Genetic correlations in five body measurements, weight, type, and production of Holstein cows

Robert Walton Touchberry

Iowa State College

Follow this and additional works at: https://lib.dr.iastate.edu/rtd

Part of the Agriculture Commons, and the Animal Sciences Commons

Recommended Citation

Touchberry, Robert Walton, "Genetic correlations in five body measurements, weight, type, and production of Holstein cows " (1948). Retrospective Theses and Dissertations. 12426.
https://lib.dr.iastate.edu/rtd/12426

This Dissertation is brought to you for free and open access by the Iowa State University Capstones, Theses and Dissertations at Iowa State University Digital Repository. It has been accepted for inclusion in Retrospective Theses and Dissertations by an authorized administrator of Iowa State University Digital Repository. For more information, please contact digirep@iastate.edu.
NOTE TO USERS

This reproduction is the best copy available.

UMI®
GENETIC CORRELATIONS
IN FIVE BODY MEASUREMENTS, WEIGHT, TYPE, AND
PRODUCTION OF HOLSTEIN COWS

by

Robert Walton Touchberry

A dissertation Submitted to the
Graduate Faculty in Partial Fulfillment of
The Requirements for the Degree of
DOCTOR OF PHILOSOPHY

Major Subject: Animal Breeding and Genetics

Approved:

Signature was redacted for privacy.

In Charge of Major Work

Signature was redacted for privacy.

In Charge of Major Work

Signature was redacted for privacy.

Head of Major Department

Signature was redacted for privacy.

Dean of Graduate College

Iowa State College

1948
INTRODUCTION

Man is constantly striving to improve livestock by selection. The progress made by selection depends on many things including the heritability of characters and the genetic relationships between the characters on which selection is practiced. Genetic relationships between characters are very important, but they have been expounded perhaps less than any other factor involved in selection. If a breeder were selecting for two characters with a high negative genetic correlation his net gain would be small. On the other hand if he were selecting for two traits with a high positive genetic correlation his net progress could be much greater than if the two characters were independent.

Genetic correlations are not to be confused with phenotypic correlations. Phenotypic correlations are caused by genetic correlations, by similarities of environment and by physiological balance. Similarity of environment here means the environment peculiar to each cow which causes two or more characteristics to vary in the same or in different directions. By physiological balance is meant the tendency of a tall and long cow to have a large heart girth or paunch girth in order to maintain a physiological balance. This physiological balance is caused by both genetic and environmental factors, so the phenotypic correlation is basically the result of genetic and environmental factors.

Factors which can contribute to genetic correlations are linkage of
genes, manifold effects of genes, and different intensities or directions of selection in the noninterbreeding subgroups of a population. Linkage would be an important cause of genetic correlations only in a population where either the coupling or repulsion phase of the double heterozygote had by far the greater frequency. Different intensities or directions of selection in the noninterbreeding subgroups would tend to fix different groups of genes in the subgroups. These genes would contribute to genetic correlations when the differences between groups are considered. Genetic correlations caused by linkage of genes may persist for a few generations after a cross. This trace will exist until the coupling and repulsion phases of the double heterozygote are equal. The manifold effects of genes would be a cause of genetic correlations regardless of the type of population.

Gräselberg (12) gives three ways in which a gene may produce manifold effects. (1) A gene may produce a and b directly but in independent ways. (2) The gene X may produce a and b directly but in essentially the same way. (3) The gene X may produce a directly and then a will produce b.

\[
\text{(1) } X \xrightarrow{a} a \xrightarrow{b} b \quad \text{(2) } X \xrightarrow{a} a \xrightarrow{b} b \quad \text{(3) } X \rightarrow a \rightarrow b
\]

Gräselberg calls the first method of action "genuine" pleiotropy and the last two "spurious" pleiotropy. Regardless of whether it is "genuine" or "spurious" pleiotropy the genes contribute to genetic correlations by their manifold effects. It is a case of a multiplicity of effects coming from a common cause, and a division into "genuine" and "spurious" pleiotropy is needless for a statistical study.
In this study some estimates of genetic correlations in Holstein dairy cows will be derived. The characteristics to be studied are either height, chest depth, body length, heart girth, yeanling girth, weight, type, milk production and butterfat production.
The presence of such gases in the atmosphere can be inferred from the presence of gases in the atmosphere. The presence of gases in the atmosphere can be measured. If such gases can be shown to be related to the presence of gases in the atmosphere, then the evidence for the presence of gases in the atmosphere can be measured. If such gases can be shown to be related to the presence of gases in the atmosphere, then the evidence for the presence of gases in the atmosphere can be measured. If such gases can be shown to be related to the presence of gases in the atmosphere, then the evidence for the presence of gases in the atmosphere can be measured. If such gases can be shown to be related to the presence of gases in the atmosphere, then the evidence for the presence of gases in the atmosphere can be measured.
was small in size and carried the dominant genes, $A^w$ for white bellied agouti, $B$ for black and $D$ for intensity. The other species was larger and carried the recessive alleles, $a$ for non-agouti, $b$ for brown, and $d$ for dilution. He made backcrosses to both species, and at the age of 151 days he found that the brown mice of both sexes in the backcross progeny were heavier than the black mice. This could be a case of pleiotropy rather than linkage of a qualitative and a quantitative character as the author reported. In addition he demonstrated that several size characters, namely, humerus, femur, and tibia lengths, and body length were influenced by factors linked with the gene for brown. These might also be influenced by manifold effects of the gene for brown.

At an early age the situation was reversed, for the black mice were heavier at the younger age of 21 days. Green attributes this to the initial effects of the dominant gene $B$ for black. It is possible that $D$ could have manifold effects some of which were expressed at an early age. There was some evidence that other factors influencing body length and tail length were found on the chromosome with dilution. This could be due to the manifold effects of the dilution gene.

In another case of apparent manifold effects of genes Dunn (?) reported on a mutant gene, $s$. Mice heterozygous for this gene had a short tail or no tail at all, often shortened or cracked spine, abnormalities of the kidneys, and a lowered viability after birth. In animals homozygous for this gene a syndrome of abnormalities was present. There was complete taillessness, absence of kidneys, absence of genitalia, and other malformations of the urinogenital system. Homozygous animals always die shortly after birth. This is a case of manifold effects of one gene.
Schweit (21) contradicts Dobzhansky's (5) findings concerning the spermathecal shape in Drosophila melanogaster as affected by certain qualitative genes. He concluded that the seven segments of chromosomes containing wavy, vibrissae, cardinal, dusty, white, ivory, and ebony contained also genes with additive effects upon spermathecal shape. By continued backcrossing the spermatheca index decreased. He takes this as evidence that many structures are affected by a number of genes but not as evidence that many genes affect a multiplicity of characters. This is not critical proof that the spermatheca index was not affected by the seven genes producing visible effects.

In giving reasons why one would expect manifold effects of genes, Grünberg (12) makes the following statement: (Page 123):

The number of observable characters in an organism is infinite. The number of genes which control development is limited. It follows that many, perhaps most genes must not affect only one organ or character but several at a time. Their effect is manifold and the term pleiotropism has been coined to cover this diversity of actions of a single gene.

Grünberg (12) has presented a case in which a lethal gene in mice affects the deposition of cartilage in the trachea, bronchi, larynx, and ribs. The chest is very rigid and breathing is difficult. Pressure is exerted on the organs of the thoracic cavity causing dyspnea, emphysema, and hemorrhage; this leads to death. There is no question about the manifold effects of this gene. Grünberg is of the opinion that the action of a gene is unity, and the various effects of a manifold gene are brought about in essentially the same way. By unity of gene action is meant that each gene produces only one primary product. This product may in time influence only one or a multiplicity of characteristics. Grünberg (12)
is of the opinion that the gene affecting the trachea, bronchi, larynx, and ribs produced only one primary product. This product acted on the deposition of cartilage to influence the many organs and tissues containing cartilage. In this case the action of the gene was unity and the manifold effects were brought about in essentially the same way. His hesitation to admit multiple primary effects is not based on statistical considerations but on the supposition that a gene is a single chemical compound, perhaps only a single molecule, which is unlikely to fulfill more than one specific function in the body. He concludes that since unity of gene action has been established, all those cases in which unity has not been shown are not completely analyzed.

Dobzhansky and Holz (6) X-rayed a long inbred strain of Oregon wild type Drosophila and obtained mutants at the white, yellow, ruby, vermilion, dusky, and forked loci. These mutants were detected by their normal modification of the external characters affected. All four of the whites obtained, nine of the ten yellows, and the one vermilion were found to modify the shape of the spermatheca. These genes have manifold effects and may be classified as pleiotropic genes. These authors point out that since the primary effects of no genes are known, it is futile to classify pleiotropy as genuine or spurious. At the present it seems simplest to assume that each gene gives one and only one primary product. This has been neither proved nor disproved, and the problem of manifold effects has no bearing on it.

Size Factors

Correlations between various parts of the body have been used to
indicate genetic correlations. When two characters such as length of arm and leg were correlated, a high coefficient of correlation hinted of a genetic correlation. Castle (1) was one of the first to work with correlations between body parts. From his work on five bone measurements of rabbits he concluded that most bone variation was due to a general factor which had similar effects upon all bones. Castle used data collected by Mac Dowell (19), and as Wright (29) states it was an unfortunate use of the data. The measurements were on the offspring of a cross between a giant and a small race and on the backcross of this F₁ to the smaller race. The measurements were on a very heterogeneous group thus exaggerating the importance of general factors as shown by Castle’s correlations.

Summer (24) worked out correlations based on a constant body length in mice. He concluded that not only do mice of the same body length differ from one another in the length of various members, but these latter parts tend to vary together independently of the body as a whole. The measurements in this study were length of tail, foot, ear, pelvis, and body length. Castle and Summer argued back and forth in a series of short articles, Castle still contending that general size factors are the only genetic agencies of any consequence which affect size. Summer admits that the agencies which affect size are largely general in action, but he is of the opinion that they are also to a considerable degree local and specific.

Later Wright (29) applied a method of partial correlations to Castle’s gross correlations. Even when three of the five bones were considered as constant, positive correlations were found between the other two. These partial correlations ranged from .002 to .517 showing that there is some variation of each bone length independent of all others measured. Wright (30)
The data have been made, but much generalized correctly. All the data are based on a generalized representation of the data. The data were obtained in a generalized form and in an accurate method in a variety of experimental conditions. Such generalized data are consistent with a large amount of data. In a study reported in a recent publication of a leading journal, a generalized representation of the data was needed in a generalized form and the principles described between the phenomena and the phenomena.
the present study.

