GENETIC AND ENVIRONMENTAL VARIATION IN TEN-WEEK BODY WEIGHT, TEN-WEEK BREAST ANGLE, HATCHABILITY AND RESISTANCE TO DEATH TO TEN WEEKS

OF AGE IN THE DOMESTIC FOWL

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INTRODUCTION

The broiler industry has become a highly competitive segment of the poultry industry in the United States. In order for broiler growers to prosper, they must have birds that will produce a large amount of meat with a relative low intake of feed per pound of meat produced. Several factors are of primary concern, but the most important single factor is growth rate. Growth rate in broilers is usually measured by body weight attained at broiler age.

In order for the hatcheryman to prosper, he must be able to supply broiler growers with chicks that will meet their needs. In addition, he must have birds that reproduce efficiently. The measuring stick here is the number of eggs laid per bird and the hatchability of these eggs.

Development of these qualities in broiler strains rests primarily upon the breeders of these strains. To the extent that these characters are influenced by heredity, the breeder is solely responsible. Nost of the characters that concern poultry breeders are quantitative in nature; that is, they depend upon several or many pairs of genes, and there is continuous intergradation between the extremes of their expressions. For this reason, the development of an efficient breeding system will be greatly facilitated by knowledge of the mode of inheritance of these traits.

Probably the most important statistic from the breeder's standpoint is the degree of heritability of each trait considered in his breeding program. Other useful information includes the interrelationship between traits, types of gene action involved and the relative importance

of non-additive gene effects and maternal effects.

This experiment was designed to determine some of the answers to these problems in New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds. The objectives were as follows:

- To determine any heterotic effect on 10-week body weight, 10-week breast angle, resistance to death to 10 weeks of age and hatchability resulting from crossing the breeds used in this investigation.
- 2. To calculate heritability estimates for 10-week body weight and 10week breast angle, and to calculate types of gene action and maternal effects involved with these two traits.
- 3. To calculate phenotypic, genetic and environmental correlations between 10-week body weight and 10-week breast angle.
- 4. To calculate heritability estimates of hatchability and the maternal effects on hatchability.
- 5. To determine heritability estimates of resistance to death to 10 weeks of age and the maternal effects on resistance to death to 10 weeks of age.

DISCUSSION OF PROBLEM

The purpose of this investigation was to study the nature of the variance that is observed in some traits in chickens. Since there are several types of variance that are likely to be involved, it seems advisable to devote a section of this thesis to a discussion of the types of variance and some of the other factors essential to the understanding of this investigation.

Symbols and Definitions

The symbols used in genetics and breeding literature are quite diverse. Often this is very confusing to the reader. Since there are no recognized standard symbols for many of the items used in this study, those presented by Lerner (1950) will be used. These symbols and definitions with a few alterations are as follows:

- A Subscript to indicate sire 1 of a diallel mating.
- B Subscript to indicate sire 2 of a diallel mating.
- C The component of E which is common to members of the same family but which varies from family to family.
- D Indicates the dam; in most cases it represents the component of variance derived from the mean squares between dams.
- E The environmental component of variance.
- G The additively acting genotype or the expected value.
- G The non-additive portion of Ge.
- Ge The total genotype; includes the additively acting component (G) and non-additive effects (G').
- h² The square of the correlation between G and P or the degree of heritability.

- I Represents the component of variance derived from the interaction mean squares in a diallel mating.
- L The number of diallel sets of matings.
- N Number of individuals involved in the instances used.
- p Fraction of the individuals that die.
- P Phenotype.
- Q The component of the mean square containing the environmental and half of the genetic variance.
- r Coefficient of correlation.
- r Phenotypic correlation between 10-week body weight (X) and 10-week breast angle (Y).
- rG_XG Genetic correlation between 10-week body weight (X) and 10-week ^Ybreast angle (Y).
- rE Environmental correlation between 10-week body weight (X) and X^{Y} 10-week breast angle (Y).
- S Indicates the sire; in most cases represents the component of variance derived from the mean squares between sires.
- T Sum components of variance derived from the mean squares or S+D+Q and in the case of diallel matings S+D+T+Q.
- X 10-week body weight.
- x Number of sires.
- Y 10-week breast angle.
- y Number of dams per sire.
- z Number of offspring per dam.
- Z The height of the ordinate which truncates p of the area of the normal curve.

Types of Variance

Most, if not all, of the characteristics with which we are concerned in poultry breeding vary among individuals. In some cases, this variance is absent or so slight that mating like phenotypes will produce like offspring. An example of this is plumage color. In other cases, mating like phanotypes does not insure offspring with the same phenotype. An example of this type is body weight at a given age. The expression of the latter trait is said to be continuous; that is, the body weights of offspring of such a mating show continuous variation and do not fall into a few distinct classes.

The phenotypic variation that we observe among individuals may be due to hereditary or genotypic differences and to differences in environment to which the individuals are exposed. Variation in simply inherited traits such as comb type is almost completely due to differences in genotypes. Such traits are said to have a high heritability. On the other hand, a trait like egg production may be influenced more by environment than by genotype. This trait is said to have a low degree of heritability. The portion of the observed variance that is due to heredity, whether large or small, is the raw material with which the breeder works.

The hereditary variance can be further subdivided into (1) the genic or additively genetic variance, (2) dominance deviations, and (3) epistatic deviations. Additive genetic variance for all practical purposes is the only type of genotypic variance transmitted from parent to offspring.

If we let σ_p^2 = the actually observed variance, σ_{Ge}^2 = that part of the variance due to hereditary differences and σ_E^2 = that part of the variance due to differences in the environment under which different individuals develop, we can write the equation

$$\mathcal{T}_{\mathbf{p}^2} = \mathcal{T}_{\mathbf{Ge}^2} + \mathcal{T}_{\mathbf{E}^2}.$$

Actually this is true only when we assume there is no non-linear interaction between genotype and environment. However, for most practical purposes the interaction term can be neglected.

The genetic component can be further subdivided into additive effects (\mathcal{T}_{G}^2) and non-additive effects $(\mathcal{T}_{G}^{\prime 2})$ and the equation

JGe2= JG 2 + JG 2

may be written. Most data do not lend themselves to the type of statistical analysis necessary to separate genetic variance into these two components. When the genetic component is expressed as a percentage of the total variance, it is referred to as heritability in a broad sense. Heritability in a narrow sense is the percentage of the total variance due to additive gene action.

Additive gene effects: Generally we assume that genes affecting characters under selection are additive in their effects. This means that each gene has an average additive effect, either plus or minus, when in combination with other genes in a genotype. Thus any genotype would have an expected value which could be determined by adding all these average effects, provided the number of genes and the value of each were known. Stated in another way, it means that if gene A has a given effect, the genotype AA will be as different from genotype Aa as the latter is from the genotype aa.

<u>Dominance effects</u>: Dominance deviations are due to allelic genes not having additive action in genotypic combination. If dominance is complete, genotypes AA and Aa will have identical phenotypes. Dominance is not always complete. One deviation from complete dominance is over-dominance in which case the heterosygote has a superior phenotype to either homosygote. Dominance deviations are not transmitted from parent to offspring, thus they tend to reduce heritability in the narrow sense and reduce the effectiveness of selection.

Epistatic effects: Epistatic variations are due to non-additive effects between non-allelic genes in genotypic combination. These effects are similar to dominance effects except that epistasis refers to non-allelic genes, while dominance effects refer to allelic genes. Epistatic deviations are transmitted to some degree from parent to offspring. If the desirable gametic combination is AB, the genotypic combination Aa Eb will transmit the desirable gametic combination $\frac{1}{4}$ of the time. As the number of pairs of epistatic genes increases, the fraction of transmitted epistatic gene combinations decreases until it becomes negligible with many pairs of genes.

<u>Sex-linked effects</u>: Males among birds are homogametic and females are heterogametic. This means that males have two sex chromosomes; females have only one sex chromosome. If sex-linked genes are additive in their effects, males should show twice the effect for any given gene. Thus males will contribute more than females to the genetic variance of traits affected by sexlinked genes.

<u>Maternal effects</u>: In addition to the environmental component of variance, there is evidence of extra-chromosomal influences. One theory advanced to explain this phenomenon is a cytoplasmic contribution to the sygote. Since most of the cytoplasm involved in reproduction is of maternal origin, this is usually designated as maternal cytoplasmic inheritance. The dam may also contribute to the variance of characters through environmental effects not common to all progenies concerned. Since most chicks are "raised" separately from their dams, this factor is more easily controlled in chickens than in most farm animals. However, this does not rule out the possibility of dams contributing some maternal effects through the eggs they lay. This would be particularly true during embryonic life, but it seems that this influence should be overcome within a short time after hatching. Regardless of the mode of contribution, maternal effects are evident in several traits.

Concept of Heritability

From the equation

we can calculate the portion of the phenotypic variance due to genetic

differences by the fraction

$$\sigma_{Ge^2}/\sigma_{P^2}$$

This fraction is designated as heritability (h^2) in the broad sense. Under most conventional systems of breeding only the additive portion of the genotypic variance can be utilized by the breeder. Thus we must base our heritability estimates upon the equation

$$\mathcal{T}P^2 = \mathcal{T}G^2 + \mathcal{T}E^2$$

from which can be derived the formula

$$h^2 = \frac{\mathcal{T}G^2}{\mathcal{T}G^2 + \mathcal{T}E^2} = \frac{\mathcal{T}G^2}{\mathcal{T}P^2}$$

This fraction is heritability in the narrow sense because the non-additive effects have been removed from the genetic component and incorporated into the environmental component of variance.

The degree of heritability for each trait is of exceedingly great importance. It influences the amount of gain which selection can accomplish in a breeding program and dictates the choice of an efficient breeding system. Thus it is highly desirable for breeders to have these estimates for their breeding flock.

Heritability applies to a particular population and to a particular trait within that population. It is a ratio, and as such can change as the numerator or denominator changes. For this reason, it becomes necessary to calculate heritability estimates for different populations and periodically within each population. It is doubtful if the environmental component of variance ever remains constant from year to year or for that matter between seasons of a year. The genetic component can be expected to remain more constant than the environmental component but it too will change. If selection is effective, there will be a gradual fixation of the desirable alleles accompanied by a slight reduction of the term $\int Q^2$. Since selection will not affect $\mathcal{T} \mathbb{E}^2$, this term remains relatively constant over a long period of time. Therefore, we must expect some decline in heritability of metrical traits. The forces of mutation and rare recombination of genes oppose this decline in $\mathcal{T} \mathbb{G}^2$. These forces are not likely to be of any great importance unless the frequency of all desirable alleles approaches 1.

Methods of Estimating Heritability

All methods of estimating heritability depend in one way or another on how closely phenotypic resemblance parallels genetic resemblance. In other words, they are based on the correlation between genotype and phenotype. Because it is usually difficult to calculate this correlation directly, analysis of variance is usually used to separate the variance into its components to get the correlation indirectly. Genetic resemblance is inferred from relationship rather than calculated.

Several methods of estimating heritability exist. Different methods have different uses and all are subject to different kinds of biases. The major difficulty of these methods is knowing and discounting that fraction of the phenotypic resemblance which comes from a common environment. This common environment is more easily discounted in poultry than other types of farm animals since chicks are separated from their dams during the rearing period. By brooding all chicks together or randomly distributing them in the necessary number of houses, the environment can for all practical purposes be considered the same for all chicks. Another difficulty may arise from a correlation between dominance and epistatic effects in certain kinds of relatives. However, this is usually minor. We assume that estimates are based on random mating which is not always true. This can cause an overestimate or underestimate of genetic likeness between relatives being studied. If the mating system and degree of inbreeding are known, corrections can be made for any divergence from random mating.

Brief mention will be made of the different methods of estimating heritability, with emphasis placed on the more useful methods for poultry. For a more detailed discussion, the reader is referred to Lush (1948).

Since heritability estimates are based on how closely genotype parallels phenotype, it becomes necessary to determine the genotype as accurately as possible. The greater the degree of genetic relationship, the greater will be the accuracy of determining it, since the effect of sampling error will be reduced with an increase in genetic relationship. For this reason heritability estimates are determined from such data as full-sib correlations, paternal half-sib correlations, intra-sire offspring-dam correlations, intrasire regressions of offspring on dam, regressions of variance on genetic relationship, and regressions of offspring on the mean of the parents.

The most widely used method of estimating heritability in poultry is referred to as the method of intra-class correlation between full and half sibs. It is based on the fact that in a randomly breeding population, the sire and dam each contributes $\frac{1}{4}$ of the genetic variance to their offspring. By use of analysis of variance to partition the variance into its components, three estimates of heritability may be derived as shown in table 40 of the appendix.

An adaptation of the above method involves the use of diallel matings. This method permits the determination of non-additive genetic variance, sexlinked gene effects and maternal effects. For a detailed design and analysis see table 40 of the appendix. To the best of the writer's knowledge, there are only two reports in the literature dealing with this type of analysis in chickens.

Lerner (1945) reported results of a series of 31 diallel sets of matings using Single Comb White Leghorns to study age at sexual maturity. Herita-

bility of this trait was within the range of 16 to 33 percent. Non-additive deviation accounted for only 0.9 percent of the total variance. It was concluded that non-additive effects did not play an important part in determining sexual maturity.

Hazel and Lamoreux (1947) reported a similar study on age at sexual maturity and body weight at 22 weeks of age in Single Comb White Leghorns. Their data were collected from the mating of 60 pens of 6 females each to 60 males in each of 3 different series. Thus each male had 6 mates, all in one series of matings, and each hen had 3 mates, each of them in a different series. Estimates of heritability were 27 and 32 percent for sexual maturity and 22-week body weight respectively. Non-additive gene effects were a minor factor in the determination of both characters. There was no evidence that sex-linked genes were involved with either trait. About 5 percent of the variation in body weight was due to maternal effects, but sexual maturity was not influenced by maternal effects.

Correlation Between Traits

If a correlation exists between two or more traits that are under selection in a breeding program, it will influence the effectiveness of selection. A high positive correlation between two traits permits selection for either with a simultaneous improvement in the other. A negative correlation between two traits has an opposite effect. If a positive correlation exists between a trait of major importance and one or more traits of lesser importance, selection intensity may be increased for the major trait with a resultant reasonable amount of improvement in the ones of lesser importance.

The causative forces for a correlation between traits may be genetic or environmental in nature. The genes causing such a relationship may be the same genes or they may be linked. These genes may also be associated

EXPERIMENTAL PROCEDURE

The stocks used in this investigation were from the Oklahoma A. and M. College Poultry Farm. The New Hampshires have been bred as a closed flock for a number of years. The Silver Oklabars were developed by the Oklahoma A. and M. Poultry Department and have also been bred as a closed flock for a number of years. Inbreeding in both breeds has been purposely avoided.

This experiment was conducted by making a series of diallel matings. This type of mating is defined as the mating of two or more animals at different times to the same two or more animals of the opposite sex. For the purpose of this study, the same dams were used and mated to different sires.

The use of diallel matings has one great advantage over the use of single male matings. By partitioning the variance of the offspring separately for each pen, it is possible to isolate any interaction or non-additive gene effects that might be involved. Removal of the interaction component gives a more accurate estimate of the additive gene effects and permits a more accurate determination of maternal and sex-linked gene effects. The greatest disadvantage of diallel matings is that they cannot be made concurrently. For this reason size and hatch effects will be confounded. This confounding cannot be removed but single male matings can be made concurrently with the diallel matings to give an indication of its importance.

On March 30, 1953, twenty-two single male mating pens were selected from the pedigree matings on the Oklahoma A. and M. College Poultry Farm. Ten New Hampshire females and 10 Silver Oklabar females were selected and randomly placed in each pen. Most of these females had been used in the 1953 pedigree matings, and the remainder were randomly picked from the laying houses. Eleven New Hampshire males and 11 Silver Oklabar males were selected and randomly assigned to head these 22 single male matings.

After the matings were made, 7 days were allowed to assure good fertility. Then all eggs were pedigreed and saved during a period of 10 days which extended from April 6 through April 15, 1953. Only eggs from hens with a minimum of 4 eggs were set and in no cases were more than 7 eggs set per hen. Eggs were trayed and set in a Cugley setting unit during the evening of April 15.

The first shift of males was removed from their respective pens on April 14, and with the exception of one male of each breed, all males were replaced by a randomly chosen male of the same breed on April 17. One pen headed by a New Hampshire male and one headed by a Silver Oklabar male were mated to the same females throughout the experiment. These were control pens.

The 2 shifts of males comprised one series of diallel matings. Another series was run in the same manner. Pertinent dates regarding these matings were as follows:

Hatch	Male In	Eggs Saved	Eggs Set	Date Hatched
1	March 30	April 6 - April 15	April 16	Nay 7
2	April 17	April 21 - April 30	May 1	May 22
3	May 2	May 8 - May 21	May 22	June 12
_4	May 23	May 29 - June 11	June 12	July 3

Exact dates are given for the reason that fertility declined with succeeding hatches. This is the usual case with the onset of hot weather during the summer months.

On the 18th day of incubation, all eggs were candled and the infertiles and dead germs removed. The remaining eggs were placed in wire baskets according to dam numbers and placed in a Cugley separate hatcher. The infertile eggs were "broken out" to detect any sign of embryonic development, and those showing signs of development were recorded as fertile.

On the day of hatching, all chicks were wing banded and pedigreed by sires and dams. They were vaccinated for Newcastle disease with a live virus

hatch was brooded in the following manner: 575 chicks in each of two 30 ft. x 30 ft. pens and 178 chicks in each of three 12 ft. x 12 ft. houses. The second hatch was brooded as follows: 575 chicks in each of two 30 ft. x 30 ft. pens and 243 chicks in a 12 ft. x 12 ft. house. Natural gas was used as a source of heat for all groups except the group of 243 chicks, which was brooded under an electric canopy. The third hatch was brooded by placing 600 chicks in each of two 30 ft. x 30 ft. pens and 182 chicks in a 12 ft. x 12 ft. house. The fourth hatch was small, so the chicks were equally divided into two groups of 442 chicks each and brooded in two 30 ft. x 30 ft. pens. Hatches 3 and 4 were brooded under infra-red lights.

A high efficiency broiler ration was fed throughout the experiment. Water was supplied in gallon containers for a period of about 2 weeks after which the gallon containers were replaced with automatic waterers or large pan_type waterers in the small pens.

A respiratory disorder was observed in all houses of the first hatch on July 5. The most noticeable symptoms were sneezing, watery eyes, and a rasping noise when the birds breathed. Mortality showed no increase and there was no decrease in feed consumption. The affected birds appeared to be less active than the non-affected birds. The symptoms increased in severity during the last week of the experiment.

The same type of respiratory disorder broke out in chicks of the second hatch, but was not quite as severe as in the first hatch. The symptoms were first noticed on August 1 and had largely disappeared by August 21.

On the morning of July 17, several chicks in the fourth hatch showed symptoms of Newcastle disease. Three affected chicks were sent to the diagnostic laboratory of the School of Veterinary Medicine. This disease was diagnosed as Newcastle disease. These chicks had been vaccinated at day-old with a live virus intranasal Newcastle vaccine which was a few days older than the expiration date. Apparently the vaccine was too old to give complete immunity, but virulent enough to cause a few cases of the disease that spread among the non-immunized chicks. Mortality was heavy for a period of 10 days.

At 10 weeks of age all birds were weighed to the nearest tenth of a pound. Breast angle was measured with the West Virginia breast meter. The usual 5 degree gradations were subdivided for this experiment into 2.5 degrees gradations. Sex was also determined for each bird at this time.

HETEROSIS, HERITABILITY, TYPES OF GENE ACTION, AND MATERNAL EFFECTS IN RELATION TO TEN-WEEK BODY WEIGHT IN BROILERS

PART I

To keep abreast of the rapidly expanding broiler industry, breeders have found it necessary to select for faster growing birds. To-day's broiler must attain a body weight in about 9 weeks equal to a 12 to 15-week weight in the early days of the broiler industry. It has been necessary to investigate more thoroughly the mode of inheritance of body weight at broiler age in order to develop an efficient breeding program. One of the most important statistics needed is the degree of heritability of body weight. To determine the most efficient breeding system to produce broiler chicks, it is desirable to know more about the types of gene action involved so that this system can be properly evaluated.

This part of the experiment was designed to determine the following information in New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds.

1. If heterosis was involved in determining 10-week body weight in the crosses.

2. Heritability of 10-week body weight.

3. Types of gene action involved in determining 10-week body weight.

4. Maternal effects on 10-week body weight.

REVIEW OF LITERATURE

Much of the early work on the inheritance of body weight was designed to show that inherent differences exist. Punnett and Bailey (1914) were two of the earliest workers to demonstrate that such an inherent difference did exist. They made crosses between Gold-pencilled Hamburgs and Silver Sebright Bantams through 3 generations of selection and matings. The F_1 was intermediate between the parental breeds in body weight. The F_2 resulted in variation which exceeded the extremes of both the original parents. In the F_3 , tests were made to see if the largest and smallest F_2 birds would breed true. These matings produced progenies which varied considerably among themselves, but neither the small nor the large birds produced the extremes that resulted in the F_2 . These workers concluded that size in poultry depends upon definite factors, and that these factors segregate in gametogenesis.

May (1925) made reciprocal crosses between White Cornish and Silver Spangled Hamburgs, and obtained body weights at 10 months of age. The average parental body weights were 2390 grams for Cornish males, 1885 grams for Cornish females, 1480 grams for Hamburg males, and 1160 grams for Hamburg females. The F_1 and F_2 progenies weighed on the average, almost as much as the average weights of the Cornish. Neither of these progenies was more variable in weight than the purebred parental stocks. May stated that the increased weight of F_1 hybrids in relation to the parental averages could be explained on the basis of heterosis. Without heterosis the average body weight would have been intermediate between the parents. Waters (1931) disagreed with this explanation but agreed that part of the increase might have been due to heterosis. Since the number of offspring used in May's study was small, chance alone could have caused this unexpected increase in body

weight. At 10 months of age, the number of offspring in each group ranged from 8 to 83. In general it can be stated that the small number of birds makes it difficult to draw definite conclusions regarding the inheritance of body weight.

Jull and Quinn (1931) studied the inherent nature of body weight in chickens by making reciprocal crosses between Barred Plymouth Rocks and Rose Comb Black Bantams. Body weights were taken of the F_1 and F_2 progenies at approximately 30 weeks of age. F_1 offspring showed less variability than the F_2 offspring. The latter group did not include birds as large as the larger parent breed nor as small as the smaller parent breed. If 4 pairs of factors were functioning as suggested earlier by Punnett, 256 birds would have been necessary to recover all possible combinations of weight characters. However the 124 F_2 progeny that were produced seem sufficiently large to have included some of the extreme classes. These data provide evidence for a genetic difference in 30-week body weight, but give no information regarding the number of pairs of genes involved.

Waters (1931) reported one of the most extensive early studies of inheritance of body weight using White Leghorns, Brahmas and their reciprocal crosses. This study extended over a period of 10 years and included a total of 2966 birds. All chicks were weighed at weekly intervals during the first 3 months and then at monthly intervals until 10 months of age. The F_1 reciprocal hybrids were intermediate in weight at 10 months of age between the parental averages. Variability was no greater than that of either parent breed. The mean weight of the F_2 hybrids was also intermediate between the parental breeds, but their variability was significantly greater than that of the F_1 progeny. From the F_2 progeny, large, intermediate and small-sized birds were selected to be mated within their own size group. These 3 groups produced progenies with different means and variabilities. Waters stated that

this was evidence for genetic as well as phenotypic differences, and it is certain that segregation for large and small size took place in the F_2 generation. Variability curves based on monthly weighings showed that the differences in variability between the original breeds and the F_1 and F_2 hybrids demonstrated no significant genetic differences until growth was nearly complete. At 10 months of age these differences were clearly shown. There was no evidence of hybrid vigor at 10 months of age but there was evidence for it during early growth. The maximum amount of hybrid vigor was manifested in the F_1 with decreasing amounts in subsequent generations. Waters made the assumption that differences in weight were dependent primarily upon 2 pairs of genes each with equal and cumulative effects. Fossibly many other genes of lesser influence also operated.

