>Bb-</td>
</tr>
<tr>
<td>Bh-</td>
<td>9% (3)</td>
<td>Bh-</td>
</tr>
</tbody>
</table>

The only Bucks available for classification were 2½ year old Bucks born and reared under project conditions. These are not strictly comparable with the Adult Doe results for the reasons outlined earlier but they were not selectively bred.

There were 21 Does and 12 Bucks that were born in October 1988 included in the March 2000 assessment. These had been selected visually as herd replacements from the total drop of 89 kids sired by 3 bucks.
- Z124 – 53 kids
- Z125 – 35 kids
- Z131 – 1 kid

Both Z124 and Z125 were high yielding bucks with very little Guard Hair.

**Table: 3.2/4 March 2000 Hair Growth – by Segment - for Selectively Bred Animals:**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1½ Year Old Does: [n =21]</th>
<th>1½ Year Old Bucks: [n = 12]</th>
</tr>
</thead>
<tbody>
<tr>
<td>W+</td>
<td>100% (21)</td>
<td>100% (12)</td>
</tr>
<tr>
<td>K+</td>
<td>57% (12)</td>
<td>100% (4)</td>
</tr>
<tr>
<td>Bb+</td>
<td>29% (6)</td>
<td>58% (7)</td>
</tr>
<tr>
<td>Bh+</td>
<td>76% (16)</td>
<td>75% (9)</td>
</tr>
<tr>
<td>W-</td>
<td>nil</td>
<td>W-</td>
</tr>
<tr>
<td>K-</td>
<td>43% (9)</td>
<td>K-</td>
</tr>
<tr>
<td>Bb-</td>
<td>71% (15)</td>
<td>Bb-</td>
</tr>
<tr>
<td>Bh-</td>
<td>24% (5)</td>
<td>Bh-</td>
</tr>
<tr>
<td>Bb-</td>
<td>42% (5)</td>
<td>Bb-</td>
</tr>
<tr>
<td>Bh-</td>
<td>25% (3)</td>
<td>Bh-</td>
</tr>
</tbody>
</table>
These figures can be broken down by Sire:
Sire Z131 contributed 1 Doe W+ Bb- K+ Bh+ which is not included in the tables following.

### C. 1½ Year Old Does: [n =20]

<table>
<thead>
<tr>
<th></th>
<th>Z124</th>
<th>Z125</th>
</tr>
</thead>
<tbody>
<tr>
<td>W+</td>
<td>85</td>
<td>15</td>
</tr>
<tr>
<td>K+</td>
<td>45</td>
<td>10</td>
</tr>
<tr>
<td>Bb+</td>
<td>20</td>
<td>15</td>
</tr>
<tr>
<td>Bh+</td>
<td>60</td>
<td>15</td>
</tr>
<tr>
<td></td>
<td>%</td>
<td>%</td>
</tr>
<tr>
<td></td>
<td>n</td>
<td>n</td>
</tr>
</tbody>
</table>

### D. 1½ Year Old Bucks: [n = 12]

<table>
<thead>
<tr>
<th></th>
<th>Z124</th>
<th>Z125</th>
</tr>
</thead>
<tbody>
<tr>
<td>W+</td>
<td>75</td>
<td>25</td>
</tr>
<tr>
<td>K+</td>
<td>75</td>
<td>25</td>
</tr>
<tr>
<td>Bb+</td>
<td>58</td>
<td>17</td>
</tr>
<tr>
<td>Bh+</td>
<td>58</td>
<td>17</td>
</tr>
<tr>
<td></td>
<td>%</td>
<td>%</td>
</tr>
<tr>
<td></td>
<td>n</td>
<td>n</td>
</tr>
</tbody>
</table>

### Exploring the inheritance of Mane, HHbib and HHbritch

**Discussion and Conclusions** …

1. **Withers Mane** is very prevalent, being always present (ON) to some extent, in all animals assessed. Animals with Withers Mane OFF may possibly exist.

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>HHwithersMane: Very persistent</td>
<td>Unknown</td>
<td>Medium</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

   Comment (Sex Linked?)  Sex Linked – Unlikely
   Other References Suggest equivalent remnant still in today’s sheep population.

   Further Questions Why is this so persistent?

2. **Back Mane** (K) is sometimes absent. Table:3.2/3 shows the relationship over 34 unselected does as being 85% ON (K+) and 15% OFF (K-). The Buck Z124 produced a relatively high percentage of K- doe progeny - of a total of 17 daughters assessed 8 (47%) were K-. Starting with the assumption that the inheritance of Back Mane may be a simple dominant/recessive relationship where ON “KK” or Kk is dominant to OFF “kk” the theoretical population distribution will be …

   KK (25%) – Kk (50%) – kk (25%)

   In practice the distribution in a small population may differ significantly from the theoretical.

   Assuming the Buck Z124 was a homozygous recessive (kk). When bred into the population represented by the 34 Unselected Does this Buck would produce the following theoretical progeny (per 100 does mated):

   - Buck kk x 15kk does = 15kk progeny
   - Buck kk x 56Kk does = 28kk progeny and 28Kk progeny
   - Buck kk x 28KK does = 28Kk progeny

   Thus 43% (28 + 15) of the progeny would exhibit K- characteristics. This is in close agreement with the actual result of 47%.

   It is notable no buck is recorded as K-. It is uncertain if this is a reflection of the small Buck sample size or a sex-linked characteristic.

   The data in Table 3.2/1 and to a lesser extent in Table 3.2/2 demonstrate the wide variation in prominence of the Back mane when it is seen to exist. This suggests some related influence that regulates Back Mane growth once activated.
A study of photographic archives suggests this same “Hair Growth Regulator” is common to all hair patches on the animal. Further work is required to answer this question.

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>HHbackMane: On/Off ?</td>
<td>Single Locus</td>
<td>High</td>
<td>None</td>
</tr>
<tr>
<td>Comment (Sex Linked?)</td>
<td>K+ dominant, Sex Linked – ?.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other References</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Further Questions</td>
<td>Once switched ON – what regulates growth activity? Can a Buck be K-?</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

3. **Neck Mane** (not distinguished from the Withers Mane in observations) is nevertheless sometimes absent. (Photo of D036, Fig: 3.2/3) General observations suggest this may have a similar mode of inheritance to the Back mane. This requires clarification.

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>HHneckMane: On/Off ?</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
<tr>
<td>Comment (Sex Linked?)</td>
<td>Is the presence of Neck Mane sex-linked? – not sure.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other References</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Further Questions</td>
<td>Suggested single locus control - requires clarification. Are Neck Mane and Back Mane controlled by the same growth processes?</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Fig: 3.2/3 D036 has no Back Mane, no Neck Mane**

The photograph shows one of the project progeny D036 that has no Back Mane, no Neck Mane and only a small vestigial Withers Mane. This animal has been examined in detail and there is not even a suggestion of the other Mane segments, although of course some guardhair is present arising from the short haired version of the AAgarb.

It is interesting to note, that it is general sheep-classing practice, in the fine wool industry, to class sheep on the back, at a position that corresponds exactly to the Withers Mane. The accepted wisdom is that “good wool” at this point is “good wool” all over the body. It seems likely that a remnant influence of the Withers Mane still exists in a proportion of today’s finewool sheep. This would suggest that while it can be eliminated it may not be an easy task. The mode of inheritance can only be guessed at...
4. **Britch Hair** (Bh) would seem to follow a pattern similar to that of the Back Mane (K).

Table 3.2/3 shows the relationship over 34 does as being 91% ON (Bh+) and 9% OFF (Bh-).

The Buck Z124 produced a relatively high percentage of Bh- doe progeny - of a total of 17 daughters assessed 5 (29%) were Bh-. Using an argument similar to that outlined for Back Mane, Z124 could, when mated into a population with 9% Bh- females, be expected to produce around 39% (9 + 30) of his daughters with Bh- characteristics. The actual figure of 29% is in reasonable agreement with the theoretical considering the low sample sizes involved. *He produced 5 Bh- progeny. To match the theory he had to produce 6.6 Bh- progeny.*

Table 3.2/4 lists similar Bh+/Bh- ratios for both Does and Bucks suggesting the mode of inheritance is independent of the sex of the animal.

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
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<td>6</td>
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Comment (Sex Linked?) Bh+ is dominant to Bh-. Sex Linked – Unlikely.

5. **The Bib (Bb)** would also seem to follow a pattern similar to that of the Back Mane and the Britch Table 3.2/3 shows the relationship over 34 does as being 53% ON (Bb+) and 47% OFF (Bb-).

Again Buck Z124 produced a relatively high percentage of Bb- doe progeny - of a total of 17 daughters assessed 13 (76%) were Bb-. Using an argument similar to that outlined for Back Mane, Z124 could, when mated into a population with 47% Bb- females, be expected to produce around 65% (47 + 18) of his daughters with Bb- characteristics. The actual figure of 76% is in reasonable agreement with the theoretical considering the low sample sizes involved. *He produced 13 Bb-progeny. To match the theory he had to produce 11.2 Bb-progeny.*
The differences in Bb+/Bb- ratios for both Does and Bucks shown in Table: 3.2/4 considering the numbers involved are not considered significant. It is suggested the mode of inheritance is independent of the sex of the animal.

### Ref No FPU HHbibHair: On/Off ? Genetic Control Certainty Environmental Modifiers

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<th>HHbibHair: On/Off ?</th>
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Comment (Sex Linked?) Bb+ is dominant to Bb-. Sex Linked – Unlikely.

Other References

Further Questions

### Hair Segment Associations

**Table: 3.2/4 March 2000 Hair Growth Associations.**

Explores the associations between the various Hair Segments for the two datasets.

**Adult Does: [n = 34]**

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<td>W+ &amp; Bb+</td>
<td>40% (22)</td>
<td>Bb- 60% (33)</td>
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<td>Bb- nil</td>
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<tr>
<td>W+ &amp; Bh+</td>
<td>76% (42)</td>
<td>Bh- 24% (13)</td>
</tr>
<tr>
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<td>Bh- nil</td>
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</tr>
<tr>
<td>K+ &amp; Bb+</td>
<td>38% (21)</td>
<td>Bh- 44% (24)</td>
</tr>
<tr>
<td>K- &amp; Bb+ 2%</td>
<td>Bb- 16% (9)</td>
<td></td>
</tr>
<tr>
<td>K+ &amp; Bh+ 60%</td>
<td>Bb- 15% (8)</td>
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</tr>
<tr>
<td>K- &amp; Bh+ 16%</td>
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**Adult Bucks: [n = 4]**

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<td>53% (8)</td>
<td>Bb- 47% (7)</td>
</tr>
<tr>
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<tr>
<td>W+ &amp; Bh+</td>
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<td>Bh- 27% (4)</td>
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<td>Bb- 47% (7)</td>
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<tr>
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**1½ Year Does: [n = 21]**

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<td>W+ &amp; Bb+</td>
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<td>Bb- 60% (33)</td>
</tr>
<tr>
<td>W- &amp; Bb+ nil</td>
<td>Bb- nil</td>
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</tr>
<tr>
<td>W+ &amp; Bh+</td>
<td>76% (42)</td>
<td>Bh- 24% (13)</td>
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<tr>
<td>W- &amp; Bh+ nil</td>
<td>Bh- nil</td>
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</tr>
<tr>
<td>K+ &amp; Bb+</td>
<td>38% (21)</td>
<td>Bh- 44% (24)</td>
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<td>K- &amp; Bb+ 2%</td>
<td>Bb- 16% (9)</td>
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</tr>
<tr>
<td>K+ &amp; Bh+ 60%</td>
<td>Bb- 15% (8)</td>
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</tr>
<tr>
<td>K- &amp; Bh+ 16%</td>
<td>Bb- 9% (5)</td>
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</table>

**1½ Year Bucks: [n = 12]**

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<td>W+ &amp; Bb+</td>
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<td>Bb- 47% (7)</td>
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<tr>
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<td>Bh- 27% (4)</td>
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<td>K+ &amp; Bb+ 53%</td>
<td>Bb- 47% (7)</td>
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<td>K- &amp; Bb+ nil</td>
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<tr>
<td>K+ &amp; Bh+ 73%</td>
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</tr>
<tr>
<td>K- &amp; Bh+ nil</td>
<td>Bh- nil</td>
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</table>

### Conclusions on Associations

The On and OFF status of these hair garblets was perceived to be independent in terms of gene control, from the AAgarb, which was present, in one form or another, in all assessed animals.

- The Withers Mane W+ would seem to be inherited quite independently of the Bib (Bb) in both Bucks and Does. As both W+ & Bb+ and W+ & Bb- occur frequently and independently, no relationship can be seen to exist between these characteristics.
- The Withers Mane W+ would seem to be inherited quite independently of the Britch (Bh) in both Bucks and Does.
- If present - the Back Mane K+ would seem to be inherited quite independently of the Bib (Bb) in both Bucks and Does. There is a suggested correlation between absence of Back Mane (K-) and absence of Bib (Bb-), at least in Does.
- If present - the Back Mane K+ would seem to be inherited quite independently of the Britch (Bh) in both Bucks and Does. There is a possible correlation between absence of Back Mane (K-) and absence of Britch (Bh-), at least in Does.
3.3 Down and Other “Non-cashmere” Patterns

- Full Body Cover – the ZZgarb and the YYgarb
- The ‘Non Hair’ Garblets - DDgarblets (Down Garblets) and MMgarblets (Mohair-like Garblets)

From observations and heritability measurements by other authors (see Table 2.2/1) there is little doubt that the overall down cover of an animal is under genetic control. The data from this project suggests that of the down fibre populations under consideration (like the guardhair populations) there may be two types – those covering the whole body (with, perhaps, the exception of the extremities) – the Garbs and those which are regional – the Garblets.

