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SOME ASPECTS

OF

GENE DOSAGE EFFECTS

IN

N-TYPE SHEEP.

Thesis submitted in part
fulfilment of the degree of
Master of Science.

By

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PART I

PART I.

CHAPTER I.

G E N E R A L I N T R O D U C T I O N.

Section I. DR. DRY'S EXPERIMENTAL ROMNEY FLOCK.

In 1929 Dr. Dry at Massey College started simple breeding experiments on the inheritance of fleece characters in the New Zealand Romney. These included pronounced hairiness, i.e., substantial medullation in coarse fleeces. In newborn lambs with coarse hairy birthcoats, long coarse, hairy fibres, called by Dry Halo-hairs (1933, 1935) project above the rest of the birth coat. Lambs born were graded on halo-hair abundance (Dry 1933, 1935) Grade I having no halo hairs on the back and grades II, III, IV, and V an increasing number up to Grade VI, which had many. Experiments showed that in these lambs halo-hair abundance was inherited in multifactorial fashion.

However in 1931 a search for lambs with many halo-hairs was made in several stud Romney flocks, this leading to the discovery of oligogenes producing a high abundance of halo-hairs. One ram was received from Mr. N. P. Nielson of Tiakitahuna and became the founder of a stock carrying an incompletely dominant gene producing a great abundance of halo-hairs in the birthcoat far surpassing that shown by Grade VI. lambs showing this birthcoat were called N-grade in gratitude to Mr. Nielsen. The same gene appears to have been brought on to the College property in 1929 in a hairy ewe from which the foundation N-grade ram of the Massey-N stock was descended.

A Recessive-N gene, ordinarily producing N-grade halo-hair abundance in the homozygotes only, was also discovered. In 1935 the original Recessive-N ram was born, the double grandson of a hairy ram, bought and used in 1929

genotype lambs sustained a full abundance of halo-hairs at the front of the body much better than in the heterozygous Dominant-N genotype. In 1947 A. S. Fraser's analysis of stored data showed how to distinguish between homozygous and heterozygous Dominant-N sheep with a very small margin of error and to do this with maximum efficiency on birthcoat detail in newborn lambs. (Dry and Fraser 1947.) In heterozygous Dominant-N's there is almost always a rdduction in halo-hair abundance in a small armpit area just behind the shoulder called the shoulder patch. About 1 in 70 heterozygous Dominant-N lambs have no shoulder patch reduction. Homozygous Dominant-N lambs never show any reduction below N-grade in halo-hair abundance in the shoulder patch region. Even in the sheep studied in this thesis, one sheep, 300/48, a homozygous Dominant-N which possessed a weakly medullated array on the shoulder patch still had a full abundance of halo hairs.

Breeding experiments carried out by Dry (P.C.) have shown that the Recessive-N and the Dominant-N genes are certainly not allelic but the genetic analysis has not yet been carried far enough to show whether or not they are linked. The mating homozygous Dominant-N x homozygous Recessive-N thus produces animals of a fourth genotype, carrying one Dominant-N and one Recessive-N gene and called double heterozygote.

All told five genotypes were available for study, namely Non-N or ordinary flock Romney, heterozygous Dominant-N, homozygous Dominant-N, homozygous Recessive-N, and double heterozygote. Heterozygous Recessive-N's were not studied as their phenotype was very little different from that of ordinary Non-N Romneys. An exception to this is seen in Dry's "Dominoes", (Dry P.C.) but these, although of great theoretical interest are not typical heterozygous Recessive-N's. No sheep known to be of any other particular

abundance in lambs at birth and also of the presence or absence of horns in sheep of different genotypes, except for the rather anomalous position of the data relating to horns in the homozygous Recessive-N's,(Dry & P.C.) has shows that there seems to be a graded series in abundance of halo-hairs, and in horn characterization, in sheep of different genotypes.

The ordinary Non-N Romney genotype has the least abundance of halo-hairs over the body, these always, except in one doubtful case being less than N-grade in abundance on the back position, and it is usual for neither rams nor ewes to grow horns.

Heterozygous Dominant-N lambs show great variation in abundance of halo-hairs. About one lamb in seventy shows no reduction in abundance of birthcoat halo-hairs in any part of the body including the shoulder patch region. About 1 lamb in 9 shows a reduction in the shoulder patch region only, while about 3 in 4 have a reduction in halo-hair abundance in some other region of the body as well, generally showing itself in reduced halo-hair abundance over the front of the body and sometimes along the side. About 2 in 13 of the heterozygous Dominant-N lambs are less than N-grade on the back, including cases less than grade VI halo-hair abundance in this position. Horns in Romney N-type sheep are sex-influenced, and are present in heterozygous Dominant-N ramb but not in ewes, except that 1 in 10 rams failed to grow horns, while about 1 ewe in 10 grows horns.

Homozygous Recessive-N lambs have N-grade abundance of halo-hairs better sustained at the front of the body than heterozygous Dominant-N's. About 1 lamb in six shows no reduction below N-grade in halo-hair abundance on any part of the body including the shoulder patch. About 1 in 5 show a reduction on the shoulder patch region only, while about 3 in 5 show a reduction in other body regions as

all these have been grade VI.

However horns as mentioned before are, in Recessive-N ewes, less well developed than in heterozygous Dominant-N ewes. No ewes in the former genotype have grown horns, these being defined as horny projections more than an inch long. Only one ewe in 57 grew scurs, horny projections less than an inch long, while the majority were clean-polled, not even possessing lumps under the skin.

In double heterozygotes, although the records are less detailed as many of the observations were made before the significance of the shoulder-patch was discovered, they show that about one lamb in six or seven has no shoulder patch, 11 out of 14 have a shoulder patch or greater reduction, while one out of 21 is classed as grade VI. However, the horns position is different from that in Recessive-N. For ewes, in comparison with heterozygous Dominant-N's, it is seen that the proportion of sheep with horns or scurs is not significantly greater but that the proportion clean-polled is very distinctly lower. Thus in double heterozygotes there seems to be an increase, both in halo-hair abundance and in ability to produce horns when compared with the heterozygous Dominant-N's while there is only an increased ability to produce horns when compared with Recessive-N's.

In homozygous Dominant-N lambs, there has never been seen any reduction of halo-hair abundance in any region of the body, while both ewes and rams grow horns, the only exception to this being one ewe that grew very poorly in her first year and only had scurs at three years. Thus sheep of this genotype surpass those of all other genotypes in that there is a complete covering of halo-hairs in all parts of the body and both sexes grow horns. Whether the fullest possible abundance of halo-hairs, is, however, reached with this genotype is not known.

born which had N-grade abundance of halo-hairs on the body. Breeding tests showed that this was not due to a Recessive-N gene being present in the Non-N stock but that some other explanation is needed. Even in ordinary heterozygous Recessive N's however, the single Recessive-N gene has some phenotypic expression as a quarter or more of the ram lambs have horns mostly quite small. Also, although very few lambs of this genotype have full N-grade abundance of halo-hairs, on analysis of data supplied by Dry it was found that there are more lambs of Grades II and III and less of Grade I for halo-hair abundance than with normal flock Romneys.

Section II: GOLDSCHMIDT'S THEORY OF GENE DOSAGE EFFECTS.

Goldschmidt & Hoener (1937), and Mohr (1932) have formulated a theory of gene dosage effects as a result of study of the vestigial wing, no wing series of alleles. Here there is a series of alleles, +, normal wing; ni, nicked; no, notched; vg, vestigial wing, and Nw, no wing, which is incompletely recessive. Different combinations of these alleles produce different degrees of wing reduction and to explain the facts the following theory was put forward by Mohr. The scalloping effect was known to be due to the destruction of already existing wing area due to either inefficiency of some growth substance or by accumulation of some lytic stuff. Mohr suggested that, assuming that the first possibility is correct, all the alleles produce the same growth substance, but some do it less efficiently. If it is supposed that the threshold for wild type phenotype is 40, then different genotypes produce different amounts of growth substance which in turn produces different phenotypes according to the following scheme:

$\frac{vg^{Nw}}{vg^{Nw}}$	$\frac{vg}{vg^{Nw}}$	$\frac{vg}{vg}$	$\frac{vg^{no}}{vg^{Nw}}$	$\frac{vg^{no}}{vg}$	$\frac{vg^{ni}}{vg^{Nw}}$	$\frac{vg^{no}}{vg^{no}}$	$\frac{vg^{ni}}{vg}$	$\frac{+}{vg^{Nw}}$	$\frac{vg^{ni}}{vg^{no}}$	$\frac{+}{vg}$	$\frac{vg^{ni}}{vg^{ni}}$	$\frac{+}{vg^{no}}$	$\frac{+}{vg^{ni}}$	$\frac{+}{+}$
12	16	20	21	25	28	30	32	36	37	40	44	45	52	60
										wild type.				

No wing = 6; vestigial = 10; notched = 15; nicked = 22; wild = 30 for 1 gene. This theory fits all the facts about the vestigial wing alleles found by Goldschmidt.

From this Goldschmidt has put forward a theory of gene action as follows (Goldschmidt 1938): A gene acts by catalysing the production of a certain substance which has a certain effect on the biochemical system of the individual carrying it. Mutant genes may either produce more or less of the same substance than the wild type gene, and the mutant effect is seen when there is not enough of a substance produced by the two alleles to give threshold value to produce the wild phenotype. This explanation works equally as well if the mutants in the case of vestigial wing produce a lytic substance that dissolves away the already formed wing, except that here the series of mutants must produce successively more and more of the substance.

Goldschmidt (1928) also discusses dominigenes which he describes as non-allelic genes, the action of which is to alter the action of other mutant or wild type genes. In the vestigial wing series he has found three dominigenes which shift the dominance of the normally completely recessive vestigial wings to-wards the vg type if all three are present, although each one individually has a small effect. It is suggested by Goldschmidt as an explanation that the dominigenes affect the rates of reaction of the substance's produced by vestigial wing series in some way, thus affecting the phenotype in a similar way to that suggested for the mutant genes themselves.

In this theory dominance is also seen to be a subphenomenon of the same system of reactions of different speed. Dominigenes change this speed or one of the concomitant processes controlling threshold etc. with the same quantitative effect upon the result as different alleles. (Goldschmidt 1938.) Referring again to Mohr's explanation

phenotypically intermediate condition whenever the threshold for wild type is not transgressed. If this threshold for wild type is transgressed in the heterozygote the allele behaves as a complete recessive, but if not, then it is partially dominant. This partial dominance may be caused by failure of the two alleles to produce enough substance to cross the threshold value or by the influence of dominigenes as above.

If there is suggested another threshold value at the other end of the scale it can easily be seen how a mutant gene can be fully dominant. Also if it further suggested that this speed or rate of production of a substance by the gene can also be altered by the whole genotype in which it finds itself placed, as well as by dominigenes, this theory of dominance can well harmonize with that of Fisher (1930).

Section III: APPLICATION OF GENE DOSAGE THEORY TO N-TYPE SHEEP.

In view of the nature of the effects produced by the two N-genes it was thought that they would provide material for a study of dosage effects. Certainly the facts about halo-hair abundance at birth and horns in N-type sheep, except for the anomalous position of horns in Recessive-N's, would seem to merit examination in the light of the theories of Goldschmidt and Mohr as outlined above.

The position of horns in relation to birthcoat halo-hairs is, however, somewhat obscure, for while both seem to be effects of the same gene and increase with increasing gene dosage, within a genotype high birthcoat halo-hair abundance does not necessarily mean good growth of horns, or vice versa. (Dry P.C.) This variation would also seem to be partly genetic. Thus, it could well be suggested that, as the correlation between the two effects is not absolute, the Recessive-N gene produces better halo-hair

view that the theories postulated by Goldschmidt fit the known facts about N-genes are: (a) The discovery by Dr. Dry of a probable dominigene that shifts the expression of the heterozygous Recessive-N gene towards that of N-type. The animals are thought to be Domino, e.g. nr/+.Do/+ and on halo-hair distribution, and horn size in males are of weak N-type characterization. (b) There is evidence that genetic factors hinder the expression of the N-gene in heterozygous Dominant-N sheep, and very likely one or several such modifying factors are quite powerful.

The aim of the present thesis was to provide new facts as a basis for the study of dosage effects in N-type sheep, and to learn something about dosage effects. With the two separate N-type genes present, the Recessive-N designated nr and the Dominant-N designated N, together with their wild type alleles, the following genotypes, arranged in increasing order of dosage of the N-type genes, could theoretically be attained:

(i) +/+.+/+ wild type Romney; (ii) +/+.nr/+ heterozygous Recessive-N; (iii) N/+.+/+, heterozygous Dominant-N; (iv) +/+.nr/nr. homozygous Recessive-N; (v) N/+.nr/+. double heterozygote; (vi) N/+.nr/nr not yet identified; (vii) N/N.+/+ homozygous Dominant-N; (viii) N/N.nr/+ not yet identified; (ix) N/N.nr/nr not yet identified. Only the genotypes (i), (iii), (iv), (v) and (vii) were studied. Genotype (ii) was omitted as it was much like genotype (i), while no lambs or samples from lambs known to be of genotypes (vi), (viii) and (ix) were available. The effect of increasing gene dosage on hairiness was studied by the fibre type array method (Dry 1935; Sutherland 1939) to be described later, and also by means of the medullometer which gives a measure of total percentage hairiness in the fleece.

Sections of skin were also made from some of the genotypes to see if increasing gene dosage had any effect on

to secondary follicles (Fraser, Ross & Wright I.P.) but their study had been limited to one position of the body.

Section IV: GRADIENTS OVER THE BODY.

Galpin (1936) studied the fibre type array gradient in the New Zealand Romney lamb and found a gradient in hairiness over the body, the most hairy arrays being found on the britch and the least hairy on the poll. As in the heterozygous Dominant-N, Recessive-N, and double heterozygote genotypes, there was a great variation in birthcoat halo-hair abundance in different regions of the body, it was decided to study the fibre type array, total medullometer hairiness, and follicle population in different regions of the body to see if and how this variation changed in different genotypes. Also it was thought that differences between genotypes in any one position might not be truly representative of changes over the fleece with increasing dosage of N-type genes. Finally, the changes and gradients in fibre type array, hairiness and follicles over the body were studied and the findings compared with those of Galpin.

Section V: GENERAL.

The number of animals studied in each genotype is too few to allow any separation on fibre type array detail, hairiness as measured by the medullometer or on percentages of individual fibres present of the three intermediate genotypes heterozygous Dominant-N, Recessive-N, and double heterozygote. No real difference between any of these genotypes in any of the above measurements could be detected. However, Dry's information on birthcoat halo-hair distribution would suggest that there is a real difference between heterozygous Dominant-N and Recessive-N, but none between double heterozygotes and Recessive-N. Double heterozygotes, heterozygous Dominant-N's and Recessive-N's differ in ability to grow horns.

with regard to one measurement, but it was thought better in this thesis work to make preliminary studies in several directions instead of piling up data on a single point.

As mentioned previously the three genotypes of high dosage, namely N/+.nr/nr, N/N.nr/+ and N/N.nr/nr have not yet been identified. However it is hoped that the present work on known genotypes may ultimately provide a basis for tackling dosage effects in lambs so bred that some of them must carry these heavier dosages.

As already indicated, another problem of interest which has not been tackled at present, is the study of dosage effects in lambs provisionally called "dominoes".

PART II

PART II.

CHAPTER II.

I N T R O D U C T I O N

For this work the individual fibres in a small lock of wool were sorted into classes depending on tip shape and presence or absence of medulla. The various classes and also their significance in the fibre type array are described below while the materials and method are discussed in that chapter. (See Chapter 3.)

Section I.

Dry (1933 & 1935) described the fibre types of the Romney sheep, placing them in a number of classes depending on the shape of the fibre tip and also the presence or absence of medulla in both the pre- and post-natal region. These fibre types have also been described by Sutherland (1939) and Goot (1940), but as they are fundamental to the work they will be described here. Also in this work the curly-tip fibres were further divided into two extra types.

A. Pre-curly-tip fibre group.

I. (i) Halo-hairs designated HH. So long as they continue their growth these are either the longest and stoutest fibres found, or are amongst them, and are the first to appear on the foetus. They project above the rest of the coat of the newborn lamb, but in N-grade birthcoats they are so numerous that they form a thick mat. These fibres consist of a stout end which may be straight or curved, a medullated pre-natal region, apt to be slightly wavy, and a stout, strongly medullated post-natal region, generally straight The pre-curly-tip region is generally larger than in super-sickle fibres. Halo-hairs are sometimes, although only occasionally, less medullated than hairy-tip-curly-tip fibres or of less total fibre area than peak-curly-tip fibres.

at the junction between the curly-tip and post-natal regions, supposed to mark the point of fibre formation when the lamb was born and thus called the birth point. (Goot 1940.)

II. Super-sickle-fibres and Sickle-fibres: These as a group are distinguished from halo-hairs in that the pre-curly-tip region is shorter and forms a distinctly sickle-shaped end which is of greater area of cross section than the neck region of the following curly-tip portion of the fibre. As with halo-hairs they are sub-divided on the presence or absence of medulla in their various regions. However, sickle-fibres may be so "weak" that all the fibre is non-medullated. Also the degree of medullation here is generally less than in the halo-hair group.

(i) Super-sickle A fibres (designated SSA): These are shorter and less stout than halo-hairs but, like them, they are medullated throughout their length. Sometimes they are discontinuous from halo-hairs and this has led Sutherland (1939) to suggest that they are fundamentally different. However, in other arrays halo-hair and super-sickle-A fibres would seem, on eye-grading, to grade into each other, and are very difficult to separate. Intermediate fibres were sometimes put into another class, called halo-hair$_2$, HH_2, but these were not really distinct from halo-hairs at one end of the scale or super-sickle As at the other.

(ii) Super-sickle A' designated SSA': These resembled super-sickle As except for a break in medulla at the birth point. (c/f halo-hair'.)

(iii) Super-sickle B designated SSB: These are of three types. Type (a) has a break in medulla below the sickle-shaped end as well as another break at the birth point, but medulla is present in the middle of the curly-tip region, between these two breaks. Type (b) has the non-medullated region next to the birth point extended up towards the sickle-end but there is always some medulla present in the curly-tip region just below

(iv) Sickle-fibres designated Sk: These are distinguished by having no medulla in the curly-tip region of the fibre. The sickle end may or may not be medullated.

(v) and (vi) Super-sickle (generally SSB) and sickle fibres may or may not have medulla in the post-natal region. If medulla is absent they are termed fine super-sickle or sickle fibres respectively.

B: Curly-tip fibres. These fibres consist of only two regions, a curly pre-natal region and a post natal region which may or may not be crimped and/or medullated. As with other groups they are sub-divided according to the predence or absence of medulla.

(i) Hairy-tip-curly-tip fibres designated HTCT: These have medulla present in the curly-tip region in amounts varying from a trace to complete medullation throughout, except the extreme apical end. Generally medulla is also present post-natally but occasionally it is absent when the fibres are termed checked-hairy-tip-curly-tips.

(ii) Curly-tip fibres designated CT: These have no medulla in the curly-tip region; which may consist of many curls in fibres next to the pre-curly-tip series down to slight curling in those fibres next to the histerotrich series which lack a curly-tip region. The length and number of curls present in the curly-tip region is taken as a measure of the order in which these fibres appeared in the foetus and allows them to be arranged in a series depending on time of appearance. Curly-tip fibres are sub divided as follows:

a. Medullated post-natally.
These may include the bulk of the curly-tip fibres or only a very small percentage; medulla may be strong or weak.

b. Non-medullated post-natally:
These may be either at the beginning or the end of the curly-tip series or at both places. If the fibres non-medullated post-natally precede medullated fibres in the array the non medullated ones are termed "checked" and are considered to be next to fine sickle fibres. However, non-medullated fibres occurring later than medullated ones in the array are considered to be a result of lack of basic medulla producing ability of follicles, and are termed curly-tips non-medullated.

This division of the hairy-tip-curly-tips and curly-tips may be further complicated if a discontinuous drop in length or diameter of the fibres of the series occurs. This is termed a precipice and fibres fall into dis-- tinct groups according to whether they are "above" or

of the hairy-tip-curly-tip fibres matters are not so complicated, but often there are present pre-precipice curly-tip fibres discontinuous from the post-precipice ones, and generally stouter and more strongly medullated although in one exceptional case (178/48 side) this was not so. Very occasionally some of the post-precipice fibres belong to the hairy-tip-curly-tip fibre type, and this creates another anomaly. There may be some merit in attempting to divide arrays into precipice and non-precipice ones as the classification of fibres in the two arrays is somewhat different. All the fibres in the precipice type array can be put into the fibre types of the non-precipice ones but some valuable data is thereby lost. (See later.)

C. Histerotrich Fibres designated Hi: These fibres consist only of a post-natal region, i.e. lack a curly-tip. Goot (1940) has done work which would suggest that they first start to appear about two or three days before birth. As they are still appearing at the time the samples were collected they were not considered in the analysis of the data to the extent that the other fibre types were. However, they were divided into medullated and non-medullated histerotrichs. This sub-classification was sometimes important, especially when most or all of the curly-tip fibres were medullated, in that it helped to show the strength of the basic medulla producing ability in the array; but the information was not complete as not all histerotrichs were present.

The action of the N-genes is to increase the hairiness, i.e., to increase the medullation of the individual fibres. This increase in medullation can be measured as the proportion of various fibre types in each of the groups halo-hairs, super-sickle and sickle, curly-tip and histerotrich. Also, with increased medullation the proportion of fibres in the various groups themselves may change, but this is not so marked as the changes of

while the classification of the various groups is based on tip form and is more probably related to time of appearance of the fibre groups in the age of the foetus than to medullation. However, the halo-hair group is very often absent from the less medullated arrays; and in these an increase in the proportion of fibres in the curly-tip group has also been postulated (Goot 1940), this being attributed to the "promotion" of the histerotrichs. The secondary follicles it is thought face less severe competition when the primary follicles are growing less stout fibres.

Section 2:

This includes the main ideas that have emerged in work on the coat of the Romney lamb when the fibre types are considered, not separately, but as collections or arrays. When a lock of the birthcoat of a lamb, is, some time after birth, pulled to pieces and the fibres laid out on black velvet, it is seen that there are usually pre-curly-tip, curly-tip (including hairy-tip-curly-tip) and histerotrich fibres present. These fibres can be arranged in their order of appearance in the lamb and this series of fibres is called a fibre type array. Halo-hairs are believed to be the first constituents of the fleece to begin their development prior to birth (Dry 1935). Consequently they are placed at the front end of the array. Following are the other pre-curly-tip fibres, which possess a sickle-end above the curly-tip position of the fibre. Curly-tips lacking a sickle-end, occur next in the array, those curly-tips with many curls in the tip being thought to arise first on the foetus and these are consequently put at the front end of the curly-tip series of fibres. Those with few curls are similarly thought to appear late and are placed last in the curly-tip series. Histerotrich fibres lack a curly-tip region and most would appear to arise after birth. (Goot 1940). These fibres are placed last in the array.

I. Plateau array: Possesses no sickle or checked curly-tip fibres but of the other fibre types, halo-hairs, hairy-tip-curly-tips, curly-tips and histerotrichs are always present. Super-sickles may or may not be found. This array has been extensively studied by Sutherland (I939), who distinguishes between strong Plateau, no super-sickle B fibres present, and weak Plateau where such fibres are present. Both types on Sutherland's classification may have a few sickle-fibres "in parallel".

II. Saddle array: Possesses sickle fibres not"in parallel" but no fine sickles or checked curly-tips. Of the other fibre types, halo-hairs, super-sickles and hairy-tip-curly-tips may or may not be present.

III. Ravine array: This is distinguished by possessing fine sickle fibres but no checked curly-tips.

IV. Valley array: Possesses both fine sickle-fibres and checked curly-tips but is more medullated than the Plain array in that it possesses medullated curly-tip fibres following the checked curly-tips.

V. Plain arrays: These possess no medullated curly-tips following what are probably checked curly-tips. Thus there is just a straight series of fibres from fine sickles, through non-medullated curly-tips to non-medullated histerotrichs. In all except one Plain array studied these were the only fibre types present, the possible exception being an array classed as Ravine bordering on Plain present on the shoulder patch of heterozygous dominant-N, I04/48, where an occasional halo-hair and super-sickle B were present in addition to the other three fibre types.

Two other array types, Escarpment and All-In, have been found. The former was not met with in this work and will not be discussed further and only a possible case of the latter on the withers of 80/47, was found. The All-In array is described as having a transition from small ended sickle-fibres to medullated curly-tips. Together with the above Saddle characteristics are superimposed Valley characteristics. These are an association between large and small ended fine sickle-fibres and a small number of checked curly-tip fibres.

Those fibre types previous to the essential fibres, e.g. the super-sickles and medullated sickle-fibres, may or may not be present in a Valley array. If they are absent the array is termed"truncated".

This fibre type array classification of Dry's is thus a direct measure of what Goot (I940) calls the head check which is supposed to operate in the following way. An array with no head check would possess only halo-hairs, super-sickle As and hairy-tip-curly-tips down to non-medullated histerotrichs and/or curly-tips. This is what

the head check operates, causing first the pre-curly-tip fibres and if stronger the curly-tip fibres next to the pre-curly-tip series, to be non-medullated. Thus a very weak head check only causes some of the super-sickle A fibres to become super-sickle A'. A stronger head check produces successively super-sickle B, sickle and fine sickle- and super-sickle fibres. A very strong head check finally affects the curly-tip fibres next to the pre-curly-tips causing them to be checked. When the checked curly-tips are followed later in the array by medullated curly-tips a Valley is produced but when the head check is such as to include many checked curly-tips and/or the basal medullation is so weak that no medullated curly-tips are found in the middle of an array, a Plain is produced.

As the head check gets stronger in the array the basal medullation generally, but not always, becomes weaker. (See array 178/48 later.) The exceptions to this generalization would seem to suggest that head check and basal medullation are independent variables but that the N-genes affect both causing increase in basal medullation and decrease of the power of the head check.

The fibre type array classification is based only on the presence or absence of fibres affected by the "head check". Unfortunately there is no convenient measure of basal medullation but some research should be devoted to the problem. (However, see Chapter 6.)

Increased dosage of N-genes also causes the curly-tips next to the pre-curly-tip series to become long and strongly medullated and separated from the other curly-tips series by a precipice. The final result is seen when all these pre-precipice curly-tip fibres become hairy-tip-curly-tips but this only occurs in hairy or "tough" arrays. According to the theories of Fraser, Ross and Wright (I.P.) the primary lateral follicles form the hairy-tip-

it is not absolutely correlated with the strength of the "head" check. Some effort could well be made to correlate the effects of all these different measurements of increasing medullation.

CHAPTER III.

MATERIALS AND METHOD

Section 1: SAMPLING POSITIONS

For each fibre type array of the homozygous Dominant-N, heterozygous Dominant-N and Non-N stock a small sample of wool, consisting of about three locks, was taken from each of seven standard sampling positions on the sheep. These positions are as follows:

1. Standard Back Position: In the mid-dorsal line at the level of attachment of the last rib.
11. Withers Position: In the mid-dorsal line immediately above the shoulder position and level with the 5th rib.
111. Side Position: On the point of the last rib.
1V. Shoulder Patch Position: For this sample one of the smallest and shortest locks from the armpit region were selected.
V. Shoulder Position: Mid-way between the elbow joint and the shoulder joint on the fore limb.
V1. Neck Position: Mid-way between the shoulder position and the ear; i.e. on the side of the neck.
V11. Britch Position: As found on the leg by the present observer, this position is between the stifle joint and the projection of the pelvis on the side of the tail. The sample was taken from where lines of equal length drawn at right angles to each other from the above-mentioned positions meet.

The back, withers, side and britch positions have been described by Galpin (1936). The Figure following shows the seven sampling positions in relation to the sheep. (See Fig. I.)

All the wool samples, except those from the Non-N genotype were collected from lambs born in Dr. Dry's experimental Romney flock. Samples 13/50, 14/50, 30/50 and

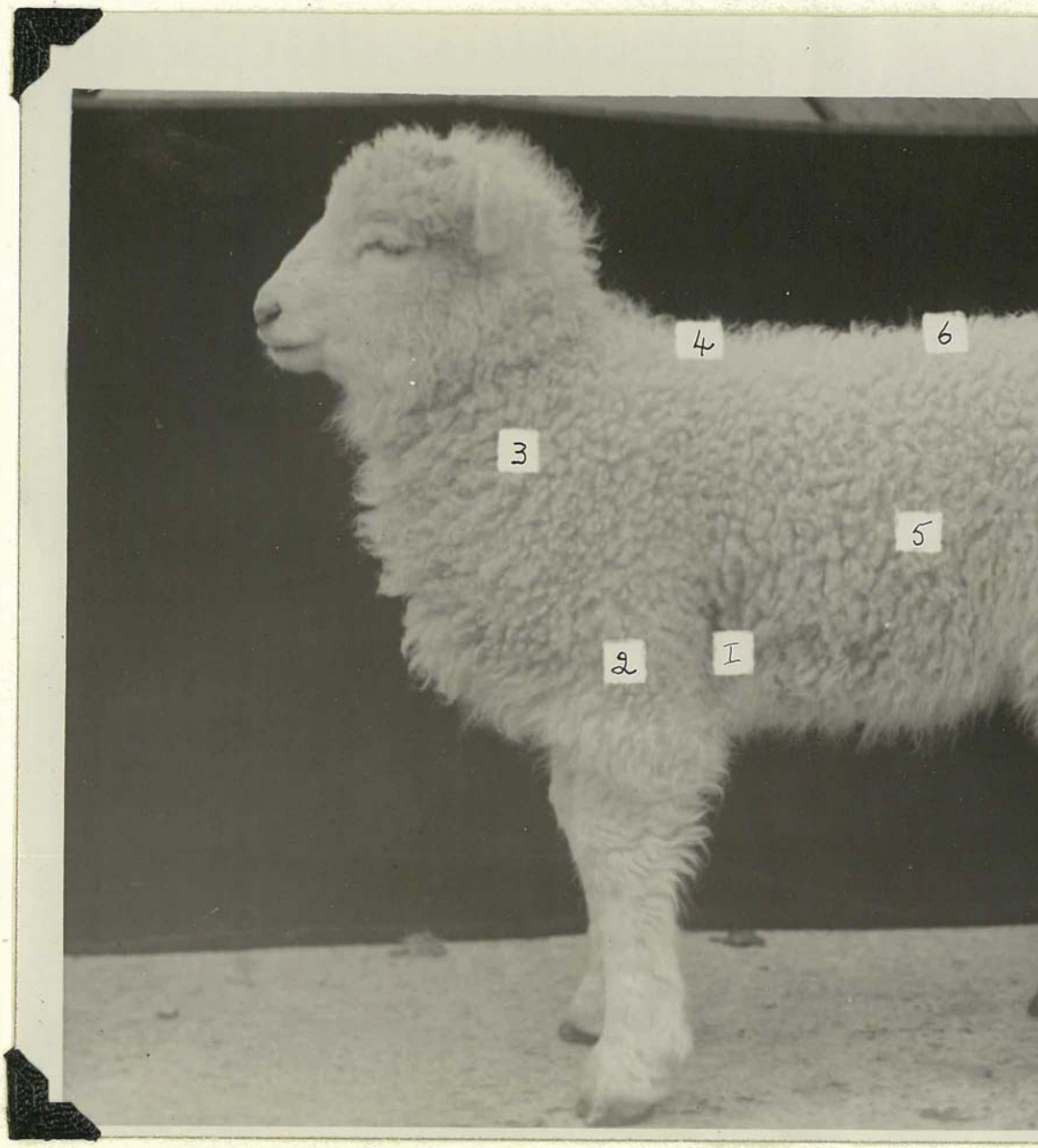


FIGURE I.

I. Shoulder patch 2. Shoulder 3. Neck 4. Withe

the flock belonging to Mr. R. A. Buchanan of Kerere.

Samples from the Recessive-N genotype were collected from lambs born in 1948 and 1947. The 1948 Recessive-N lambs were sampled in every position except the britch, while the 1947 lambs were not sampled from the shoulder patch. By sorting out fibre type arrays in this genotype from samples collected in both years a measure of the arrays in all seven positions could be taken.

The only samples available from lambs of the double heterozygote genotype were from lambs born as long ago as 1944 and these were only sampled in the back, withers, side and britch positions. Samples from any of the other positions were unfortunately not available from this genotype.

Section 2 : SAMPLING METHOD

For sampling the sheep was held by the neck with its head between the operator's legs and its back in front. The sampling position was then found and the sample, including about three locks of wool was then taken by cutting back from this position. Sometimes however a second person held the lamb, while the first person did the sampling and when this occurred the sample was cut off from in front of and including the sampling position. How much error was incurred through this difference in technique is not known, but any error variance included here is included in the statistical analysis, in the error variance between individual sheep. After sampling the samples were packed, dusted with D.D.T. powder to prevent moth larvae from causing destruction and stored until use.

All of the samples analysed were taken from lambs about two months after birth. This was before the pre-curly-tip fibres had been shed and lost, but not all of the histerotrich fibres had appeared at this time. (Coot 1940.) Thus the proportions of pre-curly-tip and curly-tip

Section 3.

To find the fibre type array of a particular sample the materials needed were, some black velvet cloth, a pair of blunt tipped forceps, benzol, a microscope, slide and cover slip. From the sample a small sub-sample of approximately 400 fibres was taken, and, with the blunt tipped forceps, each individual fibre was sorted out on to the black velvet. If the sub-sample contained less fibres than estimated an additional sub-sample was taken so that at least 400 fibres were sorted. If there was any doubt as to which class or type a fibre belonged, it was placed on a slide under a cover slip, the whole was irrigated with benzol and examined under a microscope. Medullated fibres contain air which has a different refractive index from benzol and thus shows white to the naked eye or black under the microscope. Non-medullated fibres however contain no air and the refractive indices of benzol and this fibre are very similar. Consequently in benzol non-medullated fibres appear colourless and invisible to the naked eye and transparent under the microscope. In this way it was possible to tell with absolute accuracy in which parts of a fibre medulla was present or absent. (Elphick 1932). Fibres were then sorted into the classes described in the Introduction and the fibre type array studied.

CHAPTER IV.

FIBRE TYPE ARRAYS AND GENE DOSAGE

In this chapter fibre type arrays, as described in the introduction for Part II (Chapter 2) are used for a study of gene dosage. Comparisons are made between arrays present on the same position between different genotypes and between different positions in the same genotype. Finally the interaction of these two comparisons is studied, giving qualitative or quantitative changes in fibre type array gradients in different genotypes. As no mathematical measurement of fibre type array could be made, all the observations here recorded are without statistical backing, a fact to be kept in mind throughout this chapter. The relative tables are at the back of this work. In this work, as Plateau arrays covered a fairly wide range they were sub-divided as follows: Plateau P_1 is a very strong plateau possessing neither super-sickle A', super-sickle B nor sickle-fibres. Plateau P_2 possesses neither super-sickle B nor sickle-fibres while Plateau P_3 has no sickle-fibres. Saddle arrays as stated before (Chapter 2) possess sickle-fibres. As a result this classification is more rigid than that of Sutherland (1939) who includes in Plateau those arrays with a few sickle-fibres following on from the super-sickle B's these being described as "in parallel" with the array. On the above classification these arrays would be classed as strong Saddle. Sickle-fibres "in parallel" do occur however and are sometimes seen in a fairly "tough" Plateau containing super-sickle A and a few super-sickle A' fibres but no super-sickle B's.

In all work in the present chapter, in comparisons between individual fibre types (Chapter 5), and in the medullometer work (Part III), in the heterozygous Dominant-N

and 194/48 were, in addition, included.

The term "toughness" is used to denote the degree of hairiness of an array while "weakness" is used in the opposite sense.

Section 1: COMPARISONS BETWEEN ARRAYS PRESENT IN THE SAME POSITION BETWEEN DIFFERENT GENOTYPES.

A: Back Arrays (See Tables I & 2 - 35 and Graph I.)

The fibre type array in all the Non-N sheep on the back is Valley, a very characteristic feature of this genotype. However Dry (P.C.) and Galpin (1936) have found that, although Valley is the most common array on the back of Non-N Romneys, Plain is common and Ravine and Saddle are found easily. This would suggest that all possible variation in the Non-N genotype has not been encountered in this work, due probably either to the small numbers taken or else to variation in the flock the lambs were selected from being less than normal. The only other Valley on the back occurs in the heterozygous Dominant-N, 178/48, but this sheep is unusual as described later. (Chapter 6).
Heterozygous Dominant-N's show much variation, the weakest back array found being the above-mentioned Valley and the strongest a Plateau P_1 in 48/48. However the majority of the wool samples analysed were Saddle or weak Plateau.
Recessive-N's and double heterozygotes are similar except that two out of four Recessive-N back arrays are strong Plateaus while no double heterozygote arrays are Plateau and one is Ravine. Thus, if anything, Recessive-N arrays would seem to be less and double heterozygotes more checked on the back. The six homozygous Dominant-N's are all Plateaus. Four are strong (grade P_1), while the other two are grades P_2 and weak P_2.

B: Withers Arrays. (See Tables I & 2 - 35 and Graph I)

position and these overlap with the Non-N withers arrays.

C: Side Arrays. (See Tables I & 2-35 and Graph I.)

Side arrays are of similar "toughness" to those of the back.

D: Shoulder Patch Arrays. (See Tables I & 2 - 35 and Graph I

These show differences in comparisons between genotypes when compared with back, withers and side arrays. All Non-N shoulder patch arrays are Plain and contain only the fibre types, fine sickle, non-medullated curly-tip, and non-medullated histerotrich. The heterozygous Dominant-N shoulder patch arrays all contain some medullated fibres. Arrays range from truncated Valley of 178/48 and Ravine bordering on Plain of 104/48 to Saddle found in 48/48 and 65/48. Sheep 93/48 and 16/5 0 have Valley arrays in this position and all other heterozygous Dominant-N's Ravine. The typical array for a heterozygous Dominant-N on the shoulder patch region is thus Ravine. In the Recessive-N genotype the four shoulder patch arrays are two Valleys, a Ravine and a Saddle. Thus here the typical arrays would also appear to be about the "toughness" of a Ravine, thus showing no difference from heterozygous Dominant-N's. Homozygous Dominant-N's are the only genotypes to show Plateau arrays on the shoulder patch. Of the six homozygous Dominant-N shoulder patches studied five were weak Plateaus and one a Ravine. However this sheep 300/48 showed very weak arrays for N/N on the side, shoulder patch and britch. The reason for this is not known but the phenomenon will be discussed below. Double heterozygote shoulder patches as stated earlier were not available.

E: Shoulder and Neck Arrays. (See Tables I & 2 - 35 and Graph I.)

Shoulder and Neck arrays are very similar except that of the two if there is any difference the shoulder is usually the weaker. This does not agree with the halo-hair distributions over the body in heterozygous Dominant-N's

on Plain, having fibres that are definitely checked curly-tips but no medullated peak curly-tips following.

In the heterozygous Dominant-N's both shoulder and neck arrays vary in toughness from Valley to strong Saddle bordering on Plateau except the neck array of 35/48 which is a weak Plateau. The average array for shoulder appears to be about the border between Ravine and Saddle while that for the neck is Saddle.

Recessive-N genotype arrays in these positions are of similar but slightly greater "toughness" ranging from border between Ravine and Valley to Saddle on the neck and weak Plateau on the shoulder. However, this difference in toughness between Recessive-N's and heterozygous Dominant-N's is very slight and is probably of no significance. It is seen mainly in the lack of Valley arrays in Recessive-N's and in the presence of a shoulder Plateau but against this however is the lack of a neck Plateau array.

All the homozygous Dominant-N shoulder and neck arrays are Plateaus, ranging from strong in 239/48 to weak in 15/50, 14/50, 245/48 and 300/48. Thus the average array for this genotype in these positions is a Plateau of grade P_2 or P_3 and this is much tougher than the arrays present in other genotypes.

F: Britch Arrays. (See Tables I & 2 - 35 and Graph I.)

Britch arrays were studied in the Non-N, heterozygous Dominant-N, Recessive-N, double heterozygote and homozygous Dominant-N genotypes. Non-N britches, in contrast with arrays in this genotype on other parts of the body, are very variable and range in toughness from Valley, present in two sheep, through weak Saddle, (1 case), to weak Plateau (also 1 case). The average array would therefore appear to be a weak Saddle or a Ravine. In the heterozygous Dominant-N genotype two britch arrays were not Plateau, one in 178/48 being a Saddle and the other in 16/50

Grade VI, and 16/50 being Grade III. All other heterozygous Dominant-N and all double heterozygotes and homozygous Dominant-N sheep had Plateau arrays on the britch. These showed no increase in "toughness" in the homozygous Dominant-N genotype where three of the six arrays studied were weak Plateau. It is concluded that in all N-grade sheep a certain threshold in britch hairiness, as shown by the fibre type array, has been reached and that increase in gene dosage does not result in increased "toughness" of the array. Variation in the "toughness" of Britch arrays as seen in N-grade sheep is due to a factor or factors unknown.

The one Recessive-N britch array studied was also a strong Plateau so there does not seem to be any anomaly in the position there, although the data does not permit generalisation.

Section 2: COMPARISON BETWEEN POSITIONS WITHIN GENOTYPES.

Galpin (1936) has studied fibre type array gradients in the Non-N N.Z. Romney. She has found that the extent to which the fibre type arrays were depressed varied over the body, giving a general gradient from britch to poll, the most depressed arrays being found on the poll and the least depressed on the britch. This gradient was gradual, no sudden transition taking place on any part of the body. Subsidiary gradients up the side of the body, accompanying the posterior anterior gradients were also found most noticeably on the limbs. In these gradients, the array on the inferior position limited the array on the superior position; thus the array on the britch limited the arrays in the rest of the body to being no less depressed than that of the britch, but they could be more depressed.

A: In the Non-N Romneys studied (Tables I & 2 - 5 and Graph I) the shoulder patch was in all cases the most checked region, the array here being straight Plain as

followed by coarser non-medullated curly-tips so the array was slightly less checked than on the shoulder patch. On the other two sheep, arrays are truncated Valleys, containing medulla in the curly-tip fibres, except in B 5 neck, where one medullated sickle-fibre is present.