Lerner and Asmundson (1932) studied the inheritance of growth in chickens by making a cross between a Light Sussex male and Ancona females. F_1 crosses and backcrosses were made. The formula

$$R = \frac{W_2 - W_1}{\frac{1}{2}(W_2 + W_1)} X_{100}$$

was used to determine rate of growth for the periods 2 to 8 weeks and 8 to 12 weeks. In this formula $W_{1=}$ 2-week weight and $W_{2=}$ 8-week weight. The Light Sussex showed a higher growth rate than the Anconas. Males in the F_1 generation showed a higher mean growth rate than those of the F_2 and were less variable. Results for the F_1 and F_2 females did not agree with data for the males in that the growth rates of the 2 groups were equal or even lower for the F_1 females than for the F_2 females. Backcross data indicated that rapid rate of growth was dominant over slow growth. The authors stated that due to the small numbers available, their data were not adequate for a precise genetic analysis but they point to inherent differences in growth rate between the two breeds. Assundson and Lerner (1933) made a study of the genetic difference in growth rate of Single Comb White Leghorns. They divided 340 chicks into 4 lots on the basis of sex and time of hatching. Growth from 2 to 8 weeks was computed using the formula given in the preceding paragraph. Comparisons between the progenies of 3 males revealed no significant difference in growth rate. Six more or less closely-related families were divided into rapid, intermediate, and slow growing lines. There was no significant difference between families of different classes. These workers concluded that a genetic difference in growth rate was evident and this difference was dependent upon multiple factors. The small number of sire families and progeny probably was responsible for the lack of a significant difference in some cases. The sires could have possessed about the same genotypes.

In a similar study by Asmundson and Lerner (1934) with Single Comb White Leghorns and Barred Plymouth Rocks, it was concluded that from 2 to 8 weeks of age is the best period to study genetic differences in growth rate.

Maw (1935) studied the inheritance of skeletal dimensions in Light Brahmas, Golden Sebright Bantams and reciprocal crosses between these breeds. Although body weight was not used as a criterion of size, weight was obtained to compare with the results of other investigators. These breeds vary greatly in body size and approach the extremes in body weight that have been attained in domestic fowl. The Brahma males weighed approximately 10 pounds more than the Bantam males and the Brahma females weighed approximately 8 pounds more than the Bantam females. Matings were accomplished by means of artificial insemination. At approximately 10 months of age, the Brahmas were weighed, killed, and the meat removed from the skeleton. Measurements were taken of the long bones of the leg and wing and cranial length and breadth. Similar data were collected on all other birds after 180 days of age. The F_1 and F_2

progenies were slightly smaller in mean body weight than the mean body weight of the 2 parental breeds. Maw stated that these results supported the findings of Jull and Quinn (1931) which indicated the presence of dominant or partially dominant genes for small body size. The mean lengths of bones of the F_1 and F_2 birds were intermediate between the mean bone lengths of the parents. Linkage was found to exist between factors for body size and the sex-linked genes for silver and gold, and fast feathering. This study gives support for the presence of sex-linked genes that affect body size. One criticism that can be made about this work is the widely different ages at which the data were collected. Light Brahmas are noted for a slow rate of growth but it is doubtful if the rate is sufficiently slow to warrant an additional 4 months to be comparable with the growth of the Bantams. Most domestic breeds of fowl attain their mature body size between 10 and 12 months of age regardless of their mature weight. It seems that the data from the different groups would have been more comparable if all the birds had attained their mature weights.

Schnetzler (1936) demonstrated that inherent differences in body weight are present at 8 or 9 weeks of age. From a group of 242 Barred Plymouth Rocks he selected the heaviest males and females and the lightest males and females on the basis of 8 or 9-week weight. Keeping these lines separate and continuing this type of selection for several generations, Schnetzler was able to establish a fast and a slow growing line.

Jaap and Morris (1937) by means of analysis of variance showed the important causes of variation in 8-week body weight of 6 varieties and some crossbred chickens. These causes and their relative importance were as follows:

Cause		Percent of Total Variation
Varieties		
Pen (mostly sire)		19
Dams within males		27
Sex		23
Remainder		18
	Total	100

These results clearly demonstrate that a genetic difference occurs in 8-week body weight.

Kaufman (1948) concluded from data on Polish Greenleg X Bantam crossbreds that sex-linkage was involved in adult body weight. Reciprocal crosses failed to give the same result for 8-month body weight. The weight of F_1 females approached the weight of Bantam hens when Bantam males were used. When Greenleg males were used, the offspring were intermediate between the parental breeds. No males were available in the first cross due to some of the data being lost. Kaufman concluded that 2 pairs of genes were involved in 8-month body weight. One pair was autosomal and the other pair was located on the sex chronosomes. The number of birds involved in this study was exceedingly small and appear to be inadequate for drawing such definite conclusions. This investigation was carried out in Foland during the years 1937-1939, and most of the data were lost during the war.

Godfrey (1953) presented further evidence for the presence of a sexlinked gene that affects growth rate. This evidence was obtained from a study involving 69 Rose Comb Elack Bantams, 87 Barred Plymouth Rocks, 110 F₁ (RCB X EPR) crossbreds, 879 F₂ crossbreds, 82 F₃ chicks, and 1172 birds from a backcross of F₁ males to New Hampshire females. Evidence for sex-linked effects upon growth rate was apparent when F₁ females fell below the intermediate parental body weight at an earlier age than males. In addition, the mature shank length values of the F₁ females were considerably below the female parental intermediate, while the males were nearly intermediate when compared to the mean shank length of the male parents. Further evidence resulted from linkage studies involving 5 pairs of marker genes in the backcross. The barring and slow feathering loci marked the sex chromosome near both ends and silver served as a supplementary sex-linked marker. The rose comb and white skin loci marked separate autosomes. This study suggested that a sex-linked gene for growth is located approximately half-way between the silver and slow feathering loci. Godfrey concluded that there is one sexlinked gene which affects growth rate to 9 weeks of age, and at least 15 pairs of genes are involved in the overall genetic difference.

Lerner, Asmundson and Cruden (1947) determined heritability estimates for 12-week body weight in a randomly selected sample of New Hampshires. The data were analyzed separately for males and females, but due to the low numbers in each mating, the results would be of questionable statistical validity. For this reason the data were transformed into respective standard deviations for the two sexes and then pooled. The heritability analysis was based on the methods of Whatley (1942) and Hazel et al (1943) with a few modifications called for by the nature of the data. The heritability estimate for 12-week body weight based on the sires contribution was 0.42; based on the dam's contribution, the estimate was 0.60, and a combination of the 2 gave an estimate of 0.51. The authors stated that due to the small numbers involved, sampling error was likely to be large. However, there was rather close agreement among the 3 estimates. El-Ibiary and Shaffner (1951) criticized these workers for using only 230 birds and for combining sexes. They stated that under normal conditions there would be a 15 to 20 percent sex difference in body weight. Lerner and his associates recognized both of these shortcomings. Their method of transforming the data to standard deviations was an attempt to overcome the sex difference. Granted that such a method might lead to some error in calculation, it tends to overcome sampling error in that the numbers should be approximately doubled by combining sexes.

Shoffner and Sloan (1948) calculated heritability of 300-day body weight among inbred lines of chickens. The method of analysis was that of intra-sire regression proposed by Lush (1940). When the estimate was corrected for 16.2 percent inbreeding, h^2 equaled 0.75. This estimate appears to be high in relation to other estimates of the heritability of body weight. The authors stated that the high estimate could very likely be correct. A large part of the data were derived from crosses of breeds differing inherently in body size. Segregation in succeeding generations probably provided a larger portion of genetic variance than normally is the case within closed flocks.

El-Diary and Shaffner (1951) calculated heritability estimates for body weight in New Hampshires at 2, 4, 6, 8, and 10 weeks of age. These estimates were based on data collected from 2 randomly distributed groups of chicks treated in different ways. One group was fed an adequate ration plus 0.2 percent thiouracil, and the other group received the same ration without the thiouracil. Only dams having at least 2 male or 2 female chicks and sires with chicks from at least 2 dams were used in the analysis. Data were analysed separately for sexes by means of analysis of variance and covariance. Heritability estimates were calculated from the sires contribution to the genetic variance (g^2) and from the combined contribution of sire and dam (h^2) . Their estimates of heritability were:

	ودورة كانفناك فتقوير سويت	Fena	les		Males						
	Tre	ated	Contr	rols	Trea	ted	Controls				
Age	hZ	g2	h ²	g ²	հ2	g2	h ²	g ²			
2 Weeks	•574	.017	•314	0	•357	.039	•445	•056			
4 Weeks	.361	.217	.278	.143	•255	•055	•381	.131			
8 Weeks	•352	.194	•369	•225	•379	•033	.270	.107			
10 Weeks	•392	.231	•540	.2 59	.452	•038	.210	.128			
The authors	stated	that g ²	is herit	tability	in a rat	her narr	ow sense,	, and that			
h ² is herit	ability	in a bro	ad sense	. This	is not a	n estima	te in the	narrow			

sense as used by Lerner (1950) to include only the additive genetic variance. Lush and associates (1948) stated that the combined estimate leads to a smaller sampling error since the sampling errors due to sire and dam contributions tend to cancel each other. Lush and his associates also point out that the combined estimate includes one-fourth of the variance from dominance deviation in the component which he calls extra variance within groups of paternal half sibs as well as any likeness between full sibs caused by environmental variations which are alike for daughters of the same dam but can be different for paternal half sibs. Hence,more confidence can be placed on the estimate from the sires contribution when the data are numerous enough to make sampling errors small.

Godfrey and Williams (1952) reported heritability of body weight in chickens based on a selection experiment using Silver Oklabars. One line was selected for rapid growth while another line was selected for slow growth as measured by body weight at 6 and 12 weeks of age. Original selection for the 2 lines was made from the same population. Results of 2 generations of selection yielded heritability estimates of .19 and .30 for body weight at 6 weeks of age, and estimates of .31 and .32 for body weight at 12 weeks of age. Estimates calculated for males were consistently lower at both ages than those calculated for females. Selection solely for body weight at 6 and 12 weeks of age resulted in significant differences in adult body weight and egg size between the selected parents of the rapid and slow growth lines.

When the available estimates of heritability of body weight in chickens are considered as a group, there is considerable variation among them. Since sampling error and various other types of errors may be operating, considerable variation in estimates can be expected. Other discrepancies might arise from using different stocks and from using different methods of calculation. It seems that numerous estimates from numerous sources would tend to give a

rather reliable average estimate of heritability.

Some estimates of heritability of body weight in chickens have been based on weights of birds older than broilers. Others have been published only in tabular form with no description as to the method of calculation or source of data. Because of these reasons, some of these estimates have not been reviewed but will be presented in tabular form. The available heritability estimates of body weight in chickens are as follows:

<u>h</u> 2	Investigator	Year	Method	ge of Birds
.19	Godfrey and Williams	1952	Selection Expt.	6 weeks
.30	Godfrey and Williams	1952	Selection Expt.	6 Teeks
54	El-Thiary and Shaffner	1951	2(S+D)/T	10 weeks
.21	El-Ibiary and Shaffner	1951	2(S+D)/T	10 weeks
.26	El-Ibiary and Shaffner	1951	LS/T	10 weeks
.13	El-Ibiary and Shaffner	1951	LS/T	10 weeks
.51	Lerner et al	1947	2(S+D)/T	12 Woeks
.60	Lerner et al	1947	2D/T	12 weeks
-42	Lerner et al	1917	2D/T	12 weeks
.31	Godfrey and Williams	1952	Selection Expt.	12 weeks
-32	Godfrey and Williams	1952	Selection Expt.	12 weeks
-80	Lerner and Cruden	1951	D/D Begression#	8ª months
1.9	Lerner and Cruden	1951	D/D Regression#	St months
.).7	Lemen and Graden	1051	2(SAD)/T	
941 77	Lemen and Canden	1051	Le /m	
+エ! ッピ	Lerner and Uruden	1921		
•12 61	Shoilner and Sloan	1940	Intra-Sire Aegression	
•01	Comstock et al***	1947	**	**
•00	Comstock et al	1947	**	**
•56	Comstock <u>et al</u>	1947	**	**
•54	Comstock et al	1947	**	**
•52	Constock et al	1947	**	**
•48	Comstock et al	1947	**	**
•43	Comstock et al	1947	4 4	44
.42	Comstock et al	1947	**	**

* Daughter-Dam regression **Not known *** Quoted from Shoffner & Sloan (1948)

MATERIALS AND METHODS

The design of the experiment and method of collecting data are discussed on pages 14 through 17 and demonstrated in table 40 of the appendix. Ten-week body weights were analyzed for this part of the study.

To simplify the statistical analyses, subgroups of equal numbers were used; that is, equal numbers of dams per sire and equal numbers of offspring per dam were used. Due to the small number of each sex in some cases, the female weights were converted to the equivalent of male weights. This was accomplished by dividing the total weight of males within each breed and cross by the total weight of the females within the same breed or cross to get a factor to multiply each female weight by. Any errors made in weighing would be magnified when multiplied by the conversion factor, but it is hoped that by increasing the numbers of sires, dams, and offspring, sampling error was reduced to compensate for this possible error.

The numbers of offspring per dam used in the analyses were 4 in the case of some breeds and crosses and 3 in others. Thus the sire with the least number of mates with the appropriate number of offspring automatically determined the number of dams that were used per sire. A table of random numbers was used to select the appropriate number of dams needed. Two samples of data were selected for each breed and cross for each of the 2 series of matings. For the first sample, the first 3 or 4 chicks were used. For the last sample, the last 3 or 4 chicks were used. All chicks had equal chance of being banded in any sequence at hatching time, thus these were random samples.

The first step in the analysis of these data was to figure the average 10-week weight of all breeds and crosses by sexes within pens. This was done to see if any noticeable heterotic effect was present, and also to
compare the performance of the purebreds in relation to the crossbreds.

The data from the control pens were analyzed by breeds and crosses and sexes within each breed and cross by means of analysis of variance to see if there was a hatch effect. In no case did this hatch effect approach significance at the 5 percent level. For this reason it seemed justifiable to pool hatches when the analysis warranted it. Due to the nature of a diallel mating, sire and hatch effects are confounded. Since the sires must be mated to the same dams, there is no way to relieve this situation by making the matings concurrently. This discrepancy is one criticism of a diallel mating scheme.

In order to calculate heritability and other important estimates, it was necessary to separate the variance components. For this purpose analysis of variance was used, and the total variance was separated into the following parts: (1) differences between sires, (2) differences between dams, (3) interaction, and (4) remainder. The mean squares of these parts were reduced to the components of variance as outlined by Lerner (1950). The details of this reduction are presented in table 40 of the appendix. The remainder (Q) is the component of variance containing the environmental component and half of the genetic variance. It is that variance expected between full sibs. Interaction (I) indicates the interaction component between the genes contributed by the sire and by the dam. The dam's contribution (D) is the extra variance occurring within groups of paternal half sibs. This contribution is in addition to the variance found among full sibs. Sires contribute additional variance (S) to non-sibs as compared to paternal half sibs.

A sample of data was taken, and the steps in its analysis are presented in table 41 of the Appendix. For this reason the details of the analysis will not be discussed here.

From the components S and D, heritability estimates of body weight were calculated. These calculations are based on the theory that S and D each contain one-fourth of the genetic variance, thus 4S, 4D, and 2(S+D) are 3 estimates of the total genetic variance. Each of these estimates of the total genetic variance will give an estimate of heritability when divided by the total variance. These percentages are estimates of heritability in the narrow sense because the interaction component has been removed. Heritability in this sense is an indication of the additive genetic variance.

The presence of sex-linked and maternal effects were detected by inference depending upon the size of the contribution of sire and dam. Excluding sex-linked gene effects and maternal effects, the sire and dam are expected to contribute equally to the total variance. Thus when either the sire or dam components were larger than the other component, it was assumed that the difference was due to either sex-linked gene effects or maternal offects. The smaller component in each case was subtracted from the larger component and the difference was divided by the total variance to determine the percentage of either sex-linked gene effects or maternal effects. This procedure results in a value greater than zero for one of these effects and the other must take a value of zero. Actually, this is not necessarily true. sampling error can easily cause the sire and dam components of variance to >e different. In some cases, both of these effects could be contributing equally to the variance and each masking the effect of the other. In other ases, both might be contributing to the variance but not in equal amounts; hus one effect partially masks the effect of the other. In any case, sampling error might lead to a positive value for either of these effects.

Non-additive effects were determined by dividing "I" by the total variance hen "I" was a positive figure. This figure represents the percent of the otal variance that is due to genes not acting additively when in genotypic

combination.

RESULTS

The average 10-week body weights are presented in Tables 1 through 4. For the purpose of comparison, the averages for pure New Hampshire and Silver Oklabars were considered as the parental stock averages. When the data for hatches and sexes were combined, the Silver Oklabar X New Hampshire crossbreds averaged 0.05 of a pound more than the New Hampshires and 0.14 of a pound more than the Silver Oklabars. The New Hampshire X Silver Oklabar crossbreds were equal in weight to the New Hampshires and averaged 0.09 of a pound more than the Silver Oklabars. In both crosses, the crossbreds exceeded the average of both parental stocks in 10-week body weight.

These differences are small and the question might be raised as to the repeatability of these results. Strengthening evidence can be obtained by comparing the data on a hatch basis. In all 4 hatches the Silver Oklabar X New Hampshire crossbred males were superior in average weight when compared with the other breeds and cross. Females from this cross were superior in weight in 2 hatches when compared with the other breeds and crosses. The New Hampshire males showed a slight superiority in average weight over the New Hampshire X Silver Oklabar crossbred males in 2 hatches and were equal to the crossbred average in another hatch. The females of the latter cross showed superiority over all other females in 2 hatches but ranked second and third in mean body weight in the other 2 hatches. Silver Oklabars had the lowest average body weight for both sexes in all hatches.

To test the significance of the differences in mean 10-week body weight, the data were tested statistically by means of "t" tests. The data for the crosses were pooled and compared to the pooled data for the breeds for each hatch and for all hatches combined. The mean of the better cross

of the better parent (New Hampshires). The resulting "t" values are presented in the following table:

				Hatch		
Comparison	Sex	1	2	3	4	<u> </u>
Breeds vs Crosses	Nales	3 . 182 **	5•263**	2.067*	3•757 **	6•538 **
	Females	1.724	3•077**	1.915	2•021*	4•339 **
SBXINH VBNHXSB	Males	1.880	1.146	.551	1.560	2.857**
	Females	.598	.9731	1.433 ¹	2.822##	.461
SBX NH VS NH	Males	1.438	3•588**	•457	2 .216*	3.838**
	Females	1.308	•077	1•241	2 .1 4 3*	1.172

*Indicates significance at the 5% level.

****Indicates significance at the 1% level.**

INH X SB females had a higher mean body weight in these instances than SB X NH females.

These results show that the mean 10-week body weight of the crossbreds was significantly higher than the mean of the parental breeds. On a hatch basis, the means of the crosses did not differ significantly, but when the data for all hatches were pooled, Silver Oklabar I New Hampshire males had a significantly higher mean body weight than the males of the reciprocal cross. The Silver Oklabar X New Hampshire males also had a mean body weight that was significantly higher than the New Hampshire males in hatches 2 and 4 and for all hatches combined. Silver Oklabar X New Hampshire females did not differ significantly from females of the reciprocal cross or New Hampshire females in mean 10-week body weight. It can be concluded that heterosis was involved in determining 10-week body weight in the crosses used in this study.

An analysis of variance was calculated for the control pens to determine if an interaction component of variance was present. Since the same sires and dams were used for all hatches, an interaction component would be an indication of a hatch effect. The results of these analyses are presented in Table 5. Only in the cases of New Hampshires and Silver Oklabar I New Hampshire crossbreds are the interaction components positive figures. In neither of these instances do the positive figures approach significance. These results show that no significant hatch effect was present.

The analyses of variance and important estimates derived from the components of variance are presented in Tables6 through 9. Estimates of heritability for 10-week body weight ranged from 0.01 to greater than 1. It is impossible to have a true estimate that exceeds 1, and it is unlikely that estimates as low as 0.01 are correct. Using samples, and especially small samples, will lead to sampling errors that might explain this wide range. Since S or D have to be multiplied by 4 to calculate heritability estimates, it can readily be seen that any error, whether sampling or otherwise, will also be multiplied by 4.

Forty-six estimates of heritability were calculated. Twenty-six of these were in the range of 25 to 56 percent. A further break down of these estimates are as follows: 9 were in the range of 25 to 30 percent; 5 in the range of 31 to 40 percent; 11 in the range of 41 to 50 percent; and 3 in the range of 51 to 56 percent. Thirty percent of all the estimates were in the range of 40 to 56 percent. For this reason, it appears that heritability of 10-week body weight as determined by this study is in the range of 40 to 56 percent. When all the estimates were averaged, the average estimate was 0.45. Realizing that this is more or less an average of averages, it does indicate the mean of such averages, and as such, gives support for setting the range of heritability.

Heritability estimates based on the sires' contribution were the highest of the 3 estimates in general. This automatically made the estimates based on dams' contribution the lowest of the 3 estimates. Combining these 2 sources of variance to give a joint estimate resulted in estimates that fell close to the mean for all estimates. Ten out of 15 estimates were

within the range of 41 to 56 percent.

Sex-linked gene effects on body weight ranged from 0.02 to 0.24 and were evident in 13 of 16 cases. The mean for sex-linked gene effects was 0.10. Non-additive gene effects ranged from 0.025 to 0.098 and were evident in only 4 of 16 cases. Since non-additive gene effects did not occur consistently, it is difficult to draw any conclusions regarding the size of these effects. The mean for these effects was 0.02.

Based on the sire components of variance, an estimate of 0.64 was calculated for the total genetic variance in 10-week body weight. Based on dam components of variance, the estimate of genetic variance plus a small maternal effect was 0.30. The estimate calculated from sire components of variance was higher than the estimate calculated from dam components because of a relatively large sex-linked gene effect. Therefore, the most accurate estimate of the variance in 10-week body weight must be calculated from the combined sire and dam components of variance less the maternal effect. Maternal effects were evident in only 3 of 16 cases and ranged from 0.042 to 0.139. The mean maternal effect was 0.02. After the maternal effect was removed, the combined sire and dam components yielded an estimate of 0.45 for the genetic variance in 10-week body weight. About 0.02 of the genetic variance was due to non-additive gene effects; thus, the remaining 0.43 was due to additive gene effects.

The different breeds and crosses varied too much in percentages of the total variance due to different types of gene action on 10-week body weight to draw any conclusions in this respect. There was rather close agreement on the percentages of the variance due to sex-linked gene effects. There was also close agreement on the percentages of the variance due to additive gene effects except for Silver Oklabars which yielded estimates considerably less than the estimates derived for New Hampshires and the crosses.

DISCUSSION

The results of this study clearly point to the presence of heterosis in 10-week body weight when reciprocal crosses were made between New Hampshires and Silver Oklabars. When Silver Oklabar males were used in the cross there was a greater effect than when New Hampshire males were used. Since the reciprocal crosses gave different results, it is evident that the Silver Oklabars contributed more to the increased body weight than the New Hampshires. The only logical explanation for this appears to be the presence of sex-linked genes affecting 10-week body weight. Obviously it is not a case of Silver Oklabars possessing a sex-linked dominant gene for heavier body weight because the Silver Oklabar females would have transmitted this gene to their crossbred sons. This was not the case as these crossbred males were not superior to the New Hampshire males. A more logical explanation would seem to be that a sex-linked gene or genes for increased body weight at 10-weeks of age was functioning and the frequency of this gene or genes was higher in the Silver Oklabars than in New Hampshires. However, this is not demonstrated very well in the analysis of variance. Sex-linked gene effects in the first series of matings were minor in the Silver Oklabar X New Hampshire crossbreds, but this cross showed the greatest effects in the second series.

Numerous hypotheses have been advanced to explain the genetic basis of heterosis. Most of these hypotheses lead to an interpretation in terms of non-additive gene action. The results of this study failed to indicate the presence of non-additive gene effects and also failed to support the hypotheses based upon non-additive effects. This leads the writer to state that the superiority of Silver Oklabar X New Hampshire crossbreds in 10-week body weight as compared to the reciprocal cross and pure parental strains

was due to an unexplained heterotic effect, plus an additional sex-linked gene effect that is contributed more by the Silver Oklabars than by the New Hampshires.

The most important estimates derived from the analyses of variance are the heritability estimates. Most of these estimates fell within the range where individual selection is equally as effective or more effective than family selection. Lerner (1950) has shown that when full sister or brother families contain 5 members and $h^2=0.4$, the ratio of the effectiveness of family selection and individual selection is 1 to 1. As the number increases or h^2 increases, the emphasis shifts in favor of individual selection. Thus the results of this study indicate that individual selection will be slightly more effective than family selection in selecting for 10-week body weight.