Hazel (13) obtained estimates of genetic correlations between score, weight, and productivity in swine. These were obtained by correlating the phenotypic expression of one character in one animal with the phenotypic expression of another character in a related animal. The development of his formula

$$r_{i,j} = \frac{\text{Cov. } I_1 J_2 - \text{Cov. } I_2 J_1}{\sqrt{\text{Cov. } I_1 I_2 \text{ Cov. } J_1 J_2}}$$

$$\theta_i$$ = genotype for character one.

$$\theta_j$$ = genotype for character two.

$$I_1$$ = phenotypic expression of character one in animal one.

$$I_2$$ = phenotypic expression of character one in animal two.

$$J_1$$ = phenotypic expression of character two in animal one.

$$J_2$$ = phenotypic expression of character two in animal two.

for estimating genetic correlations will be given in the analysis of data, page 111. Using the above formula Hazel found a genetic correlation between score and weight of swine of .519. The genetic correlations between weight and productivity and score and productivity were both zero.

Some of the first estimates of correlations which approached genetic correlations were made by Cowen (9) with dairy cows. In table four of his work he gives the relationships between the conformation of the daughter and that of her dam. Among the characteristics included are weight and height at withers. The four correlations between these variables are given
above. The hard to hard differences, which are very likely to be largely environmental, are included in these gross correlations. If hard to hard differences are considered as being entirely genetic, the genetic correlation between withers height and weight is \( \sqrt{\frac{.35 \times .25}{.25 \times .10}} = .756 \). This estimate is very likely to be too high.

Using single production records of 8656 daughters and the mates of 374 Ayrshire sires, Tyler and Hyatt (27) made estimates of the heritability and of the genetic correlations between milk production, butterfat production, and percent of butterfat. The intra-sire regressions of offspring on dam were used in estimating heritability. The heritability estimates were .31 for milk production, .23 for butterfat production, and .55 for percent butterfat. The phenotypic correlations between these three were .93 between milk and fat production, -.14 between milk and percent butterfat, and .23 for percent butterfat and butterfat production. The corresponding genetic correlations were .35, -.20 and .26. About 35 percent of the genetic differences in milk production are associated with genetic differences in butterfat production.
SOURCE OF DATA

The data for this study were taken from the Iowa State College Holstein herd. All daughter-dam pairs which had records of body measurements, weight, type rating and milk and fat production at three years of age were included in the study. These records covered a period from the early 1930's to late in 1945. It was possible to obtain 187 daughter-dam pairs with the daughters coming from 22 different sires. The daughters and dams per sire were distributed as shown in Table 1.

Table 1. The Dams and Daughters Per Sire

<table>
<thead>
<tr>
<th>Sire Number</th>
<th>Dams Per Sire</th>
<th>Daughters Per Sire</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>17</td>
<td>19</td>
</tr>
<tr>
<td>5</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>6</td>
<td>10</td>
<td>12</td>
</tr>
<tr>
<td>7</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>8</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>9</td>
<td>7</td>
<td>6</td>
</tr>
<tr>
<td>10</td>
<td>12</td>
<td>12</td>
</tr>
<tr>
<td>11</td>
<td>10</td>
<td>11</td>
</tr>
<tr>
<td>12</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>13</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>14</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>15</td>
<td>11</td>
<td>12</td>
</tr>
<tr>
<td>16</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>17</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>18</td>
<td>19</td>
<td>19</td>
</tr>
<tr>
<td>19</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>20</td>
<td>11</td>
<td>11</td>
</tr>
<tr>
<td>21</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>22</td>
<td>14</td>
<td>14</td>
</tr>
</tbody>
</table>
The production records were based on a 213 day lactation, milking twice per day, and mature equivalent basis. This is called here the 1944 method of recording production. Most of the production figures were copied directly from the herd book, but nine of the records had to be converted from an older basis to the 1944 basis. The production record beginning nearest to or including the third birthday was used.

The type ratings were made at the third birthday of the cows, and this was usually done by a group of three men. The type rating given was a weighting of the three ratings. The ratings were not wholly independent, as a brief critique of the cows' merits was held just prior to the time of giving the ratings. Type was divided into eighteen categories by subdividing each official class into three subclasses. These were designated as low, middle, and high. For example, the official class of good is divided into low good, middle good, and high good. The classes were assigned numerical values from zero through seventeen in order to obtain a quantitative measure of the type rating.

The weights were taken just prior to the type ratings and consisted of a single weighing. The weights were recorded to the nearest two pounds. In a few instances the scales may not have been breaking properly. Weights taken then could have been forty or fifty pounds in error, but such cases were rare. In some four or five cases the cows were near calving, but no correction was made for pregnancy.

The body measurements consisted of wither height, chest depth, body length, heart girth, and paunch girth. Each measurement used was the average of three independent estimates in order to reduce the random errors of measurement. Wither height was measured at the highest part of the
withers. Chest depth was taken six or seven inches to the rear of the front legs at approximately the shallowest part of the chest. One bar of the calipers was pressed firmly against the back and the other directly below was pressed firmly against the floor of the chest. The distance between the two was recorded as the chest depth. The heart girth was measured at the smallest part of the chest by a steel tape, and the girth of the paunch was measured at the maximum circumference of the paunch. Body length was measured as the horizontal distance from the pin bone to the point of the shoulder. This measurement was taken with large calipers.
ANALYSIS OF DATA

Effects of Errors of Measuring and of Rounding

The type ratings and weights were used just as they were recorded in the books. The weights were subject to considerable error, but no means of correcting these errors was used. The production records are subject to errors in estimating monthly production from one day samples and to errors in converting to a mature equivalent basis.

The body measurements are the average of three independent estimates. These single estimates were subject to a small error variance as shown by Table 2. The average of the three single estimates would be subject to an even smaller error variance: one-third as great. For example

\[ \sigma_{\bar{x}}^2 = \frac{\sigma_x^2}{3}. \]

The averages of the three single measurements were rounded to the nearest centimeter. The errors of rounding would be distributed in a uniform distribution, and this distribution is described by the following function.

Let \( x \) be the error of rounding

\[ f(x) = \frac{1}{x} \text{ for } 0 < x < \delta \]

The mean of \( x \) would be described by the following integral,

\[ \mathcal{E}_{1/3} = \int_0^\delta x \text{d}x = \left[ \frac{x^2}{2} \right]_0^{\delta} = 0 \]
so it is proved that the rounding hasn't affected the mean of the measurements.

Table 2. The Components of Variance Contributing to the Total Variance of Each Body Measurement of 3-Year-Old Cows

<table>
<thead>
<tr>
<th>Component of Variance</th>
<th>Wither height</th>
<th>Chest depth</th>
<th>Body length</th>
<th>Heart girth</th>
<th>Paunch girth</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma_T^2$</td>
<td>13.256</td>
<td>6.258</td>
<td>22.985</td>
<td>54.582</td>
<td>131.757</td>
</tr>
<tr>
<td>$\sigma_B^2$</td>
<td>.258</td>
<td>.127</td>
<td>1.365</td>
<td>.697</td>
<td>.522</td>
</tr>
<tr>
<td>$\sigma_R^2$</td>
<td>.083</td>
<td>.083</td>
<td>.083</td>
<td>.083</td>
<td>.083</td>
</tr>
<tr>
<td>$\sigma_0^2$</td>
<td>13.597</td>
<td>6.468</td>
<td>23.533</td>
<td>55.362</td>
<td>132.342</td>
</tr>
<tr>
<td>$\sigma_T^2 + \sigma_B^2$</td>
<td>13.514</td>
<td>6.385</td>
<td>23.450</td>
<td>55.279</td>
<td>132.299</td>
</tr>
<tr>
<td>$\sigma_0^2$</td>
<td>3.697</td>
<td>2.543</td>
<td>4.851</td>
<td>7.441</td>
<td>11.504</td>
</tr>
<tr>
<td>$\sqrt{\sigma_T^2 + \sigma_B^2}$</td>
<td>3.676</td>
<td>2.527</td>
<td>4.843</td>
<td>7.435</td>
<td>11.500</td>
</tr>
</tbody>
</table>

$\frac{\sigma_0^2}{\sqrt{\sigma_T^2 + \sigma_B^2}}$ = 1.003 1.006 1.002 1.001 1.0003

$\sigma_T^2$ = Variance due to differences between cows.

$\sigma_B^2$ = Variance due to 1/3 random errors of a single measurement.

$\sigma_R^2$ = Variance due to rounding the figures to nearest centimeter.

$\sigma_0^2$ = Total variance.

$\sigma_T^2 + \sigma_B^2$ = Total variance before rounding.

The variance of $x$ can be found by finding the second moment of $x$ about the origin as follows:
\[ \mu_2^{-1} = \int_0^{\infty} x^2 e^{-x^2} \, dx = \left[ \frac{x^3}{3} \right]_0^{\infty} = \frac{1}{12} \]

\[ \mathcal{J}^2 = (\mu_2^{-1}) - (\mu_1^{-1})^2 \quad \text{and} \quad \mathcal{Y}^2 = \frac{1}{12} \]

so the error variance brought in by rounding is 1/12 or .083. This has long been known as "Shepard's Correction" (23). This is shown in Table 2 with the random errors of measuring and the true variance of the cows.

The error variances and cow variances were taken from a previous study on the measurements of cows in this same herd by Touchberry (26). Table 2 shows that the errors of measurement and the errors due to rounding are small as compared with the variance due to the differences between cows.

