SELECTION METHODS FOR GENETIC IMPROVEMENT OF INDONESIAN FOWL COMPARED BY SIMULATION

By

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A DISSERTATION

Submitted to
Michigan State University
in partial fulfillment of the requirements
for the degree of

DOCTOR OF PHILOSOPHY

DEPARTMENT OF DAIRY SCIENCE

1978

ABSTRACT

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Effectiveness of four methods of selection, mass selection, selection index, restricted selection index and independent culling levels, was studied for each of nine simulated native chicken populations.

The nine populations were chosen arbitrarily out of the possible combinations of three levels of heritability of body weight (.4, .3, .1), heritability of egg production (.3, .2, .1), heritability of egg weight (.5, .3, .1), genetic correlation between body weight and egg production (-.6, -.4, -.2) and genetic correlation between body weight and egg weight (.5, .3, .2).

Nine generations of selection were performed by truncation, where upper 1.25% males and 12.5% females were saved for breeding.

The economic value per unit of body weight was 25 times the economic value per unit of egg production.

Mass selection showed that predictions of direct responses were more accurate than those for correlated responses. When negative genetic correlation and heritabilities were low, the correlated responses were predicted more accurately than when both were high.

Selection index showed that within the same combination of heritabilities, mean genetic change of body weight was highest when genetic correlation between body weight and egg production was lowest, but on the contrary the smallest negative change in egg production occurred in the population with the lowest negative genetic correlation. As in selection index, restricted selection index and independent culling levels also showed that the magnitude of negative genetic correlation affected the mean genetic change of the two traits in opposite ways.

Mean body weight response was largest when mass selection was used, and was about doubled at generation ten when heritability was .4, but egg production was decreased 1.7% per generation.

Comparable responses on mean body weight were obtained by selection index and restricted selection index, and independent culling levels showed slightly smaller responses.

Selection index showed no decrease in egg production in populations with genetic correlation equal to -.2.

Restricted selection index produced decreases in egg production 40%-50% less than mass selection when genetic correlation was strong (-.6 or -.4) regardless of heritabilities.

When selection index was considered 100% efficient, mass selection was 20% less efficient and independent culling levels were 10% less efficient, especially when genetic correlation was strong.

Examination of genetic correlations showed that during selection experiments in all populations and for all methods of selection the initial genetic correlation was maintained.

Mass selection and independent culling levels produced genetic correlation in the selected offspring somewhat weaker than in the unselected offspring, but the difference was clear only when the genetic correlation was strong. Selection index and restricted selection index maintained genetic correlation in all cases.

ACKNOWLEDGMENTS

I am deeply indebted to Dr. John L. Gill, my major professor for his patient assistance and invaluable suggestions in the preparation of this manuscript. I would like to express my appreciation for his guidance and encouragement in my graduate program.

I am grateful to Dr. C. E. Meadows, Dr. T. H. Coleman, Dr. W. T. Magee and Dr. R. W. Erickson for their participation and suggestions in my graduate program, to Dr. R. R. Neitzel for his assistance in computer programming.

I am also grateful for the leave of absence provided by the Gadjah Mada University, for the financial support provided by the Midwest Universities Consortiums for International Activities (MUCIA, Inc.) and for the facilities provided by the Department of Dairy Science at Michigan State University.

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INTRODUCTION

Nature has provided that animals will reproduce, but if we let them reproduce naturally, we arrive at the problem of lack of nutritious food from animals. This problem we observe now in part of the world (underdeveloped and developing countries) where men haven't interfered much in the life pattern of animals. On the other hand, in developed countries lack of production from animals is not a problem since for many decades men with science and knowledge have been able to improve and change animal production and reproduction to suit their needs.

Improvement in animal production is brought about primarily by the change in genetic composition of animals through careful selection of breeding stock. So it's obvious if developing countries want to solve their food problem, an effort toward the increase of animal production should be put forward.

Ideas to increase production by crossbreeding, upgrading, linebreeding and entire replacement with exotic breeds have been suggested, but all of these can't be justified and wholly adapted without first conducting a study of the genetic potential of the existing populations.

The author is interested in planning and working toward the improvement of the native chickens in Indonesia. The native chicken population is a good example of producing and reproducing as nature provided. They are raised widely in the traditional way, well adapted to local conditions and characterized by low production of meat and eggs. Yet they provide nearly 90% of chicken meat supply for the nation.

An extensive and intensive study of the population of chickens by survey and experiment is necessary for estimation of genetic parameters. The author is interested in improving body weight of chickens at market age (sexual maturity). Most studies with other breeds of chickens have indicated that body weight has a moderate to high heritability and the variability of body weight is due primarily to additive genetic variance. Therefore the author believes that selection within the native chicken population should give a good response.

As the practical studies can't be conducted for the time being, a Monte Carlo simulation process may be used to mimic the native chicken population. In this study three different levels of heritability of body weight, egg production and egg weight, and three different levels of genetic correlation between body weight and egg production, and between body weight and egg weight are used in combinations to simulate potential progress.