**Full-body cover**

**The ZZgarb**

It is suggested that the primary and predominant down population, and that of most interest to the Cashmere industry, is an overall “undercoat” of fine down fibres that cover the whole body. This has been termed the ZZgarb. These are the fibres that dominate in a symmetrical way the 5 to 25 micron range of any cashmere histogram. They are the fibres that in the “unimproved” goat commence growing in early summer and shed in late winter. They are also the fibre population that the authors believe, form the basis (in sheep) of the superfine and ultrafine quality merino wools. Vickers (1990) made an attempt to isolate and describe this population and to foster the identity of a “Fine Fleeced Cashmere Goat”. She described the visual fleece properties expected in such an animal.

It is possible that more than one population makes up the observed ZZgarb, but the evidence suggests this is very unlikely.

---

**Fig: 3.3/1 The ZZgarb in all its glory!**

This is a standard histogram produced from OFDA data in the range 1 to 175 microns from the midside sample of Tag:C23.

![Histogram](image)

Every goat examined by the authors during the expected cashmere growth period has shown some evidence of the ZZgarb. This applies to many “breeds” of goat in many countries. Goats selected for milk and meat still display a ZZgarb. In some cases the fibres may appear to be outside the accepted cashmere diameter range, but they appear to be down type fibres none-the-less.
The mode of inheritance of the ZZgarb remains unknown. Evidence from this study suggests it responds to selection in an additive way. Winter (1985) proposed a simple way to improve down weight by selection for down length. Graham & Bell (1990) explain the relationship between down production and fibre diameter and provide “expected performance” tables for 1, 2 and 3 year old bucks. These tables were compiled from a survey of 509 AWTA tested bucks from all parts of Australia. The Patrick Index (Snippet May 1989 p28) quantifies this relationship in the form of a regression curve, such that animals of different down diameter can be compared for relative genetic performance. With some reservations as explained under the heading YYgarb these references were likely quantifying the performance of the ZZgarb.

In Table 2.2/1 originally presented in Section 2.2 “What Do We Know About Down Production?” reports heritability figures from three different flocks of three different origins.

| Table 2.2/1 Heritability estimates for Cashmere characteristics (with standard errors) |
|-------------------------------------|----------------|----------------|----------------|----------------|
| Total Flick Wt | Down Wt. | Down Diam. | Down Lngth. |
| Couchman & Wilkinson (1988) | 0.14 ±0.08 | 0.20 ±0.06 | 0.32 ±0.11 |
| Gifford et al (1989) | 0.42 ±0.16 | 0.36 ±0.13 | 0.70 ±0.19 |
| Pattie & Restall (1989) | 0.29 ±0.11 | 0.61 ±0.18 | 0.47 ±0.15 | 0.70 ±0.19 |

Those of Gifford et al (1989) from selected down bearing animals of South Australian origin, heavily classed for traditional style. Those of Pattie & Restall (1989) were sampled at random from the Cobar region of Western NSW and mated at random to produce the next generation, because of this they had a low average annual down production of 49.6g. Both these estimates were likely derived from fibre populations predominantly based on the ZZgarb.

The estimates of Couchman & Wilkinson (1988) on the other hand, are around half the average of the other two estimations in all characters under consideration. These estimates were obtained from selected down bearing animals with some angora ancestry and an average annual production of 172.3g down. Couchman & Wilkinson were very likely dealing with the product of two (or perhaps more) combined populations the (ZZgarb + YYgarb). Given that these are probably inherited independently (and it seems likely), this would explain the lower measured heritability.

The YYgarb
This is the base fibre population from which the Mohair goat was probably derived. It is proposed that the YYgarb can exist in Cashmere, Cashgora and Mohair goats. These animals all belong to the one species, Capra hircus, the primary difference between each of these classifications is in the mean fibre diameter and range of the YYgarb population.

Project investigations suggest that the ZZgarb and the YYgarb both coexist and are independently inherited. It is suspected that all goats have a ZZgarb, but some may not have the YYgarb

At the cashmere end the YYgarb is very refined, and due to selection, produces a fairly cashmere-like fibre. The YYgarb shows as a tail on a normal cashmere histogram (ZZgarb + YYgarb). The tail results from the combination of the high population numbers of the ZZgarb with the generally smaller population of the YYgarb, extending the total fibre population into the higher micron range. Moylan & McGregor (1991) describe in detail the fleece properties of the Fauré Island goat (an island off the coast of Western Australia). These goats produce a range of attractive, commercially usable fibre, in the Strong Cashmere to Fine Mohair range. They are a specialised selection of what is more generally known as the Cashgora goat. This goat is still described as (ZZgarb + YYgarb) with both populations contributing in varying proportions to the total effect, depending on whether the animal is strong cashmere or fine mohair. The normal cashmere histogram will have a more prominent tail, becoming broader as the influence of the YYgarb increases.
At the extreme end of the YYgarb range is the Mohair goat. The fate of the ZZgarb at this point has not been investigated. Theory would suggest it is still there – buried and totally overshadowed by mohair.

**Fig: 3.3/2 The (ZZgarb + YYgarb)**
This is a standard histogram produced from OFDA data in the range 1 to 175 microns from the midside sample of Tag:B103. Note the two marked fibre populations that combine to produce the skewed histogram

---

**The ‘Non Hair’ Garblets - DDgarblets (Down Garblets) and MMgarblets (Mohair-like Garblets)**
At the time of writing more work was required to fully delineate the “Non-hair” garblets. It seems unlikely that these correspond exactly to the Hair-garblets. The only exception seems to be the Bib and maybe an area around the britch. There is no garblet equivalent of the Trousers. The Trousers are thought to be exposed areas of the underlying garbs.

**The Scarf Garblet**
Project observations suggest that the strongest (higher diameter) down fibre will always be found on the neck of the animal. This has been confirmed by fibre sampling at each point and subsequent fibre diameter measurement. This particular garblet would seem to be fairly persistent. It would seem to be independently inherited. The animal photographed has a ‘cashmere style’ DDscarf although on close examination it is 2 to 3 microns stronger than the main fleece. It is proposed there is an MMscarf form, in which fine mohair mingles with the underlying ZZgarb to produce a ‘Cashgora Neck’
The Bib Garblet
The Bib area in some animals can display prominent fibres of at least 3 types, depending on the time of year – short guardhair (HH), ‘cashgora’ type (MM), and down (probably the underlying garbs). The Bib is usually the point where shedding begins. An animal with good down coverage sheds to expose coarser down or ‘cashgora’ coverage, which in turn, may shed to expose hair. It is tentatively proposed that an MMbib capable of independent inheritance exists. More work is needed to define its relationship with the HHbib and the three garbs.

The Waistcoat Garblet
The position of the Waistcoat is shown in Fig: 3.3/4. There is considerable variation amongst animals in the type of fibre covering this region. The most desirable types have a dense even coverage of cashmere over the entire body with little variation in mfd from front to rear. Less desirable types have a range of stronger fibres covering the Waist Coat region. This suggests basic genetic control.

There are some complicating environmental influences – age, nutrition, health and sex all affect the degree to which this characteristic is accentuated when present.

The MMwaistcoat is a clearly defined garblet. It is suggested there is no DD or HH equivalent. The fibre population of this garblet varies from obvious mohair fibre down to cashmere. In many cashmere animals the MM fibres are so fine as to be acceptable as a component of the cashmere fleece. A more extreme example is shown in the accompanying photograph.

---

Fig: 3.3/3
The Scarf Down Garblet

Fig: 3.3/5 Graphic illustration of sudden change in fleece type
### ‘Non-Hair’ Garblet FPU’s

<table>
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<th>Genetic Control</th>
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<td>Mechanism that determines DD/MM fibre diameter is unknown.</td>
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4. The Down/Guardhair Microcosm

This was explored using three separate techniques …

1. The Fibre Draw – a time honoured textile technique in which the fleece sample is carefully laid out in an orderly manner on a black velvet board. This assists visual appraisal and allows an assessment of composition, fibre length, fibre diameter and surface morphology.

2. The manipulation and study of raw OFDA Fleece Test Data – a computer data manipulation technique that yielded a wealth of valuable information on the relative contributions of fibres of different diameter.

3. Growth Pattern Measurement – a technique in which changes in down length at a midside sample point were measured and charted on a monthly basis.

The combined data from these explorations was used to develop an understanding of the Down/Guardhair Microcosm.

4.1 Fibre Draw Measurement Technique

As a part of this project, a 'mapping' technique was developed from the "fibre draw' used for many years by Topmakers to examine the length structure of fibres in a Top.

In the procedure as developed, a small sample of fleece is clipped from the animal at skin level from the Midside position. (Position of test was standardised to mid side 10cm to the rear of the shoulder bone, on the Left Hand Side – see diagram.) This position is well clear of the influence of any “Waistcoat”.

The sample fibres were then carefully drawn over a black velvet covered board, such that the fibres are spread evenly, ie. at constant density, across the board aligned on a base line from the longest to the shortest. The individual fibres that make up the staple can then be readily seen, enabling measurement of their length and a quantitative assessment made of the relative percentages of Down and Guardhair. Measurements were taken with the same ruler as outlined under Fleece Growth Pattern.

Fig:4.1/1 Midside Fibre Draw – mixed Down/Guardhair fibres arranged by fibre length.
This technique would be of considerable use to Growers in assessing, by comparison, the finer fleece differences between two or more apparently similar animals. For example in selecting Bucks. It is similar to the technique taught to Growers by Mr. Geoff Smith (Technical Director, Dawson International Plc.) in the early 1980s. Its major drawback is the high degree of skill required to prepare a draw that will accurately and reproducibly reflect the true nature of the sample. We were fortunate that Robert Pearce had developed this skill from many years practice in the Wool Topmaking industry.

Fibre Draw Mapping enables direct evaluation of the relative fibre contributions to the total fleece. Length relationships and distributions, can be studied - for fleeces from the same animal over the growing period, or individual animal fleeces at a similar point in the growth cycle.

The draw can highlight in a qualitative way the different components of mixed fibre populations. Figure 4.1/2 shows a sudden change in length of the down fibre – suggesting two distinct down populations.

Draws of this nature were noted for both down and guardhair. (See discussion of results – later in this section.)

**Limitations of the Draw**

Two limitations of the fibre draw had to be addressed – quantifying the result and storage of the drawn sample for future reference. The draw can be stored for future reference by photography, or transferring it from the velvet board to a sheet of black card using a strip of clear adhesive tape. The tape system was found to be clumsy and required a lot of additional handwork. Photography was deemed to be impractical. Some effort was made to record the image using a digital scanner with limited success. Three years on - the advent of the inexpensive digital camera would seem to be the ideal tool. In the end it was decided to store the samples in their raw form and quantify the observed physical characteristics of the draw by measurements that could be stored and manipulated.

Longest, Median, and Shortest lengths for both Down and Guardhair were recorded. These lengths are measured from the base line to the tip of the fibres at the respective positions along that base line. The median point is the baseline midpoint for each of the fibre types. This is usually a simple matter as the two types are generally clearly separated into distinct distributions. If, as occasionally occurs, some intermingling of the distributions is evident, it is necessary to assess the relative midpoints by judgement, or in difficult cases to separate the mixed fibres into their places using small tweezers.

A visual estimate was made of the down yield for each draw. (Visual “volume” of down relative to “volume” of total fibre.)

**Fibre Diameter measurements**

A fibre diameter measurement was taken, and recorded to one decimal place, on samples of fibre drawn from each of the longest median and shortest down populations. This was done using an optical microscope with calibrated graticule following the technique proposed by Browne & Cooper (1985). 100 fibres were measured and the mean fibre diameter and Coefficient of Variation of diameter calculated by computer. A provisional trial was run to establish the accuracy of the optical microscope in this situation and it was found that mfd results were repeatable (at worst) ±0.25 micron. The absolute microscope calibration was done using a calibration slide marked in 0.001 mm intervals. The results from this microscope were generally comparable with measurements taken using the OFDA and LASERSCAN systems.
Storage and Assessment Software

A special software segment was added to the Cashstud Program to speed collection and aid analysis of this data. This program performed any necessary calculations on each record.

Fig: 4.1/3 Draw Analysis – recorded information could be "tagged" A and/or B and/or C.

Fig: 4.1/4 Draw Analysis – data tagged “A” saved as Group4 and ready for export to MSExcel.
The software was designed to allow the draw data to be sorted into “sub-sets” these sub-sets could be given a group number and exported to MS Excel for graphing and further analysis. This concept of groups allowed the draw data to be “mixed and matched” in a series of sometimes exclusive and sometimes overlapping combinations that could be explored in a wide variety of graphical ways. The Cashstud Ver: 6.05 program, the original entry data, and all derived data files are available on the CD that comes as part of this report.