The influence of these errors upon the observed correlations between characteristics can be shown as follows. Let one variable be represented by \( X \) and another by \( Y \). Let \( \mathcal{J}_X^2 \) be observed variance of \( X \) and \( \mathcal{J}_Y^2 \) the observed variance of \( Y \). \( \Sigma_{XY} \) is the sum of the cross products. \( \mathcal{J}_X^2 = \sqrt{\Sigma_{XY}^2 + \Sigma_{XX} \mathcal{J}_X^2} \) where \( \Sigma_{XX} \) is the variance due to random errors of measuring. Likewise \( \mathcal{J}_Y^2 = \sqrt{\Sigma_{XY}^2 + \Sigma_{YY} \mathcal{J}_Y^2} \).

\[ r_{XX} = \frac{\Sigma_{XX}}{\mathcal{J}_X^2 \mathcal{J}_Y^2} \quad \mathcal{J}_X^2 = \sqrt{\Sigma_{XX}^2 + \Sigma_{XX} \mathcal{J}_X^2} \quad \mathcal{J}_Y^2 = \sqrt{\Sigma_{YY}^2 + \Sigma_{YY} \mathcal{J}_Y^2} \]

\[ r_{XY} = \frac{\Sigma_{XY}}{\mathcal{J}_X \mathcal{J}_Y} \quad r_{XY} = \frac{\Sigma_{XY}}{\mathcal{J}_X \mathcal{J}_Y} \quad \sigma_{XY} = \frac{\mathcal{J}_X \mathcal{J}_Y}{\mathcal{J}_X \mathcal{J}_Y} \]

A very thorough discussion of this is given by Sheehart (22).

From the above relationships one can see the true correlation is larger than the observed correlation unless \( \mathcal{J}_{XX} \) and \( \mathcal{J}_{YY} \) are zero. The
amount by which the true correlation exceeds the observed correlation
depends upon the magnitude of the random errors of measuring. In the
present study the errors of measuring are relatively small as is seen in
Table 2.

The errors of rounding affect the correlations just as random errors
of measuring do. From Table 2, $\sqrt{\sigma^2 + \sigma_r^2}$ is the observed variance before
rounding, and $\sqrt{\sigma^2}$ the variance after rounding. Line 5 of Table 2 gives
the ratio of $\frac{\sigma}{\sqrt{\sigma^2 + \sigma_r^2}}$. In a correlation involving any two of
the variables in Table 2, the effect of rounding may be determined by
multiplying the observed correlation by the product of the corresponding
two ratios in line 5. For example, suppose the observed correlation be-
tween body length and palm girth is .407. The product of the correspond-
ing ratios in line 5 is 1.002, and 1.002 x .407 equals .4076. Rounding
has reduced this correlation by .0008 which is a very small amount.
Rounding also had very little effect on any of the other correlations.
The correlation .407 when corrected for random errors of measuring and for
rounding, becomes 1.002 x .407 = .421. The true correlation has been
reduced by the amount .014 which is trivial.

No estimates of error were made for weight, type, and production, so
no correction for random errors can be made on these variables. In a
correlation involving one of the above variables and a body measurement,
the appropriate figure in line 5 of Table 2 may be used to correct the
correlations, but such corrections are of little importance.

General, Group, and Special Factors

In order to give this study more of a biological interpretation, an
example is used. This example is very much simplified and is by no means as complicated as the actual problem of general, group, and special factors will be. The example is as follows. Suppose X and Y represent two different characteristics of an animal and that each has both genetic and environmental factors acting upon it. These factors are given below.

\[ A = \text{Gene which when present adds 10 to } X. \]
\[ B = \text{Gene which when present adds 10 to } X \text{ and 10 to } Y. \]
\[ C = \text{Gene which when present adds 10 to } X \text{ and 10 to } Y. \]
\[ D = \text{Gene which when present adds 20 to } Y. \]
\[ E = \text{Environmental factor which adds 5 to } X. \]
\[ F = \text{Environmental factor which adds 5 to } X \text{ and } -5 \text{ to } Y. \]
\[ J = \text{Environmental factor which adds 5 to } Y. \]
\[ G_X = \text{Genotype of } X. \]
\[ G_Y = \text{Genotype of } Y. \]
\[ E_X = \text{Environment affecting } X. \]
\[ E_Y = \text{Environment affecting } Y. \]

Given the above information the ratio of the possible genotypes for each characteristic was found. It was then assumed that, one, neither, or both of the environmental factors had an equal chance of appearing with each genotype to which they apply. For example, the genotype AAEECC could appear with \( I, E, \text{ neither}, \text{ or with } E + I; \text{ thus there were four levels of environment for each genotype.} \)

With such a system as outlined above the variance of \( X \) and that of \( Y \) would be due to heredity and environment. The total variance of \( X \) was 164.93 and that of \( Y \) was 345.79. Of the variance of \( X, 152.38 \text{ was genetic variance and } 12.55 \text{ was environmental. Likewise } Y \text{ had a genetic variance of} \)
333.24 and an environmental variance of 12.55. The heritabilities of X and Y are .924 and .961 respectively. From this information paths from the genetic and environmental sources of variance to X and Y can be evaluated. These values are shown in the path coefficient diagram which follows.

From the genetic and environmental factors it is known that Gx and Gy are correlated and that Ex and Ey are correlated. The covariance between Gx and Gy is 101.59 and this is caused by B and G. The correlation between Gx and Gy is \[ \frac{101.59}{\sqrt{152.36 \times 333.24}} = .450 \] and this is a true genetic correlation. The correlation between Ex and Ey can likewise be found and it is \[ \frac{6.475}{\sqrt{12.350 \times 12.350}} = -.500 \]. This environmental correlation is caused by I which has a positive effect on X and a negative effect on Y. With this information the value of the paths in the diagram below can be found.

From the diagram above the correlation between X and Y is found to be made up of a genetic and environmental component. This correlation is
\[ 0.425 - 0.019 = 0.406 \], and it can be attributed to a general or group factor. The covariance of \( X \) and \( Y \) is the amount of variance in each that can be attributed to a general or group factors or both. This covariance is approximated by \( 101.59 - 6.175 = 95.115 \). Fifty-eight percent of the variance of \( X \) and 25 percent of the variance of \( Y \) is traced to common sources which may be general or group factors or both. This leaves 72 percent of the variance of \( Y \) and \( 32 \) percent of the variance of \( X \) which must be accounted for by special factors or sources to which both \( X \) and \( Y \) are not common. The division of the variance of \( X \) and \( Y \) may be diagrammed as group and special factors as shown below. From this one can see the

![Diagram](image)

\( V \) Special factor affecting \( X \) alone.

\( Z \) Group factor affecting \( X \) and \( Y \).

\( W \) Special factor affecting \( Y \) alone.

distinction between genetic and environmental correlations and general and group factors.

To get back to the actual problem of general, group, and special factors a few terms must be explained. The term factor includes those genetic and environmental forces which produce variation in the variables studied. The work factor as used here is not synonymous with the word gene. By a general factor is meant those factors which affect all characteristics...
although perhaps at different magnitudes. A group factor is one which
causes variation in a group of the variables but not in all of them.
Special factors are those which produce variation in only one of the vari-
ables. In this section on General, Group and Special Factors, no attempt
is made to differentiate between the genetic and non-genetic factors.

The statistical method used in this study to analyze the influence of
general, group and special factors is one of least squares and path coef-
ficients. The method was developed by Wright (30) while studying
MacDowell's (19) data on body measurements of rabbits. Nelson (20) also
used this method in studying five body measurements and weight of dairy
 cows. The present study includes type, milk production, and fat production
in addition to the variables studied by Nelson.

The data used in studying general, group, and special factors are
those taken on the daughters. Let the variables be represented as follows:

\[ A = \text{Wither height} \]

\[ B = \text{Chest depth} \]

\[ C = \text{Body length} \]

\[ D = \text{Heart girth} \]

\[ E = \text{Rumah girth} \]

\[ F = \text{Weight} \]

\[ G = \text{Type rating} \]

\[ N = \text{Milk production} \]

\[ I = \text{Butterfat production} \]

\[ S \text{ is the general factor which affects all the variables. Let the path from} \]
\[ S \text{ to } A \text{ be represented by } S_A, \text{ the path from } S \text{ to } B \text{ by } S_B, \ldots, \text{ and the path} \]
\[ S \text{ to } I \text{ by } S_I. \text{ A diagram of these paths is shown in figure } 1. \]
\[ V_x = V_y = 0, \quad V_z = \frac{\partial \phi}{\partial z} = \frac{\partial V}{\partial z} \]

So we have

\[ V_x^2 + V_y^2 + V_z^2 = V^2 \]

where

\[ E_x = \frac{\partial^2 \phi}{\partial x^2} = \frac{\partial^2 V}{\partial x^2} \]

\[ E_y = \frac{\partial^2 \phi}{\partial y^2} = \frac{\partial^2 V}{\partial y^2} \]

\[ E_z = \frac{\partial^2 \phi}{\partial z^2} = \frac{\partial^2 V}{\partial z^2} \]

so that

\[ E_x + E_y + E_z = V^2 \]

Thus the

\[ \Delta x \cdot \Delta y \cdot \Delta z = \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} + \frac{\partial^2 \phi}{\partial z^2} = \frac{\partial^2 V}{\partial x^2} + \frac{\partial^2 V}{\partial y^2} + \frac{\partial^2 V}{\partial z^2} = V^2 \]

Assume that

\[ \Delta x = \Delta y = \Delta z \]

and

\[ E_x = E_y = E_z \]

then

\[ E_x V_x + E_y V_y + E_z V_z = V_x V_y + V_y V_z + V_z V_x \]

Hence

\[ E_x V_x + E_y V_y + E_z V_z = 0 \]

Thus the

\[ \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} + \frac{\partial^2 \phi}{\partial z^2} = \frac{\partial^2 V}{\partial x^2} + \frac{\partial^2 V}{\partial y^2} + \frac{\partial^2 V}{\partial z^2} = \nabla^2 V \]

Hence

\[ \nabla^2 V = 0 \]

Thus the

\[ \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} + \frac{\partial^2 \phi}{\partial z^2} = 0 \]

Hence

\[ \Delta x \cdot \Delta y \cdot \Delta z = \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} + \frac{\partial^2 \phi}{\partial z^2} = \frac{\partial^2 V}{\partial x^2} + \frac{\partial^2 V}{\partial y^2} + \frac{\partial^2 V}{\partial z^2} = \nabla^2 V = 0 \]

Hence

\[ \Delta x \cdot \Delta y \cdot \Delta z = 0 \]

Thus the

\[ \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} + \frac{\partial^2 \phi}{\partial z^2} = 0 \]

Hence

\[ \Delta x \cdot \Delta y \cdot \Delta z = 0 \]
Figure 1: Path Coefficient Diagram of General Factor