Next in increasing order of "toughness" are the withers and side samples which also have very similar arrays. These are all Valleys in some cases truncated, but the side positions are consistently "tougher" than the withers as shown by their possessing more medullated curly-tip fibres. In sheep B 1 there is no medulla present in the withers array, but it is seen in curly-tip fibres on the side.

Back arrays are next in order of toughness. All are Valley arrays but B 5 has an odd hairy-tip-curly-tip fibre at the peak of the curly-tip series. B 4 back array is, if anything, slightly weaker, as shown by it possessing less medullated curly-tip fibres, than the side and withers arrays on the same sheep, but in all the other Non-N sheep studied the reverse was the case. Besides having a greater percentage of medullated curly-tip fibres following the checked curly-tips, all the Non-N back arrays except B 4 possessed pre-curly-tip fibres other than fine sickles, and B 5 shows super-sickle B and sickle fibres in this position.

Britch arrays were the "toughest" found in Non-N sheep, two of which had Valley arrays in this position, one a Saddle bordering on a Ravine, and one a Plateau grade P_3. The "weakest" britch Valley, found on B 1, was stronger than the back array on the same sheep as it had more medullated curly-tips and less checked curly-tips as well as halo-hair, super-sickle B and fine super-sickle B fibres present. The next stronger britch Valley, that on B 5 had, except for a very small number of medullated histerotrich fibres, the same fibre types as were present on the back but more of the

noticeable however, was that sheep possessing the "toughest" britch arrays namely B 4 and B 6 did not possess the "toughest" arrays on other parts of the body, as can be seen by the (Tables Nos. 2 - 5). B 6 arrays in other positions were all very weak yet the britch array was Plateau while B 5 arrays on the back, withers and side positions were tough compared with these positions in other Non-N sheep studied, yet the britch array was only a Valley. Because of this anomalous position it is suggested that for fibre type array detail in Non-N sheep, the britch sample does not give a true measure of the hairiness of the fleece and at least one other position should be sampled.

It is seen that in the individual sheep there is very little variation over the body or gradient in "toughness" in the Non-N sheep studied. All possess weak and in many cases truncated Valley or Plain arrays in all body positions except the britch. Thus these sheep possess a very even fleece with regard to fibre type array detail except for a small area on the britch, where a tougher array is often found. However, it is also possible that this lack of variation over the body in Non-N lambs was due to selection with regard to this character having been practised in the flock from which these lambs came.

B: In the heterozygous Dominant-N genotype (Tables I & 6 - 17 and Graph I) the "weakest" arrays are again found in the shoulder patch position. These range from a Ravine bordering on a Plain array present in 104/48, which is however "tougher" than the Plains present in the Non-N shoulder patches, as it possesses halo-hairs and super-sickle B fibres, through three Valleys, and Ravines, up to two Saddle arrays. Thus the typical heterozygous Dominant-N shoulder patch array is Ravine.

The body positions next in ascending order of "toughness" are the shoulder and neck, but exceptions to this

different gradient is 65/48 where though the shoulder array is the weakest next to that on the shoulder patch the next array in ascending order of "toughness" is a strong Saddle found on the back. In this sheep the neck, and withers arrays are about of equal "toughness" being on the border between Plateau and Saddle. However, on closer inspection it is seen that the neck array has no halo-hairs, a moderate number of super-sickle A fibres and many super-sickle B's while both the back and withers arrays possess halo-hairs, a moderate number of super-sickle As and fewer super-sickle B fibres than found on the neck. Thus, although the back array has more sickle fibres than are found on the neck, thus technically making it a Saddle, yet taking all things into consideration it is the "tougher".

On the shoulder the arrays range from Valley, present in 16/50 and 178/48, through Ravine of which array three are present and Saddle, six present, up to one array present on 35/48 on the border between Plateau and Saddle. On the neck the arrays range from a truncated and very weak Valley present in 16/50 through one Valley in 178/48, one Ravine in 104/48, six Saddles, two arrays in 65/48 and 48/48 on the border between Plateau and Saddle up to one array in 35/48 which is a Plateau of grade P_3. Thus although in both positions the majority of arrays are Saddle, in the shoulder there are three Ravines while the " toughest" array is on the border between Plateau and Saddle. On the neck however only one Ravine is present, while the "toughest" array is a Plateau.

Of the withers, side and back positions the withers would appear to possess the weakest arrays. Sometimes indeed as in sheep 6/48, 35/48 and 93/48 the withers array is weaker than that on the neck while in 104/48 and 90/48 it is stronger than the side array. However, arrays in this position in heterozygous Dominant-N sheep range from two

Plateau and Saddle up to two arrays in 48/48 and 90/48 classified as weak P_1 Plateaus. Thus when compared with neck arrays those on the withers are seen to be "tougher" in that no true Ravine was present but that two fairly strong Plateaus were found. However, the significance of this difference in view of the small numbers, although it cannot be subject to statistical analysis, is doubtful.

Side arrays are weaker in "toughness" compared with those on the withers in the cases mentioned above and in sheep 41/48, 12/48, 65/48, and 16/50 they are "tougher" than the back arrays. In the twelve heterozygous Dominant-N sheep studied, the side arrays ranged from one Valley in 178/48 through one array on the border between Saddle and Ravine in 104/48, three Saddle arrays, up to seven Plateau arrays. Of these latter, four were classed as P_3, two borderline cases between P_2 and P_3 and one as P_1 with one super-sickle B in parallel. Here the majority of arrays are classed as Plateaus in contrast with those of the withers but the average array would probably be about the border between Plateau and Saddle.

Back arrays are weaker in "toughness" than those of the side in the above-mentioned cases. In 16/50 the back array is tougher than the britch array. These arrays vary in toughness from Valley in 178/48 through strong Ravine in 16/50, four Saddle arrays up to six Plateaus of which two are classed as P_3, one as a border-line case between P_2 and P_3, two as P_2 and one as P_1. Here as on the side, the majority of arrays are Plateaus although many Saddles are present and the average toughness would appear to be about the level of the border between Plateau and Saddle. In the four cases mentioned, the back arrays are "weaker" than on the side, in sheep 90/48, 78/48, 104/48 and 6/48 they are "tougher" while in the remaining four cases no marked

both the back and side arrays. Here the britch array is Valley, the back Ravine, and the side Saddle, this being the "toughest" region of the body studied. This is in contrast with Dry's halo-hair grading of this lamb which was classed Grade III in the back, while on the britch there was a full N-grade abundance of halo-hair over a restricted range. Arrays in this region of the body range from Valley in 16/50 through Saddle on 178/48 to Plateau in the other ten cases. Of these, two are classed as P_3, one as a borderline case between P_2 and P_3, one as P_2 and six as P_1. The average "toughness" of heterozygous Dominant-N britch arrays would therefore be a Plateau of about Grade P_2 or P_3.

In this genotype therefore, the increasing order of " toughness" of the various positions studied would appear to be shoulder patch < shoulder < neck < withers < side = back < britch. However, in any individual sheep this order does not necessively hold good. Shoulder patch arrays are always the weakest of any of the positions studied with regard to any single sheep, but in all the other positions the order in an individual sheep may or may not hold.

Fibre type arrays in the individual sheep in the heterozygous Dominant-N genotype also show great variation between different positions of the body, or in other words, the fibre type array gradients are much more marked than in the Non-N sheep studied. Even the average arrays for the whole genotype in the different positions studied show this: e.g.:

Shoulder Patch	average	array	: Ravine
Shoulder	"	"	: Saddle
Neck	"	"	: Saddle
Withers	"	"	: Strong Saddle
Side	"	"	: border between Plateau and Saddle
Back	"	"	: border between Plateau and Saddle
Britch	"	"	: Plateau of grade P_2 or P_3.

When individual sheep were studied a similar type of gradient

In four sheep arrays are:

SHEEP ARRAYS:	178/48	104/48	78/48	48/48
Sh. Patch.	Truncated Valley	Ravine bordering on Plain	Ravine	Saddle
Sh.	Valley	Ravine	Ravine	Saddle
Nk.	Valley	Ravine	Saddle	Plateau-Saddle border.
W.	Valley	Saddle	Plateau/ Saddle border.	Plateau P_1.
S.	Valley	Ravine/ Saddle border	Plateau P_3	Plateau P_2
Bk.	Valley	Saddle	Plateau P_2	Plateau P_1
Br.	Saddle	Plateau P_1	Plateau P_2	Plateau P_1

Here the heterozygous Dominant-N genotype is seen to produce great variation in the fleece characters as measured by the fibre type array. This is so far as gradients over the body are concerned is in keeping with Galpin's (1936) findings that it is in the intermediate coated lambs, as distinct from the fine-even-coated lambs, or uniformly coarse coated ones that marked gradients occur in fibre type arrays over the body.

C: In the Recessive-N genotype (Tables I & 20-24 & Graph I) the shoulder patch is again the "weakest" position studied. The range, although only four sheep were studied in this position, is from Valley in 351/48 and 353/48 to weak Saddle seen in 332/48.

Next in ascending order of "toughness" are arrays found on the shoulder and neck positions. Arrays found here are mostly Saddle and in three sheep 351/48, 332/48 and 353/48 there is no difference in toughness between the two positions. Saddle arrays are present in the two former sheep while the latter has an array bordering between Ravine and Valley in both positions. In 343/48 a Plateau grade P_3 is present on the shoulder and a Saddle on the neck, while in 80/47 a Ravine is present on the Shoulder and a Saddle on the neck. Thus it is seen that, on fibre

The back, withers, and side arrays are very similar. In 80/47 the withers array is weaker than the other two, which are Saddle, possessing fine sickle, and both checked and non-checked hairy-tip-curly-tip, and curly-tip fibres. It is in fact a most unusual array possessing features of a Ravine, Saddle and Valley and might best be termed "All-in". However, see Chapter 6, Section I. In the other four sheep the withers array is similar in "toughness" to the weaker of the other two arrays. Thus in 351/48 the withers array is a Plateau Grade P_3, similar to that on the side. The same position is seen in 343/48 while in 332/48 the back and withers arrays are Saddle and the side is on the border between Plateau and Saddle. In 353/48 Saddle arrays are present in all three positions. From the above description it will be seen that there is practically no difference between the back and side arrays. Side arrays are weaker in 351/48 and 343/48 while the reverse is true in 332/48. In sheep 353/48 and 80/47 arrays are similar in both positions. On the withers, the average array grading would be about the strength of a strong Saddle, on the side and back about the border between Plateau and Saddle. Back arrays may show slightly greater over-all "toughness" in that two Plateau arrays of grade P_1 are present but it is probably of no significance, especially as in one sheep side is "tougher" than back. However withers arrays would, over the whole picture, appear to be slightly "weaker".

The one Recessive-N britch array studied showed nothing unusual, being a Plateau grade P_1 like those found in many heterozygous Dominant-N sheep.

D: In the double heterozygote genotype (Tables I & 25 - 29 & Graph I) the arrays were collected from sheep born in 1944 and, as the significance of the shoulder patch was not then realised (Dry and Turner 1947) [illegible]

that in the Recessive-N genotype. On the back, withers, and side positions there is remarkable uniformity in the sheep studied and practically no difference between positions. Saddle arrays of very similar "toughness" are present in all three positions of sheep 129/44, 88/44, and 155/44 and the back and withers (the only positions studied) of 9/44. In 42/44 Ravines of approximately similar strength are present on the back and withers, except that in the latter a checked hairy-tip-curly-tip fibre was found, while the array on the side was a Saddle.

Britch arrays in the double heterozygotes studied are all Plateau and these range from one on the border between Grades P_2 and P_3 through one on the border between Grades P_1 and P_2 up to two of grade P_1.

Recessive-N and double heterozygote genotypes are very similar, and in all except one sheep marked gradients occur in fibre type array. The exception is 332/48 which is unusual in that arrays in all positions are Saddle. Whether there is any significance in this or not is not known, but a study of distribution of fibres in 353/48 and 80/47 (Tables 20 & 22) shows that there is not the variation in presence or absence or numbers of various fibre types commonly encountered in heterozygous Dominant-N sheep. Thus there would appear to be a slight suggestion that there may be less variation in arrays from different parts of the body in Recessive-N sheep. Certainly the back, withers, and side arrays in both of these genotypes and more markedly in the double heterozygotes show remarkable uniformity, but then so do some on the heterozygous Dominant-N sheep.

E: In the homozygous Dominant-N genotype (Tables I & 30 - 35 & Graph I) the gradients in most of the sheep studied seem to be much less marked and in some cases altered. Except in sheep 300/48, a very special case which will be described later, all arrays found in all positions of the

other arrays. In sheep 245/48 the shoulder patch array is on the border between Plateau grade P_2 and P_3 and apparently "tougher" than the shoulder array. However, on closer inspection it shows other weaknesses, such as the possession of many halo-hair' fibres, and no super-sickle A fibres, which are completely medullated, while the shoulder array possesses many of the latter and none of the former.

Arrays found on the shoulder and neck positions range from Plateau grade P_3 in 14/50, 245/48, and neck of 15/50, through an array on the border between Plateau P_2 and Plateau P_3 on the shoulder of 15/50, Plateaus grade P_2 on 263/48 up to Plateau grade P_1 on 239/48.

The side arrays in sheep 263/48 and 15/50 are weaker than arrays found in both the shoulder and neck positions. In the formmer grade P_2 Plateaus are found in all positions, but the array on the side possesses a higher percentage of super-sickle A' fibres. In the latter sheep a weak grade P_3 Plateau is found on the side and a strong grade P_3 Plateau is on the shoulder and neck. Sheep 14/50 and 239/48 show side arrays of comparable "toughness" with those on the shoulder, but in both cases slightly "weaker" than the neck arrays. However, this difference is so slight, it is probably of no significance. In sheep 245/48 the side array is "tougher", being a grade P_2 Plateau, than either the shoulder or neck arrays which are grade P_3. Thus in this genotype, there would appear to be no real difference in "toughness" between arrays found in these three positions, a fact of considerable interest in comparison with the findings in other genotypes.

A very anomalous situation is seen when the arrays on the back, withers, and britch are compared. In all the other genotypes, as before shown, the array found on the britch, is, with the exception of sheep 16/50, the

and P_3, on the back, and one on the border between grades P_1 and P_2 on the withers. Here the withers array is the "toughest" found, next comes that on the back, and then that on the britch. This britch array is of comparable "toughness" with that on the neck position possessing a higher percentage of super-sickle A' fibres but fewer super-sickle B. In sheep 14/50 the britch array is a strong grade P_3 Plateau again of comparable "toughness" with that found on the neck. Here the withers array is a grade P_2 Plateau and the back grade P_1. Thus the arrays in ascending order of "toughness" are britch < withers < back compared to britch < back < withers in 15/50.

In the other three sheep 245/48, 239/48 and 263/48 Britch arrays are as tough or tougher as those found on the back and withers except that in 263/48 the back and withers arrays possess only halo-hairs and no super-sickle A fibres but both are present on the britch. If, as suggested by Sutherland (1939) halo-hairs are a fundamentally different type from super-sickle A fibres, this may perhaps indicate a difference between the back and withers and the britch arrays. However there is no difference in the medullation present in the two fibre types so one type of array cannot be said to be "tougher" than the other in that respect.

Back and withers arrays are very similar, the differences being small and contradictory. Thus in 14/50 the withers array is weaker than that on the back, possessing many super-sickle A' fibres but in 15/50 and 239/48 the back arrays are weakest.

Arrangement of arrays in different body positions of homozygous dominant sheep in ascending order of "toughness" would therefore appear to be shoulder patch < shoulder = side = neck < britch < back = withers. Plateaus were found in all positions on all sheep except in

l.	Shoulder Patch	:	Grade P_3
ll.	Shoulder	:	Border between grade P_2 & P_3.
lll.	Side	:	" " " "
lV.	Neck	:	" " " "
V.	Britch	:	Strong grade P_2.
Vl.	Back	:	Border between grade P_1 & P_2.
Vll.	Withers	:	Weak grade P_1.

The arrays of 300/48 (Tables I & 30) show two peculiarities:

(i) Compared with those of other homozygous Dominant-N sheep marked weaknesses can be found, sickle-fibres being present in the side and neck arrays and fine sickles in that of the shoulder patch.

(ii) In contrast with arrays in other genotypes but in keeping with the position in homozygous Dominant-N sheep, the gradients over the body found in the former do not hold.

In this sheep the arrays seem to be divisible into two groups:

(a): Those on the back and withers which are grade P_1 Plateaus, as "tough" as any found in these positions on other homozygous Dominant-N's, and containing only halo-hairs, super-sickle A, hairy-tip-curly-tip, medullated curly-tip, non-medullated curly-tip and non-medullated histerotrich fibres.

(b): Arrays on the side, shoulder patch, shoulder, neck and britch positions which all possess super-sickle B or even more checked fibres. The most checked array included here is a Ravine, with many fine sickles found on the shoulder patch. Next are a strong Saddle found on the side, and an array on the border between Plateau and Saddle found on the neck. The shoulder array is a weak Plateau, grade P_3, with many super-sickle B fibres while that on the britch is a stronger P_3 Plateau.

Section lll:

GRADIENTS OF DIFFERENT GENOTYPES.

There is very little variation over the body in the Non-N genotype but as before stated this is very probably

either Valley or Plain. As far as gradients were found to exist there seemed to be a gradient round the shoulder region cumulating in the extremely checked shoulder patch. Next a fairly well-checked area was found on the side of the neck and another on the side. Back arrays were found to be "tougher" than those on the side but this is only an overall average and does not hold in every case, so that the results here may not be in contradiction with those of Galpin (1936). Withers arrays while less"tough" than those on the back are "tougher"than those on the shoulder. Britch arrays, the "toughest", show much variation.

B: In contrast the heterozygous Dominant-N genotype shows great variation both in fibre type arrays in different parts of the body of the same sheep, as before shown, and between different sheep in the same body positions. e.g. Shoulder patch arrays range from Ravine bordering on Plain in 104/48 and three Valleys up to two Saddle arrays, shoulder arrays range from Valley to one on the border between Plateau and Saddle, neck arrays from truncated and very weak Valley up to a grade P_3 Plateau and withers, sides, back and britch arrays from Valley to grade P_I Plateau. Apart from the anomalous case, seen in 16/50 however, the fibre type array gradients found in other genotypes hold. In this genotype they are just more marked.

C: In the Recessive-N and double heterozygote genotypes the position is very similar to that in the heterozygous Dominant-Ns in all respects, except for some slight suggestion that there may be less of a marked gradient between different body positions than in the heterozygous Dominant-N genotype. If this is so it would be very interesting from the theoretical point of view if the gradients could be genetically reduced when the medullation of the fleece was at a half way stage. e.g. would it be possible to produce a uniformly moderately hairy fleece?

D: In the homozygous Dominant-Ns, apart from sheep 300/48, the fibre type array gradients are much reduced and in some cases reversed. Apart from the shoulder patch being the weakest array, all other positions are fairly uniform

and here the britch array is no longer the "toughest" present; this position being taken in three of the six sheep studied, by the back and withers arrays. Furthermore the side arrays, which in other genotypes are classed next to the withers and back arrays in "toughness" classification, are here relatively much "weaker", and are similar to arrays found on the shoulder and neck. A clue to the situation may be gathered from a study of sheep 300/48, a homozygous Dominant-N but possessing several weak arrays. Here as in other sheep studied the shoulder patch array is weakest. Next in "toughness" come the shoulder, side, neck and britch arrays while the back and withers arrays are again "tougher".

Section IV:

DISSCUSSION AND CONCLUSIONS

A theory to explain these facts is as follows: In the Non-N genotype there exists a very slight gradient in fibre type arrays in different parts of the body. One marked gradient, is as found by Galpin (1936), that extending from the britch to the withers or a posterior anterior gradient. Another is the gradient on the shoulder culminating in the reduced shoulder patch while the neck and side regions also seem to be fairly weakly medullated. Here the basal medulla producing ability of the genotype is insufficient to produce any great degree of fleece hairiness except on the britch. Next with increasing dosage of N-genes this medullation extends over the body, showing its effect first in the areas which possess the "tougher" arrays but extending more and more to those areas where "weaker" arrays are found. As the ability to produce fleece hairiness seems to be expressed more readily in those areas of the body where "tougher" arrays are found, it can easily be seen how gradients would increase in steepness with increasing ability of the genotype to produce fleece hairiness. The heterozygous Dominant-N genotype produces this second stage. Arrays in

Non-N sheep, are "weak" arrays still found. A similar position is found in the double heterozygote and Recessive-N genotypes except for the suggestion before-mentioned, that here the body gradients may be less marked. If this is not a fortuitous result due to small numbers, it does not fit into the theory as above-suggested, but could be due to :

(i) A theoretical postulated effect of the recessive-gene on the body gradients causing these to be less marked.

(ii) Polygene combinations linked to the recessive gene whose effect is to damp down the gradients.

(iii) A chance collection of polygenes, not linked with the Recessive-N gene, in a small stock.

All explanations are unsatisfactory in that they are theoretical attempts to explain away a suspected phenomenon whose real cause if the above is a real effect is unknown.

In the homozygous Dominant-N genotype ability to produce a Plateau array in every region of the body studied has been reached, consequently gradients do not follow the same pattern as in other N-grade genotypes. However if no other complications occurred this would mean a uniform fibre type array all over the body, except for some last lingering effects of lack of ability to produce fully medullated fibres, seen in shoulder patch arrays being slightly weaker than the rest and with the same gradients still present but very much less obvious, as in Non-N sheep but at the opposite extreme of the "toughness" range. However this latter condition is not realised.

In the homozygous Dominant-N's the gradients seem to be altered to some extent and to be in increasing order of "toughness", shoulder patch $<$ shoulder $=$ side $=$ neck $<$ britch $<$ withers $=$ back. In 300/48 there is apparently a lack of ability to produce medullated fibres, but this produces "weakness" in arrays in accordance with the postulated gradients in homozygous Dominant-N's not in

to be known of the mechanism of the productions of gradients themselves and of the physiological and developmental effects of the N-genes, a matter for future research. However, from this it is seen that in contradiction to the findings of Galpin (1936) that when the various N-grade genotypes are taken into account, that the array in the inferior position does not limit the array in the superior position to being no less depressed than itself. The array on the britch does not limit the arrays on the rest of the body to being no less depressed than that on the britch. However, the only lambs studied by Galpin were ordinary flock Romneys, of Non-N genotype and in the few Non-N Romneys studied her findings, are, in the main, supported. It is only in the N-type sheep, more especially in the homozygous Dominant-N that any marked anomalies are found.

However, in heterozygous Dominant-N's one sheep, 16/50, where the britch array was Valley, the back Ravine and the side Saddle, was found to have gradients not according to the general pattern so that even here the statement that arrays in the inferior position limit arrays in the superior position to not being more "tough" than themselves is not an inviolable law, but does not hold in the great majority of cases. Other slight anomalies are found in that arrays in one of the body positions that is classed as "weaker" in fibre type array detail when an average of all cases is taken may possess "tougher" arrays than the "tougher" position placed next to it on the scale, in individual cases. Conversely a "tougher" position may possess an array weaker than the one in "weaker" position next to it on the scale. This overlapping is seen to occur between shoulder and neck, neck and withers, withers and side, and side and back positions.

CHAPTER V.

COMPARISONS BETWEEN INDIVIDUAL FIBRE TYPES, BETWEEN POSITIONS AND BETWEEN GENOTYPES.

Section I. INTRODUCTION.

The purpose of the investigations included in the present chapter was to study the differences in the percentages of the individual fibre types present, between genotypes and between different positions of the body. The differences between the different fibre type arrays Plateau, Saddle etc. are based on the presence or absence of only one or two different fibre types (Chapter 2), the rest being ignored. A study by Ross and Wright (I.P.) has shown that real differences do exist between percentages of different fibre types present on the standard back position. For statistical purposes in the present chapter all percentages were transformed by using Bliss's transformation : angle = arc sin $\sqrt{\%}$ (Snedecor 1946 P. 447) as most percentages were under twenty and the data was heavily skewed. For the following work the fibres were all placed in the fibre type groups halo-hair, halo-hair', super-sickle A, super-sickle A', super-sickle B, fine super-sickle B, sickle, fine sickle, checked curly-tip, hairy-tip-curly-tip, medullated curly-tip, non-medullated curly-tip, medullated histerotrich and non-medullated histerotrich. The fibre type curly-tip big as hairy-tip-curly-tip, i.e. those pre-precipice-curly-tip fibres in arrays where precipices occurred, was here placed with the smaller medullated curly-tips in the medullated curly-tip fibre group. This was because these fibres could only be distinguished in arrays where a precipice occurred. They will be dealt with later under the chapter on precipice.

In the present chapter the statistical method was similar to that in the analysis of the medullometer

A. Comparisons of the means of halo-hair percentages present between different genotypes in all regions of the body show that differences at the 1% level exist in all positions.

On the shoulder patch the only real difference is that between the homozygous Dominant-N and all other genotypes which is at the 1% level of significance. Similarly on the neck position although here there is also a real difference at the 1% level between halo-hair abundance in the Non-N and Recessive-N genotypes.

On the shoulder position there is only a real difference, again significant at the 1% level between the means of the Non-N and the Recessive-N and homozygous Dominant-N genotypes while on the withers position there is a separation of the genotypes into three groups on halo-hair abundance. The Non-N genotype has the least abundance of halo-hairs and the mean of the percentage in this genotype differs at the 5% significance level from the means of all other genotypes. There is no real difference between the means of the percentage of halo-hairs present in the three genotypes heterozygous Dominant-N, double heterozygote, or Recessive-N, these forming a group intermediate in halo-hair abundance. The homozygous Dominant-N genotype's mean of halo-hair percentage differs significantly at the 1% level from the mean of all other genotypes, being of a greater order of magnitude.

On the side, back and britch positions the halo-hair abundance in the Non-N genotype differs significantly at the 1% level, in being much lower than that in the N-grade genotypes. Among the N-grade genotypes themselves in these positions the only real difference in halo-hair abundance is that between the heterozygous Dominant-N and homozygous Dominant-N on the back position, the heterozygous Dominant-N genotype possessing fewer halo-hairs.

before suggested there is probably less variation than normal in the flock from which the samples were taken. Common observation would suggest that there are more halo-hairs in these Non-N lambs where there is an appreciable number of these fibres, on the back than on the side and withers. However, significant differences at the 1% level exist between positions in all other genotypes.

In the heterozygous Dominant-N genotype no significant differences are seen in halo-hair abundance between the shoulder patch, neck, shoulder and withers positions or between the side and back positions. However the former group of positions possesses less halo-hairs than the latter, the difference being at the 5% significance level. Also the mean of the percentage of halo-hairs present on the britch is found to be significantly greater than the mean of halo-hair percentage present on any other region of the body.

In the double heterozygote genotype the withers and side positions form one group of lower halo-hair abundance than another group formed by the back and britch positions but no other real differences are seen.

In the Recessive-N genotype the mean of the percentage of halo-hairs present on the shoulder patch position is significantly lower, at the 5% level, than that found on any other position of the body studied. The means of all the other positions however form a graded series, in ascending order, neck, withers, shoulder, side and back, not divided into any groups but having the extremes significantly different from each other. Thus the back position mean is significantly different, at the 5% level from that on the neck and withers, but this procedure should be adapted cautiously as stated elsewhere, (See Part III; also Tukey 1949).

In the homozygous Dominant-N genotype the means

back. In this series the back position mean is seen to be significantly greater at the 5% level than the means of all other positions but between other positions there are only significant differences between the means at extremes of the series such as between those of the britch, and those of the shoulder and shoulder patch position.

C. Changes in the differences between positions between genotypes show that the greatest differences between positions are found in the heterozygous Dominant-N genotype and the least in the Non-N and homozygous Dominant-N genotypes. All the Non-N sheep positions show a very low abundance of halo-hairs and there is no real difference between the means of halo-hair percentage in any position.

The Recessive-N, heterozygous Dominant-N and double heterozygote genotypes form a group, intermediate in halo-hair abundance and no real difference between these genotypes is seen in halo-hair abundance in any body position. In the heterozygous Dominant-N genotype the body positions are in three groups as regards halo-hair abundance. Shoulder patch, neck, shoulder and withers positions form one group of low halo-hair abundance, side and back positions another group of intermediate halo-hair abundance while the britch possesses a significantly greater abundance of these fibres than any other position. Of the four positions studied in the double heterozygote genotype the withers and side positions form a group of significantly lower-halo-hair abundance than the back and britch positions. In the Recessive-N genotype the shoulder patch mean of halo-hair percentage is significantly lower than that of all other positions but the means of the latter form a graded series with real differences existing between extremes of this series.

The homozygous Dominant-N genotype possesses the highest halo-hair abundance of any genotype studied. It

fact is that here the back position possesses significantly more halo-hairs than all others positions including the britch. This however is in keeping with what is found in regard to gradients over the body in fibre type array in homozygous Dominant-N sheep. For the other positions a graded series, with increasing halo-hair- abundance, is found from the shoulder patch to the britch. The differences between the positions found in the heterozygous Dominant-N, Recessive-N and double heterozygote genotypes seem to be removed by the halo-hair abundance increasing on those body regions where it is low.

Section III.

COMPARISONS BETWEEN HALO-HAIR' FIBRES.
(See Table 37 A & B)

In all except the comparisons between genotypes on the shoulder patch and comparisons between positions in the homozygous Dominant-N genotype halo-hair' fibres were too few in number to give any real difference between the means of percentages of fibres present. In the above-mentioned cases, however, real differences do exist.

In the comparisons between genotypes on the shoulder patch it is seen that the homozygous Dominant-N genotype possesses far more halo-hair's than are found in any other genotype, the difference here being significant at the 1% level. Indeed, halo-hair' fibres are hardly present at all in any other genotype studied on this position.

In comparisons between positions in the homozygous Dominant-N genotype differences at the 5% level exist. On all positions except the shoulder and shoulder patch very few of these fibres are found and even the shoulder does not possess significantly more than other body positions. However on the shoulder patch of this genotype the mean of the percentage of halo-hair' fibres is significantly greater than that of any other position.

Section IV:

the shoulder, neck and side positions and at the 1% level on the back and britch positions. However, on closer examination it is seen that in all cases it is the Non-N genotype that possesses significantly less super-sickle A fibres than any of the N-grade genotypes. The differences here are of the same level of significance, as those found between genotypes as a whole. No real differences are found between any of the N-grade genotype.

B: However in contrast to between positions within genotype analysis shows that real differences occur between positions in all the N-grade genotypes, but not in the Non-N. These differences are at the 5% level in the homozygous Dominant-N genotype and at the 1% level in the rest. In the heterozygous Dominant-N genotype the positions can be arranged in ascending order of super-sickle A abundance as follows: shoulder patch, withers, neck, back, side, shoulder and britch. Not much besides the fact that significant differences in super-sickle A abundance do occur between these positions, can be said, for there are no sharply defined groups of positions. Features of interest, however, are the low abundance of super-sickle As on the withers and the high abundance on the shoulder in comparison with the position with regard to over-all hairiness as measured by the medullometer. However the result may be explainable on the grounds that there are less pre-curly tip fibres on the withers position and a greater abundance on the shoulder. (See later.)

In the double heterozygote genotype the withers position is low in the number of super-sickle A fibres present and differs from the other three positions in this factor at the 1% significance level. The side and back positions form another group of intermediate super-sickle A abundance while on the britch position the mean of the percentage of super-sickle A fibres present is significantly

a graded series in super-sickle A abundance occurs, with overall significant differences between the means of the percentages, but no sharply defined groups being present. In the Recessive-N genotype the series is in increasing order of super-sickle A abundance: shoulder patch, withers, neck, back, shoulder and side, while in the homozygous Dominant-N genotype it is withers, shoulder patch, back, neck, side, shoulder and britch. Here again as in the heterozygous Dominant-N genotype there is a low percentage of super-sickle A fibres on the withers and a high percentage on the shoulder position.

Section V: COMPARISONS BETWEEN SUPER-SICKLE A' FIBRES. (See Table 39)

There are real differences between the different genotypes only in the means of the percentages of super-sickle A' fibres on the shoulder patch and side regions. These differences are at the 1% level in the case of the shoulder patch position and at the 5% level on the side. Closer inspection shows that on the shoulder patch the mean of the percentage of these fibres is higher in the homozygous Dominant-N genotype than in any other, this difference being at the 5% level. The other three genotypes form a series in increasing order of fibre abundance as follows: Non-N, heterozygous Dominant-N, Recessive-N. The only real difference is between the means of the Non-N and Recessive-N genotypes. On the side position the genotypes also form a series, in increasing order of abundance of fibres as follows: Non-N, heterozygous Dominant-N, Recessive-N, double heterozygote and homozygous Dominant-N. No sharply defined groups are found but differences at the 5% level do exist between genotypes.

The only real differences between positions are found in the heterozygous Dominant-N genotype. Here again only a series of means is formed with no sharply defined

these positions. The order of the series is different from that found in halo-hairs and super-sickle A fibres and the change is probably due to these fibres being characteristic of neither very "tough" nor yet very "weak" medullation.

Section V1:

COMPARISONS BETWEEN SUPER-SICKLE B FIBRES.
(See Table 40 & Graph 4)

A: Comparisons between genotypes in different positions show that real differences exist here on all positions except the side and britch.

On the shoulder patch region differences at the 5% significance level exist between genotypes. The Non-N genotype possesses less super-sickle B fibres on this position than the N-grade genotypes and this difference is significant. None of the N-grade genotypes show any real differences among themselves.

On the shoulder and neck positions, differences at the 1% level of significance exist between genotypes. On both positions there are no fibres of this type present in the Non-N genotype and this is significantly less, at the 5% level than the number present in any N-grade genotype. On the shoulder the Recessive-N genotype also contains significantly more super-sickle B fibres than are found in the homozygous Dominant-N but no other real differences exist in either position.

On the withers and back positions the order of genotypes in a scending order of abundance of this fibre type is: Homozygous Dominant-N, Non-N, heterozygous Dominant-N, Recessive-N and double heterozygotes. On the withers there is a difference significant at the 5% level between the percentages of these fibres present in the Non-N and Heterozygous Dominant-N sheep. All the other genotypes in this position and all genotypes in the back form a graded series, but between which real differences do exist, no distinct groups being found.

Non-N and homozygous Dominant-N genotypes.

B: A between position within genotype analysis shows that significant differences do exist between positions in all genotypes except Recessive-N. In the Non-N genotype the britch position possesses a significantly greater percentage of super-sickle B fibres than any other position, but no real differences exist elsewhere. In the heterozygous Dominant-N and double heterozygote genotypes the position is the reverse to that found in the Non-N. The britch position in both cases possesses the lowest abundance of super-sickle B fibres. In the heterozygous Dominant-N genotype there is just a graded series in increasing order of fibre abundance: britch, back, withers, side, shoulder patch, neck and shoulder between which positions, differences at the 1% significance level do exist. In the double heterozygote the britch mean of the percentage of super-sickle B fibres present is significantly lower than that on the withers, side and back positions but between the latter no real differences exist. In the homozygous Dominant-N genotype the abundance of super-sickle B fibres forms a graded series in increasing order: withers, back, britch, side, neck, shoulder and shoulder patch. The shoulder patch shows a significantly greater (at the 5% level) abundance of these fibres than any other position. The other positions only form a graded series between which only a doubtfully significant difference between the extreme members exists.

C: When the differences in the percentage of super-sickle B fibres present between positions are studied between genotypes the interaction is seen to be very complex and interesting and emphasizes the position of these fibres denoting intermediate medullation. In the Non-N genotype these fibres denote "toughness" and are found mainly on the britch position, the most hairy region studied in this

denote "weakness" as seen in the heterozygous Dominant-N, double heterozygote and more especially in the homozygous Dominant-N genotype. Here the least abundance of these fibres is found on the most hairy parts of the fleece, in those positions studied, namely on the britch position and the back and withers of homozygous Dominant-N sheep.
In the heterozygous Dominant-N genotype the greatest abundance is found on the shoulder, neck and shoulder patch positions. Unfortunately these positions in the double heterozygote were not available for study. An interesting point is the lack of any real differences between positions with regard to these fibres in the Recessive-N genotype, but this may be partly due to the britch position not having been studied.

Section V11:

COMPARISONS BETWEEN FINE SUPER-SICKLE B FIBRES. (See Table 37 C.)

In all comparisons of fine super-sickle B fibres except that between positions in the heterozygous Dominant-N genotype too few of these fibres were present to give any real differences. However in the above-mentioned case real differences at the 5% significance level do exist between positions. On closer examination it is seen that the shoulder patch position contains appreciably more of these fibres than any other position except the neck where the mean of the percentage of finesuper-sickle B fibres is intermediate between that on the shoulder patch and that on other regions. The t test shows that a real difference exists between the mean of the shoulder patch position and the means of all other positions except the neck. No other significant differences exist.

Section V111:

COMPARISONS BETWEEN SICKLE-FIBRES.
(See Table 41 & Graph 5)

A: Comparisons between genotypes in different

characteristic of the genotypes intermediate in hairiness. i.e.: the heterozygous Dominant-N, Recessive-N and double heterozygote. However on the most hairy position namely the britch, these fibres are characteristic of the least hairy Non-N genotype.

On the shoulder patch, neck and shoulder positions both the very weakly hairy Non-N genotype and the very strongly hairy homozygous Dominant-N form one group possessing very few of these fibres. The Recessive-N and heterozygous Dominant-N genotypes form another group in all three cases possessing a significantly greater number. On the withers and side positions a series in increasing order of sickle fibres abundance is found as follows: Homozygous Dominant-N, Non-N, heterozygous Dominant-N, Recessive-N, and double heterozygote. No sharply defined groups are found here but between the genotypes real differences, at the 1% level on the withers and at the 5% level on the side do exist. As in previous cases of this nature the extremes of the series show real differences upon application of the t test, but these are obscured by overlapping from adjacent genotypes.

On the britch position, however, the Non-N genotype shows a significantly greater, at the 1% level, percentage of sickle-fibres, than any other genotype. No real differences however are found to exist between any N-grade genotype.

B: Between positions within genotypes real differences in sickle-fibres abundance are only found in the heterozygous Dominant-N and double heterozygote genotypes. In the heterozygous Dominant-N genotype a series is formed, in increasing order of sickle-fibres abundance, as follows: britch, side, back, withers, neck, shoulder and shoulder patch. Real differences at the 1% significance level exist between these positions but no sharply defined

difference is significant at the 1% level but no real differences are found between any of the other positions.

In the Recessive-N genotype, as with the super-sickle B fibres a uniformly high abundance of sickle-fibres with no real differences between positions is found while there is a low abundance of these fibres in both the Non-N and homozygous Dominant-N genotypes.

Section 1X:

COMPARISONS BETWEEN FINE SICKLE-FIBRES.
(See Table 42 & Graph 6)

On studying the means of the percentages of these fibres present between positions within genotypes and between genotypes within positions it is found that they are characteristic of very weakly medullated genotypes and positions; namely the Non-N genotype and the shoulder patch position in the heterozygous Dominant-N and Recessive-N sheep. Statistical tests of significance give the following results:

A: Between genotypes within positions significant differences are found to exist in all positions except the shoulder patch. On these positions namely the neck, shoulder, withers, side, back and britch positions, the Non-N genotype is found to possess a significantly higher (in all cases at the 1% probability level) percentage mean of fine sickle fibres than is found in N-grade genotypes. No real differences are found within any of the N-grade genotypes themselves, and they all contain in all positions except the shoulder patch, very few of these fibres.

B: In the between position within genotype analysis real differences between positions are found in only the heterozygous Dominant-N and Recessive-N genotypes. In both these cases the mean of the shoulder patch position is significantly higher than the mean of all other positions at the 1% probability level. In the Recessive-N genotype no real differences exist between any of the other positions.

difference between the extreme members of this series. However as already stated this result must be accepted with caution.

In the Non-N genotype there is a uniform high abundance of fine sickle-fibres and in the homozygous Dominant-N and the positions studied in the double heterozygote genotype a low abundance is present throughout. There is no real difference between positions in any of these genotypes.

Section X:

COMPARISON BETWEEN CHECKED CURLY-TIP FIBRES.
(See Table 43 & Graph 7)

As with the fine sickle-fibres, these fibres are characteristic of the Non-N genotype but they are however not found in any great quantity on the shoulder patch position in any genotype.

Between genotypes within positions significant differences are found on all positions except the shoulder patch. On the neck, shoulder, withers, side and back positions, the Non-N genotype has a high abundance of checked curly-tip fibres and all the N-grade genotypes a low abundance, this difference being significant at the 1% level. On the britch a similar position is found but there are fewer checked curly-tip fibres in the Non-N genotype and the difference here is only at the 5% probability level.

Between positions within genotypes real differences only exist in the Non-N genotype. In all the N-grade genotypes studied abundance of these fibres is too low to give any real differences in any comparison which could be made.

In the Non-N genotype however, a low abundance of checked curly-tip fibres is found on the shoulder patch and britch regions and a high abundance on every other position. The low abundance of checked curly-tips on the

genotype. The reason for the reduced abundance of these fibres on the britch was however due to this position being "tougher" than the other regions studied. A significant difference at the 1% level exists between these two groups of positions but there are no real differences within either of the groups.

Section XI:

COMPARISONS BETWEEN HAIRY-TIP-CURLY-TIP FIBRES. (See Table 44 & Graph 8)

These fibres are found mainly on the N-grade, more especially the homozygous Dominant-N, genotypes. The only appreciable number found on the Non-N genotype were on the britch but even on the shoulder patch position of the heterozygous Dominant-N and Recessive-N genotypes these fibres were found.

A: In comparisons between genotypes within positions significant differences are found to exist on all positions. On the shoulder patch a real difference at the 5% significance level exists between the mean of the percentage of hairy-tip-curly-tip fibres found in the homozygous Dominant-N genotype and those of all other genotypes. No real differences are found within the latter however.

On the neck position the Non-N differs at the 5% level from the N-grade genotypes in possessing less of this fibre type. Between the N-grade genotypes the means form a graded series and between the members of this series real differences at the 5% level exist. Between genotypes on the neck, as on the shoulder, withers, side, back and britch, significant differences at the 1% level exist.

On the shoulder the homozygous Dominant-N genotype possesses significantly more hairy-tip-curly-tips than any other genotype, as on the shoulder patch, but there are also real differences here between a graded series of means formed by the Non-N, heterozygous Dominant-N, and Recessive-N genotypes. On the withers, the Non-N genotype

series with a real difference existing between the heterozygous Dominant-N and Recessive-N genotypes and the homozygous Dominant-N. On the side, back and britch the means in the Non-N genotype are lower than those of the N-grade genotypes this difference being significant at the 5% level on the side and the 1% level on the back and britch. No real difference between the means of the N-grade genotypes in any of these positions is seen.