The results of this study also indicated that most of the genetic variance involved in 10-week body weight was additive in nature. Non-additive gene effects were negligible as compared with additive gene effects. Since sex-linked gene effects may be additive too, it may be stated that the statistical analyses of these data revealed that most of the genetic variance was due to genes with additive effects.

Estimates of sex-linked gene effects were evident in most cases but the estimates varied considerably among hatches. There was rather close agreement among breeds and crosses in the size of these effects. Since these effects are determined by inference, the only statement that appears justifiable is that they exceed the maternal effects and give support to the idea that sex-linked genes influence body weight. Actually this measure of sex-linked gene effects measures only the differences between the sire's contribution and the dam's contribution to the variance of 10-week body weight. The consistency of the larger contribution from sires rather than

the amount is the important factor. This is exceedingly strong evidence to indicate the presence of sex-linked gene effects.

Non-additive gene effects were not important based upon the number of times they were positive (4 out of a possible 16) and upon the fact that the 4 positive numbers were not significant. Thus "nicking" as determined by non-additive effects was not important in this study of 10-week body weight.

The above statement might not hold when placed on an individual bird basis. Some individual birds were superior to their sibs and non-sibs because they received a genotypic combination that was not wholly additive in nature and not uniformly transmitted to the rest of the family. In some cases individual dams might have "nicked well" with a given size to produce effects not common to other members of that size family but was common to all within that particular dam family. Selection of these superior individuals for breeding purposes would probably lead to less improvement than was expected in the following generation.

Maternal effects were evident in only 3 cases. This indicates that maternal effects were unimportant in determining 10-week body weight in the breeds and crosses used in this study.

The results of this study point to continuance of our conventional types of breeding program with emphasis on individual selection for body weight at or near broiler age. The results fail to give support to such systems as recurrent reciprocal selection that rely largely upon non-additive gene action. If these systems have a place in breeding programs, it must be with traits other than body weight. An exception to this might occur when one of the so-called genetic ceilings have been reached. If such a situation developed, any improvement would be welcomed and it might be attained by sorting out those individuals that "nick well".

Heritability in a narrow sense is the portion of the total phenotypic

variance which is due to additive gene effects. Thus traits with high heritabilities are dependent to a large extent upon additive gene effects and breeding systems designed to utilize non-additive gene effects will not be as efficient as individual selection. On the other hand, traits with low heritabilities are not greatly influenced by additive gene effects and breeding systems designed to utilize non-additive gene effects might be useful. Heritability estimates for body weight in chickens are of the magnitude that much of the phenotypic variance is due to additive gene effects. The present conventional system of using individual selection or individual and family selection for body weight in chickens is to be recommended.

SUMMARY

From 2 series of diallel matings random samples were studied to calculate heterotic effects, estimates of heritability, types of gene action, and maternal effects in relation to 10-week body weight among New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds. The study involved 82 sires, 440 dams, and 5,355 chicks. A total of 16 samples were used which varied in number from 10 sires, 10 dams and 60 chicks, to 16 sires, 32 dams, and 256 chicks per sample.

The data were analyzed by analysis of variance as outlined by Lerner (1950). The results were as follows:

1. Both crosses showed a heterotic effect, but only when Silver Oklabar males were mated with New Hampshire females, were the crossbreds equal to the better parent. Silver Oklabar males contributed more to the increased body weight than did the New Hampshires males. It has been postulated that this difference is due to sex-linked genes with the frequency of the desirable genes being higher in Silver Oklabars than in New Hampshires.

2. Heritability estimates for 10-week body weight ranged from 0.01 to greater than 1. The mean estimate was 0.45.

3. Sex-linked gene effects were evident in 13 of 16 cases and ranged from 0.02 to 0.241 with a mean of 0.10. Non-additive gene effects were evident in 4 of 16 cases and the mean effect was 0.02. Additive gene effects accounted for 0.43 of the total variance.

4. Maternal effects were evident in 3 of 16 cases and the mean effect was 0.02.

AVERAGE TEN-WEEK BODY WEIGHT OF PROGENY BY PENS FOR FIRST HATCH

	New Hampshires		New Hampshire I Silver Oklabars				5	Silver Lew Ham	Oklat	ar I		Silver	Okl	bars			
•	У	ales	Fei	ales	Y	ales	Fer	ales		i i	ales	Pen	ales	ľ	ales	Fei	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	'n	Mean	n	Mean	n	Mean	n	Mean
2	22	2.74	23	2.35	19	2.83	22	2.40	n	30	2.97	23	2.43	30	2.80	24	2.29
12	16	2.91	15	2.34	19	2.84	28	2.26	21	31	2.89	21	2.40	19	2.76	16	2.34
13	19	2.88	17	2.44	15	2.85	17	2.46	22	19	2.69	15	2.13	10	2.46	12	2,19
14	22	2.81	23	2.29	22	2.83	18	2.32	23	13	2.90	17	2.32	16	2.47	15	2.35
15	14	2.86	14	2.32	16	2.86	15	2.33	24	22	2.80	20	2.34	12	2.65	17	2.29
16	17	2.90	16	2.39	11	2.90	13	2.31	25	19	2.71	24	2.25	19	2.79	15	2.31
17	26	2.72	14	2.11	19	2.56	18	2.20	27	23	2.94	14	2.44	15	2.66	26	2.27
18	9	3.03	27	2.36	15	2.79	16	2.36	28	0		0		0		0	
19	25	2.89	21	2.30	18	3.08	9	2.47	29	16	3.09	21	2.48	23	2.80	21	2.44
20	20	2.34	10	2.42	14	2.91	22	2.41	30	20	3.05	31	2.43	16	2.93	17	2,32
Total	190	2.85	180	2.33	168	2.84	178	2.34	Total	193	2.89	173	2.34	160	2.73	163	2.30
1*	20	2.82	12	2.25	18	2.83	20	2.33	26*	23	2.94	18	2.27	29	2.64	17	2.16

*Control Pens

AVERAGE TEN-WEEK BODY WEIGHT OF PROGENY BY PENS FOR SECOND HATCH

		New H	ampsh	ires	N S	ew Ham ilver	pshir Oklab	ire X Silver Oklabar X Abars New Hampshires			ar I es		Silver	Okla	bars		
•	M	ales	Fem	ales	Ľ	ales	Pet	ales		ľ	ales	Fei	ales	ľ	lales	Pen	ales_
Pen	'n	Mean	n '	Mean	n	Mean	n	Mean	Pen	n	Mean	<u> </u>	Mean	n	Mean	<u>n</u>	Mean
2	16	2.56	16	2,14	n	2.53	16	2.17	11	22	2.66	22	2.17	24	2.59	13	2.11
12	7	2.73	16	2.21	18	2.68	16	2.23	21	19	2.74	19	2.18	13	2.70	ш	2.05
13	15	2.64	13	2.31	10	2.68	15	2.27	22	9	2.69	24	2.08	0		8	2.09
1)4	23	2.60	17	2.18	14	2.81	20	2.24	23	13	2.81	14	2.04	10	2.51	17	1.98
15	2	2.90	6	2.12	3	2.63	9	2,21	24	12	2.80	18	2,20	18	2.52	ш	2.03
16	15	2.33	19	2.07	9	2.78	13	2.12	25	16	2.61	ш	2.05	7	2.64	14	2.12
17	19	2.71	17	2.20	18	2.71	23	2,12	27	24	2.71	19	2.17	19	2.52	23	1.99
18	10	2.99	8	2.24	6	2.77	5	2.12	28	12	2.74	11	2.25	9	2.59	7	2.03
19	24	2.47	21	2.12	17	2.71	20	2.17	29	20	2.89	8	2.38	11	2.80	15	2.33
20	12	2.54	15	2.29	14	2.81	16	2.29	30	24	2.90	21	2,35	10	2.75	17	2.09
Total	143	2.62	148	2.18	120	2.71	153	2.24	Total	171	2.76	167	2.18	121	2.61	136	2.08
1*	10	2.99	7	2.23	15	2.89	16	2.29	26*	19	2.85	15	2.17	26	2.55	14	2.16

*Control Pens

AVERAGE TEN-WEEK BODY WEIGHT OF PROGENY BY PENS FOR THIRD HATCH

		New H	lampsh	ires	N S	iew Han Silver	oklat	re I Dars		8	lew Han	Oklat	oar I res		Silve	- Okla	ibars
_	ľ	ales	Fes	ales)	lales	Fei	ales			ales	Fei	ales]	ales	Fe	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Moan	n	Mean	D	Mean
11	20	2.61	21	2.15	23	2.70	17	2.11	2	19	2.42	17	1.84	15	2.21	18	1.89
21	10	2,82	20	2.11	18	2.48	16	2.11	12	10	2.62	13	2.12	13	2.49	19	2.12
22	17	2.48	17	2.21	4	2.58	5	2.18	13	25	2.74	17	2.12	7	2.39	14	2.01
23	8	2.70	ш	1.99	13	2.50	18	1.99	זע	16	2.30	16	2.16	13	2.24	16	1.88
24	30	2.63	13	2.08	14	2.48	25	2.11	15	0		0		0		0	
25	15	2.56	25	2.11	18	2.56	18	2.19	16	8	2.25	9	1.86	6	2.72	1	1.90
27	19	2.69	13	2.19	18	2.48	22	2.19	17	22	2.93	19	2.22	14	2.64	16	1.99
28	ш	2.86	5	2.26	9	2.68	4	2.20	18	15	2.91	6	2.30	13	2.66	14	2.10
2 9	15	2.51	15	2.11	15	2.55	19	2.14	19	7	2.63	12	2.18	3	2.83	3	2.07
30	25	2.61	31	2 .2 0	22	2.85	18	2.26	20	12	2.67	13	2.21	15	2.55	17	1.99
Total	170	2.63	171	2.14	144	2.58	162	2.14	Total	134	2.64	122	2.11	99	2.49	118	2.00
1*	5	2.76	5	2.14	11	2.88	6	2.40	26 *	16	2.69	30	2.10	17	2.54	16	1.99

*Control Pens

AVERAGE TEN-WEEK BODY WEIGHT OF PROGENY BY PENS FOR FOURTH HATCH

		New H	ampsh	ires	N	ew Hamp ilver (oshir Malal	e X ars		Silver Oklabar X New Hampshires			oar I		Silver	Okla	bars
	M	ales	Fen	ales	M	ales	Fer	ales		ī	lales	Fei	ales	X	lales	Fen	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Mean	n	Mean	n	Mean
ш	10	2.81	12	2.25	6	2.80	17	2.28	2	9	2.83	12	2.35	6	2.45	10	2.14
21	9	2.50	8	2.13	7	2.60	7	1.78	12	3	2.27	2	2.05	2	2.85	10	2.04
22	6	2.65	10	2.01	1	2.10	3	1.97	13	ш	2.91	20	2.28	3	2.53	3	2.20
23	7	2.71	6	2.15	10	2.55	9	2.06	14	10	2.80	9	2.27	4	2.45	4	2.18
24	15	2.94	16	2.19	10	2.82	5	2.04	15	5	2.88	5	2.12	13	2.11	6	1.88
25	10	3.04	17	2.23	3	2.83	3	2.27	16	8	2.80	14	2.36	7	2.80	6	2.18
27	8	2.75	4	2.45	12	2.85	6	2.28	17	10	2.87	11	2.35	13	2.59	13	2.12
28	13	2.57	12	2.09	4	2.67	3	1.83	18	2	3.20	3	2.47	6	2.68	7	2.17
2 9	7	2.47	6	2.17	6	2.65	9	1.91	19	2	2.95	4	2.25	0		0	
30	9	2.43	12	2.25	9	2.71	8	2.23	20	8	2.95	16	2.21	16	2.88	17	2.15
Total	94	2.71	103	2.18	68	2.71	70	2.10	Total	68	2.85	96	2.29	80	2.59	76	2.12
1*	3	3.00	5	2.06	8	3.09	n	2.33	26 ≭	18	2.77	15	2,11	n	2.44	13	2.02

*Control Pens

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ANALYSIS OF VARIANCE FOR TEN-WEEK BODY WEIGHT FOR CONTROL PENS

New Hampshire												
Source	d.f.	S.S.	¥.S.	F Values								
Total	23	2.5329										
Between Sires	1	•07 04	.0704									
Between Dams	3	.2340	.0780									
Interaction	3	. 8004	.26 68	2.988								
Remainder	16	1.4281	.0893									
	New Hamps	hire I Silver Ok	labars									
Total	23	1.7677										
Between Sires	l	.0022	.0022									
Between Dams	3	. 2520	.0840									
Interaction	3	.2022	.0674	.822								
Remainder	16	1,3113	.0820									
	Silver Okla	abars X New Hamp	shires									
Total	58	4.4684										
Between Sires	2	.1377	•0689									
Between Dams	8	1.6706	. 2088									
Interaction	8	. 4650	•0581	1.058								
Remainder	40	2.1951	•0549									
		Silver Oklabars										
Total	46	4.8031										
Between Sires	2	.1000	•0500									
Between Dams	6	•5158	•0860									
Interaction	6	.1836	•0306	•245								
Remainder	32	4.0037	.1251	• • • • • • • • • • • • • • • • • • •								

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BODY WEIGHT AMONG NEW HAMPSHIRES

Source of	Sam	ole 1	Sam	ole 2	Sam	ple 3	Sam	ple 4
Variation	d.f.	N.S.	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Total	217		186		119		119	
Between Sires	7	.2200	6	.4027	7	•2257	7	.1919
Between Dams	21	.1480	18	.1134	14	.0995	14	.1514
Interaction	21	•0832	18	.0936	14	.0757	14	.0754
Remainder	168	.0661	144	.0653	84	.0625	84	.0764

ANALYSIS OF VARIANCE

Statistics	Symbols	Sample 1	Sample 2	Sample 3	Sample 4
Contribution from sires	S	.0086	.0193	.0167	•0128
Contribution from dams	D	.0081	.0025	.0040	.0125
Interaction	I	.0043	.0071	.0044	.0
Remainder	Q	.0661	•0653	.0625	.07 64
Total	T	.0871	.09 42	.0876	.1017
Heritability	ЦS/T	•39	. 82	.76	•50
	ЦD /Т	•37	.11	.18	-49
	2(S+D)/T	•38	.46	•47	•50
Sex-linked effects	S-D/T	•006	.178	.145	.003
Maternal effects	D-S/T	ο	ο	0	ο
Non-additive effects	I/T	.049	•075	. 050	ο
			1		

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BODY WEIGHT AMONG NEW HAMPSHIRE X SILVER OKLABAR CROSSBREDS

ANALYSIS OF VARIANCE

Source of	Samp	ole 1	Sam	ole 2	Sam	ole 3	Sample 4	
Variation	d.r.	M.S.	d.r.	¥.5.	d.i.	N.S.	d.I.	I.S.
Total	184		184		77		77	
Between Sires	8	•3060	8	.2056	77	. 1526	7	.1232
Between Dams	24	.1300	24	.1040	7	. 0592	7	.1471
Interaction	24	•0800	24	.0457	7	.0236	7	.0515
Remainder	128	.0590	128	.0563	56	•0582	56	.0759

Statistics	Symbols	Sample 1	Sample 2	Sample 3	Sample 4
Contribution from sires	S	.0182	.0124	.0157	.0079
Contribution from dams	D	.0070	.0080	•0002	.0119
Interaction	I	.0097	ο	0	о
Remainder	Q	•0590	•0563	. 0582	•0759
Total	T	•0939	.07 67	.0741	•0957
Heritability	ls/T	•78	.65	•85	•33
	ЦD/Т	.30	. 42	.01	•50
	2(S+D)/T	•54	•53	.43	. µг
Sex-linked effects	S-D/T	.119	•057	•209	0
Maternal effects	D-S/T	o	0	0	.042
Non-additive effects	I/T	•103	0	0	o
		1	1		

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BODY WEIGHT AMONG SILVER OKLABAR X NEW HAMPSHIRE CROSSBREDS

ANALYSIS OF VARIANCE

Source of	Sam	ole 1	Sam	ole 2	Sam	le 3	Sample 4	
Variation	d.f.	N.S.	d.f.	¥.S.	d.f.	¥.S.	d.f.	¥.S.
Total	211		248		102		85	
Between Sires	7	.1871	8	.1755	6	.4018	5	•4141
Between Dams	21	.25 89	24	.1229	12	•1249	10	.1293
Interaction	21	.0672	24	.0543	12	.1177	10	.0512
Remainder	162	•0832	192	.0743	72	•0809	60	.0758

Statistics	Symbols	Sample 1	Sample 2	Sample 3	Sample 4
Contribution from sires	S	.0065	.0063	.0316	.0376
Contribution from dams	D	.0220	•0061	.0012	. 0089
Interaction	I	0	0	.0123	0
Remainder	Q	.0832	.0743	•0809	•0758
Total	T	.1117	.0867	.1260	.1223
Heritability	4s/t	•23	•29	1.00	1.23
	ЦD/T	.78	•28	. 04	.29
	2(S+D)/T	.51	•29	•52	.76
Sex-linked effects	S -D/T	0	.002	•241	•235
Maternal effects	D-S/T	.139	0	0	ο
Non-additive effects	I/T	0	0	•098	0
		1	1		·

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BODY WEIGHT AMONG SILVER OKLABARS

Source of	Sam	Sample 1		Sample 2		Sample 3		le 4
Variation	d.f.	M.S.	d.f.	X.S.	d.f.	¥.S.	d.f.	¥.S.
Total	184		184		55		55	
Between Sires	8	.1750	8	.1704	5	•4134	5	. 2236
Between Dams	24	. 2210	24	.1232	5	•0805	5	.1864
Interaction	24	. 0770	24	. 0568	5	.1 458	5	.1120
Remainder	128	•0900	128	.0861	40	.1178	40	.1435

ANALYSIS OF VARIANCE

Statistics	Symbols	Sample 1	Sample 2	Sample 3	Sample 4
Contribution from sires	S	.0071	•0070	.0 446	.0134
Contribution from dams	D	.0218	•0062	0181	.0072
Interaction	I	ο	0	.0093	0
Remainder	Q	•0900	.0861	.11 78	.1435
Total	T	.1189	•0993	. 1536	.1541
Heritability	цs/т	.24	•28	1.16	•33
	ЦD/Т	.73	•25	47	.18
	2(S +D)/T	-49	.27	•35	•25
Sex-linked effects	S-D/T	0	.008	.408	•038
Maternal effects	D-S/T	.124	0	0	0
Non-additive effects	I/T	0	0	0	0
			1	1	

PART II

HETEROSIS, HERITABILITY, TYPES OF GENE ACTION, AND MATERNAL EFFECTS IN RELATION TO TEN-WEEK BREAST ANGLE IN BROILERS

Dressed fryers with broad breasts present a highly desirable carcass from the consumers' point of view. There is a generally accepted belief that broad-breasted birds yield a higher percentage of edible meat than do the so-called "slab-sided" birds. Meat yield studies have shown that this is not always true (Jaap et al., 1950). Nevertheless, an endeavor must be made to meet the consumers' demands.

The trend toward "cut-up" poultry in recent years has helped to market narrow-breasted birds to better advantage. By removing the breast bone, breast meat can be displayed in a manner that gives birds a broad-breasted appearance. Since many of the market birds are still sold as whole birds, other means must be sought to improve breast width.

The most logical means of improving breast width is by selective breeding. The literature contains numerous examples to show that breast width is an inherited characteristic in poultry. Thus improvement can be expected if broad-breasted birds are selected as parents. This adds another characteristic to an already overburdened breeding program with which most breeders are confronted. For this reason it is highly desirable to know something about the mode of inheritance of breast width in chickens in order to make selection and mating as efficient as possible.

This part of the experiment was designed to determine the following information in New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds :

1. If heterosis was involved in determining 10-week breast angle in the crosses.

- 2. Heritability of 10-week breast angle.
- 3. Types of gene action involved in determining 10-week breast angle.
- 4. Maternal effects on 10-week breast angle.

REVIEW OF LITERATURE

Two deficiencies are noted in reviewing the literature on the inheritance of breast width in poultry. In the first place, much of the work has been confined to turkeys and there is no assurance that these data are applicable to chickens. The second deficiency is the lack of an adequate, standard method or procedure of measuring breast width.

Most of the genetic studies on breast width in turkeys have considered body conformation rather than breast width alone. Conformation includes breast width as a component part, but also includes many other factors that are important in determining a desirable market carcass.

One of the earliest means used to measure breast width was a solder wire molded around the breast to determine its curvature (Jaap and Penquite 1938; Asmundson, 1944 and 1945; Collins <u>et al</u>, 1950; and others). Bird (1945) developed an instrument that measured one-half the breast width and body depth simultaneously. Knox and Marsden (1944) and others have used subjective grades to determine breast width. El-Ibiary and Jull (1948), Kish (1953), and others have used calipers to take this measurement. Various workers have employed a device with expandable jaws that measures the angle of the breast in degrees. This latter type is presently being used rather widely as the West Virginia breast angle meter. Its greatest advantage is the speed with which measurements can be made.

Jaap and Penquite (1938) used solder wire to measure breast width in chickens and turkeys. Dressed birds were suspended by the feet and a wire was molded around the breast from the anterior end of the keel toward the point of insertion of the femurs. The solder wire was then placed on a piece of paper and a drawing made of the interior curvature. The curve was then transposed to graph paper and the width measured at successive points of one-half inch from the apex. A satisfactory point for measuring

breast width to demonstrate differences was found to be 12 inches from the anterior end of the keel. This method of measuring breast width was also accurate for live birds as shown by a correlation of 0.998 between live and dressed measurements. The greatest disadvantage in using this system is the length of time required to obtain individual measurements.

Asmundson (1944) used the "molded solder wire" technique to determine breast width in turkeys but criticized it for being relatively crude. Repeatability of measurements obtained by Jaap and Penquite (1938) demonstrated that this method can be used to good advantage when used properly.

Knox and Marsden (1944) studied the inheritance of width of breast in turkeys by mating Beltsville Small White toms with Broad-breasted Bronze hens. Both the F1 and F2 progenies of this cross had an average breast width intermediate between the parental averages. They concluded that breast type was inherited in a manner typical of quantitative characters. This work demonstrated an apparent genetic difference for breast width but their method of classifying birds for these differences can be severely criticized. Their method involved a combination of touch and sight. One person held the turkeys with breasts up while an assistant cupped both hands over the breast, one hand on either side. Each bird was given a numerical value for breast type ranging in value from 1 to 9 with 1 being the most desirable and 9 being the least desirable. Human error could be an important factor and subject such data to considerable bias. Statistical analyses of such data would be of questionable validity.

Asmundson (1945) studied the inheritance of breast width in turkeys by reciprocally crossing 2 strains of Bronze turkeys and backcrossing the F_1 progeny to the parental strains. Breast width was measured at 24 weeks of age using the solder wire method. An analysis of variance of the data showed a significant difference between the means of the 2 strains. The

 F_1 and backcross progeny for the most part were intermediate between the parental means. The author stated that the data indicated that differences in breast width were due to multiple genes and that these genes were autosomal.

Lerner and associates (1947) calculated heritability estimates for 12-week breast angle using a randomly selected sample of New Hampshire fryers. Breast width was determined by molding a solder wire over the birds breast about 1 centimeter back of the anterior point of the keel and measuring the width about 1 centimeter laterad and dorsad to the keel. Due to the small numbers involved, the data were transformed into standard deviations for the 2 sexes and then combined. The heritability analysis was based on the methods of Whatley (1942) and Hazel et al (1943) with a few modifications called for by the nature of the data. Heritability estimates obtained were as follows: 0.126 based on the sire's contribution, 0.293 based on the dam's contribution, and 0.210 based on a combination of the two. The authors stated that due to small samples used, sampling error was probably large and estimates should be considered as approximations.

El-Ibiary and Jull (1948) studied the genetic variation in live body conformation in turkeys. Beltsville Small White females were mated to Broad-breasted Bronze toms in the first mating. F_1 females were mated to either F_1 toms or Beltsville Small White toms. Breast width was measured at 28 weeks of age using an instrument devised by Bird (1945). This instrument measured one-half the breast width at one-fifth of the body depth. Analysis of variance revealed a genetic difference among individuals in width of breast. In all cases sires contributed more to the variance than did the dams. The authors stated that this was due to using purebred and F_1 crossbred sires but only F_1 crossbred dams to produce the F_2 . The inference was that the purebreds contributed more to the genetic

variance than did the crossbreds. This appears to be the author's own supposition rather than factual information derived from their data.