The objectives of this study are:

1. To design an optimal breeding plan to improve body weight at sexual maturity.
2. To compare effectiveness of four different methods of selection:
    (a) Selection on body weight by truncation on phenotypic

value and monitoring the change of egg production and egg weight as correlated response.

(b) Selection on body weight and on egg production simultaneously.

(c) Selection on body weight with the imposed restriction of no change in egg production.

(d) Selection at two stages, first on body weight then on egg production.

3. To predict direct response to selection under different combinations of parameter values and selection methods.
4. To examine correlated responses under different combinations of parameter values and selection methods.

LITERATURE REVIEW

Improvement of native stock

Recently there has been considerable interest and effort in improving animal production in developing countries.

From the genetic standpoint animal improvement can be achieved through selection and breeding.

Although suggestions have been made for genetic improvement via crossbreeding, upgrading, replacement of native stock by imported animals or selection within the native populations, they do not lead to an easy decision. However McDowell (1972) cited a recommendation from an expert on animal breeding and climatology of F.A.O. who recommended the following procedures:

1. Objectively evaluate presently available animals and the environments to which they are exposed.
2. Experimental work should be conducted to assess the merits of indigenous animals, and their ability to respond to improved environments. When sufficient merit exists, then programs of improvement through selection should be implemented.
3. When evaluation indicates the need for grading up, then animals that will be likely to contribute the desired end result should be chosen.

From this recommendation it is obvious that a careful study of genetic potential of native animals is a prerequisite for a plan for further improvement.

Most improvements of native stock have been done by crossbreeding or upgrading, primarily in dairy cattle and in swine. However, a number of native stocks that have been improved without infusion of foreign blood are Arabian horses, Brahman and Boran beef cattle, Karakul sheep, Angora goats, several Chinese breeds of pig and the Awassi sheep in Israel.

The improvement of Awassi sheep as dairy animals is interesting. The program was initiated 50 years ago with local stock. Epstein (1977) reported that the improvement in the course of 30 years from 1943 to 1973 was reflected by the number of ewes with actual lactation yields of more than 400 kg. In 1943 only 0.08% of all milk recorded animals yielded more than 400 kg but by 1973 the percentage had increased to 18.9%. Some important things to note from this report are:

1. milk yield is an additive trait
2. selection was practiced within the native flock by selecting the additive genetic variation
3. improvement was achieved without introducing outside genetic material.

In chickens it has been reported that the variance of body weight is mainly due to additive genetic variance and the heritability is quite high (Martin et al., 1953; Brunson et al., 1956; Kan et al., 1959 and Siegel, 1962).

Varieties of native chickens are found in developing countries, and dominate the chicken populations in the rural areas.

Uddin (1962) and McArdle (1972) suggested the improvement of native chickens for egg production by crossbreeding or upgrading.

El-Issawi (1973) reported that in Egypt, Baladi, Fayoumi and Dandarawi were developed as layers from indigenous breeds.

No reports were noted on selecting native chickens for meat production.

Genetically there is a similarity between body weight in chickens and milk production in Awassi sheep. Although the heritability of milk production in Awassi sheep was not reported, the author believes that the heritability is moderate because of the long term response to selection. If the improvement of native chickens is concentrated on body weight instead of egg production, then selection on additive genetic variation of body weight within the native population seems very promising.

Monte Carlo studies in genetics

Monte Carlo technique has been introduced in genetic and selection studies to confirm genetic theories and to predict results. Monte Carlo methods comprise that branch of experimental mathematics which is concerned with problems using random numbers. As the genetic systems obey the laws of probability, they can be investigated using probabilistic Monte Carlo methods.

Fraser (1957a) introduced the first techniques for the simulation of genetic systems by high speed electronic digital computers. The genetic framework was presented as a binary system in which the symbols 0 and 1 were regarded as identifying the two alleles of a single locus. An array of alleles in the chromosome was generated by adopting the binary representation of the generated random numbers.

Fraser (1957b) studied the effects of linkage on the rate of advance under selection. His results indicated that linkage in large populations caused a correlation of rate of advance with degree of linkage when the recombination is less than .5%. However, in small populations the effect of linkage is considerably exaggerated. In his next three papers on the subject Fraser (1960, a, b, c) discussed the effects of linkage, dominance and epistasis. The study on epistasis was extended by considering the effects of reproductive rate and intensity of selection. Fraser also simulated selection against phenotypic extremes.

Since the works by Fraser, many simulation studies have been reported, which primarily were concerned with artificial selection theory. These studies contributed to the understanding of some of the operating genetic mechanisms.

A detailed review of these studies is not warranted, but examples of types of studies may serve to summarize.

Barker (1958a, b) investigated selection between alleles at an autosomal locus and at a sex linked locus.

Martin and Cockerham (1960) reported the effect of linkage on the progress from mass selection in small populations.