B: Between position within genotype analysis shows that real differences occur between the means of the percentages of hairy-tip-curly-tip fibres, at the 1% significance level in the heterozygous Dominant-N and double heterozygote genotypes and at the 5% level in the homozygous Dominant-N genotype. In the latter case the shoulder patch position possesses significantly less of the fibre type than any other position but no other real differences are found.

In the double heterozygote genotype the britch possesses significantly more, (at the 5% level) hairy-tip-curly-tip fibres than are found on the back, withers and side. There are no real differences between these latter positions however. In the heterozygous Dominant-N genotype the means in the various positions form a graded series as follows: Shoulder patch, shoulder, neck, withers, back, side and britch in increasing order of abundance of this fibre type. No groups of positions are found to be separable but real differences at the 1% level do exist.

No real differences exist between positions in the Non-N and Recessive-N genotypes.

C: When the changes in the differences between positions between different genotypes are studied not much information can be found. To begin with, as stated above, real differences between positions only occur in three N-grade genotypes. In the Non-N genotype a uniformly

homozygous Dominant-N genotype a uniformly high abundance of these fibres is found on all positions except the shoulder patch while in the double heterozygote and heterozygous Dominant-N genotype the abundance shows more variability with a tendency for the britch to possess more fibres of this type than other positions. The only thing this would tend to show is that these fibres denoting fleece hairiness have reached their full abundance in the homozygous Dominant-N genotype on all positions except the shoulder patch, but have not done so in the less hairy genotypes.

Section X11:

COMPARISON BETWEEN MEDULLATED CURLY-TIP FIBRES. (See Table 45)

These fibres were in most arrays present in large numbers. A considerable error variance combined with fairly high, uniform means in the N-grade genotypes meant that few real differences were found here.

A: Between genotypes within positions real differences exist on the shoulder patch, neck, withers and side positions. On the shoulder patch and neck the non-N genotype possesses a lower abundance of medullated curly-tips fibres than is found on any N-grade genotype, this difference being significant in both cases at the 1% level. No real differences are seen between any N-grade genotypes in these positions.

On the withers a similar distribtution of means to that on the shoulder patch and neck is found except that here the difference is at the 5% significance level only.

On the side position the means form a series in ascending order of fibre abundance, as follows: Non-N, Recessive-N, heterozygous Dominant-N, double heterozygote and homozygous Dominant-N. No groups of positions with means distinct from the rest are found but statistical analysis shows that differences at the 1% level do exist

genotypes of intermediate "toughness" are distinct. Although there is only one chance in twenty that this result is due to random variation this possibility cannot be ignored, together with the fact that here means at the extremes of a graded series are being compared.

Section XIII:

COMPARISONS BETWEEN NON-MEDULLATED CURLY-TIP FIBRES. (See Table 46)

As with medullated curly-tip fibres and as is also found with non-medullated hysterotrichs large error variances occur here together with a fairly high and uniform value of the means for these fibres. Consequently statistical analysis shows very few significant differences between means.

Between genotypes within positions real differences are only found on the shoulder patch and side positions. On both positions no genotypes are significantly different from all other genotypes but a series is formed, between which in both cases differences at the 5% significance level exist. Here the abundance of these fibres is low in heterozygous Dominant-N and homozygous Dominant-N genotypes in both cases and in the double heterozygote on the side while it is high in the Non-N genotype. On the side here as with medullated curly-tips a real difference exists in abundance of fibres in the heterozygous Dominant-N and Recessive-N genotypes.

Between position within genotype comparisons show that real differences at the 5% significance level exist in the Non-N and Recessive-N genotypes. Here as in comparisons between genotypes the means just form a graded series. In the Non-N genotype there is seen to be a low abundance of these fibres on the britch and back and a high abundance on the neck and shoulder patch. In the Recessive-N genotype there is a low abundance on the back and withers and a high abundance on the shoulder and shoulder patch.

positions in some genotypes. Thus it would seem, as is expected, that these fibres denote lack of hairiness if anything, but against this there is a slightly higher abundance in the Recessive-N genotype in some positions.

Section XIV:

COMPARISONS BETWEEN HISTEROTRICHS.
(See Tables 47 & 48)

It should be borne in mind that the results for this class of fibre where they differ from the findings of others, should be treated with extreme caution as not all histerotrich fibres were present when the wool samples were collected. Furthermore many histerotrich fibres were very small and extreme care was needed so that none should be lost when sorting out fibres into arrays.

No real differences were found in any comparisons between medullated histerotrichs and between non-medullated histerotrichs, the only real difference found is between positions on the homozygous Dominant-N genotype where differences at the 1% significance level do exist. Here a graded series is found with a low abundance of these fibres on the britch and shoulder and a high abundance on the shoulder patch. Thus here, histerotrich abundance does not run parallel to degree of "toughness" of the various positions.

As most investigators have only studied total histerotrich fibres, the total of the medullated and non-medullated histerotrich fibres added together was studied to give the following result. (Table 49)

Between genotypes within positions the only real difference is found on the shoulder position. Here the means form a graded series, in increasing order of fibre abundance: homozygous Dominant-N, Recessive-N, heterozygous Dominant-N, Non-N. Between the means differences at the 5% level exist and further examination shows the homozygous Dominant-N mean to differ significantly from

and homozygous Dominant-N genotypes. In the former the means again form a graded series with a low abundance of histerotrichs on the shoulder and britch and a high abundance on the withers and shoulder patch. In the homozygous Dominant-N genotype a similar position exists. This is also similar to the position found in this genotype when the non-medullated histerotrichs alone were studied.

Other investigators have found (Goot 1940, Sutherland 1939) a high abundance of histerotrich fibres in the more hairy arrays, especially in Plateau. Although the study here is between different body regions and different genotypes rather than between different arrays, between genotypes on the shoulder the greatest abundance of histerotrichs is found in the least hairy genotype, and the least abundance in the hairiest genotype. In the two cases where real differences are found between positions within genotypes the abundance of histerotrichs does not seem to run parallel to the degree of "toughness" of arrays on a position.

Thus it is found that there is very little difference in histerotrich abundance between any genotype or between any position within a genotype. The one significant difference between positions within genotypes seems to be directly contrary to the findings of Sutherland and Goot while between positions as stated above, histerotrich abundance does not parallel "toughness".

The reasons for this discrepancy may be as follows:

1. The histerotrichs were not all present when the samples were taken and the differences observed by Goot and Sutherland were due to histerotrichs appearing for a longer period of time in the more hairy arrays. This theory is supported by the theory of Goot's (1940) that during the development of the fleece the growth of histerotrichs has

early February, those studied by Sutherland were taken in October and November as were the samples studied in this work and when not all histerotrichs were present.

2. Variation in the number of histerotrichs in arrays of varying "toughness" is obscured by error variance within positions and genotypes. There may be a slight effect of this kind but it would be unlikely to obscure the variation in relative histerotrich number found by the two authors quoted above.

Section XV:

COMPARISONS BETWEEN TOTAL PRE-CURLY-TIPS.
(See Table 50 & Graph 9)

As Galpin (1934) has studied differences in the abundance of pre-curly-tip fibres (Halo-hairs, super-sickles, sickles and fine sickles) in different regions of the body it was thought that additional information on this point could be provided by the present work.

Between genotypes within positions it is found that on the shoulder patch, shoulder and back positions, the Non-N genotype possesses less pre-curly-tip fibres than are found in other genotypes this difference being significant at the 1% level. However too much importance should not be attached to this difference as in the Non-N genotype many baby sickle fibres, shed before birth, (Dry 1935), occurred so that the total here may be somewhat less due to these being lost.

Between positions within genotypes, in the Non-N genotype, the one studied by Galpin (1934), it was found that there was a series in ascending order of pre-curly-tip abundance as follows: Shoulder patch, withers, neck, back, shoulder, side and britch with an over-all analysis giving 1% differences between positions. The shoulder patch differs, at the 5% level from the means of all positions except the withers, the withers mean differs from those of the side and britch. No other real differences are found.

Withers, neck, side, back, shoulder patch, shoulder and britch. In both cases the withers position possesses significantly fewer of these fibres than are found on all other positions except the neck. In the heterozygous Dominant-N genotype the means of the withers and neck positions differ significantly at the 1% probability level from the means of all other positions. There are no real differences within either of these two groups. In the homozygous Dominant-N genotype the means form a series between which differences at the 1% level exist but no well defined groups of means are seen.

In the double heterozygote genotype the withers mean is significantly lower, at the 1% level, from those of the side, back and britch. Between the latter no real differences exist.

In the Recessive-N genotype the order of positions in increasing order of means, is withers, neck, shoulder patch, side, back and shoulder. Here differences at the 1% level exist between positions but again no distinct groups are found. The shoulder patch occupies a relatively lower place in this series than in the other N-grade genotypes but this may not be significant.

In the Non-N genotype a low abundance of pre-curly-tip fibres is found in the shoulder position and a high abundance on the side. In all N-grade genotypes the outstanding factor is the low abundance of these fibres on the withers and neck, and the fact that the order of positions arranged in increasing mean value is very similar although the significance of this latter effect is in doubt.

Galpin (1934) in studying abundance of pre-curly-tip fibres in the New Zealand Romney grouped the positions in order of diminishing counts as follows:

Poll	A area
Ventral Neck	B area
Shoulder Point	C area

Her theory to account for variation in the abundance of pre-curly-tip fibres is that when fibres and follicles appear earlier on the body region of the foetus there are a greater proportion of pre-curly-tip fibres in the array. This is supported by a detailed exaimination of the time of appearance of follicles on the foetus in the New Zealand Romney, (Galpin 1935.). Carter and Hardy (1947) studying the Merino also found that from the poll posteriorly to the sacrum development became less advanced. Compared with the work of Galpin, broadly speaking, the stage relations were the same and the regional variations very similar.

As the gradients in pre-curly-tip abundance discovered here were not similar to those discovered by Galpin it is suggested that the above theory should be thoroughly investigated. The low abundance of pre-curly-tip fibres on the Non-N shoulder patch may be a false effect due to shedding of baby sickles, but the main discrepancy in comparison with the results of Galpin is the low abundance on the withers. Unfortunately the side of the neck was not studied by Galpin, so no comparison is possible here. However, Wildman (1932) in different British breeds of sheep and Carter and Hardy (1947) in the merino have found that follicles development appears first on the head and neck. This, if it occurs in N-type Romneys would seem to invalidate Galpin's theory, but as stated above a full investigation is necessary. Another anomalous fact, but whose significance is doubtful is the high abundance of pre-curly-tips on the back and britch. As stated by Galpin, the pre-curly-tip fibre gradients do not parallel the fibre type array gradients over the body and variations in "toughness" do not seem to have much, if any, effect.

Section XVI:

and genotypes, the fibres intermediate in hairiness on those positions and genotypes intermediate in hairiness while fibres showing little or no hairiness are found in the least hairy positions and genotypes.

The distribution of the means of the percentages of fibres present in the halo-hair and hairy-tip-curly-tip fibre types closely parallels the result obtained from a comparison of the fibre type arrays (Chapter 4) and the results of the medullometer tests. These fibre types are, together with super-sickle A fibres, the hairiest fibres seen in the pre-curly-tip and curly-tip fibre groups. Super-sickle A fibres however seem to reach their full abundance in the genotypes and positions intermediate in hairiness after which no significant differences between means are seen. This would seem to suggest that these fibres are an indication of slightly less "toughness" than halo-hairs and hairy-tip-curly-tips.

The position in the super-sickle A' fibres is similar to that seen in the super-sickle As except that here there are very few real differences seen between means and a very even distribution of fibres is seen in the double heterozygote, Recessive-N and homozygous Dominant-N genotypes. The heterozygous Dominant-N genotype possesses greater differences between positions.

The super-sickle B fibres are characteristic of genotypes and positions intermediate in hairiness and as such in the Non-N genotype they denote strength being found mainly on the britch. In the N-grade genotypes, except the homozygous Dominant-N, there is a tendency for more of these fibres to be found on the shoulder patch and fewer on the britch. In the homozygous Dominant-N genotype these fibres more strongly denote weakness, the greatest number being found on the shoulder patch, and the least number on the withers and back, the positions which on

except that practically none of these fibres are found in the homozygous Dominant-N genotype. This may be taken as indicating that these fibres are characteristic of greater "weakness" of medullation. However their appearance in this genotype would seem to suggest that the coat of these animals is still far from that characteristic of the primitive sheep such as the Mufflon.

Fine sickle-fibres and checked curly-tips are the fibres only found in the "weakest" positions and genotypes the only anomaly here being that the "weakest" position of the "weakest" genotype namely the Non-N shoulder patch has no checked curly-tips. This is because the "weakest" array Plain has none of these fibres but they are characteristic of the tougher Valley array. This is due to the fact that to separate the checked curly-tips from those non-medullated through lack of basic medulla producing ability, some medullated curly-tips must be present. When these were absent, as in the Plain array all curly-tip fibres were called curly-tips, non-medullated. Apart from this discrepancy these two fibre types are found mainly in the Non-N genotype in all positions and on the shoulder patches of the heterozygous Dominant-N and Recessive-N sheep. They also occur on a few other of the "weaker" positions in the heterozygous Dominant-N sheep.

Medullated curly-tips and non-medullated curly-tips occur in abundance in all except a few arrays and consequently there is not much real difference between either positions or genotypes. Where real differences do occur however, medullated curly-tips are found in greater abundance on the more hairy positions and genotypes and the non-medullated curly-tips on the less hairy.

Histerotrich abundance, both that of medullated histerotrichs, non-medullated histerotrichs and the total for this fibre group showed very little variation either

more hairy arrays possess greater histerotrichs abundance, are not supported although this conclusion is very tentative.

Abundance of total pre-curly-tips was also studied and the most outstanding feature here was the low abundance of these fibres on the withers and neck positions and on the Non-N shoulder patch. This is in contrast to the findings of Galpin (1934) who discovered a fairly high abundance of these fibres on the withers. Her theory to account for differences in pre-curly-tip abundance in different body positions is that where fibres and follicles appear early on the foetus a greater abundance of pre-curly-tips fibres will be found. No study was made, in the present work, of the time of appearance of fibres or follicles in the foetus but Ross (1945) has investigated this question and found that in the N-type the time and order of appearance of the follicles on the foetus is similar to that in the Non-N Romney (Galpin 1935). However it is suggested that the whole position should be investigated, especially in relation to Galpin's theories.

CHAPTER VI

UNUSUAL ARRAYS FOUND

Section I: The array on the withers of 80/47.

This array was found on only one of the Recessive-N withers studied and no significance is attached to its appearance. It is however, interesting as a curiosity.

80/47 WITHERS ARRAY.

FIBRE TYPES

HH.	SSA.	SSA'.	SSB.	SK.	SK FINE.	HTCT CHKD.	CT CHKD.	HTCT.	CT MED.	CT NON-MED.	HI NON MED.
.87	.65	-	.43	I.30	.43	.43	.22	I.0%	38.04	I7.I7	29.35

The array contains a few halo-hairs, super-sickle As, and super sickle Bs. The first appreciable number of fibres is contained in the sickle-fibre group, and these are followed by a few fine sickles, checked hairy-tip-curly-tips, and checked curly-tips. Medullated curly-tips, non-medullated curly-tips, and histerotrichs complete the array. If these were all the fibre types present, the array could be classed as a Valley although unusual in that checked hairy-tip-curly-tip fibres are present. However, beside these fibres an appreciable number of hairy-tip-curly-tips, not checked, are also present. These could perhaps be considered as the peak of the curly-tip series and on inspection it was found that three of the hairy-tip curly-tip fibres found had fewer curls in the curly-tip region than some of the curly-tip fibres. However, there are two other hairy-tip-curly-tip fibres which did not belong in this category. These however, resembled the sickle-fibres and may be classed as sickles with a curly-tip rather than a sickle end.

If the above reasoning is correct then the whole array can be regarded as a Valley bordering on Ravine with anomalous hairy-tip-curly-tip fibres in parallel.

The other alternative is to regard the array as a true "All-In", with both the characters of a strong Valley, containing fine sickle, checked hairy-tip-curly-tip and

checked curly-tip fibres and of a Saddle containing sickle and hairy-tip-curly-tip fibres.

The first alternative is more tenable in view of the idea of a single head check acting on the array, and the facts are not sufficient to contradict it, but care must be exercised in drawing any conclusions on such limited data.

Section 2:

ARRAYS ON SHEEP 178/48

(See Table 7.)

Other arrays studied of considerable interest are those on sheep 178/48 a border-line-N of grade VI halo-hair abundance on the back at birth. This sheep had arrays in all body positions that were Valley, except the britch where a Saddle array was found.

However in all these arrays the basal medullation was very strong, and medullated histerotrichs occur throughout. The greatest development of this extreme was seen in the side array, a Valley with a precipice. Here the pre-precipice fibres were all long and fairly thin, including one hairy-tip-curly-tip fibre in the array. However, in contrast with the normal finding, the post-precipice fibres were on eye grading coarser and much more stoutly medullated than the pre-precipice fibres although shorter. This medullation continued well into the histerotrich fibres. Although a sharp precipice such as above only occurred in the side and britch arrays, all other arrays in this sheep exhibited the same type of phenomenon, namely a well checked array in the pre-curly-tip and some of the curly-tip fibres with fine sickles and checked curly-tips in all positions except the britch, the fibres all being thin and weakly medullated showing the effects of the check, followed by stout fibres with strong medullation that continued right into the histerotrich fibres.

The degree of "toughness" as shown by the first half of these arrays was generally only encountered in weakly medullated fleeces and where a strong head check

basal medullation. What seems to have occurred here is that a strong head check is operating on strong basal medullation showing that there are indeed as Goot (1940) and Sutherland (1939) have suggested, two independent forcexs at work producing medullation in the fleece.

One other interesting sidelight in the above is that here the head check has been able to influence fibres as far down the array as the precipice but no further.

Section 3:

OTHER ARRAYS.

Cases of arrays showing the other extreme from those of 178/48 were also studied. Sheep 300/48 (See Table 30) a very weakly medullated homozygous Dominant-N showed the most extreme form of a moderate or weak head check operating on a very reduced basal medullation. In the shoulder patch of this sheep a moderately strong head check produced a Ravine array but basal medullation was so weak that no curly-tip fibres below the precipice were medullated and 8.5% above the precipice were also non-medullated.

Side and neck arrays in 300/48, classed as Saddle and Plateau respectively, showed the same type of effect for not more than about 3% in the former and 0.4%in the latter of the post-precipice curly tip fibres were medullated. The side array of 353/48, back array of 9/44, neck array of 35/48, neck array of 90/48, and side array of 343/48 also show a similar phenomenon, so the effect is not restricted to any one genotype. In the homozygous Dominant-N 300/48 there seems to be little effect on basal medullation produced by two doses of the dominant-gene so far as can be measured with the rather inaccurate method available, as there is little difference between the basal medullation of this sheep and the Non-N's studied. However, an effect is produced by the N-genes in that there the head check is very much weaker than in non-N sheep producing mostly Plateau, but one

CHAPTER VII.

THE HETEROZYGOUS DOMINANT-N SHEEP OF LESS THAN N-GRADE BIRTHCOAT HALO-HAIR ABUNDANCE AND VARIATION IN THIS GENOTYPE.

Dry (P.C.) has found, see also Chapter I, that when homozygous Dominant-N rams are mated to ordinary Non-N flock Romney ewes about I6% of the offspring possess birthcoat halo-hair abundance less than N-grade. Most of these lambs are classed Grade VI, V, IV, or III, for halo-hair abundance although occasional grade II and probable grade I lambs occur, but the evidence on this latter point is not conclusive. In this present work four of these lambs were studied, one from each of the grades VI, V, IV, III, for birthcoat halo-hair abundance. Of these lambs I78/48 was a borderline-N of grade VI, I58/48 a low-N of grade V, I94/48 a low-N of grade IV and I6/50 a low-N of grade III. This is not really sufficent material for a very thorough analysis but it does give some indication of the arrays and medullation to be found in borderline and low-N's.

Section I.

RESULTS.

Fibre type array analyses (See tables I & 6, 7, I8 & I9) show that the arrays here are weaker than those found on N-grade hererozygous Dominant-N's. In lambs I78/48 and I94/48 arrays on all positions except the britch are Valley. In I6/50 Valley arrays are found on the withers, shoulder patch, shoulder, neck, and britch, but the back array is Ravine and the side Saddle. In I58/48 a Valley is found on the shoulder patch, Ravine on the withers, shoulder and neck, Saddle on the back and side, and Plateau on the britch. This is also considerably weaker than the arrays found in N-grade heterozygous Dominant-N's except I04/48 and 6/48, two sheep with a big reduction of halo-hair abundance on the front of the body.

Basal medullation, except in I78/48, is also weak in so far as it is possible to measure it at present. This is especially true in I94/48 and I6/50, the two lambs of

lowest halo-hair abundance, where in most positions many non-medullated and few medullated curly-tip fibres were found. Lamb 158/48 has stronger basal medullation but nothing unusual like that found in 178/48. Thus on fibre type array data it would seem that, omitting the borderline-N grade lamb 178/48, the low-N lambs possess arrays that are weak in every respect in comparison with those of N-grade heterozygous Dominant-N's. It is highly probable that the arrays found here would be similar in all respects to those on the Non-N Romneys of higher halo-hair grades but none of these latter were studied in the present work.

Medullometer tests also show (Table 54) that the fleece, in the various positions studied, is less medullated in the low-N's than in the N-grade lambs in this genotype, except again that 104/48 possesses a fleece as weakly medullated as that of the low-N's. Within the low-N's themselves those lambs of lowest halo-hair abundance namely 194/48 and 16/50 also have the lowest medulla content of the fleece.

Section 2:

VARIATION IN THE HETEROZYGOUS DOMINANT-N GENOTYPE.

The birth-coat halo-hair abundance in this genotype has been found by Dry (P.C.) to show great variation. The Non-N genotype has never been known to show greater than Grade VI halo-hair abundance on the back position while every homozygous Dominant-N so far studied has full N-grade halo-hair abundance in all body regions. It is notable that in 300/48, studied in this work, there is a full abundance of halo-hairs in all body regions studied even although the arrays show other weaknesses.

In contrast in the heterozygous Dominant-N lambs halo-hair abundance ranges from Grade III, (with a few grade II and possible grade I) on the standard back position to

istic of the Non-N genotype to that of the homozygous Dominant-N.

For comparitive purposes heterozygous Dominant-N lambs were phenotypically graded as follows:

A. No reduction in halo-hair abundance in any region.
B. A small reduction in the shoulder patch region only.
C. A small reduction on the side of the neck and a separate shoulder patch reduction. There may or may not be a slight reduction on the side of the body.
D. Nox or a small reduction on the side of the body but a big reduction on the side of the neck continuous with the shoulder patch reduction.
E. A fair or big reduction both on the side of the body and the side of the neck, the latter continuous with the shoulder patch reduction.
F. A fair or big reduction on both the side of the body and the neck but a small separate shoulder patch reduction.
G. Heterozygous Dominant-N lambs of less than N-grade birthcoat halo-hair abundance.

Of the above about 1-2% of heterozygous Dominant-N lambs are in Class A, 10% in Class B, 48% in Class C, 4% in classes D, 2% in Class F, 19% in Class E, and 16% in Class G. Fromthis it can be seen that there are numberous sheep in very widely separated classes and the variability is not just seen in an occasional sheep of a different phenotype. As well as great variation between different lambs great variation is also seen over the body in different regions of the same lamb. (Photographs 11 to 15). As can be seen from the above classes some lambs have full N-grade abundance of halo-hairs in all body regions or a small reduction on the shoulder patch region. Others have reductions on the side of the neck and side of the body, these may be big or small (see Photographs 12 to 15), but still N-grade abundance in other body regions. Finally there are the lambs classed as less than N-grade which have not full abundance of halo-hairs on the standard back but may or may not possess this number elsewhere on the body.

Increasing phenotypic abundance of halo-hairs however seems to be an orderly process. N-grade abundance

abundance causes an N-grade birthcoat to be produced on all body regions except for reductions on the side of the body and the side of the neck, this latter being continuous with the shoulder patch reduction. The next step towards a full N-grade birthcoat is the reduction of these areas of reduced abundance and the separation of the shoulder patch area of reduction from that of the neck and side. Finally these reduced areas are obliterated, the first to disappear being that on the side, next that on the side of the neck, and lastly that on the shoulder patch.

As is mentioned elsewhere fibre type array analysis and medullometer tests show this same pattern. As is pointed out the hairy positions here show much difference between the Non-N and N-grade genotypes while in the least hairy positions the heterozygous Dominant-N, Recessive-N, and double heterozygote genotypes are more like the Non-N than the homozygous Dominant-N genotype. This tendency shows an orderly progression from the hairy britch position to the very reduced shoulder patch. Within the heterozygous Dominant-N genotype itself the same tendency is discernable. Fibre type array analysis shows that in the low-N's, except for 16/50 where the position is unique, the britch position shows the most marked variability and the greatest differences from other body positions. With increasing fleece medullation the side, back and britch positions come to have more and more similar types of arrays. In 48/48 the "toughest" heterozygous Dominant-N studied the withers, side, back and britch positions all possess Plateaus grade P_1 while Saddle arrays are found on the weaker shoulder and shoulder patch positions. In the hairier sheep in this genotype in general it is the shoulder and neck and more especially the shoulder patch region where the differences occur. See Table I.

With the medullometer readings comparisons

genotype the britch is sharply distinct showing greater fleece medullation. In the N-grade genotypes of intermediate toughness differences are found between both "tough" and "weak" positions while in the homozygous Dominant-N genotypes fewer real differences are seen between positions, as the less hairy positions have greatly increased medullation. Unfortunately the variation between positions in individual sheep in the heterozygous Dominant-N genotype as fleece medullation increased was obscure as widely different medullometer deflection results were obtained between different samples from the same sheep, and these were not orderly when different sheep were studied.

The Recessive-N and double heterozygote genotypes also show much phenotypic variation. Unfortunately in both these genotypes an insufficient number of sheep were studied to give much idea of the variation in fibre type arrays or in total medullation as measured by the medullometer. However on birthcoat halo-hair abundance both genotypes are very similar and show slightly greater overall abundance than the heterozygous Dominant-N genotype. Thus in both genotypes about one lamb in six has full halo-hair abundance in all body regions including the shoulder patch, one in five has a shoulder patch reduction only, three out of five have a shoulder patch and other reduction and odd borderline-N's of grade VI halo-hair abundance on the back occur.

Section 3:

DISCUSSION

The variation seen in the genotypes of intermediate fleece hairiness, namely the heterozygous Dominant-N Recessive-N and double heterozygote is interesting in view of the result of Goldschmidt (1923) who when studying intersexuality in the Gipsy Moth, Lymantria dispar, found greater phenotypic variation in the crosses that gave intersexes than

effect is removed, giving a greater variation. This may be due either to genetic modifiers or phenotypic variation, which factors are allowed to express themselves to the full as no threshold value for reaction velocity has to be passed. The threshold effect gives stability against phenotypic variation in pure males and females as if the reaction velocity is slightly altered.

A similar explanation in regard to the various hair producing genotypes in the Romney sheep as discussed above would seem to fit a similar phenomenon. In the Non-N genotype lambs especially those from the better stud flocks continual phenotypic selection by farmers would tend to reduce variation to a minimum whether this reduction was caused by selection of modifiers to produce a threshold effect or whether it was due to lack of genetic variation. Unfortunately in this present study no data was available to help decide this question.

However increasing dosage of N-genes does produce at first genotypes showing great phenotypic variation. When the hairy positions of the fleece are showing great medullation and N-grade halo-hair abundance, and the less hairy positions less medullation and lower halo-hair abundance, it would appear that any slight variation, both phenotypic and genotypic that affects the reaction velocities which may be involved in the production of a medullated fleece, can produce great variation in final fleece medullation and halo-hair abundance. From the work of Dry (P.C.) it would appear that some of the variation in the heterozygous Dominant-N genotype is genotypic as the low-N's breed in such a manner as to suggest that this is the case.

With a greater increase in the dosage of N-genes it would appear highly probable that a threshold value is passed when all the fleece shows full abundance of halo-hairs. Even although when this is the case, the medullometer tests

N-gene dosage is present. Here this lack of variation is caused by the "weak" body positions increasing in hairiness until a relatively evenly medullated fleece is produced. i.e. a threshold for fleece hairiness has been passed.

CHAPTER VIII

THE PRECIPICE AND RELATED PHENOMENA

Galpin (unpublished paper) defines the precipice as follows:

> "Precipice is the term give to a sudden change along the array from the coarse hairy-tip-curly-tips to fine curly-tip fibres without the presence of intermediate fibres."

The phenomenon has also been discussed by Goot (1940) and Sutherland (1939) who have made measurements of lengths of fibres above and below the precipice. However, in the present work arrays were only classed as possessing a precipice if the discontinuity as described by Galpin was visible to the eye. No measurements of fibre length or medulla diameter were made so the arrays were only described as showing a precipice if the discontinuity appeared to be absolute by eye.

The presence of a precipice was found in the sheep and genotypes studied to be highly correlated with the degree of "toughness" of the arrays, although as no numerical measurement of "toughness" could be obtained no statistical work could be done to give correlation coefficients.

Phenomena related to the occurence of a precipice are the occurence of pre-precipice curly-tip fibres and post-precipice hairy-tip-curly-tip fibres. The pre-precipice curly-tip or curly-tips big as hairy-tip-curly-tips are only found in less medullated arrays as when these become "tough" all pre-precipice fibres in the curly-tip group are hairy-tip-curly-tips. The position with regard to post-precipice hairy-tip-curly-tips fibres is more obscure. They seem to occur, in so far as the limited data available is correct, when the post-precipice fibres are long and strongly medullated and are found, but in no great abundance throughout the N-grade genotypes.

Section 1.

RESULTS.

(See Tables I & II p. 5)

in these sheep but the britch array of B 4 was classed as a Saddle bordering on Ravine yet had no precipice. In both the above arrays pre-prexcipice curly-tip fibres occur, these being a sign of "weakness".

In all N-grade genotypes the precipice occurs in many arrays being very characteristic of the Plateau where it is found in three quarters of these arrays. It occurs in about one-third of the Saddles, one-fifth of the Ravines and about one-twelfth of the Valleys.

When the different positions are studied it is found that a precipice is most prevalent on the britch and side positions being present here in 70-80% of the cases. The back, withers and neck regions show a precipice in about half of the N-type arrays studied while it is very much less common on the shoulder patch and shoulder. However as not all positions were studied in all genotypes this result may be somewhat biassed. A sounder result is obtainable by studying the precipice phenomena within a genotype as follows:

In the heterozygous Dominant-N genotype (Tables I & 6 - 17) the precipice is formed mainly on the britch and side positions where it occurs in 70-80% of the cases. It is also found on about 30-40% of the back, withers and neck positions but very rarely on the shoulder and not on any of the shoulder patches. When only those arrays in which a precipice occurs are studied it is seen that on the shoulder only one array, in sheep 35/48, comes into this category and here there is a big percentage of pre-precipice curly-tip fibres and few hairy-tip curly-tips this showing "weakness".

On the neck it is found that all precipicexxarrays here are of the weaker type, showing some and in some cases many pre-precipice curly-tip fibres. In the neck arrays of 48/48, 90/48, and 6/48, there are many pre-precipice curly-tip fibres and very few hairy-tip curly-tips, but in 41/48,

proportion of the pre-precipice fibres hairy-tip-curly-tips supports the findings from fibre type array analysis in Chapter 4 that the neck is slightly "tougher" than the shoulder, although this is the reverse of the position seen when the areas showing halo-hair reduction in the "tough" heterozygous Dominant-N's were studied. This lends further emphasis to the suggestion that the relation between the neck and shoulder may vary in a study of halo-hair abundance, fibre type array and precipice.

On the withers and back as few precipices occur as on the neck and on the withers all the precipice arrays possess pre-precipice curly-tips, these being on sheep 35/48, 12/48, 65/48 and 41/48. On the back, however, although arrays on sheep 90/48, and 48/48 possess these fibres, none are found in 65/48 and only a very low percentage in 35/48. Thus the back would appear "tougher" than the withers, as was found when fibre type arrays were compared, although the differences here may be due to chance variation. On the side a precipice is found much more frequently than on the back and withers but fibre type array analyses show that the side is not markedly "tougher" than the back. Consequently there is here a definite indication that the occurrence of a precipice is not absolutely correlated with "toughness". Also on the side a precipice occurs in a very "weak" array namely the Valley in borderline-N 178/48. However as described elsewhere this sheep is a curiosity with some N-type fleece characters.

All the other side arrays with a precipice are either Plateau or Saddle. Precipice arrays on the side are similar to the back as regards "toughness" measured by the presence or absence of pre-precipice curly-tips. In sheep 12/48, 65/48 and 41/48, and 78/48, none of these fibres are found but in 178/48, 6/48, 16/50, 158/48 and 90/48 they are

possess precipices. However here greater "toughness" is indicated by the fact that in most cases the pre-precipice fibres are hairy-tip-curly-tips except on 178/48 and 78/48 where pre-precipice curly-tips occur. A few of these fibres are also found in sheep 48/48.

In the Recessive-N genotype (Tables I & 20-24) the back, withers and side and neck arrays all show a precipice in about 60-80% of the cases but it is rare on the shoulder and shoulder patch. On the back, withers and neck this is a greater abundance than is seen in the heterozygous Dominant-N genotype, but this difference may be due to chance variation.

In the only shoulder array with a precipice, that on 343/48, pre-precipice curly-tip fibres occur. Also in all the withers and neck arrays showing a precipice these fibres occur although they are not numerous in the withers of 351/48, and 343/48 or on the neck of 351/48. Back arrays with a precipice show these fibres in sheep 353/48 and 343/48 but not in 351/48. The only britch array studied, that of 80/47 showed a precipice but no pre-precipice curly-tips.

In the double heterozygote genotype (Tables I & 25-29) the back, withers, and side and britch positions possess arrays with a precipice in 50-75% of the cases studied. On the back, withers and side all precipice arrays were found to possess pre-predpice curly-tip fibres, but all of the britch arrays in this category showed only hairy-tip-curly-tips above the precipice. Hence there is a sharp distinction in "toughness" between the britch and other arrays when the classification is on the presence or absence of the pre-precipice curly-tips. Compared with the Recessive-N and heterozygous Dominant-N genotypes it is seen that the back and side of the double heterozygotes would appear "weaker" in that no arrays with only hairy-tip-curly-tip fibres above the precipice were present. However in view of the small numbers taken the

shoulder patch arrays where it occurs in about 60% of the cases. It also occurs in about 60% of the shoulder arrays, 80% of the back and withers arrays and in all the side, neck and britch arrays. However in view of the small numbers studied there may be no real difference between these results.

Shoulder patch arrays possessing a precipice show many pre-precipice curly-tip fibres in sheep 300/48, a few in sheep 15/50 and 239/48 and none in sheep 245/48. Shoulder arrays with a precipice show a few of these fibres in 263/48 but none in sheep 15/50, 239/48 and 245/48. In the back and withers arrays a precipice and pre-precipice curly-tips are found in sheep 15/50 but there are no pre-precipice curly-tips in sheep 263/48, 239/48, 14/50 and 245/48. Side, neck and britch arrays studied all possess a precipice. The side and neck arrays in sheep 15/50 and 300/48 possess pre-precipice curly-tips while those on sheep 239/48, 263/48, 14/50 and 245/48 do not. The only britch array with these fibres is that in sheep 300/48.

Thus it is seen that the main difference between the homozygous Dominant-N and the other genotypes is that here a far greater proportion of arrays on the shoulder patch and shoulder show a precipice. Also in this genotype the precipice arrays on the "weaker" positions such as the withers, shoulder and neck seem to be "tougher" in that fewer arrays with pre-precipice curly-tip fibres are found.

Post precipice hairy-tip-curly-tip fibres are also found in four sheep in the homozygous Dominant-N genotype. They seem however to be more characteristic of certain sheep than certain positions. They occur in all positions in sheep 239/48 and on all positions except the side of 245/48. They are also found on the back of 14/50 and the back, side and britch of 263/48. However in no case are many of these fibres present/and along the array they quickly pass into medullated

double heterozygote genotype the britch array of 155/44; and in the heterozygous Dominant-N genotype the britch arrays of 93/48, and 65/48, the side and neck and britch of 12/48, and the back and britch of 90/48.

Thus it would seem from the limited data available that the post-precipice hairy-tip-curly-tip fibres do increase in abundance in the more hairy positions and genotypes and they would therefore denote "toughness" of any array.

Section 2:

DISCUSSION.

From the above it is seen that with increasing dosage of N-genes from Non-N to Homozygous Dominant-N along with increasing fleece medullation a precipice appears in fibre length, and often in diameter and medulla diameter as well, in the curly-tip class of fibres. In 178/48 the side array, with a very strong "head" check and strong basal medullation, the pre-precipice curly-tip fibres seem more checked and thinner, but still longer than the post-precipice ones. However in most arrays the reverse is the case.

At first the precipice, when it occurs in fairly weak arrays, separates the curly-tips into two classes, pre- and post-precipice fibres. However, with increasing medullation all the pre-precipice fibres tend to become hairy-tip-curly-tips and this is well seen when arrays in homozygous Dominant-N sheep are compared with those in sheep of other N-grade genotypes. Finally with increasing dosage of N-gene a few post precipice fibres tend to become hairy-tip-curly-tips but this effect is sporadic and not well marked.

Fraser, Ross and Wright (I.P.) have suggested that the primary central follicles of the skin produce the pre-curly-tip fibres, the primary lateral follicles hairy-tip-curly-tips and the secondary follicles curly-tips and histerotrichs. However with regard to the pre-curly-tip fibres both the findings of Galpin (1934) and those in the present work (Chapter

(Galpin (1935) and Ross (1945) show that while the various follicle types commence development at different ages of the foetus in different parts of the body, this development is essentially similar in all body regions. The differences in the ratiox of primary to secondary follicles in different positions at the same age, due to follicles commencing growth in the foetus at different times of foetus age in different regions, may partly or wholly explain the differences in the percentages of pre-curly-tip fibres. Galpin's suggestion (1934) that the time of appearance of the follicles on the foetus determines the percentage of pre-curly-tip fibres would seem to be worth further attention in the light of the new facts, but as suggested elsewhere the position needs investigating.

The further suggestion by Fraser, Ross and Wright (I.P.) that the primary lateral follicles produce hairy-tip-curly-tips is, it is suggested, only true as a limiting case, but instead it is suggested that, where a precipice occurs, all pre-precipice fibres are produced in the primary follicles and post-precipice fibres in the secondary follicles and that this is the real significance of the precipice. Pre-precipice curly-tip and hairy-tip-curly-tip fibres may be confined to the primary lateral follicles, but the suggestion is that pre-precipice curly-tips are produced in the primary and not the secondary follicles. This might well explain the discrepancy in the number of hairy-tip-curly-tip fibres found by Fraser, Ross and Wright. Support for this view is obtained from the fact that the precipice seems to occur at a fairly constant distance along the array. Also skin sections show (see later) that although there are no apparent differences in the proportions of follicle types with increasing dosage of N-genes, it is seen that the fibres in the primary follicles tend to become very much larger and distinct from those in the secondary follicles. This shows all gradients from very similar fibres in all follicles in the Non-N sheep to very different fibres in the primary and secondary

A study of the birthcoat of the lamb of the Scottish Blackface by Lockner (1931) shows that here fibres, called by Lockner, heterotype A, heterotype B and wool fibres exist. Heterotrype A fibres are long, not shed and have curly tips while heterotype B fibres, which appear first in the birthcoat, have a sickle-shaped end and are shed after an interval of about two months, being replaced by kemps. Wool fibres Lockner divides into Medium Wool and Fine Wool, but states that it is not always easy to separate the two classes completely. He also mentions that wool fibres, being shorter than the longer growing hairy fibres, have no influence on the external appearance of the coat, so it would appear probable that a precipice occurs in length between the heterotype A fibres and the Medium Wool.

Goot (1940) has suggested that the N-type birthcoat is an example of an "atavistic" reversion towards the coat of the primitive sheep. Certainly it appears from Lockner's description that Heterotype B fibres can be said to homologous with halo-hairs and/or super-sickle As and it is also possible that Heterotype A fibres are homologues of pre-precipice curly-tips and hairy-tip-curly-tips. The wool fibres found by Lockner could also be homologous with post-precipice curly-tips and histerotrichs. The fact that some of the post-precipice fibres in N-type sheep are medullated is not a fact that contradicts this hypothesis as some of Lockner's "wool" fibres are also medullated, and they are coarser and more medullated than the same fibres in the Urial Ovis Vignei and other sheep with more primitive coats than the Blackface. The facts of shedding of pre-curly-tips in N-type sheep also support the view that Heterotype Bs are homologous with halo-hairs and super-sickle A fibres.

However in the Blackface, the curly tips of the Heterotype A fibres are non-medullated and as, if the above hypothesis is correct, the arrays on this sheep are approximately

It should be stressed however, that the facts here are not known.

Another anomalous fact is that in the Blackface the wool fibres are shed annually in the Spring, whereas no such phenomenon with regard to the post-precipice fibres in N-type sheep is seen. However no explanation of this fact is given as more research would have to be done to determine its cause.

CHAPTER IX

THE DISCRIMINANT FUNCTION AS APPLIED TO FIBRE TYPE ARRAYS.

Section 1: INTRODUCTION.

In earlier work, as in this thesis, comparisons between arrays of different "toughness", whether made between different regions of the body of the same sheep, or between sheep of a similar genotype (Galpin 1936), orbetween sheep of different genotypes in the same position, have been empirical observations, the overall data being of such a kind that statistical analysis was not applicable. To find a mathematical measurement of toughness as at present shown by Plateau, Saddle, Ravine, Valley and Plain arrays is a matter for future research.

Another attack on the problem has been made by Ross and Wright who have compared fibre types individually between the Recessive-N, heterozygous Dominant-N and homozygous Dominant-N genotypes on the standard back position. (Ross, Wright I.P.). Their results have shown that real differences do exist between genotypes in the percentages of some fibre types present although their results are complicated as they have further divided their fibres into Kemps and those not shed.