Z = General Factor

Z₁ = Paths from Z to Variables
<table>
<thead>
<tr>
<th>θ (°)</th>
<th>β (°)</th>
<th>θ = 0° - 10°</th>
<th>β = 10° - 20°</th>
<th>β = 20° - 30°</th>
<th>β = 30° - 40°</th>
<th>β = 40° - 50°</th>
<th>β = 50° - 60°</th>
<th>β = 60° - 70°</th>
<th>β = 70° - 80°</th>
<th>β = 80° - 90°</th>
</tr>
</thead>
</table>

Legend: θ is the angle at which optical elements meet.
αύξησαν καθώς είχαν λείψανα επιστήμη να την καταλάβει 

δυσμενής προκειμένου καθώς τον είχε σέστησε αυτή την κατάλογο στον θάνατο εκείνη την πρώτη φορά που το έβλεπε.
\[ \Delta_\text{BA} + \Delta_\text{AB} = \Delta_\text{BA} \]

\[ \Delta_\text{BD} + \Delta_\text{DB} = \Delta_\text{BD} \]

\[ (\Delta_\text{BA} + \Delta_\text{AB}) = \Delta_\text{BD} \]

\[ \Delta_\text{BA} \text{ and } \Delta_\text{AB} \text{ are very small so their product approaches zero. Assuming that the product of the two deltas is zero we may write the equations,} \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

Adding the eight equations we get the following equation:

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

\[ E_3(\Delta_\text{BA} + \Delta_\text{AB}) \]

\[ E_3(\Delta_\text{BD} + \Delta_\text{DB}) \]

If we let \( E_3(\Delta_\text{BA} + \Delta_\text{AB}) \) and all to the right of the equality sign in equation (1) equal to \( E_3 \) and then divide both sides through by \( E_3 \) we get the following equation
Table 4. The Estimated and Least Squares, Values of the Paths from the General Factor Z

<table>
<thead>
<tr>
<th>Variable to which path leads</th>
<th>$z_1'$</th>
<th>$\Delta_z'$</th>
<th>$\delta_z$</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>.655</td>
<td>-2.15</td>
<td>.739</td>
</tr>
<tr>
<td>B</td>
<td>.755</td>
<td>-2.25</td>
<td>.585</td>
</tr>
<tr>
<td>C</td>
<td>1.024</td>
<td>-2.35</td>
<td>.766</td>
</tr>
<tr>
<td>D</td>
<td>.569</td>
<td>-1.34</td>
<td>.585</td>
</tr>
<tr>
<td>E</td>
<td>.419</td>
<td>-1.70</td>
<td>.565</td>
</tr>
<tr>
<td>F</td>
<td>.816</td>
<td>-1.90</td>
<td>.560</td>
</tr>
<tr>
<td>G</td>
<td>.206</td>
<td>-1.01</td>
<td>.225</td>
</tr>
<tr>
<td>H</td>
<td>.533</td>
<td>-1.03</td>
<td>.065</td>
</tr>
<tr>
<td>I</td>
<td>-.014</td>
<td>.011</td>
<td>-.003</td>
</tr>
</tbody>
</table>

$z_1'$ = First estimate of the paths

$\Delta_z$ = Correction for first estimate

$\delta_z$ = Least squares solution values for paths

$$\Delta_z = \left[ \frac{T - z^2}{S_z} \right] + z_B \Delta z_B + z_G \Delta z_G + z_D \Delta z_D + z_E \Delta z_E + z_F \Delta z_F +$$

$$z_B \Delta z_B + z_E \Delta z_E + z_I \Delta z_I = \frac{R_2}{S_z} \tag{2}$$

Now taking all of the equations involving $z_B$ and $\Delta z_B$, and treating them as was done above, we get a set of equations whose sum gives equation 3.

$$\Delta z_B = \left[ \frac{T - z^2}{S_z} \right] + z_A \Delta z_A + z_G \Delta z_G + z_D \Delta z_D + z_E \Delta z_E + z_F \Delta z_F +$$

$$z_B \Delta z_B + z_E \Delta z_E + z_I \Delta z_I = \frac{R_2}{S_z} \tag{3}$$

Subtracting equation 3 from equation 2, the following equation is obtained.

$$\Delta z_A = \left[ \frac{T - z^2}{S_z} \right] + z_B \Delta z_B + \Delta z_B \left[ \frac{T - z^2}{S_z} \right] = \frac{R_2}{S_z} \frac{R_2}{S_z} = \frac{R_2}{S_z} \tag{4}$$
Solving this equation for \( \Delta_{2A} \), an answer in terms of \( \Delta_{2B} \) is found. Next the eight equations involving \( \Delta_{G} \) and \( \Delta_{2G} \) are solved for in terms of \( \Delta_{2A} \). This process continues until all \( \Delta_{i} \) are in terms of \( \Delta_{2A} \). Having found these values one can substitute in equation 1 and get the numerical value of \( \Delta_{2A} \). Once \( \Delta_{2A} \) is found the other \( \Delta_{i} \) are easily found by substitution in equations of the type (4). With the corrections found the \( (z_{i})'s \) can be corrected to the \( (z_{i})'s \) or the least square values. These values are given in column 3 of Table 4.

From these least square values of the paths the correlations between any two variables can be calculated. For example, the calculated correlation between \( A \) and \( B \) is \( z_{A}z_{B} \). These calculated values are given in column 2 of Table 3. The third column of this same table is the difference between the actual intra-cies correlations and the calculated correlations. Some of the residuals are quite large and should be tested.

Perhaps the best way to test these residuals is by deriving partial correlations for each pair of variables. Each path is the correlation between \( A \) and the corresponding variable to which the path leads. \( z_{A} \) is the correlation between \( A \) and \( A \). From this it follows that \( r_{AB} = z_{A}z_{B} \) is the numerator of the partial correlation \( r_{AB} \). The necessary numerators are in column 3 of Table 3, so all that has to be calculated are the denominators of the fractions similar to \( r_{AB} = \frac{r_{AB} - z_{A}z_{B}}{\sqrt{(1-z_{A}^{2})(1-z_{B}^{2})}} \).

\( r_{AB} \) is the correlation between \( A \) and \( B \) in a hypothetical case where \( z \) is constant. A partial correlation was calculated for each of the 36 pairs of variables, and these are given in column 4 of Table 3.

One thing to be noted about these partial correlations is the great
This process gave the adjusted calculated values in column 5 of Table 3. It will be noted that the high negative residuals of CI, DK, FH, and H were omitted in determining the factor .613. These intra-sire correlations \( r_{CI}, r_{DH}, r_{FH}, \) and \( r_{H} \) are very small and non-significant and the high partial correlations resulting from them are likely to be mechanical in source.

Column 6 of Table 3 is found by subtracting the adjusted values in column five from the intra-sire correlations in column 1. Column 7 gives the partial correlations based on the \( S_i^2 \) values. One significantly large negative partial correlation \( r_{DH, S} \) still persists along with four other fairly large negative correlations. Only one of these \( r_{AE, S} \) is based on a significant intra-sire correlation, and this partial correlation is not significant. The factor .613 has succeeded in disposing of the important negative residuals.

In column 7 of Table 3 there are several large, positive, partial correlations. The general factor has left a large part of the variance of these variables involved in large partials unaccounted for. Either height is involved in three such correlations. The partial correlations between A and B, A and C, and A and D are all significant. These four variables, A, B, C, and D are hereafter termed the skeletal group because they are largely measurements of skeletal growth. By grouping the six residuals which result from combinations of these four measurements one gets the first column of Table 5. Let \( Y \) represent the sensitive factor which is common to these four variables. This can be called the skeletal group factor.

The evaluation of paths from \( Y \) to each of the variables A, B, C, and
B is done by the same method used in evaluating the paths from R to each of the variables. The values of the paths are given in Table 7. By examining column 6 of Table 7 one can see that the residuals are very small. Column 7 gives a test of these and none is significant. No further adjusting of these paths is necessary in evaluating the skeletal group factor.

Table 5. The Residuals, Calculated and Partial Correlations Used in Determining the Skeletal Group Factor

<table>
<thead>
<tr>
<th>Variables</th>
<th>Residual</th>
<th>$Y_{ij}$</th>
<th>$\Delta_1$</th>
<th>$r_{ij.\hat{y}}$</th>
<th>$Y_{ij}$</th>
<th>$\Delta_1$</th>
<th>$r_{ij.\hat{y}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>AB</td>
<td>.210</td>
<td>.217</td>
<td>-.007</td>
<td>-.009</td>
<td>.184</td>
<td>.026</td>
<td>.032</td>
</tr>
<tr>
<td>AC</td>
<td>.203</td>
<td>.173</td>
<td>.026</td>
<td>.032</td>
<td>.151</td>
<td>.052</td>
<td>.062</td>
</tr>
<tr>
<td>AD</td>
<td>.103</td>
<td>.113</td>
<td>-.004</td>
<td>-.005</td>
<td>.096</td>
<td>.013</td>
<td>.015</td>
</tr>
<tr>
<td>BE</td>
<td>.143</td>
<td>.155</td>
<td>-.011</td>
<td>-.013</td>
<td>.131</td>
<td>.012</td>
<td>.014</td>
</tr>
<tr>
<td>BD</td>
<td>.170</td>
<td>.098</td>
<td>.072</td>
<td>.082</td>
<td>.083</td>
<td>.087</td>
<td>.097</td>
</tr>
<tr>
<td>CD</td>
<td>.017</td>
<td>.086</td>
<td>-.063</td>
<td>-.069</td>
<td>.068</td>
<td>-.051</td>
<td>-.055</td>
</tr>
</tbody>
</table>

Examining again the partial correlations in column 7, Table 3, one discovers that the variables D, E, and F vary together as evidenced by the positive significant correlations. It is noted that D varied with G independent of the general factor. Because of this sizeable residual (.101) based on a significant intra-sire correlation (.208) it seems logical to include G in the group with D, E, and F. This necessitates including the two small residuals, $34 = .048$ and $36 = .071$. This gives a group of four characteristics with variance in each coming from a common source other than the general factor. The three body measurements
$D$, $E$, and $F$ are essentially measurements of flesh, while $G$ is the measurement of type. It seems logical to call this group the flesh and type group and to call their common source of variance the flesh and type factor. This factor will be symbolized by the letter $X$. With four variables and six residual correlations a least squares solution of the paths from the flesh and type factor $X$ to each of the variables $D$, $E$, $F$, and $G$ is possible. These paths are evaluated by the same method as was used previously in evaluating the paths from $Z$ and from $T$. The calculated values $X_iX_j$ are given in column 5 of Table 6 and the residuals in column 6 of the same table. These residuals are small and column 7 of Table 6 gives a test which shows that none is significant. No further adjustment of these paths is necessary as the negative residuals are trivial.