Gill (1965a, b, c) studied the effects of population size, linkage, selection intensity and environmental variation upon genetic change in simulated populations. In other studies Gill and Clemmer

(1966) reported the effect of selection and linkage on degree of inbreeding. And a similar study was reported by Bogyo and Ting (1968).

Young (1966) presented the results from simulation studies on the rate of decay of the additive genetic variance due to selection and the resulting change in heritability.

Hill and Robertson (1966) studied the effect of linkage on limits to artificial selection.

Parker et al. (1969, 1970a, b) examined selection response and genetic correlation in simulated populations.

Bereskin (1969, 1972) reported the effect of inbreeding on genetic and phenotypic trends and selection response.

Bulmer (1976) studied the effect of selection on genetic variability.

Sather et al. (1977) reported the effects of population size, selection intensity, mating system and selection method in simulated populations.

Data for those studies were generated on the assumption of known initial gene frequencies and number of loci affecting the traits.

However in other studies Monte Carlo methods were used to generate data for metric traits for which realistic specification of gene frequencies and number of loci can't be made. The generation of data was based on a specified biological model and statistical estimates of biological parameters. Several studies using this procedure have been reported.

Magee (1965) studied the estimation of response to selection when selection was applied for two traits.

Everett et al. (1967) used simulated records of milk production to estimate the genetic and environmental trends.

Strohbehn (1974) evaluated response to selection and mating systems with different levels of heritability, selection intensity and progeny testing.

Bruns and Harvey (1976) studied the effects of varying selection intensity for two traits on estimation of realized genetic parameters.

These studies show that when data can't be made available from a real experiment, then Monte Carlo methods for generation of biological data make possible selection studies, which can serve as guides for establishing long term experiments that will have optimal chance of success.

Genetic correlation and correlated response

Genetic correlation between traits is important when dealing with metric traits, as selection applied to one trait generally results in correlated response in other traits not under selection.

The most important underlying cause of genetic correlation appears to be pleiotropy, i.e., some genes affect two or more traits. Other possible causes of genetic correlation are usually considered to be minor or transient such as linkage (Falconer, 1960).

Two traits can be correlated genetically either positively or negatively and theoretically in selection experiment the correlated response can be predicted if the genetic correlation and the heritabilities of the two traits are known.

Many studies on genetic correlation and correlated response have been reported, with considerable emphasis on

1. whether the theoretical treatment of correlated response to selection in terms of the genetic correlation is adequate to explain the responses realized in experiments
2. asymmetrical correlated response
3. the effect of selection on genetic correlation
4. negative genetic correlation between traits

Falconer (1954) experimented with mice to check the validity of the theory of genetic correlation. Two way selection was made for body weight in one pair of lines and for tail length in another pair. The results showed an agreement between the two independent estimates of the genetic correlation between weight and tail length, one from each pair of lines. This agreement showed that the theoretical treatment of the genetic correlation between two traits adequately accounts for the observed correlated responses.

Reeve and Robertson (1953), selected for wing and thorax length in Drosophila melanogaster for fifty generations. The genetic correlation between traits is .7. A good agreement was found between estimates of the genetic correlation between the two characters in their base population and the correlated responses when either of the two were selected separately.

Clayton et al. (1957), working with Drosophila melanogaster, observed the correlated response on number of sternopleural bristles, when selection was practiced on number of abdominal bristles. The genetic correlation between abdominal bristles and sternopleural bristles in the base population was small but slightly positive (.05 to .10). They reported that a moderate agreement with predicted correlated response was observed in earlier generations but the correlated response became entirely unpredictable with further selection in later generations. They suggested that the magnitude of genetic correlation affects the accuracy of the expected response and the effect of random drift in the correlated trait causes the response somehow to deviate from the expectation when the genetic correlation is weak.

Asymmetrical correlated response in selection experiments have been reported, where discordance of the pattern of correlated response with the expectation was observed.

Falconer and Latyszewski (1952) experimented with mice, where mice were selected for growth rate on high and low planes of nutrition. They considered the same measurement made under two different environments as two separate traits. Genetic correlations observed were equal in early generations but were markedly different in later generations. They attributed this asymmetry to changes in the basic parameters due to selection applied.

Bell and McNary (1963) and Yamada and Bell (1963) also observed asymmetry of genetic correlations when selection was applied to Tribolium castaneum under two different environments.

Clayton et al. (1957) reported asymmetry in correlated response of sternopleural bristle number in Drosophila melanogaster when selection was practiced to increase or decrease abdominal bristle number.

Siegel (1962) reported results of a double selection experiment which provided a comparison of the genetic correlations obtained between body weight and breast angle at eight weeks of age in white Plymouth Rock chickens. The results showed that selection for body weight apparently resulted in greater changes in breast angle than selection for breast angle did for body weight. The relative efficiency of changing breast angle through selection on body weight as compared to direct selection for breast angle was 71% in males and 94% in females, but, the percentage efficiency for changing body weight through selection for breast angle as compared to direct selection for body weight was 33% for males and 29% for females. He concluded that the asymmetrical response could be due to unequal heritabilities, where the realized heritability of eight week body weight (.31 for males and .28 for females) was approximately one third larger than the respective value for breast angle (.24 for males and .21 for females).