In the present chapter the discriminant function as developed by Fisher (1936) is applied to fibre type arrays to see if a significant difference exists between genotypes in the types of fibres present in an array. The function was originally developed by Fisher as a means of finding which of all possible linear compounds of a set of measurements will best discriminate between two different groups. In a fibre type array the percentage of each fibre type present can be taken as a measurement of that array which can be compared with the percentage of the same fibre type present in another array. (In this work as previously mentioned percentages were

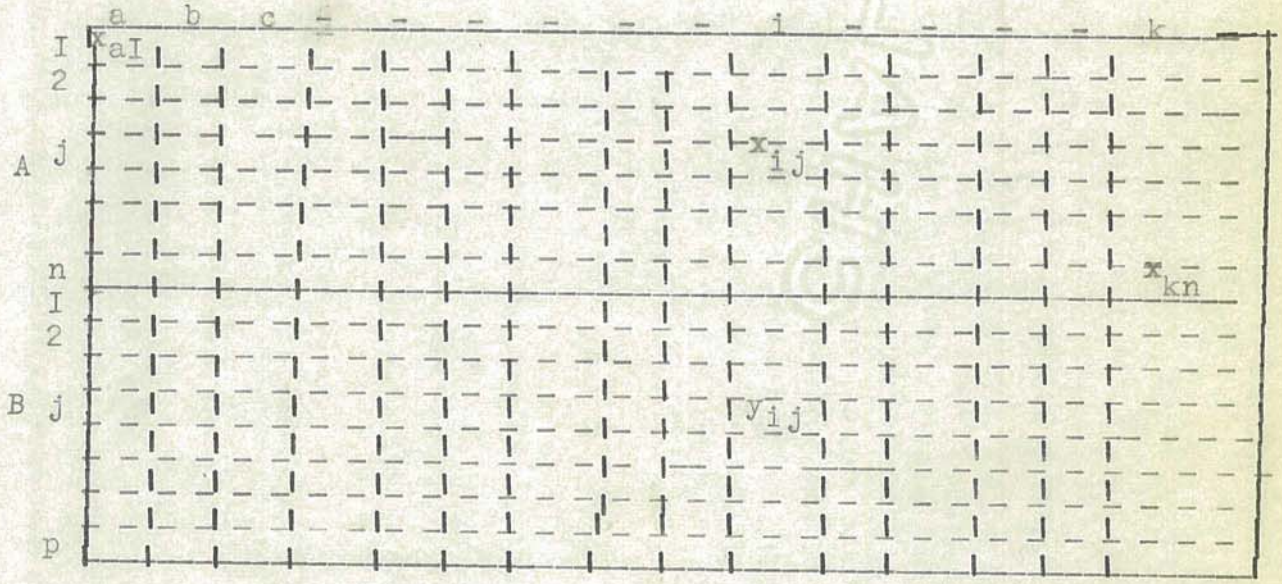
discriminant fuction to fibre type array comparisons was made by Mr. G. M. Wright of the Applied Mathematics Laboratory, Wellington (Personal Communication) while throughout the work Mr. Glenday, also of the Applied Mathematics Laboratory, has been a source of constant help and advice.

Section 2:

THE DISCRIMINANT FUNCTION.

When multiple measurments can be made on a group of data and the same measuremements on another group the discriminant function is the linear compound which best discriminates between the two groups.

To derive the discriminant function let us suppose that there are a,b ----- i, ----- k fibres found on 1,2, ----- j -----n sheep in class A and 1,2 ----- P sheep in Class B.



Xij : measurement for Class A i^{th} fibre, j^{th} sheep.

Yij : measurement for Class B i^{th} fibre, j^{th} sheep.

Where X's and Y's are %ages transformed to arc.sin $\sqrt{\%}$ (Snedecor 1946 P. 449). The first step in the calculation is to derive the difference of the means between genotypes for all fibre types present. These quantities are denoted d_a, d_b, ----- d_i, ----- d_k where

d_i : difference of the means for the i^{th} fibre.

The next calculation is the sums of squares and the sums of products within classes.

e.g.:

$$
\begin{array}{ll}
 & S_{aa}X_a + S_{ab}X_b \text{ -----} S_{aj}X_j \text{-----} S_{ak}X_k = d_a. \\
(1) & S_{ba}X_a + S_{bb}X_b \text{ -----} S_{bj}X_j \text{-----} S_{kk}X_k = d_b. \\
 & \text{----------} \\
 & S_{ka}X_a + S_{kb}X_b \text{ -----} S_{kj}X_k \text{-----} S_{kk}X_k = d_k.
\end{array}
$$

Then solve for X's and the discriminant function is:

$$Z_i = X_aZ_a + X_bZ_b \text{ -----} X_jZ_j \text{ -----} X_kZ_k.$$

Where Z_a, Z_b ----- Z_k are the transformed percentages of fibres for the sheep Z_i.

In matrix notation the set of equations (1) can be written

$$KX = d \text{ ——————} \quad (2)$$

To solve for X we must find K^{-1} the inverse of K and pre-multiply (2) throughout, giving:

$X = K^{-1} d$ (The equations to give the X's).

The inversion of K(a symmetric Matrix) is here done by Dwyer's method (1945) : e.g.:

Suppose K=

a_{11}	a_{12}	a_{13}	a_{14}
	a_{22}	a_{23}	a_{24}
		a_{33}	a_{34}
			a_{44}

Then inversion:

a_{11}	a_{12}	a_{13}	a_{14}	a_{15}	1		
	a_{22}	a_{23}	a_{24}		a_{26}	1	
		a_{33}	a_{34}			a_{37}	1
			a_{44}				a_{48} 1
b_{11}	b_{12}	b_{13}	b_{14}	b_{15}			
	b_{22}	b_{23}	b_{24}	b_{25}	b_{26}		
		b_{33}	b_{34}	b_{35}	b_{36}	b_{37}	
			b_{44}	b_{45}	b_{46}	b_{47}	b_{48}
				c_{55}	c_{56}	c_{57}	c_{58}
					c_{66}	c_{67}	c_{68}

Where inverse matrix:

$$k^{-1} : \begin{vmatrix} c_{55} & c_{56} & c_{57} & c_{58} \\ c_{56} & c_{66} & c_{67} & c_{68} \\ c_{57} & c_{67} & c_{77} & c_{78} \\ c_{58} & c_{68} & c_{78} & c_{88} \end{vmatrix}$$

Calculations are:

$$b_{jj} = \sqrt{a_{jj} - b_{1j}^2 - b_{2j}^2 \text{ -----} b_{(j-1)j}^2}$$

$$b_{jk} = \frac{a_{jk} - b_{1k}b_{1k} - b_{2j}b_{2k} - b_{3j}b_{3k} \text{ ---} b_{(j-1)j}\, b_{(j-1)k}}{b_{jj}}$$

and

$$C_{st} = \sum_i b_{is}\, b_{it}.$$

Equations giving X are $X = K^{-1} d$.

The method can be extended to cases of more than two classes of sheep A and B, but the set of formulae (1) applies only to the two class (A and B) case.

The discriminant function thus derived will only give information as to whether statistically significant differences exist between fibre types present on two classes of sheep, in this case, two different genotypes. No interpretation can be given to these differences. e.g.: as to whether they are differences in proportion of medullated fibres, toughness of arrays, proportions of pre-curly-tip curly-tip, or histerotrich fibres, etc.

Section 3:

RESULTS.

In this work, as calculating a discriminant function between any two genotypes for one body position is a tedious business, only comparisons between homozygous Dominant-N, Recessive-N and heterozygous Dominant-N genotypes on the shoulder patch position were made, but here statistically significant differences were found between the means of the arrays of the homozygous Dominant-N and the other two genotypes.

(The function separating the homozygous and hetero-

As can be seen from the preceding section the work is greatly increased by having more classes of fibres and it proved impossible to work out a function in a reasonable amount of time containing more than nine fibre types. Consequently all pre-curly-tip and curly-tip fibres were put into the classes halo-hair and super-sickle A, super-sickle A' and super-sickle B, sickle normal, fine pre-curly-tip, curly-tip checked, hairy-tip-curly-tip, curly-tip big as hairy-tip-curly-tip, curly-tip medullated and curly-tip non-medullated. Histerotrichs were ignored.

For the discriminant function calculated from fibre type percentages in the Recessive-N and heterozygous Dominant-N genotypes, only 8 fibre types were included, the curly-tips big as hairy-tip-curly-tips were placed with medullated curly-tips in the one class. As even this proved to be very cumbersome in the comparison between the Recessive-N and homozygous Dominant-N genotype, only the fibre types Halo-hair and super-sickle A, sickle normal, fine pre-curly-tip and hairy-tip-curly-tip were included in the discriminant function and this gave a difference between genotype means, statistically significant at the 1% probability level.

The results are shown in tables 51, 52 and 53. One function (Table 51) separates the homozygous Dominant-N and heterozygous Dominant-N genotypes at the 1% level. Between the Recessive-N and homozygous Dominant-N genotype means (Table 53) as stated above, the function was only calculated for four fibre types but these showed a real difference significant at the 1% level.

Between the heterozygous Dominant-N and Recessive-N genotypes (Table 52) a real difference between the means at the 5% significance level is just apparent. However the suggestion that this difference is real should be accepted with caution as a closer examination of the numerical values of the fibre type arrays shows that one of these values for the Recessive-N geno-

be interpreted with extreme caution.

No function was worked out to see if any real difference existed between the fibre types present on the shoulder patches of ~~t~~the Non-N and N-grade genotypes (see before) but these are readily separable on other grounds. All the Non-N genotype arrays only possess three fibre types, fine sickles, non-medullated curly-tips and non-medullated histero-trichs, but all the N-grade genotype arrays contain in addition, some medullated fibres. Also differences are readily apparent when the fibre type arrays are compared by simple observation, (see Chapter 4) and when individual fibre types themselves are compared. (Chapter 5).

Section 4:

DISCUSSION.

The results of this analysis are very similar to those of empirical comparisons made between fibre type arrays and to those of comparisons made between individual fibre types as far a s a limited application of the discriminant function to one position between genotypes will permit the drawing of conclusions.

Empirical comparisons between fibre type arrays showed that:

I: All Non-N shoulder patch arrays are Plain,

II: Recessive-N and heterozygous Dominant-N shoulder patch arrays are on the average, about Ravine,

III: Most homozygous Dominant-N shoulder patch arrays are Plateau

Statistical comparisons between individual fibre types show that real differences at the 1% significance level exist between the means of the Non-N and N-grade genotypes in medullated curly-tip fibres. Real differences at this level also occur between Non-N and homozygous Dominant-N genotypes in the abundance of halo-hair and super-sickle A' fibres and between the heterozygous Dominant-N and Recessive-N, and the homozygous Dominant-N genotypes in abundance of halo-hairs and sickle fibres. No real differences in any comparison between

types present on the heterozygous Dominant-N and Recessive-N sheep and those on the homozygous Dominant-N sheep. Analysis of differences between individual fibre types and empirical comparisons of arrays has shown the nature of these differences.

The position between the Recessive-N and heterozygous Dominant-N genotypes is obscure and no real differences may exist between the two genotypes in the fibre types present on the shoulder patch. No real differences are found between these two genotypes in individual fibre type comparisons on the shoulder patch and no difference is seen in empirical comparisons made between fibre type arrays. Any real differences that may exist would be a very slight one and would need a greater number of anaylses to establish it, beyond reasonable doubt, than have at present been carried out.

PART III

PART III

HAIRINESS AS MEASURED BY THE MEDULLOMETER

CHAPTER X.

INTRODUCTION .

A visual estimation of the degree of medullation of a wool sample can be made by the benzol test introduced by Elphick (1932). In this test a small sample of wool is washed in petrol and then immersed in benzol in a flat dish over a black background. Non-medullated fibres become invisible while medullated ones stand out white and chalky. McMahon collected the light so reflected from the medulla on to the cathode of a photo-electric cell and this gives an approximately linear relation between the index so obtained and the percentage air space in the fibre calculated from specific gravity determinations in benzol. (McMahon 1937). By this method therefore a measurement of the total medulla percentage present in a wool sample can be made.

The aim in this section was:

A: To study the medulla distributions over the body.

B: To study the medulla differences between the genotypes.

C: To study the relationship between medulla and fibre type array.

CHAPTER XI.

MATERIALS AND METHOD.

Section 1: GENERAL METHOD

The wool samples used were those approximately ten weeks old, on which fibre type arrays were ascertained except for the following alterations. In the heterozygous Dominant-N genotype analyses on samples from lamb 21/48 were included in the analysis and samples from lambs 78/48 and 90/48 were omitted. The medullometer which had recently been overhauled and altered in the manner described by Ross (1950) was used. As the degree of deflection produced by a certain amount of medulla was not known, comparisons were made between degrees of deflection produced by a standard weight of wool. The high sensitivity range was used throughout the work.

The routine method employed for medulla tests was as follows:

1: Wool samples were first washed in petrol and then left to dry for 24 hours.

2:(a) The medullometer was turned on and left to warm up for a minimum of fifteen minutes.

(b) The tray was half filled with benzol and the glass cover plate placed in position. Enough benzol was always added to cover the glass plate.

(c) The machine was adjusted to zero.

(d) A test plate was placed on the lamenoid with which the medullometer was standardised to give a reading of 50 on the high sensitivity. This was always placed under the glass plate.

When this was completed the medullometer was ready for carrying out tests on the wool samples.

3:(a) A wool sample was taken of such a size that when the fibres were spread in the lamenoid as few crossed as possible.

(b) The glass cover plate was placed in position over the wool fibres.

5: The samples were placed in the humidity room for 24 hours and then weighed.

Repeats were done on at least two samples from each sheep and a 5% margin of error was tolerated. Agreement in most cases was found to be good. However in some repeat medulla tests done in May, about a month after the original readings were taken, the repeats were all lower than the originals. D.A. Ross (1950) found that in samples stored for one year there had been a 14% increase in percentage medullation and suggested as an explanation that the changes were due to changes in the machine. It is not known what caused the above decrease in readingsbut in view of Ross's work it would appear likely that the machine may have altered.

D.A. Ross states that on the high sensitivity range the relationship between the amount of light incidence on the cathode and deflection was found to be curvilinear. However the deflection scale is a logarithmic one, and, using silver coins of different sizes it was found that the relationship between the amount of light incidence on the cathode and deflection reading on the scale was linear.

6: The degree of deflection produced by a certain weight of wool was then calculated and these figures were then used for comparitive purposes.

Section 2:

STATISTICAL METHOD.

When untransformed numbers, corresponding to different degrees of deflection, were analysed it was found that the standard deviation was proportional to the mean when the latter was low but was independent when the means were high. (See Table 55). As the situation was complicated in this fashion a simple transformation could not be appliedto all the data. As a result all the between genotype analyses were made on untransformed data as here the majority of means were high. Statistical analysis between positions within genotypes were

analysis was carried out on log. transformed data, the transformation being the logarithm to the base 10 of the number. (Snedecor 1946)

The results are shown in tables 54, 55, 56, and 57, in which are included the means, the overall F values and their significancesand d for the 5% and 1% level of significance This last value is calculated from the following formula:

$$\text{For the 5\% level } d = t.05\sqrt{\frac{2 \times ems}{ko}}$$

$$\text{For the 1\% level } d = t.01\sqrt{\frac{2 \times ems}{ko}}$$

Where t is the value of the t ratio at the 5% or 1% level of probability for n_2 degrees of freedom, that is, the number of degrees of freedom within classes.

ems = Error mean square
ko = The harmonic mean of the number of measurements within classes.

d is $\sqrt{2}$ x the fiducial interval (Snedecor 1946), and is the least figure the class means have to differ by for there to be a significant difference at the 5% or 1% level respectively. It is derived from a definition of t (Snedecor 1946) and instead of doing each analysis separately and finding the t value and its significance level, d gives the amount the means have to differ by for t to be significant.

In the following chapter a double asterisk ** against the F value indicates that this is significant difference at the 1% probability level. Similarly a single asterisk * denotes that significant differences exist at the 5% level.

CHAPTER XII

RESULTS.

Section 1:

BETWEEN GENOTYPE ANALYSES.

(See Tables 56 & 57)

Between genotype analyses gave F values which were all found to be significant at the 1% level. Data was obtainable from all the five genotypes: non-N, +/+, heterozygous Dominant-N, N/+, Recessive-N, nr/nr, double heterozygote N/+.nr/+, and homozygous Dominant-N N/N in only the back, withers and side positions. A full set of comparisons between all seven positions could only be made in the non-N, heterozygous Dominant-N and homozygous Dominant-N genotypes. No shoulder patch, shoulder or neck samples were available in the double heterozygotes, and the one Recessive-N britch studied was not included in the analysis as more data than this was necessary for statistical calculations.

A: Means in the shoulder patch Region between genotypes:

+/+	N/+	nr/nr	N/N	F	d
16.5	64	65	268	27.69** $n_1 = 3$ $n_2 = 21$	5% level = 65.48 1% level = 89.09

Data from the shoulder patch region showed that the mean of the homozygous Dominant-N genotype differed at the 1% level of significance from all other genotypes but that these remaining genotypes did not differ significantly among themselves.

B: Means in the withers and neck positions : Genotypes:

Withers:

+/+	N/+	N/+.nr/+	nr/nr	N/N	F	d
20.25	183.5	203	205	364	9.83** $n_1 = 4$ $n_2 = 26$	5% level: 107.18 1% level: 151.27

Neck:

+/+	nr/nr	N/+	N/N	F	d
17.25	173	192	383	13.84** $n_1 = 3$ $n_2 = 22$	5% level: 111.29 1% level: 151.27

However no real difference is observed between the means of intermediate genotypes, heterozygous Dominant-N, double heterozygote and Recessive-N in the withers samples and heterozygous Dominant-N and Recessive-N in those from the neck.

C: Means on the shoulder position:

+/+	N/+	nr/nr	N/N	F	d
18.25	204	250	378	11.86** $n_1 = 3; n_2 = 22$	5%level:116.70 1%level:158.63

On the shoulder position the Non-N genotype mean also differs from those of all other genotypes at the 1% probability level, but the homozygous Dominant-N genotype mean only differs from all others at the 5% level. Again there is no real difference between heterozygous Dominant-N and Recessive-N means.

D: Means on the side, back and britch positions.

Side:

+/+	N/+.nr/+	nr/nr	N/+	N/N	F	d
25.75	278	341	354	474	11.42** $n_1 = 4$ $n_2 = 25$	5%level=136.12 1%level=184.16

Back:

+/+	N/+	N/+/nr/+	nr/nr	N/N	F	d
38.5	340	347	373	477	12.86** $n_1 = 4$ $n_2 = 26$	5%level : 119.82 1%level : 161.96

Britch:

+/+	N/+	N/+.nr/+	N/N	F	d
116	403	453	516	14.79 $n_1 = 3$ $n_2 = 21$	5% level : 123.70 1% level : 168.36

On the side, back and britch positions the Non-N genotype means differ from those of all other genotypes at the 1% level. However here the means of all other genotypes form a series of increasing order of medullation and there is no real differenee between the mean of any one genotype and the one next to it in the series. On the side position the homozygous Dominant-N genotype mean differs at the 1% significance level from that of the double heterozygote, but not from that of the heterozygous Dominant-N or Recessive-N. On the back the homozygous Dominant-

between any of the N-grade genotypes on the britch.

Thus, taking the mean of the untransformed numbers being a measure of the medullation of the fleece samples, it is seen that this mean increases in value, denoting increasing medullation on all positions from low values in the Non-N genotype to high values in the homozygous Dominant-N's. The Non-N means differ significantly from those of the N-grade genotypes in all positions except the shoulder patch. The homozygous Dominant-N means differ significantly from those of all other genotypes (including the N-grade genotypes) on the shoulder patch, withers, neck and shoulder positions. On the side and back positions the homozygous Dominant-N means only differ significantly from some of the lower of those of other N-grade genotypes while in the britch position no real differences are observable between N-grade genotypes. Over the whole fleece there are seen to be significant differences in medullation between the Non-N genotype, the heterozygous Dominant-N, double heterozygote and Recessive-N genotypes and the homozygous Dominant-N genotype. However there are no observable differences in the sheep studied between the three intermediate genotypes, namely heterozygous Dominant-N, Recessive-N and double heterozygote.

CONCLUSION.

In conclusion on the shoulder patch, shoulder, neck and withers the five genotypes are divisible into three groups:

1: The Non-N genotype with wool very little medullated.

2: The heterozygous Dominant-N, double heterozygote and Recessive-N genotypes with wool intermediate in medullation and,

3: The homozygous Dominant-N genotype with wool strongly medullated. In the positions side, back and britch, with the body positions possessing greater medullation (see next section) there is less difference between the homozygous Dominant-N and the three intermediate genotypes of Class 2. This phenomenon reaches its climax on the britch position where no differences

types gave the following results:

The F test shows that in all of the five genotypes, differences at the 1% significance level do exist between the means of the various positions studied. d values showed the individual positions to differ significantly from each other in the following way:

A: THE NON-N GENOTYPE.

Shoulder Patch	Withers	Shoulder	Neck	Side	Back	Britch
1.25	1.208	1.225	1.229	1.389	1.546	2.000

d

5% level = .308
1% level = .419

F Values:

F 7.77 **
$n_1 = 6$; $n_2 = 21$.

As before explained the analysis was here carried out on the log. transformed data. The britch mean in the Non-N genotype differs from the mean of all other positions at the 1% level of significance. Also the back mean differs significantly from the means of all other positions which are as small as, or smaller than, that on the neck.

B: THE HETEROZYGOUS DOMINANT-N GENOTYPE.

Shoulder Patch	Withers	Neck	Shoulder	Side	Back	Britch
64	183.5	192	204	354	340	403

d

5% level = 93.16
1% level = 123.71

F Values:

F 13.39 **
$n_1 = 6$; $n_2 = 70$.

In the heterozygous Dominant-N genotype the shoulder patch mean differs from that of all other positions at the 5% level. The means of the withers, neck and shoulder positions form one group, all of whose means differ at the 1% level from those of a group consisting of the side, back and britch positions, the latter showing the greater medullation. No real medulla differences within each of the above two groups are seen.

C: THE DOUBLE HETEROZYGOTE GENOTYPE.

Withers	Side	Back	Britch	F	d

available from the back, withers, side and britch positions. However, this shows that the britch mean is just significantly different at the 5% level, from those of all other positions. Also the back and withers means differ at the 5% level. In this genotype the withers and side show the least, the back intermediate, and the britch the greatest medullation. This is the only N-grade genotype where the britch mean differs significantly from those of all other positions, but this is probably a real difference as there is only one chance in twenty that the result is fortuitous.

D: THE RECESSIVE-N GENOTYPE.

Shoulder Patch.	Neck	Withers	Shoulder	Side	Back	F Value.
65	173	205	250	341	373	F 9.09 ** $n_1 = 5$; $n_2 = 23$

d

5% level : 106.74
1% level : 144.81

In the Recessive-N genotype no britch sample was available for study. Here the shoulder patch mean, the lowest in the series, differs from the means of all other positions at the 5% level. The means on the other positions form a series neck, withers, shoulder, side and back in increasing order of medullation. No sharply defined groups are found but the highest means differ significantly from the lowest. Thus the withers and neck positions differ at the 5% level from the side and back. Also the shoulder position from the back, but this comparing of means at extremes of a graded series is a procedure which should be adopted with caution. (Tukey 1949).

E: THE HOMOZYGOUS DOMINANT-N GENOTYPE.

Shoulder Patch.	Withers	Shoulder	Neck	Side	Back	Britch
268	364	378	383	474	477	516

F Value.

F 5.89 **
$n_1 = 6$
$n_2 = 35$

d

5% level = 101.01
1% level = 135.55

between positions in this genotype, but no means show themselves to be clearly different from all the others. The shoulder patch mean differs at the 5% level from those on the shoulder, neck, side, back and britch but not from the withers mean. Similarly the britch mean differs at the 5% level from that of any position lower in the scale than the neck, but not from the side and back positions.

CONCLUSION;

Thus in conclusion it is seen that in the Non-N genotype the mean of the britch is much higher than the mean of the other positions, this difference being significant at the 1% level. The back mean differs significantly from the means of all other positions which are smaller than or as small as that on the neck. With the heterozygous Dominant-N genotype the means form three groups, the lowest containing the shoulder patch position, the next highest containing the neck, shoulder, and withers positions, and the final group consisting of the side, back and britch positions containing the highest means. Differences between these groups are at the 5% level between the first and second and at the 1% level between the second and third. In the Recessive-N and double heterozygote genotypes, the means, in increasing series are still arranged in the same order but in the double heterozygotes only the britch position and in the Recessive-N's only the shoulder patch are clearly separable from the rest. In the homozygous Dominant-N genotype the means form a graded series, not three sharply defined groups, arranged, in the order of increasing medullation, shoulder patch, withers, shoulder, neck, side, back and britch. This is very similar to the order in other genotypes.

Section 3;

COMPARISONS OF DIFFERENCES IN POSITION BETWEEN GENOTYPES.

The following facts emerge when comparisons between genotypes and comparisons between positions within genotypes

would have made a full analysis very difficult to carry out. As a result the following is just an empirical observation.

1: The Non-N genotype differs signficantly from the N-grade genotypes in all positions, except that on the shoulder patch it does not do so when compared with the heterozygous Dominant-Ns and Recessive-Ns. The means of all the medullometer determinations in all samples of the Non-N genotypes are low except on the britch, as are the shoulder patch means of the heterozygous Dominant-N and Recessive-N genotypes.

The Non-N britch determination is higher than, and differs significantly from the other Non-N positions but it is also lower than and significantly different from britch medulla determinations in N-grade genotypes.

2: The heterozygous Dominant-N genotype differs significantly from the Non-N in all positions except the shoulder patch, being more medullated as is shown by the means of the medullometer readings. It also differs significantly from the homozygous Dominant-N genotype on the withers, neck, shoulder and back positions, being less medullated.

In comparisons between positions it is seen that fleece medullation in the withers, shoulder and neck regions has risen significantly compared to the Non-N genotype, while that of the side and back has risen still more. The britch fleece medullation has risen significantly compared to that present in the Non-N genotype, but not to the extent that a real difference is still present between the britch and back and side positions.

3: The Recessive-N and double heterozygote genotypes do not differ significantly in any position in comparisons with the heterozygous Dominant-N. In the position analysis it is seen that there are not three sharply defined groups as in the heterozygous Dominant-N genotype but the shoulder patch, neck, withers, shoulder, side, back and britch positions form a series, when present, increasing in medullation. However

ly from those on all other positions also at the 5% level. Thus there is here a suggestion that there is not the same amount of variation between positions as found on the heterozygous Dominant-N genotype, but there were here fewer samples and this may partly explain the results.

4: The homozygous Dominant-N genotype differs significantly from all other genotypes on the shoulder patch, withers, neck and shoulder positions, but not on the side, back or britch. The means of the medullometer readings are however in this genotype higher than those of the intermediate genotypes in all cases and with sufficient numbers all these differences might have become significant.

Position analysis shows that the positions shoulder patch, withers, shoulder, neck, side and back and britch form a series of increasing medullation, the boundaries between the three groups (found in N/+) being obliterated by overlapping. That this obliteration has been caused by all the positions becoming more medullated is suggested by the fact that as with the heterozygous Dominant-N genotype there are no real differences between the back, side and britch positions, but in addition the back and side do not differ significantly from the shoulder and neck and differ from the withers only at the 5% level. As in the heterozygous Dominant-N genotype there are no real differences between the shoulder, neck, and withers positions, but in addition the shoulder patch does not differ significantly from the withers. The hairiness in the adult sheep at shearing time has been studied by Dry (P.C.) and for comparative purposes the results are shown in Chapter 17.

Section 4:

CONCLUSIONS.

In conclusion it is seen that the effect of increasing gene dosage from 0 to 1 to 2 alleles of the Dominant-N gene is to increase significantly the amount of medullation present in the fleece. However the increase is not uniform over the

increase in medullation of the fleece on the withers, neck and shoulder positions also ~~x~~occurs.

With increase of the Dominant-N gene dosage from 1 to 2 alleles the greatest increases in medullation of the fleece occur on the less hairy parts of the body, namely in the fleece covering the withers, shoulder, shoulder patch, and neck positions as is shown by the differences here between the means of the medullometer readings for the two genotypes all being significant, in all except one case at the 1% level. No real difference however is seen between sheep carrying 1 or 2 doses of the Dominant-N gene in the side and britch positions while the difference on the back is at the 5% significance level only.

The Recessive-N gene in a single dose has not been studied but in two doses it produces the same amount of hairiness as is produced by the one dose of the Dominant-N gene. As mentioned before there is a slight suggestion that in the double heterozygote and Recessive-N genotypes the medullation is more evenly distributed over the body although the range of the means is similar. However this may be a purely fortuitous result.

If the theory of gene dosage effects is a correct interpretation of the facts one dose of the Dominant-N together with one dose of the Recessive-N gene, as present in double heterozygotes, should produced more hairiness than either two doses of the Recessive-N gene or one dose of the Dominant-N but less than two doses of the latter. Unfortunately medulla tests could only be made on the back, withers, side, and britch position samples but these do not show any real difference in medullation from that produced by the Recessive-N or heterozygous Dominant-N genotypes. The means are seen to differ somewhat from the two latter genotypes but none of the differences are significant. As with the Recessive-N genotype the position analysis shows that here the data also forms a graded series

born in 1944 while those from other genotypes were from lambs born in 1947, 1948 or 1950. It is conceivable that there may be a seasonal effect on medullation.

2: Position effects could account for the failure to produce more medullation than two doses of the Recessive-N gene, but not for the failure to produce more medullation than one dose of the Dominant-N gene. To account for the latter it would be necessary to postulate that the Recessive-N gene in a single dose has no effect in the presence of a single dose of the Dominant-N gene. In view of the halo-hair distributions in lambs of the two genotypes at birth and also the data relating to the growth of horns in rams, (Dry P.C.,) this is unlikely

3: Insufficient numbers of medullometer readings have been taken to establish the significance of any determinations of medullation made between the genotypes. In view of Dry's information in (2) above, this is suggested as the most likely explanation.

CHAPTER XIII

THE RELATIONSHIP BETWEEN HAIRINESS AS MEASURED BY THE FIBRE TYPE ARRAY METHOD AND BY THE MEDULLOMETER.

In general the correspondence between hairiness as measured by the fibre type array method and by the medullometer is seen to be fairly close. In the following chapter however, as there is no numerical measurement of an array, the following observations are not supported by any statistical work.

Section 1:

Comparisons between genotypes, using the two methods give very similar results but discrepancies do occur.

On the shoulder patch region in medullometer tests there is only a real difference between the mean of the homozygous Dominant-N genotype and those of all other genotypes. However fibre type array comparisons show that whereas Plain arrays exist on this position in the Non-N genotype, Ravine is the average arr ay in the heterozygous Dominant-N and Recessive-N genotypes and Plateau Grade P_3 in the homozygous Dominant-N.

On the withers, shoulder and neck regions a similar result is obtained from the two measurements. Medullometer readings show that the Non-N genotype, the heterozygous Dominant N, Recessive-N and double heterozygote genotypes and the homozygous Dominant-N genotype form three distinct groups in ascending order of medullation. Fibre type array analysis shows the same three groups, Valley being the array found in the Non-N genotype, Saddle the characteristic array for the heterozygous Dominant-N, Recessive-N, and double heterozygote genotype on the withers, and Plateau in the homozygous Dominant-N.

On the back and side medullometer readings show the Non-N genotype to possess significantly less hairiness but that no sharply defined groups are found in a study of the N-grade

and Plateau arrays in the homozygous Dominant-N genotype. However, here the difference between the N-grade genotypes may not be real as there is some overlapping between arrays and the results should be accepted with caution.

Both measurements show that on the britch the Non-N genotype is less "tough" or hairy than the N-grade ones but there is no real difference between any N-grade genotypes. Ravine is about the average array for Non-N britch while Plateaus are found here in N-grade genotypes.

Section 2:

Between positions within genotypes some more marked differences in the results of the medullometer tests and those of the fibre type array analyses are seen.

In Non-N genotype Plain arrays are found in all shoulder patches studied and Valley on all other regions except the britch where the average array is about Ravine. Medullometer tests show that the britch region is significantly more hairy than other regions and also that the back is significantly hairier than the shoulder patch, withers, shoulder and neck. No real difference is seen between the other positions.

In the heterozygous Dominant-N genotype medullometer tests show the shoulder patch to be the least hairy, the withers, neck and shoulder positions intermediate in hairiness and the side, back and britch the most hairy. Fibre type arrays however are Ravine on the shoulder patch and then grade up to Plateau on the britch, positions being arranged in ascending order of "toughness" as follows: shoulder, neck, withers, side, back and britch. In the Recessive-N and double heterozygote genotypes a fairly close correspondence between array classification and medullometer hairiness is seen.

However in the homozygous Dominant-N genotype the means of the medullometer tests for positions show an increase in medullation from the shoulder patch to the britch in very much the same order as that for other genotypes except that

gradients in fibre type arrays in homozygous Dominant-N sheep has been fully dealt with in Chapter 4 but it is seen to be restricted to fibre type array detail and does not appear in the medullometer tests.

Section 3:

In this section a few comparisons between the medullometer tests and fibre type array classification on individual sheep were made. However as these measurements were subject to an unknown amount of error variance none but the broadest conclusions can be drawn.

In arrays found in 178/48 (Table 7) as already mentioned in Chpter 6, a very strong head check was found combined with a strong base, Valley arrays being found on all positions except the britch, yet medullated histerotrichs were found in all positions. Medullometer tests, (Table 54) on the samples from this sheep show, however, that although this sheep is a borderline-N of grade VI halo-hair abundance besides having a very strong head check, that readings are here higher than those of a weak N-grade sheep 104/48. whose arrays range from Ravine on the shoulder path, shoulder and neck, through Saddle on the withers, side and back up to Plateau on the britch. However the readings for this sheep are lower than those for all other heterozygous Dominant-N's of N-grade birthcoat abundance of halo-hairs.

Conversely the homozygous Dominant-N sheep 300/48 a weak base is combined with a weak head check (Tables 1 & 30). Here medullometer readings are much higher than are found in 178/48 although basal medullation would here appear to be much less. Alsow with a few exceptions medullometer readings are here higher than those found in most cases on corresponding positions in the heterozygous Dominant-N sheep.

In most other cases individual variation in the single medullometer measurements is too great to allow any conclusions to be drawn. However the above would tend to

big effect on medullometer readings and this is also suggested by the fact that in 300/48 where halo-hair abundance is well sustained in all regions, (Table 30) although the arrays themselves are weak, medullometer readings are high, but in 178/48 both medullometer readings and halo-hair abundance are low. Further support to this suggestion is given by the fact that halo-hair and hairy-tip-curly-tip fibre percentages follow the distributions of tatal medullation as measured by the medullometer fairly closely. (See Tables 36,44 & 56)

Section 4:

In conclusion it is seen that there is a fairly close correspondence between medullometer measurements and the results of the fibre type array analysis. Where the two methods give different results, they are probably due to the fact that fibre type array classification only depends on the presence or absence of one or two fibre types. Other factors affecting total medullation such as the basal medullation, abundance of fibre types other than those directly affecting array classification, especially halo-hairs, degree of medullation of a medullated fibre etc., are ignored in the classification of arrays but all would affect medullometer readings. Total medullation as measured by the medullometer is probably still the best test of overall medullation of the fleece.

PART IV

PART IV.

SKIN FOLLICLES IN THE N-TYPE SHEEP.

CHAPTER XIV

INTRODUCTION.

The follicle development in the N-type foetus has been studied by Ross (1945) on the poll, central and dorsal neck, stomach, brisket, withers, britch, side and back. In comparison with the position in the ordinary Non-N New Zealand Romney as studied by Galpin (1935) and the studies of other finer wooled sheep such as the Merino, (Carter 1943), no difference has been found in the age at which follicle initiation begins, nor in the fundamental group arrangement. However Ross has found in the positions which she has studied that in the N-type sheep there is a rapid rate of growth of follicles after the 92 day stage of foetal development. Also the constituents of the individual follicle bundle in N-type were found to show great differences in size. The large primary follicles particularly those of the central trio are in striking contrast with the small secondary follicles. These extremes of vigour within the same bundle are marked when the follicles are compared with those of the finer breeds as illustrated by Carter (1943).

This paper by Carter (1943) gives a detailed description of the structure of the skin and follicle system in the Merino sheep which, apart from minor details as pointed out above, is very similar to that found in the New Zealand Romney, both Non-N and N-type. He found that at birth the follicle group possessed all the essential features of the adult arrangement. This is as follows:

"The follicle group in the skin of the Merino consists typically but not exclusively of a basic group of three primary follicles and a variable number of secondary follicles. The primary follicles represent an original trio group composed of one central (primary X or Y) and two lateral (primary x or y) follicles established during the primary phase (or protophase) in the pre-natal development of the

(c) A large bi-lobar or multi-lobar acinous sebaceous gland.

Of these structures the first two belong exclusively primary follicle.

The secondary follicles are composed of all those follicles which are established after the completion of the two group of primary follicles, that is during the secondary phase (or neophase) in the pre-natal development of the follicle population. The only accessory structure associated with a secondary follicle is the sebaceous gland which is small and generally unilobar. It may even be absent." (See Figure 2.)

In another section of his work, Carter states that in development the first secondary follicles are formed on the opposite or ectal side of the bundle to the primaries which are found on the ental side, and later secondary follicles develop between these and the primaries. The first secondary follicles to develop are the largest and it is usually these which possess the sebaceous gland.

"A small proportion of primary follicles may never have been grouped in "trios" but remain either as solitary (Primary X or Y) follicles or as couplet groups (primary Xx or Yy). For this reason it is not strictly accurate to express the relation between primary and secondary follicles entirely in terms of the "classical group".

Burns (1949) has made a study of Romney and Leicester lamb skin sections from 1 month to 9 months after birth, and she has also found that here the main lines of follicle population development are similar to those described in the Merino breed by Carter (1943). However she has also found that accessory structures (sweat glands and arrector muscles) usually associated with primary follicles only, may occasionally be found in follicles situated on the ectal side of the follicle bundle and apparently corresponding to large secondary follicles. However where both a sweat gland and an arrector muscle are present she has classed the follicle as a primary suggesting that it may have become displaced in development, but it would appear that a large secondary follicle on the ectal side of the bundle can possess an arrector pili muscle.

The aim of this part of the work was to study the follicles, their contained fibres, and the ratio of primaries

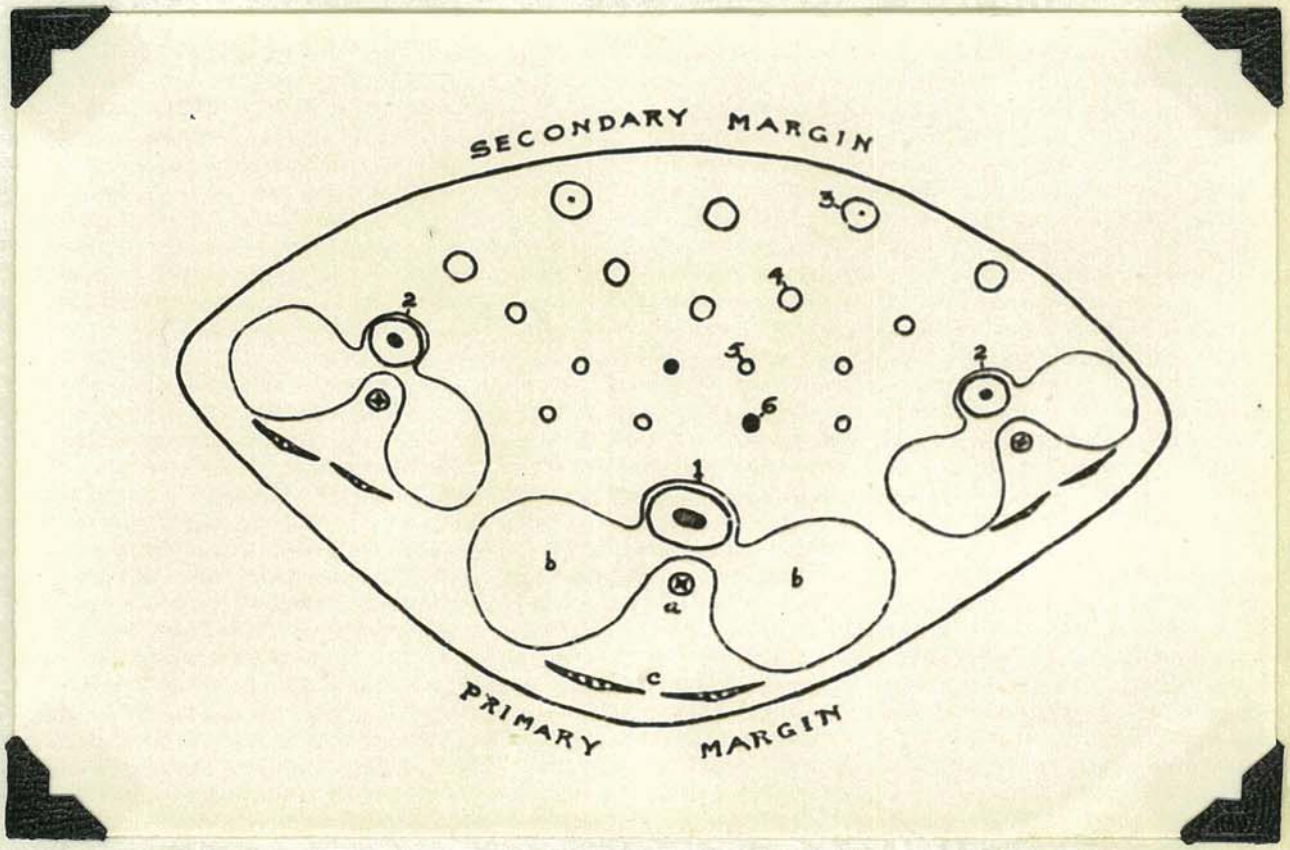


Fig.2. Diagram of the merino follicle group showing its relation to the original trio group.

1. Primary (central trio) fibre.

2. Primary (lateral trio) fibre.

3, 4 & 5 Secondary fibres numerically in order of their establishment.