Results:
A total of 336 Fibre Draws were produced over the first two years of the project. All animals were represented - most up to 3 times. Fibre draws were done for all animals twice in 1998. The first samples were taken 6th January 1998 the second set 3 months later on the 5th April 1998. A comparison of the two draw series provided a picture of the changes taking place at the Midside over an acknowledged growth period. A third series of draws were done for all animals the following year as a guide to consistency and annual variation.

The data for the two draw series was sorted using the Cashstud program and exported as two CSV (comma separated value) files readable in Microsoft Excel:
- DrawSub1 AllAdult6_1_98.CSV. (n = 85)
- DrawSub2 AllAdult5_4_98.CSV. (n = 109)

The data for each series was then combined into a common file (DrawChange JanToApl98.xls). Only animals with data in both series were included. Columns were added to the file to calculate the Change in all measured characteristics over the three-month period and the Change%.

The relationship between the various columns of data was examined graphically using the wide array of tools available in MS Excel. Correlations reported are expressed graphically.

The results of these exploratory ventures were interesting and in some cases surprising.

Down - Comparing Median and Mean
Part of the planned investigation was to explore the relationship in each animal, between measured characters at the Median (physical mid-point of the fibre draw), as well as at the Long and Short ends. On full analysis of all data, an examination of the errors involved led to the conclusion that the raw Median data was unreliable except in general terms.

Down - Comparing Long and Short
The investigation of the Long and Short end of the draw was more productive. The longest fibres could easily be extracted and measured. The results were very reproducible. In practice, the Short end was all fibres left when the decision was taken to terminate the draw. So the Short measurement was of a group of fibres that contained, but was not necessarily representative of, the shortest fibre. For the purpose of this analysis this error was considered acceptable and the Short end fibres were treated as being of uniform length.

The Chart (Fig 4.1/5) plots the change in length over a 3 month period (representative of the growth rate) of the ‘Long’ end and the ‘Short’ end of the fibre draw. There are about 7 animals in which the Long and Short end of the down population increased at the same rate, possibly suggesting that just one fleece population is involved. At higher growth rates of the Long end, there seems to be no relationship between Long and Short. This may suggest, that in these animals, there may be independent fibre populations associated with either end of the draw.

Growth rates measured by this method, show that around 70% of the project animals grew down at better than 10 mm per month, the best animals doing over twice this rate.
Change in down length of ‘Long’ & ‘Short’ fibres over a 3 month period

Animals in order of increasing change in ‘Longest Down’

Fig 4.1/5: Plots the change in Down Length (over a 3 month period) for the longest fibres in a draw and the shortest fibres in the same draw. The ‘Long’ and ‘Short’ plot for each animal are aligned side by side. The animal pairs are then aligned in order of increasing ‘Change in Long Down’.

Down - Comparing Fibre Length and Mean Fibre Diameter

Within Animal Comparisons
All draw results, without exception, show that within the down components of an individual animal fleece there is a direct relationship between the fibre length and the mean fibre diameter of the sub-sample under consideration. As the down gets longer the mfd increases. Table 4.1/14, for example gives figures for two bucks Z124 and Z125.

This is a well known fact and novice breeders typically fall into the trap of thinking a “longer fleece is a stronger fleece”. This is not actually the case!

Between Animal Comparisons
Figures 4.1/6-7-8 examine the relationship between the mean fibre diameter of a data-subset (Long or Short) and its length. The first two charts show the result for the ‘Long’ fibre end of the draw and the ‘Short’ fibre end of the draw respectively. The third chart plots the ‘Change in Length’ (representative of the growth rate) of the ‘Long’ fibre end of the draw against the mean fibre diameter of the Long data-subset as measured at the end of the measurement period (5th April 1998).

Between animals - there is no apparent correlation between fibre length and fibre diameter for either the Long end, or the Short end down data-subsets in a fleece. This fact has major implications for the industry. Given the commercial reality that it is important to hold the mfd of fleece within certain limits – the only practical options for increasing clean down production are to produce more fibres per unit area of skin, or to increase down length which requires increasing fibre growth rate (length/unit time).
Fig 4.1/6: Plots the down length of the ‘Long’ end of the fibre draw against the mean fibre diameter of the sub-sample. The animal pairs are then aligned in order of decreasing MFD. As sampled at 5/4/1998.

Fig 4.1/7: Plots the down length of the ‘Short’ end of the fibre draw against the mean fibre diameter of the sub-sample. The animal pairs are then aligned in order of decreasing MFD. As sampled at 5/4/1998.
Fig 4.1/8: Plots the length of 3 months down growth (representative of Growth Rate) for the ‘Long’ end of the fibre draw, against the mean fibre diameter of the sub-sample. The animal pairs are then aligned in order of decreasing MFD. As sampled at 5/4/1998

**Down – Growth Rate**

Figure 4.1/8 shows clearly the, between animal, comparisons for fibre growth rate plotted against mfd for the Long draw data-subset of the 85 measured animals.

*There is also no apparent correlation between fibre growth rate and fibre diameter. It should be possible to select for fast growing, long down while holding mfd constant.*

In view of the importance of this finding it was decided to investigate further the possibility that the lack of correlation between growth rate and diameter may have been due to inaccurate data.

Measurements for mean fibre diameter of the long end of the draw were taken at the beginning and end of the 3 month growth measurement period. These mfd measurements were made on two independent samples taken from the midside sample site. For this reason there was some variation of the ‘before and after’ results in some animals. Of the 85 animals, 59 had ‘before and after’ measurements that fell within ± 1 micron of their average result. The measurements for these animals are listed in full in Table 4.1/1, and charted in descending order of average mean fibre diameter in Figure 4.1/9.

It can be seen from the chart that there is no correlation between fibre growth rate and average mfd of the selected data subset. A regression analysis of the data subset confirmed this, producing a value of $R^2 = 0.0395$. 
Table 4.1/1: Fibre length and mean fibre diameter measurements of the ‘Long’ draw data subset – for the 59 animals that had ‘before and after’ measurements that fell within ± 1 micron of their average mfd result.

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Coping with what seems a contradiction

To better understand the apparent conflicts in the ‘down length (growth rate) / mfd relationships’ … consider the analogy of two pine plantations, both with the same ‘genetic potential’. Within each, there is a range of trees. Consider one growing on poor soil and one growing on good soil. There is a relationship between height and diameter within a plantation, governed by a set of ‘within plantation’ genetic rules.

Between plantations, it is the soil fertility that governs the growth rate and height and this has nothing to do with the ‘within plantation genetic’ rules.

This is an imperfect analogy, because the natural systems under consideration are driven by different fundamental mechanisms, but it serves to illustrate that height/diameter relationships can be controlled by more than one mechanism.

Aspects of Down Growth Rate

Several aspects of down growth rate were investigated. Fig 4.1/10 charts the subsequent increase in down length, over a 3 months period, against the “Starting Length” as at 6/1/1998. This chart is for the ‘Long’ end of the fibre draw. The chart shows something of the different growth rhythms between animals, even under the tightly controlled nutritional and environmental conditions of the project. The animals with the longest down on the 6th of January in general terms grew less down over the next three months than did the animals with the shortest down on the 6th of January.
Subsequent change in down length against Start Length at 6/1/98 (Long)

Animals arranged in decreasing order of Start Length

Fig 4.1/10: Plots (for the ‘Long’ end of the fibre draw) the subsequent increase in down length over a 3 months period against the “Starting Length” as at 6/1/1998. The animal pairs are then aligned in order of decreasing Start Length.

Change in Guardhair Length Vs Change in Down Length

Animals arranged in decreasing order of Down Length

Fig 4.1/11: Charts change in Guardhair Length over a 3 months period, starting on 6/1/1998; against change in Down Length over the same period. The animal data-pairs are aligned in order of decreasing Down Length.
Guardhair

Fig 4.1/11: charts change in Guardhair Length (growth rate of guardhair) against change in Down Length (growth rate of down) over a 3 months period, starting on 6/1/1998 – on a between animal basis. There would appear to be no correlation between the growth rates of the two fibres. This suggests that the down and guardhair populations are independent in their actions and independent in their inheritance.

Fig 4.1/12: plots data-pairs for each animal - the length of Guardhair at the ‘Long’ end and ‘Short’ end of the guardhair fibre draw. There is no obvious relationship or pattern between the two. This could suggest different fibre populations influencing each end of the draw.

The AAgarb

A better understanding is needed of the workings and inheritance of the AAgarb. A midside draw diagram of the Buck A011 shows two distinct length distributions in the Guardhair population, this is suggestive of a second overall Hair Garb (BBgarb). This is also supported in the discussion on Fig:4.1/12.

Fig 4.1/13 Midside draw of Buck A011 showing two separate guardhair populations that did not overlay each other in any way.
The short haired guardhair coat was the most common in the project animals. Long and intermediate forms of guardhair do exist. The question arises, are they all manifestations of a variety of alleles at the same locus – or – are the observed phenotypes combinations of additional populations (e.g. AAgarb + BBgarb) – or – both. Earlier in this report (Section 3.2) the possibility of a BBgarb was considered on circumstantial evidence. The draw of Buck A011 is definitive and there is no doubt that two guardhair populations separated by a significant gap of some 20 mm in length exist. This would be one of the aspects worthwhile investigating as a future project. The basic data should be fairly easy and cheap to collect. The elucidation may provide some clues to the action of loci covering the down populations.

The use of the Fibre Draw in investigating the consequences of mating decisions is illustrated in Section 3.2 Draw diagrams for the Sire Dam and Progeny of a mating show how it is possible to trace the changes in fibre populations.

**Further evidence in support of the concept of the ZZgarb and YYgarb**

The principal bucks used for mating in the first year of the project investigations were Z124 and Z125 these were both high yielding bucks with very little guardhair. Their pedigree was not known, they could have been related. At first glance they looked like twins, but they were not identical twins. The fibre draws of both bucks, taken as 1½ year olds, are of interest. Both show two down populations.

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The shorter (Down 2) population seems to be the same in both cases (within the ± 0.25 micron limits of accuracy of the diameter measurements). The fibre diameter measurements taken show a tight range around a mean of 14.0 microns. The actual population mean fibre diameters are shown in the attached table. The Down 2 mfd’s were taken at the ‘Long’ and ‘Median’ position on the actual draw (see Fig 4.1/2), the Down 1 mfd at the ‘Short’ position.
4.2 The Innovative Use of OFDA Data

Developing a good understanding of the Down/Guardhair Microcosm was difficult. The seemingly endless array of apparent fleece types was hard to quantify. A crucial aid to developing some understanding of the situation turned out to be the Raw Data delivered by the OFDA (Optical Fibre Diameter Analyser).

The OFDA is a computer controlled optical microscope that feeds its image to a television camera and from there to the controlling computer for analysis. Its primary advantage is its ability to measure at a reasonable cost and with acceptable accuracy the full spectrum of fibre diameters found on a cashmere goat. (Browne, 1991). The OFDA was originally developed by BSC Electronics in West Australia in conjunction with Melden Laboratories. An initial trial (Browne, 1990, personal communication) in April 1990 demonstrated its potential value for cashmere measurement. With the encouragement of the ACGA and project funding from RIRDC the OFDA was eventually developed to provide a method of fibre diameter measurement and a calculated estimate of yield (Peterson and Gherardi, 1994). It is now widely used by growers for routine fibre measurement on breeding animals.

A number of organizations offer a fibre measurement service using OFDA equipment. The Project measurements were carried out by Performance Wool Testing Service. The Project is indebted to Mr Grant Hornell for his assistance in providing the raw data in addition to the test results.

The full value of the Raw OFDA Data has not previously been recognised

To date OFDA measurement data has only been used to produce a Cashmere Fibre Histogram with an upper limit of 35 micron and an estimate of Yield. The raw data contains, in addition, valuable information on the entire fibre population of an animal and the relationship between the various components.

A technique for converting and charting the raw data using an excel spreadsheet on a normal home computer was developed. This technique, which we have named an “Ofdagram”, became the primary tool used to explore the Down/Guardhair Microcosm. The technique is fully described in Appendix A.

In addition to being an excellent investigational tool the Ofdagram would be useful in any on-farm breeding program. It provides a graphical depiction of all the fibre populations at the sample site. It draws attention to fleece differences not easily seen by the human eye. It would be particularly applicable to the selection of bucks. Here, there is an opportunity to apply selection pressure to characteristics, which for practical “number” reasons, may be deemed unacceptable in breeding does.

With a sires 50% influence on any breeding program, a little care taken with their selection will pay big dividends. Under the current, widely used “macro” selection methods, a buck’s fleece is often only considered in terms of colour, Mean Fibre Diameter, Yield and Down Weight. Often the final choice is a “hunch” selection from a large group of generally acceptable animals. Information gleaned from the Ofdagram will enable selection pressure to be applied to a number of important additional fleece characteristics.

Raw OFDA data – what you get.