Nordskog and Festing (1962), also experimenting with chickens, reported an asymmetry of the realized genetic correlation between body weight and egg weight when selection was applied for both high and low directions for body weight and egg weight.

Bohren et al. (1966) and Parker et al. (1970a) reported asymmetrical correlated response from simulation selection experiments.

Bohren et al. (1966) suggested that in experiments it is unlikely and more surprising to find symmetrical than asymmetrical correlated response.

Parker et al. (1970a) reported asymmetrical response in later generations although the response was symmetrical in early generations.

The effect of selection on genetic correlation has been of considerable interest to research workers. Falconer (1960) theorized that if selection has been applied to two traits simultaneously the genetic correlation between them should be expected eventually to become negative, because those pleiotropic genes that affect both traits in the desired direction will be strongly acted on by selection and brought rapidly toward fixation. They will then contribute little to the variances or covariances of the two characters. The pleiotropic genes that affect the traits in opposite ways are less strongly influenced by selection and will contribute most of remaining covariances of the two traits, and the resulting genetic correlation will be negative.

Friars et al. (1962), Lentz and Gowe (1974), Emsley et al. (1977), from selection experiment with poultry, reported a decline over time in estimates of genetic correlation for traits related to egg production.

Parker et al. (1969, 1970a, b) examined the effect of truncation selection of a primary trait upon the genetic correlation and the correlated response in a secondary trait in simulated populations. Results from an additive model indicated that high selection intensity resulted in a decline in genetic correlation while low selection intensities maintained the genetic correlation. A model with complete dominance showed that the change in genetic correlation where selection was by upper truncation followed the same patterns as for the additive model. Selection by lower truncation with high intensity of selection showed a more rapid decrease in genetic correlation.

Cheung and Parker (1974) conducted an experiment with mice over 14 generations. They reported that estimates of realized genetic correlation between 6-week body weight and 6-week tail length showed that more intense selection led to some decrease in genetic correlation between the two traits.

Knowledge of the magnitude of the genetic correlation and the direction of the change of the correlated response in a secondary trait upon selecting the primary trait is important. Breeders are more concerned with the existence of negative genetic correlation as simultaneous selection for two traits with negative genetic correlation may produce little progress and selection to improve one trait will cause a decrease in the other trait.

Evidence of negative genetic correlation among economic traits in livestock and poultry has been reported by research workers.

In dairy cows a negative genetic correlation between milk yield and butterfat percentage was reported by Johansson (1950), Freeman and Dunbar (1955), Tabler and Touchberry (1955), Farthing and Legates (1957) and Johnson (1957). The values reported were in the range of -.58 to -.20.

Fredeen and Jonsson (1957), as cited by Falconer (1960), reported a genetic correlation of -.47 between body length and backfat thickness and -.96 between growth rate and feed efficiency (lbs feed/lb gain) in pigs.

In chickens, evidence of negative genetic correlation between body weight and egg production has been reported. This means that joint selection for body size and egg production in a given flock reduces progress in each trait as compared to that made with the same selection differential provided no selection pressure is placed on the other trait. This has special importance in the poultry industry for broiler producers. The broiler strains have large body size but are low in egg production, so it would be impossible for the broiler breeders to improve both traits significantly by simultaneous selection.

A wide range of values of negative genetic correlation between body weight and egg production has been reported.

When experimenting with New Hampshire chickens, Dillard et al. (1953) reported genetic correlations of -.17 and -.20, Jerome (1956) obtained a correlation of -.59 and Shimizu et al. (1968) observed a moderately negative genetic correlation.

Nordskog (1960) studied White Leghorns and reported a positive correlation of +.08, not significantly different from zero. In the heavy breeds he obtained a highly significant negative genetic correlation of -.35.

Siegel (1963), using White Plymouth Rocks in his study, reported a range of negative correlation from -.01 to -.71.

Gowe et al. (1973), measuring the genetic correlation in White Leghorns chickens, reported values in the range of -.17 to -.37.

Working with broiler chickens, Mehta et al. (1975) reported a correlation of -.14.

These studies indicated that negative genetic correlation between body weight and egg production is obvious and substantial. To improve native chickens in developing countries for meat production, attention should be given to the existence of the negative correlation, especially because it is known that egg production in native chickens is relatively low. Both traits should be considered when one formulates selection schemes.

Methods of selection

In plant or animal breeding three methods of selection can be used if breeders are interested in selecting more than a single character.

1. Tandem method.

   Selection is practiced for only one trait at a time until satisfactory improvement has been made in this trait. Selection efforts for this trait are then relaxed, and efforts are directed toward the improvement of a second trait, then a third, and so on.

2. Independent culling method.

   A certain level of merit is established for each trait and all individuals below that level are discarded regardless of their superiority or inferiority in other traits.