6. Follicle anlage in which a fibre has not yet been ~~trans~~formed.

Associated structures figured with primary follicles are:

a. Duet of sudoriferous Gland.

b. Lobes of the sebaceous Gland.

c. The m.arrector pili.

Sebaceous glands associated with secondary follicles have not been drawn. From Carter.

just a basis to provide material to work on in the future. The ratio of primary to secondary follicles and follicle anlagen was studied in different regions, building on the work of Fraser, Ross and Wright (I.P.) who studied the Non-N and heterozygous Dominant-N genotypes on the standard back position. As fleece characters vary so greatly in different body regions it was necessary to know if the ratio changed over the body as well as in different genotypes; consequently skin samples from the seven standard positions (Chapter 3) were studied. It was hoped that the study would provide results that could be used to build on in later studies of dosage effects on skin follicles.

CHAPTER XV

MATERIALS AND METHOD.

The material consisted of whole skins collected from lambs which died at birth. The two Recessive-N, the homozygous Dominant-N and the heterozygous Dominant-N skins were from Dr. Dry's experimental Romney flock while the Non-N skin was donated by Mr. H. Jackson of Te Akau, being from an ordinary grade Romney flock. These skins were stored in formol saline for two months when samples were removed from the seven standard positions, back, withers, side, shoulder patch, shoulder, neck and britch. The sampling was at times a little inaccurate as only the skin was a guide to the positions, but in most cases this was fairly satisfactory. These samples were first washed in running water for twenty-four hours; then placed in 30% and 50% alcohol for a similar period of time and finally stored in 70% alcohol.

It was found that, for sectioning purposes the skin could be cut quite well if embedded in B.D.H. paraffin wax, melting point 54°-55°C. provided the microtome knife was kept sharp. Sections were cut at 8μ on a Cambridge rocker across the surface of the skin this showing the arrangement of the follicles.

Sections were stained with haemotoxylin and eosin (Guyer 1936) but the haemotoxylin used was iodine ripened using the method of Cole (1943). With this method of staining with haemotoxylin the sections needed no mordanting. The method was to remove the wax in xylol and take the sections down through the alcohols to water. They were then stained with iodine ripened haemotoxylin for one hour rinsed in water and taken up to 50% alcohol. Next the haemotoxylin stain was removed from the cytoplasm by 0.5% nitric acid in 50% alcohol. The remainder of the method was similar to that set out in Guyer.

The sections were studied under the low power of

relevant secondary follicles seen were counted. Follicle anlagen in which the fibre was not yet formed were not numerous but where present they were counted and their total added to that of the secondary follicles. However on the back and shoulder patch positions the follicle anlagen were counted separately and both the ratio of primary to secondary follicles and the ratio of primary to secondary follicles and follicle anlagen were calculated. However as these anlagen were in no case numerous and the proportion present was never found to vary markedly a further study was not made.

In counting it was in most cases easy to distinguish the m.arrector pili and the sudoriferous gland ducts of the primary follicles. Where a follicle with both these accessory structures was present on the ectal side of the bundle the follicle was classed as a primary but where only an arrector-pili muscle was present the follicle was classed as a secondary. This is in accordance with the results of Burns (1949) who found follicles with these accessory structures on the ectal side of a bundle and concluded that a secondary follicle may possess an arrector muscle, but thought that a follicle possessing sudoriferous gland was a displaced primary. In the sample from the neck of heterozygous Dominant-N, Q, the skin had somewhat decomposed and here the separation of follicles was more difficult.

From a section approximately ½ a square c.m. in area two areas were counted and this process was repeated on a similar section cut from another sample from the same area. Approximately 400 follicles were thus counted from the one sampling position.

When calculating results on the back and withers positions, both the ratios $\frac{P+p+S+s}{P+p}$ and $\sqrt{\frac{P+S}{P}}$ (Carter 1943), & the simple ratio of primary to secondary follicles as used by Burns (1949) were calculated for comparative purposes.

CHAPTER XVI

RESULTS.

The ratios of primary to secondary follicles and follicle anlagen are shown in table 59 but the numbers studied are too few to give much of an indication as to whether any real differences occur between positions within genotypes or between genotypes. An F test was carried out between positions including data from all the lambs studied, genotype being ignored, but no real differences were found to exist here.

Between genotypes in all cases except the Recessive-N only one lamb was studied in each genotype so no information as to whether any variability found was due to the genetic constitution, or was just normal variation found between individual lambs, could be obtained. However the results do show that there is a higher proportion of secondary follicles in the Non-N lambs studied, an intermediate proportion in the heterozygous Dominant-N lamb and a low proportion in the homozygous Dominant-N lamb and Recessive-N lambs, but whether these results are just a chance effect or not is not known.

Fraser, Ross and Wright (I.P.) have estimated the primary / secondary follicle ratio at birth just in front of the standard back position in the heterozygous Dominant-N and Non-N genotypes. They found that there was no real difference in the ratio between genotypes and that the average ratio was 1 to 2.37 with variation from 1/1.8 to 1/3.8. As the results found in this work in the heterozygous Dominant-N and Non-N genotypes are within these limits it is probable that any variation here is due to chance. However in the Recessive-N and homozygous Dominant-N genotypes the ratio is outside these limits being 1/1.13 in the former and 1/1.35 in the latter on the standard back position, but in view of the limited number of skin sections studied no definite conclusions can be drawn.

All things taken into account it is seen that no outstanding differences are found to exist in the ratio of primary to secondary follicles present, but a real clarification of the position must await the study of larger numbers. This is in keeping with the findings of Fraser, Ross and Wright mentioned above.

However when comparisons are made with the results of studies of fine wool sheep such as the Merino (Carter and Hardy 1947), it is found that there is a greater proportion of secondary follicles and follicle anlagen in the Merino foetus just before birth than in the Non-N and Netype Romneys studied at birth. Thus it would appear that in the finer wooled sheep and breeds there may be a greater proportion of secondary follicles and secondary follicle anlagen at birth.

No information could be gained from the present work on the proportion of primary central to primary lateral follicles as at birth these are not distinguishable.

As found by Ross (1945) it is seen in the sections studied that in the N-grade genotypes the fibres in the primary follicles are very much greater in diameter and more stoutly medullated than those in the secondary follicles. In contrast fibres in all follicles in the Non-N genotype are very similar both in diameter, and medullation if present. (See Photographs 1 to 4.) It is interesting in view of this fact, that Spöttel and Tänzer (1923) have found that in primitive sheep such as the Mufflon the fibres in the primary follicles are very much greater in diameter than those in the secondary follicles, while in fine-wooled sheep such as the Merino all follicles contain fibres of a very similar diameter. (Photographs 7 to 8). The significance of this in relation to the precipice has been explained earlier, Chapter 8. However this fact is also interesting in view of the suggestion of Goot's (1940) that the N-type birthcoat is similar to that of the primitive sheep.

birth, but are very much lower than the $\frac{P+p+S+s}{P+p}$ ratio for the Merino. From this it can be seen that in the Merino foetus a much higher proportion of secondary follicles anlagen are present than in the Romneys at birth. As previously stated (Chapter 15) very few of the secondary follicle anlagen found to be present in the Romney material studied here, but the reasons for these differences are not known.

In conclusion it is seen that the only outstanding feature of the N-type Romney skin sections studiedis the larger size of the fibres in the primary follicles. The numbers studied were too few to clarify the position with regard to the ratio of primary to secondary follicles present or any other features.

In the material taken in the present work, the trio structure had become distorted as is mentioned by Carter (1943) in the post natal characters of the Merino follicle group. Instead of distinct trio groups being present, the primary follicles all tended to be arranged in a row with their accessory structures on one side next to the connective tissue strands or major trabeculae, and the secondary follicles on the opposite side. (See Photographs 1 to 6). Primary follicles on the ectal side of the bundles and secondary follicles with m.arrector pili were also found to be present. (Photographs 5 to 6).

PART V.

PART V.

GENERAL DISCUSSION AND SUMMARY.

CHAPTER XVII

DISCUSSION.

In this study of gene dosage effects in the N-type sheep it is seen that there is an orderly change in certain fleece characters with increasing gene dosage. The Non-N genotype shows all the characteristics of non-medullated fleeces. The arrays except in the britch position are all weak, fibre types analysis showing that non-medullated fibres are characteristic of this genotype and medullometer tests show that little overall medullation is present.

The lowest dosage of N-genes obtainable is one dose of the Recessive. This genotype, namely nr/+, or Carrier, was not studied in this present work as the fleece was very little different from that of the Non-N genotype. However, from data supplied by Dry (P.C.) it has been found that a significantly greater proportion of lambs in this genotype are of Grades III and II and less are of Grade I halo-hair abundance on the standard back position than in the Non-N genotype. Also here Dry has found that a quarter or more of the carrier rams when raised to maturity have horns, mostly quite small.

Another indication that this genotype is more capable of producing a more medullated fleece than the Non-N is the fact that whereas an N-grade birthcoat is never produced by the Non-N genotype, Carrier lambs occasionally show this feature. Here it has been shown by breeding experiments that these sheep were not homozygous Recessive-N's and Dry (P.C.) has suggested that a dominigene, an oligogene acts on the single dose of the Recessive-N gene to produce an N-grade birthcoat. In this connection classification of the fleeces at shearing time into z grades by Dry (see later) also shows that there is here a greater degree of hairiness found on some Carrier sheep than is

and total medullation as measured by the medullometer all show mean values much higher than those for the Non-N genotype. Also the mean values for the percentages of non-medullated fibres is lower in this genotype than in the Non-N. However it should also be emphasised that this first increase in hairiness occurs most markedly in the more hairy regions of the fleece and very little difference is seen between this genotype and the Non-N in the shoulder patch position. Another feature of this genotype is the extreme variability encountered in it in all measurements made. Halo-hair abundance varies from Grade III on the standard back position similar to Grade III on the Non-N genotype, with a few Grade II and probable Grade I lambs to a full N-grade abundance of halo-hairs in all parts of the body as is characteristic of the homozygous Dominant-N genotype. About 16% of the heterozygous Dominant-N lambs are less than N-grade and an estimated 1 in 70 show no reduction anywhere on the body. Dry has found that at least some of this variability in the heterozygous Dominant-N genotype has a genetic basis. (P.C.)

This variation is also shown in fibre type arrays. These vary from Valley in most positions of the body in lambs 16/50 and 178/48 up to Saddle and Plateau arrays in 48/48. In the medullometer tests too, the standard deviation and hence the variance is greatest in this genotype.

Gradients over the body are similar to those in the Non-N genotype but they are much more pronounced. As hairiness increases within this genotype the hairy body positions first become very medullated and this gross hairiness gradually spreads over the body to the "weaker" positions as medullation increases.

Fibre types characteristic of this genotype are, especially in the pre-curly-tip class those of intermediate medullation; e.g. super-sickle B and sickle-fibres. Horns are here present in the rams but not in the ewes except that about 1 ram in 10 failed to grow horns while about 1 ewe in 10

readings show no marked differences between these genotypes. However Dry (P.C.) has found that there is a slightly greater average halo-hair abundance in the Recessive-N's and double heterozygotes than in the heterozygous Dominant-N's. The only sheep found on the borderline between N-grade and Non-N in the two former genotypes are of grade VI halo-hair abundance on the back while about 1 lamb in 6 has no reduction of halo-hair abundance on any region of the body. The horns position varies in the two genotypes, the Recessive-N ewes showing poorer ability to grow horns than those in the heterozygous Dominant-N genotype, while the double heterozygote ewes show greater ability to produce horns than the heterozygous Dominant-N's. Another item of interest is the suggestion that the Recessive-N's and double heterozygotes show less variation between body positions in fibre type array detail than is found in the heterozygous Dominant-N's.

Another big increase in fleece medullation is seen when two doses of the Dominant-N gene are present in the genotype. Here there is a full N-grade abundance of halo-hairs on all body regions in all lambs studied and both ewes and rams grow horns. Fibre type array analyses in this genotype do however show variation but there is a great increase in "toughness" compared with other genotypes studied. The greatest increase in "toughness", percentage of medullated fibres, or in hairiness as measured by the medullometer is however in the "weaker" body positions.

Nearly all arrays in all positions are Plateau with the exceptions being in sheep 300/48. Gradients over the body are also different on fibre type array classification. In comparison with other genotypes, the britch position shows itself to be "weaker" in three of the six cases studied than the back and withers. Also the side tends to be comparatively weaker than in other genotypes.

ence again being most noticeable in the "weaker" body positions. However here the britch position is found to possess the greatest degree of medullation in the fleece and no differences in the order of positions in increasing hairiness when compared with other genotypes, are seen.

In the follicles the only readily observable effect of increasing N-gene dosage is the increase in the relative size of fibres in the primary follicles.

Dry (P.C.) has classified the adult fleeces of sheep of various genotypes for hairiness at shearing time in the following way:

a. Z_3 : fleece grossly hairy and hairiness well maintained at the front of the body.

b. Z_2 : fleece still very hairy but some weaknesses at the front of the body.

c. Z_1 : fleece less hairy.

d. Z^- : fleece hairy by ordinary flock romney standards but poorly hairy by N-type standards.

e. ordinary flock romney fleece.

In finding the average Z grade in the following, Dry (P.C.), has ignored all Z^- and less hairy fleeces and given Z_3 fleeces the value of 3, Z_2 fleeces the value of 2 and the Z_1 fleeces the value of 1. In all except the double heterozygote genotype the fleeces were from ewes of mixed ages born later than 1946 but in this genotype some ewes of greater age were present. However the average Z grades for the various genotypes are set out in table 58. In the Carrier genotype it is seen that the average Z grade is 0.05,,this being due to the presence of a few Z_1 fleeces. In the other genotypes the average Z grade in the Recessive-N and heterozygous Dominant-N genotypes is 1.31 and 1.12 respectively while the homozygous Dominant-N genotype it is 2.19. Borderline and Low N's in the heterozygous Dominant-N genotype average 0.28 while in the double heterozygote genotype, omitting three ewes born in 1944, which had less hairy fleeces due to age, the average Z grade is 1.31. This

that the homozygous Dominant-N genotype contained significantly more sheep with fleeces graded Z_2 and Z_3 and less sheep with fleeces graded Z_1, Z^- and non-hairy than in the heterozygous Dominant-N and Recessive-N genotypes. For the analysis the data was combined into the two groups as outlined above. Similarly the Recessive-N and heterozygous Dominant-N genotypes conatin significantly more sheep with fleeces graded Z_1, Z_2 or Z_3 and less sheep with fleeces graded Z^- or Non-hairy than the Carrier, nr/+, genotype. All differences are at the 1% significance level. (See Table 58).

It is seen that Goldschmidt's theory of gene dosage (see introduction) provides a suitable theoretical basis on which to explain the above results of different N-gene dosage in Romney sheep. A similar theory to that proposed by Mohr (1932) for the facts discovered about the vestigial wing gene could explain many of the discoveries in the N-type sheep as follows:

In the Non-N genotype the genotype is below a certain threshold necessary to produce an N-grade birthcoat on the standard back position. Variation does exist here as the birthcoats show Grades I to VI of halo-hair abundance on the back, but the majority of lambs were grades I, II and III, the average for all that were studied being grade 1.66. Horns are seldom produced in either sex.

Fibre type arrays and medullometer tests in the limited material studied in this work, also show very little variation except on the britch. Except for this position the fibre type arrays are all Valley or Plain and the means of the medullometer measurements areall low. However on the britch there is considerable variability both in the arrays and in the medullometer readings, the averages in both cases showing greater "toughness" than elsewhere. Follicles are seen in the few skin sections studied to show no great differences in the

follicles had a much greater diameter than those in the secondary follicles.

In the Recessive-N heterozygotes or Carriers there is just one very weak gene tending to produce horns and fleece medullation. On the average its only known effect on fleece medullation is to slightly increase the abundance of birthcoat halo-hairs. However in the Carrier rams this gene causes the threshold value of some substance or substances necessary for the production of horns to be passed in about a quarter of the cases. This variability is probably due to both genetic and environmental factors but has not been studied. Also in a few cases Dry (P.C.) has suggested that a dominigene acts in concert with the single Recessive-N gene to cause the threshold value for the production of a substance or substances, necessary for the production of an N-type birthcoat, to be passed. This may also be considered as the greatest possible reaction of a single Recessive-N gene shown when it is placed in a genotype most favourable to its activity.

The next increase in N-gene dosage is seen in the heterozygous Dominant-N genotype. Here all the fleece characteristics as stated above show great variability, but in all except about 16% of the cases the threshold value suggested above as being necessary for the production of an N-grade birthcoat on the standard back position, is passed. However in only about 1 lamb in 70 born in this genotype is the genotype sufficient to cause the production of a full abundance of halo-hairs in all body regions. Similarly the fibre type array analyses show all ranges from that characteristic of non-medullated genotypes to that of weak homozygous Dominant-N's. A similar situation is found in regard to medullometer tests and percentages of the fibre types present. Horns, with odd exceptions are produced in the rams but not in the ewes.

Thus in this genotype it would appear that the

acting on the single Dominant-N gene is able to express itself. That this is the normal situation when a genotype producing a phenotype intermediate between two extremes is bred is suggested by Goldschmidt's (1923) work on Lymantria dispar. Here the full male or female type is phenotypically stable and it is suggested that this stability is due to a threshold value having to be passed to produce intersexuality. However when a cross producing intersexes is made great variability is seen in the resulting progeny, as all variability, both genetic and environmental comes to expression.

In the heterozygous Dominant-N genotype a similar situation is found except that here the variability is such that the threshold value characteristic of both the Non-N and homozygous Dominant-N genotypes can be passed. The horns position however seems more stable and one interesting point is that horn production although thought to be a pleiotropic effect of the N-gene, is found by Dry (P.C.) within this genotype to be independent of fleece medullation. Whether this is due to different genes, acting on a common precursor produced by the N-genes, to produce horns in one case and fleece medullation in the other is not known.

In the Recessive-N and double heterozygote genotypes a slightly higher level of ability to produce a substance or substances necessary for the production of a hairy fleece is found, as about 1 in 6 lambs born in these genotypes pass the threshold value necessary for the production of a full birth-coat abundance of halo-hairs in all body regions, and only a few borderline N's of grade VI halo-hair abundance on the back are seen. However fibre type array analyses and medullometer tests show no real differences between these two genotypes, and the heterozygous Dominant-N. With simple gene dosage it would be expected that the heterozygous Dominant-N, Recessive-N and double heterozygote genotypes should, in that order, be able to produce increasingly medullated fleeces. However

and this latter genotype in turn shows less ability than the double heterozygote genotype. These differences would suggest that the productions of horns and medullation of the fleece are not simple pleiotropic effects of the same gene but the position needs investigating. It is also suggested that there is less variability in the Recessive-N and double heterozygote genotypes but unless this is due to the lack of lambs with a very weakly medullated fleece no theoretical explanation can be advanced. However the effect is not marked and in view of the small numbers may not be real.

Finally in the homozygous Dominant-N genotype it is found that horns are grown in both sexes and a full abundance of birthcoat halo-hairs is produced. Here N-gene dosage is sufficient to pass the threshold necessary for the production of both the above characters in all cases studied. However fibre type array analyses show that in not all cases is there fully a medullated fleece as possible produced in all regions of the body. Also here gradients do not follow those seen in other genotypes so some new factor or factors may be operating. Medullometer tests, while also showing "weaknesses" in various body positions do <u>not</u> show that gradients are different from those in other genotypes. Whether it would be possible with still higher N-gene dosage to produce a more medullated fleece or whether the total possible fleece medullation in the New Zealand Romney has been produced in the homozygous Dominant-N genotype is a subject for future research.

The other effect of increasing N-gene dosage is that the fibres in the primary follicles increase greatly in diameter relative to those in the secondary follicles. It has been suggested previously that this causes the precipice to appear in "tough" arrays, a feature also characteristic of arrays on sheep carrying a high dosage of N-genes.

The physiological and embryological effects of the N-genes have not been studied. It is most probable in view of

any research on this subject it would be as well to leave the matter until more is known.

CHAPTER XVIII

SUMMARY AND CONCLUSIONS.

A study of gene dosage effects in N-type sheep has been made using the fibre type array method and the medullometer method developed by Elphick and McMahon. As the position was complicated by gradients occuring in the fibre type arrays and total fleece medullation over the body, the study on each sheep was made in the seven positions: back, withers, side, shoulder, shoulder patch, neck and britch, this being to see what gradients were present and how these changed with increasing N-gene dosage.

Fibre type arrays show that there is an increase in "toughness" with increasing dosage of N-genes. Threshold effects prevent this from being a straight linear arrangement, there being greater variation in genotypes of intermediate "toughness." With weak medulla producing genotypes the first increase in medullation is seen in the more strongly medullated parts of the fleece, namely, the britch, back and side, but with increasing N-gene dosage this increase in "toughness" spreads to positions showing "weaker" arrays finally producing a fairly uniformly "tough" fleece.

Fibre type array gradients studied by Galpin (1936) were, in all genotypes except the homozygous Dominant-N, in most cases similar to her findings. There was a posterior anterior gradient in toughness, tougher arrays being found on the britch, back and side, and weaker ones on the withers, neck and shoulder, in that order. It was in addition, found that the shoulder patch was the "weakest" positions studied. However the order of increasing "toughness" of positions especially those where similar types of arrays were found was seen to be somewhat variable. In one outstanding case, 16/50, a heterozygous Dominant-N lamb of Grade III halo-hair abundance, the back and side positions were found to be "tougher" than the

Gradients were not so marked in the homozygous Dominant-N sheep as here the fleece tended to be uniformly "tougher", but where they occurred they seemed to differ from those of other genotypes, in that the britch was less tough than the back and withers positions and the side was relatively weaker.

A discriminant function, to separate genotypes on the different types of fibres present, has been worked out to separate all genotypes except the Non-N on the shoulder patch position. However this gave very similar results to those obtained by other methods in that the homozygous Dominant-N genotypes was found to differ significantly from the Recessive-N and heterozygous Dominant-N genotypes, but the latter two are only barely significantly different at the 5% level. The Non-N is separable from the N-grade genotypes on this position as here, in all cases studied, arrays only contain fine sickle-fibres and non-medullated curly-tips and histerotrichs, while all N-grade genotypes arrays studied contain at least a few medullated fibres. The mathematical calculations were too laborious to permit the widespread use of this method in the limited time available.

A statistical analysis of the percentages of fibre types present in different genotypes has been made. With genotypes showing little hairiness, non-medullated fibres, e.g. fine sickles and checked curly-tips are mainly present this being especially noticeable in the pre-curly-tip fibre group. Increasing N-gene dosage causes those fibres showing intermediate medullation, namely super-sickle B and sickle-fibres, to be present in the heterozygous Dominant-N, Recessive-N and double heterozygote genotypes. Finally in the homozygous Dominant-N genotype the majority of fibres are those showing the greatest degree of medullation found, namely halo-hairs, super-sickle As and hairy-tip-curly-tips.

The N-genes did not however appear to greatly affect

"toughness" of arrays. However in view of the fact that all histerotrich fibres were not present at the time of sampling this result cannot be regarded as final. The percentage of pre-curly-tip fibres also did not differ markedly fr between genotypes within positions. However between positions it was found that there was a lower percentage of these fibres on the withers and neck. These findings are somewhat contradictory to those of Galpin (1934) as explained elsewhere but the reason for this is not known. Data relating to the precipice is also analysed. It is found that with increasing N-gene dosage and "toughness" of arrays a precipice occurs in the curly-tip fibres. It would appearthat this is due to the increasing difference in size between fibres produced in the primary and the secondary follicles. As N-gene dosage increases further, the pre-precipice curly-tips become hairy-tip-curly-tips.

Measurements with the medullometer show a similar type of increase in total fleece medullation to the increase of "toughness" as found by the fibre type array method. In very weakly medullated sheep and genotypes the first increase in fleece medullation is in the hairy body positions and later increases in hairiness with increasing N-gene dosage follow in the "weaker" positions. Comparisons between positions also show similar differences to those observed by fibre type array measurements in that the order of positions in most cases, in ascending order of medullation, is shoulder patch, withers, shoulder, neck, side, back and britch. The only unusual feature is the relative "weakness" of the withers position. However the order of positions in increasing order of fleece hairiness in the homozygous Dominant-N genotype is similar to that in the other genotypes. Here the fibre type array method (see above) gives a different result from that obtained by medullometer measurements.

Sections have been cut of both N-type and Non-N

genotypes in the ratio of primary to secondary follicles at birth.

It is seen that the theory of gene dosage, as put forward by Goldschmidt (1938) provides a suitable theoretical basis for the facts so far discovered about gene dosage effects in N-type sheep.

Related to dosage effects, were, in this study several items of significance with regard to the architecture of the fleece.

The borderline-N lamb 178/48 would, with the strong head check and strong basal medullation seen here, suggest that there are two distinct forcers acting to produce fleece hairiness. Further evidence to support this is obtained from the homozygous Dominant-N lamb 300/48, where it would appear that a weak head check acts on a weak base. It is probable that both an increase in basal medullation and a decrease in the power of the head check occur with increasing hairiness, but owing to the lack of a suitable measurement of "base" this cannot be ascertained for certain.

In the study of the neck and shoulder regions it is seen that while Dry (P.C.) has found that there is generally a reduction of halo-hair abundance on the neck before a reduction is seen on the shoulder, yet shoulder arrays are generally the "weaker". This suggests that the fibre type array and halo-hair abundance are not absolutely correlated. This difference may be due to the "damping" of halo-hairs to super-sickles on the neck, seen in lambs in the genotypes of intermediate hairiness. Whereas this damping may well affect the abundance of halo-hairs present, it may not affect the "toughness" of the fibre type array. Also in the N-type birthcoats Dry (P.C.) has found that the halo-hairs form tufts and curls these forming the units of patterns over the surface of the fleece. In the less hairy N-grade genotypes, especially where damping occurs, the tufts at the front end of the body and on the neck region

have been studied here, it would seem that, if changes are similar to those found in the genotypes studied in the present work, any further increase in fibre type array "toughness" or medullometer hairiness in November samples, would only be likely to occur in the "weaker" body positions. Also it may be noted that in adult sheep it is often seen that there is an area of wool round the poll, even although the rest of the fleece is markedly hairy. In a study of higher dosages it would probably be well worth while to study the poll.

As the trend in basal medullation as seen in the samples studied is not well known it would be unwise to predict the effect on it of higher gene dosage. However, Dry (P.C.) has found that in very hairy adult sheep the hairiness in the proximal or butt end of the staple is well sustained down to the skin in the "weaker" body positions. Although this is a rather different effect from the sense in which "basal medullation" has been used in this thesis, a study of this feature might well be useful in higher N-gene dosages.

Other features that should be watched for in a study of higher gene dosages are the situation with regard to fibre types denoting slight "weakness" on the less hairy positions and data relating to the precipice.

With regard to fibre types, in the weaker positions of the homozygous Dominant-N genotype super-sickle A' and super-sickle B fibres are frequently found while occasional sickles and fine sickles are also present. In genotypes of higher N-gene dosage, these may not be found. Pre-precipice curly-tips, sometimes present on some positions in homozygous Dominant-N sheep, may also be lacking with higher N-gene dosage, while post-precipice hairy-tip-curly-tips may become more numerous!

The precipice is found, in the homozygous Dominant-N genotype, to be present much more frequently than in lambs of lower N-gene dosage. This is especially true on "weaker" body

effects different to any seen in the sheep so far studied. This however is a matter for future research.

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TABLES

TABLE I.

CLASSIFICATION OF PRE NATAL CHECKS AS;

TABLE I.

EAU P_I (NO SSA' SSB or SK); PLATEAU P_2 (No SSB or SK); PLATEAU P_3 (No SK); SADDLE (SK All Medullated); RAVINE e SK); VALLEY (Fine SK, Chkd CT); PLAIN (No Medullated CT).

BODY POSITIONS

S	SHEEP	SHOULDER PATCH	SHOULDER	NECK	WITHERS	SIDE	BACK	BRITCH
	B/6	Plain	Border between Valley & Plain	Border between Valley & Plain	Truncated & weak Valley	Truncated & weak Valley	Valley	Plateau P_3
	B/I	Plain	Border between Valley & Plain	Border between Valley & Plain	Border between Valley & Plain	Truncated & weak Valley	Valley	Valley
	B/4	Plain	Truncated Valley	Truncated Valley	Truncated Valley	Truncated Valley	Truncated Valley	Weak Saddle
	B/5	Plain	Truncated Valley	Weak Valley	Valley	Valley	Strong Valley	Very strong Valley
	I6/50	Valley	Valley	Truncated & very weak Valley	Valley	Saddle	Strong Ravine	Very strong Valley
	I78/48	Truncated Valley	Valley	Valley	Valley	Valley	Valley	Saddle
n	I04/48	Ravine bordering on Plain	Ravine	Ravine	Saddle	Saddle/ Ravine border	Saddle	Plateau P_3
	6/48	Ravine	Ravine	Saddle	Saddle / Ravine border	Saddle	Plateau P_3	Plateau P_2
	I2/48	Ravine	Saddle	Saddle	Strong Saddle	Plateau P_2/P_3 border	Strong Saddle	Plateau P_I

SHEEP	SHOULDER PATCH	SHOULDER	NECK	WITHERS	SIDE	BACK	BRITCH
41/48	Ravine	Saddle	Saddle	Saddle	Plateau P3	Saddle	Plateau P 1
93/48	Strong Valley	Saddle	Strong Saddle	Saddle	Plateau P3	Weak Plateau P 3	Strong Plateau P 3
78/48	Ravine	Ravine	Saddle	Border between Plateau & Saddle	Plateau P3	Plateau P 2	Plateau P 1
65/48	Saddle	Saddle	Border between Plateau & Saddle	Border between Plateau & Saddle	Plateau P3	Strong Saddle	Plateau P 1
35/48	Ravine	Border between Plateau & Saddle	Plateau P 3	Saddle	Plateau Border between P2 & P3	Plateau Border between P2 & P3	Plateau P 1
90/48	Ravine	Saddle	Saddle	Weak Plateau P 1	Saddle	Plateau P 2	Plateau Border between P 2 & P 3
48/48	Saddle	Saddle	Border between Plateau & Saddle	Plateau P 1	Weak Plateau P 1	Plateau P 1	Plateau P 1
158/48	Valley	Valley bordering on Ravine	Valley bordering on Ravine	Ravine	Saddle	Saddle	Plateau P 3
194/48	Valley Truncated.	Valley	Valley	Valley	Valley	Valley	Ravine

CLASSIFICATION OF PRE-NATAL CHECKS. Table I a.

B O D Y P O S I T I O N S

ES	SHEEP	SHOULDER PATCH	SHOULDER	NECK	WITHERS	SIDE	BACK	BRITCH.
	42/44	——	——	——	Weak Ravine	Saddle	Ravine	Plateau Border Between P 2 & P 3.
	88/44	——	——	——	Saddle	Saddle	Saddle	Plateau Border Between P 1 & P 2.
	9/44	——	——	——	Saddle	——	Saddle	——
	129/44	——	——	——	Saddle	Saddle	Saddle	Plateau P 1.
	155/44	——	——	——	Saddle	Saddle	Saddle	Plateau P 1.
	353/48	Valley	Border Between Ravine & Valley	Border Between Ravine & Valley	Saddle	Saddle	Saddle	——
	80/47	——	Ravine	Saddle	Valley or All-In	Saddle	Saddle	Plateau P 1.
	332/48	Saddle	Saddle	Saddle	Saddle	Border between Plateau & Saddle	Saddle	——
	351/48	Valley	Saddle	Saddle	Plateau P 3.	Plateau P3	Weak Plateau P.1.	——
	343/48	Ravine	Plateau P 3.	Saddle	Plateau P 3.	Plateau P3	Plateau P 1.	——
	300/48	Ravine	Plateau P 3.	Weak Plateau P3	Plateau P 1.	Strong saddle	Plateau P 1	Plateau P_3
	15/50	Plateau P 3.	Border between Plateau P 2 & Plateau P 3.	Plateau P3	Plateau Border between P1 & P2	Plateau P 3	Plateau Border between P2 & P 3.	Plateau P 3.

142b.

SS	SHEEP	SHOULDER PATCH	SHOULDER	NECK	WITHERS	SIDE	BACK	BRITCH.
	14/50	Plateau P 3	Plateau P 3	Plateau P3	Plateau P 2	Plateau P 3	Plateau P1	Plateau Strong P 3
	245/48	Border between P 2 & P 3	Plateau P 3	Plateau P3	Plateau P 1	Plateau P2	Plateau P 1	Plateau P 1
	239/48	Plateau P 3	Plateau P 1	Plateau P1	Plateau P 1	Plateau P2	Plateau P 2	Plateau P 2
	263/48	Plateau P 3	Plateau P 2	Plateau P2	Plateau P 1	Plateau P2	Plateau P 1	Plateau P 1

TABLE 2. B 4 +/+.+/+ GENOTYPE.

HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non-Med	Hi Med	Hi Non-Med	Precipice.
						.48							72.55		26.97	No
						6.57	9.53					34.32	20.34		29.24	No
						6.61	13.98					4.30	40.25		34.87	No
						4.44	13.71					26.81	25.00		30.04	No
						8.42	7.58					31.58	18.32		34.11	No
						8.19	6.67					24.83	34.10		26.67	No
			.68		9.55	.23						45.45	16.82		27.27	No

Table 3 B 5. +/+.+/+ GENOTYPE

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd.	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non-Med	Hi Med	Hi Non-Med	Precipice.
							1.89							77.13		20.98	No
							4.08	13.27					5.36	61.48		15.82	No
						.23	2.52	15.60					3.21	55.96		22.48	No
				.22		.44	1.96	6.32					5.23	49.02		36.82	No
				1.10		.44	4.19	8.96					9.91	55.73		24.67	No
				.20		.60	1.40	5.61		.40			19.64	43.09		29.06	No
				1.49		1.49	3.71	5.20		. 50		13.86	12.13	53.22	.25	8.17	Yes Slight

TABLE 4. B 6. +/+.+/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
					.48			4.60	10.65					9.61	30.02		34.62	No
								3.08	5.54					6.15	56.92		28.31	No
								5.18	6.74					8.03	44.04		36.01	No
								2.55							68.11		29.34	No
								3.85	9.52						54.65		31.97	No
								2.66	6.30						63.92		27.12	No
	3/68		.41	.21	.82						10.22		5.11	19.63	28.43		31.49	Yes, Slight

TABLE 5 B.I +/+.+/+ GENOTYPE.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Postpce HTCT	Prepce CT	CT Med	CT Non-Med	Hi Med	Hi Non-Med	Precipice.
							.46							68.19		31.35	No
							2.04	9.04						49.85		39.07	No
							2.75	6.78						46.82		43.64	No
							2.08	9.11						64.32		24.48	No
							5.05	14.11					3.79	54.74		22.32	No
						.20	1.37	9.99					44.81	22.11		22.50	No
	.50			.25	.25	.50	5.03	1.01					51.26	21.11	1.01	19.10	No

16/50 N/+ GENOTYPE TABLE 6

	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Postpce HTCT	Prepce CT	CT Med	CT Non-Med	Hi Med	Hi Non-Med	Precipice.
						2.37	3.66	3.45					12.72	46.12		31.68	No
				.40	.40	1.61	3.02	6.64					5.03	62.78		20.12	No
							.19	1.30					2.60	69.02		26.90	No
				.23	.23		2.09	5.10		.93			7.66	58.24		25.52	No
			.22	2.82		3.25						14.54	8.03	45.77		25.38	Yes
			.43	1.30		4.56	.43			.22			10.63	53.80		28.63	No
5		2.05	1.30	1.68		.74	.19	1.30		6.33			13.78	51.40		20.67	No

178/48 N/+ GENOTYPE TABLE 7

H	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT	HTCT Chkd	Post Pce HTCT	Pre Pce	CT	CT Med	CT Non-Med	Hi Med	Hi Non-Med	Precipice.
							7.49	5.35						37.97	16.22	.36	32.62	No
				1.37		6.39	.68	2.05						67.58	4.11	1 .83	13.70	No
				.79	.16	4.40	.47	1.89						61.01	1.26	4.56	25.47	No
				.61		1.02	1.63	5.30						44.40	.81	19.14	27.09	No
			.20	2.44		2.03	.41	1.83	.20			14.86		46.95	.20	12.80	18.09	Yes
		.52	1.04	.87		3.83	.52	.87	.17					53.39	.87	17.74	20.17	No
67		3.47	.20	.41		.41			7.96			5.51		56.94	4.69	1.43	15.31	Yes Slight

104/48 N/+ GENOTYPE TABLE 8

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Pce HTCT	Pre pce CT	CT Med	CT None Med	Hi-Med	Hi Non Med	Precipice.
.85				.28			3.94							72.96		21.40	No
		.37		2.22		2.77	1.48						1.11	77.26		14.42	No
				1.89	1.44	.44	1.11		.22				17.56	58.67		20.67	No
1.57		.26		.52		.79							38.48	34.55		23.56	No
1.14		.85		2.85		1.99	.28			8.26			47.86	26.21		10.54	No
2.46		1.57	.45	.89		1.79				.22			30.43	39.82		22.37	No
3.13		1.99		.57						20.17			4.55	40.91		28.69	Yes.