Bird (1948) used the device he developed in 1945 to measure breast width in Barred Plymouth Rocks and White Leghorns. He secured measurements from the progeny of 5 Barred Plymouth Rock sires each of which had been mated to 2 or 3 dams. The data were analyzed by calculating the regression of breast width on depth of body. The regression equation was found to take the approximate form

$$\bar{X} = 85 - 0.2 X$$

 $\overline{\mathbf{Y}}$ was the expected width proportionate to the depth X when measurements were expressed in millimeters. When roundness of breast was expressed as I-Y, that is the observed minus the expected, a positive residual value indicated a better than average roundness. Negative values indicated a sharp and narrow breast width. Only in the case of 1 dam and 1 sire was there evidence of any material influence of parents upon the mean breast width of their progeny. This male provided evidence for a true genetic difference. Among the progeny of 5 White Leghorn sires there was no evidence for genetic segregation for breast width. Bird concluded that breast width was inherited chiefly from the sire with, at best, an incipient influence from the dams. He further stated that it was possible to progeny test sires on the basis of roundness of breast of their sons and thereby achieve improvement in this important character. If breast width is inherited chiefly from the sire, it would of necessity be a sex-linked trait. Therefore. selection of broad-breasted sires should give rapid improvement in breast width. This has not proved to be true in selective breeding programs. Perhaps if these data had been subjected to an analysis of variance, any genetic differences would have been more clearly demonstrated.

Asmundson (1948) crossed strains of turkeys differing widely in mean

body weight and breast width in order to study the mode of inheritance of several traits. Measurements were taken at 24 weeks of age. The data were subjected to an analysis of variance. The strains differed significantly in width of breast. The F_1 progeny were in all cases intermediate between the parental means and there were no consistent differences between the F_1 progeny from reciprocal crosses; hence, the differences in breast width were determined by autosomal genes. There was no indication of dominant genes. There was a highly significant difference between dam families, while those between sires were not. The lack of significance between sires was probably due to using only a few highly selected sires. A large randomly selected sample probably would have given different results.

Collins and associates (1950) studied the genetic differences in breast width and fleshing in a strain of Rhode Island Reds in which no previous selection for these traits had been practiced. These workers selected narrow-breasted and broad-breasted birds so that like-to-like and unlike -to -unlike matings could be made. Breast width was determined by using a lead tape and with a breast angle measuring device. The former method of measuring was discarded in favor of the latter when correlations between measurements were found to be high. Measurements were taken at 8 and 12 weeks of age and the 8-week measurements were converted to 12-week measurements by means of a regression equation. Data for sexes were pooled when a "t" test revealed no significant difference between sexes in all but one of the mating periods. Differences between dams were not consistent. It was evident that a small but significant genetic difference existed between the broad-breasted and narrow-breasted sires used in this study. The authors stated that the apparent absence of differences in breast width among progenies of unlike dams could be attributed in part to the small number of progeny, but more to confounding of dam and period. It was not

implied that dams exert no influence on breast width as claimed by Bird (1948).

Kish (1953) selected narrow-breasted and broad-breasted New Hampshire breeders on the basis of 14-week breast width and made all possible combination of matings of like-to-like and unlike-to-unlike. Vernier calipers were used to measure breast width to the nearest one-sixteenth of an inch. The point of measurement was approximately 1 inch posterior to the cranial process of the sternal crest at a distance one-half inch dorsad to the crest. Analysis of variance showed highly significant differences between means of sexes and between means of mating types. The experiment was repeated with selection of breeders being based on individual and family records. In a span of 3 years (4 generations) it was possible to develop wide and narrow breast lines that differed from each other on an average of 0.09 to 0.11 inches. The most effective breeder selection was combined individual and family selection. Progeny resembled the sires in breast width to a greater degree than they resembled the dams. Kish stated that this would permit a breeder to divide his breeding program into 2 parts. Concentration of effort toward meat type could be used in male lines, and high egg production in female lines. To accomplish this, a breeder would have to divide his flock into 2 lines thus reducing his facilities and effective breeding population by one-half for each of the 2 traits. Kish failed to consider the genetics of the differences in breast width. To this writer's knowledge there are no known cases where the sire contributes more to the progeny's genotype than the dam, except in cases of sex-linked genes. All the evidence available on the inheritance of breast width point to quantitative inheritance with the possible influence of some sex-linked genes. For this reason a sounder approach to this problem appears to be a breeding program combining individual and family selection for both traits, with

emphasis placed on the one deemed most important by the breeder.

Although there are few estimates of heritability of breast width in chickens, there is ample evidence to show that this trait is influenced by heredity. All evidence points to a typical quantitative trait with evidence strongly in favor of sex-linked gene effects.

MATERIALS AND METHODS

The data on breast angle, measured as described previously in the section on "Experimental Procedure", were secured from the same populations described in Part I. The methods of analysis are the same as for those used to analyze 10-week body weight data, and thus will not be reported

RESULTS

The data on 10-week breast angles are summarized in Tables 10 throug 13. The averages for the New Hampshires and Silver Oklabars were conside to be indicative of the parental averages for the purpose of comparing th crossbred averages.

In all hatches the Silver Oklabars had a higher average breast angle than the New Hampshires and crossbreds. In all hatches except the fourth hatch, the average for New Hampshires was the lowest average of all group The average for New Hampshire females of the fourth hatch equalled the average for the New Hampshire X Silver Oklabar crossbred females of that hatch. The crossbreds had an average breast angle intermediate between the parental breeds. The cross utilizing Silver Oklabar males was slight superior in average breast angle to the reciprocal crossbreds.

To test the significance of the differences in mean 10-week breast angle, the data were tested statistically by means of "t" tests. The dat for the crosses were pooled and compared to the pooled data for the breed for each hatch and for all hatches combined. The better cross (SB X NH) mean was also compared to the parental mean for each hatch and for all hatches combined. In no case was there a significant difference between the means tested. It can be concluded that no heterotic effect was prese on 10-week breast angle.

An analysis of variance was calculated for the control pens to deter if an interaction component of variance ware present. Since the same sire and dams were used for all hatches, an interaction component would be an indication of a hatch effect. The results of these analyses are presente in Table 14. Only in the case of New Hampshires was the interaction component a positive figure, and in this instance it did not approach

statistical significance. On this basis, it seemed justifiable to state that there was no hatch effect on 10-week breast angle.

The analyses of variance and important estimates derived from the components of variance are presented in tables 15 through 18. Estimates of heritability for 10-week breast angle ranged from -0.23 to 0.91. The mean estimate was 0.46. Estimates of heritability based on the dams' contributions averaged 0.55 and those estimates based on the sires' contriputions averaged 0.37. This wide range can most likely be explained on the basis of sampling error since the samples used were relatively small. Since S and D have to be multiplied by 4 to calculate estimates from them, it can readily be seen that any error, whether sampling or otherwise, will also be multiplied by 4 and contribute to this wide range.

Mean estimates for the different breeds and crosses were as follows: 0.47 for New Hampshires, 0.52 for New Hampshire X Silver Oklabars, 0.41 for Silver Oklabar X New Hampshires, and 0.44 for Silver Oklabars.

Sex-linked gene effects ranged from 0.04 to 0.24 and were present in 4 of 8 cases. Non-additive gene effects were also evident in 4 of 8 cases and ranged from 0.02 to 0.10. It is difficult to draw any conclusions regarding the magnitude of these effects because of the inconsistency of their occurrence. Perhaps the most satisfactory method of deciding what value to give to each of these effects would be to obtain an average effect in each case. The average sex-linked gene effect was 0.08 and the average non-additive gene effect was 0.02.

Based on the sire components of variance, an estimate of 0.39 was calculated for the total genetic variance. Based on the dam components of variance, an estimate of 0.57 was calculated for the total genetic variance plus a fraction of the total variance due to maternal effects. Maternal

effects ranged from 0.08 to 0.36 and were evident in 4 of 8 cases. The average maternal effect was 0.14. Removal of the maternal effect from the dams' contributions to the variance resulted in an estimate of 0.43 for the total genetic variance. The estimate from sire and dam contributions was 0.41. Two percent of the genetic variance was due to non-additive gene effects and the remaining 0.39 was due to genes with additive effects. Sexlinked gene effects accounted for 0.08 of the total variance. These effects can be additive and need not be separated from the autosomal additive gene effects.

The different breeds and crosses varied too much in percentages of the total variance due to different types of gene action on 10-week breast angle to draw any conclusions in this respect.

DISCUSSION

The results of this study indicate that heterosis was absent or played an exceedingly small role in the determination of 10-week breast angle in the breeds and crosses used in this study. In some cases the average breast angle of the crossbreds exceeded the mean for the parental breeds. This may be considered as a heterotic effect, but not sufficiently high to be of practical importance. However, since the Silver Oklabar X New Hampshire cross demonstrated a worthwhile heterotic effect on body weight and a slight effect on breast angle, the latter effect becomes more important. The heterotic effect on body weight is sufficient to make the Silver Oklabar X New Hampshire mating economically sound, thus any secondary improvement such as increased breast width makes the cross more desirable.

Since the reciprocal crosses failed to produce the same results in 10-week breast angle, it appears that the slight difference was due to sex-linked genes rather than heterosis. This was not supported by the results of the analyses of variance which indicated that sires and dams contributed about equally to this trait.

The most important statistics derived from this study are the heritability estimates for 10-week breast angle. Most of these estimates fell in the range of 42 to 68 percent. This is a range in which individual selection is slightly more effective than family selection. If a breeder includes breast angle as a trait in his breeding program, measurement at broiler age and selection on the basis of individual measurements are to be recommended.

Most of the genetic variance in 10-week breast angle was due to genes with additive effects. Non-additive gene effects were indicated in 4 out

of 8 cases, but never exceeded 10 percent of the total variance. Sampling error might have caused these small effects. If non-additive gene effects were present, they were too small to be of any great importance. However, non-additive gene effects might be of importance on an individual bird basis. Some individuals were superior to their sibs and to non-sibs because they received a genotypic combination that was not wholly additive in nature and not uniformly transmitted to the rest of the family. This could lead to the selection of some individuals for breeding purposes that would not produce progeny with the expected amount of improvement in breast width.

On the basis of the results of this investigation, it appears that 10-week breast angle, among the breeds and crosses studied, is inherited in a manner characteristic of a quantitative trait. Most of the genetic variance is due to additive gene effects. Sex-linked gene effects apparently influence this trait too, but these genes may also be additive in their effects. Maternal effects were indicated but did not occur consistently. Since maternal effects and sex-linked gene effects were detected by inference, the magnitude of these effects is questionable.

SUMMARY

From 2 series of diallel matings random, samples were studied to alculate heterotic effects, estimates of heritability, types of gene ction, and maternal effects in relation to 10-week breast angle among lew Hampshires, Silver Oklabars, and reciprocal crosses between these reeds. The study involved 82 sires, 440 dams, and 5,355 chicks. A otal of 8 samples were used which varied in number of birds from 10 sires, 0 dams, and 60 chicks to 16 sires, 32 dams, and 256 chicks per sample.

The data were analyzed by analysis of variance as outlined by Lerner (1950). The results were as follows:

1. Heterosis was absent or negligible in determining 10-week breast ugle. Silver Oklabar males contributed slightly more to the average breast ridth than the New Hampshire males. Apparently sex-linked genes were functioning, and the frequency of the desirable genes was higher in Silver Neglabars than in the New Hampshires.

2. Heritability estimates for 10-week breast angle ranged from -0.23 to 0.91. The mean estimate was 0.46.

3. Sex-linked gene effects were evident in 4 of 8 cases, and the mean ffect was 0.08. Non-additive gene effects were evident in 4 of 8 cases and the mean effect was 0.02. Approximately 39 percent of the total variunce was due to genes with additive effects.

4. Maternal effects were evident in 4 of 8 cases and the mean effect ras 0.14.
AVERAGE TEN-WEEK BREAST ANGLE OF PROGENY BY PENS FOR FIRST HATCH

	New Hampshires			ires	N	lew Ham ilver	pshir Oklal	e I Dars		S	ilver Iew Han	Oklat	oar I 'es		Silver	Okla	bars
1	Ņ	ales	Fen	ales	N	ales	Fer	ales			lales	Fen	ales)	ales	Fen	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Mean	n	Mean	n	Mean
2	22	72.5	23	73.2	19	72.4	22	72.8	11	30	75.3	23	74•7	30	76.2	24	78.0
12	16	72.8	15	71.5	19	74.2	27	73.1	21	31	74.9	21	75.6	19	74.2	16	76.9
13	19	72.2	17	73.8	15	74.3	17	74.7	22	19	74.6	15	73.2	10	73.5	12	75.6
14	22	73.5	23	73 .2	22	75.0	18	74.2	23	13	73.3	17	72.5	16	74.1	15	75.3
15	14	70.9	14	71.8	16	73.1	15	72.7	24	22	72.6	20	74.0	12	75.2	17	76.9
16	17	74.6	16	75.5	11	74.3	13	73.7	25	19	73.3	24	75.4	19	74.9	15	76.3
17	26	75.3	14	72.3	19	75.1	18	75.7	27	23	72.8	14	73.4	15	74.5	26	75.2
18	9	75.6	27	73.1	15	74•3	16	74.5	28	0		0		0		0	
19	25	73.8	21	73.0	18	75.6	9	75.8	29	15	73.8	21	76.9	23	75.1	21	76.4
20	20	71 .1	10	72.8	14	75.2	22	75.3	30	20	74.4	31	74.7	16	75.9	17	76.3
Total	190	73.2	180	73.1	168	74.4	177	73.7	Total	192	74.2	186	74.6	160	75.0	163	76.4
<u>1</u> *	20	72.9	·12	71.5	18	73.1	20	72.5	26*	23	75.2	18	76.5	29	76.8	17	77.5

*Control Pens

AVERAGE TEN-WEEK BREAST ANGLE OF PROGENY BY PENS FOR SECOND HATCH

	New Hampshires			ires	N S	ew Ham ilver	pshir Oklab	e I ars		S N	ilver ew Ham	Oklab pshir	ar I es		Silver	Okla	bars
4	M	ales	Fem	ales	Ĩ	ales	Fem	ales		M	ales	Fem	ales	M	ales	Fem	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Mean	n	Mean	n	Mean
2	16	72.2	16	70.9	11	72.1	16	71.6	11	22	73.2	22	74.3	24	75.8	13	75.8
12	7	73.9	16	71.4	18	71.9	16	71.9	21	19	75.9	19	77.1	13	75.8	11	76.4
13	15	73.0	13	72.9	10	73.8	15	73.0	22	9	75.0	24	73.4	0		8	77.5
14	23	71.6	17	71.8	14	70 .9	20	73.4	23	13	75.6	14	72.3	10	75.5	17	75.0
15	2	70.0	6	71.7	3	70.8	9	71.9	24	12	75.4	18	76.0	18	75.8	11	77.3
16	15	69.3	19	70.0	9	72.2	13	71.7	25	16	72.7	11	72.7	7	74.3	14	76.4
17	19	70.5	17	71.9	18	72.5	23	72.2	27	24	72.8	19	73.2	19	74.0	23	73.9
18	10	72.8	8	70.9	6	75.8	5	73.5	28	12	72.9	11	73.2	9	72.2	7	73.6
19	24	72.3	21	•72.1	17	74.7	20	74.0	29	20	74.3	8	77.2	11	74.8	15	74•7
20	12	73.1	15	72.0	14	73.6	16	74•4	30	24	72.4	21	72.6	10	73.3	17	74.6
Total	143	71.9	148	71.6	120	72.9	153	72.8	Total	171	73.8	167	74.1	121	74.9	136	75.4
1*	10	74.3	7	72.5	15	74.8	16	72.8	26#	19	75.1	15	76.0	26	77.2	14	76.8

*Control Pens

A VERAGE TEN-WEEK BREAST ANGLE OF PROGENY BY PENS FOR THIRD HATCH

	New Hampshires		nires	New Hampshire X Silver Oklabars				Silver Okla New Hampshi			bar X Silver Ok res			Okla	bars		
)	ales	Fei	ales)	lales	Fen	ales)	ales	Fen	ales	X	ales	Fen	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Mean	n	Mean	n	Mean
11	20	69.5	21	69.4	23	71.5	17	72.8	2	20	69.5	21	69.4	23	71.5	17	72.8
21	10	7.20	20	72.3	18	72.9	16	71.6	12	10	72.0	20	72.3	18	72.9	16	71.6
22	17	72.1	17	73.4	4	75.6	5	74.5	13	17	72.1	17	73.4	4	75.6	5	74.5
23	8	71.6	11	70 .7	13	73.1	18	72.5	14	8	71.6	11	70.7	13	73.1	18	72.5
24	30	70.6	13	70.2	14	72.0	25	72.7	15	30	70.6	13	70.2	14	72.0	25	72.7
25	15	72.7	25	71.6	18	73.1	18	74.7	16	15	72.7	25	71.6	18	73.1	18	74.7
27	19	73.7	13	72.7	18	73.2	22	75.9	17	19	73.7	13	72 .7	18	73.2	22	75.9
28	11	71.8	5	71.0	9	72.5	4	73.1	18	11	71.8	5	71.0	9	72.5	4	73.1
29	15	73.2	15	71.5	15	72.3	19	71.3	19	15	73.2	15	71.5	15	72.3	19	71.3
30	25	70.9	31	71.2	12	73.1	18	72.8	20	25	70.9	31	71.2	12	73.1	18	72.8
Total	170	71.6	171	71.4	144	72.7	162	73.2	Total	170	71.6	171	71.4	144	72.7	162	73.2
1*	5	73.0	5	74.7	11	72.7	6	72.1	26*	5	73.0	5	74.7	11	72.7	6	72.1

A VERAGE TEN-WEEK BREAST ANGLE OF PROGENY BY PENS FOR FOURTH HATCH

	+														_		
		New H	lamps h	ires		lew Hamj	pshir Oklah	e I			Silver '	Oklat	ar I		Silver	Okla	bars
	L N	lales	Fen	ales	ľ	lales	Fei	ales	-	Ì	lales	Fei	ales		lales	Fem	ales
Pen	n	Mean	n	Mean	n	Mean	n	Mean	Pen	n	Mean	n	Mean	n	Mean	n	Mean
11	10	69.8	12	71.5	6	72.5	17	72.5	2	9	74.7	12	71.9	6	72.9	10	74.0
21	9	70 .8	8	72.2	7	69.3	7	69.3	12	3	70.8	2	72.5	2	77.5	10	76.8
22	6	69.2	10	70.8	1	75.0	3	71.7	13	11	72.1	20	73.8	3	71.7	3	75.0
23	7	72.5	6	70.0	10	72.8	9	73.3	יור	10	73.5	9	72.5	4	73.1	4	75.0
24	15	72.7	16	71.7	10	74.3	5	73.0	15	5	73.0	5	73.0	13	73.1	6	76.7
25	10	71.3	17	72.9	3	73.3	3	74.2	16	8	71.3	14	73.9	7	75.0	6	75.8
27	8	72.5	4	74.4	12	74.4	6	70.4	17	10	75.5	11	73.9	13	74.6	13	75.8
28	13	70.4	12	70.6	4	71.3	3	73.3	18	2	73.8	3	71.7	6	72.9	7	70.6
29	7	69.3	6	68.8	6	72.5	9	66.7	19	2	72.5	4	73.8	0		0	-
30	9	68.3	12	69.8	9	74.4	8	70.3	20	8	71.3	16	70.9	16	73.9	17	73 .7
Total	94	70.8	103	71.3	68	73.1	70	71.2	Total	68	73.0	96	73.0	69	74.9	76	74.7
1*	3	75.0	5	68,5	8	73.8	11	70.9	26#	18	75.7	15	71.7	11	74.8	13	77.3

*Control Pens

ANALYSIS OF VARIANCE OF TEN-WEEK BREAST ANGLE FOR CONTROL PENS

		new mampenires		
Source	d.f.	S.S.	N.S.	F Values
Total	23	248.96		
Between Sires	1	26.83	26.830	
Between Dams	3	86.46	28.820	
Interaction	3	44.00	14.677	2.562
Remainder	16	91.67	5.729	
	New Hamp	shire X Silver (Oklabars	
Total	23	195.83		
Between Sires	1	4.16	4.160	
Between Dams	3	89.58	29.860	
Interaction	3	14.59	4.863	•889
Remainder	16	87.50	5.469	
	Silver O	clabar X New Ha	ampshires	
Total	58	623.41		
Between Sires	2	5.41	2.705	
Between Dams	8	235.41	29.426	
Interaction	8	40.42	5.053	•591
Remainder	40	342.17	8.554	
		Silver Oklabara	1	
Total.	46	539.32		
Between Sires	2	28.38	14.190	
Between Dams	6	167.44	27 •907	
Interaction	6	35.16	5.860	•608
Remainder	32	308.34	9.636	

SOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEP BREAST ANGLE AMONG NEW HAMPSHIRES

ource of	First	t Series	Secon	d Series
ariation	d.f.	¥.S.	d.f.	¥.S.
otal	248		102	
stween Sires	8	42.7488	6	12.6733
etween Dams	24	24.0963	12	23.4958
nteraction	24	12.2804	12	10.4167
emainder	192	7.6715	72	9.6642

ANALYSIS OF VARIANCE

tatistics	Symbols	First Series	Second Series
ontribution from sires	S	1.9043	.2507
ontribution from dams	D	1.4770	2.1799
iteraction	I	1.1522	•2508
emainder	Q	7.6715	9.6642
otal	T	12,2050	12.3429
eritability	ЦS/Т	.62	•08
	цо/т	•48	•71
	2(S+D)/T	•55	•39
ex-linked effects	S-D/T	•035	0
aternal effects	D-S/T	0	.156
on-additive effects	I/T	•094	.020

POOLED ANALYS IS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BREAST ANGLE AMONG NEW HAMPSHIRE X SILVER OKLABAR CROSSBREDS

Source of	First	Series	Second Series			
Variation	d.f.	¥.S.	d.f.	M.S.		
Total	184		55			
Between Sires	8	24.6088	5	18.5440		
Between Dams	24	9.7658	5	16.0440		
Interaction	24	7.2479	5	7.2880		
Remainder	128	6.8360	40	7.2917		

ANALYSIS OF VARIANCE

Statistics	Symbols	First Series	Second Series
Contribution from sires	S	1.4467	1.8753
Contribution from dams	D	•4197	1.4587
Interaction	I	•1373	0
Remainder	Q	6.8360	7 •2917
Total	T	8.8397	10.6257
Heritability	ЦS/T	• 65	.71
	ЦD/T	.19	•55
	2(S+D)/T	•42	•63
Sex-linked effects	S-D/T	.116	•235
Maternal effects	D-S/T	0	0
Non-additive effects	I /T	.016	0

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BREAST ANGLE AMONG SILVER OKLABAR X NEW HAMPSHIRE CROSSBREDS

Source of	First	Series	Second Series			
Variation	d.f.	¥.S.	d.f.	¥.S.		
Total	155		85			
Between Sires	⁻ 5	12.6960	5	36.1120		
Between Dams	15	19.7273	10	11.5370		
Interaction	15	5.7147	10	10.6960		
Remainder	120	6.0808	60	8.8887		

ANALYSIS OF VARIANCE

Symbols	First Series	Second Series
S	4395	2.8240
D	1.7058	.1402
I	0	.6024
Q	6.0808	8.8887
Т	7.7606	12.4553
45/T	23	•91
4D/T	•88	•05
2(S+D)/T	•33	. 48
S-D/T	O ,	.215
D-S/T	•276	0
I/T	0	•048
	Symbols S D I Q T LS/T LD/T 2(S+D)/T S-D/T D-S/T I/T	Symbols First Series S 4395 D 1.7058 I 0 Q 6.0808 T 7.7606 LS/T 23 LD/T .88 2(S+D)/T .33 S-D/T 0 D-S/T .276 I/T 0

POOLED ANALYSIS OF VARIANCE, COMPONENTS AND IMPORTANT ESTIMATES FOR TEN-WEEK BREAST ANGLE AMONG SILVER OKLABARS

Source of	First	Series	Secon	d Series	
Variation	d.f.	¥.S.	d.f.	M.S.	
Total	138		33		
Between Sires	6	12.6350	3	10,5900	
Between Dams	18	17.4355	3	27.2600	
Interaction	18	3.0217	3	1.5600	
Remainder	96	7•5955	24	10.0695	

ANALYSIS OF VARIANCE

Statistics	Symbols	First Series	Second Series
Contribution from sires	S	.4200	•0868
Contribution from dams	D	1.6400	2.8650
Interaction	I	0	0
Remainder	Q	7•5955	10.0695
Total	T	9.6555	13.0213
Heritability	4s/T	.17	•03
	4d/T	•69	•88
	2(S+D)/T	•43	•45
Sex-linked effects	S-D/T	0	0
Maternal effects	D_S/T	•497	.213
Non-additive effects	I/T	0	0

PART III

PHENOTYPIC, GENETIC, AND ENVIRONMENTAL CORRELATIONS BETWEEN TEN-WEEK BODY WEIGHT AND TEN-WEEK BREAST ANGLE IN BROILERS

The importance of early growth rate in broilers as reflected in body weight at broiler age and the desirability of broad breasts in broilers have been discussed in Parts I and II. Selection for body weight is of primary importance in the breeding program of any breeder of broiler strains. Selection for breast width is also desirable but does not compare with the importance of body weight. The more competitive the broiler industry becomes, the greater will be the necessity for broilers with wide breasts which present more eye appeal to the customers.