**Table 6. Residuals, Calculated $r^2$s, and Partial Correlations of Flesh Type Group**

<table>
<thead>
<tr>
<th>Variables</th>
<th>Residual</th>
<th>$X_iX_j$</th>
<th>$\Delta_1$</th>
<th>$r_{ij}X$</th>
<th>$X_i'X_j'$</th>
<th>$\Delta_1'$</th>
<th>$r_{ij}'X$</th>
</tr>
</thead>
<tbody>
<tr>
<td>DI</td>
<td>.184</td>
<td>.190</td>
<td>-.006</td>
<td>-.008</td>
<td>.184</td>
<td>-.002</td>
<td>-.003</td>
</tr>
<tr>
<td>DF</td>
<td>.185</td>
<td>.179</td>
<td>.006</td>
<td>.007</td>
<td>.174</td>
<td>.011</td>
<td>.014</td>
</tr>
<tr>
<td>DG</td>
<td>.048</td>
<td>.037</td>
<td>.011</td>
<td>.011</td>
<td>.036</td>
<td>.012</td>
<td>.012</td>
</tr>
<tr>
<td>EF</td>
<td>.428</td>
<td>.429</td>
<td>-.001</td>
<td>-.002</td>
<td>.417</td>
<td>.012</td>
<td>.020</td>
</tr>
<tr>
<td>Eo</td>
<td>.161</td>
<td>.090</td>
<td>.012</td>
<td>.015</td>
<td>.087</td>
<td>.014</td>
<td>.018</td>
</tr>
<tr>
<td>EG</td>
<td>.071</td>
<td>.083</td>
<td>-.014</td>
<td>-.018</td>
<td>.082</td>
<td>-.012</td>
<td>-.015</td>
</tr>
</tbody>
</table>

**Figure 2 gives a path coefficient diagram of the variables and the general, skeletal, and flesh-type factors. The square of any path is the fraction of variance in that particular variable that is caused by**
variance in the source from which the path leads. For example, the variance in \( \sigma \) that is caused by variance in \( z \) is \( (\sigma_{z\sigma})^2 \). The values of all the lettered paths in figure 2 are given in Table 7. It will be noted in figure 2 that a \( F \) is given as a group source of variance for type, and milk and fat production. By observing the residuals in Table 3, one can see that there is a common source of variance for these three variables, but with three unknowns and only three primary equations an exact solution is impossible. Some of the paths have values over one, and this does not fit the proportion of variance hypothesis for the path.

Table 7. Adjusted Values of the Paths from General and Group Factors

<table>
<thead>
<tr>
<th>Variable to which path leads</th>
<th>Source from which path leads</th>
<th>( z )</th>
<th>( y )</th>
<th>( x )</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td></td>
<td>.659</td>
<td>.460</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td></td>
<td>.802</td>
<td>.400</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td></td>
<td>.709</td>
<td>.328</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td></td>
<td>.728</td>
<td>.208</td>
<td>.277</td>
</tr>
<tr>
<td>E</td>
<td></td>
<td>.531</td>
<td>.664</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td></td>
<td>.731</td>
<td>.628</td>
<td></td>
</tr>
<tr>
<td>G</td>
<td></td>
<td>.202</td>
<td>.131</td>
<td></td>
</tr>
<tr>
<td>H</td>
<td></td>
<td>.039</td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td></td>
<td>-.002</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The phenotypic expressions of type and production are related, but a description of this common variance must be left to the partial correlation of Table 3.

The path coefficients are measures of the extent to which the source
Figure 2. Path Coefficient Diagram of General and Group Factors

1. General factor
2. Skeletal group factor
3. Flesh and type group factor
4. Factor which seems to tie up type and production
and variable tend to vary in the same or in a different direction. Table 8 gives the portion of variance in each variable that is caused by variance in the different sources. Where there is no value given the portion of the variance for that particular source is zero. The special factors, W, are factors which affect each variable independently of the other characteristics.

Table 8. Partition of the Variance of the Variables Amongst the Sources.

<table>
<thead>
<tr>
<th>Variable affected</th>
<th>Z</th>
<th>Source of Variance</th>
<th>X</th>
<th>W</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td></td>
<td>.434</td>
<td></td>
<td>.325</td>
</tr>
<tr>
<td>B</td>
<td></td>
<td>.643</td>
<td></td>
<td>.197</td>
</tr>
<tr>
<td>C</td>
<td></td>
<td>.403</td>
<td></td>
<td>.399</td>
</tr>
<tr>
<td>D</td>
<td></td>
<td>.637</td>
<td></td>
<td>.282</td>
</tr>
<tr>
<td>E</td>
<td></td>
<td>.232</td>
<td></td>
<td>.441</td>
</tr>
<tr>
<td>F</td>
<td></td>
<td>.610</td>
<td></td>
<td>.394</td>
</tr>
<tr>
<td>G</td>
<td></td>
<td>.041</td>
<td>.017</td>
<td>.948</td>
</tr>
<tr>
<td>H</td>
<td></td>
<td>trace</td>
<td></td>
<td>1.000</td>
</tr>
<tr>
<td>I</td>
<td></td>
<td>trace</td>
<td></td>
<td>1.000</td>
</tr>
</tbody>
</table>

S General factor.
F Skeletal group factor.
X Type flesh group factor.
W Special factors.

The portion of the variance attributed to each special factor was determined indirectly by subtraction. It will be noted that most of the variance in type, milk production, and fat production has been attributed to special factors. If one assumes milk and butter to be determined by a
production factor, 67.3 percent of the variance in each can be attributed to this group factor. The assumption is a very logical one as butterfat is an integral part of milk.

Another interesting feature of the proportions of variance in Table 8 involves the variable F, or weight. The proportions, .610 due to the general factor, and .394 due to the flesh-type factor, add up to 1.004. This excess is probably due to the rounding of figures in calculating weight is completely determined by the general and the flesh-type factors.

Variance in the general factor is more important in causing variance in the body measurements and weight than it is in determining variance in type and production of milk and butter. The general factor G could very logically be called a general size factor as it exerts most of its influence on size. The least squares method of evaluating the paths has maximized them, but the adjustment to get rid of the significant negative residuals has lowered the paths from the general and group factors. The adjusted values given in Table 7 are perhaps nearer to the actual value of the paths. It remains that the general factor is largely a size factor.

The skeletal group factor, Y, accounts for 24.9 percent of the variance in wither height, 16.8 percent of the variance in chest depth, and 12.7 percent of the variance in body length, but only 5.1 percent of the variance in heart girth. Chest depth, wither height, and body length are more direct measures of the skeleton than is heart girth. Heart girth is an expression of the fleshiness of the animal as well as being an indication of the skeletal size.

The flesh-type group factor, X, contributes more to ymunch girth
and weight than to any other variables. The paunch girth variance is 45.4 percent determined by variance in \( X \), while 40.6 percent of the weight variance is traced to variance in \( X \). Heart girth and type have only 7.9 percent and 1.8 percent, respectively, of their variance attributed to \( X \). Type is only slightly related to the factor \( X \) as is shown by the value of the path \( X^2_0 \) which is only .131.

Milk and fat production are largely independent of the variables other than type as shown in Table 3. These correlations with type are relatively small even though they are significant. Milk and fat production are highly correlated with each other, but are independent of body measurements and weight. Gaines (8) has shown that production of F.S.N. is correlated with weight. His study was on a larger volume of data, and his weights were taken 30 days after calving. He has also shown that correcting for age is approximately equivalent to correcting for weight. In the present study there was some variation in the ages at which the records were made, and consequently they were age corrected. This correction would have tended to remove any weight-production correlations that might have existed.

Type is more closely related to production and weight than to any other variables. These relationships are small, \( r_{F0} = .229 \), \( r_{OY} = .182 \), and \( r_{G1} = .255 \), and 94.2 percent of the variance of type is determined by a special factor. This special factor is perhaps largely balance of parts, condition of animal, and opinion of the judge. The genetic part of this special factor is not known at present. The general, skeletal, and flesh-type factors are unimportant sources of variance for type, milk production, and fat production.
Estimates of Genetic Correlations and Heritability

An estimate of the genetic proportion of each observed intra-sire correlation between characteristics given in column 1 of Table 3 may be made by using the following method. To explain the method consider the variables wither height and chest depth. Correlate wither height in the dam with chest depth in the daughter and then wither height in the daughter with chest depth in the dam. The average of these two will give the phenotypic correlation due to genetic causes. It will not be a true genetic correlation because of the phenotypic variance in the denominator. That is, its numerator is one-half the genetic covariance, but its denominator is the phenotypic variance. A true genetic correlation involves only genetic variances as will be shown later.

Using the above method the figures in columns 2 and 3 of Table 9 were obtained. Column two gives the phenotypic correlations due to genetic causes. Column 3 shows what fraction of each intra-sire phenotypic correlation is genetic. This table helps to explain the meaning of the various correlations. For example, the correlation between chest depth and wither height is .738, and .675 of this is due to genetic causes. The correlation between type and butterfat production is .250, and none of it is due to genetic causes. Phenotypic correlations are not certain indicators of a common genetic cause.

A true genetic correlation is the correlation between two genotypes in the same animal. For instance the correlation between the genotype for wither height and the genotype of the same animal for chest depth is a true genetic correlation. The method used to estimate genetic correlations is that developed by Hazel (13). This author shows that we may
There are several approaches to estimating the correlation coefficient. In one approach, the correlation coefficient is defined as

\[ r_{xy} = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2 \sum (y_i - \bar{y})^2}} \]

where \( x_i \) and \( y_i \) are the individual observations, and \( \bar{x} \) and \( \bar{y} \) are the sample means. This formula gives a measure of the linear dependence between the two variables.

In another approach, the correlation coefficient is defined in terms of the covariance and the standard deviations:

\[ r_{xy} = \frac{\text{Cov}(x, y)}{\sigma_x \sigma_y} \]

where \( \text{Cov}(x, y) \) is the covariance between \( x \) and \( y \), and \( \sigma_x \) and \( \sigma_y \) are the standard deviations of \( x \) and \( y \), respectively.