6/48 GENOTYPE N/+ TABLE 9.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post ppce HTCT	Pre ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice.
				2.51	1.04	3.55	1.46						32.15	25.05		34.23	No
.22		2.02	1.57	3.14		.67	.45			.45			31.61	35.87		23.99	No
		2.67	1.23	1.23		1.03				1.23		11.09	21.97	29.16	.62	29.77	Yes
.68		2.05	.34	1.54		2.05	.34			1.54			33.50	25.98		31.97	No
5.51		2.57	.37	.37		.74				13.97		4.41	11.03	33.46		27.57	Yes
7.19		1.24	.50	.50						11.91			31.76	25.06		21.34	No
2.29		7.55	.23							14.65			24.49	21.05		29.75	Yes

12/48 N/+ GENOTYPE TABLE 10

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post ppce HTCT	Pre ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med.	Precipice.
	.21	.21		2.74	.21	6.54	.21			6.54			38.40	9.07	.63	35.23	No
2.71		1.94	.78	1.36		.78				16.09			43.41	4.26	.58	28.10	No
		.83	.21	2.07		2.07				8.06	7.64	.41	45.66	1.24	3.51	28.31	Yes Very slight
2.20	1.32	1.76		.44		.22				9.69	[illegible]	3.30	45.81	4.85	1.98	28.41	Yes Very slight
2.41		3.50		.22						14.88	7.88		39.17	2.84	3.06	26.04	Yes
5.52		1.15	.69	.69		.23				15.40			46.90	2.30	.92	26.21	No
4.24		3.06								11.53	14.82		37.65	2.35	2.12	24.24	Yes Big

41/48 N/+ GENOTYPE TABLE 11

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post ppce HTCT	Pre ppce CT	CT Med	CT Non-Med	Hi-Med	Hi Non Med	Precipice.
				6.15		5.85	.62		.62	6.15			7.70		40.92	31.69	No
		2.05	1.28	3.07		2.56				5.63			49/88		28.39	5.88	No
		.56	.75	2.44		.75				13.51		.56	37.52		38.84	5.07	Yes
				.79		2.36				16.75		3.66	28.27		36.65	11.52	Yes
8.46	.22	2.23	.67	.22						15.37			34.30		29.62	8.91	Yes
4.74		1.18	1.42	.24		.71				13.27			41.71		26.54	10.19	No
6.68		4.59								12.11			38.20		24.22	14.20	Yes

93/48 N/+ GENOTYPE TABLE 12

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post ppce HTCT	Pre ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice.
38		1.91		.19	.57	4.78	2.1o	.96		.76			37.67	20.46	1.15	29.06	No
		8.14	.88	1.42		1.06				13.98			57.17	2.48	2.12	12.74	No
35		3.39	.85	2.55		.42				13.01			53.18	4.67	3.25	17.82	No
00		1.39	.20	1.00		1.39				10.76			57.97	7.37	1.79	17.13	No
55		7.47	.18	2.19						17.12		.18	47.36	.91	4.37	19.67	Yes
31		3.75		1.36			.51			14.48			51.96	1.87	3.24	20.61	No
68		4.15	.23	.46						18.43	3.00		47.00	.46	3.00	16.59	Yes Big

78/48 N/+ GENOTYPE TABLE 13

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post ppce HTCT	Pre ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice.
1.01		.51	.51	2.02	.25	2.27	.51			.76			13.13	50.25		28.79	No
6.08		7.14	3.70	.26			1.32	.26		3.17			2.12	47.62		28.31	No
2.11		3.17	.53	.88		2.46				3.35			10.04	58.27		19.19	No
.48	1.45			.24		.24				9.40			4.82	36.14		47.23	No
4.86	1.08	1.98	1.08	.54						5.41			12.79	31.71		40.54	Yes
7.80		3.41	.49							11.71			34.15	13.17	.49	28.78	No
6.05	6.63									25.94		4.61	8.65	32.56	.58	14.99	Yes

TABLE 14 N/+ GENOTYPE 65/48.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	2.23		1.82		1.21		.40				12.96			43.32	3.44	7.49	27.13	YES Slight
	1.31		1.09	.22	.66		.22				12.45		3.28	39.30	8.52	2.18	30.79	YES
	2.52		1.44		.72						13.69			45.95		16.94	18.74	YES
	.86				1.29		4.09				3.44			47.10		15.05	28.17	NO
	.50		3.15	.17	1.16		1.16				.99			59.11	.83	7.45	25.50	NO
			1.67	.21	2.50		.21				11.67			49.58	1.46	8.33	24.38	NO
	4.76		.95								16.19	5.52		42.10		11.43	19.05	YES Big

TABLE 15 35/48 N/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	2.77		3.20	.64	.21						11,94		.21	17.91	26.65		36.46	YES
	.87		1.21	.35	1.04		.52				8.13		2.25	20.76	2.11		43.77	YES Big
	4.95		1.16		.17						13.53		.17	18.15	18.48	.33	43.07	YES
	.16	.16			1.61	.48	4.66	.32						13.02	29.10		50.48	NO
	.64		4.29	1.27	1.91		.16				1.91		7.63	4.29	37.36		40.54	YES
	.16		2.76	.65	1.30						8.28		.81	2.44	42.69		40.91	YES
	5.17		2.58								13.92			14.31	21.27	.40	42.35	YES Big

TABLE 16 90/48 N/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	6.35	1.26		.91							19.27	.23	1.36	14.51	31.75		24.26	YES
	.74	3.72	.74				.50				8.68			12.40	46.15		27.04	NO
	3.63		.20	1.41	1.41		.40				18.95		2.42	17.74	31.45		22.38	YES
	.17			.17	3.60		1.03	.69			6.86			25.38	32.59		29.50	NO
			4.92	.70	1.87		1.17				2.81			16.16	46.37		25.99	NO
	.15	2.47			2.16		1.23				1.39		11.42	.31	48.46		32.41	YES
	5.78		4.20	.88	.18						20.84			19.26	30.30	.35	18.22	NO

TABLE 17 48/48 N/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	3.78	2.62	.87								13.08		2.03	16.57	28.78		32.27	YES
	1.99	.22	.66								6.84			4 .19	41.50		44.37	NO
	2.21		3.10		.22						14.82			42.92	6.42	2.86	27.43	NO
	.21		5.75		.21		4.05				.85			7.46	37.74		43.71	NO
	2.59		.94	.24	.71		.94				1.65			29.65	28.94		34.35	NO
	1.67				.48		.24				.96		7.89	22.97	31.10		34.69	YES
	7.90		.91								17.33		.30	27.05	20.97		25.53	YES

TABLE 18 158/48 N/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	.37		.56	.37	4.48		7.09				1.87			39.55	25.00		20.71	NO
					1.12		7.16	1.79			1.57			52.57	19.46		16.33	NO
	.41		.61	2.65	2.65		3.05				4.89		7.94	31.77	25.66		20.37	YES
					.21		3.17	6.13	4.02					13.32	41.65		31.50	NO
			.73	.24	2.92		7.06	4.14	.24		.24			28.22	39.90		16.30	NO
					.84		4.40	1.05	.21		.42			32.49	34.80		25.79	NO
	2.86	.44	3.30	.88	1.32						16.08			33.48	20.70	.44	20.48	YES Big

TABLE 19 194/48 N/+ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	Ct Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	.	.19	.19	.19	1.50	.56	2.82	2.63	3.76		.37			27.64	28.95		31.20	NO
	.16			.32	.32	.16	.32	2.89	6.10					.16	51.36		38.20	NO
					2.40	.57	1.84	1.41	1.27	.14	.28			32.11	23.90		36.07	NO
	.22							7.56	7.56					.43	45.14		39.09	NO
				.26	.40	.53	1.06	6.34	6.34					10.70	46.90		27.48	NO
					.49	.74	3.94	4.93	2.22					40.89	28.08		18.72	NO
	1.32			1.54	2.86	.22	2.42	.88			2.64			38.33	22.91		26.87	NO

TABLE 20 353/48 nr/nr GENOTYPE.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
3.05		.76	.38	4.19		1.33				8.95		5.14	23.24	16.00	.19	36.76	YES Slight
		.18	.18	.36		3.58				3.76		7.33	20.39	18.25		45.97	YES Slight
1.14		2.66	.76	2.66		2.85				2.28		9.30	2.85	46.87		28.65	YES
				2.16		2.88	2.16	2.16					7.69	64.18		18.75	NO
		.27	.40	3.61		3.48	.13	.27		.13			10.58	61.45		19.68	NO
.40				.80		5.38	.20	.20				9.36	1.00	63.55		19.12	YES Slight

TABLE 21 nr/nr GENOTYPE 332/48.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	4.97		3.24	1.73	4.10		1.30				20.09			41.90	7.78	.22	14.69	NO
	.96	.24	.48	.96	.96		2.17				16.63			39.28	8.67	1.69	27.95	NO
	2.94		3.78	1.26	1.47		.21				20.59			35.08	19.12		15.55	YES
					3.01		5.82				5.62			31.33	16.67		37.55	NO
	2.49		4.98	1.36	3.39		.90				11.54			30 .77	28.73		15.84	NO
			.39	.19	2.33		3.70				11.09			49.03	13.42	.19	19.65	NO

TABLE 22 80/47 nr/nr GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	1.66		1.48	.37	.37		3.33				4.81			32.90	21.81		33.27	NO
	.87		.65		.43		1.30	.43	.22	.43	1.09			38.04	17.17		39.35	NO
	2.08		.83	.63	.83		1.46				1.88			31.67	23.33		37.29	NO
	2.52		2.13		1.36	.19	4.07	.39			.19			36.05	29.26		23.84	NO
	1.56		.69	.17	.69		3.13				.52			33.51	29.34		30.38	NO
	4.67		1.72								14.50	9.34		24.82	17.69	.25	27.03	YES

TABLE 23 351/48 nr/nr GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	8.26		2.17		.22						18.26			29.57	24.35		17.17	YES
	2.89		.87		.87						12.55		.58	24.68	24.39		33.19	YES Slight
	3.62		5.43	.20	.60						16.90		.40	4.43	51.31		17.10	YES
	.47		.47	2.83	2.59		1.42	2.36	.71	.71	2.83			5.66	53.77		26.18	NO
	5.26		3.95	1.10	2.19		.88				8.11			8 .11	47.15		23.25	NO
	1.90		3.04		.76		.57				12.33		.38	12. 14	48.58		20.30	YES

TABLE 24 343/48 nr/nr/ GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	3.79		2.01								14.06		.67	26.79	22.32		30.36	YES Slight
	1.71		1.07		.64						13.92		.21	23.77	22.91	.64	35.12	YES Slight
	1.09		5.24		.87						13.32		3.06	1.53	50.00		24.89	YES
	.25			.25	1.72	.98	2.70	1.23						7.62	52.83		32.43	NO
	2.59		3.11	.17	1.38						7.94		2.59	10.71	47.32		24.18	YES Slight
	1.53		1.34	.38	1.34		.57				11.66		.76	17.78	34.80		29.83	YES Slight

42/44 N/+/nr/+ GENOTYPE. TABLE 25.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd.	HTCT Chkd.	HTCT	PostpceHTCT	Prepce CT	CT MED	CT NON-MED	HI MED	HI NON-MED	Precipice.
1·48		1·48	·56	·74	·19	·37	·37			9·08		3·70	31·67	8·15	8·89	33·33	Yes Slight
·49		·99		·66		1·48	·33		·16	3·13		11·18	42·76	1·97	8·22	28·62	Yes Slight
·42		1·91	1·06	1·27		1·91				3·40		5·94	56·05	·42	6·79	20·81	Yes Slight
4·70		3·47	·25	·25						14·36			56·19	1·49	3·22	16·09	No

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88/44 n/+/nr/+ GENOTYPE. TABLE 26.

HH	HH&	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Postpce HTCT	Prepce CT	CT MED	CT NON-MED	HI MED	HI NON-MED	Precipice.
2·12		2·12	·58	·96		·96				4·23			38·85	20.00	.19	30.00	No
1·25		·36	·36	·71		2·14				3·92			33·33	26·56	·18	31·19	No
2·13		1·49	·43	1·06		1·28				2·13			30·85	28·30		32·34	No
2·36		6·09	·20							12.77			11.98	24.95		41.65	Yes

9/44 N/+/nr/+ GENOTYPE. TABLE 27.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	Postpce HTCT	Prepce HTCT	CT	CT MED	CT NON-MED	HI MED	HI NON-MED	Precipice.
4·87	2.12			1.27		1.69				14.83		2.97	2.12	44.70		25·42	Yes
1·73	·25			·25		·99				10·12		3·70	20·25	37·04		25·68	Yes

129/44 N/+/nr/+ GENOTYPE. TABLE 28.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Postpce HTCT	Prepce CT	CT MED	CT NON-MED	HI MED	HI NON-MED	Precipice.
4·58		2·50		1·04		1·88				9·79		5·42	24·79	12·08	·63	37·29	Yes
·78		1·36	·39	·97		3·31				7·78		7·98	23·35	17·32	·39	36·38	Yes
2·17		5·12	·16	1·55		1·09				6·15		9·61	17·83	24·50		31·47	Yes
5·58		5·81								13·26			36·51	13·26	1·40	24·19	Yes Big

155/44 N/+/nr/+ GENOTYPE. TABLE 29.

HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	PostpceHTCT	PrepceCT	CT Med	CT Non-Med	Hi Med	Hi NoneMed	Precipice.
5·53		3·53		1·86		·56				9·46			39·52	2·41	10·39	28·76	No
3·77		·58	·38	1·54		1·35				6·35			48·08	3·85	10·00	27·12	No
1·64		2·26	·62	1·64		2·46				4·52			43·33	7·19	4·93	31·42	No
6·03		2·77								12·54	6·68		41·86	2·61	3·75	23·78	Yes big.

TABLE 30 300/48 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	5.36		2.49								20.50			24.90	20.50		26.26	NO
	3.13		1.37								16.41			26.37	27.93		24.80	NO
	3.61		3.26	.17	.86		.34				.52		15.81	3.09	44.85		27.49	YES
	3.52		1.51	.50	2.51	1.51		3.52			.50		1.01		8.54 PrePpce 46.23		30.65	YES Slight
	2.91		3.27	1.09	1.64						2.73			13.82	56.55		18.00	NO
	2.61		1.74	.70	3.13		.17				2.43		11.13	.35	53.39		24.35	YES Slight
	4.60		3.75	.85	.85						8.91		2.56	8.86	36.46		23.17	YES

TABLE 31 15/50 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	4.43		1.27	.95	.16						14.87		1.27	28.16	22.63		26.27	YES
	1.73		.58	.14							12.27		3.17	27.27	24.82		30.01	YES Big
	2.28		1.67	1.98	1.83						14.31		1.67	36.83	16.89		22.53	YES
	2.13			1.14	2.84						9.53		.43	17.21	31.58		35.14	YES Slight
	2.46		.88	2.99	.18						11.42			30.93	30.40		20.74	YES
	2.83		.81	.54	.40						15.25		1.35	24.70	30.09		24.02	YES Slight
	2.69		2.87	2.51	.36						16.88			34.47	24.96		15.26	YES Slight

TABLE 32 14/50 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	4.45		.47								16.63	.94		48.48	5.39	3.51	20.14	YES
	3.29		.78	1.94							19.77			54.07	1.55	1.74	16.86	YES
	2.55			2.97	1.70						20.17			56.05	.21	4.88	11.46	YES
	1.32	.19		2.47	2.47						10.27			30.23	23.57		29.28	NO
	1.30		1.73	1.30	3.90						18.61			43.29	19.05		10.82	NO
	2.05		.68	1.60	.68						15.98			53.20	4.79	1.37	19.63	YES Big
	4.36		2.18	4.36	.44						18.08			49.24	11.33		10.02	YES Big

TABLE 33 245/48 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	6.28	.20	2.43								16.19	.61		40.28	8.70	.81	24.49	YES Slight
	4.41	.23									13.92	.46		41.07	9.05	1.39	29.47	YES Slight
	2.22		4.11	.47							15.19			39.56	6.17	2.37	29.91	YES
	1.28	1.28	.26	.89	.13						8.16	.26		30.87	15.31	.64	40.94	YES Slight
	2.67		5. 21	.15	.27						15.91	.27		40.31	14.17	.13	20.72	YES
	2.93		4.13	.13	.40						14.11	.13		47.00	3.20	1.07	26.90	YES
	3.23		4.95								16.56	1.51		54.62	.43	1.51	17.20	YES Big

TABLE 34 239/48 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	5.59		2.45	.17							17.66	.35		46.15	10.49		17.13	YES
	3.30		.44								14.76	.44		45.81	7.49	1.54	26.21	YES
	5.14		2.34	.23							20.09	.47		48.36	3.74	1.64	17.99	YES
	2.03	1.13	3.61	.68	.45						7.45	1.13	.23	41.53	17.83		23.93	YES
	4.84	2.53									19.82	.46		57.60	5.07	.46	9.22	YES
	3.94		1.62								17.13	9.95		45.14	.69	5.09	16.44	YES Slight
	4.88		4.65								14.65	.93		54.42	2.33	3.26	14.88	YES Big

TABLE 35 263/48 N/N GENOTYPE.

	HH	HH'	SSA	SSA'	SSB	Fine SSB	SK	Fine SK	CT Chkd	HTCT Chkd	HTCT	Post Ppce HTCT	Pre Ppce CT	CT Med	CT Non Med	Hi Med	Hi Non Med	Precipice
	8.41										15.89	.70		46.73	10.98		17.29	YES
4	.50										14.41			33.33	26.13		21.62	YES
	3.99		1.91	.52							15.94	.17		53.21	3.29	.87	20.10	YES
	2.39	.96		2.39	5.74						1.91			30.46	29.19		26.95	NO
	.70		7.91	.23							12.79		.23	47.44	16.05		14.65	YES
	2.71		1.67	.21							18.16			40.71	17.33		19.21	YES
	4.03		4.61								15.16	3.45		57.56	4.41		10.75	YES Big

TABLE 36 ANALYSIS OF HALO-HAIRS.

GENOTYPES

+/+	N/+	N/+/nr/+	nr/nr	N/N	F Values	D
0	2.53	-	1.70	8.31	20.26** n_1= 3 n_2= 22	5% level = 2.37 1% level = 3.22
0	4.20	5.62	5.65	10.51	9.90** n_1=4 n_2= 27	5% level = 3.33 1% level = 4.50
0	2.13	-	5.17	9.67	14.76** n_1= 3 n_2= 23	5% level = 3.21 1% level = 4.36
0	3.69	-	8.15	8.72	4.93** n_1= 3 n_2= 23	5% level = 5.07 1% level = 6.87
0	8.67	6.99	8.25	10.34	5.31** n_1= 4 n_2= 26	5% level = 4.72 1% level = 6.37
0	8.66	10.26	11.65	13.80	7.52** n_1=4 n_2= 27	5% level = 5.04 1% level = 6.81
2.77	12.19	12.31	-	11.43	6.82** n_1= 3 n_2= 22	5% level = 4.19 1% level = 5.69
1.00 n_1= 6 n_2= 21	10.14** n_1=6 n_2= 77	8.79** n_1=3 n_2=14	4.41** n_1=5 n_2=23	6.52** n_1=6 n_2=35		
5% level = - 1% level = -	5% level = 3.39 1% level = 4.49	5% level = 3.11 1% level = 4.32	5% level = 4.59 1% level = 6.23	5% level = 2.07 1% level = 2.78		

** Indicates F value significant at the 1% probability level.

* Indicates F value significant at the 5% probability level.

TABLE 37 A

ANALYSIS OF HALO-HAIR' FIBRES.

	Genotypes						
	+/+	N/+	N/+.nr/+	nr/nr	N/N	F Value	d
Sh. Pt.	0	0.41	-	0	3.45	6.34** n_1:3 n_2:22	5% : 2.03 1% : 2.75

TABLE 37 B.

HALO-HAIR' FIBRES.

	Sh.Pt.	Sh.	Nk.	W.	S.	Bk.	Br.	F Value	d
N/+ Genotype.	3.45	1.53	0	0.46	0	0.43	0	2.67* n_1:6 n_2:35	5% : 2.24 1% : -

---

TABLE 37 C.

FINE SUPER-SICKLE B FIBRES

Between Positions N/+ Genotype.

	Sh.Pt.	Nk.	Sh.	W.	S.	Bk.	Br.	F Value	d
N/+	1.64	0.77	0.30	0.23	0	0	0	2.89* n_1: 6 n_2: 77	5% : 1.00 1% : -

---

TABLE 38 ANALYSIS OF SUPER-SICKLE A FIBRES.

GENOTYPES

	+/+	N/+	N/+	n r	N/N	F Values	D
	0	2.38	-	.98	3.49	.78 n_1= 3 n_2= 22	5% level = - 1% level = -
	0	3.95	4.04	4.46	3.33	2.09, n_1= 4 n_2= 27	5% level = - 1% level = -
	0	4.73	-	5.01	7.32	3.15* n_1= 3 n_2= 23	5% level = 4.54 1% level = -
	0	8.38	-	9.18	8.81	3.57* n_1= 3 n_2= 23	5% level = 6.01 1% level = -
	0	7.80	9.17	10.51	7.71	3.95* n_1= 4 n_2=26	5% level = 5.56 1% level = -
	0	6.28	8.73	7.80	6.24	5.64** n_1= 4 n_2= 27	5% level = 3.65 1% level = 4.93
	0.92	9.12	12.14	-	11.19	10.58** n_1= 3 n_2= 22	5% level = 4.09 1% level = 5.56
	- n_1= n_2=	3.87** n_1=6 n_2= 77	9.86** n_1= 3 n_2=14	6.57** n_1=5 n_2=23	3.27* n_1= 6 n_2=35		
	5% level = - 1% level = -	5% level = 3.66 1% level = 4.86	5% level = 3.28 1% level = 4.55	5% level =3.88 1% level =5.27	5% level = 4.48 1% level = -		

TABLE 39 SUPER-SICKIE A' FIBRES.

GENOTYPES

	F/+	N/+	N/+	nn/nr	N/N	F Values	D
	0	0.54	-	3.14	6.38	11.34** n_1= 3 n_2= 22	5% level = 2.76 1% level = 3.75
	0	1.90	2.11	1.61	1.69	.73 n_1= 4 n_2= 27	5% level = - 1% level = -
	0	2.56	-	1.68	3.50	2.27 n_1= 3 n_2= 23	5% level = - 1% level = -
	0	4.31	-	3.74	4.55	2.18 n_1=3 n_2= 23	5% level = - 1% level = -
	0	2.39	4.12	3.71	5.20	3.41* n_1= 4 n_2= 26	5% level = 3.01 1% level = -
	0	3.60	1.73	2.92	1.33	2.30 n_1= 4 n_2= 27	5% level = - 1% level = -
	0.66	1.67	1.36	-	4.41	1.55 n_1= 3 n_2= 22	5% level = - 1% level = -
	- n_1= - n_2= -	3.97** n_1=6 n_2=77	1.68 n_1=3 n_2=14	.45 n_1=5 n_2=23	1.84 n_1=6 n_2=35		
	5% level = - 1% level = -	5% level = 1.91 1% level = 2.54	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -		

TABLE 40 SUPER-SICKLE B FIBRES.

GENOTYPES

	F/+	N/+	N/+/nr/+	nr/nr	N/N	F Values	D
	0	6.17	-	8.81	7.94	4.51* $n_1=3$ $n_2=22$	5% level = 4.87 1% level = -
	0.67	3.87	5.03	4.55	0	11.07** $n_1=4$ $n_2=27$	5% level = 2.00 1% level = 2.70
	0	6.61	-	6.06	3.70	6.89** $n_1=3$ $n_2=123$	5% level = 3.26 1% level = 4.42
	0	6.88	-	8.71	4.03	9.10** $n_1=3$ $n_2=23$	5% level = 3.38 1% level = 4.59
	1.51	5.56	6.73	6.28	3.43	2.62 $n_1=4$ $n_2=26$	5% level = - 1% level = -
	1.63	3.72	6.14	5.94	0.38	4.33** $n_1=4$ $n_2=27$	5% level = 3.487 1% level = 4.68
	4.96	1.81	.72	-	2.09	2.68 $n_1=3$ $n_2=22$	5% level = - 1% level = -
	5.02** $n_1=6$ $n_2=21$	4.87** $n_1=6$ $n_2=77$	19.26** $n_1=3$ $n_2=14$	1.71 $n_1=5$ $n_2=23$	4.04** $n_1=6$ $n_2=35$		
	5% level = 2.34 1% level = 3.17	5% level = 2.31 1% level = 3.16	5% level = 1.80 1% level = 2.50	5% level = - 1% level = -	5% level = 3.81 1% level = 5.12		

TABLE 41 SICKLE FIBRES.

GENOTYPES

	~~+~~/+	N/+	N/+ ~~N~~/+	~~nr/nr~~	N/N	F Values	D
	0	9.28	-	10.01	0	13.57** n_1=3 n_2= 22	5% level = 4.69 1% level = 6.37
	0.95	4.28	7.66	5.19	0	6.50** n_1= 4 n_2= 27	5% level = 3.46 1% level = 4.67
	0.69	4.96	-	8.67	0.39	8.36** n_1= 3 n_2= 23	5% level = 3.80 1% level = 5.16
	0	6.39	-	6.64	0	8.43** n_1= 3 n_2= 23	5% level = 3.95 1% level = 5.36
	0.95	2.94	7.36	3.86	0.56	3.12* n_1= 4 n_2= 26	5% level = 4.13 1% level = -
	1.75	3.54	5.75	4.74	0	2.26 n_1= 4 n_2= 27	5% level = - 1% level = -
	7.27	0.72	0	-	0	5.68** n_1= 3 n_2= 22	5% level = 3.93 1% level = 5.34
	2/48 n_1= 6 n_2= 21	6.24** n_1=6 n_2=77	21.51** n_1=3 n_2=14	1.37 n_1=5 n_2=23	- -		
	5% level = - 1% level = -	5% level = 3.07 1% level = 4.06	5% level = 2.25 1% level = 3.13	5% level = - 1% level = -	5% level = - 1% level = -		

TABLE 42 FINE SICKLE FIBRES.

GENOTYPES

	+/+	N/+	N/+	nr/nr	N/N	F Values	D
	6.24	6.07	-	5.91	1.80	1.45 n_1=3 n_2= 22	5% level = - 1% level = -
	9.65	1.58	0.66	0.75	0	13.86** n_1= 4 n_2= 27	5% level = 2.75 1% level = 3.72
	10.75	1.04	-	0.51	0	36.61** n_1= 3 n_2= 23	5% level = 2.19 1% level = 2.97
	11.51	2.68	-	1.13	0	15.73** n_1=3 n_2= 23	5% level = 3.39 1% level = 4.60
	13.71	0.56	0	0	0	123.67** n_1= 4 n_2= 26	5% level = 1.44 1% level = 1.94
	10.64	1.00	0.70	0	0	21.27** n_1= 4 n_2= 27	5% level = 2.54 1% level = 3.43
	6.71	0.21	0	-	0	8.64** n_1= 3 n_2= 22	5% level = 3.03 1% level = 4.12
	2.09 n_1= 6 n_2= 21	6.14** n_1=6 n_2=77	- n_1=+ n_2=-	6.33** n_1=5 n_2=23	- n_1= - n_2= -		
	5% level = - 1% level = -	5% level = 2.29 1% level = 3.04	5% level = - 1% level = -	5% level = 2.45 1% level = 3.32	5% level = - 1% level = -		

TABLE 43 CHECKED CURLY-TIP FIBRES.

GENOTYPES

	T/+	N/+	N/+	nr/nr	N/N	F Values	D
	0	2.48	-	3.32	0	1.13 n_1= 3 n_2= 22	5% level = - 1% level = -
	16.87	2.20	0	0.54	0	18.24** n_1= 4 n_2= 27	5% level = 4.34 1% level = 5.86
	18.71	1.20	-	0.51	0	54.82** n_1=3 n_2= 23	5% level = 3.18 1% level = 4.31
	18.70	2.17	-	0.60	0	31.29** n_1= 3 n_2=23	5% level = 4.11 1% level = 5.58
	16.15	0.65	0	0	0	50.39** n_1=4 n_2= 26	5% level = 2.65 1% level = 3.58
	16.29	0.45	0	0	0	140.28** n_1= 4 n_2= 27	5% level = 1.57 1% level = 2.11
	4.74	0.55	0	-	0	3.20* n_1= 3 n_2= 22	5% level = 3.39 1% level = -
	15.57** n_1=6 n_2= 21	.72 n_1=6 n_2=77	- n_1= - n_2= -	1.15 n_1=5 n_2=23	- n_1= - n_2= -		
	5% level = 5.60 1% level = 7.67	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -		

TABLE 44 HAIRY-TIP-CURLY-TIP FIBRES.

GENOTYPES

	t/+	N/+	N/+nr/+	nr/nr	N/N	F Values	D
	0	5.86	-	5.85	13.76	4.65* $n_1=3$ $n_2=22$	5% level = 7.53 1% level = -
	0	13.46	14.19	16.78	23.06	8.54** $n_1=4$ $n_2=27$	5% level = 7.64 1% level = 10.32
	0	11.01	-	12.82	22.38	6.01** $n_1=3$ $n_2=23$	5% level = 10.14 1% level = 13.75
	0	8.68	-	11.47	21.04	7.53** $n_1=3$ $n_2=23$	5% level = 8.75 1% level = 11.87
	0	18.54	11.52	17.84	21.10	5.52** $n_1=4$ $n_2=26$	5% level = 9.92 1% level = 13.41
	.91	16.96	17.64	20.81	24.62	9.20** $n_1=4$ $n_2=27$	5% level = 7.75 1% level = 10.46
	5.68	24.26	22.64	-	24.86	15.31** $n_1=3$ $n_2=22$	5% level = 6.40 1% level = 8.70
	1.53 $n_1=6$ $n_2=21$	7.62** $n_1=6$ $n_2=77$	9.20** $n_1=3$ $n_2=14$	1.93 $n_1=5$ $n_2=23$	2.80* $n_1=6$ $n_2=35$		
	5% level = - 1% level = -	5% level = 6.43 1% level = 8.53	5% level = 4.61 1% level = 6.40	5% level = 0 1% level = -	5% level = 6.44 1% level = -		

TABLE 45 MEDULLATED CURLY-TIP FIBRES.

GENOTYPES

	+/+	N/+	N/nr/+	nr/nr	N/N	F Values	D
	0	26.46	-	19.98	28.58	6.45** $n_1=3$ $n_2=22$	5% level = 14.31 1% level = 19.45
	14.69	31.21	37.95	33.63	38.24	3.87* $n_1=4$ $n_2=27$	5% level = 12.63 1% level = -
	5.58	31.30	-	28.97	37.08	5.99** $n_1=3$ $n_2=25$	5% level = 14.83 1% level = 20.12
	12.31	31.61	-	25.50	38.22	2.78 $n_1=3$ $n_2=23$	5% level = - 1% level = -
	20.06	35.16	39.61	23.21	40.41	4.44** $n_1=4$ $n_2=26$	5% level = 12.44 1% level = 16.82
	31.05	34.54	32.08	34.41	38.71	.67 $n_1=4$ $n_2=27$	5% level = - 1% level = -
	37.15	31.41	36.58	-	40.80	1.05 $n_1=3$ $n_2=22$	5% level = - 1% level = -
	6.95** $n_1=6$ $n_2=21$	.59 $n_1=6$ $n_2=77$	.50 $n_1=3$ $n_2=14$	2.05 $n_1=5$ $n_2=23$	1.12 $n_1=6$ $n_2=35$		
	5% level = 14.82 1% level = 20.18	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -		

TABLE 46 NON-MEDULLATED CURLY-TIP FIBRES.

GENOTYPES

	F/+	N/+	N/+	nr/nr	N/N	F Values	D
	57.78	29.18	-	42.78	31.95	4.77* $n_1=3$ $n_2=22$	5% level = 17.59 1% level = -
	44.19	26.19	22.50	25.02	22.18	2.27 $n_1=4$ $n_2=27$	5% level = - 1% level = -
	46.02	28.31	-	37.50	22.09	1.95 $n_1=3$ $n_2=23$	5% level = - 1% level = -
	42.76	28.78	-	40.72	27.81	1.36 $n_1=3$ $n_2=23$	5% level = - 1% level = -
	40.73	19.58	20.27	37.76	17.49	3.40* $n_1=4$ $n_2=26$	5% level = 17.84 1% level = -
	34.51	22.34	22.88	25.08	20.69	1.04 $n_1=4$ $n_2=27$	5% level = - 1% level = -
	32.66	21.25	16.91	-	18.58	1.09 $n_1=3$ $n_2=22$	5% level = - 1% level = -
	3.77* $n_1=6$ $n_2=21$	.62 $n_1=6$ $n_2=77$	.21 $n_1=3$ $n_2=14$	3.54* $n_1=5$ $n_2=23$	1.14 $n_1=6$ $n_2=35$		
	5% level = 12.56 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level = 12.12 1% level = -	5% level = - 1% level = -		

MEDULLATED HISTERIOTRICH FIBRES. TABLE 47

Genotypes: +/+	N/+	N/+.nr/+	nr/nr	N/N	F Values	d
0	7.29	8.22	2.41	3.58	.86	5% = -
					$n_1 = 4$; $n_2 = 27$.	1% = -
0	9.45	6.99	0	5.72	1.77	5% = -
					$n_1 = 4$; $n_2 = 26$.	1% = -
0	7.64	8.64	1.04	2.66	1.43	5% = -
					$n_1 = 4$ $n_2 = 27$	1% = -

TABLE 48 NON-MEDULLATED HISTEROTRICH FIBRES.

GENOTYPES

	+/+	N/+	N/+nr/+	nr/nr	N/N	F Values	D
	31.35	34.98	-	32.24	33.85	.91 n_1= 3 n_2= 22	5% level = - 1% level = -
	33.10	32.78	33.04	36.99	29.79	1.35 n_1= 4 n_2= 27	5% level = - 1% level = -
	34.31	29.83	-	29.12	27.73	1.19 n_1= 3 n_2= 23	5% level = - 1% level = -
	32.32	27.96	-	27.46	23.11	2.04 n_1= 3 n_2= 23	5% level = - 1% level = -
	32.65	28.87	32.50	29.51	27.44	.77 n_1= 4 n_2= 26	5% level = - 1% level = -
	32.02	29.69	33.76	30.60	27.84	1.44 n_1= 4 n_2= 27	5% level = - 1% level = -
	27.04	28.01	30.62	-	22.76	1.75 n_1= 3 n_2= 22	5% level = - 1% level = -
	.82 n_1= 6 n_2= 27	2.17 n_1=6 n_2=77	.45 n_1=3 n_2=14	2.33 n_1=5 n_2=23	6.41** n_1=6 n_2=23		
	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level =4.33 1% level =5.81		

TABLE 49 TOTAL HISTEROTRICH FIBRES.

GENOTYPES

+/+	N/+	N/+ mr/+	mr/mr	N/N	F Values	D
31.35	37.87	-	32.24	33.91	1.56 n_1= 3 n_2= 22	5% level = - 1% level = -
33.10	36.07	35.35	37.28	30.31	2.00 n_1= 4 n_2= 27	5% level = - 1% level = -
34.31	33.30	-	29.14	28.63	2.61 n_1= 3 n_2= 23	5% level = - 1% level = -
32.32	30.47	-	27.46	23.20	3.62* n_1= 3 n_2= 23	5% level = 6.20 1% level = -
32.65	32.84	34.39	29.51	28.66	1.22 n_1= 4 n_2= 26	5% level = - 1% level = -
32.02	32.84	36.17	30.66	28.33	2.60 n_1= 4 n_2= 27	5% level = - 1% level = -
27.28	30.46	32.08	-	23.37	2.76 n_1= 3 n_2= 22	5% level = - 1% level = -
.77 n_1= 6 n_2= 21	2.60* n_1=6 n_2=77	1.64 n_1=3 n_2=14	2.53 n_1=5 n_2=23	7.04** n_1=6 n_2=35		
5% level = - 1% level = -	5% level = 4.78 1% level = -	5% level = - 1% level = -	5% level = - 1% level = -	5% level = 4.09 1% level = 5.49		

TABLE 50 TOTAL PRE-CURLY-TIP FIBRES.

GENOTYPES

	F/+	N/+	N/+/m/+	m/m	N/N	F Values	D
	6.24	16.35	-	16.73	16.31	16.08** n_1= 3 n_2= 22	5% level = 3.43 1% level = 4.66
	9.97	11.43	12.41	12.00	11.88	1.15 n_1= 4 n_2= 27	5% level = - 1% level = -
	10.85	12.61	-	14.42	14.02	1.36 n_1= 3 n_2= 23	5% level = - 1% level = -
	11.51	16.86	-	18.73	16.43	5.56** n_1= 3 n_2= 23	5% level = 3.36 1% level = 4.56
	14.22	15.69	16.27	16.89	15.73	1.05 n_1= 4 n_2= 26	5% level = - 1% level = -
	11.35	16.23	16.60	17.96	15.85	4.28** n_1= 4 n_2= 27	5% level = 3.09 1% level = 4.17
	15.44	17.20	17.81	-	17.79	1.23 n_1= 3 n_2= 22	5% level = - 1% level = -
	4.72** n_1= 6 n_2= 21	8.42** n_1=6 n_2=77	7.12** n_1=3 n_2=14	6.45** n_1=5 n_2=23	6.05** n_1=6 n_2=35		
	5% level = 4.03 1% level = 5.49	5% level = 2.18 1% level = 2.89	5% level = 2.73 1% level = 3.80	5% level = 2.92 1% level = 3.96	5% level = 2.25 1% level = 3.01		

TABLE 51

DISCRIMINANT FUNCTION BETWEEN N/N, N/+, & */+ SHEEP.
Fibre Type Arrays (Transformed %ages of fibres types.)
SHOULDER PATCH POSITION.

SHEEP	HH +SSA	SSA'+SSB	SK Nml	SK Fine	PreCT HTCT	CTBig as HTCT	CT Chkd	CT Méd	SMALL MEDCT	CT NON-MED	
245/48	9.3	11.5	-	-	21.3	-	-	-	46.7	30.9	
239/48	12.7	13.8	-	-	18.3	3.1	-	-	48.1	29.2	
300/48	15.6	12.0	-	15.6	4.9	21.8	-	-	-	54.8	N/N
14/50	8.4	15.7	-	-	22.1	10.8	-	-	38.9	35.4	
15/50	10.5	14.3	-	-	22.6	4.7	-	-	31.1	44.3	
263/48	-	23.3	-	-	9.3	-	-	40.2	-	39.2	
90/48	2.8	13.4	6.9	5.7	18.2	22.5	-	-	27.6	42.8	
48/48	18.4	3.5	15.3	-	7.0	-	-	23.5	-	53.9	
41/48	6.0	28.3	27.5	8.6	29.8	-	-	32.0	-	-	
115/48	-	19.3	14.7	4.6	6.6	-	-	43.0	-	34.8	
6/48	-	11.2	13.4	11.2	-	-	-	44.4	-	38.1	
104/48	-	3.4	-	13.1	-	-	-	-	-	76.5	N/+
30/50	-	-	9.5	18.4	-	-	4.4	32.7	-	49.4	
35/48	3.2	11.4	17.9	7,3	-	-	-	30.7	-	50.00	
12/48	5.7	12.5	18.5	4.6	18.5	-	-	50.4	-	22.0	
65/48	7.0	8.7	15.8	-	14.4	-	-	68.0	-	-	
93/48	10.5	3.0	15.2	11.3	6.0	-	6.7	47.3	-	32.8	
194/48	3.4	-	-	20.6	3.4	-	20.6	4.8	-	59.4	
158/48	-	3.2	12.0	17.5	-	-	14.1	26.2	-	51.4	
B 1	-	-	-	4.7	-	-	-	-	-	85.6	
B 6	-	-	-	10.9	-	-	-	-	-	78.9	+/+
B 5	-	-	-	8.9	-	-	-	-	-	80.9	
B 4	-	-	-	4.6	-	-	-	-	-	84.6	

$Z_1 = x_1 2.4468 + x_2 3.0607 - x_3 3.1201 + x_4 1.3397 - x_5 .8214 - x_6 .5736 - x_7 .3468 + x_8 .4724 + x_9 1.0000 + x_{10} 0.0000$

WHERE:

x_1 = arc.sin % of HH+SSA Fibres.

x_2 = " " SSA'+SSB "

x_3 = " " SK Normal "

x_4 = " " Fine Pre CT "

x_5 = " " HTCT "

x_6 = " " CT Big as HTCT Fibres.

x_7 = " " CT Chkd. Fibres.

x_8 = " " CT Med "

x_9 = " " Small Med CT Fibres.

x_{10} = " " Non Med CT " .

The scores given to the 23 sheep used by this function are:

N/N	245/48	87	
	239/48	105	
b	300/48	79	86.0
	14/50	83	
	15/50	79	
	263/48	83	

N/+

90/48	34	
48/48	13	
41/48	18	
115/48	34	
6/48	28	
104/48	28	
30/50	9	
35/48	11	19.1
12/48	9	
65/48	15	
93/48	18	
194/48	28	
158/48	3	

+/+

B I	6	
B 6	15	9.8
B 5	12	
B 4	6	

/d : 9.3
t : 1.7
n : 15

DISCRIMINANT FUNCTION BETWEEN N/+ AND nr/nr SHEEP.

Table 52

Fibre Type Arrays : (Transformed %ages of Fibre types) Shoulder Patch Position.

	SHEEP	HH & SSA	SSA' & SSB	SK Nml.	FINE PRE CT	CT CHKD	HCTC	CT MED	CT NON MED.
N/+	6/48	-	11.24	13.44	11.24	-	-	44.37	38.12
	104/48	-	3.63	-	13.05	-	-	-	76.44
	48/48	18.72	3.63	15.34	-	-	7.04	23.42	53.79
	90/48	2.56	13.44	7.04	5.74	-	18.15	36.87	42.88
	78/48	8.33	10.78	10.31	6.02	-	6.02	25.40	57.17
	35/48	4.44	10.47	17.85	7.27	-	-	30.85	49.95
	12/48	4.80	11.97	18.63	4.80	-	18.63	50.71	22.06
	65/48	7.04	8.72	15.56	-	-	14.30	65.65	-
	93/48	10.47	3.14	15.12	11.24	6.80	6.02	47.29	32.77
	158/48	-	3.14	11.97	17.46	14.06	-	26.21	51.35
	16/50	-	-	10.78	13.44	13.05	-	25.55	55.30
nr/nr	332/48	-	12.66	17.76	-	-	17.46	45.11	31.11
	353/48	-	9.46	10.78	9.46	9.46	-	17.95	62.72
	351/48	6.55	15.68	7.92	10.31	7.92	11.24	16.11	58.63
	343/48	3.63	9.81	11.54	10.47	-	-	19.64	62.17

Discriminant Function:

$$Z_1 : X_1\ 1.5274 * X_2\ 4.2787 + X_3\ 0.2735 + X_4\ 1.3235 - X_5\ 0.3928 + X_6\ 1.0511 - X_7\ 0.1262 + X_8\ 0.1992.$$

Where:

X_1 : HH & SSA
X_2 : SSA' + SSB
X_3 : Sk Normal
X_4 : Fine Pre Ct.
X_5 : HTCT
X_6 : CT Chkd.
X_7 : CT Med
X_8 : CT Non Med.

Totals for sheep:

N/+ Sheep

6/48	69	58
104/48	48	
48/48	53	
90/48	68	
78/48	75	
35/48	72	
12/48	61	
65/48	38	
93/48	54	
158/48	62	
16/50	42	

nr/nr Sheep

332/48	53	77
353/48	76	
351/48	106	
343/48	74	

d : 19
t : 2.16*
n : 13

DISCRIMINANT FUNCTION BETWEEN N/N & nr/nr SHEEP

Table 53

N/N SHEEP

SHEEP	HH + SSA	SK Nml.	FINE PRE CT	HTCT	TOTAL After D.F.applied Nos. coded by adding	
245/48	12.66	-	-	22.30	134.4	(100.
263/48	12.39	-	-	9.28	133.5	
239/48	17.36	-	-	19.64	147.0	
300/48	15.56	-	15.56	4.80	125.7	1322
14/50	8.91	-	-	22.38	124.3	
15/50	10.47	-	-	22.53	128.5	

nr/nr SHEEP

SHEEP	HH +SSA	SK Nml.	FINE PRE CT	HTCT		
332/48	-	17.76	-	17.46	26.6	
353/48	-	10.78	9.46	-	45.4	49.3
351/48	6.55	7.92	10.31	11.24	74.2	
343/48	3.63	11.54	10.47	-	51.0	

$\bar{d}$: 82.9
t : 9.39**
n : 8

Discriminant Function:

$Z_1 : x_1\ 2.69 - X_2\ 4.15 - X_3\ 1.04 + X_4\ .015$

Where:

X_1: HH +SSA
X_2 :Sk Normal
X_3 :Fine Pre CT.
X_4 :HTCT.

DEFLECTION PRODUCED PER GRAM OF WOOL IN DIFFERENT GENOTYPES. ARBITRARY UNITS.

TABLE 54

A. +/+ GENOTYPE

SHEEP		Positions. Sh. Pt.	W.	Sh.	Nk.	S.	Bk.	Br.
H	B I.	16	9	14	22	20	20	67
E	B 6.	14	9	9	13	20	42	238
E	B 5.	19	19	21	18	22	29	73
P	B 4.	17	44	30	16	41	63	86

B. N/+ GENOTYPE

SHEEP	Positions. Sh.Pt.	W.	Sh.	Nk.	S.	Bk.	Br.
158/48	36	131	80	63	147	222	290
194/48	6	23	24	19	56	63	109
	(Included only in Chapter on Low-N's.)						
16/50	18	43	20	18	198	125	220
178/48	26	94	105	106	156	221	254
104/48	20	33	50	21	140	146	298
6/48	74	177	190	235	387	384	457
12/48	41	183	234	122	313	306	353
41/48	154	351	308	319	537	504	606
93/48	92	253	283	257	402	362	494
21/48	68	304	212	243	372	444	364
35/48	33	185	206	198	362	368	420
65/48	78	142	308	282	518	412	483
48/48	100	253	328	308	510	469	484

C. N/+.nr/+ GENOTYPE

SHEEP	Positions. Sh.Pt.	W.	Sh.	Nk.	S.	Bk.	Br.
129/44	-	288	-	-	351	329	408
88/44	-	154	-	-	219	267	440
42/44	-	113	-	-	194	311	450
155/44	-	341	-	-	349	440	515
9/44	-	181	-	-	-	390	-

D. nr/nr GENOTYPE

SHEEP	Positions. Sh.Pt.	W.	Sh.	Nk.	S.	Bk.	Br.
351/48	65	239	241	183	303	472	-
332/48	126	253	375	316	484	412	-
353/48	24	118	102	60	259	278	-
343/48	44	221	262	168	385	375	-
80/47	-	193	269	139	273	330	497

E. N/N GENOTYPE

SHEEP	Positions. Sh.Pt.	W.	Nk.	Sh.	S.	Bk.	Br.
300/48	222	334	294	255	398	462	458
15/50	294	322	323	335	452	406	456
14/50	321	541	425	437	591	625	621
245/48	199	343	357	361	372	387	475
263/48	215	255	407	343	473	448	470

RELATION OF STANDARD DEVIATION TO MEAN IN MEDULLOMETER TESTS.

Table 55.