If a breeder adds breast width to his selection program, chances are he will reduce his selection pressure for body weight in order to select for a trait of lesser importance. However, if a sufficient positive genetic relationship exists between body weight and width of breast, breeders could continue selecting solely for body weight and still obtain a reasonable amount of improvement in breast width.

This portion of the experiment was designed to determine the phenotypic, genetic, and environmental correlations between 10-week body weight and 10-week breast angle.

REVIEW OF LITERATURE

Published data dealing with the interrelationship between body weight and width of breast in chickens are very limited. Several references are available on this relationship among turkeys, but most of these papers are directed toward body conformation in general. To this writer's knowledge the paper of Lerner <u>et al</u> (1950) is the only published work in which genetic and environmental as well as phenotypic correlations were determined.

Asmundson (1944) calculated phenotypic correlations between body weight and various body measurements in 3 strains of Bronze turkeys. Strain 1 was selected primarily for egg production and was comparatively poor in market conformation. Strain 2 was selected for good conformation and early development, but was not of the broad-breasted type. Strain 3 was the broad-breasted type of Bronze turkey. Correlation coefficients between breast width and body weight ranged from 0.435 to 1.0. These values are high in comparison with those reported elsewhere.

Lerner and associates (1947) studied the interrelationship between breast width and body weight at 12 weeks of age among New Hampshire fryers. The statistical techniques of Hazel <u>et al</u> (1943) were used to determine phenotypic, genetic, and environmental correlations between these traits. Correlations based on a combination of sire and dam contributions were 0.099, 0.157, and 0.132 respectively for genetic, environmental and phenotypic correlations. Additional genetic correlation coefficients of -0.134 based on sire's contribution, and 0.228 based on dam's contribution were calculated.

El-Ibiary and Jull (1948) made observations on body weight and various characters affecting conformation among 28-week old Beltsville Small White turkeys, Broad-breasted Bronze turkeys, and crossbred progeny of these

two varieties. These workers found a positive phenotypic correlation of 0.066 between body weight and breast width among these turkeys.

El-Ibiary (1948) published a more complete analysis of the data discussed above. The phenotypic correlations between body weight and breast width at 28 weeks of age among the turkeys studied were calculated separately for sexes. The resulting correlation coefficients were 0.392 for males and 0.390 for females as compared with a value of 0.066 for the combined sexes. Since turkeys show such a wide sex difference in body weight, analyzing the data for sexes separately seems a more accurate measure of the true relationship.

Asmundson (1948) studied the genetics of weight and conformation in 2 strains of Bronze turkeys which differed in weight and width of breast. Data were collected from purebred progeny, crossbred progeny, and backcross progeny at 24 weeks of age. These data revealed positive phenotypic correlations of 0.430 for the female progeny and 0.447 for the male progeny.

Collins and co-workers (1950) found a positive relationship between body weight and breast angle among Rhode Island Reds. Their data were taken from a series of matings in which a narrow-breasted line and a broad-breasted line were selected and all possible matings of like-to-like and unlike-to-unlike were made. A regression of breast width on body weight revealed that breast width tended to increase as body weight increased. This result was based on measurements taken at 8 and 12 weeks of age. These workers found a significant phenotypic correlation of 0.261 between breast width and body weight in the female parent stock. The combined male and female progeny showed a correlation of -0.288 at 8 weeks and of 0.075 at 12 weeks. When the data for sexes were analyzed separately, the correlations at 8 and 12 weeks of age respectively, were 0.226 and 0.352 between the 2 traits studied for males, and 0.141 and 0.125 for females.

MATERIALS AND METHODS

The design of the experiment and method of collecting data were disissed previously under "Experimental Procedure" and demonstrated in Table) of the Appendix. From these data, random samples were taken for this irt of the study.

To simplify the statistical analyses, subgroups of equal numbers were sed; that is, equal numbers of dams per sire and equal numbers of offspring or dam were used. Due to the wide range of variation in body weight otween sexes, and the small range of variation in breast angle between oxes, the data were analyzed separately for each sex.

When the raw data were examined, it was found that a majority of the Ire families contained at least 3 dams that had 3 or more offspring of le sex or the other. The average number of offspring per dam was less lan 6; therefore, it was impossible to find many dams with 3 chicks of lch sex. In order to utilize as many sire families as possible, 3 dams er sire were used for each sex. A table of random numbers was used to slect the dams and the first 3 chicks of the approporiate sex were selected er each dam used. All chicks had equal opportunity of being banded in ty sequence at hatching time, thus these were random samples.

The data for the different hatches were pooled for the analyses. alyses of variance, as described in Parts I and II, showed that there was significant difference between hatches in 10-week body weight and 10-week east angle. For this reason the data from different hatches were pooled.

Lerner (1950) stated that so long as the purportedly correlated traits 'e measured in the same individual, the common environment to which they 'e subjected will tend to conceal the true nature of their interrelationip. To avoid a common environmental effect, the traits under investigation

were correlated between full sibs.

These data were analyzed using the method of Hazel <u>et al</u> (1943). It is essentially an extension of the analysis of variance to include covariance between the traits studied. The total variance for body weight and breast angle and the covariance between these 2 traits were separated into the following parts: (1) differences between sires, (2) differences between dams mated to the same sire, and (3) remainder. The mean squares and covariance components were reduced to their component parts as outlined by Lerner (1950).

The remainder (Q) is the component of variance or covariance containing the environmental component and one-half the genetic component of variance or covariance. It is the variance or covariance expected between full sibs. The dam's contribution (D) is the extra variance or covariance occurring within groups of paternal half sibs, and is in addition to that component found among full sibs. Sires contribute additional variance or covariance (S) to non-sibs as compared to paternal half-sibs.

Proper manipulation of the variance and covariance components will yield phenotypic, genetic and environmental correlation coefficients. The procedure for calculating these statistics is outlined in Table 42 of the Appendix.

RESULTS

The results of the analyses of variance and covariance as well as the resulting correlation coefficients between 10-week body weight and breast angle are presented in Tables 19 through 22.

Phenotypic correlations ranged from 0.01 to 0.41. Although these values approached 0 in some cases, they were positive in all cases. From these results it appears that a low, but consistent, positive phenotypic correlation existed between 10-week body weight and 10-week breast angle among the breeds and crosses studied.

The genetic correlation coefficients were not as consistent as the phenotypic correlations. Based upon the sire's components of variance and covariance, the genetic correlation coefficients ranged from .14 to 1.02. The mean coefficient was .49. Based upon the dam's components of variance and covariance, the genetic correlation coefficients ranged from -.19 to 2.38. The mean coefficient was 1.07. When the sire and dam components were combined, the correlation coefficients ranged from .27 to 1.05 and the mean was .65. It is difficult to draw any conclusions about the magnitude of these correlations since the estimates varied so greatly among themselves. It can be stated, however, that a positive genetic relationship did exist between 10-week body weight and 10-week breast angle in the breeds and crosses used in this study.

Based upon the sire's components of variance and covariance, the environmental correlation coefficients ranged from -2.31 to 6.51. The mean coefficient was .45. Based upon the dam's components of variance and covariance, the environmental correlation coefficients ranged from -1.72 to .60. When the sire and dam components were combined, the correlation coefficients ranged from -1.40 to .43 and the mean was -.73. The normally

expected range for correlations was exceeded at both extremes. The only statement that can be made regarding the environmental correlations is that the majority of them was negative. It can be concluded that a negative environmental relationship existed between 10-week body weight and 10-week breast angle in the breeds and crosses used in this study.

DISCUSSION

The phenotypic correlations found in Tables 19 through 22 are consistently positive, but they signify very little as to the true nature of those relationships. It might be erronously concluded that positive correlations of this magnitude would assure a breeder of improvement in the correlated traits while selection was being practiced for only one trait. This is not necessarily true. If the relationship is largely environmental in nature, selection progress may be impeded since the animals selected on the basis of phenotypic performance for one of the traits involved may be superior only because of the environmental effects associated with the possession of the other trait. The importance of phenotypic correlations lies in the relative importance of environmental and genetic influences.

The genetic correlations derived from this study would tend to indicate that a breeder could practice rigid selection for body weight and also increase breast width simultaneously. This undoubtedly is true to some extent, but it is doubtful if any drastic changes could be made in either characteristic simply by practicing rigid selection for the other trait.

The dams' components of variance and covariance contain any maternal effects that might be influencing breast angle and body weight. This effect would cause correlations that were based upon the dams' components to be too high. It has been shown in Parts I and II that some maternal effects are involved with these traits. For this reason, those correlations based upon the sires' components will be more indicative of the true genetic correlations between body weight and breast angle.

In an attempt to determine what caused these exceedingly high values, the data for different hatches were analyzed separately, and numerous

samples were taken from within these hatches. The results showed that it was not due entirely to sampling error. Different samples changed the individual coefficients somewhat but the trend remained the same. Apparently these high correlations are due to the inherent nature of the data which the author cannot explain.

Even though there is a positive relationship between body weight and breast angle, it would be possible to select for body weight without materially changing breast angle. Figures 1 and 2 are supporting evidence for this statement. In the case of purebred New Hampshire and Silver Oklabar females, as the average body weight increased, the mean breast angle increased. Although the range of breast angle values within different weight classes fluctuated considerably, it did not change appreciably as the body weight increased. It would be relatively simple to select some breeding females that had desirable body weight but fell below the average for breast angle if no attempt was made to select for breast angle. Possibly enough of these females would be selected to become breeders to counteract any change in mean breast angle.

The data for males are not presented but it followed a pattern similar to that of the females. Greater selection pressure could be practiced here and more emphasis could be placed on breast width. However, when the data were plotted on a hatch basis, the largest weight classes often contained only 1 or 2 males which were in many cases below the breed average for breast angle. Certainly these males would have been saved as potential breeders if they met other qualifications. It is possible that enough males and females with breast angle values below the breed mean could be selected to counteract the tendency of the mean breast angle to increase as body weight increases and thereby keep the mean breast angle for a breed relatively constant.

It is not likely that the environmental correlations will affect the progress of selection for body weight and breast angle to any great extent. Any effect should be to accelerate progress since selection for one of the characters will partially compensate for the effects of the environmental difference on the other since the traits are negatively correlated.

It would be difficult to make any recommendations for a breeding program from these data because of the inconsistent results obtained in this study. If a breeder desired to improve breast width in broiler stocks, the most logical approach would seem to be individual selection based on measurements at broiler age.

The inconsistency of the results obtained in this study leads the writer to question the reliability of this method of calculating genetic and environmental correlations. More research in this field might lead to a more satisfactory statistical method or methods for calculating correlations. Like the methods of calculating heritability estimates, different methods of calculating genetic and environmental correlations would be subject to different biases. The application of more than one statistical method to the same data should give more reliable correlations. Similarily, numerous correlations from different sources should give a more reliable average correlation coefficient between 2 traits.

SUMMARY

From 4 hatches of chicks, random samples were studied to determine the phenotypic, genetic, and environmental correlations between 10-week body weight and 10-week breast angle in New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds. The study involved 82 sires, 440 dams, and 5,355 chicks. Random samples of 3 chicks per dam and 3 dams per sire were taken for each sire that produced sufficient chicks. Data for sexes were analyzed separately as outlined by Hazel et al (1943). The results were as follows:

1. Phenotypic correlations ranged from 0.01 to 0.41.

2. Based upon the sire components of variance and covariance, genetic correlations ranged from .14 to 1.02 with a mean of .49. Based upon the dam components, genetic correlations ranged from -.19 to 2.38 with a mean of 1.07. Genetic correlations based upon combined sire and dam components ranged from .27 to 1.05 with a mean of .65.

3. Based upon the sire components of variance and covariance, environmental correlations ranged from -2.31 to 6.51 with a mean of .45. Based upon the dam components, environmental correlations ranged from -1.72 to .60 with a mean of -.42. Environmental correlations based upon combined sire and dam components ranged from -1.40 to 40 with a mean of -.73.

4. These results indicate that a low positive phenotypic correlation, a positive genetic correlation of questionable magnitude, and a negative environmental correlation of questionable magnitude exist between 10-week body weight and 10-week breast angle among the breeds and crosses studied.

ANALYSES OF VARIANCE AND COVARIANCE AND CORRELATIONS BETWEEN TEN-WEEK BODY WEIGHT (x_1) AND BREAST ANGLE (x_2) AMONG NEW HAMPSHIRES

ANALYSES

			Males		1	Females			
Source of	Ι	Mean	Squares	Cov.		Mean	Squares	Cov.	
Variation	d.f.	X ₁	X2	X ₁ X ₂	d.f.	X ₁	X ₂	X1X2	
Total	206	ļ			179				
Between Sires	22	•3673	25.8782	1.1127	19	.1578	38.9821	1.0510	
Between Dams	46		16.8478	•7537	40	.0755	11.5277	.5310	
Between full sibs	138	.1263	8.5447	.4203	120	.0416	6.7014	0014	

COMPONENTS OF VARIANCE AND COVARIANCE

		Males			Females		
Components	Symbols	Xl	12	X ₁ X ₂	I 1	1 2	1 1 1 2
Contribution from sire Contribution from dams Within families Total	s S D Q T	.0256 .0036 .1263 .1555	1.0028 2.7677 8.5447 12.3152	.0399 .1111 .4203 .5713	.0091 .0177 .0416 .0624	3.0504 1.6090 6.7014 11.3608	.0578 .1773 0014 .2337

Туре	Derived From	Males	Females	
Phenotypic	T	.41	.28	
Genetic	ЦS	•25	•35	
	<u>L</u> D	1.11	1.29	
	2(S+D)	.45	.76	
Environmental	T-lis	.62	01	
	$\mathbf{T} = \mathbf{J}_1 \mathbf{D}$	- 30	-1.72	
	$Q_{-}(S_{+}D)$	10	-1.15	

ANALYSES OF VARIANCE AND COVARIANCE AND CORRELATIONS BETWEEN TEN-WEEK BODY WEIGHT (X1) AND BREAST ANGLE (X2) AMONG NEW HAMPSHIRE X SILVER OKLABAR CROSSBREDS

			Males		Females				
Source of		Mean	Squares	Cov.		Mean	Squares	Cov.	
Variation	d.f.	X1	I ₂	I 1 I 2	d.f.	<u> </u>	I 2	X ₁ X ₂	
Total	161				233				
Between Sires Within Sires	17	.2724	26.1435	1.2306	25	.1404	23.1236	.9076	
Between Dams Between full sibs	36 108	.1181 .0788	9.6475	.3256 0216	52 156	.0山0 .0370	8.6806 7.7381	.0415 1158	
	1	1							

COMPONENTS OF VARIANCE AND COVARIANCE

	Symbols		Males		Females		
Components		X ₁	X2	I ₁ I ₂	X ₁	12	I 1 I 2
Contribution from sires Contribution from dams Within families Total	s S D Q T	.0171 .0131 .0788 .1090	1.8329 .6825 7.6000 10.1154	.1006 .1157 0216 .1947	.0107 .0023 .0370 .0500	1.6048 .3142 7.7381 9.6571	.0962 .0524 1158 .0328

Туре	Derived From	Males	Females	
Phenotypic	т	.19	.04	
Genetic	45	•57	•73	
	4D	1.22	1.94	
	2(S+D)	•79	•99	
Environmental	T-4S	62	-2.31	
	T-4D	41	30	
	Q-(S+D)	48	71	

ANALYSES OF VARIANCE AND COVARIANCE AND CORRELATIONS BETWEEN TEN-WELK BODY WEIGHT (X1) AND BREAST ANGLE (X2) AMONG SILVER OKLABAR X NEW HAMPSHIRE CROSSBREDS

ANALYSES

Males				Females				
	Mean	Squares	Cov		Mean	Squares	Cov.	
d.f.	X ₁	X ₂	x ₁ x ₂	d.f.	X ₁	12	1 12	
179				197				
19	•3527	21.1458	.7742	21	.2462	27.8924	.7276	
40	.1353	13.9585	.1750	44	.0707	12.2789	.1420	
120	.0705	7.6736	.0854	132	.0449	6.0941	1218	
	d.f. 179 19 40 120	Mean d.f. X1 179 .3527 19 .3527 40 .1353 120 .0705	Males Mean Squares d.f. X1 X2 179 .3527 21.1458 40 .1353 13.9585 120 .0705 7.6736	Mean Squares Cov. d.f. X1 X2 X1X2 179 .3527 21.1458 .7742 40 .1353 13.9585 .1750 120 .0705 7.6736 .0854	MalesMeanSquaresCov.d.f. X_1 X_2 X_1X_2 d.f.1 X_2 X_1X_2 179.352721.1458.774219.352721.1458.774240.135313.9585.1750120.07057.6736.0854	MalesMeanSquaresCov.Meand.f. \underline{X}_1 \underline{X}_2 $\underline{X}_1 \underline{X}_2$ d.f. $\underline{1}_1$ 179.352721.1458.774221.246240.135313.9585.175044.0707120.07057.6736.0854132.0449	MalesFemalesMeanSquaresCov.MeanSquaresd.f. \underline{X}_1 \underline{X}_2 $\underline{X}_1 \underline{X}_2$ d.f. \underline{X}_1 \underline{X}_2 179.352721.1458.774221.246227.892440.135313.9585.175044.070712.2789120.07057.6736.0854132.04496.0941	

COMPONENTS OF VARIANCE AND COVARIANCE

		Males			Females		
Components	Symbols	X ₁	X ₂	X ₁ X ₂	X _l	X2	X ₁ X ₂
Contribution from sire Contribution from dams Within families Total	s S D Q T	.0243 .0216 .0705 .1164	.7986 2.0950 7.6736 10.5672	.0666 .0299 .0854 .1819	.0195 .0086 .0449 .0730	1.7348 2.0616 6.0941 9.8905	.0651 .0879 1218 .0312

Туре	Derived From	Males	Females	
Phenotypic	T	.16	.O4	
Genetic	45	. 48	•35	
	ЦD	. 14	•66	
	2(S+D)	•27	•47	
Environmental	T-4S	22	-	
	Т–ЦD	.24	42	
	Q-(S+D)	03	-1.40	

ANALYSES OF VARIANCE AND COVARIANCE AND CORRELATIONS BETWEEN TEN-WEEK BODY WEIGHT (X1) AND BREAST ANGLE (X2) AMONG SILVER OKLABARS

ANALYSES

			Males		Females				
Source of		Mean	Squares	Cov.	[Mean	Squares	Cov.	
Variation	d.f.	X1	I 2	X ₁ X ₂	d.f.	X ₁	I 2	I 1 I 2	
Total Between Sires Within Sires	98 10	•3700	27 .8920	.1730	116 12	•3600	20.0950	.8425	
Between Dams Between full sibs	22 66	.1323 .0742	14.6463 6.8182	.5100 1818	26 78	.1177 .0612	11.6984 9.8291	.6412 1314	

COMPONENTS OF VARIANCE AND COVARIANCE

			Males		Females		
Components	Symbols	x _l	X ₂	X ₁ X ₂	X ₁	12	X1X5
Contribution from sire Contribution from dams Within families Total	s S D Q T	.0264 .0194 .0742 .1200	1.4717 2.6094 6.8182 10.8993	0374 .2306 1818 .0114	.0269 .0188 .0612 .1069	.9330 .6231 9.8291 11.3852	•0224 •2575 -•1314 •1485

Туре	Derived From	Males	Females	
Phenotypic Genetic Environmental	T 45 4D 2(S+D) T-45 T-4D Q-(S+D)	.01 1.02 19 .45 6.51 .60 -1.35	.14 .14 2.38 1.05 80 -1.66 -1.15	



Figure 1

\$

RANGE OF VARIATION AND MEANS FOR BREAST ANGLE FOR DIFFERENT WEIGHT CLASSES AMONG SILVER OKLABAR FEMALES

Figure 2



PART IV

HERITABILITY OF ALL-OR-NONE TRAITS: HATCHABILITY AND RESISTANCE TO DEATH TO TEN WEEKS OF AGE

The economic loss resulting from poor hatchability of eggs amounts to several million dollars annually in the United States. A much greater loss results from mortality. In broilers, the loss from mortality includes the cost of raising birds to the age of death, plus the potential income that the producer would have received if the birds had lived to market age.

The development of new drugs, vaccines, and better feeds have done much to decrease the death loss among domestic birds. Improved management practices, refrigeration and better incubators have improved the percentage hatch of fertile eggs. However, there is still a need to improve these conditions in commercial flocks.

There is some evidence that both hatchability and viability are inherited; thus, some improvement can be made by selecting for these two characteristics in breeding programs. Present evidence indicates that the heritabilities of hatchability and viability are low; hence, the rate of improvement by selection will be a slow process.

This portion of the experiment was designed to determine the following information in New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds :

1. If heterosis was involved in determining hatchability of fertile eggs and total eggs, and resistance to death to 10 weeks of age.

2. Heritability of hatchability and resistance to death.

3. Maternal effects on hatchability and resistance to death.

REVIEW OF LITERATURE

Hatchability

Hatchability is influenced by numerous factors, many of which are known to be hereditary. Nineteen lethal genes are known which, if present in populations, reduce the hatchability of fertile eggs (Landauer, 1948 and Jull, 1952). There is considerable evidence that a relationship exists between such traits as egg size, egg shape, and shell quality and hatchability. Since these traits are known to be hereditary, it is apparent that hatchability is hereditary at least to the degree that it is influenced by such traits. For a more detailed description of lethal genes and egg characteristics that affect hatchability, the reader is referred to Jull (1952) and Landauer (1948).

Shoffner and Sloan (1948) used the intra-sire regression method to calculate the heritability of hatchability of fertile eggs. In order to circumvent the difficulties brought about by the skewness of percentage data, the percentage hatch data were transformed to degrees before analysis. After the estimate was corrected for 16.1 percent inbreeding, the heritability estimate was 16 percent.

Wilson (1948a) calculated heritability estimates of fertility in an inbred flock of White Leghorns using the regression of offspring on dam method. Based on data unadjusted for inbreeding, heritability was .10; data adjusted for 34 percent inbreeding yielded an estimate of .06.

Wilson (1948b) calculated heritability estimates of embryonic mortality and hatchability in an inbred flock of White Leghorns using intraclass correlations between progenies of full sibs. The results were as

	Heritability		
Trait	Adjusted for Inbreeding	Unadjusted	
lst week embryonic mortality	•006	.012	
2nd week embryonic mortality	•007	بلده.	
3rd week embryonic mortality	•012	•025	
Hatchability	•019	•039	

Resistance to Death

Considerable data are available which indicate that breed, strain, and family differences exist with respect to their ability to withstand ertain diseases and adverse environmental conditions. For a thorough veview the reader is referred to Jull (1952). Genetic differences in susceptibility and/or resistance have been demonstrated for the following liseases: pullorum, infectious coryza, avian diphtheria, "blue-comb" isease, coccidiosis, fowl typhoid, the lymphomatosis complex, and Neweastle disease.

Lush and associates (1948) calculated heritability estimates for esistance to death from records of more than 20,000 Leghorn pullets huring their first year of production. Using the observed percentages of nortality, heritability estimates of .083 for total mortality, .068 for nortality due to the lymphomatosis complex, and .031 for mortality from auses other than lymphomatosis were calculated from the sires' components of variance. Estimates based on the combined contribution of sires and ams were .083, .083 and .032 respectively. Transformation of these values to the Bliss probit scale (Finney, 1952) resulted in slightly higher stimates. The resulting estimates based on the sires' contribution to the genetic variance were .145, .156, and .074 respectively for total mortality, lymphomatosis and other causes. Corresponding estimates based on a combination of the sire and dam contributions were .081, .093, and .038 respectively. Dams had about the same influence as sires upon the fate of their offspring. The incidence of mortality from all causes ranged from 24.1 to 33.2 percent with a mean incidence of 29.8 percent. The incidence of mortality from lymphomatosis ranged from 8.9 to 22.2 percent with a mean of 15.7 percent. Heritability estimates on the probit scale were not presented by years and could not be related to the incidence of mortality. In the following table the incidence of total mortality was related to heritability estimates before they were transformed to the probit scale.