3. Selection Index method.

   Extra merit in one trait may offset defects in another. Each trait is weighted by its relative economic value and a linear function of such values gives an index value for net merit based on all the traits. Then animals with the highest index value will be kept for breeding purposes.

The selection index method has been the subject of number of studies either theoretical or experimental.

Smith (1937) developed an index designed for the selection of plant lines, using Fisher's concept of discriminant functions to derive a linear equation based on observable characteristics as the best available guide to the genetic value of each line.

Hazel (1943) by use of Wright's path coefficients, developed a selection index which maximized the correlation between the index and the aggregate genetic value of the traits selected for. Hazel's selection index is defined as:

$$I = b_1x_1 + b_2x_2 + - - - - - + b_nx_n$$

where the b_i's are the derived optimum weighting coefficients for the characters x_i.

The aggregate genetic value of the index is defined as

$$H = a_1g_1 + a_2g_2 + - - - - + a_ig_i + - - - - + a_ng_n$$

where the a's are economic values corresponding to one unit of the x_i. The problem is to obtain a set of values for the b_i's which maximizes the correlation between I and H. The desired solution to the b_i's is obtained from a set of simultaneous linear equations which can be presented in matrix notation as:

$$\underline{Pb} = \underline{Ga}$$

where $\underline{b}$ is a column matrix of unknown b_i's

$\underline{P}$ is the phenotypic variance covariance matrix

$\underline{G}$ is the genotypic variance covariance matrix

$\underline{a}$ is the column matrix of economic weighting factors

Hazel and Lush (1942), Young (1961) and Finney (1962) presented theoretical papers comparing the three methods: tandem selection, independent culling, and selection index. They theorized that selection index is never inferior to tandem selection or independent culling. However, Rasmuson (1964), found contrary to theoretical expectations, that selection based on independent culling levels was superior in two experiments to selection index for increasing the total number of bristles in *Drosophila melanogaster*. On the other hand, Sen and Robertson (1964) compared index, independent culling levels, and tandem methods for increasing both abdominal and sternopleural bristles, and concluded from their results that the index method was superior as predicted by selection theory.

In practice there are situations when we want to change the mean of one trait while holding the mean of a second trait constant. For this purpose the concept of a restricted selection index has been derived mathematically by Kempthorne and Nordskog (1959). The idea is that the usual index equations be solved subject to the simultaneous conditions that the covariance between the index and a linear function of the genotypes involved be zero, thus preventing selection on the index from causing any genetic change in this function.

In solving for the index weighting factors, Kempthorne and Nordskog (1959) did not retain the equations carrying the restriction explicitly in the system.

The index weighting factor is obtained by solving the final form of equation:

$$\underline{b} = \left[\underline{I} - \underline{P}^{-1}\underline{GC}\ (\underline{C}'\underline{GP}^{-1}\underline{GC})^{-1}\underline{C}'\underline{G}\right] \underline{P}^{-1}\underline{Ga}$$

where: $\underline{b}$ is a column vector of index weighting factors

$\underline{I}$ is identity matrix

$\underline{P}$ is phenotypic variance-covariance matrix

$\underline{G}$ is genotypic variance-covariance matrix

$\underline{C}$ is a column vector of zero's with a *one* in the i^{th} position, where the i^{th} trait is the trait subject to the restriction

$\underline{a}$ is a column vector of economic values

The effect of restriction is to multiply the unrestricted selection index by a matrix, obtained after performing a sequence of matrix operations.

Cunningham et al. (1970) presented a paper on restricted selection index and showed a different procedure for the solution of index weighting factors. The procedure has proved to be very practical and simple. A matrix equation taking the original form of unrestricted selection index with a modification of rows and columns is used. In this method the equation carrying the restriction is retained.

The equation is:

$$\begin{bmatrix} \underline{P} & \underline{G}_j \\ \underline{G}_j' & \underline{O} \end{bmatrix} \begin{bmatrix} \underline{b} \\ \underline{b}_d \end{bmatrix} = \begin{bmatrix} \underline{G} \\ \underline{O} \end{bmatrix} \begin{bmatrix} \underline{a} \end{bmatrix} \qquad \text{or}$$

$$\underline{P}^*\underline{b}^* = \underline{G}^*\underline{a}$$

where $\underline{P}$ is the phenotypic variance-covariance matrix

$\underline{G}$ is the genotypic variance-covariance matrix

$\underline{G}_j$ is the j^{th} column of the genetic variance-covariance matrix for the j^{th} trait, the trait subject to restriction

$\underline{b}$ is a column vector of index weighting factors

$\underline{b}_d$ is a column vector of dummy weighting factors

$\underline{a}$ is column vector of economic values

Cunningham's method is equivalent to Kempthorne and Nordskog's as the solution for $\underline{b}$ in Cunningham's equation is:

$$\underline{b} = \left[\underline{I} - \underline{P}^{-1}\underline{G}_j\ (\underline{G}_j'\ \underline{P}^{-1}\ \underline{G}_j)^{-1}\underline{G}_j'^{\,1}\right] \underline{P}^{-1}\underline{GV}$$

where $\underline{G}_j$ is the j^{th} column of the genetic variance-covariance matrix, expressed as $\underline{G}\ \underline{C}$ in Kempthorne and Nordskog's method.