The Raw data delivered by the OFDA is presented in a comma-delimited format. As originally presented the data file, which has an “.SP1” extension, can be opened in a spreadsheet program such as Microsoft Excel. It contains …

A header - which details:
- OFDA machine identification.
- Last calibration date and details.
- Name of the Testing Service.
- Customer Name, Test Operator.
- Date of measurement.
Measurement records (the actual measurement dataset):

- Each record is one cell or field. It contains the animal Tag Number (or other identification number) followed by the fibre count for each fibre diameter step. This data is separated by commas and starting at 1, rises in 1 micron steps.
- Multiple measurements may be taken for each fleece. These appear as additional records. The acceptable number of test records for each fleece is determined by the level of agreement between measurements.

The fleece measurement service uses this information to print a histogram, plotting fibre count for each diameter step against diameter.

**Calculating Yield**

To calculate Yield, the assumption is made that Down and Guardhair are of a similar specific gravity and their volumes are then directly related to the contribution of each to overall Fleece Weight. It is also assumed that the length of all fibres in a “Minicored” sample, prepared for measurement using the OFDA, are the same. Therefore length can be neglected and the cross-sectional area of fibres in each Micron Step can be used to represent the relative contributions of each Micron Step to overall fleece weight.

After the elimination of constants the formula to calculate OFDA Yield is as follows:

\[
\text{OFDA yield (\%) = } \frac{\text{(Sum together in 1 micron steps to 35\(\mu\) (} d^2 \times n \text{) )}}{\text{(Sum together in 1 micron steps to 175}\mu \text{ (} d^2 \times n \text{) )}} \times 100
\]

Where:  
\[d = \text{diameter of fibre} \]
\[n = \text{number of fibres}\]

The above formula assumes a figure of 35 microns as the transition point between down and guardhair – this is a fairly arbitrary figure. Initially Histograms covering the full diameter range from 1 to about 175 microns were printed. Selecting a scale suited to the far more numerous down population means the coarser fibres, which are much fewer in number register as small valueless blips. As a result most measurement services chose to present a printout cropped at an upper limit of 35 micron.

The importance of knowing something about the other fibres that contribute to total fleece weight was recognised, but not resolved. Nixon (1999), suggested plotting the values using a Logarithmic scale for fibre count. This in itself has some limitations.

**Converting and Charting the Data**

The raw data from the OFDA measurements on the project animals for the July 2000 shearing was converted into a row and column format and saved as a Microsoft Excel file. For this report, a format where each record is a row and each micron level a column, was adopted.

The OFDA measures and counts a relatively large sample – usually between 3,000 and 4,000 fibres per run, which equates to between 12,000 and 24,000 fibres per sample. The measurement process requires that there be reasonable agreement between runs. Where agreement is poor, more measurement runs are done on each sample. It is normal practice to discard individual runs that vary widely from their contemporaries. For this project it was decided the most accurate picture would emerge from averaging the results of all runs.

The data and subsequent calculations were charted using Microsoft Excel. The steps involved are described in detail in Appendix A.
Results
OFDA measurement data based on a mid-side fleece sample taken at shearing in July 2000 was processed and analysed in detail. The data was drawn from 66 animals (18 bucks and 48 does). Four measurement runs were done on 44 of the 66 samples. Six measurement runs were done on 22 of the 66 of animals.

Some 230 charts were created and examined. The amount of data collected and analysed is too extensive to present in the body of this report. The base data and a selection of 198 charts are included on the attached CD.

The project animals had been deliberately selected to cover a range of “High Producing” fleece types, including Strong Cashmere and one or two in the “Downey Cashgora” range.

The charts created for each animal, based on the average of all runs for that sample (a Dataset) is shown in Figure 4.2/1

![Figure 4.2/1 A Plot of Fibre Count against Diameter, for the Diameter Range 1 – 175 micron](image)

This is a traditional, full range Histogram. Its main purpose is to give an overview and to show clearly the distribution of the down population.

To get a better understanding of the “Non-down” components of the fleece the vertical (Y or value axis) was adjusted to a more suitable scale. This scale depended a little on the fleece under investigation, but usually had a maximum value of 20. (Figure 4.2/2)
Fig: 4.2/2 A Plot of Fibre Count against Diameter, for the Diameter Range 1 – 175 micron Using enhanced vertical scale.

Fig: 4.2/3 An Ofdagram - a Plot of Fibre Area (Volume) against Diameter for range 1-175µ
THE OFDAGRAM (Figure 4.2/3):
This plot represents the relative contribution of each “Micron Step” to total fleece weight.
Strictly this plot is based on Fibre Area. As it can be assumed that the “Minicored” fibres used for
OFDA measurement are all of the same length, this plot can be considered as Fibre Volume against
Diameter. Assuming further that the Specific Gravity of Down and Guardhair fibres are similar, this
plot can be considered as fibre weight against diameter.

A variety of other charts were often created during the process of investigating individual areas of
interest. These were quickly and easily created using the same raw data. The beauty of this
technique, as an exploratory process, is the quality of the graphic output and the ease and speed at
which a data set can be manipulated.

Discussion
The graphical evidence examined demonstrated in all cases that the total fleece is made up of at least
two distinct fibre populations – the Down and the “others fibres”. This is not new information. Wal
Clark, in the very early days of the industry told new growers that the Down grows from secondary
follicles and the Guardhair from Primary follicles.

It is an obvious deduction that the “other fibres” include at least one population of guard hair. A
close examination of the charts suggests that “guardhair” could itself be a composite population -
made up from, say, an independent population of short “kemp” fibres and another population of
longer hairs. Figure: 4.2/3 is an Ofdagram of the combined product of six separate OFDA
measurements on the midside sample of Tag: C21. How many “non-down” populations can you
see?

A considerable time was spent trying to discover a mathematical process that could be used to
separate and define these possible populations. The authors are deeply indebted to Professor John
Browne (whose lifetime interest has been the probabilistic modelling of systems) for his help, advice
and experience in trying to extract the maximum value from this data. Unfortunately no such
mathematical process could be found.

The fine “mohair like” fibres present on some animals were easier to see, but again ‘impossible’ to
prove mathematically. There was however, sufficient evidence from other sources to define the
concept of the YYgarb. Fig: 3.3/2 The (ZZgarb + YYgarb) shows the two outlined fibre populations
that combine to produce the skewed histogram.

The Ofdagram could be a very valuable tool for aiding decisions in on-farm breeding programs. A
discussion of the application of Ofdagrams is covered in Sections 5 & 6.
4.3 Down Growth Patterns

- Measurement Techniques
- Rates of Growth
- Discussion

To date the discussion of the inherited components of fleece production has been based in one dimension. At the most favourable point in time – does a genetically controlled “consequence” happen or does it not?
In practice this is simplistic – with cashmere fleece production there is an element of … “now you see it! – now you don’t!”

Time-Rate of Growth
Superior forms of growth rate (eg. continuous throughout the year) if identified, would potentially favour greater fleece weights and provide a valuable selection characteristic - if genetically based. Additionally, knowledge of such rate/s may provide guidance for fleece weight maximisation through identification of appropriate shearing times and frequency.

As environment factors such as feed levels and climate stress were largely controlled, this component of the investigation sets out to consider if time/rate growth patterns are genetically controlled.

Measurement technique:
- Equipment and method of use.

The equipment used for this test consisted of a specially prepared ruler with the measuring end commencing exactly at 0 mm., graduated at 1mm., 5 mm., and 10 mm. intervals and 150 mm in length to allow for ease of use. The animals were restrained, as for shearing, to restrict their movement and allow for more accurate measurement.

The position of measurement was standardised to mid side 10cm to the rear of the shoulder bone, on the LHS.
Measurements were made of down fibres, from skin level to point at which tip taper commences, with the end of the ruler being positioned at a staple root end as it joins the skin. The staple was laid out with just sufficient tension to straighten it along the ruler, and the length noted. Guard hair fibre (which may be longer or shorter) was ignored. The length of staple was then recorded against date and animal tag number, together with fleece shedding status (if present) and other relevant observations such as kidding or sickness.

- Accuracy and reliability.
A 'blocky' down fibre tip allows for more reliable measurement to nearest 1 mm. The more usually occurring, less well defined down fibre tip, was more difficult to measure with this accuracy; measurements being taken to the nearest 5 mm.

Measurement error was minimised by ensuring the one operator took all measurements. The reliability of the comparative month to month result was similarly enhanced.

- Frequency of test.
Tests were taken monthly within 2 days of each mid month date
Measurements of this type were commenced after Aug.1998 shearing on 13 selected animals (11 does and 2 bucks), and extended to all adult animals (juvenile, maiden and mature) after shearing July 1999.
Rates of Growth (Results)
A total of approximately 2000 measurements, together with associated observations on fleece shedding status at time of measurement, and month of shearing and kidding etc., were taken. As all measurements were taken at one point on the mid side they are only truly representative of the down population covering that region. Further if more than one down population is active at this site they represent the combined activity of all populations, with the longest fibres of any population at the time of measurement determining the result.

These measurements together with notes assisting the evaluation were entered in a Microsoft Excel Spreadsheet in a format suitable for graphical representation. A series of charts were created depicting the measured fleece length against time, for each animal. These are included on the CD attached to this report.
Ref: Monthly Time Rate of Growth Spreadsheet, Sheet 1 including comments, and Charts 1 - 10.

NOTE: the Excel graphical representation of the point of shearing or shedding is a sloping line, joining the ‘before’ and ‘after’ plot. This can be confusing - to be strictly correct, the line should drop vertically.

Time-Rate of Growth patterns were examined:
1. To identify similar and repeating growth rate patterns, if any, including any 'growth pause' period.
2. To examine correlation of growth pattern with animal status (fleece shedding, kidding, age, sex).
3. To determine if growth rate patterns may be genetically controlled.

Year 1999/00, was the first year in which complete measurements of monthly fleece growth were taken on a significant number of animals. It is also the first year in which a significant amount of 'double shearing' was undertaken.

‘Double shearing’ is defined as shearing twice per year, a traditional July/August time, plus mid-cycle at February/March. The decision to shear an animal was based on observed fleece length and visual evidence of shedding. Shearing was not undertaken at a down length under 40mm. This length was considered a minimum commercial requirement. It was thought desirable that such 'double shearing' should occur at 70 - 80mm. – well within the capability of many of the animals. Ref. Charts.

Time-Rate of Growth - Discussion
In general terms the animals followed the typically understood growth pattern originally outlined by McDonald (1985). The does tended to shed in response to kidding stress and often did not resume down growth until after weaning. Bucks slowed their growth and often shed in March/April in response to the onset of the rut. Non pregnant young females tended to grow at a constant rate with little change throughout the year.

Measured Growth Rates
Rates of growth were interesting and seem to have a genetic base, but there was insufficient data to quantify relationships between groups. The worst average rates recorded were around 10 mm down growth per month. The best was provided by Z002, a 4 year old doe who consistently grew at the rate of just over 20 mm/month. The ‘B’ Tag does, mostly sired by the one buck Z124, were very consistent in their performance, and for most of the growing season, averaged around 15 mm/mth. Allowing for differences due to ill health or social upset, animals seemed to be consistent between years in their average fibre growth rate, suggesting that growth rate was under some form of genetic control.

These measurements were confirmed by those taken using the Fibre Draw (Section 4.1). The ‘Long’ end of the draw in over 70% of measured animals grew at greater than 10 mm/month. The fastest growing down was on Z092 with an average measured growth rate of 23 mm/month over a 3 month period. This compares very favourably with feral does that typically grow at 4-8 mm/month.
**Length Trigger**

There is a suggestion of a “length” trigger that stops growth when a certain length is reached. This limit appears to be somewhere between 10 cm and 12 cm.

---

**THE KEY TO INCREASING DOWN PRODUCTION**

For a given mfd and a given fibre density per unit skin area – ‘Growth Rate' (down fibre produced/unit time) is the fundamental component of down production.

The ‘Time-Rate of Fibre Growth’ and Fibre Draw measurements, together, lead to one of the most important findings of this project.

‘Down Growth Rate' and Down Mean Fibre Diameter are independently inherited traits that do not seem to be correlated in any way.

- For a given mfd ‘Down Growth Rate’ is easily measured as ‘Change in Length’.
- There is considerable potential for selection - the measured growth rate in the best project animals was up to 3 times the growth rate of better feral animals.

---

**On Farm Usage**

There is some potential to refine this technique for use in an on-farm situation. It is simple to implement and may highlight the differences in fibre production between animals. One refinement of this, used with great success at Karakan for many years, was to collect a small sample following measurement (cut where the fleece leaves the skin). These samples were taped in a book with clear tape and provided a pictorial record of fleece growth. This aid proved invaluable in aiding culling and mating decisions.
5. Outcomes

5.1 Getting it all together – Conclusions

The race is not always to the swift – nor the battle to the strong, but that’s the way to bet!

This pearl of wisdom from an unknown author encapsulates the spirit of these conclusions?

The authors propose a new way to view animal fleece production. They propose a model, that based on their investigation, conforms completely with their understanding of the intricacies of the Cashmere, Cashgora, Mohair and Merino wool growth. The proposals are unproven in detail although supported in fact. They may not be correct - but that’s the way to bet!