		Heritability		
Incidence	Year	2(S+D)/T	45/T	
•241	1942	•094	•094	
•304	1939	•076	•089	
.315	1941	•125 *	•082	
•332	1940	•079	•066	

*Unduly large due to individual culling.

Excluding the high estimate for the year 1941, the tendency was for heritability to decrease as the incidence of mortality increased.

Wilson (1948b) calculated heritability of chick mortality to 8 weeks of age in an inbred flock of White Leghorns using intra-class correlations between progenies of full sibs. Before the data were adjusted for inbreeding, heritability was .118 and when the data were adjusted for 34 percent inbreeding, heritability was .052.

Robertson and Lerner (1949) calculated heritability estimates of mortality for the production flock of the University of California. The data were analyzed using the probit transformation. The resulting heritability estimates were as follows: .089 for total mortality, .026 for deaths due to reproductive disorders, .048 for deaths from lymphomatosis, and .066 for deaths from causes other than lymphomatosis. The mean incidences of mortality were 0.416 for total mortality, 0.081 for lymphomatosis, 0.234 for reproductive disorders, and 0.335 for causes other than lymphomatosis. The relationship between heritability estimates and the incidence of total mortality is presented in the following figure:



These data fail to show a consistent change in heritability as the incidence of mortality changed.

The hatchability data used in this study were collected on the parents rather than the first generation progeny. Mortality data were collected on the first generation progeny from 2 series of diallel matings. Most of the parental birds were selected for hatchability and this leads to a bias since the samples were not completely random. There is no way to determine the magnitude of this bias, but it probably is not sufficiently large to seriously affect the results of the analyses. Previous work (Shoffner and Sloan, 1948 and Wilson, 1948b) indicated that 16 percent or less of the variance in hatchability was genetic. For this reason, it is not likely that hatchability in those birds selected to be parents will deviate much from the flock average from which they were selected.

All data were analyzed by hatches after an analysis of variance showed that a hatch effect was present for the hatchability data and percent mortality. In order to circumvent the problem of proper weighting for families which differed greatly in size, the smallest families were excluded (Lush et al, 1948). Regarding mortality data, only sire families with 3 or more dams, each of which had hatched 3 or more chicks, were used. The number of sire and dam families eliminated from the analyses was small in all hatches except the fourth. For example, in the first hatch no New Hampshire sire families were eliminated and only 7 dam families were eliminated. Five of the dam families were eliminated because they contained only 1 or no chicks. The other 2 families were eliminated because they contained only 2 chicks. Seven out of 57 dam families were eliminated in this instance. With few exceptions, sire families were eliminated because they contained no chicks or only 1 dam with more than 2 chicks. In the fourth hatch, 3 or 4 sire families were eliminated from each analysis.

Since a minimum of 4 eggs was set per dam, the only data excluded from the hatchability analyses were sire families with hatchability percentages of zero or extremely low percentages.

Excluding some dams and sires from the analyses because of the mortality level or because of hatchability biased the samples to some extent. It is doubtful if these samples were biased to the extent that they would have been biased by including all sires and dams. For example, if a dam hatched 2 chicks and 1 died, 50 percent mortality resulted. In other cases, all the dams in some pens showed hatchability percentages of less than 20 percent when mated with certain sires. It was felt that such low percentages of hatchability were due to poor fertility of the male and placed too great a penalty on the females. This was substantiated by the fact that in all cases of poor hatchability in a given pen, the same females gave high percentages of hatchability when mated with other males. It is doubtful if any breeding experiment will ever result in a desirable number of progeny for each dam and sire used; thus, the nature of the experiment dictates that some of the data collected cannot be used in the analyses.

The statistical technique used to extract the desired information from these data was outlined by Lush <u>et al</u> (1948). It is essentially an analysis of variance based upon percentages. However, the data are of an all-or-none type, in that each chick either lived or died and each egg hatched or failed to hatch. Thus each chick or egg had to go into one or the other of two mutually exclusive classes. Such data are distributed binomially rather than normally.

The actually observed variance in binomial data is correlated with the mean and becomes very small when the average percentage in either class approaches zero. For this reason, heritability estimates derived from binomial data will depend, to some extent, upon the average incidence of

mortality or hatchability. Within a given flock where all birds are subjected to approximately the same environment in regard to diseases, management and other factors, these estimates should be adequate. Before such data can be compared with data from other sources where the percentage mortality or hatchability are likely to be different, some correction for the average incidence of mortality or percentage hatchability must be made.

One method of making this correction is the transformation of the data to the probit scale. The basic assumption for this transformation is that resistance to death, whether it be embryonic or post-embryonic, among individual birds is a continuous and normally distributed variable with death being a threshold that separates the population into two fractions. Heritability estimates calculated on the observed percentage scale can be transformed to the genetically more accurate heritability on the probit scale by multiplying it by

where p is the fraction which dies and Z is the height of the ordinate which truncates p of the area of the normal curve. p can be calculated and Z can be determined from statistical tables (Table V, Finney, 1952).

The details of the analysis and transformation to the probit scale are presented in Table 43 of the Appendix.

RESULTS

Hatchability

Hatchability data are presented by hatches in Table 23 for each breed and cross. Hatchability percentages are presented by pens in Tables 24 through 27. Percentages of hatchability varied so much between hatches, it is difficult to draw any conclusions regarding which breed or cross had the best average. When the data were combined for all hatches, the crosses showed a slightly higher percentage hatch of fertile eggs and total eggs than the breeds. The differences were small in all cases. To test the significance of these differences, "t" tests were made on a hatch basis and on the pooled data for all hatches. The mean of the crosses was compared to the mean of the breeds, and the mean of the better cross in each instance was compared to the mean of the breeds. The resulting "t" values were as follows:

	Hatch				
Comparison	1	2	3	4	All
Crosses vs breeds-%HF SB X NH vs breeds-%HF	•513 1•000		•547	،للبا 2 .1 60#	1.611 1.348
NH X SB vs breeds-%HF		.312	1.062		
Crosses vs breeds-%HT SB I NH vs breeds-%HT	.169	•358	.007		
NH X SB vs breeds-%HT			•945		.215

--Indicates that the breed mean was equal to or slightly greater than the cross mean.

*Indicates significance at the 5% level.

These data fail to show a significant difference between the crosses and breeds in hatchability. Thus no heterotic effect on hatchability was evident.

Heritability estimates for hatchability and the maternal effects on
hatchability are presented in Tables 28 through 31. It is obvious from the size of the size and dam contributions in relation to the total variance and from heritability estimates based upon observed hatchability percentages, that a rather large maternal effect was present in the dam's contribution to the variance. Hence any heritability estimate based upon the dam's contribution to the variance or a combination of sire and dam contributions will be in excess of the true estimate. For this reason, heritability estimates based on the sire components of variance were considered to be more indicative of the true estimates; thus, only these estimates were transformed to the probit scale. Heritability based upon the observed hatchability percentages and calculated from 4S/T ranged from -.017 to .365 for hatchability of all eggs, and ranged from -.104 to .333 for hatchability of fortile eggs with means of .107 and .047 respectively. Heritability estimates on the probit scale ranged from -.03? to .581 with a mean of .201 for hatchability of all eggs and ranged from -.366 to .580 with a mean of .076 for hatchability of fertile eggs.

Mean heritability estimates were calculated for the different breeds and crosses, and are presented in the following table:

		Heritability						
	Obse	rved %	Probi	t Scale				
Breed or Cross	% HT	% HF	%HT	% HF				
NH	.128	•058	. 270	.141				
NH X SB	.101	•037	. 190	•073				
SB X NH	•078	051	•131	136				
SB	•117	•124	•195	•226				

Heritability estimates were higher in both breeds than in the crosses.

In order to determine the effect of percentage hatchability upon heritability, mean estimates were calculated for various levels of hatchability. The results were as follows:

	Heritability							
Percentage	Obsei	rved %	Probi	t Scale				
Hatchability	75HT	% HF	% HT	X HF				
Below 65 65-69.9	•155	.110	•250	.189				
70-74.9 75-79.9 80-84.9 85-89.9 90-95.0	.065 .148 .036	.110 .011 029	.134 .314 .075	.244 040 –086				

In general, heritability was lower at the higher hatchability percentages.

Maternal effects were evident in all cases except among Silver Oklabars in the fourth hatch. When expressed as a percentage of the total variance, maternal effects calculated on the observed percentages ranged from .10 to .33 with a mean of .176 for percentage hatch of all eggs, and ranged from .045 to .231 with a mean of .138 for percentage hatch of fertile eggs. Values for maternal effects were considerably higher when transformed to the probit scale. The range for maternal effects upon percentage hatch of all eggs was .157 to .655 with a mean of .358, and the range for these effects upon percentage hatch of fertile eggs was .097 to .621 with a mean of .342. There was considerable variation among breeds and crosses in regard to the magnitude of the maternal effects. When the maternal effects from the dams of each breed were pooled, there was no breed difference.

Resistance to Death

Mortality data are presented in Tables 32 through 35. New Hampshires showed the lowest percentage of mortality of all breeds and crosses in all hatches except the fourth hatch. Silver Oklabars showed the highest percentage of mortality of all breeds and crosses in all hatches. The average mortality percentage for the breeds was less than 1 percent greater than the average for the two crosses.

To test the significance of these differences, the mean mortality rate for the crosses was compared to the mean for the breeds by means of the "t" test. No significant differences were noted on a hatch basis or when the data for the 4 hatches were pooled. Since there were no significant differences, the "t" values have been omitted. These results indicated that no heterotic effect was present on resistance to death to 10 weeks of age.

When the data were analyzed on a pen basis, it was difficult to draw definite conclusions regarding the superiority of one breed or cross over the other in viability. Due to the small numbers of chicks involved, an increase of one in the number of chicks that died often more than doubled the mortality percentage. The results are similar to those obtained on a hatch basis, and tend to substantiate the conclusion that no heterotic effect was evident on viability to 10 weeks of age.

Heritability estimates and the maternal effects involved with resistance to death to 10 weeks of age are presented in Tables 36 through 39. Dams rather consistently contributed more to the total variance than did sires. It is apparent that a maternal effect was exerted on livability to 10 weeks of age. Since the dams' contribution to their offspring contained maternal effects, heritability estimates based upon the dams' contribution will be in excess of the true estimates. For this reason, heritability estimates based upon the sires' contribution to the genetic variance were considered to be more indicative of the true heritability estimates for resistance to death. Only estimates based upon the sires' contribution were converted to the probit scale.

Heritability estimates based on the sires' components of variance ranged from -.110 to .457 with a mean of .048 when calculated on the observed percentages of mortality. On the probit scale, these estimates ranged from -.845 to 1.719 with a mean of .162. Based on observed percentage of mortality, mean estimates for breeds and crosses were as follows: .013 for New Hampshires; .116 for New Hampshires X Silver Oklabars; .030 for Silver Oklabars X New Hampshires, and .034 for Silver Oklabars. Transformation of these estimates to the probit scale resulted in the following means: -.052 for New Hampshires; .224 for New Hampshires X Silver Oklabars; .316 for Silver Oklabars X New Hampshires, and .161 for Silver Oklabars. The crosses as a group gave higher heritabilities than the breeds in both cases.

In order to determine the effect of level of mortality upon the heritability of resistance to death, mean heritabilities were calculated for various levels of mortality. The results were as follows:

	Heritability				
Mortality	Observed %	Probit Scale			
2.0 - 2.9	038	334			
3.0 - 3.9 4.0 - 4.9	•041 •090	•292 •463			
5.0 - 5.9 6.0 - 6.9	110*	-。 山5*			
7.0 & above	.158	•454			

*Only one estimate

With the exception of mortality at the 6.0 - 6.9 percent level, heritability was higher at the higher mortality levels.

Maternal effects were evident in 10 of 16 cases. Based on the observed mortality percentages, maternal effects ranged from .001 to .257 with a mean of .095. When these figures were transformed to the probit scale, the range was .007 to 1.039 with a mean of .416. Mean maternal effects by breeds and crosses based on observed mortality percentages and the probit scale respectively were as follows: .105 and .582 for New Hampshires ;.020 and .145 for New Hampshires X Silver Oklabars; .144 and .625 for Silver Oklabars X New Hampshires; and .131 and .436 for Silver Oklabars. New Hampshire females contributed a greater maternal effect than Silver Oklabar females.

DISCUSSION

Hatchability

Each cross yielded a higher percentage hatch of fertile eggs than the better parental average. In each hatch one or the other cross had a higher average than the better parental average. Each cross yielded a slightly higher percentage hatch of total eggs than the combined parental average, but less than the better parental average. These results indicated the presence of heterosis, but "t" tests failed to show a significant difference in any of these comparisons. New Hampshires yielded approximately a 5 percent better hatch of all eggs set than the Silver Oklabars, but the results were reversed regarding hatchability of fertile eggs. The Silver Oklabars yielded a 5 percent better hatch in this respect than the New Hampshires. These results show that the New Hampshires produced more fertile eggs than the Silver Oklabars, but the latter breed hatched a higher percentage of their fertile eggs than did the New Hampshires. Hence, it is possible that any heterotic effect upon hatchability of all eggs set could have been masked by infertility of the eggs set. It is also possible that preferential matings caused some of the observed infertility. Since there were approximately equal numbers of females of each breed in each pen, but only one male of a breed in a given pen, it is possible that some or all males showed a preference for their own breed causing the crosses to produce a lower percentage of fertile eggs.

These results lead the writer to conclude that heterosis in hatchability needs to be investigated more thoroughly. The use of larger numbers of experimental birds than were used in this study would be of great value. Performing these studies at different times of the year would also be beneficial. This study was conducted at the time of year when fertility

and hatchability were declining.

The size of the heritability estimates presented in Tables 28 through 31 are of the magnitude that family selection will be more efficient than individual selection in improving hatchability. It is also evident that due to low heritability estimates obtained, improvement will be a rather slow process. Since the maternal effects were of such magnitude, it might be advantageous to place more emphasis on the selection of dams rather than sires.

Heritability of hatchability varied considerably among the different breeds and crosses. Regarding hatchability of all eggs, New Hampshires gave the highest estimate of heritability with Silver Oklabars giving the lowest estimate. In the case of hatchability of fertile eggs, Silver Oklabars gave the highest estimate of heritability and New Hampshires gave the second highest. The only explanation the writer can advance to explain this is the effect of level of hatchability. Breeds and crosses with the higher hatchability percentages gave lower heritability estimates with the exception of New Hampshires in regard to percentage hatch of total eggs. In this instance, New Hampshires yielded a slightly higher percentage hatch of all eggs than the other groups, and also gave the highest heritability estimate. Due to the small numbers of birds involved in this study, sampling error could have caused this deviation.

The nature of the maternal effects obtained in this study cannot be ascertained from these data. The dam contributes through the egg she lays all the nutrients necessary for the development of the chick. It is possible that some dams fail to supply the proper balance of nutrients in their eggs. There is a possibility that chemical substances such as hormones and antibodies are deposited in different amounts in eggs, and the growth and development of chicks might be hindered or stimulated as

the case might be. Some inherited egg characteristics such as size, shape, and shell thickness very likely are contributing factors to maternal effects. If cytoplasmic inheritance is involved, it is another source of the maternal influence upon hatchability.

Regardless of the nature of the maternal influences, some or all of it is undoubtedly affected by heredity and some improvement can be expected as a result of selection (Srb and Owen, 1952). In fact, some improvement in hatchability might be obtained indirectly by the selection for egg size, shell quality and other egg characteristics (Landauer, 1948, and Jull, 1952).

Resistance to Death

The results of this investigation indicate that resistance to death to 10 weeks of age was inherited in the manner typical of a quantitative trait. No apparent heterotic effect was involved, but a maternal effect was present.

The heritability estimates based on the observed percentages of mortality are comparable with the estimates reported by other investigators. Heritability estimates on the probit scale are considerably in excess of those previously reported. One possible reason for this discrepancy is that the previously reported estimates were calculated on laying house mortality and might not be comparable with mortality to 10 weeks of age. A more likely explanation is that due to small numbers involved in this study, sampling error was great.

When transformed to the probit scale, many of the estimates were greatly increased. The increase due to the transformation to the probit scale was caused by the low incidence of mortality. As the incidence of mortality approaches zero, the height of the ordinate (Z), which truncates the percentage of chicks that died (p) on the normal curve, decreases considerably. Since p (1-p) must be divided by Z^2 to obtain a figure to multiply each heritability estimate by, it is clear that the figure will increase as Z decreases. As an example, when the incidence of mortality is about 1.5 percent, the transformation figure is slightly less than 10. When the incidence of mortality increases to 12 percent, the transformation figure drops to less than 3. When heritability estimates of the magnitude obtained in this study are multiplied by transformation values of from 5 to 10, some heritability values greater than 1 will result. In the case of laying house mortality, which is likely to run between 15 and 25 percent annually, the transformation figures would be greatly reduced.

Heritability of resistance to death varied considerably among the different breeds and crosses. New Hampshires gave the lowest estimates with a mean of -.052 on the probit scale. The Silver Oklabar X New Hampshire cross gave a mean estimate of .224, and the Silver Oklabars gave a mean estimate of .161. There are two possible explanations for these results. Crossing two breeds which have been bred as closed flocks for several years could very easily increase the genetic variance by introducing new genes from each breed. Increasing the genetic variance would increase heritability. Silver Oklabars were developed from several breeds and have not been bred as a closed flock as long as the New Hampshires. Thus it is likely that the Silver Oklabars have more genetic variability than the New Hampshires and would give higher heritabilities. Another explanation for the variation of heritability estimates among breeds and crosses was the effect of level of mortality. As the level of mortality increased, the heritability also increased. New Hampshires showed the lowest mortality percentage and would be expected to give the lowest

heritability on this basis. Silver Oklabars were the only exception to this explanation. Mortality was highest in the latter breed, but heritability was the second lowest estimate. It is possible that both of these explanations are valid and function at the same time.

An inconsistent maternal effect was evident regarding resistance to death to 10 weeks of age. The nature of these maternal effects has seve possible explanations which have been discussed in connection with hatchability.

SUMMARY

Hatchability and mortality data were studied in 4 hatches of New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds. The data were analyzed as outlined by Lush and associates (1948) to determine heterotic effects, heritability estimates, and maternal effects for hatchability and resistance to death to 10 weeks of age. The results were as follows:

1. No heterotic effect was evident upon the percentage hatch of fertile eggs or upon the percentage hatch of total eggs.

2. Heritability estimates based upon the sires' contribution to the genetic variance ranged from -.017 to .365 with a mean of .107 for percentage hatch of all eggs. The range was -.104 to .333 and the mean was .047 for percentage hatch of fertile eggs. When the heritability estimates were transformed to the probit scale, the range was -.037 to .581 and the mean was .201 for hatchability of all eggs. The range was -.366 to .580 and the mean was .076 for hatchability of fertile eggs.

3. Maternal effects were present in all cases except among Silver Oklabars in the fourth hatch. Based upon observed hatchability percentages, maternal effects ranged from .10 to .33 with a mean of .176 for hatchability of all eggs. These effects ranged from .045 to .231 with a mean of .138 for hatchability of fertile eggs. When transformed to the probit scale, maternal effects ranged from .157 to .655 and the mean was .358 for hatchability of all eggs. The range was .097 to .621 and the mean was .342 for hatchability of fertile eggs.

4. No heterotic effect was evident upon the resistance to death to 10 weeks of age.

5. Heritability estimates based upon the sire's contribution to the

genetic variance ranged from -.110 to .457 with a mean of .048 for resistance to death to 10 weeks of age. When these values were transformed to the probit scale, the range was -.845 to 1.719 and the mean was .162.

6. Maternal effects were evident in 10 of 16 cases. Based on the observed mortality percentages, these effects ranged from .001 to .257 with a mean of .095. Transformed to the probit scale the range was .007 to 1.039 and the mean was .416.

PERCENT HATCHABILITY BY BREEDS AND CROSSES FOR EACH HATCH

	and a state of the s	Fir	st Hatch		
Breed or	Eggs	No.	No.	% Hatch of	% Hatch of
Cross	Set	Infertile	chicks	Fertile Eggs	Total Eggs
NH	522	18	422	83.7	80.8
NH X SB	537	72	410	88.2	76.4
SB X NH	539	54	447	92.2	82.9
SB	501	57	405	91.2	80.8
Total	2099	201	1684	88.7	80.2
		Seco	ond Hatch	L	
NH	427	64	327	90.1	76.6
NH X SB	455	92	333	91.7	73.2
SB X NH	508	50	407	88.9	80.1
SB	436	72	333	91.5	76.4
Total	1826	278	1400	90.4	76.7
		Thi	rd Hatch	1	
NH	507	цц	379	81.9	74.8
NH X SB	501	81	364	86.7	72.7
SB X NH	537	136	342	85.3	63.7
SB	545	175	302	81.6	55.4
Total	2090	Ц36	1387	83.9	66.4
		Four	ath Ustab		
NH	480	65	234	56.4	48.8
NH X SB	404	112	195	66.8	48.3
SB X NH	500	164	232	69.0	46.4
SB	467	144	223	67.0	47.8
Total	1851	485	884	64.7	47.8

PERCENT HATCHABILITY BY PENS FOR THE FIRST HATCH

	N	ł	NH	X SB		S.	В	SB	X NH	
Pen	% HF	% HT	% HF	% HT	Pen	% HF	% HT	% HF	% HT	
2	87.0	85.5	86.5	81.8	11	88.9	87.5	91.7	88.8	
12	80.5	75.0	94.1	92.3	21	94.9	84.1	88.3	85.5	
13	90.2	90.2	71.7	61.1	22	83.9	76.5	94.9	94.9	
14	95•7	93.8	95.8	86.8	23	85.4	76.1	91.4	86.5	
15	78.4	74•4	88.6	75.6	214	91.9	68.0	93.9	80.7	
16	80.0	78.3	89•7	78.8	25	97•3	81.8	95•7	80.4	
17	90.0	90.0	95.2	93.0	27	94.1	81.4	91.3	73.7	
18	67.3	62.7	97.0	71.1	28	0**	0	0	о	
19	87.3	82.8	88.2	50.8	29	94.4	83.6	95.1	81.3	
20	77•5	75.6	88.1	82.2	30	78.0	66.7	91.5	78.3	1
Total	83.7	80.0	88.2	76.4	Total	91.2	80.8	92.2	82.9	ļ
1*	87.2	81.0	80.8	75.0	26*	100.0	98.0	93.6	84.6	

*Control Pens **Male was infertile. Not figured in totals 臣

Table	25
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PERCENT	HATCHABILITY	BY	PENS	FUR	THE	SECOND	HATCH	
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	N	H	NH	K SB		S	В	SB 2	X NH
Pen	% HF	% HT	% HF	% HT	Pen	% HF	% HT	% HF	% HT
2	85.7	83•7	94.1	82.1	11	93.3	87.5	90.2	79•3
12	83.3	64.1	85•7	85•7	21	93.1	87.1	87.1	84.0
13	88.2	83.3	90•3	82.4	22	91.7	55.0	87.2	82.9
<u>1</u> 4	93.2	93.2	92.7	84.4	23	86.1	79•5	97.0	97.0
15	90.0	28.1	82.4	32.6	24	94•4	85.0	88.6	83.0
16	90.2	86.0	89•7	70 •3	25	91.7	59•5	93 •5	53•7
17	94•7	94•7	97•7	91.3	27	93.8	84.9	86.5	78.9
18	90.9	45.5	80.0	28.6	28	100.0	65.4	78.1	75.8
19	100.0	100.0	97.6	77•4	29	88.6	62.0	81.1	75.0
20	84.8	84.8	96.9	86.1	30	80.0	66.7	90•4	90.4
Total	90.1	76.6	91.7	73•2	Total	91.5	76 . 4	88.9	80.1
1*	81.8	64.3	89.2	86.8	26*	95•7	90.0	92.7	88.4