Several experiments have been devoted to verification of the theory of the restricted selection index. Abplanalp et al. (1963) selected Broad Breasted Bronze turkeys for seven generations using an index calculated to produce maximum gains in 9-week weight while holding 24-week body weight constant. The results were in fair agreement with predicted values.

Scheinberg et al. (1967) compared relative efficiency of restricted index selection and unistage tandem selection on three traits in *Tribolium castaneum*. They reported that the results in general confirm the biological validity of the restricted selection index theory.

Okada and Hardin (1967) experimenting also with *Tribolium castaneum*, reported results from 7 generations of selection. Restricted selection index was effective for increasing 14-day larva weight while holding 30-day adult weight constant, and when selection was continued into 13 generations, the results showed the same trend. They suggested that the restricted selection index is biologically valid (Okada and Hardin, 1970).

Eisen (1977) conducted a study on bidirectional restricted index selection for 10 generations in mice. His goal was to maximize genetic change in postweaning weight gain from 3 to 6 weeks of age, while keeping genetic response in feed intake at zero. The results indicated that the first four generations of selection appeared to verify the biological validity of the restricted selection index since genetic gain in feed intake was essentially zero. The overall regressions of feed intake on generation number or on index units were not significantly different from zero, but nevertheless subsequent to generation four feed intake tended to change in the same direction as post weaning gain in both index lines. He explained that the failure of the intended complete genetic restriction on change in feed intake may have been the result of a biological incompatibility between the goals of the restricted index and the genetic correlation between the traits in the index.

In summary, most studies have shown that, theoretically and experimentally, index selection is superior to other methods of selection, and that a restricted selection index is effective in permitting genetic progress in one trait without substantial genetic change in a correlated trait.

Most selection studies have involved two traits with positive genetic correlation, but no studies have been noted in which the genetic correlation between two traits under selection is negative.

METHODS AND PROCEDURES

Parameters used in simulated populations

Values of genetic parameters used in this simulation process are based on reviews of literatures concerned with other populations of chickens. It's been assumed that the genetic variability of body weight is only due to the additive genetic variance, i.e., dominance and epistasis play a trivial role.

Three levels of heritability for each trait and three levels of genetic correlation between body weight and egg production and between body weight and egg weight were selected. The selected heritability parameters for body weight were .1, .3, .4, for egg production .1, .2, .3, and for egg weight .1, .3, .5. The selected genetic correlations for body weight and egg production were -.2, -.4, -.6, and for body weight and egg weight .2, .3, .5.

The parameters used for mean body weight, 12 month egg production and egg weight were 1.6 kg, 104 eggs, 38 g, respectively and the standard deviations were .2 kg, 5 eggs, 4 g respectively, based on recent studies reported by Wartomo et al. (1976). For each trait the environmental variances corresponding to different heritability values were calculated easily, as the additive variance was the only genetic variance.

Simulated mating system

The size of breeding flock was kept constant through all generations: 12 males and 120 females were divided into three groups, I, II, and III, with 4 males and 40 females in each group. Within each group, males and females were assigned randomly and equally to four pens; therefore 1 male and 10 females were in each pen.

To simulate 4 rotations of mating in one year, within each group the males were shifted from pen to pen, so each male mated with 40 females to make a sire's family. From each mating, each sire had 4 offspring, 2 males and 2 females, so the sire's family consisted of 80 males and 80 females. To continue the next generation 1 male and 10 females were selected from each sire's family, so that 1.25% males and 12.5% females were saved for breeding. The next mating of the selected parents in each generation was done by shifting the males in group II to group I, selected males in group III to group II, and selected males in group I to group III, while the females remained in assigned groups.

With this mating system, inbreeding was assumed to be zero or trivially small.

Generation of base parental population

A repetitive pseudo-random number generator was used to simulate the probabilistic genetic mechanism. A library program, RANF, was available in the MSU Computer system (CDC 6500) for the generation of uniformly distributed random numbers in the range $0 \leq r_i \leq +1$.

For the uniform distribution, variance is equal to the square of the range divided by 12.

Therefore, $V(r_i) = (1)^2/12 = 1/12$

Twelve random uniform numbers (r_i) were added together to form a random sum in the range 0 to 12.

Then the variance of the sum equals 12 (1/12) = 1, so the standard deviation of the sum also is 1.

By subtracting six from any sum of twelve r_i, one obtains random numbers in the range of $-6 \leq e_j \leq +6$, and the e_j are normally distributed with a mean of zero and standard deviation of 1, providing standard normal random deviates (RND). It is well known that the deviates so produced do not conform well to the normal distribution in the extreme tails, but that is of little consequence in studies of this type.