Both approaches yield the same result, but the latter is more convenient when working with population parameters.
Figure 3. Diagram of a Genetic Correlation

$x_1$ = Phenotypic expression of wither height in dam.

$x_1^j$ = Phenotypic expression of wither height in daughter.

$x_j$ = Phenotypic expression of chest depth in dam.

$x_j^j$ = Phenotypic expression of chest depth in daughter.

$e$ = Environment in all cases.

$g_1$ = Genotype for wither height in dam.

$g_1^j$ = Genotype for wither height in daughter.

$g_j$ = Genotype for chest depth in dam.

$g_j^j$ = Genotype for chest depth in daughter.

$r$ = Relationship of animals, dam and daughter.

$y$ = The genetic correlations to find.
Figure 4. Path Coefficient Diagram of Desired Correlations

From figures 3 and 4 it is apparent that the problem of estimating 
$r_{G_fG_j}$ is one of evaluating $y$. From daughter and dam comparisons it is 
possible to get two estimates of $y$. These will be called $y_1$ and $y_2$.

These are derived as follows:

$$\hat{y}_1 = \sqrt{\frac{r_{G_fG_j} \cdot r_{X_fX_j}}{r_{G_fI} \cdot r_{X_fI}}}$$

$$\hat{y}_2 = \sqrt{\frac{r_{G_fG_j} \cdot r_{X_fX_j}}{r_{G_fI} \cdot r_{X_fI}}}$$

and $y$ can now be defined as the geometric mean of these two estimates.

This is expressed below in terms of correlations and covariances.

Hazel (19) has shown that

$$y = \sqrt{\frac{r_{X_fX_j} \cdot r_{X_fX_j}}{r_{X_fX_j} \cdot r_{X_fX_j}}} = \sqrt{\frac{\text{Cov. } X_fX_j}{\text{Cov. } X_fX_j}} \cdot \sqrt{\frac{\text{Cov. } X_fX_j}{\text{Cov. } X_fX_j}}$$
it may be expressed in regressions also. Then one variable is selected
regressions may be preferred, but it makes no difference because all
variances are in the denominator and numerator alike. The only factors
that don’t cancel out are the covariances.

How do environmental errors and non-random mating with different
intensities of selection in the subgroups affect the estimates of \( \gamma \)? The
effects of non-random mating with different intensities of selection in
the subgroups of a population would be in both numerator and denominator
alike and would tend to cancel out. The effects of selection in these
data are negligible as dam and daughter are selected to about the same
degree. If the effects of selection were important they would be in both
numerator and denominator. Correlations arising from environmental
sources might be in both numerator and denominator, but it is a question
whether they would influence both in the same magnitude. For example,
environment conceivably could cause the covariance of \( X_1X'_1 \) to be higher
than that of \( X_2X'_2 \). Suppose \( X_1 \) were milk production and \( X_2 \) were wither
height. It seems logical that good environment could influence production
more than it would wither height and would tend to make the denominator
larger than the numerator. This study was done on an intra-sire basis so
as to take out any environmental time trends. Any other environmental
components could be estimated roughly by correlating the dam with the
stall mates of the daughter. These environmental portions were assumed
to be small in this study and were not considered because all the data
were from one herd and in each correlation the two items were not many
years apart.

Nine estimates of heritability were made and environmental errors
can affect these very much. The closer the relatives used in estimating heritability the smaller will be the errors due to environment. This is because the environmental error between relatives is relatively smaller as the relative pairs are more closely related.

The raw graph shows heritability changes. To show this observe Figure 5, which is taken from Lush's (19) monograph on genetics. Figure 5 is a genetic diagram that shows the relationship between genetic and environmental effects on a phenotype. The figure illustrates the concepts of additive, dominance, and epistatic effects.

Figure 5: Genetic Diagram of the Relationship Between Phenotype

- Phenotype value
- Environmental effects
- Additive genetic effects
- Dominance effects
- Epistatic effects

In the diagram, the phenotype value is influenced by the additive genetic effects, dominance effects, and environmental effects. The relationship between these factors is complex and requires detailed analysis to understand fully.
The value is very near 180°. The vector is not described in the text, but it is clear that the vector is composed of two components, $\vec{A}$ and $\vec{B}$. The angle between these two vectors is given by $\theta = \arccos \left( \frac{\vec{A} \cdot \vec{B}}{\|\vec{A}\| \|\vec{B}\|} \right)$.

The magnitude of the vector $\vec{C}$ is given by $|\vec{C}| = \sqrt{\vec{A}^2 + \vec{B}^2 - 2\vec{A} \cdot \vec{B}}$. The components of $\vec{C}$ are $C_x = A_x B_y - A_y B_x$ and $C_y = A_x B_x + A_y B_y - C_z$. This implies that the projection of $\vec{C}$ onto the $x$-axis is $A_x B_y - A_y B_x$.
The correlation coefficients given in Table 1, the correlation coefficients given in Table 2, and the correlation coefficients given in Table 3 are all positive. However, the correlation coefficients given in Table 4 are all negative. The correlation coefficients given in Table 5 are all zero.

The correlation coefficients given in Table 6 are all positive, except for the correlation coefficient between the variables X and Y, which is negative. The correlation coefficients given in Table 7 are all positive, except for the correlation coefficient between the variables Z and W, which is negative. The correlation coefficients given in Table 8 are all positive, except for the correlation coefficient between the variables U and V, which is negative. The correlation coefficients given in Table 9 are all positive, except for the correlation coefficient between the variables T and S, which is negative. The correlation coefficients given in Table 10 are all positive, except for the correlation coefficient between the variables R and Q, which is negative.
<table>
<thead>
<tr>
<th>0</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>I</td>
</tr>
<tr>
<td>7</td>
<td>X</td>
</tr>
<tr>
<td>00</td>
<td>0</td>
</tr>
<tr>
<td>06</td>
<td>6</td>
</tr>
<tr>
<td>26</td>
<td>2</td>
</tr>
<tr>
<td>61</td>
<td>1</td>
</tr>
<tr>
<td>96</td>
<td>0</td>
</tr>
<tr>
<td>100</td>
<td>0</td>
</tr>
<tr>
<td>76</td>
<td>7</td>
</tr>
</tbody>
</table>

**Table:**

The inter-column correlations were higher when the following:

- Temperature
- Humidity
- Light intensity
- Wind speed
- Soil moisture

**Note:**

The values in this table represent the correlation coefficients between the variables listed above. Higher values indicate a stronger correlation. The exact implications of these correlations would depend on the specific context of the study. The table suggests that certain environmental factors may influence each other in complex ways, which could be explored further in future research.

---

*To some researchers and keep conducting to gather these estimates more.*
Table 10 were used. The figures on the diagonal from upper left to lower right went into the denominator of the formula, and those off this diagonal went in the numerator. For example, the genetic correlation between either height and weight involved four figures.

\[ r = \sqrt{\frac{.212 \times .154}{.363 \times .185}} = \sqrt{.437} = .698. \]

Where all of the intra-sire correlations were positive there was no trouble in deriving the genetic correlations given in Table 11. When both members of the numerator were negative there was no trouble. In some cases the numerator of the radical included a positive and a negative number. In most of these cases the intra-sire correlations were not significant and the genetic correlation could be called zero. An attempt was made to evaluate the genetic correlations based on these small positive and negative intra-sire correlations by using the method developed by Hazel (13).

The intra-sire correlation -.085 between type of dam and type of daughter was called zero. It was assumed that this \( r \) was due mainly to large errors that can creep into single classifications and to sampling errors. Tylor (28) found a heritability of 0.30 for single type ratings, but his volume of data included 3,738 daughters out of 1,601 dams. His estimate is no doubt a better estimate of type in general. The arithmetic or geometric means of the intra-sire correlations of Table 10 involving type are all smaller than the value .157 required for significance. By calling the genetic variance of type zero no valuable information has been lost, for type seems to be genetically independent, or nearly so, of
the other variables studied.

If the -0.085 were significant or had meaning, what would it mean?
It would mean that the lower type dams would have higher type daughters
and the higher type dams would have lower type daughters. It would also
mean that 0.025 of the variance in daughter type would be produced by
genetic variances of type in the dam. The biology of a negative herit-
bility is very hard to explain. The following explanation was suggested
by Lush. If overdominance were real and the poorest dams had been culled,
a negative heritability would result. This is best shown by the follow-
ing diagram. The curved line is the regression of phenotype on genotype

Desirability of
Phenotype

Desirability of Genotype

in an unselected population while the straight line is the regression of
phenotype on genotype when the poorest dams are allowed to have no calves.
There is no proof that this is the cause of the negative correlation, so
the heritability of type was given a value of zero.

Grouping the genetic correlations on the basis of the number of
significant intra-sire correlations on which they were based, three groups
were found. In one group the combinations of the variables A, B, C, D,
and F are found. All of the correlations between these five were based
on four significant intra-sire correlations except for one. This one
was $r_{gd}$ which involved three significant intra-sire correlations. This
group is composed of skeletal measurements and weight. The highest
genetic correlation .883 was found between heart girth and weight, and
the correlation .936 between chest depth and heart girth is the next
largest. These two are followed closely by the correlation .831 between
body length and weight.

Comparing these genetic correlations (column 2, Table 12) to the
phenotypic correlations given in column 1 of Table 12, one can see close
agreement. The genetic correlations are larger than the phenotypic corre-
lations in all cases except one. The smaller phenotypic correlations
can be attributed to the action of environment on the animals. The en-
vIRONMENT causes the phenotypes of the various characteristics to vary
more independently of each other than they would if heredity were the
only source of variance. The effect is similar to introducing an error
in measurements or weight. In the case of the one genetic correlation,
$r_{gd}$, which was smaller than the corresponding phenotypic correlation
there may be a strong environmental component at work. A cow with a
long body would seemingly have a larger heart girth. The two correla-
tions are not significantly different, so the difference could be purely
a mechanical one.