Means. $\bar{x}$	Standard Deviation. s	n	Genotype	Position.
16.5	2.08	4	+/+	Sh. Pt.
17.25	3.775	4	+/+	Neck
18.5	9.11	4	+/+	Shoulder
20.25	16.52	4	+/+	Withers
25.75	10.20	4	+/+	Side
38.5	18.66	4	+/+	Back
116	79.79	4	+/+	Britch
64.0	41.80	11	N/+	Sh. Pt.
191.8	108.72	11	N/++	Neck
204	105.73	11	N/+	Shoulder
183.5	101.2	11	N/+	Withers
354	141.2	11	N/+	Side
340	127.2	11	N/+	Back
403	116.79	11	N/+	Britch
64.8	43.14	4	nr/nr	Sh. Pt.
173.2	92.87	5	nr/nr	Neck
249.8	97.62	5	nr/nr	Shoulder
204.8	53.45	5	nr/nr	Withers
340.8	93.78	5	nr/nr	Side
373	74.49	5	nr/nr	Back
203.4	87.68	5	N/+.nr/+	Withers
278.25	83.48	4	N/+.nr/+	Side
347.4	67.04	5	N/+.nr/+	Back
453.25	44.90	4	N/+.nr/+	Britch
268.3	79.18	6	N/N	Sh. Pt.
383	72.39	6	N/N	Neck
377.67	96.56	6	N/N	Shoulder
364	97.00	6	N/N	Withers
474	86.69	6	N/N	Side
477	88.59	6	N/N	Back
516	79.98	6	N/N	Britch

TABLE 56.

GENOTYPES

Numbers means used for all between genotype analy

POSITIONS		+/+	N/+	N/+. nr/+	nr/nr	N/N
	SHOULDER PATCH	16.5	64	___	65	268
	WITHERS	20.25	183.5	203	205	364
	NECK	17.25	192	___	173	383
	SHOULDER	18.5	204	[illegible]	250	378
	SIDE	25.75	354	278	341	474
	BACK	38.5	340	347	373	477
	BRITCH	116	403	453	___	516
	F VALUES	4.83** n_1=6 n_2=21	13.39** n_1=6 n_2=70	9.16** n_1=3 n_2=14	9.09** n_1=5 n_2=23	5.89** n_1=6 n_2=3
	d	5%Level = 48.19 1%Level = 65.59	5% Level = 93.16 1% Level = 123.71	5% Level = 106.16 1% Level = 147.33	5% Level = 106.74 1% Level = 14481	5% LEVEL = 101 1% Level = 135

TABLE 57. COMPARISONS BETWEEN POSITIONS WITHIN THE NON N GENOTYPE WHERE LOG TRANSFORMED DATA WAS USED.

1·215 */+

1·208

1·225

1·229

1·389

1·546

2·000

F = 7·77 **
N1=6 N2=21

5% Level= ·308
1% Level= ·419

TABLE 38

NO. OF FLEECES IN Z GRADES IN DIFFERENT GENOTYPES.

(Hoggets excluded, the sheep being ewes of 2 to 6 yrs. of age.)

	N/N	N/+ N-grade	N/+ VI	N/+ low-N	N/+ VI & Low-N	Total N/+	nr/nr	nr/+
Z_3	20	8	0	0	0	8	2	0
Z_2	24	65	0	0	0	65	11	0
Z_1	10	57	5	2	7	64	6	2
Z_-	0	39	2	7	9	48	6	9
NH	0	0	5	4	9	9	1	29
Totals	54	169	12	13	25	194	26	40
av.Z Grade	2.19	1.25			0.28	1.12	1.31	0.05

N/+.nr/+ Genotype. Taking highest Z grade recorded for a fleece for each ewe. Some were born before 1946 and are getting old and less hairy.

Average Z : 1.81

Z Grades of 1951 Fleeces.

(3) born in 1944, 1,Z2; 2 Z^- excluded)

Average Z : 1.31.

If 1944 ewes included average Z : 1.19

Sheep born later than 1945

Average Z : 2.33

Ewes of 1945

Average Z : 0.9

For Chi Square Test.

N/N compared with N/+ and nr/nr.

Data placed in two groups.

Group A.: No. of fleeces graded Z_2 or Z_3.
Group B.: No. " " " Z_1, Z_- or NH

N/N Group A : 44
Group B : 10

N/+ Group A : 73
Group B :121

Between N/+ and N/N
Chi Square : 32.6

nr/nr Group A : 13
Group B : 13

Between nr/nr and N/N
Chi Square : 8.49

nr/+ compared with nr/nr and N/N.

Data placed in two groups:

Group A : No. of fleeces graded Z_3, Z_2 or Z_1.
Group B : No. " " " Z^-, or NH.

nr/+ Group A : 2
Group B : 38

n/+ Group A :137
Group B : 57

Between nr/+ and N/+
chi square : 58.98

nr/nr Group A : 19

Between nr/+ and nr/nr
chi square : 33.66

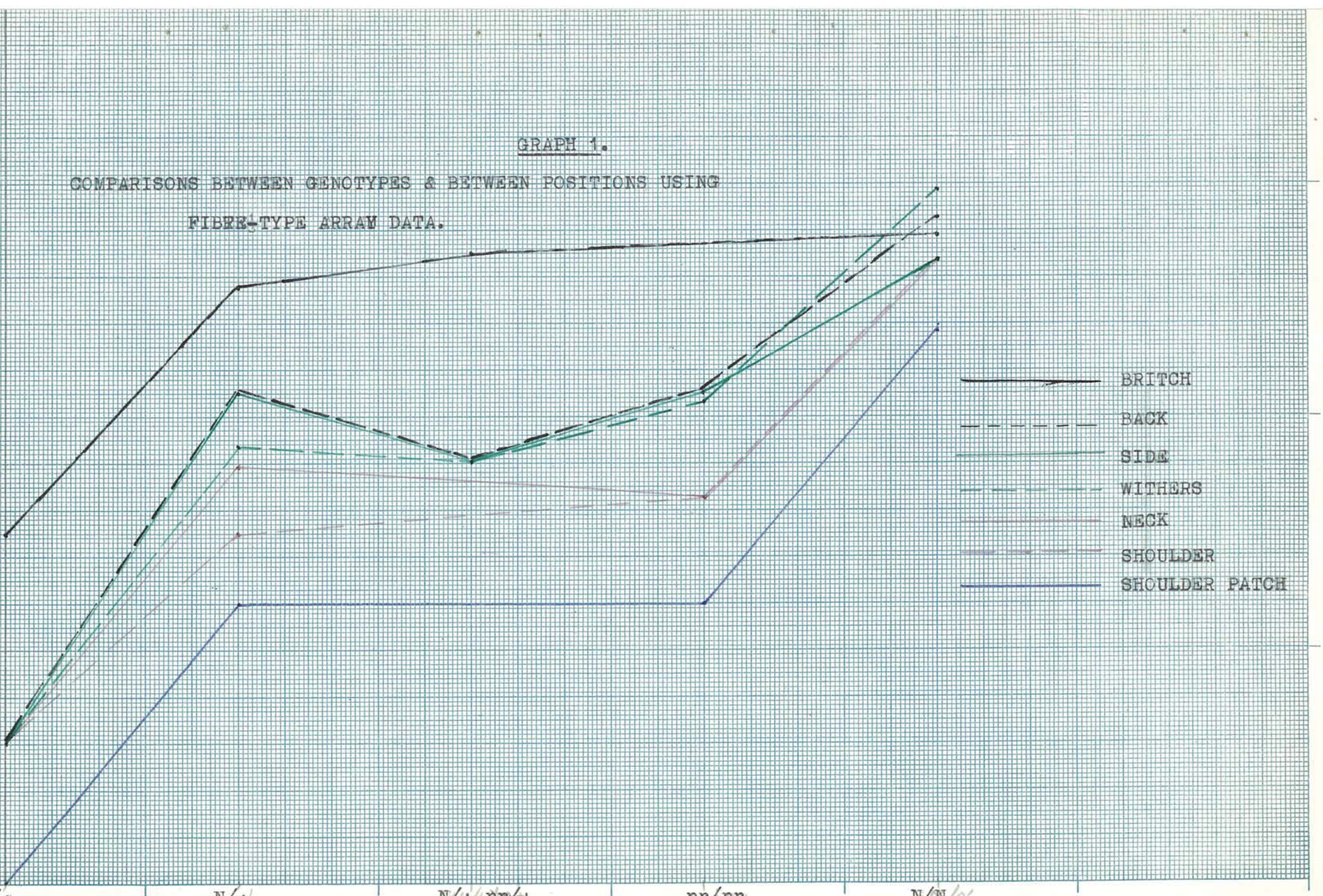
TABLE 59. FOLLICLE POPULATION COUNTS.

SHEEP POSITION		P/s Ratio Inc.Sec.Foll. Anlage.	P/s Ratio Exc.Sec. Foll. Anlage.	Carters $\frac{P+p+S+s}{P+p}$	Ratios $X\frac{P+S}{P}$
	Bk.	1 to 1.13	1 to 0.92	2.13	1.92
	W.	1 to 1.20		2.20	
	S.	1 to 1.85		2.85	
x	Sh.Pt.	1 to 2.00	1 to 1.66	3.00	2.66
nr/nr	Sh.	1 to 1.74		2.74	
Geno-	Nk.	1 to 1.58		2.58	
type.	Br.	1 to 1.65		2.65	
	Bk.	1 to 1.12	1 to 0.86	2.12	1.86
	W.	1 to 1.56		2.56	
	S.	1 to 1.39		2.39	
Z	Sh.Pt.	1 to 2.18	1 to 1.93	3.18	2.93
nr/nr	Sh.	1 to 1.86		2.86	
Geno-	Nk.	1 to 2.29		3.29	
type.	Br.	1 to 1.98		2.98	
	Bk.	1 to 2.23	1 to 1.83	3.23	2.83
	W.	1 to 2.98		3.98	
	S.	1 to 2.07		3.07	
Q	Sh.Pt.	1 to 3.04	1 to 2.78	4.04	3.78
N/+	Sh.	1 to 2.79		3.79	
Geno-	Nk.	1 to 2.14		3.14	
type	Br.	1 to 2.20		3.20	
	Bk.	1 to 1.35	1 to 1.12	2.35	2.12
	W.	1 to 2.23		3.23	
P	S.	1 to 1.71		2.71	
N/N	Sh.Pt.	1 to 2.21	1 to 1.89	3.21	2.89
Geno-	Sh.	1 to 2.34		3.34	
type	Nk.	1 to 2.82		3.82	
	Br.	1 to 1.73		2.73	
	Bk.	1 to 3.48	1 to 3.12	4.48	4.12
	W.	1 to 3.45		4.45	
J.H.J.	S.	1 to 3.64		4.64	
*/+	Sh.Pt	1 to 5.02	1 to 4.61	6.02	5.61
Geno-x	Sh.	1 to 3.80		4.80	
type.	Nk.	1 to 4.14		5.14	
	Br.	1 to 4.13		5.13	

GRAPHS.

GRAPH 1.

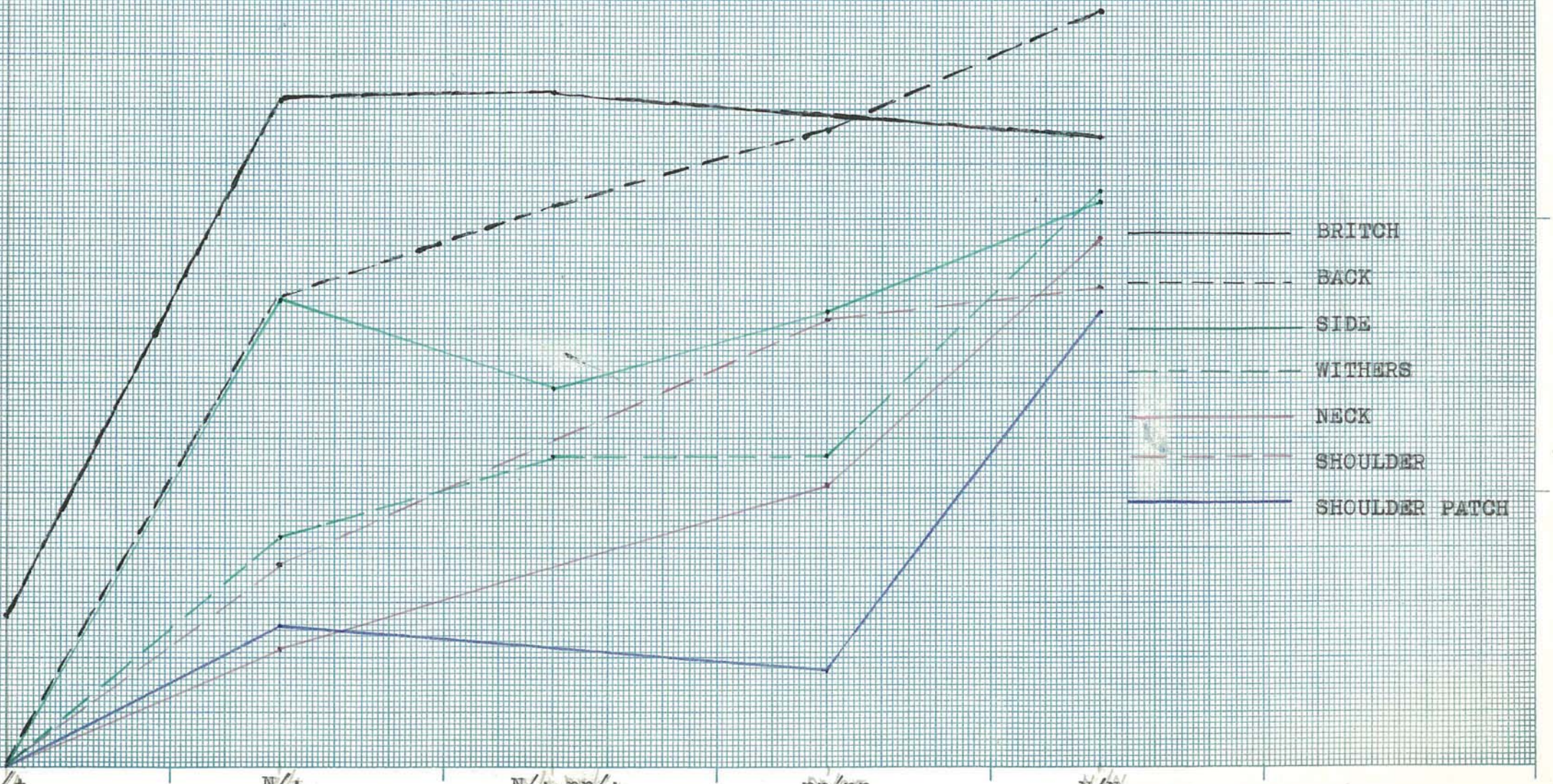
COMPARISONS BETWEEN GENOTYPES & BETWEEN POSITIONS USING FIBER-TYPE ARRAY DATA.



No. 2D: Metric (19 x 30 cm.)

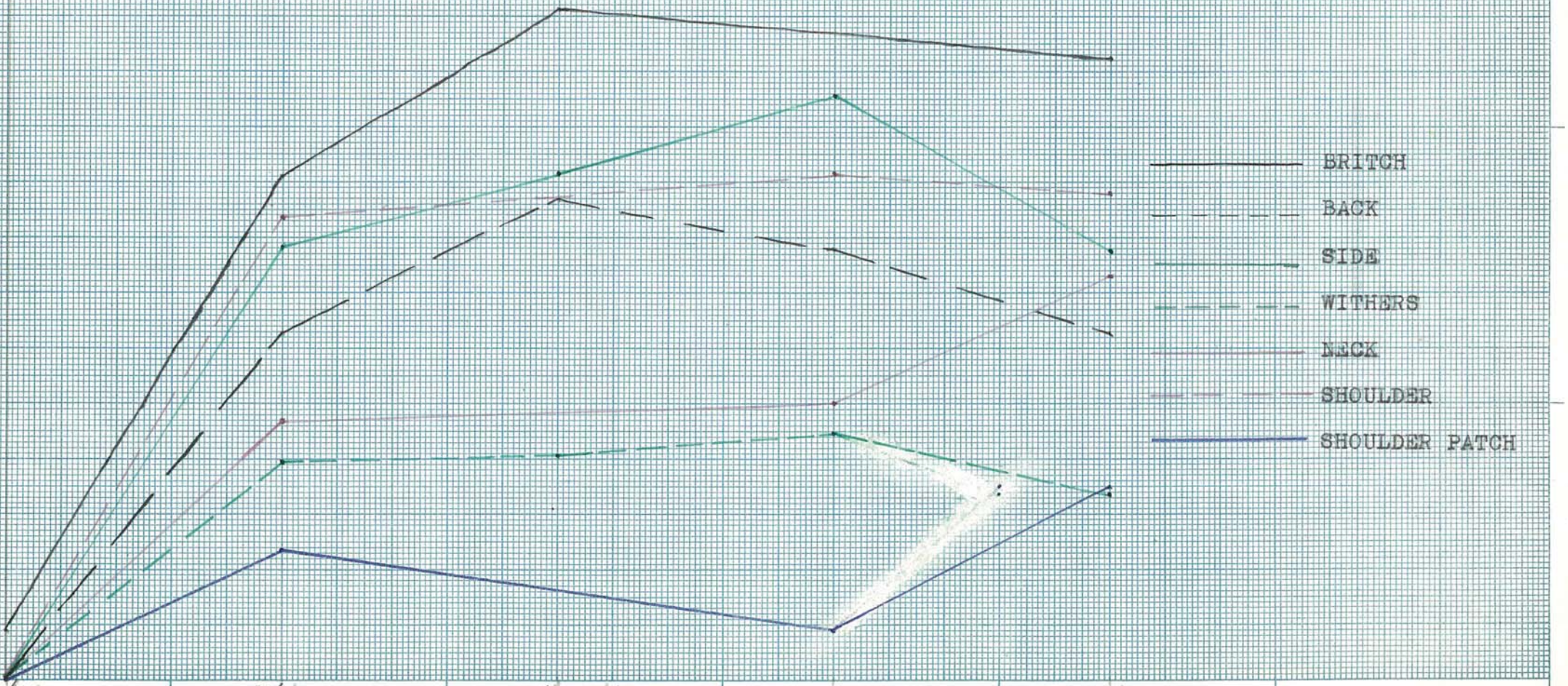
GRAPH 2.

COMPARISONS BETWEEN HAKO-HAIR FIBRES.



GRAPH 3.

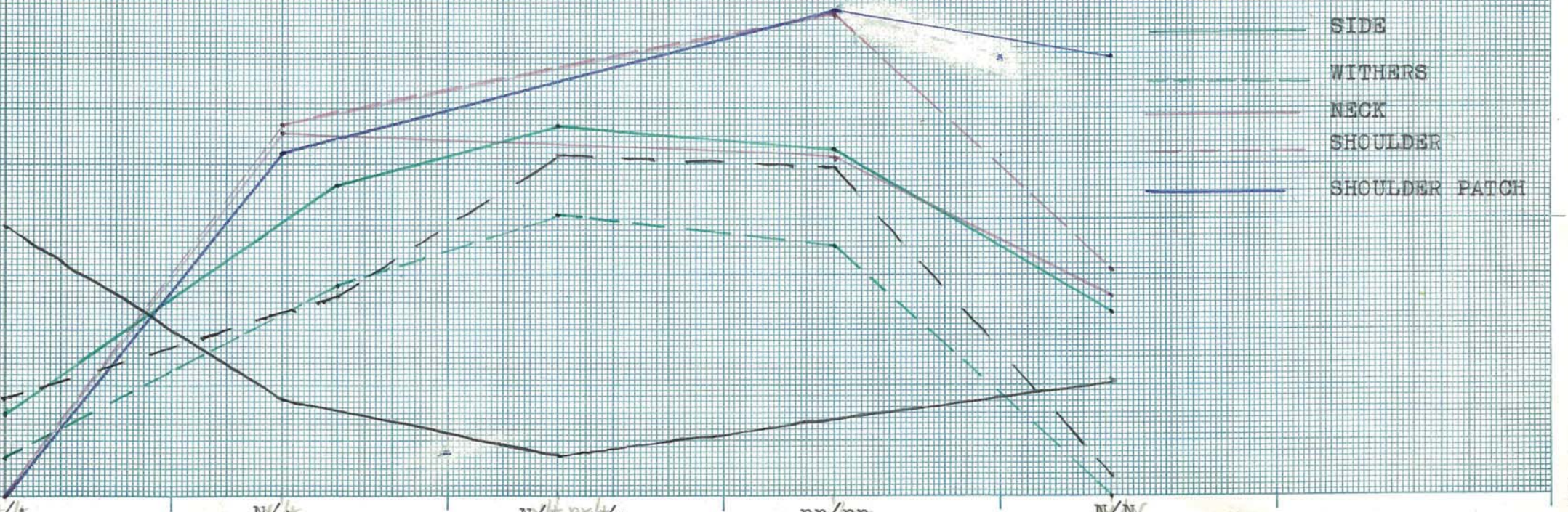
COMPARISONS BETWEEN SUPER-SICKLE A FIBRES.



No. 2D: Metric (19 x 30 cm)

GRAPH 4.

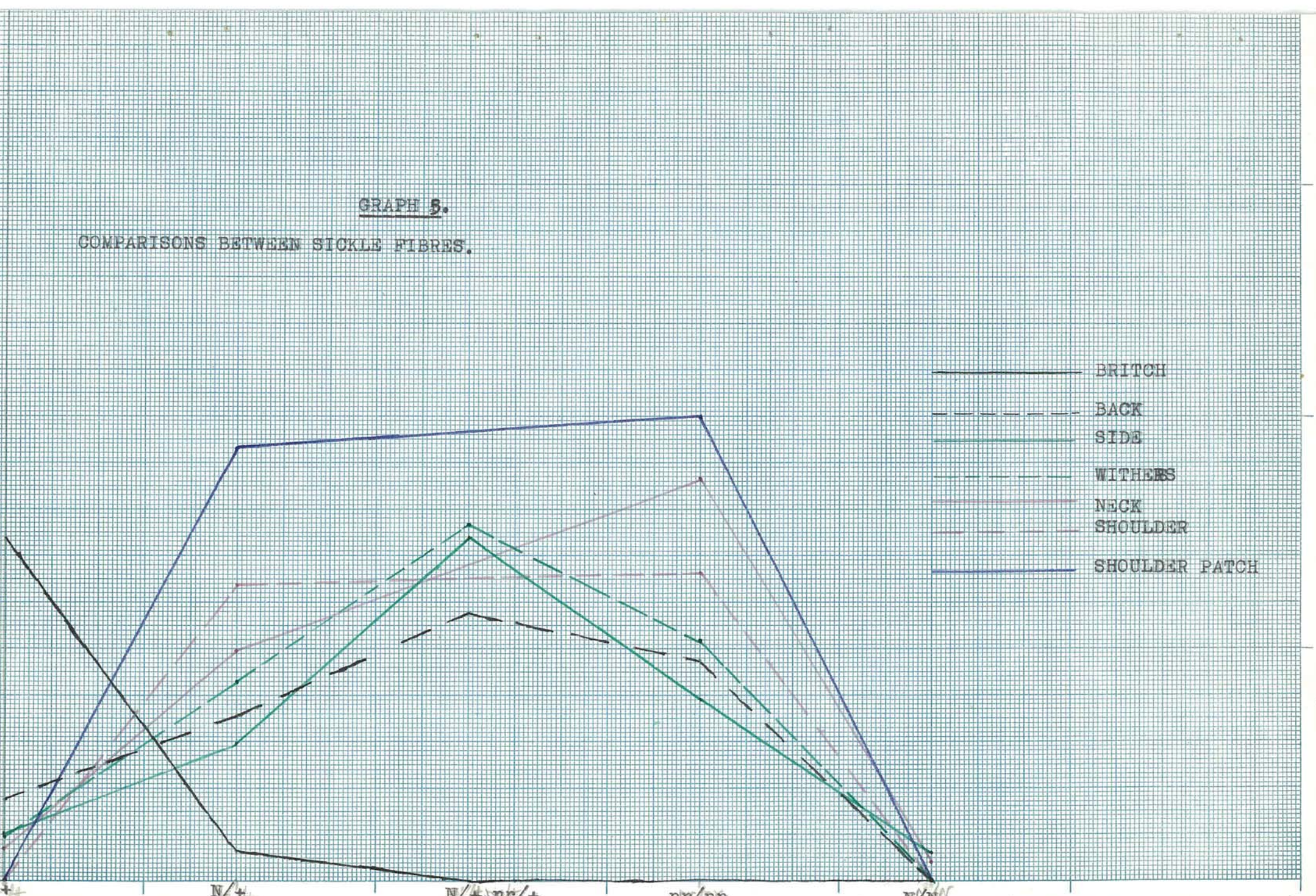
COMPARISONS OF SUPER-SICKLE B FIBRES.



No. 2D: Metric (19 x 30 cm.)

GRAPH 5.

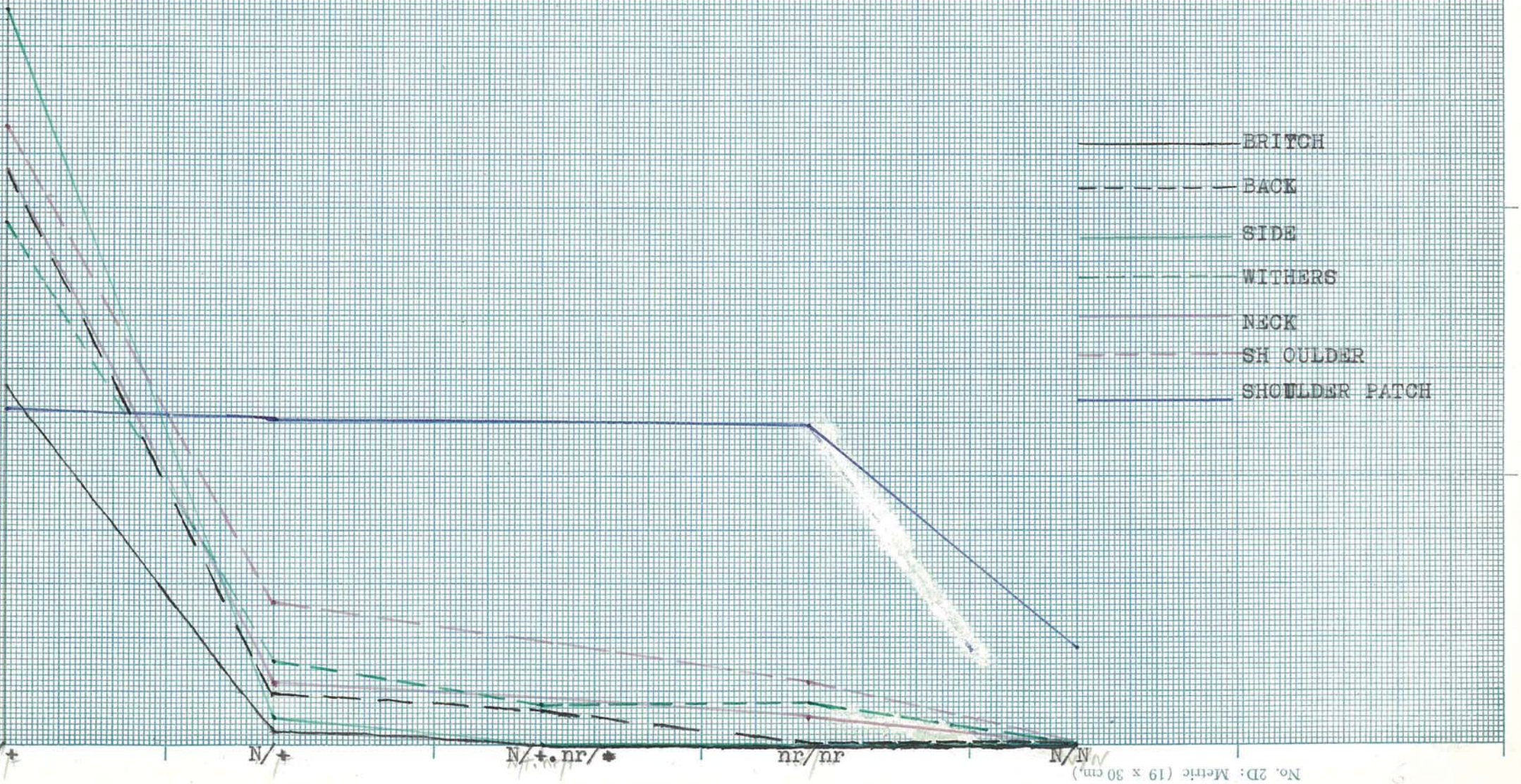
COMPARISONS BETWEEN SICKLE FIBRES.



No. 2D: Metric (19 x 30 cm)

GRAPH 6.

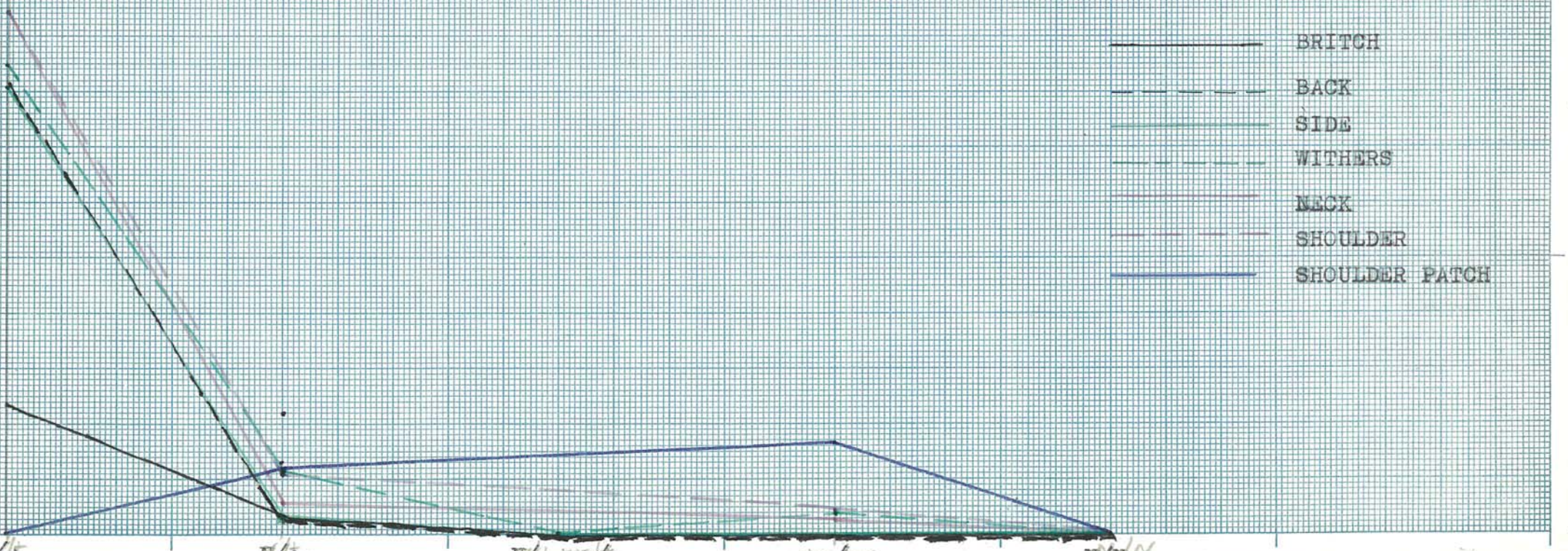
COMPARISONS BETWEEN FINE-SICKLE FIBRES.



No. 2D: Metric (19 x 30 cm.)

GRAPH 7.

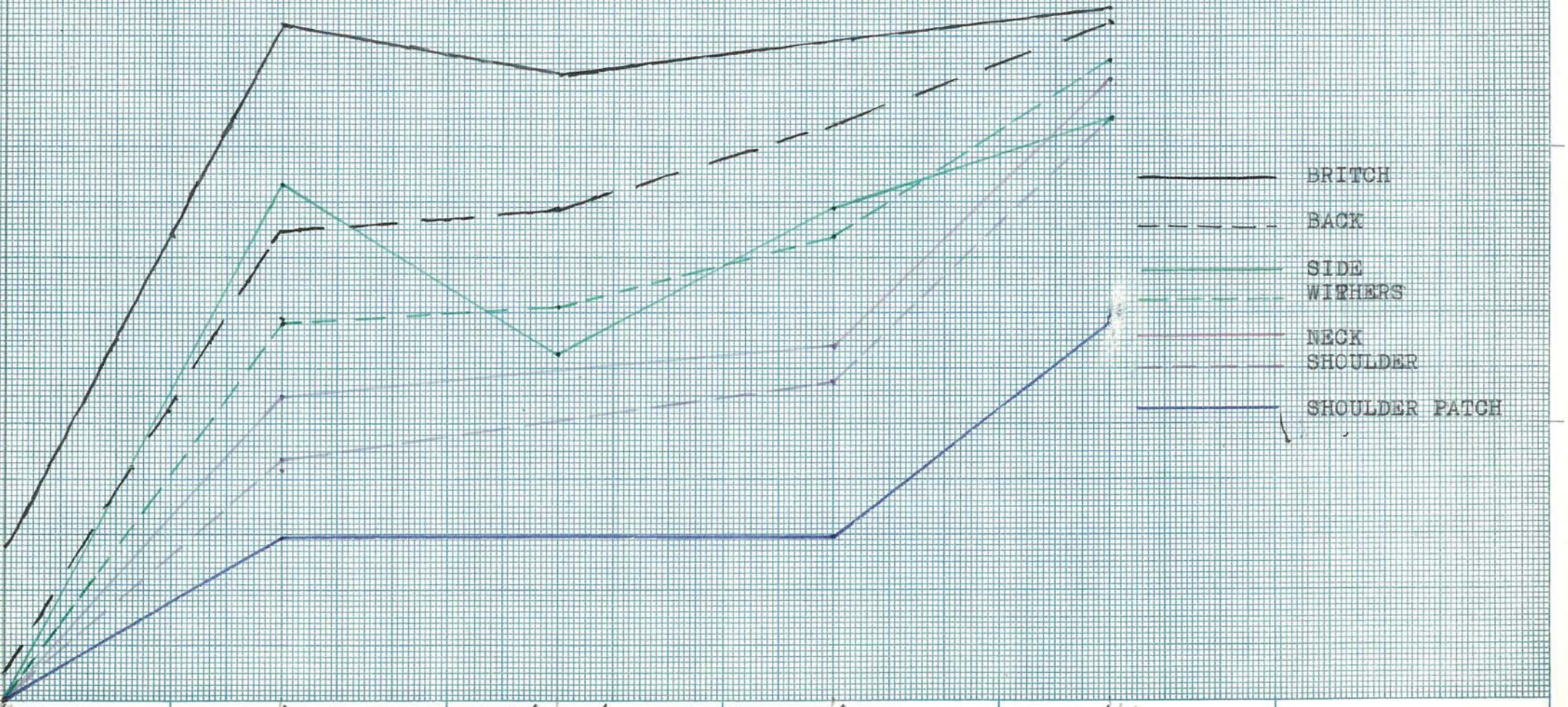
COMPARISONS BETWEEN CHECKED CURLY-TIP FIBRES.



No. 2D: Metric (19 x 30 cm)

GRAPH 8.

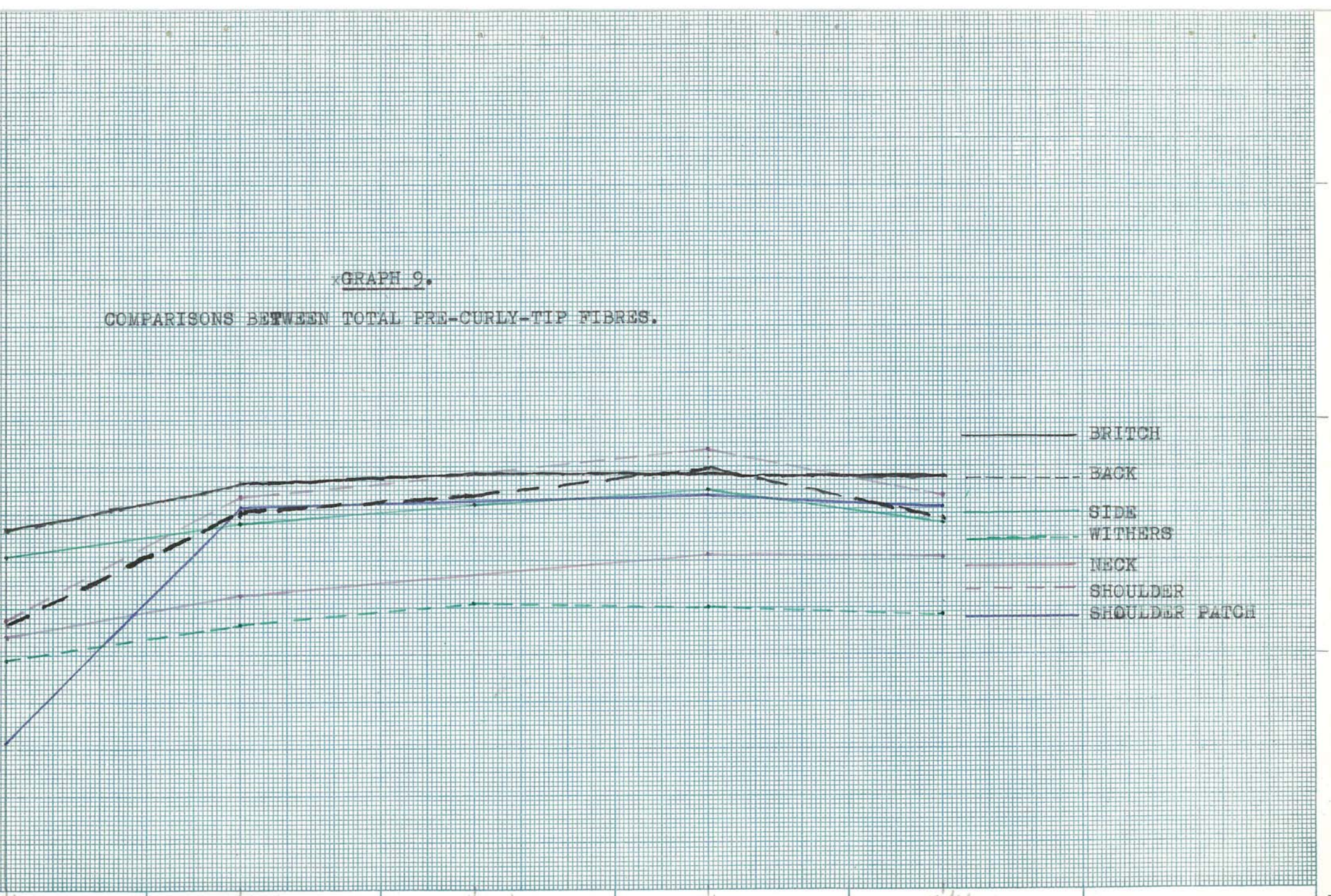
COMPARISONS BETWEEN HAIRY-TIP-CURLY-TIP FIBRES.



No. 2D: Metric (19 x 30 cm.)

GRAPH 9.

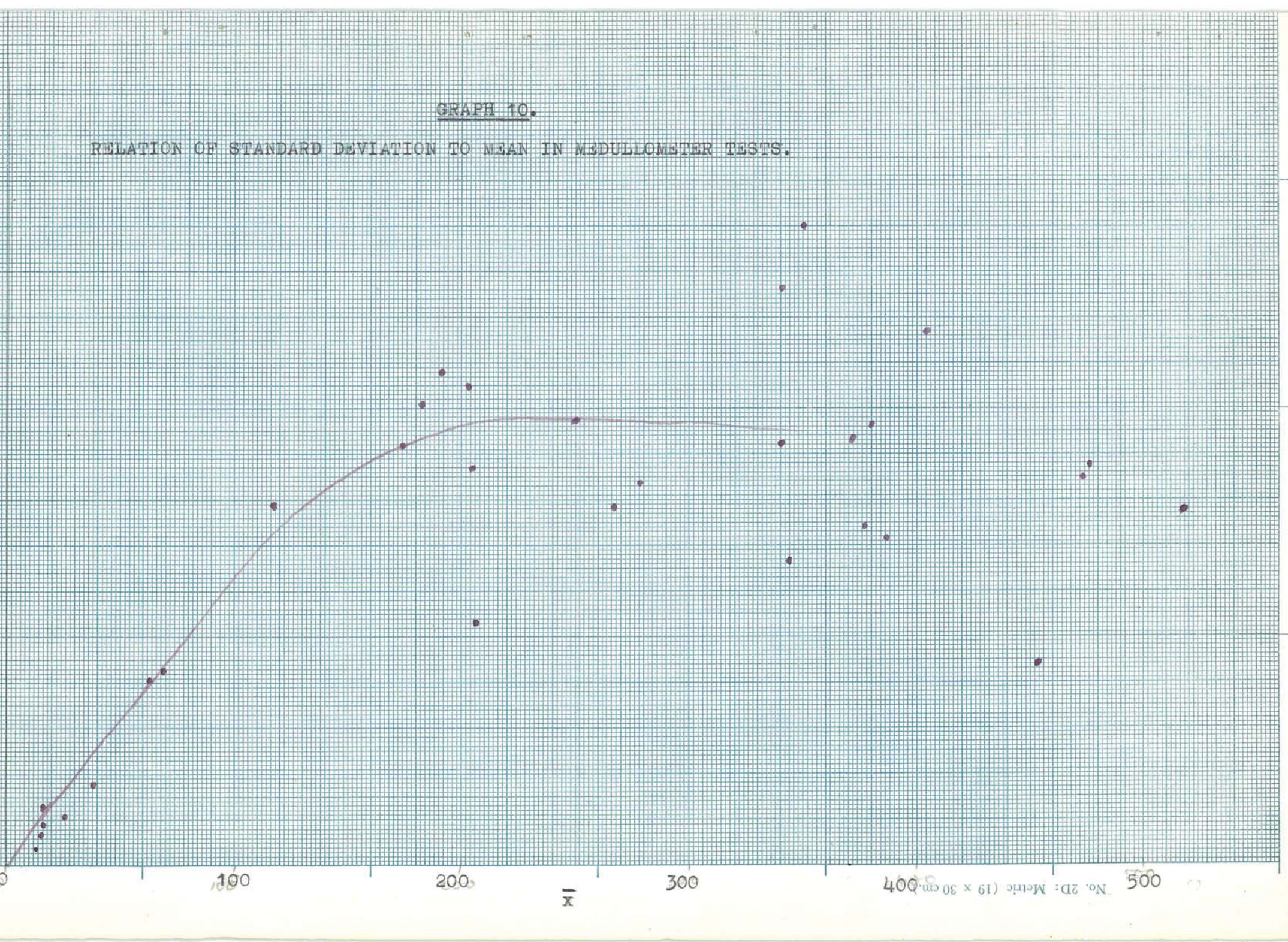
COMPARISONS BETWEEN TOTAL PRE-CURLY-TIP FIBRES.