The base populations were generated to provide genotypes of the male and female parents from which to generate the progeny from which selections were made. For convenience in notation, subscripts 1, 2 and 3 are used for body weight, egg production and egg weight respectively on symbols for genetic and phenotypic parameters. Subscripts on random normal deviates are consecutive as deviates are introduced into simulation methodology. Similar numbering applies to constants introduced.

Genetic deviation of body weight in an individual is

$$G_1 = G_1 (RND)_1$$

where σG_1 = additive standard deviation of body weight and

RND = a random normal deviate

The genetic deviation of egg production in the same individual must include a term $\sigma G_1 (RND)_1 \; C_1$, where C_1 is a constant value and $C_1 = \text{Cov } G_1 G_2 / \sigma^2 G_1$.

Therefore the genetic covariance between body weight and egg production is Cov $G_1 G_2$, which can be calculated for the required genetic correlation. But the genetic deviation of egg production cannot be generated simply as: $G_2 = \sigma G_1 (RND)_1 \; C_1$

From this expression $\sigma^2 G_2 = \sigma^2 G_1$, but in fact $\sigma^2 G_2 \neq \sigma^2 G_1$

To restore the variance of egg production to $\sigma^2 G_2$ another term is then added to the expression so that

$$G_2 = \sigma G_1 \; (RND)_1 \; C_1 + (RND)_2 \; C_2$$

The variance of this expression is

$\sigma^2 G_2 = \sigma^2 G_1 \; (C_1)^2 + (C_2)^2$, and the value of C_2 can be calculated.

The phenotypic value of body weight is:

$$P_1 = \mu_1 + G_1 + (RND)_3 \; \sigma E_1$$

where μ_1 = mean genetic value of body weight (1.6 Kg), and

σE_1 = environmental standard deviation of body weight

Phenotypic value of egg production is:

$$P_2 = \mu_2 + G_2 + (RND)_4 \; \sigma E_2$$

where μ_2 = mean genetic value of egg production (104 eggs), and

σE_2 = environmental standard deviation of egg production

With the same procedure the genetic deviation of egg weight can be obtained: $G_3 = \sigma G_1 \; (RND)_1 \; C_3 + (RND)_5 \; C_4$

The value of C_4 can be calculated from

$$\sigma^2 G_3 = \sigma^2 G_1 \ (C_3)^2 + (C_4)^2$$

The phenotypic value of egg weight is

$$P_3 = \mu_3 + G_3 + (\mathrm{RND})_6 \ \sigma E_3$$

where μ_3 = mean genetic value of egg weight (38 grams), and

σE_3 = environmental standard deviation of egg weight

In this study the standard deviations used for body weight, egg production and egg weight are .2 kg, 5 eggs, and 4 g, respectively.

Twelve males and 120 females were generated as the base parental population.

Generation of offspring

The genotypic value of male and female parents was used to generate the offspring.

The genetic deviation of body weight in an offspring is generated as

$$GO_1 = \tfrac{1}{2} \ (GM_1 + GF_1) + (\sqrt{.5}) \ (\sigma G_1) \ (\mathrm{RND})_7$$

where symbols M and F stand for male and female.

Genetic deviation of egg production of the same individual must include a term $(\sqrt{.5}) \ (\sigma G_1) \ (\mathrm{RND})_7 \ (C_5)$ where $C_5 = \mathrm{Cov} \ G_1 G_2 / \sigma^2 G_1$. The genetic covariance between body weight and egg production is $\mathrm{Cov} \ G_1 G_2$, and can be calculated for the required genetic correlation.

But the generation of genetic deviation for egg production can't be expressed simply as:

$$GO_2 = \tfrac{1}{2}(GM_2 + GF_2) + (\sqrt{.5})\ (\sigma G_1)\ (RND)_7\ (C_5)$$

The variance of this expression gives $\sigma G_2^2 = \sigma G_1^2$, but in fact $\sigma G_2^2 \neq \sigma G_1^2$, so another term is then added to restore σG_2^2, and the genetic deviation for egg production is generated as:

$$GO_2 = \tfrac{1}{2}(GM_2 + GF_2) + (\sqrt{.5})\ (\sigma G_1)\ (RND)_7\ (C_5) + (RND)_8\ (C_6)$$

Further $\sigma^2 G_2 = \tfrac{1}{2}\ \sigma^2 G_2 + \tfrac{1}{2}\ \sigma^2 G_1\ (C_5)^2 + (C_6)^2$, so the value of C_6 can be calculated.

The phenotypic values for body weight of male and female offspring and egg production of female offspring were generated as

$$PO_1 = \mu_1 + GO_1 + \sigma E_1\ (RND)_9 \quad \text{and}$$

$$PO_2 = \mu_2 + GO_2 + \sigma E_2\ (RND)_{10}$$

With the same procedure the genetic deviations of egg weight for male and female offspring were generated as

$$GO_3 = \tfrac{1}{2}(GM_3 + GF_3) + (\sqrt{.5})\ (\sigma G_1)\ (RND)_{11}\ (C_7) + (RND)_{12}\ (C_8)$$

Then the phenotypic deviation of egg weight for female offspring is:

$$PO_3 = \mu_3 + GO_3 + \sigma E\ (RND)_{13}$$

Based on the breeding scheme that was presented before, each male was mated to 40 females during the four rotations of mating in one year and each mating gave 2 male and 2 female offspring. The contribution of each male parent to the offspring population is then, 80 males and 80 females. Twelve males were used as parents, therefore 1920 offspring, 960 males and 960 females, were generated in each generation.