The next two groups include those genetic correlations based on two
and one significant intra-sire correlations. The variables involved are
$H$, $S$, and $I$ in combination with each other and in combination with the
skeletal measurements and weight. These estimates of genetic correlations
are not very reliable, especially those involving $H$ and $I$ in combina-

Figure 6. Path Coefficient Diagram of the General, Group, and Special Genetic Factors
### Table 12. Correlations And Residuals For The General Genetic Factor

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>r</th>
<th>Genetic r</th>
<th>$v_{ij}$</th>
<th>$\Delta_{ij}$</th>
<th>$r_{ij}U$</th>
<th>$v'_{ij}U$</th>
<th>$\Delta'_{ij}$</th>
<th>$r'_{ij}U$</th>
</tr>
</thead>
<tbody>
<tr>
<td>FA</td>
<td>.738</td>
<td>.307</td>
<td>.755</td>
<td>.052</td>
<td>.230</td>
<td>.575</td>
<td>.233</td>
<td>.557</td>
</tr>
<tr>
<td>AG</td>
<td>.670</td>
<td>.301</td>
<td>.679</td>
<td>.122</td>
<td>.379</td>
<td>.517</td>
<td>.284</td>
<td>.538</td>
</tr>
<tr>
<td>AD</td>
<td>.634</td>
<td>.546</td>
<td>.707</td>
<td>-.061</td>
<td>-.209</td>
<td>.596</td>
<td>.108</td>
<td>.234</td>
</tr>
<tr>
<td>AN</td>
<td>.274</td>
<td>.137</td>
<td>.424</td>
<td>-.277</td>
<td>-.566</td>
<td>.315</td>
<td>-.178</td>
<td>-.285</td>
</tr>
<tr>
<td>AT</td>
<td>.534</td>
<td>.692</td>
<td>.763</td>
<td>-.065</td>
<td>-.304</td>
<td>.581</td>
<td>.117</td>
<td>.285</td>
</tr>
<tr>
<td>AG</td>
<td>.135</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AK</td>
<td>.021</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AI</td>
<td>.009</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BG</td>
<td>.721</td>
<td>.758</td>
<td>.753</td>
<td>.005</td>
<td>.021</td>
<td>.573</td>
<td>.185</td>
<td>.440</td>
</tr>
<tr>
<td>BD</td>
<td>.810</td>
<td>.838</td>
<td>.784</td>
<td>.055</td>
<td>.263</td>
<td>.597</td>
<td>.242</td>
<td>.604</td>
</tr>
<tr>
<td>BE</td>
<td>.425</td>
<td>.514</td>
<td>.659</td>
<td>.055</td>
<td>.139</td>
<td>.349</td>
<td>.165</td>
<td>.305</td>
</tr>
<tr>
<td>BF</td>
<td>.665</td>
<td>.715</td>
<td>.846</td>
<td>-.131</td>
<td>-.653</td>
<td>.644</td>
<td>.071</td>
<td>.200</td>
</tr>
<tr>
<td>BG</td>
<td>.183</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BE</td>
<td>.015</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BI</td>
<td>.009</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GD</td>
<td>.583</td>
<td>.555</td>
<td>.705</td>
<td>-.150</td>
<td>-.513</td>
<td>.537</td>
<td>.012</td>
<td>.039</td>
</tr>
<tr>
<td>GE</td>
<td>.404</td>
<td>.179</td>
<td>.413</td>
<td>-.234</td>
<td>-.477</td>
<td>.314</td>
<td>-.136</td>
<td>-.294</td>
</tr>
<tr>
<td>GF</td>
<td>.701</td>
<td>.631</td>
<td>.761</td>
<td>.069</td>
<td>.320</td>
<td>.580</td>
<td>.251</td>
<td>.611</td>
</tr>
<tr>
<td>GG</td>
<td>.151</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GH</td>
<td>.022</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GI</td>
<td>.098</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EB</td>
<td>.647</td>
<td>.788</td>
<td>.450</td>
<td>.358</td>
<td>.302</td>
<td>.327</td>
<td>.460</td>
<td>.771</td>
</tr>
<tr>
<td>EF</td>
<td>.608</td>
<td>.693</td>
<td>.792</td>
<td>.091</td>
<td>.463</td>
<td>.609</td>
<td>.280</td>
<td>.709</td>
</tr>
<tr>
<td>EG</td>
<td>.210</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EH</td>
<td>.003</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EI</td>
<td>.086</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BT</td>
<td>.542</td>
<td>.685</td>
<td>.464</td>
<td>.221</td>
<td>.673</td>
<td>.353</td>
<td>.332</td>
<td>.625</td>
</tr>
<tr>
<td>BT</td>
<td>.208</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BH</td>
<td>.002</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BI</td>
<td>.026</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BS</td>
<td>.289</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BS</td>
<td>.044</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BI</td>
<td>.060</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BX</td>
<td>.182</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BI</td>
<td>.258</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HI</td>
<td>.571</td>
<td>.707</td>
<td>.009</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
beginning of the section on general, group, and special factors so that
he may see how general, group, and special genetic factors arise.

In determining the general genetic factor the genetic correlation
between milk and butterfat is not included, for M and I are not
geneically related to any of the other variables. This left A, E, C,
B, E, and F to determine the general genetic factor. The method was
the same as that used to determine the general factor for the phenotypes.
A discussion of this method can be found on pages 23 to 30. Column 6 of
Table 12 gives the genetic relationships between the variables that can
be attributed to a general genetic factor. Column 7 of this same table
contains two rather large negative residuals. Both of these involve
paunch girth. As was discussed earlier, the genetic correlations in-
volving paunch girth are based on only 1 and 2 significant intra-sire
correlations. The two negative residuals, rAB and rCF, are based on
only one significant intra-sire correlation so such could be expected.
The paths from the general genotype to each genotype are given in
Table 13.

Some of the genetic residuals in column 7 of Table 12 are large and
positive. The residuals involving A, E, C, B, and F were considered as
a skeletal-weight group, and H and I formed a production group. The
least squares solution for the skeletal-weight group paths is given in
Table 13. The genetic correlations that can be attributed to the genetic
skeletal-weight group factor are found in column 5. The paths from the
skeletal-weight genetic group are given in Table 14.

Milk production and fat production are not related to the general
genetic factor or to the skeletal-weight genetic factor, but are highly
From 21.6 to 65.1 percent of the general population in those countries in which
the body measurements a, b, c, d on the General Chart are

Table IJ gives the proportion of minutes of rotation of each General Palance

| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
|-------------------------------|
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  
| 1° 2° 6° 6° 1° 1° 1° 9° 2° 9° | a  

Table IJ. Least Square Solution for General-Weight Group Factor

and weight.

several to depression with other weights, above depth, body length, height.

and weight.

and weight.

and weight.

and weight.

and weight.

and weight.

and weight.

and weight.

and weight.
due to a general factor. This is evidence of the manifold effects of genes for linkage and non-random mating have an infinitesimal influence in a population of this nature. The effects of the genes are manifold as have been observed because the genes affect the size of the body in general and therefore affect all or most of the measurements of size.

The skeletal-weight genetic factor accounts for 6 to 16.6 percent of the genetic variances in the variables A, B, C, D, and F. Most of the genetic relationship between these five variables is that due to a general genetic factor. From 24.5 to 38.1 percent of the genetic variance in these five is due to special genetic factors. Each variable has a special genotype independent of the others which accounts for approximately one-third of its genetic variance. Some of this variance may be due to sampling errors.
If the production genetic factor can be taken as valid, it shows some interesting things. Here is a genetic factor accounting for .706 more than two-thirds of the genetic variance in each milk production and butterfat production. The rest of the genetic variance of each variable, 29.3 percent, is determined by special genetic factors. From this it follows that approximately 50 percent of the genetic variance of fat production is associated with changes in the genotype for milk production. When a breeder selects for one of the two he gets many genes which affect both variables. If he were selecting for butterfat production alone, approximately two-thirds of his genetic improvement would be from genes that would affect milk production also. Fat is an integral part of milk, and a high genetic correlation between the two is to be expected.

Table 15. Partitioning Each Genetic Variance Among the General, Group, and Special Genetic Factors

<table>
<thead>
<tr>
<th>Genetic Variance</th>
<th>Y</th>
<th>Z</th>
<th>Special Factors</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>.519</td>
<td>.166</td>
<td>0</td>
</tr>
<tr>
<td>B</td>
<td>.657</td>
<td>.139</td>
<td>0</td>
</tr>
<tr>
<td>C</td>
<td>.516</td>
<td>.123</td>
<td>0</td>
</tr>
<tr>
<td>D</td>
<td>.559</td>
<td>.060</td>
<td>0</td>
</tr>
<tr>
<td>E</td>
<td>.192</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>F</td>
<td>.651</td>
<td>.101</td>
<td>0</td>
</tr>
<tr>
<td>G</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>H</td>
<td>0</td>
<td>0</td>
<td>.707</td>
</tr>
<tr>
<td>I</td>
<td>0</td>
<td>0</td>
<td>.707</td>
</tr>
</tbody>
</table>


DISCUSSION

Heritabilities

The estimates show that more than one-half of the variance in skeletal measurements A, B, C, and D, is genetic variance. Environment plays a less important role on the development of the bone than it does on the size of the paunch, type rating, weight or production. This supports a theory that the growth impulse in the bone is stronger than in any other part or system of the body. The bone will grow at the expense of the other parts of the body. Just a glance at the genetic correlation between these four variables shows that they are highly related.

Observing the heritability figures for paunch girth, weight, type, milk production, and fat production, one sees that environment plays by far the larger role in determining the phenotypic variance. It is easy to visualise how the amount and kind of feed can influence the weight, paunch girth, and appearance. This will also greatly influence milk and butterfat production. The stage of pregnancy can also affect the paunch girth and weight, and it may influence the type rating. Heredity plays a lesser role in determining the phenotypic variance of the variables B, E, G, H, and I.

In this study, type was given a heritability value of zero. Judging from the phenotypic correlations, type is influenced by the size and
...
There may be a physiological reason for these correlations, for a tall, long, and heavy cow would tend to have a large udder regardless of genotype for udder. The genetic correlations involving udder are based on very small intra-breed correlations, so the estimates of these genetic correlations could easily be underestimated due to sampling errors.

One other of the five divergent correlations is that between body length and heart girth. The phenotypic correlation for $r_{xy}$ is .028 larger than the genetic correlation. This genetic correlation is based on three significant intra-breed correlations and one just smaller than the level of significance. The correlation is mechanically sound so the explanation must lie in sampling errors or environmental correlations.

One other case of a higher phenotypic than a genetic correlation is that between milk production and fat production. Tyler (27) found the same to be true. This would be expected as butterfat is an integral part of milk and the production of butterfat will depend upon the production of milk. Most environmental variations which could affect the amount of milk would affect, in the same direction, the amount of butterfat produced. The amount of butterfat would be more influenced by environment than the percent of butterfat. Tyler (27) has shown this to be true and it is in accord with popular experience generally.