There is ample documentation to prove that many aspects of Cashmere down production by individual animals are under genetic control. Cashmere down is just one component of a composite fleece that grows on a ‘Cashmere Producing’ animal. It stands to reason, that opportunities to improve down production per head, lie with the genetic manipulation of the components that make up the animals fleece.

The ultimate monetary return to the grower, from the sale of cashmere fleece, is a function of the amount and quality of down produced, less the cost of production and less the cost of downstream processing to achieve the final consumer product.

 Genetic gains can be applied to two areas:
- Increasing quantity and/or quality of saleable down.
- Manipulating guardhair to an optimum level (a trade-off between protection of the growing fleece, the downstream dehairing cost and the final product quality).

Taking it step by step from the beginning …

The FPU

It was assumed at the beginning of this project that observed phenotypic fleece production could be broken down into a number of independently inherited, contributing parts. The concept of a Fleece Production Unit (FPU) was developed. FPU’s were perceived as individual units of inheritable activity. Ten FPU’s were identified and are listed in Section 5.2 Table of Results.

Cashmere Down is of primary interest, and increasing Down production the primary goal.
This report however looks at Fleece Production as a whole. From the animals point of view Cashmere Down is just one of the components of the total fleece. It seemed important to understand all the competitive influences that might effect Cashmere Down production in order to develop an understanding of how down production could be improved. The down and guardhair populations were shown to be independent in their actions and independent in their inheritance.

Irrespective of its effect on down production, the reduction of hair content in a saleable fleece has important commercial considerations. The lighter the guardhair loading the easier the commercial dehairing process and the better and longer the dehaired product. There are significant price premiums paid by the market for higher yielding raw product and for greater fibre length in the final dehaired Cashmere.

This report has demonstrated that there are a number of contributing fibre populations that could turn up in a commercially acceptable cashmere fleece. Commercial acceptability is a function of the overall effect of the combination, which is as much a function relative to quantity, as it is of type. A full investigation of these fibre populations, their interactions, their inheritance and their quantitative operating mechanisms is an enormous task and not achievable within the scope of this project.
Sections 3, 4 and 5 of this report cover a limited investigation of some of the more prominent of these fibre populations and their interaction. Where possible an attempt is made to speculate on their form of inheritance. The investigational tools used are discussed in detail and the large amount of data collected is presented on the CD

**Between animals, there is no apparent correlation between fibre growth rate and fibre diameter.**
This fact has major implications for the industry.
It should be possible to select for fast growing, long down while holding mfd constant.

Given the commercial reality that it is important to hold the mfd of fleece within certain limits, the only practical options for increasing clean down production are to produce more fibres per unit area of skin, or to increase down length which requires increasing fibre growth rate (length/unit time). Section 4.1 provides substantial evidence to support this finding.

**Garbs and garblets**

Of the fibre populations under consideration there seem to be two types – those covering the whole body (with, perhaps, the exception of the extremities) and those which are regional.

It is proposed by this report, that all identifiable populations be named, to facilitate their common identification and further investigation. The ‘whole-body’ populations have been termed ‘garbs’. The regional populations termed ‘garblets’. Naming individual garblets is easy, and in most cases is self descriptive. Naming garbs is more complex, and a naming convention for all populations, that allows for variation in allelic performance at a population locus, has been proposed and used.

**Garbs**

It is proposed garbs exist for all types of fibre. At the time of writing three have been defined, two down garbs and one hair garb, and there is evidence to suggest a second hair garb. There may be others.

The AAgarb (overall coat of long, medium or short guardhair) is described and an example of its inheritance given. Fibre Draw and Ofdagram results suggest a second overall hair garb the BBgarb may exist. The inheritance and interaction of the hair garbs are still to be delineated. In the sheep, and the South African and Texan Mohair goat, it seems that the hair garbs have been genetically ‘switched off’. No evidence was found of a similar switch in the Cashmere goat.

The ZZgarb (classic cashmere fibre) is discussed together with comments on its operation.

The YYgarb (the likely origin of mohair) is also discussed together with the role it plays in Cashmere, Cashgora and Mohair fleeces.

Evidence of the existence of, at least, the three named garbs is compelling. They can be seen on a fibre diameter histogram manipulated in the right way (the Ofdagram) and they can be seen in the Fibre Draw (Section 4.1) of the few animals where the populations do not overlap.

**The Ofdagram**

The garbs were studied in detail using a new technique (developed during this project) to enhance and depict the previously “under-used” data available from OFDA fibre measurement devices. This technique was called an “Ofdagram”. On-farm Ofdagrams would be useful in defining more precisely the fleece characteristics of breeding animals – particularly bucks, where you often have a large choice, of seemingly similar animals. A “How-to” kit was developed for on-farm use. Details of this are given in Appendix A of this report.

It is possible that there are additional garb populations to the three mentioned. A study of Ofdagrams based on a mid-side fleece sample taken from project animals, deliberately selected to cover a range
of “high producing” fleece types, (including Strong Cashmere and “Downey Cashgora”) proved inconclusive. The eye suggests the possibility of additional garbs, but their existence was unable to be proven mathematically, despite a considerable effort in this regard.

A parallel interaction of “garbs” is presumed to operate in sheep with the ZZgarb being the dominant influence in the Superfine/Extrafine Merino, and the (ZZgarb + YYgarb) being the basis of the Peppin Merino. It is presumed that the Lincoln sheep is the equivalent to the Mohair goat and is an extreme development of the YYgarb. The AAgarb in goats seems to have been eliminated in most wool growing sheep – it is not likely to be represented by the Carpet wool alleles in New Zealand sheep, these are likely to be mutations, probably of the YYgarb.

Garblets
Garblets are regional patches of fleece that overlay the main garbs. The major garblets in the cashmere goat have been identified and named. The naming convention adopted was that of an article of clothing that might be worn in a similar manner.

Garblets are regional patches of fleece that overlay the main garbs. The major garblets in the cashmere goat have been identified and named. The naming convention adopted was that of an article of clothing that might be worn in a similar manner.

The naming of a garblet indicated whether it refers to down (DD\text{name}), mohair (MM\text{name}) or hair (HH\text{name}). For example MMbib refers to an “overlay”, sleek, shiny, fibre population that covers the front of the goat running from just under the chin down to the brisket.

The project studied in detail a number of the hair garblets. These seem capable of independent inheritance and some suggested mechanisms were proposed. A summary of these is given in Section 5.2. It is not known, at this time, whether a DD and/or MM companion garblet exists for each identified hair garblet. This seems unlikely. A great deal of work remains to define precisely garblets and their interaction.

The proposed model of garbs and garblets goes some way to explaining the development of the merino sheep from its primitive form, and the effectively kemp-free mohair goat.

\textit{It is the Authors belief that the general concepts proposed in this report will stand the test of time.}

\textit{The proof of the pudding is in the eating!}

Table 5.1/1 shows an example of the potential for rapid genetic progress that comes with the manipulation of single locus characters. The buck Z124 removed (in one generation) the BackMane garblet, the Bib garblet and the Britch garblet from a significant proportion of its progeny. The full details are covered in Section 3.2

During the course of the investigation - Buck Z124, a high yielding buck with very little guard hair, was mated to does that had been randomly selected for the characters under consideration. The estimate of character frequency for the dam group is for the group from which they came – not the dams themselves. It is approximate only.
<table>
<thead>
<tr>
<th>Character</th>
<th>Dam Group observed Frequency %</th>
<th>Progeny Group observed Frequency %</th>
<th>Expected Frequency %</th>
</tr>
</thead>
<tbody>
<tr>
<td>No Back Mane K-</td>
<td>15%</td>
<td>47%</td>
<td>43%</td>
</tr>
<tr>
<td>No HHbib Bb-</td>
<td>9%</td>
<td>29%</td>
<td>39%</td>
</tr>
<tr>
<td>No HHbritch Bh-</td>
<td>47%</td>
<td>76%</td>
<td>65%</td>
</tr>
</tbody>
</table>

The EXPECTED FREQUENCY is the expected progeny result assuming the characters recorded in the table are all recessive characters, in a simple dominant/recessive relationship. It further assumes the Buck Z124 was a homozygous recessive for all characters in the table and was mated to a dam group with the character frequency listed in the table.

Table 5.1/1  Example of rapid genetic gains possible in just one generation, for single locus characters, with simple dominant/recessive inheritance.

5.2 Table of Results

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>AAgarb: Overall guardhair long/short (and what else?)</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td>Comment (Sex Linked?)</td>
<td>Sex Linked – No</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Other References</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Further Questions</td>
<td>Intermediate forms of guardhair do exist. Are they all manifestations of a variety of alleles at the same locus – or – are the observed phenotypic combinations of additional populations? A BBgarb may exist.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>HHbackleg: Regional long guardhair/short (and what else?)</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td>Comment (Sex Linked?)</td>
<td>Sex Linked – No</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Other References</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Further Questions</td>
<td>Is this ON/OFF or are there a range of manifestations.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
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<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>HHwithersMane: Very persistent</td>
<td>Unknown</td>
<td>Medium</td>
<td>Unknown</td>
</tr>
<tr>
<td></td>
<td>Comment (Sex Linked?)</td>
<td>Sex Linked – Unlikely</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Other References</td>
<td>Suggest equivalent remnant still in today’s sheep population.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Further Questions

**Why is this so persistent?**

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>HHbackMane: On/Off ? (K)</td>
<td>Single Locus</td>
<td>High</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?)  
K+ dominant, Sex Linked – ?.

Other References

Further Questions  
Once switched ON – what regulates growth activity? Can a Buck be K-?

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>HHneckMane: On/Off ?</td>
<td>Single Locus</td>
<td>Medium</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?)  
Is the presence of Neck Mane sex-linked? – not sure.

Other References

Further Questions  
Suggested single locus control - requires clarification. Are Neck Mane and Back Mane controlled by the same growth processes?

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>6</td>
<td>HHbritchHair: On/Off ? (Bh)</td>
<td>Single Locus</td>
<td>High</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?)  
Bh+ is dominant to Bh-. Sex Linked – Unlikely.

Other References

Further Questions

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>HHbibHair: On/Off ? (Bb)</td>
<td>Single Locus</td>
<td>High</td>
<td>None</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?)  
Bb+ is dominant to Bb-. Sex Linked – Unlikely.

Other References

Further Questions

<table>
<thead>
<tr>
<th>Ref No</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>Scarf ‘Non-Hair’ Garblet: MM and possibly DD</td>
<td>Single Locus?</td>
<td>High</td>
<td>Age, nutrition, health, sex</td>
</tr>
</tbody>
</table>

Comment (Sex Linked?)  
Sex Linked – Not sure

Other References

Further Questions  
Mechanism that determines DD/MM fibre diameter is unknown.
<table>
<thead>
<tr>
<th>RefNo</th>
<th>FPU</th>
<th>Genetic Control</th>
<th>Certainty</th>
<th>Environmental Modifiers</th>
</tr>
</thead>
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<td>Age, nutrition, health, sex</td>
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<td>Waistcoat ‘Non-Hair’ Garblet: MM and possibly DD</td>
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Comment (Sex Linked?) Sex Linked – Not sure
Other References
Further Questions Mechanism that determines DD/MM fibre diameter is unknown.
6. Implications and Recommendations

- For the Industry
- For the Practical Breeder
- Suggested Future Research

6.1 For the Industry

Cashmere Goats - Understanding these concepts and using them as the basis for a selection program

The Raw Material
The first requirement for genetic production gains in any endeavour is the existence of individuals with superior performance in the characters under consideration. The wider the genetic variance the greater the potential gains. Smith Clarke & Turner (1973), first drew attention to the existence of cashmere characteristics in the Australian Feral Goat and drew attention to considerable phenotypic variance in the animals assessed. In the late 1970’s and early 1980’s entrepreneurs working on phenotypic variance of perceived production characteristics combed the Australian goat resource, both feral and domestic for superior animals. Appendix B gives the history of the Karakan herd and explains how the author Jim Browne and his wife Sheba personally assessed over 10,000 potential breeders to select 360 foundation does for the Karakan herd. In later times they were able to select from the selection of others, the Browne’s were able to purchase a small closed herd of 40 animals that dated back to the original 1972 CSIRO Selection.

Where significant phenotypic variance was not available it was created by cross breeding. Browne (unpublished) was able to ‘synthesize’ excellent cashmere progeny from carefully selected first cross Angora x Feral and Angora x Saanen animals. Bishop and Russel (1994) describe the development of a new ‘Scottish Goat’ from a very diverse base of British, Icelandic, Australian, and Siberian stock.

Major phenotypic gains have been made in Australian Cashmere breeding herds over the last 25 years by classing and selection. There is no doubt that much of the original gain in performance was made by selection. Some actual genetic gains were made by a few discerning stud breeders. These were often the result of planned cross breeding programs or in the case of Browne (unpublished) inbreeding/ linebreeding programs. For the majority of breeders, the gains made by selection were simply ‘fixed’ in perpetuity by their breeding programs. Growers quickly reached a production plateau and stayed there.