No. 2D: Metric (19 x 30 cm)

GRAPH 10.

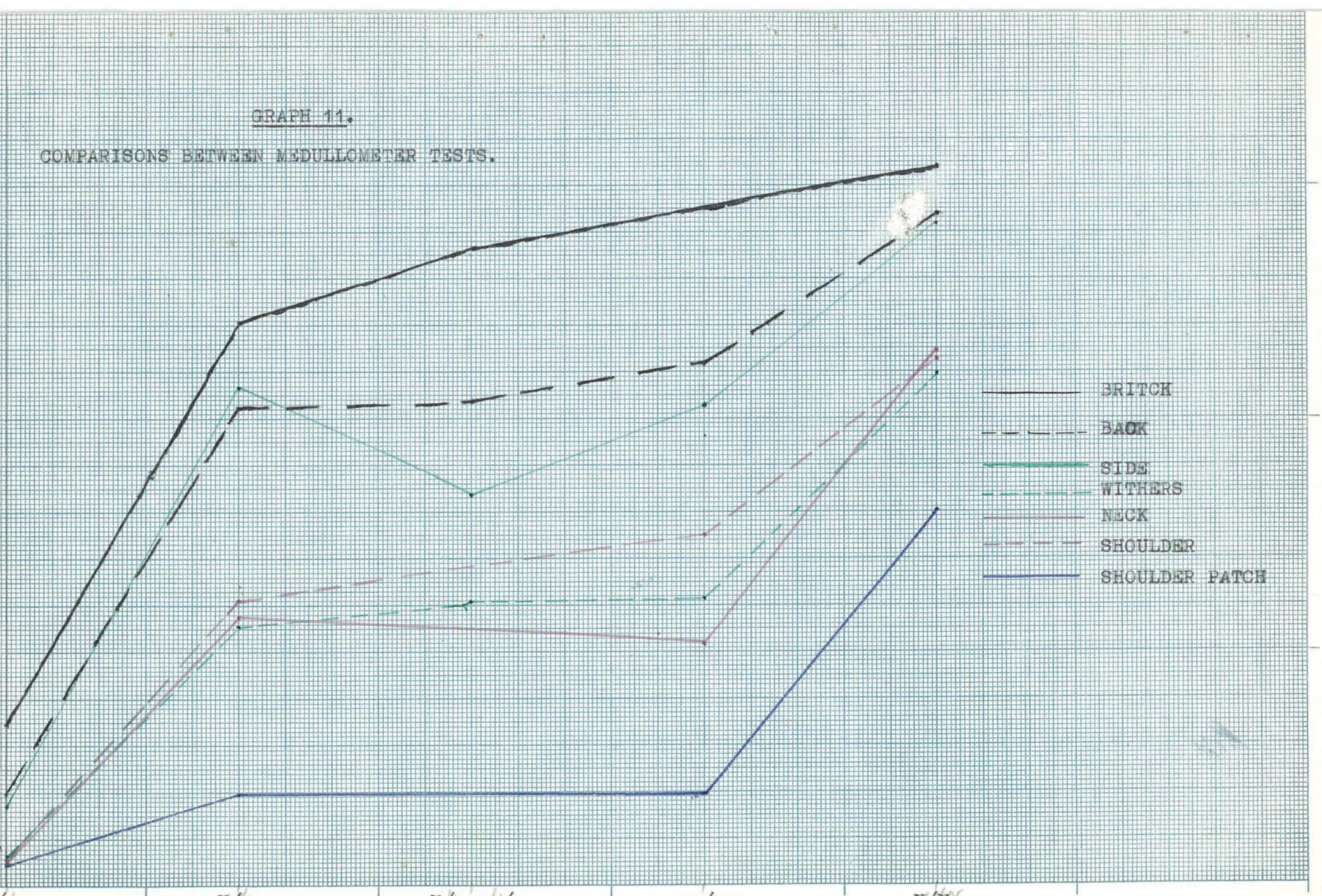
RELATION OF STANDARD DEVIATION TO MEAN IN MICROMETER TESTS.



No. 2D: Metric (19 x 30 cm.)

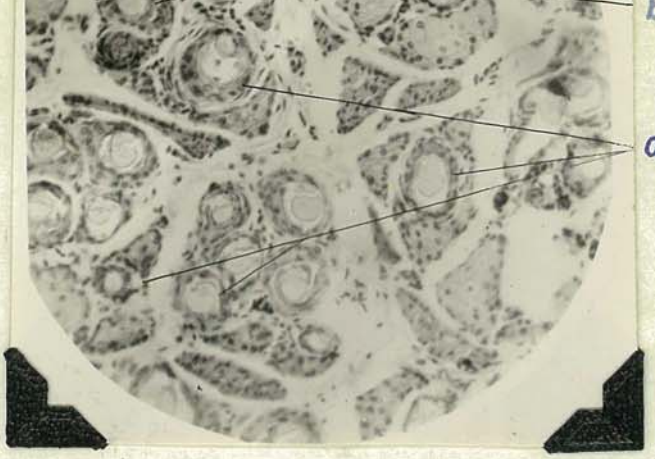
GRAPH 11.

COMPARISONS BETWEEN MEDULLOMETER TESTS.

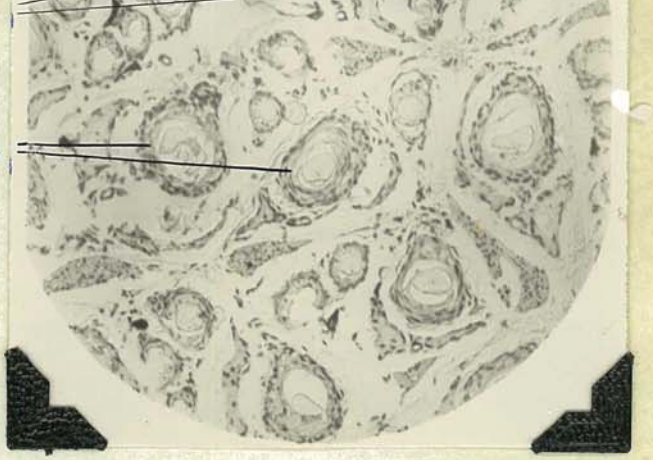


No. 2D: Metric (19 x 30 cm)

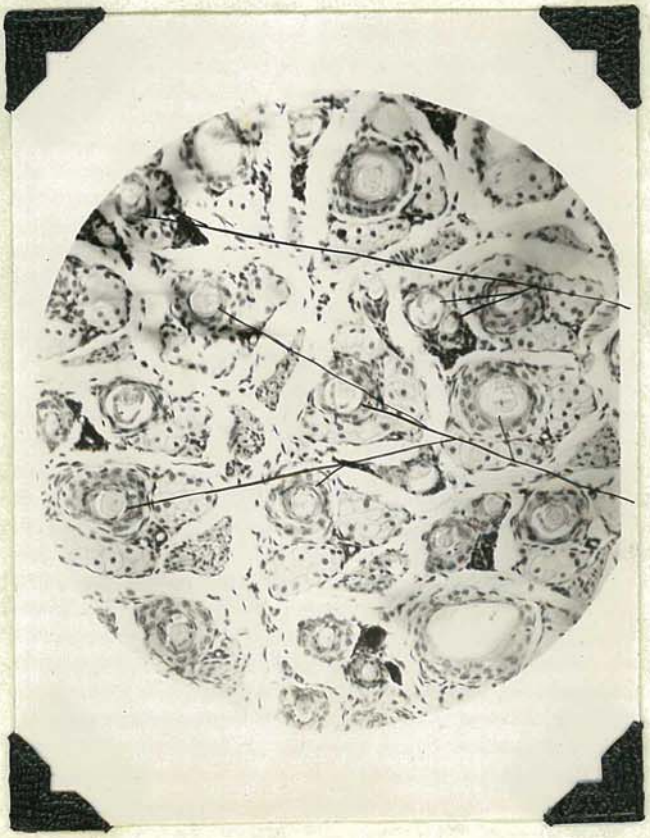
PHOTOGRAPHS.



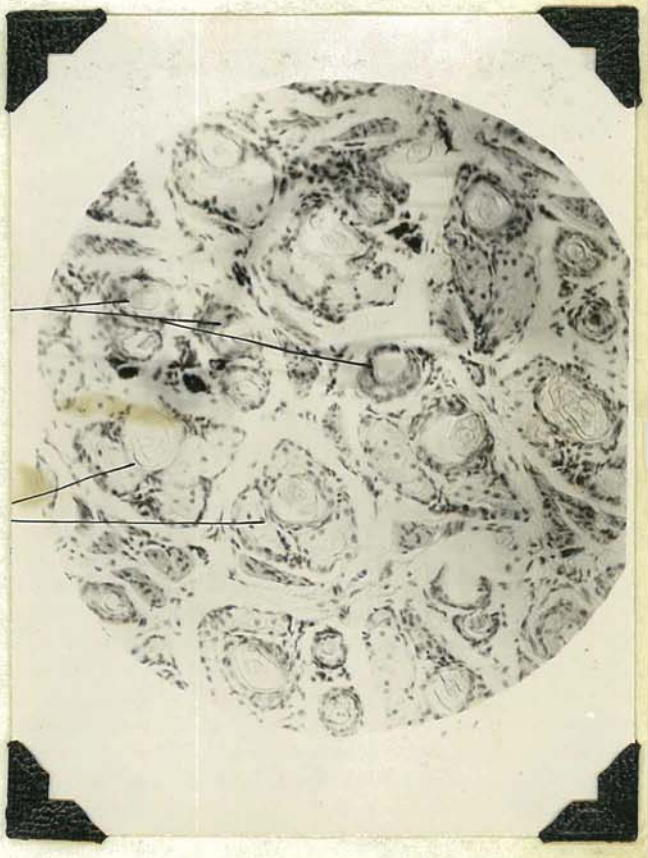
Photograph I.
Section of a Non-N Skin from the Back Position showing fibres of a similar diameter in both Primary (a) and Secondary (b) follicles.



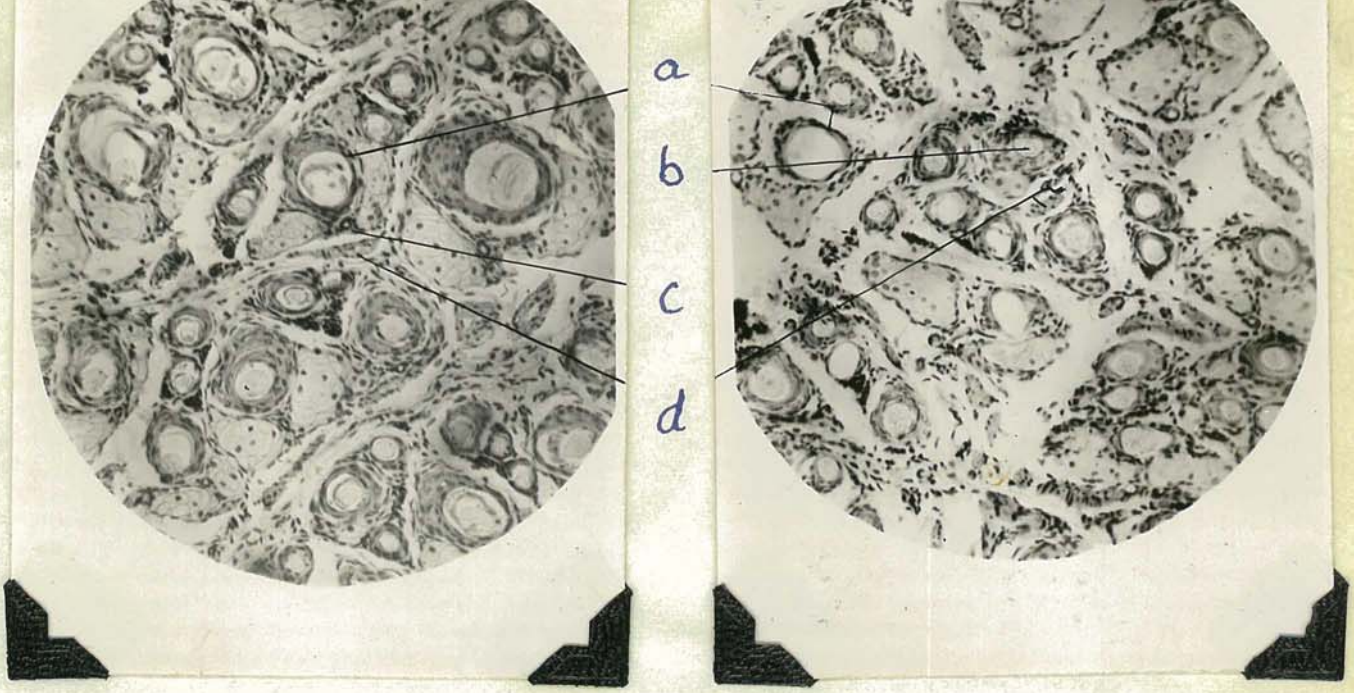
Photograph 2.
Section of an N/+ skin from the Back Position showing fibres of a greater diameter in the Primary follicles (a) than are present in the Secondary follicles (b).



Photograph 3.
Section of an nr/nr skin showing a similar relation between fibres and follicles as that found in the N/+ skin.
Primary follicle (a)
Secondary follicle (b)

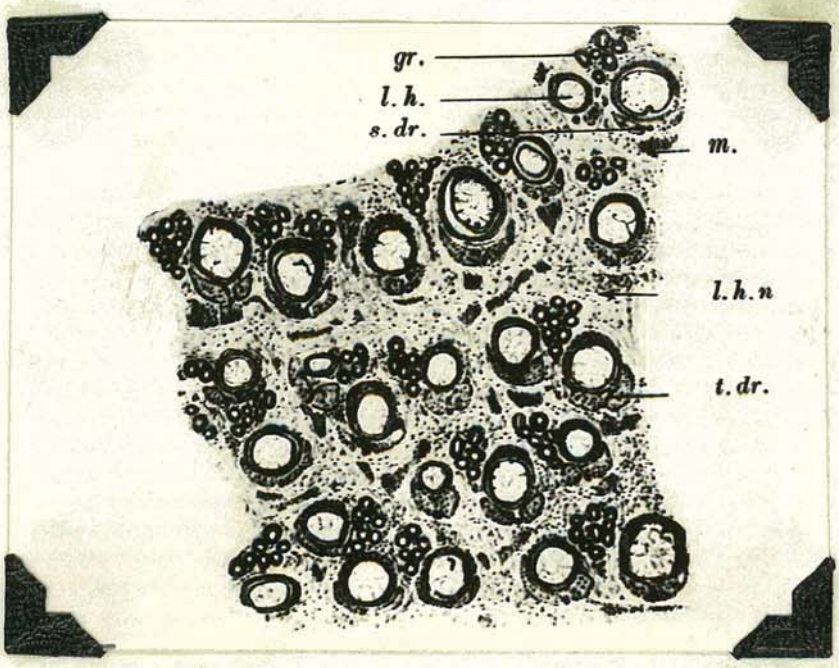


Photograph 4.
Section of an N/N skin, showing a similar relation between fibres and follicles as that found in the N/+ skin but with the difference in the diameter of the fibres growing in the Primary follicles (a) and the Secondary follicles (b) even more pronounced.

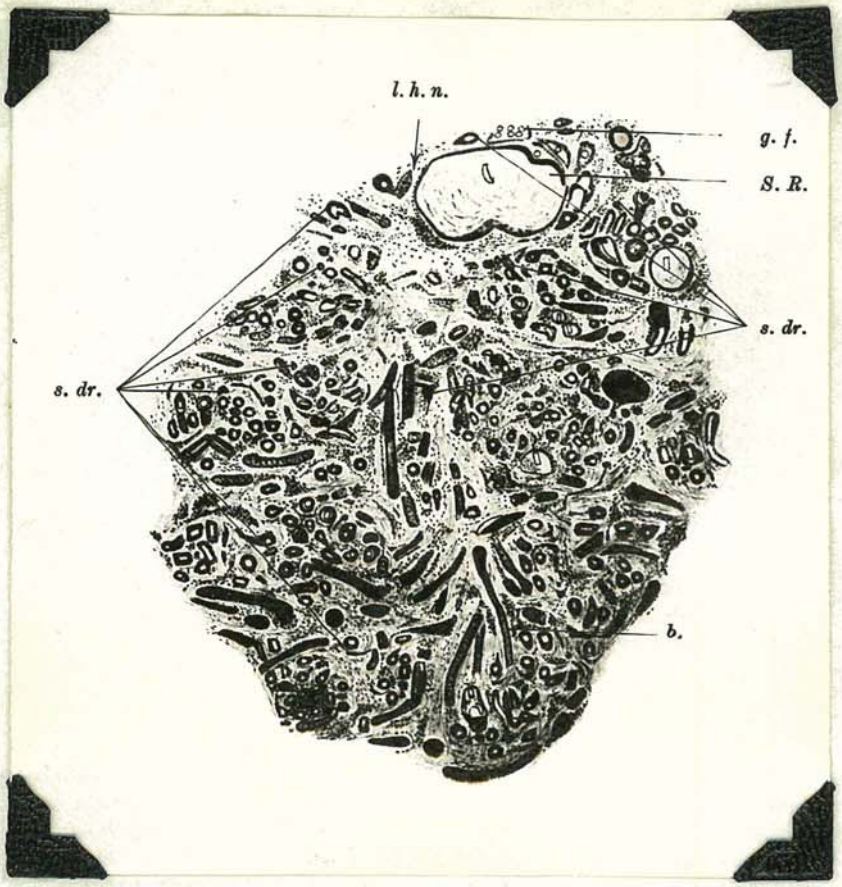


Photograph 5.
Showing a primary follicle on the ectal side of a bundle.
(a) Follicle
(c) Sudoriferous Gland Duct
(d) Arrector Pili Muscle.

Photograph 6.
Secondary follicle with an arrector muscle. No sweat gland duct is present.
(b) Secondary follicle.
(d) Arrector pili Muscle.

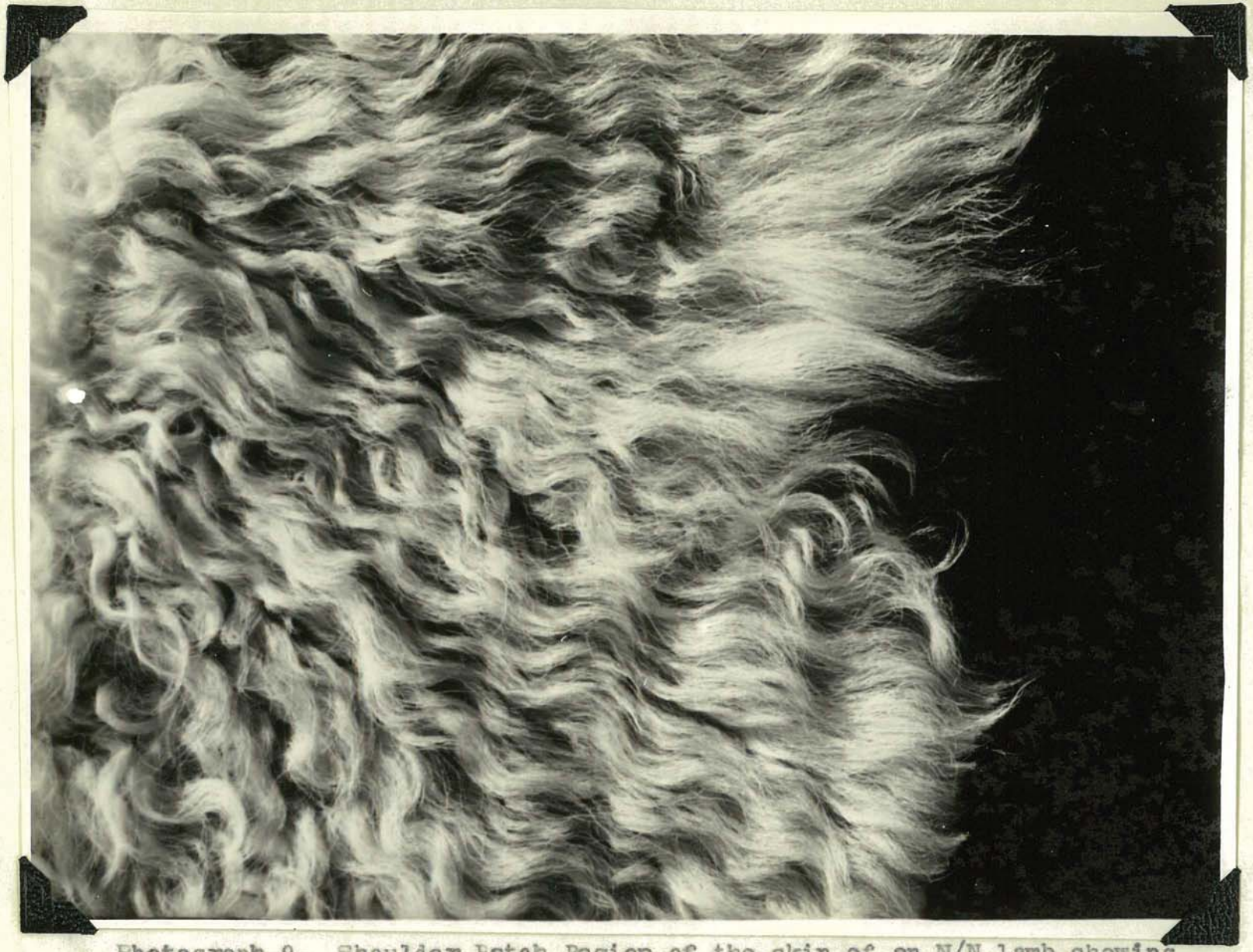


Photograph 7.
Section of skin of a Mufflon showing fibres in the primary follicles of much greater diameter than those in the secondary follicles.
gr.= secondary follicle fibre
Lh.= primary " "
s.dr=Sudoriferous Gland duct.
t.dr=Sebaceous Gland.
m. = arrector muscle.
From Spottel & Tänzer. (1923)



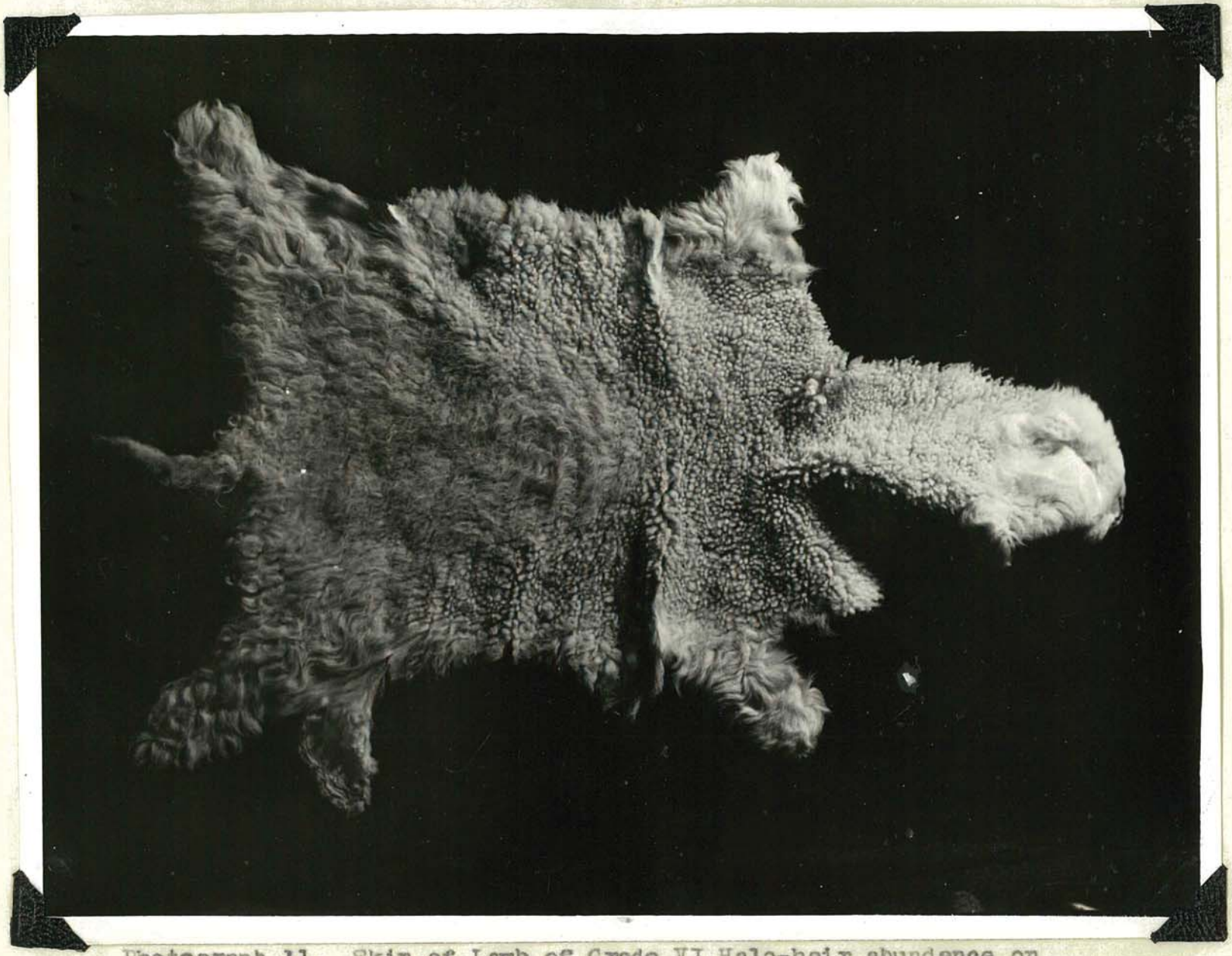
Photograph 8.
Section of a skin of a
Merino showing fibres in
all follicles very similar
in diameter.
s.dr = Sudoriferous Gland Duct.

From Spöttel & Tänzer.
(1923)

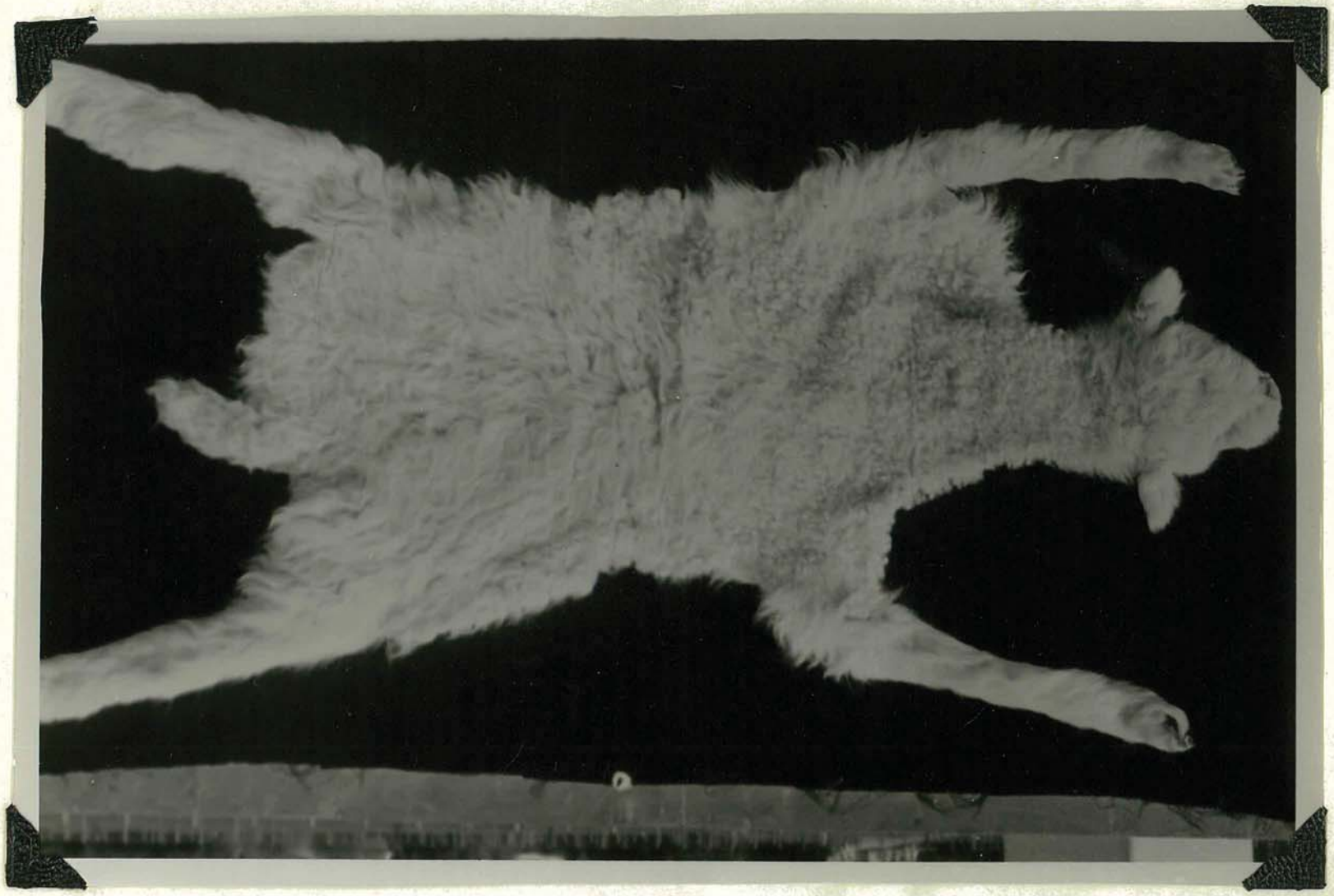


Photograph 9. Shoulder Patch Region of the skin of an N/N lamb showing a full abundance of Halo-hairs throughout.

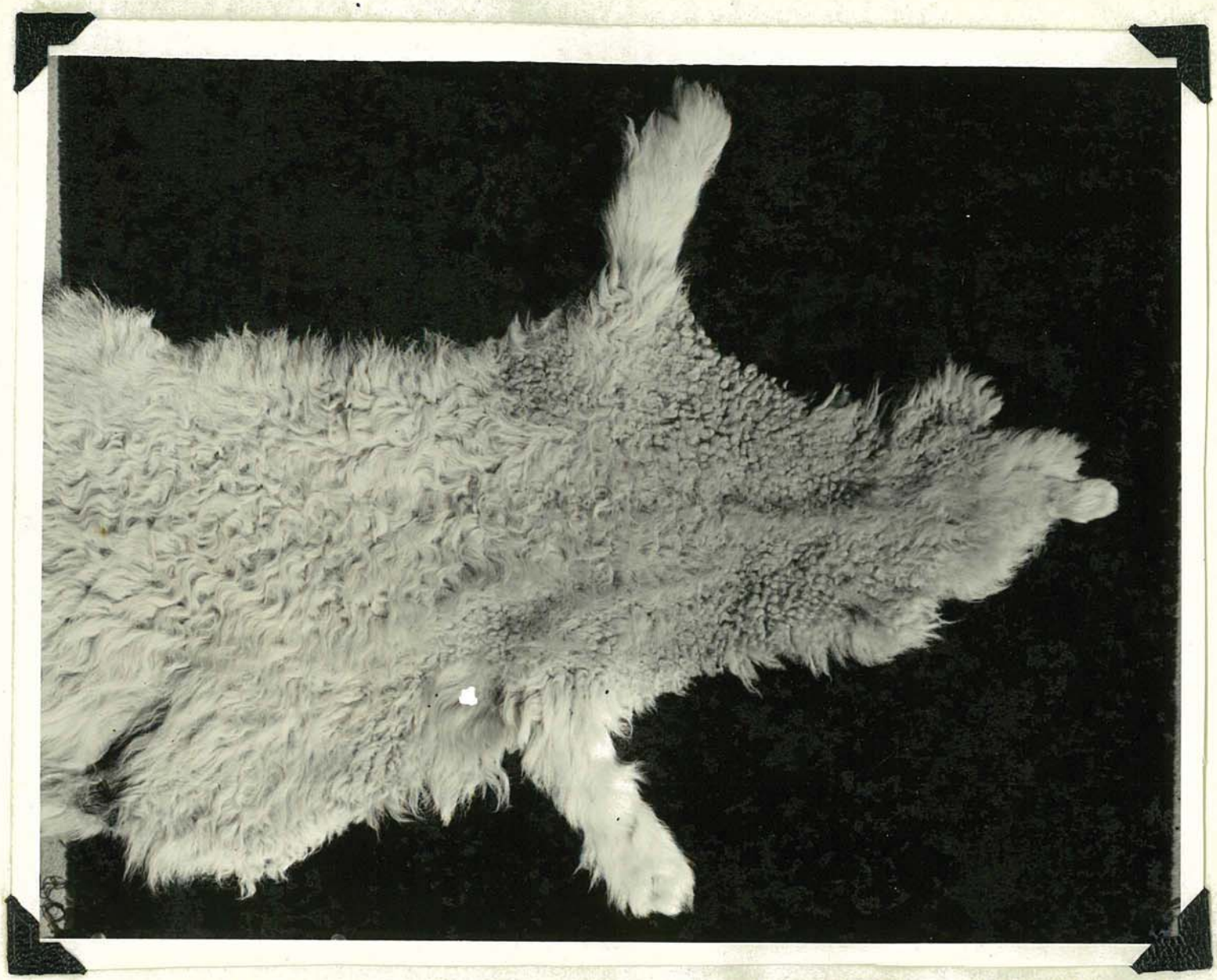
Photograph 10. Shoulder Patch Region of the skin of an N/+ lamb showing a reduced abundance of Halo-hairs in this region.



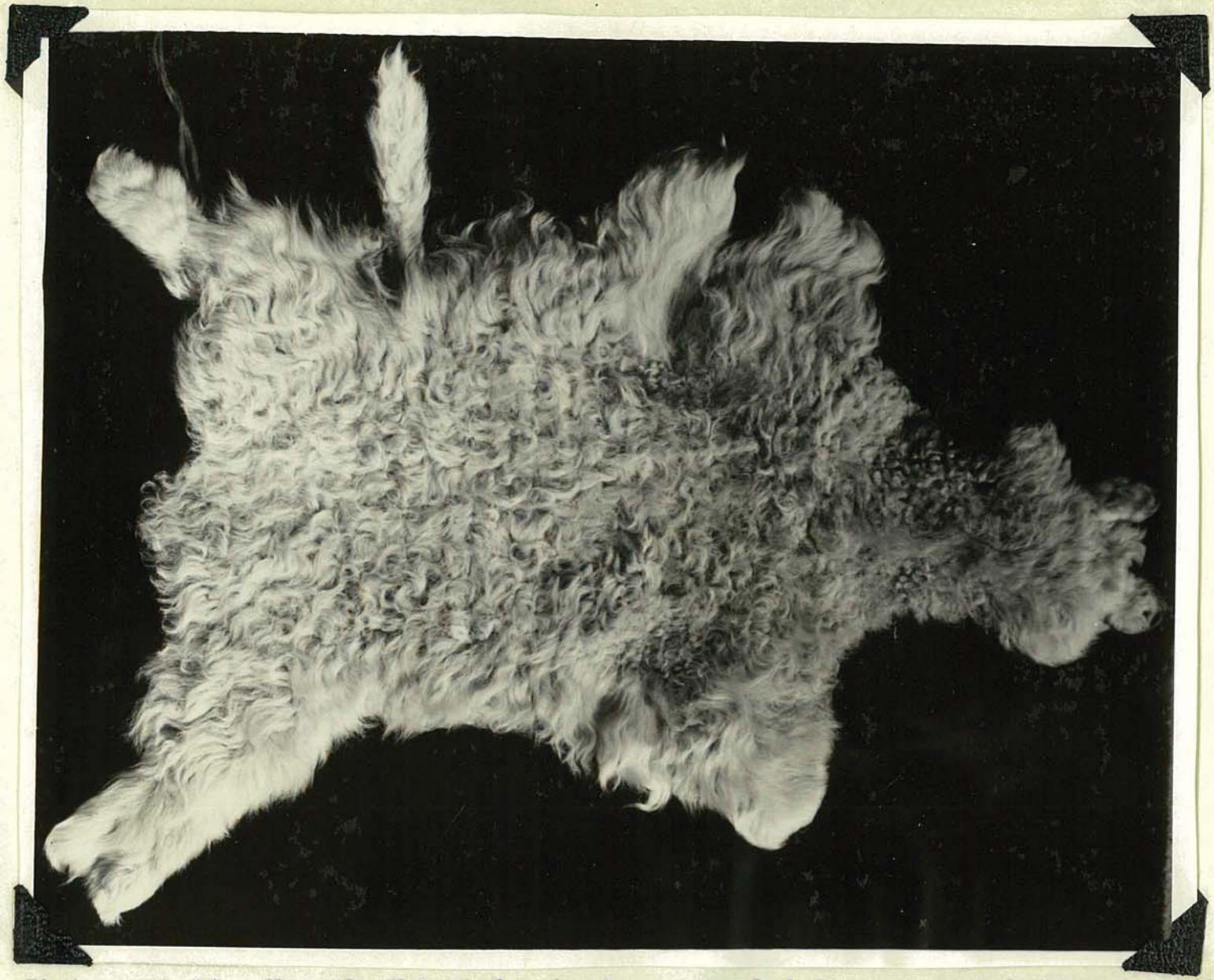
Photograph 11. Skin of Lamb of Grade VI Halo-hair abundance on the back. Note absence of halo-hairs on the front of the body and high abundance on the britch.



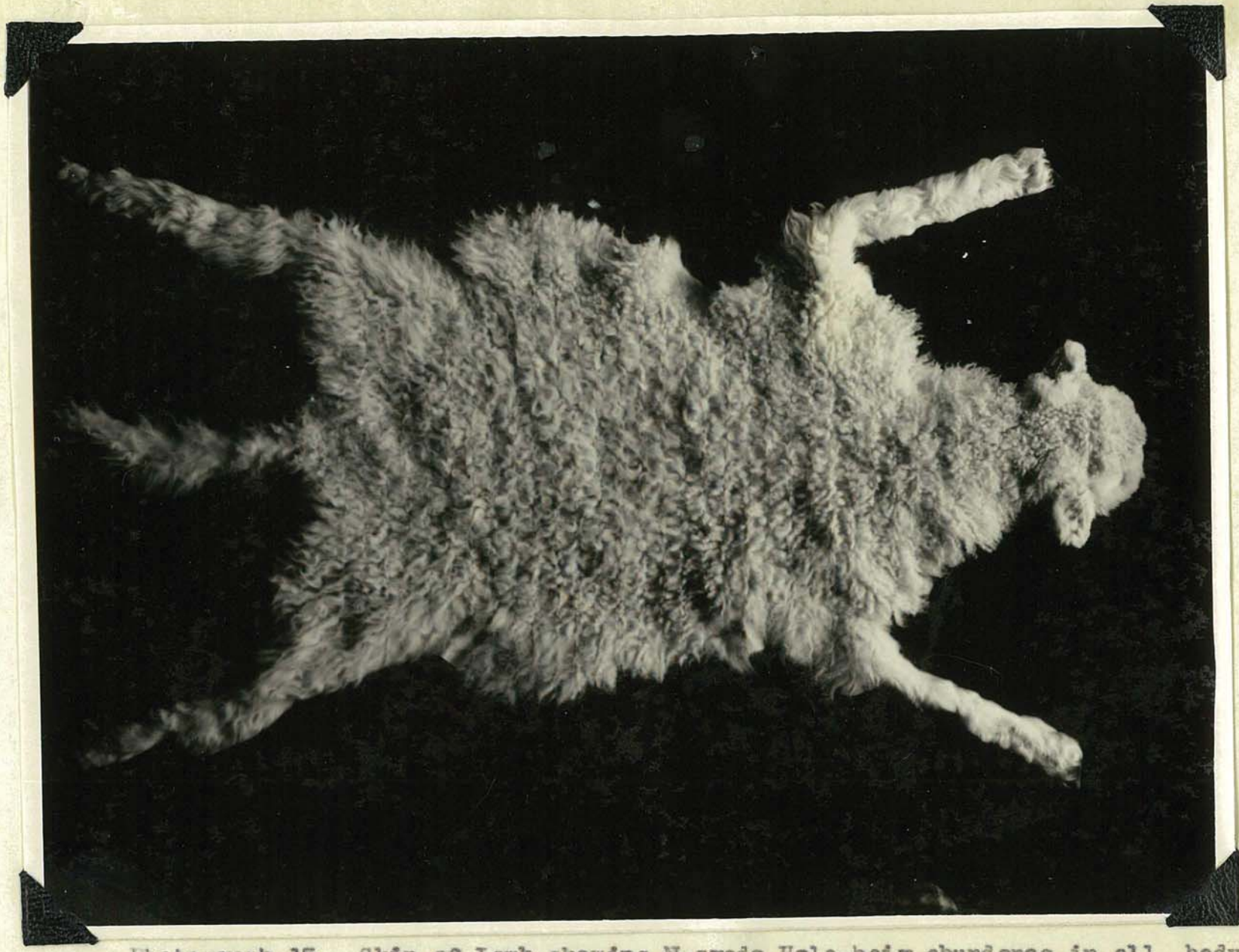
Photograph 12. Skin of a Lamb of N-grade Halo-hair abundance on the back, but with a low abundance of these fibres in the front of the body Note big drop in abundance just behind the withers position a reduction extending along the side, continuous with the shoul patch reduction.



Photograph 13. Skin of Lamb of N-grade Halo-hair abundance on the back, but still reduced in front of the body. Shoulder patch reduction continuous with that on Neck.



Photograph 14. N-grade Halo-hair abundance carried forward much better Reductions reduced to an area on each side of the neck and a separate shoulder patch reduction.



Photograph 15. Skin of Lamb showing N-grade Halo-hair abundance in all body regions. However in some places curls are small.