*Control Pens

Table 20

	NI NI	H	NH 2	<u>X SB</u>		S	B	SB.	X NH
Pen	% HF	% HT	<u>% HF</u>	% HT	Pen	% HF	% HT	% HF	% HT
ш	75.9	71.0	84.9	78.9	2	87.5	79.2	86.8	78.0
21	82.5	70•2	90 . 4	76.0	12	87.5	79.2	86.2	59.5
22	81.4	74•5	71.4	50.0	13	72.9	57.4	93.8	86.5
23	64.7	56.4	80.5	62.2	דעד	89.2	80.5	77.8	57.3
24	88.0	84.6	88.9	62.5	15	100.0	7•5	100.0	4•7
25	97.8	95•7	84.4	63.3	16	47.1	18.2	67.9	41.3
27	77-3	73.9	100.0	90.2	17	84.6	57.8	87.5	77.8
28	74.2	56.1	90.0	58.1	18	75.6	60.8	80.6	47.5
29	89.5	77.3	82.7	75•4	19	80.0	13.6	91.3	48.8
3 0	85.5	84.1	82.1	66. 7	20	84.1	78•7	79•4	61.4
Total	81.9	74•8	86.7	72.7	Total	81.6	55•4	85 . 3	63.7
1*	70.6	63.2	91.3	80.8	26 *	82.6	71.7	96.0	85•7

PERCENT HATCHABILITY BY PENS FOR THE THIRD HATCH

*Control Pens

Table	27	

PERCENT HATCHABILITY BY PENS FOR THE FOURTH HATCH

	N	I	NH .	X SB		S	В	SB.	X NH	
Pen	<u>% HF</u>	% HT	% HF	% HT	Pen	% HF	% HT	<u>% HF</u>	% HT	
11	56.0	50.9	63.4	49.1	2	65.9	55.1	64.9	58.5	
21	50.0	42.4	85.0	77.3	12	56.3	40.9	68.8	28.2	
22	62.1	60.0	14.14	30.8	13	62.5	22.7	69.4	61.8	
23	57•7	50.0	67.6	50.0	14	64.7	45.8	68.8	61.1	
24	65.3	60.4	67.9	47.5	15	82.8	58.5	61.1	27.5	
25	73.2	63.8	37.5	20.9	16	69.6	կկ-կ	73.8	63.6	
27	40.9	39.1	71.8	65.1	17	61.7	52•7	61.0	39.1	
28	68.3	54.9	61.5	30.8	18	47.5	36 •5	87.5	25.9	
29	45.7	33.3	70.8	38.6	19	75.0	7•3	77.8	14.6	
30	50.0	40.0	76.9	52.6	20	92.3	85•7	74.3	59.1	
Total	56.4	48.8	66.8	48.3	Total	69.0	47.8	69.0	46.4	117
1*	44-4	42.1	70.5	66.7	26*	85.7	76.9	69.8	59•7	

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY AND MATERNAL EFFECTS FOR HATCHABILITY IN NEW HAMPSHIRES

Analysis of Variance

	Hatch 1			Hatch 2			Hatch 3					Hato	eh 4			
Source of	8	HT	%	HF	ø	HT	¢	HF	9	HT	8	HF	8	HT	۶ ۶	HF
Variation	₫f	MS	df	MS	df	MS	d f	MS	df	MS	df	MS	df	MS	df	MS
Total Between Sires Within Sires Between Dams Remainder	523 10 71 142	.4110 .2679 .1335	506 10 71 125	.3200 .2321 .1202	350 10 49 291	•5854 •2906 •0856	330 10 49 271	•2528 •1990 •0765	469 10 67 493	•5182 •2719 •1275	145 10 67 368	•3397 •2460 •1007	403 9 54 340	•14500 •14441 •2104	350 9 54 296	.4181 .3488 .2079

Components of Variance and Estimates

		Hat	ch l	Hat	ch 2	Hat	ch 3	Hat	ch 4	-
Statistics	Symbols	% HT	% HF							
Contribution from sires Contribution from dams Within families Total	S D Q T	.0030 .0210 .1335 .1575	.0019 .0181 .1202 .1402	.0092 .0350 .0856 .1298	.0018 .0222 .0765 .1005	.0058 .0239 .1275 .1572	.0023 .0254 .1007 .1284	.0002 .0370 .2104 .2476	•0019 •0250 •2079 •2348	
Heritability (based on observed %)	ЦS/Т ЦD/Т 2 (S+D)/Т	•076 •533 30h	•054 •516	•283 1•078	•072 •884	・148 •608 378	•072 •791	•003 •598	.032 .426	
Heritability (based on Probit scale)	$4S/T \cdot p(1-p)$	•154	•117	.620	•470 •220	•300	•174	•005	•053	н
Maternal effects (based on observed %)	D-S/T	•114	.116	.119	•203	.115	•180	9بلد.	•098	18
Maternal effects (based on Probit scale)	D-S/T. <u>p(1-p)</u> Z ²	.232	.251	•436	.621	•233	•434	•236	•163	

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR HATCHABILITY IN NEW HAMPSHIRE X SILVER OKLABAR CROSSES

Analysis of Variance

	Hatch 1			Hatch 2				Hatch 3					Hate	h 4		
Source of	8	HT	%	HF	ø	HT	%	HF	%	HT	8	HF	Å	HT	\$	HF
Variation	đf	MS	df	MS	df	MS	d f	MS	df	MS	df	MS	df	MS	df	MS
Total Between Sires Within Sires Between Dams Remainder	535 10 76 1449	.8664 .5194 .1074	162 10 76 376	•2147 •1184 •0822	369 8 58 303	•3659 •3127 •1052	330 8 58 264	.0705 .1106 .0611	480 9 70 401	•4997 •4694 •1399	405 9 70 326	•1466 •2127 •0893	364 8 55 301	•9845 •4225 •1998	269 8 55 206	•5926 •2996 •1833

Components of Variance and Estimates

		Hat	ch l	Hat	ch 2	Hat	ch 3	Hat	ch 4
Statistics	Symbols	% HT	% HF	% HT	% HF	% HT	% HF	% HT	% HF
Contribution from sires Contribution from dams Within families Total	S D Q T	.0071 .0669 .1074 .1814	.0022 .0068 .0822 .0912	.0013 .0376 .1052 .1441	0012 .0100 .0611 .0699	.0006 .0548 .1399 .1953	0016 .0243 .0893 .1100	.0139 .0391 .1998 .2528	.0098 .0276 .1833 .2207
Heritability (based on observed %)	ЦS/T ЦD/T 2 (S+D)/T	•157 1.475 •816	•096 •298 •197	•036 1•0山 •540	069 .572 .252	.012 1.122	057 .867	•220 •619	•178 •500
Heritability (based on Probit scale)	$4S/T_{p(1-p)}$	•312	•257	.080	167	.022	098	•346	•300
Maternal effects (based on observed %)	D-S/ T	•330	.214	•252	•160	•278	•231	.100	•081
Maternal effects (based on Probit scale)	D-S/T. <u>p(l-p)</u> <u>Z</u> 2	•655	•574	•559	•387	•518	•398	.1 57	.136

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR HATCHABILITY IN SILVER OKLABAR X NEW HAMPSHIRE CROSSES

Analysis of Variance

		Hate	hl			Hatc	h 2			Hato	eh 3			Hatc	h 4	
Source of	8	HT	%	HF	%	HT	\$	HF	ø	HT	%	HF	ø	HT	%	HF
Variation	d f	MS	df	MS	df	MS	df	MS	d f	MS	df	MS	d f	MS	df	MS
Total Between Sires Within Sires Between Dams Remainder	508 9 71 428	.1881 .2152 .0980	470 9 71 390	•0093 •0852 •0563	401 8 63 330	•2293 •1925 •0989	387 8 63 316	.0724 .1187 .0855	493 9 70 414	•8267 •4892 •1553	398 9 70 319	.2848 .2018 .1053	424 8 58 358	.9808 .4588 .2003	318 8 58 252	•0763 •2900 •2048

Components of Variance and Estimates

		Hat	ch l	Hat	ich 2	Hat	ch 3	Hat	ch 4
Statistics	Symbols	% HT	% HF	% HT	% HF	% HT	% HF	% HT	% HF
Contribution from sires Contribution from dams Within families Total	S D Q T	0005 .0187 .0980 .1162	0016 .0050 .0563 .0597	.0008 .0168 .0989 .1165	0011 .0062 .0855 .0906	.0068 .0540 .1553 .2161	.0017 .0156 .1053 .1226	.0111 .0408 .2003 .2522	0061 .0348 .2048 .2335
Heritability (based on observed %)	ЦS/T ЦD/T 2 (S+D)/T	017 .644	107 .335	•027 •577	049 .274	•126 1•000	•055 •509 282	•176 •647	104 .596
Heritability (based on Probit scale)	$\frac{1}{4S}/T \cdot p(1-p)}{7^2}$	037	366	.065	130	.217	•131	.278	179
Maternal effects (based on observed %)	D-S/T	•165	•111	•137	.081	•218	•113	.118	.175
Maternal effects (based on Probit scale)	D-S/T. <u>p(1-p)</u> Z ²	•363	•379	•331	.216	•375	•269	.187	•300 ä

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY AND MATERNAL EFFECTS FOR HATCHABILITY IN SILVER OKLABARS

Analysis of Variance

	Hatch 1			Hatch 2			Hatch 3				Ι	Hatch	1			
Source of	%	HT	%	HF	%	HT	%	HF	%	HT	18	HF	%	HT	%	HF
Variation	df	MS	d f	MS	df	MS	d f	MS	df	MS	df	MS	df	MS	d f	MS
Total Between Sires Within Sires Between Dams Remainder	491 9 67 415	.3518 .2607 .1117	цил 9 67 365	.1066 .1014 .0571	406 10 63 333	.2864 .2796 .1203	359 10 63 286	.0818 .1176 .0712	401 7 59 335	.5331 .4270 .1637	339 7 59 273	.4954 .1889 .1203	380 9 52 319	1.1456 .2839 .2128	307 9 52 246	•7212 •1917 •1886

Components of Variance and Estimates

		Hat	ch 1	Hat	ch 2	Hat	ich 3	Hat	ch 4
<u>Statistics</u>	Symbols	% HT	% HF	% HT	% HF	% HT	% HF	% HT	% HF
Contribution from sires Contribution from dams Within families Total	S D Q T	.0019 .0233 .1117 .1369	.0002 .0079 .0571 .0652	.0002 .0290 .1203 .1495	0011 .0100 .0712 .0801	.0021 .0439 .1637 .2097	.0072 .0135 .1203 .1410	.0226 .0116 .2128 .2470	.0172 .0006 .1886 .2064
Heritability (based on observed %)	45/T 4D/T 2(S+D)/T	.056 .681 .368	•012 •485 •218	.005 .776 .391	055 .499	.040 .837	•204 •383 291	• 365 • 188	•333 •001
Heritability (based on Probit scale)	$\frac{\mu S}{T_{p}(1-p)}$.118	.049	.011	168	•439	•442	•581	•580
Maternal effects (based on observed %)	D-S/T	.156	.118	•193	•139	•199	•045	0	0
Maternal effects (based	$\frac{D-S/T.p(1-p)}{z^2}$	•330	•477	. 407	•425	•353	•097	0	0

Taoté 2c	Table	32
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PERCENT MORTALIT	Y BY	PENS	FOR	THE	FIRST	HATCH
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		NH			NH X SI	B		SI	X NH			SB	
Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.	Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.
2	46	1	2.17	43	2	4.65	11	54	l	1.85	54	0	0
12	33	2	6.06	48	1*	2.08	21	53	l	1.89	36	1	2.78
13	37	ı	2.70	32	0	0	22	36	2	5.56	22	о	0
1J4	45	0	0	45	4	8.89	23	31	1	3.23	32	1	3.13
15	29	1*	3.45	31	0	0	24	44	2	4.55	31	2	6.45
16	34	1	2.94	25	1	4.00	25	<u>14</u> 14	1	2.27	35	1	2.86
17	42	2(1*)	4.76	38	1	2.63	27	40	3	7.50	45	4	8.89
18	36	0	0	32	1	3.13	28	ο	0	0	0	0	0
19	46	0	0	28	l*	3.57	29	37	0	0	46	2(1)*	4.35
20	30	0	0	36	0	0	30	53	2	3.77	35	2	5.71
Total	378	8	2.12	358	11	3.07		392	13	3.32	336	13	3.87
1**	32	0	0	39	1	2.56	26**	43	2	4.65	48	2	4.17

*Sick at 10 weeks of age and classified as mortality. **Control Pens

Table	33
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PERCENT MORTALITY BY PENS FOR THE SECOND HATCH

		NH		Ν	IH X SI	3		5	SBX NE	I		SB	
Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.	Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.
2	32	2	6.26	28	2	7.14	11	<u>44</u>	0	0	37	ı	2.70
12	23	0	0	35	l	2.86	21	38	о	0	25	ı	4.00
13	29	1	3.45	25	0	0	22	33	0	0	9	1	11.11
과	41	1	2.44	36	2	5.56	23	28	1	3.57	29	2	6.90
15	8	0	0	12	0	0	24	37	7	18.92	33	4	12.12
16	35	1	2.86	22	0	0	25	27	ο	0	21	0	0
17	36	0	0	歫	0	0	27	<u>ұ</u> д	1	2.27	42	0	0
18	19	1	5.26	ш	0	0	28	23	0	0	16	0	ο
19	45	0	ο	37	l	2.70	29	29	1	3.45	28	2	7.14
20	27	0	0	30	0	0	30	47	2	4.26	28	l	3.57
Total	295	6	2.03	277	6	2.17	Total	350	12	3.43	268	12	4.48
1**	17	0	0	32	1	3.13	26 **	34	0	0	Цо	0	0

**Control Pens

Т	able	<u>3</u> Ь
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PERCENT MORTALITY BY PENS FOR THE THIRD HATCH

		NH		1	NH X SE	}			SBX NH	I		SB	
Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.	Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.
11	42	l	2.38	44	4	9.09	2	3 6	6	16.67	37	4	10.81
21	30	0	0	34	0	ο	12	24	l	4.17	37	5	13.51
22	34	0	0	9	0	0	13	42	0	0	21	0	0
23	19	0	0	31	0	0	יזר	32	0	0	30	ı	3.33
24	43	0	0	40	1	2.50	15	0	О	0	0	0	0
25	40	2(1 *)	5.00	37	1	2.70	16	18	1	5.56	10	3	30.00
27	32	l	3.13	42	2	4.76	17	<u>ц</u> т	3	6.82	31	ı	3.22
28	18	2	11.11	1J4	1	7.14	18	21	0	0	27	0	0
29	31	1	3.23	40	6	15.00	19	19	0	0	6	0	ο
30	56	1*	1.79	30	О	0	20	26	1	3.85	32	3	9.38
Total	345	8	2.32	321	15	4.67		262	12	4.58	231	17	7.36
1**	10	0	0	19	2	10.53	26**	46	0	0	33	0	0

*Sick at 10 weeks of age and classified as mortality **Control Pens

Table	-35
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PERCENT MURIALITI DI FENS FUR INE FUNIT NAL	PERCENT MORTA	PLLX F	RI	PENS	FUR	THE	FUURTH	HATCH
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		NH		1	нхз	В			SBX N	ł		SB	
Pen	No. Chicks	No. Dead	% Mort.	No. Chicks	No. Dead	% Mort.	Pen	No. Chicks	No. Dead	% Morte	No. Chicks	No. Dead	% Morte
11	25	3	12.00	24	1	4.17	2	21	0	0	20	4	20.00
21	17	0	0	15	ı	6.67	12	8	3	37.50	17	5	29.41
22	17	1	5.88	4	о	0	13	31	ο	0	6	0	0
23	15	2	13.33	22	3	13.67	יזר	20	1	5.00	8	о	ο
24	32	1	3.13	16	l	6.25	15	10	0	0	24	5	20.83
25	30	3	10.00	7	l	14.28	16	27	5	18.52	1 4	l	7.14
27	16	4	25.0 0	26	8	30.77	17	22	1	4.55	28	2	7.14
28	26	1	3.85	7	0	0	18	6	1	16.66	14	1	7.14
29	13	0	0	16	l	6.25	19	6	0	0	0	0	0
30	21	0	0	18	ı	5.56	20	25	1	4.00	35	2	5.71
Total	212	15	7.08	155	17	10.97	Total	176	12	6.82	166	20	12.05
1**	8	0	0	22	3	13.64	26**	33	2	6.06	26	2	7.69

**Control Pens

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR RESISTANCE TO DEATH TO TEN WEEKS OF AGE IN NEW HAMPSHIRES

Analysis of Variance

Source of	Ha	tch 1	Ha	tch 2	Ha	tch 3	Ha	tch 4
Variation	df	MS	df	MS	df	MS	df	MS
Total Between Sires Within Sires Between Dams Remainder	313 10 40 263	.0142 .0322 .0206	277 8 142 227	.0188 .0202 .0215	217 9 Ц2 2Ц6	.0308 .0183 .0235	120 6 16 98	.1877 .1375 .0764

Components of Variance and Estimates

Statistics	Symbols	Hatch 1	Hatch 2	Hatch 3	Hatch L
Contribution from sires Contribution from dams Within families Total	S D Q T	0006 .0019 .0206 .0219	0001 0002 .0215 .0212	.0003 0012 .0235 .0226	.0029 .0116 .0764 .0909
<pre>Heritability (based on observed \$) Heritability (based on Probit scale) Maternal effects (based on observed \$) Maternal effects (based on Probit scale)</pre>	$\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} $	110 .347 .119 845 .114 .875	019 038 028 155	.053 212 080 .411	.127 .510 .319 .383 .096 .289

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR RESISTANCE TO DEATH TO TEN WEEKS OF AGE IN NEW HAMPSHIRE & SILVER OKLABAR CROSSEREDS

Analysis of Variance

Source of	Ha	tch 1	Ha	tch 2	Ha	tch 3	Ha	tch 4
Variation	df	MS	df	MS	df	MS	df	MS
Total Between Sires	364 10	•0293	249 8	•0092	297 9	•0973	107 7	. 2629
Within Sires Between Dams Remainder	55 299	.0295 .0293	38 203	.0171 .0158	46 242	•0636 •0505	13 87	.0877 .0972

Components of Variance and Estimates

Statistics	Symbols	Hatch 1	Hatch 2	Hatch 3	Hatch 4
Contribution from sires Contribution from dams Within families Total	S D Q T	0 •00004 •02930 •02934	0003 .0002 .0158 .0157	.0011 .0025 .0505 .0541	.0123 0018 .0972 .1077
Heritability (based on observed %) Heritability (based on	ЦS/T ЦD/T 2 (S+D)/T ЦS/T-0 (1-р)	0 •005 •003 0	076 .051 001 746	.084 .182 .133 .370	•457 067 .195 1.270
Probit scale) Maternal effects (based on observed %)	D-S/T	.001	.032	.026	
Maternal effects (based on Probit scale)	D-S/T. <u>p(1-p)</u> Z2	•007	•314	.115	

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR RESISTANCE TO DEATH TO TEN WEEKS OF AGE IN SILVER OKLABAR X NEW HAMPSHIRE CROSSEREDS

Analysis of Variance

Source of	Ha	tch 1	Ha	tch 2	Ha	tch 3	Ha	tch 4
Variation	df	MS	df	MS	df	MS	df	MS
Total Between Sires Within Sires	394 9	•0115	336 10	•0687	270 9	•0625	143 6	•0946
Between Dams Remainder	57 328	•0319 •0296	51 275	.0285 .0217	41 220	.0246 .0408	23 114	•1110 •0466

Components of Variance and Estimates

Statistics	Symbols	Hatch 1	Hatch 2	Hatch 3	Hatch 4	
Contribution from sires Contribution from dams Within families Total	S D Q T	0005 .0004 .0296 .0295	.0013 .0013 .0217 .0243	.0008 0031 .0408 .0385	0016 .0134 .0466 .0584	
Heritability (based on observed %) Heritability (based on Probit scale)	4S/T 4D/T 2(S+D)/T 4S/T. <u>p(1-p)</u> Z ²	068 .054 007 460	.213 .213 .213 1.719	.083 322 119 .453	110 .918 .484 445	
Maternal effects (based on observed %) Maternal effects (based on Probit scale)	D-S/T D-S/T. <u>p(1-p)</u> Z ²	.031 .210			•257 1•039	128

ANALYSIS OF VARIANCE, COMPONENTS, HERITABILITY, AND MATERNAL EFFECTS FOR RESISTANCE TO DEATH TO TEN WEEKS OF AGE IN SILVER OKLABARS

Analysis	\mathbf{of}	Variance
		and the second sec

Source of	Hatch 1		Hatch 2		Hatch 3		Hatch 4	
Variation	df	MIS	df	MS	df	MS	df	MS
Total Between Sires	372 9	•0396	253 9	•0530	209 7	.1118	בי <i>ו</i> ד 6	.1900
Witnin Sires Between Dams Remainder	58 305	.0464 .0402	40 204	.0309 .0342	33 169	.1001 .0531	22 113	.1799 .0736

Components of Variance and Estimates

Statistics	Symbols	Hatch 1	Hatch 2	Hatch 3	Hatch 4	-
Contribution from sires Contribution from dams Within families Total	S D Q T	0002 .0011 .0402 .0411	.0009 0006 .0342 .0345	.0005 .0092 .0531 .0628	.0005 .0217 .0736 .0958	-
Heritability (based on observed %) Heritability (based on Probit scale)	4S/T 4D/T 2(S+D)/T 4S/T. <u>p(1-p)</u> Z ²	019 .107 .044 089	.104 070 .017 .567	.029 .585 .307 .107	.020 .907 .463 .059	
Maternal effects (based on observed %) Maternal effects (based on Probit scale)	D-S/T D-S/T. <u>p(1-p)</u> Z ²	.032 .150		.139 .514	.221 .645	129

GENERAL DISCUSSION

Heterosis

In this experiment, Silver Oklabar X New Hampshire crossbreds had a mean 10-week body weight slightly higher than the New Hampshires and considerably greater than the Silver Oklabars. The reciprocal cross yielded a mean 10-week body weight that was slightly less than the mean of the New Hampshires. Statistical analyses ("t" tests) showed that the difference between the means of the crosses as a group and the breeds as a group was highly significant. There was a significant difference between the means of the crossbred males. The mean for the males of the better cross (SB X NH) was significantly higher than the mean for the males of the better parent (New Hampshires). There was no significant difference between the means of the females in either of these comparisons. These results show that a heterotic effect on 10-week body weight was present when reciprocal crosses were made between the two breeds used in this investigation. However, the crossbreds were equal to the mean body weight of the better parent only when Silver Oklabar males were mated with New Hampshire females.

No definite conclusions can be drawn as to the cause of this heterotic effect. The statistical analyses showed that non-additive gene effects were absent or negligible; thus, heterosis cannot be explained on this basis. This leads the writer to postulate that increased heterozygosity due to crossing breeds which had previously been bred as closed flocks was the cause of this heterosis. However, this postulation is not supported by experimental evidence.

The crosses as a group did not differ significantly from the breeds in 10-week breast angle, hatchability, and resistance to death to 10 weeks of age. The means for Silver Oklabar X New Hampshire cross exceeded the

means for the breeds as a group in all of these characteristics but these differences were not statistically significant. It must be concluded that no heterotic effect was present or that this effect was too small to be significant with each of the above characteristics. Since one cross consistently averaged higher than the average for the parent breeds, these results suggest the need for a more thorough investigation of these traits.

It can be concluded that the Silver Oklabar X New Hampshire cross was superior to the reciprocal cross. A question might be raised regarding the economic soundness of using this cross commercially. It is the opinion of the writer that commercial use of this cross is economically sound. The crossbred progeny were equal to the better parental average (New Hampshires) in 10-week body weight. Since this is one of the major characteristics by which broiler stocks are evaluated, it can be seen that the cross was adequate in this respect. However, this characteristic alone would not warrant keeping two breeds to produce crossbred progeny. The deciding factor in favor of the cross is the fact that Silver Oklabars possess the sex-linked gene for silver plumage color that is dominant to the red color of the New Hampshires. The crossbred progeny will be predominantly white birds. Processors are demanding white feathered birds more and more. Since breeders cannot suddenly switch from a colored breed to a white one to supply this demand, crossbreeding seems to be the answer. This system permits the use of colored broiler strains of birds that have many years of intense selection behind them, and also maintains genetic diversity to meet the demands of producers, processors, and consumers if their demands change in the future. It is very likely that their demands will change.