Manipulation using quantitative population genetics is a ‘shotgun’ approach.
This report proposes that any rapid and economic genetic manipulation of the fleece components first requires an understanding of the factors involved. Up to now, the great majority of research in this area has concentrated on quantitative population genetics and the identification and manipulation of ‘multiple character’ variance. This should deliver positive gains, but over a very long period of time – a luxury the industry cannot afford. There has been a focus on important components like down weight, mean fibre diameter and down length. There has been equal focus on some much less tangible and composite aspects of cashmere down production, like yield and total fleece weight.

A lot of time and effort has gone into establishing the heritability and genetic correlations of the end products, rather than that of the producing components.

The quantitative genetic manipulation of Cashmere goat populations based on variance and selection is, clearly and concisely laid out, in the excellent monograph produced by Restall and Pattie (1991).
The production plateau
For the majority of breeders, after the initial gains of selection – progress was very slow! Some adopted the population genetics approach. A Group Breeding scheme was established to spearhead gains and feed improved bucks and does back to the contributing herds. This failed to deliver an economic result and was abandoned. By the mid 1990’s, for economic reasons, a large number of breeders had left the industry or changed to goat meat production, using the newly imported Boer Goat.

The tragedy of this was that so much of the initial variance captured by earlier selection was lost. However what is left tends to be “the cream of the cream”.

Not all genetic gains involve increasing production
The elimination of guardhair garblets from the individual animal, will go a long way to improving dehairing efficiency (and therefore cost). The lighter the guardhair loading, the easier the commercial dehairing process, and the better and longer the dehaired produce. Both are prime commercial considerations. For most breeders, hair coverage on paddock reared goats will be a compromise dependant on grazing conditions. This is discussed in more detail under Implications for the Breeder.

There is no doubt the industry needs some real genetic progress
The authors see the report of this project as a first step.

Successful genetic manipulation requires:
- Identification of the individual genetic components involved.
- Some idea of their mode of inheritance.
- A series of breeding goals.
- A plan to get there.

Identification of the individual genetic components involved.
The report breaks down total fleece into components. The major components are defined based on a considerable amount of circumstantial and peripheral evidence. The defined components are only partially explored. There is much more to learn.

With the limited number of animals under study, and the limited time span of the project, the investigation was one of exploration aimed at defining a structural foundation, on which others could build. The report raises many questions, and answers only a few, but it is a start. It remains for others to try and fill some of the gaps, or perhaps even rearrange the concepts.

The authors have collected a mass of data, which is provided in digital form with the report. It may still hold many secrets. While remaining the copyright of the authors and RIRDC it is available to others for the legitimate purposes of criticism, review or expanding freely available public knowledge. It is not to be used without the author’s written permission for any form of commercial gain.

Some idea of their mode of inheritance.
Ten individual FPU’s have been identified. These are not proven, but an estimate of ‘Certainty’ is given. Their mode of inheritance is discussed in detail in the text. Nine of the ten FPU’s identified are thought to operate at a single locus. Most are thought to have a fairly simple dominant/recessive relationship.
A series of breeding goals.
Breeders need to develop their own breeding goals. Each Breeder’s needs will be different and will be influenced, primarily, by their production environment. Foundation stock, target market and complimentary livestock enterprises will all influence individual breeding goals. Section 6.2 - Implications for the Practical Breeder, cover this concept in more detail.

A plan to get there.
Genetic manipulation takes time. In the planning stage some thought needs to be given to the establishment cost and on-going maintenance costs of any program. The cost of finding and purchasing outside genetic material, in the form of sires or semen, may be considerable. Breeders should only attempt a plan they know they afford and can complete. Changing the goals from year to year is a recipe for disaster. Fortunately genetic gains are permanent and additive, and a properly managed program will pay continuing dividends. Section 6.3 - Getting Started (for the Breeder), cover planning in more detail.

Also in sheep
An understanding of fleece production in the goat will go a long way towards elucidating the quantity-and-quality fleece variation in the modern sheep.

There are also a number of wool quality issues, and breeding problems, that have never really been addressed over the years. It seems no one has really understood the fundamentals involved. The concepts developed in this report if applied to sheep could provide a new way of looking at classical sheep classing problems like pockets of ‘fibre diameter variation’, ‘Doggy’ wool and ‘Bad Backs’.

Harmsworth and Page-Sharp (1970) begin their definitive text on Sheep and Wool Classing with the following …
“Primitive sheep usually possessed an undercoat of wool combined with an outer coat of long hairy fibre. After generations of careful breeding, the hair fibres have been bred out of many modern types so they now produce a heavy fleece of high quality wool. However although many wool sheep have little or no hair their wool nevertheless varies widely in type, quantity and quality.”

No doubt the Cashmere Goat has the potential to develop along parallel lines. The Genomes of the two species are so close that a study of the genetic basis of fleece production in one - becomes a study of the genetic basis of fleece production in the other – displaced in time. The Australian cashmere goat of today, represents a “genetic snapshot” of the “Australian sheep” of the early 1800’s, before the creation of the modern Australian Merino. The analogy is that of the Astronomer, who studies the birth of the Universe by looking out into space and back into time.

The mechanism of transition in sheep
So what was the mechanism of transition from primitive-fibre-producer to the modern Merino wool-sheep?

Browne (unpublished) has studied this in some detail. Assuming the Merino started from a similar base as that outlined for the Cashmere goat - there are many possibilities, the most probable would seem to be…

Possibility 1: The development of the ZZgarb into wool, the elimination of the YYgarb (longer stronger down), the AAgarb (hair), and all the hair garblets, and probably the majority of down garblets.

Possibility 2: The development of both the ZZgarb and the YYgarb into a composite wool population with a dual genetic root. The elimination of the AAgarb (hair), and all the hair garblets, and probably the majority of down garblets.
Possibility 3: The development of the YYgarb into wool with the suppression, or elimination of the ZZgarb. The elimination of the AAgarb (hair), and all the hair garblets, and probably the majority of down garblets.

Possibility 4: The development of both the ZZgarb and the YYgarb and some or all of the Down Garblets, into a composite wool population, with a multiple genetic root. The elimination of the AAgarb (hair), and all the Hair Garblets.

Possibility 5: Any one of the down fibre developments outlined in possibilities 1 to 4, combined with retention, elimination, suppression or modification of one or more of the Down garblet or Hair Garblet populations.

Browne’s studies would suggest that all these mechanisms were probably involved and that a number of parallel developments produced the major strains of the modern Australian Merino.

Superfine/Ultrafine Merino
It seems likely that the Superfine/Ultrafine ‘Saxon’ sheep of Victoria and Tasmania are the result of Possibility 1. Their wool is a very uniform population of fine fibres with a Diameter histogram very close to that of the ZZgarb illustrated in Table 3.3/1 (without the hair population). Low Mean Fibre Diameter (MFD), symmetrical distribution curve and low coefficient of variation (COV). All pointing to a single base fibre population.

Peppin Merino
The ‘Peppin’, a ‘Middle Micron Merino’, exhibits all the characteristics expected of Possibility 2. - extra clean fleece weight, higher MFD, higher COV, more visual within-staple variation of the wool fibre.

Strongwool Merino
The true South Australian Strongwool could well be a development of Possibility 3. While generally having a higher fibre diameter than the Peppin, the fibre characteristics suggest the wool has its origin in a single fibre population.

Strain differences are much more obvious in commercial sheep than they are in stud animals where heavy selection keeps the phenotypes fairly tidy. They were also more obvious thirty years ago than they are today. The heavy selection pressure placed on MFD over the last twenty five years has wrought major changes in the fibre structure of the Australian sheep flock.

The Mohair goat
The findings of this report also have some relevance to the Mohair Goat. There is an emphasis on different fibre population elements, but the principles are inherently the same. Many of the fleece faults in the mohair clip have their origin in the “primitive’ fibre populations found today in the cashmere goat. The authors believe that mohair is a development of the YYgarb. In Mohair animals of minimal fault, it is probable that all of the hairy garblet populations have been eliminated by selection.

Other fleece bearing animals
It is the authors belief that the same mechanisms and principles as discussed in this report are likely to apply to a wide range of fleece bearing animals. Not only to other members of the Family Bovidae, but even extending at least as far as the Family Camelidae. The Dromedary (Camelus dromedarius), the two humped Bactrian Camel (C. ferus bactrianus), the Lama (Lama guanicoe...
glama), the Alpaca (L. guanicoë pacos), the Vicuña (L. guanicoë vicugna): all exhibit a very similar fleece structure and a similar cycle of growth.

6.2 Implications for the Practical Breeder

The findings have many implications for the practical breeder. They provide a new way of looking at the performance of individual animals. Given that the theory has some basis (and selection using the theory will soon determine that) a breeder can now concentrate on the rapid elimination of individual, undesirable fleece characteristics from the flock.

A word of warning!
The information derived from this project will likely allow the breeder to rapidly reduce, or even eliminate, the protective guardhair covering from the goat. The authors have no doubt this is possible and some of the project animals came close to this goal. The management implications of this are considerable in un-shedded flocks. The hair plays a role in protecting the cashmere from the environmental elements, (the type of hair is an important dehairing consideration). Hair helps prevent cotting, the collection of vegetable matter and ultra-violet degradation. These problems were solved in the modern wool growing sheep by increasing the grease content of the “down” to a level of about 30%. However at the fine end of the merino clip, (in the Cashmere micron range) to get the best fibre price, sheep are either rugged or run under the ‘Sharlea’ (shedded) system. With Ultra Fine Merino they do both.

In addition, high yielding animals growing large amounts of cashmere, with very little hair seem more sensitive to post-shearing stress. In a pastoral environment, without some form of shedding or rugging, off-shears losses with this type of animal will be high.

This said – the lighter the guardhair loading, the easier the commercial dehairing process, and the better and longer the dehaired produce. Both are prime commercial considerations. For most breeders, hair coverage on paddock reared goats, will be a compromise dependant on grazing conditions.

Practical Breeders should consider adopting some of the techniques developed in this report.

Use OFDA measurement and extract additional information using an Ofdagram Extracting and using additional information from OFDA tests (as outlined in Appendix A) should be useful in identifying and quantifying “intermediate” and other unwanted fibres, such as Flexible Guardhair. The refined OFDA data should be particularly useful in buck selection, where it can be used to identify the subtle, but important, fleece differences between apparently similar animals.

Consider on-farm fibre growth measurement and start a fleece ‘Scrap-Book’ Breeders should consider introducing regular fleece length measurement (as outlined in Section 4.3) on all animals. It is simple to implement and should enable the ready identification of animals with high growth rates of down. With time, fibre growth measurement will also allow the breeder to build a picture of their flocks response to seasonal conditions. The measurements will highlight the nutritional and management conditions that maximise fibre growth. They will also define precisely when fibre stops growing prior to shedding. This may suggest a better time for shearing.

If it is considered impractical to measure all animals – breeders should create a nucleus flock and measure all animals promoted to the Nucleus. Typically replacement bucks would be selected from the Nucleus.

One refinement of regular length measurement, used with great success at Karakan for many years, was to collect a small sample following measurement (cut where the fleece leaves the skin). These
samples were taped in a book with clear tape and provided a pictorial record of fleece growth. This reference proved invaluable in aiding culling and mating decisions.

**Introduce Garb and Garblet assessment**
Consider recording a Garb and Garblet assessment on all animals. Theoretically, this need be only done once in an animal’s lifetime. In the early days of this assessment there will be much to learn and skills to develop. Breeders should run subsequent assessments on the same animal twice or more in a growing season until they are confident of their results.

**Set Breeding Goals**
The breeding goals of most cashmere flock owners could be summarized as …
(More & finer cashmere on goat) + (Bigger animals & more kids) = (more money in the bank).

Only a few breeders have given any thought to what the productive cashmere animal of the future may look like.

It is most important, before embarking on any selection practices suggested by this report that a breeder using the concepts of this report construct a “goal model” of the goat they wish to produce. They should then consider how this model will fit their management environment and adjust any selection process accordingly.

**Getting Started (for the Breeder)**

1. Decide on **YOUR** ideal goal model.

2. With this in mind review all breeding animals along the lines suggested in this report. Remember sometimes an animal is worth keeping and using, because it excels in some particular character, even though it may fall short in other aspects. By careful mating you can often ‘capture’ the excellence in progeny that have a better balance in the other characters. Animals with a ‘high down growth rate’ and a ‘high down mfd’ are an example. Mate them to very fine animals and some progeny will likely perform well in both characters.

3. Identify the contributing components to your flocks fleece production. They may be similar to those in the report, or you may find others. Remember these should be ON or OFF (present in some & absent in others) fleece components. If there seems to be too much variation – try to break the observed item into further pieces. If the component occurs in every animal in your flock, seek the opportunity to examine other flocks for its absence. If you can find just one case of an animal that does not display the character of interest, then it is likely that this is a heritable component and that it will respond to selection.

4. Consider any need to purchase outside genetic material in the form of sires or semen.

5. Record each identified component on the animal’s record.

6. Where pedigree information is available, consider reviewing a component on a pedigree basis. Look for a pattern of inheritance – this may help you make later breeding judgements.

7. Having completed all the previous steps, make a list (in priority order) of the components on which you intend to place selection pressure.