The correlations may be divided into three groups. Those involving the relationships between wither height, chest depth, body length, heart girth, udder girth, and weight can be put in one group. Another group would be composed of just those correlations involving type, and the third group would be those involving butterfat and milk production.

This grouping is essentially the same as that used in studying general,
heredity, but weight is highly correlated to the general genetic factor and influenced by the skeletal-weight genetic factor. These large effects of the general genetic and skeletal-weight genetic factors on weight are probably brought on by their effects on the skeleton, for weight would be influenced by the size of the skeleton.

The second group involves the correlations of type with the other variables. In these data, variations in type seem to have no genetic basis. This is not true in general for Tyler (26) has shown that type is inherited, and breeders have been successful in changing type over a long period of years. In swine, type has been changed in relatively short periods from big type to small type and vice versa. In these data type has no genetic relationship to any of the other variables. It is phenotypically correlated with some of the variables, for example, weight, butterfat, and milk production, but this correlation appears to have been due to common environmental variations. Type includes many things not covered in this study.

Milk and butterfat production compose the third group. These two variables are highly correlated with each other genetically and phenotypically. They are not genetically correlated with body measurements, weight, or type, and they form a group by themselves. This group is called the production group. Production is phenotypically related to type. Type includes the development of the mammary system, and this relationship could come about through this channel. The genes for production affect to a great extent both milk and butterfat production. Perhaps it is not sound to call the correlation between milk and butterfat a genetic correlation. It may be more of an automatic correlation
(Lush 16), as butter is an integral part of milk and thus the correlation of milk and fat is between a cow and one of its parts. If a cow produces a certain quantity of milk perhaps she cannot produce less than a certain amount of butterfat.

Comparing the genetic correlations found in this study with those which can be obtained from Tables 2 and 4 of Gowan’s (9) work, one finds fairly close agreement. In Gowan’s work Table 2 pertains to the correlations between the conformation of the sire and that of his daughter, while

<table>
<thead>
<tr>
<th>Genetic</th>
<th>( r_0^1 )</th>
<th><strong>Gowan’s Data</strong></th>
<th><strong>Present Data</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>AB</td>
<td>.335</td>
<td>.509</td>
<td>.907</td>
</tr>
<tr>
<td>AG</td>
<td>.712</td>
<td>.530</td>
<td>.901</td>
</tr>
<tr>
<td>AD</td>
<td>.499</td>
<td>.634</td>
<td>.646</td>
</tr>
<tr>
<td>AB</td>
<td>.384</td>
<td>.513</td>
<td>.137</td>
</tr>
<tr>
<td>AF</td>
<td>.953</td>
<td>.735</td>
<td>.698</td>
</tr>
<tr>
<td>BD</td>
<td>.709</td>
<td>.795</td>
<td>.758</td>
</tr>
<tr>
<td>BD</td>
<td>.740</td>
<td>.913</td>
<td>.638</td>
</tr>
<tr>
<td>BB</td>
<td>.712</td>
<td>.822</td>
<td>.514</td>
</tr>
<tr>
<td>BF</td>
<td>.679</td>
<td>.679</td>
<td>.715</td>
</tr>
<tr>
<td>CD</td>
<td>.894</td>
<td>.771</td>
<td>.555</td>
</tr>
<tr>
<td>CB</td>
<td>1.047</td>
<td>.797</td>
<td>.799</td>
</tr>
<tr>
<td>CF</td>
<td>.336</td>
<td>.399</td>
<td>.931</td>
</tr>
<tr>
<td>EF</td>
<td>.667</td>
<td>.923</td>
<td>.768</td>
</tr>
<tr>
<td>EF</td>
<td>.599</td>
<td>.529</td>
<td>.583</td>
</tr>
<tr>
<td>FF</td>
<td>.465</td>
<td>.527</td>
<td>.465</td>
</tr>
</tbody>
</table>

Table 4 involves the dam and daughter comparisons. These are given above along with the genetic correlations derived from the present study. The correlations \( r_{AB}, r_{CB}, \) and \( r_{CF} \) have quite different values in the

---

"*By applying the formula \[ \sqrt{\frac{XY' \cdot XY}{XX' \cdot YY'}} \] where \( X \) and \( Y \) are the characters measured and the primes indicate that it pertains to a parent instead of the offspring."
\[ \text{Εκπροσωπίζω από την ΰπτασμα του άλλου με αυτό που έγινε} \]

(1 - 260°) (€360° - ε360°) = ε360° (€360° - ε360°)

(260° - €360°) = ε360° (€360° - ε360°)

έγινε από την ΰπτασμα του άλλου με αυτό που έγινε.
Figure 7. Path Coefficient Diagram of the Paths $Z_i \rightarrow X_i$ and $G_i \rightarrow X_i$
<table>
<thead>
<tr>
<th>f10°</th>
<th>f20°</th>
<th>f30°</th>
<th>...</th>
</tr>
</thead>
<tbody>
<tr>
<td>87°</td>
<td>86°</td>
<td>85°</td>
<td>...</td>
</tr>
<tr>
<td>86°</td>
<td>85°</td>
<td>84°</td>
<td>...</td>
</tr>
<tr>
<td>85°</td>
<td>84°</td>
<td>83°</td>
<td>...</td>
</tr>
</tbody>
</table>

Note: The table represents experimental data. The correlation between the different components' properties is shown.
της σειράς των επανεμφανιστών επαναστάτων μετά την κατάρρηση της πολιτείας. Σκέφτηκε ότι ο Αθηναίοι θα προωθούσαν την κατάρρηση με την επίθεση εμπορευματικών, επιδόσεων και εισφορών, αλλά οι πολίτες της πόλης θα αντιστοίχιζαν και θα μεταμορφώνονταν σε επαναστάτες. Ωστόσο, οι Αθηναίοι δεν θα μπορούσαν να αντιστοιχήσουν στην επίθεση, αλλά θα προωθούσαν με την επίθεση εμπορευματικών, επιδόσεων και εισφορών. Ωστόσο, οι πολίτες της πόλης θα αντιστοίχιζαν και θα μεταμορφώνονταν σε επαναστάτες.
factor. Those which affect a few would be grouped under a group genetic factor, and those genetic factors affecting only one characteristic would be grouped under special genetic factors.

A breeder cannot select for the general genetic factor derived in this study and make progress in all nine of the variables studied. If he selected for the general factor his progress would be mainly an increase in the size of the body measurements and weight. Production and type would be influenced very little by selection for the general genetic factor. To improve production the breeder would do better just to consider production. Milk production and butterfat production form a group by themselves and this group is genetically unrelated to the other variables. If the breeder is mainly interested in money from production, his efforts should be exerted solely on breeding for production. If the breeder is getting returns from animals because of high type rating, then he can afford to exert some effort on improving the type of his animals. The weighting given to type and production in an index should depend on the economic value of each.

Where a breeder is mainly interested in efficiency of production, his index probably should be based on milk energy yield per unit of live weight. This would result in selecting the most economical producers on an energy basis. In some areas the breeder would want a large quantity of milk for fresh milk markets. In this case his efforts should go largely towards a large quantity of milk with the minimum amount of fat necessary to meet requirements. A breeder in another region may have a market for butterfat, so naturally his efforts should go towards improving butterfat production. There is no fixed index for all cases, but each index for
CONCLUSIONS

1. The genetic correlation of .707 between milk production and butterfat production is evidence that there are pleiotropic genes affecting both. Environmental effects cause the phenotypic expression of milk production and butterfat production to vary in the same direction more than the genetic correlation would alone.

2. The six characteristics, wither height, chest depth, body length, heart girth, paunch girth, and weight are affected by pleiotropic genes. As these characteristics are all measures of size the pleiotropic genes must be genes which affect size in general.

3. If the measures of production, milk and butterfat, are genetically correlated with body measurements and weight these correlations must be relatively small.

4. More of the variation in the skeletal measurements wither height, chest depth, body length, and heart girth is attributed to heredity than to environment. The heritabilities of these four characteristics were .728, .801, .576, and .616, respectively.

5. More of the variation in the flesh measurements, paunch girth and weight, is attributed to environment than to heredity. The heritability of these two was .265 and .370, respectively.

6. More than half of the variation in milk production and butterfat production is environmental. The heritability of these two was .254 and .350, respectively.
7. Selection for size in dairy cattle should be very successful. Progress in selecting for size should be much greater than progress in selecting for production.

8. Type is phenotypically correlated with weight, milk production, and butterfat production.
SUMMARY

The data on 137 daughter-dam pairs were used to study phenotypic correlations, genetic correlations, and heritability of five body measurements, weight, type rating, milk production and butterfat production. This gave nine estimates of heritability and 36 estimates of genetic and 36 estimates of phenotypic correlations. The measurements, weight, and type were recorded at the animal's third birthday. The production records nearest to or including the third birthday were used to estimate production of both milk and butterfat.

From the 36 phenotypic correlations between the nine variables, general, group, and special factors were derived. These factors include those genetic and environmental forces which cause phenotypic variations in the nine variables studied. The general factor had only a trace of an effect on milk production and butterfat production, and it accounted for only 0.1 percent of the variance in type rating. The general factor accounted for from 29.2 to 47.3 percent of the variance in the five body measurements and weight. The skeletal group factor accounted for 21.2, 16.0, 10.8, and 4.7 percent of the variance of either height, chest depth, body length, and heart girth respectively, while the flesh-type group factor accounted for 7.8, 44.1, 39.4, and 1.7 percent of the variance in heart girth, punch girth, weight, and type respectively. The special factors were of more importance to type, milk production, and fat production for they accounted for 94.2 percent of the variance of type and
The General Assembly and the Executive Committee of the General Assembly of the United Nations have agreed to the following:

The General Assembly has noted with appreciation the agreement reached on 24 December 1947 between the government of the United Nations and the government of the State of Israel on the status of Jerusalem.

The General Assembly has decided to hold its session in Jerusalem on 24 December 1947.
LITERATURE CITED


18. ______ Unpublished naniogaphed notes. 1948.


ACKNOWLEDGMENT

The writer wishes to express his gratitude to
Dr. J. L. Lush and to Dr. L. H. Hazel for constructive
criticisms and suggestions during the preparation of
this thesis.