Heritability

Heritability of 10-week body weight ranged from -.47 to 1.16 with a

mean of .45. Based upon the sire components of variance the mean estimate was .62 and based upon the dam components of variance the mean estimate was .28. Sire components of variance gave higher estimates of heritability because they contain sex-linked gene effects. Since sex-linked genes can be additive in their effects these estimates are correct but do not represent true estimates of heritability since they are not contributed equally by the dams. For this reason, heritability estimates based upon a combination of sire and dam components of variance are considered to be the best estimates for 10-week body weight.

Mean heritability estimates for 10-week body weight by breeds and crosses were as follows: .45 for New Hampshires; .48 for New Hampshires X Silver Oklabars; .52 for Silver Oklabars X New Hampshires, and .34 for Silver Oklabars. The higher estimates for the crosses possibly are due to increased genetic variance caused by crossing two breeds which had previously been bred as closed flocks. The difference between the mean estimates for the breeds cannot be explained. It could easily be due to sampling error.

Heritability of 10-week breast angle ranged from -.23 to .91 with a mean of .46. Based upon sire components of variance, the mean estimate was .38 and based upon the dam components of variance the mean estimate was .56. Maternal effects and sex-linked gene effects each were present in 4 of 8 cases. These effects were not consistent and it is not possible to determine the exact extent they influenced the magnitude of the heritability of 10-week breast angle. The average maternal effect was 12 percent. If this percentage of the total variance had been removed from the dam components of variance, heritability estimates calculated from the dam components would have been equal to those calculated from sire components. Heritability of 10-week breast angle would have been .38 calculated on this basis. In any event, heritability was within or at least bordering on the

range where individual selection is more efficient than family selection.

There was considerable variation among individual estimates of 10week breast angle within breeds and crosses, but the mean estimates among breeds and crosses differed only slightly. One cross (SB X NH) yielded an estimate slightly less than either parent, but the mean for both crosses was about equal to the mean for the parental strains.

Due to the presence of large maternal effects on hatchability, heritability estimates calculated from sire components of variance were considered to be more accurate estimates than those based on dam components of variance. Heritability estimates based on sire components of variance varied more for the different hatches within each breed and cross than the mean breed or cross estimates varied among themselves.

Both crosses yielded heritability estimates for hatchability that were less than those yielded by the breeds. No explanation can be offered to explain this. The Silver Oklabar X New Hampshire cross gave an estimate of $-.ll_4$ for hatchability of fertile eggs. This is even more difficult to explain since both breeds gave positive estimates.

Calculated heritabilities are only estimates of the true heritability. For this reason, mean estimates for all breeds and crosses should be better estimates of the true heritability of a trait. Mean estimates on the probit scale were .20 for hatchability of total eggs and .08 for hatchability of fertile eggs.

Heritability estimates for resistance to death to 10 weeks of age based upon sire components of variance were considered to be more indicative of the true estimates than those based on dam components because of a large maternal effect in the dam components. Only those estimates based on sire components of variance were converted to the probit scale. Mean estimates on the probit scale were as follows: -.05 for New Hampshires; .22 for New Hampshires X Silver Oklabars; 32 for Silver Oklabars X New Hampshires, and .16 for Silver Oklabars. A large negative mean estimate for New Hampshires and one large positive estimate in the case of each of the crosses caused the mean estimates for the crosses to be considerably higher than the mean estimates for the breeds. If the 3 extreme estimates were eliminated, the means for the breeds and crosses would be in a rather narrow range. Thus it seems logical to pool all estimates to obtain an average estimate of .16 for resistance to death to 10 weeks of age rather than consider each breed and cross mean as separate estimates.

Types of Gene Action

Approximately 47 percent of the total variance in 10-week body weight was genetic variation plus a small fraction due to maternal influence. Since maternal effects were detected by inference, it is not possible to calculate these effects exactly. These data show that about 2 percent of the total variance was due to maternal effects. Roughly 45 percent of the variance then was genetic in nature. About 2 percent of the genetic variance was due to non-additive gene effects; thus, 43 percent of the total variance was due to genes with additive effects. Sex-linked effects can be additive and need not be separated from autosomal genes with additive effects. In fact it would be impossible to separate sex-linked gene effects exactly or determine the exact magnitude of them since they were detected by inference.

The different breeds and crosses varied in percentages of the total variance due to different types of gene action on 10-week body weight. Four percent of the total variance in New Hampshires was due to nonadditive gene effects; no non-additive gene effects were found in Silver Oklabars. Both crosses showed non-additive gene effects in only 1 hatch

each. Sex-linked gene effects ranged from 8 percent in New Hampshires to 12 percent in Silver Oklabar X New Hampshire crossbreds. Additive gene effects were about 43 percent in New Hampshires, 47 percent in New Hampshires X Silver Oklabars, 48 percent in Silver Oklabar X New Hampshires, and 31 percent in Silver Oklabars. Since Silver Oklabars contributed as much to the additive genetic variance in the crosses as the New Hampshires, 31 percent appears to be too low for the additive genetic variance in Silver Oklabars. For this reason, an average of 43 percent appears to be more indicative of the additive genetic variance in 10-week body weight.

It can be concluded that approximately 45 percent of the variance in 10-week body weight in the breeds and crosses used in this investigation was genetic in nature. Approximately 2 percent of the genetic variance was due to non-additive gene effects and 43 percent was due to genes with additive effects. About 10 percent of the additive genetic variance was due to sex-linked gene effects. The small magnitude of non-additive gene effects and the inconsistency of their occurrence leads the writer to conclude that these effects on 10-week body weight may be ignored.

Approximately 57 percent of the total variance in 10-week breast angle was genetic variation plus a fraction due to maternal effects. Maternal effects were detected by inference and as a result, these effects could not be determined exactly. The average maternal effect was 14 percent. Removal of the average maternal effect from the genetic component of variance leaves 41 percent of the total variance as genetic variance. Two percent of the genetic variance was due to non-additive gene effects and 39 percent was due to genes with additive effects. Sex-linked gene effects accounted for 8 percent of the total variance. These effects can be additive and need not be separated from the additive genetic variance of autosomal genes.

The different breeds and crosses varied too much in percentages of the total variance due to different types of gene action on 10-week breast angle to draw definite conclusions on the different breeds and crosses. Most of the inconsistency was due to the inconsistent occurrence of sexlinked gene effects and maternal effects. This appears to be due to sampling error, to some degree, since dams in some hatches would contribute large maternal effects but the same dams in other hatches would not contribute any maternal effects. On this basis, it appears that the average percentages for all breeds and crosses are better estimates of the types of gene action than percentages for each breed and cross.

Due to the nature of the hatchability data and mortality data, these data could not be analyzed as diallel tests. As a result, the different types of gene action could not be determined. The average genetic variance in hatchability was 20 percent for percentage hatch of total eggs and 8 percent for percentage hatch of fertile eggs when expressed as a percentage of the total variance. Sixteen percent of the total variance in resistance to death was genetic in nature. These percentages are relatively small, and any non-additive gene effects might be important regardless of their magnitude.

Maternal Effects

Maternal effects on 10-week body weight were present in 2 cases out of a possible 16 cases. It can be stated that maternal effects were absent or played such a minor role in determining 10-week body weight that they may be ignored.

Maternal effects on 10-week breast angle were evident in 4 of 8 cases and contributed an average effect of 12 percent of the total variance. This is a sizable amount of the total variance but the accuracy of this percentage
might be questioned since maternal effects were not consistent in their occurrence. Silver Oklabar females contributed an average maternal effect of 36 percent when mated to Silver Oklabar males but these females did not contribute any maternal influence when mated to New Hampshire males. The results suggest that sampling error played a role in estimating maternal effects. New Hampshire females contributed an average maternal effect of 8 percent when mated to New Hampshire males and 14 percent when mated to Silver Oklabar males.

A relatively large maternal effect on hatchability was present in every hatch except in Silver Oklabars in the fourth hatch. The average maternal effect of all breeds and crosses was 36 percent of the total variance on hatchability of all eggs and 34 percent on hatchability of fertile eggs. Silver Oklabar females contributed a 17 percent greater maternal effect on hatchability than the New Hampshire females when the former breed was mated to New Hampshire males. Silver Oklabar females contributed a 3 percent smaller maternal effect than New Hampshire females when mated to Silver Oklabar males. When the maternal effects were pooled by breeds, Silver Oklabar females contributed a 7 percent greater maternal effect on hatchability of total eggs than New Hampshire females. However, New Hampshire females contributed a 2 percent greater maternal effect on hatchability of fertile eggs. Due to the methods of determining maternal effects, it is doubtful if these differences have any significance. Therefore, it can be concluded that New Hampshires and Silver Oklabars contributed approximately equal but relatively large maternal effects on hatchability.

Maternal effects contributed more to the variance in hatchability than did the genetic component. This suggests the need for a more thorough investigation of the nature of these effects. It is quite likely that some of these effects arise from egg characteristics that are hereditary and will

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permit improvement in hatchability by indirect means.

Maternal effects on resistance to death to 10 weeks of age were present in 10 of 16 cases. Calculated by breeds and crosses on the raw data, maternal effects ranged from 2 to 10 percent of the total variance. Due to the low incidence of mortality, conversion to the probit scale caused this range to increase to 11 to 33 percent. Mean maternal effects were 6 percent and 26 percent based on the raw data and the probit scale respectively. There was practically no difference in the maternal effects contributed by the females in the different breeds and crosses except among Silver Oklabar females when they were mated to New Hampshire males. It can be concluded that the ability of chicks to survive to 10 weeks of age was influenced more by maternal influence than by genetic differences. The nature of the maternal effects could not be ascertained. Undoubtedly some of the maternal effects were due to egg characteristics that are hereditary. For example, egg size might influence a chick's ability to survive, particularly during the early stage of growth. The weight of a day-old chick is largely a function of egg size. The contents of an egg are limited by the size of the egg; therefore, the amount of nutrients are also limited by the size of an egg. These egg characteristics and other characteristics possibly contribute to a chick's ability to survive to 10 weeks of age.

Correlations

Phenotypic, genetic and environmental correlations between 10-week body weight and 10-week breast angle were calculated separately for males and females by hatches. Phenotypic correlations ranged from .01 in Silver Oklabar males to .41 in New Hampshire males. New Hampshires showed the highest correlations for both sexes. The mean correlations were .19 for males and .13 for females.

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lenetic and environmental correlations varied too much to draw any ite conclusions regarding their magnitude. With few exceptions, ic correlations were positive and environmental correlations were ive. It can be concluded that positive genetic correlations and ive environmental correlations of questionable magnitude were present en 10-week body weight and 10-week breast angle in the breeds and es used in this investigation.

GENERAL SUMMARY

Data were collected from 2 series of diallel matings (4 hatches) among New Hampshires, Silver Oklabars, and reciprocal crosses between these breeds to study the genetic and environmental variation in 10-week body weight, 10-week breast angle, hatchability, and resistance to death to 10 weeks of age. This study involved 82 sires, 440 dams, and 5,355 chicks. The results were as follows:

1. Heterosis: "t" tests showed that both crosses had mean body weights significantly higher than the combined parental mean. The Silver Oklabar X New Hampshire cross equalled the better parental mean (New Hampshires) but the reciprocal cross did not. The crosses did not differ significantly from the parents in mean breast angle, hatchability, and resistance to death.

2. Heritability: Mean heritability estimates were .45 for body weight, .46 for breast angle, .20 for hatchability of total eggs, .08 for hatchability of fertile eggs, and .16 for resistance to death.

3. Gene Action: Approximate percentages of the total variance in body weight that were due to genetic differences were as follows: 45 percent for total genetic variance; 43 percent for additive genes; 2 percent for non-additive genes, and 10 percent for sex-linked genes. Similar data for breast angle were as follows: 41 percent for total genetic variance, 39 percent for additive genes, 2 percent for non-additive genes, and 8 percent for sex-linked genes. The nature of the hatchability and mortality data prevented the determination of the different types of gene action.

4. Maternal Effects: Mean maternal effects expressed as percentages of the total variance were 2 percent for body weight, 12 percent for breast angle, 36 percent for hatchability of total eggs, 34 percent for hatchability

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of fertile eggs, and 26 percent for resistance to death.

5. Correlations: Mean phenotypic correlations between 10-week body weight and breast angle were .19 for males and .13 for females. Positive genetic and negative environmental correlations of questionable magnitude existed between these traits.

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APPENDIX

Table 40

DESIGN AND ANALYSIS OF DIALLEL MATINGS

Sire Dam	A	В
a	n chix	n ch ix
Ъ.	n chix	n chix

This is the simplest design of a diallel mating. It contains 2 sires, 2 dams, and 4n chicks. Each sire and dam has 2n chicks. L sets of this design may be used.

Pooled Analysis of Variance

Source of Variance	Degrees of Freedom	Composition of Mean Square
Total	(lm-l)L	
Between Sires	L	Q+nI+2nS
Between Dams	L	Q+nI+2nD
Int-raction	L	Q4nI
Remainder	4(n-1)L	Q

- S = Between Sires M.S. Interaction M.S.* No. of Chicks per sire
- D = Between Dam M.S. Interaction M.S.* No. of Chicks per dam
- I = Interaction M.S. Remainder M.S.* No. of Chicks per dam per sire

Table 40 (continued)

Heritability

(a) estimate from sires,
$$h^2 = \frac{1}{15}$$

(b) estimate from dams, $h^2 = \frac{1}{10}$
(c) combined estimate, $h^2 = \frac{2(D+S)}{T}$
Sex-linked gene effects = $(S-D)/T***$
Maternal effects = $(D-S)/T***$
Non-additive gene effects = $1/T***$

*When the Interaction M.S. was less than the Remainder M.S. "I" was considered to be 0 and the Remainder M.S. was used to calculate S and D.

*T = Q+S+D+I

***Only components with positive figures were calculated, others were considered to be ⁰. Thus either sex-linked gene effects or maternal effects were positive and the other was 0. "I" = positive figure or 0.

Table 41

SAMPLE CALCULATIONS IN THE ANALYSIS OF DIALLEL MATINGS

		Pen 24	ŧ		
			Sires		
Dams		Sire A		Sire B	
8.		2.20		1.73	
		1.99		3.08	
		2.40		2.30	
	źI	6.59		7.11	
	źI(A+ ₿)		13.70		
	٤I ²	14.5601		17.9693	
Ъ		2.40		2.84	
		2.37		2.40	
		2.37		3.08	
	źI	7.14		8.32	
	£ X(A+B)		15.46		
	£I2	16.9938		23.3120	
Totals	/ -		<u> </u>	<u></u> אל גם	
	21	13.73		15.43	
	≤ X(A+B)		29.16		
	£I2	31.5539		41.0813	

Sample of Data: Ten-Week Body Weight

*This pen is representative of 6 pens used in this sample calculation.

Table 41 (continued)

Calculation of Sum of Squares

le 41 (continued)

1	Total	Between Sires	Between Dams	Interaction	Remainder
	1,7764	-2408	2581	.0364	1.2).11
	2.1047	.0057	2497	.4022	1.4471
	1.0451	.1657	.0520	.0019	.8255
	.6189	.1681	.0027	.0065	.4416
	.9108	.0002	•3468	.0456	.5182
	1.8949	•5377	.0227	.0674	1.2671
al	8.3508	1.1182	.9320	.5600	5.7406

Pooled Sum of Squares for Six Pens

Pooled Analysis of Variance

irce of Variation	d.f.	S.S.	M.S.
al ;ween Sires ;ween Dams ;eraction mainder	55 5 5 5 5 40	8.3508 1.1182 .9320 .5600 5.7406	.2236 .1864 .1120 .1435
: <u>Sire M.S Remainder M</u> Chicks per sire	4 <u>.5.</u> = <u>.2236</u>	<u>1435</u> = <u>.0801</u> = 6 6	.0134
: Dam M.S Remainder M. Chicks per dam	<u>.s.</u> = <u>.1864</u> -	$\frac{.1435}{6} = \frac{.0429}{6} = \frac{.0429}{6}$,0072
: 0			
$\frac{3}{T} = \frac{4(S)}{T} = \frac{4(.0134)}{.1641} = \frac{.09}{.16}$	5 <u>36</u> = .33 541		
$D = \frac{L_1(D)}{T} = \frac{L_1(.0072)}{.1641} = \frac{.02}{.1641}$	288 = .18 541		
$(S+D) = \frac{2(S+D)}{T} = \frac{2(.0134)}{.0134}$	+ .0072) = .	<u>0416 = .25</u> 1641	
:-linked gene effects = S	$\frac{D}{T} = \frac{.0134}{.160}$	<u>.0072</u> = <u>.0062</u> = . 1 .1641	038
$\texttt{vernal effects} = \frac{D-S}{T} = 0$			
-additive gene effects =	$\frac{I}{T} = 0$		

Table 42

PROCEDURE FOR CALCULATING CORRELATIONS

Example of Data

Sire A	Sire B	Sire C	Sire D
D1*	DL	D7	D1 0
D2	D5	D8	D11
D3	D 6	D9	D12

*Rach cell contains 1 dam and each dam has 3 chicks; thus each sire has 9 chicks. Data includes 4 sires, 12 dams, and 36 chicks.

Partitioning of Variance and Covariance

Source of Variance or Covariance	Degrees of Freedom	Composition of M.S. or Cov.
Total	xyz-l **	
Between sires	x-l	Q + zD + yzS
Within sires		
Between dams	x(y-1)	
Between full sibs	xy (2-1)	Q

**See pages 3 and 4 for symbols and definitions.

Step 1: Calculate analysis of variance for 10-week body weight.

- (1) Correction factor = $\frac{(\not I I)^2}{\text{total chicks}}$ (2) Total SS = $I_1^2 + \dots I_{36}^2 - C$
- (3) Between sizes $SS = \frac{(\not \in I_A)^2 + \dots (\not \in I_D)^2}{Chicks per size} C$
- (4) Between dams SS = $(\xi \mathbf{I}_{D1})^2 + \dots (\xi \mathbf{I}_{D12})^2 C$ Chicks per dam

Table 42 (continued)

- (5) Between dams within sires SS = Between dams SS Between sires SS.
- (6) Between full sibs SS = Total SS Between dams SS.
- (7) Calculate mean squares.
- (8) Reduce M.S. to their components.
 - (a) S = <u>Sire M.S. Dam M.S.</u> Chicks per sire
 - (b) D = Dam M.S. QChicks per dam
 - (c) T = S + D + Q
- Step 2: Repeat step 1 for breast angle values.
- <u>Step 3</u>: Calculate an analysis of covariance between 10-week breast angle and 10-week body weight. This is accomplished by repeating step 1 and substituting the sum of the cross products for the sum of the X's squared.

Calculation of Correlations

Phenotypic

(1)
$$\mathbf{r}_{\mathbf{X}_{1}\mathbf{X}_{2}} = \begin{array}{c} Q_{\mathbf{X}_{1}\mathbf{X}_{2}} + D_{\mathbf{X}_{1}\mathbf{X}_{2}} + S_{\mathbf{X}_{1}\mathbf{X}_{2}} \\ \sqrt{(Q_{\mathbf{X}_{1}} + D_{\mathbf{X}_{1}} + S_{\mathbf{X}_{1}})(Q_{\mathbf{X}_{2}} + D_{\mathbf{X}_{2}} + S_{\mathbf{X}_{2}})} \end{array}$$

Genetic

(1)
$$r_{GX_1 GX_2} = \underbrace{\mu_{X_1 X_2}}_{\sqrt{(\mu_{DX_1} X \mu_{DX_2})}}$$

$$(2) = \frac{4S_{\mathbf{X}_{1}}\mathbf{X}_{2}}{\sqrt{(4S_{\mathbf{X}_{1}}\mathbf{X} + 4S_{\mathbf{X}_{2}})}}$$

$$(3) = \frac{2(D\chi_1\chi_2 + S\chi_1\chi_2)}{\sqrt{2(D\chi_1 + D\chi_1)\chi + D\chi_2}}$$

Table 42 (continued)

Environmental

(1)
$$r_{E_{X_{1}}} E_{X_{2}} = \frac{Q_{X_{1}X_{2}} + S_{X_{1}X_{2}} - 3D_{X_{1}X_{2}}}{\sqrt{(Q_{X_{1}} + S_{X_{1}} - 3D_{X_{1}})(Q_{X_{2}} + S_{X_{2}} - 3D_{X_{2}})}}$$

(2) $= \frac{Q_{X_{1}X_{2}} + D_{X_{1}X_{2}} - 3S_{X_{1}X_{2}}}{\sqrt{(Q_{X_{1}} + D_{X_{1}} - 3S_{X_{1}})(Q_{X_{2}} + D_{X_{2}} - 3S_{X_{2}})}}$
(3) $= Q_{X_{1}X_{2}} - D_{X_{1}X_{2}} - S_{X_{1}X_{2}}$

$$\frac{1}{\sqrt{(Q_{\mathbf{X}_1} - D_{\mathbf{X}_1} - S_{\mathbf{X}_1})(Q_{\mathbf{X}_2} - D_{\mathbf{X}_2} - S_{\mathbf{X}_2})}}$$

Table 43

ANALYSIS OF ALL-OR-NONE DATA

Analysis of Variance

Source of Variance	d.f.	Sum of squares	Mean squares	Components of mean squares
Total	xvz-1	*	**	
Between Sires	x-1			Q+zD+yzS
Within Sires Remainder	x(y-1) xy(z-1)			Q+2D Q

Steps in Calculating

- 1. Degrees of freedom
 - (1) total = total chicks hatched 1
 - (2) between sires = no. of sires 1
 - (3) between dams = no. of dams no. of sires
 - (4) remainder = total d.f. (between sires d.f. + between dams d.f.).
- 2. Sum of squares
 - (1) total = $\frac{a(t-a)}{t}$ where a is the chicks which survived to 10 weeks

of age and t is the number of chicks that entered the brooder house.

(2) between sires = the sum of $x, \underline{a(t-a)}$ terms, one term computed t

separately for each sire family.

(3) between dams = the sum of $x, \underline{a(t-a)}$ terms, one term computed t

separately for each dam.

- (4) remainder = total S.S. between sires S.S. + between dams S.S.
- B. Mean square = the appropriate S.S./the corresponding d.f.

able 43 (continued)

. Components of the M.S.

(1) S = between sire M.S. - between dam M.S. no. of chicks per sire

(2) D = between dam M.S. - remainder M.S. no. of chicks per dam

. Heritability estimates.

- (1) $h^2 = \frac{4S}{T}$ (2) $h^2 = \frac{4D}{T}$ (3) $h^2 = \frac{2(S+D)}{T}$
- Maternal effects = $\frac{D-S}{T}$
- '. Transformation of estimates to probit scale.
 - (1) Multiply each estimate by p(1-p) where p is the fraction which $\frac{2^2}{2}$

dies and Z is the height of the ordinate which truncates p of the area of the normal curve.

(2) Calculate p and find Z in the appropriate statistical table.

VITA

Clayton C. Brunson candidate for the degree of Doctor of Philosophy

- Thesis: GENETIC AND ENVIRONMENTAL VARIATION IN TEN-WEEK BODY WEIGHT, TEN-WEEK BREAST ANGLE, HATCHABILITY AND RESISTANCE TO DEATH TO TEN WEEKS OF AGE IN THE DOMESTIC FOWL
- Major: Animal Breeding

Biographical:

Born: The writer was born near Colfax, Louisiana, November 3, 1921, the son of Andrew J. and Marie Elizabeth Brunson.

- Undergraduate Study: He attended elementary and high schools in Lasalle and Grant Parishes, and graduated from high school in May, 1939. He attended Northwestern State College of Louisiana from September, 1939 until January, 1941. After separation from the Army in 1946, the writer attended Louisiana State University from which he received the Bachelor of Science degree, with a major in Animal Industry, in May, 1949.
- Graduate Study: The writer entered Oklahoma Agricultural and Mechanical College, Stillwater, in September, 1949 and received the Master of Science degree, with a major in Poultry Breeding, in January, 1951. Requirements for the Doctor of Philosophy degree were completed in May, 1955.
- Experiences: The writer enlisted in the Louisiana National Guard in December, 1939 and was called into Federal Service in January, 1941. He was separated from the Army in February, 1946. While completing his graduate work, he was a research assistant from September, 1949 through August, 1950, an instructor from September, 1950 through August, 1952 and a research assistant from September, 1952 through August, 1953, in the Poultry Husbandry Department of Oklahoma Agricultural and Mechanical College, Stillwater. Since September, 1953, the writer has been employed as an assistant professor in the Poultry Industry Department of Louisiana State University.

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TYPIST: Hazel Brunson