8. Commence selection – remember, it may be counter-productive to select on too many components at once. Remember also, to look carefully at the culls to ensure you are not unintentionally eliminating the best examples of other useful characteristics. If you intend to work on eliminating the Mane - then March is a prime time to accurately classify animals for growth of Mane segments – late enough in the season to show reasonable growth, and early enough not to be buried.
6.3 Suggested Future Research

The new ideas and concepts presented in this report are in their very early days. Adequate and elegant additional proof of the major suppositions would provide a firm base on which to build an intimate knowledge of the genetic basis of cashmere production. This in turn would open the way to understanding all forms of animal fibre production.

Some of the following tasks could be achieved by supervised, co-operative industry effort. Perhaps as part of an industry 'Benchmarking' program. Some of the more important questions could be answered by small programs with very little overhead costs.

Tasks are listed by priority number. This is a number indicating their perceived order of importance.

1. What are the controlling factors and mode of inheritance of down fibre growth rate?

Genetic manipulation of down fibre growth rate holds the key to any major increases in down production. The key findings of this study are that fibre growth rate is independent of fibre diameter and a wide range of growth rates exist.

The identification of animals with high growth rate fibres, and a study of their follicular structure, the effects of nutrition on follicle development, and the identifications of the genetic alleles involved, would seem high priority topics. This information would be a basic requirement of any transgenic manipulation, aimed at improving production.

1. What are the down fibre growth rates on various regions of the animal – as distinct from the midside?

1. Is down growth rate a constant within the Fibre Draw subset of a Garb or Garblet population?

1. More information is required on the concept of overlaying fleece populations.

A lot of valuable information should be gleaned from a detailed (across body) Ofdagram study of selected animals. This should be a very cheap project with a prompt result. The study should try to link the observed garblet populations with the Ofdagram results.

A refinement of this would be an across body Ofdagram study of sire/dam/progeny of selected matings.

With careful subject animal selection, a great deal of new knowledge could be gained.

2. More information is required on the definition and genetic inheritance of Garblets.

This task would be a prime candidate for co-operative industry effort. Breeders who are able to keep track of progeny pedigree data, could be provided with a small software program to enable them record the sire and dam of an animal and to collect and record information on a clearly defined set of Hair Garbs and Garblets. The digital files would be emailed to a central collection analysis data base. Given that the inheritance of HHgarblets would seem to be simple, and their presence or absence easy to classify, (even without 'cross link sires') two or three generations of this data should enable the precise definition of HHgarblet inheritance.

At the time of writing more work was required to fully delineate the “Non-hair” garblets. A more ambitious project might include DD or MM garblets, although these may be harder to classify in the field. It is tentatively proposed that an MMbib capable of independent inheritance exists. More work is needed to define its relationship with the HHbib and the three garbs.

2. Nutrition and Fibre Growth

For a given animal, under a given nutritional regime …

Is (Down Production + Guardhair Production) = a constant …?

Would eliminating hair garblets allow more nutrients to be partitioned to down growth?
2. Has the AAgarb been correctly defined? What is the mode of inheritance?
A better understanding is needed of the workings and inheritance of the AAgarb. A midside draw diagram of the Buck A011 showed two distinct length distributions in the Guardhair population, this is suggestive of a second overall Hair Garb (BBgarb).

The ‘short haired’ guardhair coat was the most common in the project animals, and this was thought to be dominant to the ‘long haired’ coat. Intermediate forms of guardhair do exist. The question arises, are they all manifestations of a variety of alleles at the same locus – or – are the observed phenotypes combinations of additional populations (eg. AAgarb + BBgarb) – or – both. This would be one of the aspects worthwhile investigating as a future project. The basic data should be fairly easy and cheap to collect. The elucidation may provide some clues to the action of loci covering the down populations.

2. What fibre populations are identifiable in the Mohair Goat?
A study of fleece macrostructure, Fibre Draws and Ofdagrams of a range of Mohair goats may provide valuable confirmation of the concepts put forward in this report. The fate of the ZZgarb would be of interest. Theory would suggest it is still there – buried and totally overshadowed by mohair.

The detailed fleece differences between the traditional Australian, the Texan and the South African types may give some clue as to the existence or mechanism of ‘inheritance of ‘Kemp reduction’.

2. Is there a genetic ON/OFF switch for the AAgarb in Cashmere Goats?
There is evidence of such a gene switch in Merino sheep and Mohair goats - Texan and South African animals have quickly reduced the kemp levels of the Australian Mohair Clip. Does such a switch exist in Cashmere goats.

3. Is there a “Hair Growth Regulator”?
There is a wide variation in prominence of the Back mane, when it is seen to exist. This suggests some related influence that regulates ‘Back Main growth’, once it is ‘switched ON’. A study of photographic archives, suggests this same “Hair Growth Regulator” may be common to all hair patches on the animal. Further work is required to answer this question.

3. What is the mode of inheritance of down fibre diameter?
The authors suspect this could be complex. It is not clear what part follicle morphology, or follicle depth in the skin, play in controlling fibre diameter. It is suspected that the follicles of the ZZgarb (in its more primitive form) are not embedded very deeply in the skin, and that the classical annual shedding process is caused by the death, and sloughing, of the surface layers. It is suggested that fibre diameter may be related to follicle nutrition, which could be a function of the depth in the skin.

3. What is the cause and importance of ‘Hetero fibres’?
During the course of the investigation, notably during microscopic diameter measurement, a number of examples were observed and measured, of individual fibres which changed diameter along their length from 'hair' diameter to 'down' diameter, or from 'down diameter to 'hair' diameter. Knowledge of the contributing causes of this phenomenon may hold an important key to an understanding of fibre creation and follicle function.

4. Why is the withers mane so persistent? What is its mode of inheritance?
6.4 How relevant are the findings of this report to non-Australian goat populations?

Luikart, et al., (2001) studied the mitochondrial DNA sequences from 80 of the 105 recognised breeds of goats. They found "Goat populations are surprisingly less genetically structured than cattle populations. In goats only 10% of the mtDNA variation is partitioned among continents. In cattle the amount is 50%. This weak structuring suggests extensive intercontinental transportation of goats and has intriguing implications about the importance of goats in historical human migrations and commerce." Luikart, et al. suspect that goat genes (flow) travel rapidly because goats are more transportable and also because they represent smaller and more durable units of wealth than cattle.

Browne (from early Australian records in the Macquarie Library, Sydney) established that goats arrived in Australia with the First Fleet. In the early years of settlement they were the major domestic animal. A study of the annual variation in goat numbers of the colony of New South Wales for the period 1795 to 1805 suggests ongoing imports in considerable numbers, a major proportion of which seem to have been killed for rations. Introduced goats would appear to have come from a great variety of backgrounds and they accommodated readily to the Australian environment. Browne (Personal observation on travels in Inner Mongolia, P.R.C) recognised many phenotypes as being similar to the Australian Feral Goat. In addition to this, selected Australian Cashmere goats, have been exported for breeding purposes over the last 15 years, to USA, France, UK, and South Africa, with semen exported to USA, Canada, France UK and South Africa. - Browne (personal records).

It would seem that the findings in this report, (except where noted), could be reasonably expected to apply to most down bearing goats in most parts of the world.
7. Bibliography

Internet: On–line Databases

**GoatMap database (the mapped Genome of the Goat)** - Institut National de Recherche Agronomique, Laboratoire de génétique biochimique - 78350 Jouy-en-Josas, France.
http://locus.jouy.inra.fr/bovmap/goatmap

**Online Mendelian Inheritance in Animals (OMIA)** is a database of gene and phene (familial trait or phenotype)  http://www.angis.su.oz.au/Databases/BIRX/omia/ Editor F.W. Nicholas, Faculty of Veterinary Science, University of Sydney, NSW 2006, Australia.
email: frankn@vetsci.usyd.edu.au

The Online Mendelian Inheritance in Animals (OMIA) is the online version of MIA (Mendelian Inheritance in Animals – database). OMIA currently contains bibliographic details for 7850 publications on 1111 traits across 32 species. All of the disorders with a known molecular defect (currently 28) are included.

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7. Appendices

- A – Converting Raw OFDA data for further analysis
- B - The History of Karakan Cashmere
- C - Gestation Period – for shedded Does
- D – Communication Strategy
  - Internet Site
  - Project Visitors
Appendix A

Making an Ofdagram

(Converting raw OFDA Data for further analysis)
The raw data created during the widely accepted, industry standard, OFDA fleece test, holds the key to an in-depth understanding of the test animals fleece structure. Section 4.1.2 of this report explains the value of additional information that can be gleaned from this data. This data is available from the testing service. It is currently not utilised. It can be further analysed using the tools commonly available on most home computers.

This additional information would be of particular value in the selection of sires to be used in a mating program. With a sires 50% influence on any breeding program, a little care taken with their selection will pay big dividends. Under the current, widely used “macro” selection methods, a buck’s fleece is often only considered in terms of colour, Mean Fibre Diameter, Yield and Down Weight. Often the final choice is a “hunch” selection from a large group of generally acceptable animals. The use of this additional data will enable selection pressure to be applied to a number of important additional fleece characteristics.

The Raw data delivered by the OFDA is presented in a comma-delimited format. As originally presented the data file which has a “.SP1” extension can be opened in a spreadsheet program such as Microsoft Excel. It contains …

A header:
- OFDA machine identification.
- Last calibration date and details.
- Name of the Testing Service.
- Customer Name, Test Operator.
- Date of measurement.

Measurement records:
- Each record is one cell or field. It contains the animal Tag Number (or other identification number) followed by the fibre count for each fibre diameter step. This data is separated by commas and starting at 1, rises in 1 micron steps.
- Multiple measurements may be taken for each fleece. These appear as additional records. The acceptable number of test records for each fleece is determined by the level of agreement between measurements.

The data is of limited use in this format and must be converted into a row and column format. The instructions below use a format where each record is a row and each micron level a column. This can be reversed if desired.
**Converting the Data**

The following instructions apply in detail to the most commonly used spreadsheet program Microsoft Excel, as found in Microsoft Office 2000. Most other business spreadsheet programs have similar features. In daily use the following steps could be automated by setting up a Macro. They are outlined below in full detail to give a complete understanding of the steps involved.

Before you start – make a backup copy of your raw data (just in case!).

The data is firstly converted to a Microsoft Excel file and given a name such as “XXXXgraph.xls” derived from the original test file (eg E794graph.xls).

**To achieve this …**

*Open the raw data* – Open Excel then go to **File/Open**, locate the raw data file, (select “All Files” in the file dialogue, as the filter, to see the “sp1” files).
Process this file through the Text Import Wizard:

Step 1 of 3 … Set Original data type to Delimited, the File Origin Windows ANSI, the Start import at Row should be set on the first measurement record, (eliminating all the data in the header).

Press Next button to select the next window.

Step 2 of 3 … Set the Delimiter to Comma, all other Delimiter settings should be deleted, the balance of settings on this window can be left at their default value as illustrated.

The data should now appear in columns. Press Next button to select the next window.
Step 3 of 3 … It should not be necessary to make any changes to this window.

Press **Finish** to convert your data to a row and column format.
The OFDA data is now formatted like a normal spreadsheet. Each row is a separate OFDA run for the Tag Number listed in column A. In the example shown four sets of measurements have been run on the C21 fleece sample. This would be typical.

Each spreadsheet column lists the fibre count for a micron measurement. Column B lists the number of fibres of 1 micron diameter, column C the number of 2 micron fibres etc., rising in 1 micron steps to an upper limit of about 175 microns.

Now is probably a good time to save the imported data in its new format as an XLS file. Using File/SaveAs, save the file with a given name such as “XXXXgraph.xls” derived from the original test file (eg E794graph.xls)

The next task is to add a column header listing the micron measurement for each column.
Click on the button for Row1 – the row is highlighted. Select Insert/Rss to insert a row above Row1. This new row becomes Row1.

Type the word Micron into cell A1. Enter the value 1 in cell B1. Highlight cell B1 and all the cells in Row1 from column B to Column FT.

Select Edit/Fill/Series ... to display the “Fill” dialogue. Set Series In to Rows, Type to Linear, StepValue = 1, StopValue = 175. Click OK. This will automatically fill out the correct Micron value for each column.

While you are at it - use the Insert process to insert 3 new blank rows at the end of each set of measurements (Data set). Example: Highlight Row6, select Insert/Rows – you will need to do this 3 times.
Each OFDA run could be graphed independently. The measurement process requires that there be reasonable agreement between runs. Where agreement is poor, more measurement runs are done on each sample. It would not be unreasonable to discard individual runs that vary widely from their contemporaries. It is probable however the most accurate picture under practical conditions will be given by averaging the results of all runs.

### To average results …

In cell A6 enter a title for the line. In cell B6 insert the formula =SUM(B2:B5)/4. This will sum all the data in cells B2 to B4 and divide the result by 4. If there are 6 runs then add the 6 cells and divide by 6.

The easiest way to replicate a formula through the spreadsheet is to use **Copy** and **Paste**. When pasting to a new region, the Spreadsheet will cleverly change the cell references to suit the new conditions. Highlight Cell B6 and press **Ctrl C** (Copy). Then highlight all cells from C6 to FT6, press **Ctrl V** (Paste).

Pick a couple of cells, at random and check that the formula has been applied correctly to the entire row.

Now copy the entire row and paste it into the empty row at the foot of each data set. Check from time to time, that you are getting the correct result. This copy process will only be correct where the number of rows in a data set is the same. A convenient solution is to paste to all the “four row” data sets first, then alter the formula and paste to the “six row” data sets etc.

### Fibre count only tells part of the story …

The data averaged so far is for fibre count. That is the number of fibres counted for each micron level. As explained in Section 4.1.2 of this report there is a lot to be gained by inspecting the fibre distribution in a fleece on a volume basis. The assumption is made that Down and Guard Hair are of a similar density and their volumes are then directly related to the contribution of each to overall Fleece Weight. It is also assumed that the length of all fibres in a “Minicored” sample, prepared for measurement using the OFDA, are the same. Therefore length can be neglected and the cross-sectional area of fibres in each Micron Step can be used to represent the relative contributions of each Micron Step to overall fleece weight.

### Calculating Cross-sectional Area for each Micron Step …

In cell B7 enter the formula =B6*(3.1416*((B$1/2)*(B$1/2))). This is simply the average Micron Count multiplied by the cross sectional area of a single fibre ($\pi r^2$).

$\pi = 3.1416$. **B$1** means - use B1 as an absolute cell reference (a reference that does not change if the formula is copied to another position in the spreadsheet).

Now copy this formula to every cell in the row as explained previously. Then after spot checking the result, copy the entire row to the end of each data set as illustrated.

Remember to save your file at regular intervals. It often helps to make a backup copy from time to time. If something goes wrong there is nothing more frustrating than having to start again from the...
beginning. A simple way to do this is to highlight the XLS file in Windows Explorer then press Ctrl C (Copy) followed by Ctrl V (Paste).

The finished spreadsheet should look something like this …

The hard work is done – now to the joys of discovery …

Graphing by Fibre Count …
Excel makes it very easy to chart the output of any spreadsheet. A wizard performs the basic steps. Each component of the chart can then be changed or enhanced as required.

Highlight the row you wish to chart. Select Insert/Chart. The first window of the Wizard appears.

Enter the Title of the Chart and any axis labels you wish. The legend is not needed with this type of chart. Click the **Legend** Tab and untick the Box.

Click **Next**

3. Create the Chart as a **New Sheet**. Enter a short name for the chart access tab.

Click **Finish**.

The final result ...
On the scale automatically adopted by the wizard to show all results – the Guard Hair population may not be very obvious. There are two ways to get a better look at the Guard Hair population …

1. Change the vertical scale
With the Chart on display click on the vertical axis (Y Value axis). The axis will be marked with some small squares top and bottom. From the top line menu select Format/Selected Axis. A window appears that enables you to change the axis settings.

Change the axis settings to match the illustration, or adopt settings more suited to your requirements.

The Maximum figure is the one to play with.

Plotting on a Logarithmic scale has some limitations. The base level for a Log scale is 1. Any numbers between 1 and 0 (eg. 0.5) will appear as “negative” bars. An annoying warning message will continually appear if any cells in the row contain a 0.00 value. To eliminate this message delete the 0.00 in each cell of the row.

In the following illustration a second chart has been created using the Wizard – the scale has been modified – and the modified chart given another name.
2. Charting Cross-sectional Area for each Micron step …

This is simply a matter of highlighting one of the rows used to do the area calculation for each data set, calling the wizard and following the previously outlined steps. The chart may look something like this …

The Ofdagram - while at first glance this chart seems the same – it is showing something very different …

Each bar is an estimate of that Micron steps contribution to the total fleece weight. As the fibre diameter increases the relative contribution of each fibre to the total weight increases. Refer to section 4.1.2 of the report for a full discussion of the implications.
Appendix B

The history of Karakan Cashmere

Goats came to Australia with the First Fleet. It has even been suggested, although there is no documentary evidence, that goats were liberated on the islands off the coast of Australia by Dutch and Portuguese navigators long before the British settlement of Australia. The introduced goats would appear to have come from a great variety of backgrounds and they accommodated readily to the Australian environment.

Prior to the gold rushes flocks of grazing animals, goats and sheep were controlled by shepherds. Most abandoned their charges in favour of making their fortune on the gold fields. The landowners then had to make some attempt at fencing their runs. Rudimentary fences could be erected to control sheep, who on large runs without fences would keep to the open plains. The goats were not controlled by fences and actively sought the rougher country as their grazing environment. Thus forming the large herds of wild (or feral) goats that became well established in much of inland Australia. Eventually the spread of settlement pushed these herds back into the semi arid sparsely settled areas of the country.

Cashmere was effectively rediscovered on Australian goats in 1972 when two CSIRO researchers Dr. Ian Smith and Mr. Wal Clarke identified cashmere on some feral goats under inspection at the property of The Australian Mohair Company at Brewarrina. For a number of years the CSIRO maintained a small research herd of selected animals at their Prospect laboratory until budget restraints forced their dispersal.

By the late 1970’s a number of breeders were toying with the concept of developing and breeding an Australian cashmere goat.

The ‘Karakan Cashmere Herd’ was established early in 1979 with 50 selected feral females from the Ivanhoe area in New South Wales. The foundation bucks were a brown feral and a ”Cashmere Type” from the ”Midnight Family”.

Over the next two years, a further 360 females, from a wide variety of backgrounds, were introduced. These animals were selected by screening over 10,000 goats from all parts of New South Wales and Southern Australia. A fortunate find was a small herd of 40 animals that dated back to the original 1972 CSIRO Selection. All animals were selected for ‘fleece growing potential’, frame size, and conformation of feet, mouth and udder.

Cashmere bucks from other bloodlines were introduced at various intervals between 1979 and 1986. Karakan also participated in a Group Breeding Scheme with Cashco and Woodstock herds, (before they were both sold to New Zealand), using two common reference sires.

The Breeding Program. From 1979 to 1989 all females were single sire mated and the progeny recorded against both sire and dam. Extensive progeny testing was carried out using objective measurement. All fleece testing was done by the AWTA using ‘Shirley Analyser’ and LaserScan technology.

Over the decade every breeding technique available was used, including ‘inbreeding’ of certain superior Sires. The massive amount of information generated was originally recorded on Punch Cards. This was converted to computer in 1984.

A spin-off from data analysis was the eventual development of the CashStud IBM computer program. This program with its sophisticated analysis tools, including an EBV (Estimated Breeding Value) option became the recording system of choice for major breeding projects in Australia, New Zealand, USA and UK.
Very rapid progress was made in measured down production. The first years production from the 50 foundation animals was just under 40 g/head of 14 – 16 um cashmere down. Production gains were tracked using Annual Fleece Sale Statistics. The following table lists the average production per head of the Karakan Herd over the decade. These figures are derived by dividing the Total Sale Weight of measured Cashmere (clean down basis), by the number of contributing animals.

<table>
<thead>
<tr>
<th>Year</th>
<th>Fibre Diameter</th>
<th>Yield</th>
<th>Down Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>1979</td>
<td>15.20 um</td>
<td>23.00%</td>
<td>39.60 g</td>
</tr>
<tr>
<td>1981</td>
<td>16.86 um</td>
<td>25.55%</td>
<td>44.25 g</td>
</tr>
<tr>
<td>1985</td>
<td>16.97 um</td>
<td>32.29%</td>
<td>141.60 g</td>
</tr>
<tr>
<td>1987</td>
<td>16.81 um</td>
<td>44.04%</td>
<td>200.98 g</td>
</tr>
<tr>
<td>1989</td>
<td>16.98 um</td>
<td>41.28%</td>
<td>234.45 g</td>
</tr>
</tbody>
</table>

Table 1. Average Clean Down Production/Head in the Karakan Herd.

Individual down weights show something of the potential. Karakan R662 won the ACGA National Fleece Competition in 1987 with 509g Down at 15.79 um. 69.4% yield. The buck Karakan R5251 winning its class in 1987 with 780g at 18.74 um. 60.7% yield. Over the years of the ACGA National Fleece competition Karakan and other herds have produced many animals in the range of 500 to 850g of down. At today’s prices these figures equate to $50 - $70 annual fleece production per head.

In 1991 the Cashmere industry world wide entered a period of severely depressed pricing. Syndicate mating of the herd was commenced and tagging of offspring at birth discontinued. A system of selection at shearing time was developed based on total fleece weight and a visual scoring system. Emphasis was placed on down length, style, and fibre diameter. The aim being to hold the herd at an average around 16.8 um while increasing down production.

FROM THIS – 1979 - 50 selected feral females  TO THIS – 1989 Cashmere breeding Does

Within two years this classing program had eliminated all ‘off’ types and low producers. Classing was done to a standard not to a number. The stud herd was reduced from about 1500 animals to about 650. Numbers were held at 650 from 1993 to 1997.

This change in program seems to have had some unexpected benefits. In 1993 it was noted that the animals were holding their fleece without shedding, longer than expected. The 1993 shearing was delayed for 2 weeks. It was delayed for a further 2 weeks in 1995 and again in 1996. In 4 years, the onset of shedding in the flock had moved from the end of July to the second week in September. In 1997 the animals were shorn for other reasons at the end of August with no sign of a shedding.
Yield % also seems to be visually on the increase culminating in the appearance of two animals, which as yearlings, were growing an almost pure down fleece.

In 1997 a selection was made of an elite 120 females and 3 males for a special project named Project KKN. The balance of the herd was sold to ICM Agriculture Pty.Ltd., Hillston NSW.
Appendix C

Gestation Period for Shedded Goats

While the following results apply strictly to "Karakan" Cashmere Goats under the project feed regime, they do provide a useful guide to the Gestation Period in Australian Cashmere Goats. All Does were mated and gave birth under strictly controlled conditions.

*Frequency Bar Chart showing the length of the Gestation Period in days for all Project Does in the 1998 spring kidding program. Range 145 - 153 days.*
Appendix D

Communication Strategy.

Establish Project Internet Site
The site has been established and can be accessed through www.cashmere.au.com (Note the '.au.com' is correct). We have tried to keep the site at a "common interest" level, and have received a number of favourable comments on site presentation and the interesting nature of the Project. We receive from time to time email comments on the project and requests for further information. Most of these emanate from USA.

Visits to the Project
Details of Visits of Prominent Industry Members to the Project.

Over the course of project KKN - 1A a number of prominent industry personnel visited the facilities at Clonbinane and were able to view the operations and discuss progress. Project objectives and implementation were discussed and the visitors views and comments were sought and incorporated into the plans.

July 1998. Dr Jay Hertzel Managing Director of Genetic Solutions Pty. Ltd.
This visit was aimed at providing Dr Hertzel with a background briefing on the project. Some useful discussion took place and the following comments by him are relevant:
1. The intensive management system is well developed although a few aspects remain to be sorted out.
2. The final list of traits, are yet to be determined, and this list and scoring systems should be a priority.
3. The mapping techniques developed have promise, and the separation of the two populations of cashmere and guard hair would be very useful.
4. With the standardization of the management/nutritional environment, the next crop of bucks/does will be very important for the project since the full pedigrees will be available.
5. The data set to be collected will be unique and potentially very valuable in providing baseline data from which to develop genetic hypotheses.

June 1999. Dr Peter McInnes Research Manager RIRDC.
This visit had the objective of giving Dr McInnes an overview of the project and its management. The program for this visit included:
1. Examination of the established feeding and management systems.
2. Demonstration of the Testing and Evaluation methods in operation and being developed.
3. Demonstration of the Cashstud 6.0 recording and data manipulation computer program and its use in the project.
4. Examination of the project animals.
Dr. McInnes reported that he was impressed with the implementation of the project.

November 1999. Mr Charles Esson, President ACGA; and Mrs. Bev. Foard, Prominent Industry member and TAFE Lecturer in Goat Management.
Together, visited the project at Clonbinane, primarily to acquaint themselves with the nature of the project, to view the animals and to discuss the implications of the work on industry directions.

Both expressed great interest and made a number of valuable suggestions and comments.
March 2000. Dr. Andrew James, Vice President ACGA responsible for Fibre Sales and Marketing.
During this visit the management systems in use were demonstrated, and considerable discussion took place regarding the progress and objectives of the research, as well as examination of a range of the animals both does and mature bucks.

Many valuable comments and suggestions were made by Dr. James, in particular his suggestion that the project should look to the development of a strategy to assist industry to select animals, taking into account:
1. Correlation between back mane and britch hair.
2. Correlation between withers mane and neck hair.
3. Guard hair length v. down length, and its assessment technique.
Dr. James reported that he was impressed by the management, health and fibre growth of the goats.

In addition Robert Pearce visited the commercial testing House of Performance Wool Testing Services (then in Perth Western Australia) in July 1999. This service is one of the main ones used by the Cashmere industry, and was seen as being likely to have a major input to much of our research.

As such it was considered important that we had a detailed knowledge of the testing procedure and the evaluation programs in use, in addition to that available from research reports.

Mr Grant Hornell of PWT went to considerable trouble to address our interest and comments. The implications of our work resulting from the basic digital measurement data provided by PWT are discussed elsewhere in this report