Methods of selection

In every generation the size of breeding population was kept constant at 12 males and 120 females. For this purpose 1.25% and 12.5% of males and females respectively were saved for breeding. Four methods of selection were used and compared:

1. Within each sire family individuals were ranked. Selection of males and females was based on phenotypic value of body weight. Then one top male and 10 top females were selected. Therefore, 12 males and 120 females were selected from 12 sire families to be used as parents for the next generation.
2. Selection on body weight and egg production simultaneously, where males were selected based on their own phenotypic value and females based on Index value. For each parameter combination, an index equation was developed:

$$I = b_1x_1 + b_2x_2$$

where x_1 = phenotypic value of body weight

x_2 = phenotypic value of egg production

b_1 = weighting factor for body weight

b_2 = weighting factor for egg production

The values for b_1 and b_2 were obtained by solving the normal equations $\underline{Pb} = \underline{Ga}$

where $\underline{P}$ = phenotypic variance-covariance matrix

$\underline{G}$ = genotypic variance-covariance matrix a = vector of economic values, where economic values for body weight and egg production were set equal to 25 and 1 respectively.

In setting up the index an assumption was made that environmental correlation equals zero. The top male based on own phenotype and the top ten females based on index values were selected from each sire family.

3. Selection on body weight where no change on egg production is permitted. Males were selected on own phenotype and the top male was selected from each sire family. Selection on females was based on restricted index value. The restricted index was adapted from Cunningham et al. (1970).

The index used for selection is: $I = b_1x_1 + b_2x_2$

The index was calculated for each of the parameter combinations.

x_1 = phenotypic value of body weight

x_2 = phenotypic value of egg production

b_1 = weighting factor for body weight

b_2 = weighting factor for egg production

The values for b_1 and b_2 were obtained by solving the equation:

$$\underline{P}^*\underline{b}^* = \underline{G}^*\underline{a}$$

where $\underline{P}^*$ = is a matrix obtained by adding a row and column to the $\underline{P}$ (phenotypic variance-covariance matrix), the (n + 1) column and row of the $\underline{P}^*$ consists of the column and row vector of genetic covariances between the restricted trait (egg production) and body weight and zero in the final position.

$\underline{G}^*$ = is a matrix obtained by adding a row of zeros to $\underline{G}$ (genotypic variance-covariance matrix)

$\underline{b}^*$ = is a column vector of b's and b_d (dummy variate)

$\underline{a}$ = is a vector of economic values where economic values for body weight and for egg production were 25 and 1 respectively

Using the index values, the best 10 females were then selected from each sire family for breeding.

4. Selection at two stages, the first stage is selection on body weight then at the second stage selection is on egg production. Selection for males was based on own phenotypic value and the top male was selected from each sire family. Selection for females was done in two stages. Females were selected based on their phenotypic value for body weight and from each sire family 20 out of 80 females (25%) were saved at the first stage, then at the second stage these females were selected based on their egg production and 10 out of 20 females (50%) were saved for breeding.

In all methods of selection egg weights were monitored as the correlated response due to the positive genetic correlation between body weight and egg weight.

The process of simulation

For all methods of selections, a FORTRAN program was made general in generating the base populations and offspring populations, and a variable "input" made it possible to simulate different parameter combinations.

The process of simulations can be summarized as follows:

1. The FORTRAN program was composed of the main program and several subroutines.
2. Each run of the program started by reading the additive genetic standard deviations, and environmental standard deviations selected for study.
3. Generating males and females in the base population: The library program RANF was called to generate a Random Normal Deviate. Then 12 males and 120 females were generated in the main program according to the formula as it was explained previously.
4. Generating offspring: This generation program took place in the subroutine. The parents were mated as described before, then the offspring populations were generated according to the formula described previously.
5. The next step was selection of offspring, leaving 12 males and 120 females to be parents for the next generation. Two subroutines were used, one for selected males and the other for selected females. From this point the program was a little different for each method of selection. Males were selected in the same manner based on own phenotypic value of body weight, but selection of females was dependent on the method of selection, explained in the previous part.
6. To obtain ten generations of offspring a "do loop" was made in the main program following generation of the base population.

7. Results were stored on magnetic tape to avoid excessive printing and for statistical analysis.
8. The Stat-package program available in the MSU Computer system was used for statistical analysis.

RESULTS AND DISCUSSION

Three levels of heritability of body weight, egg production and egg weight and three levels of genetic correlation between body weight and egg production and between body weight and egg weight make 81 possible parameter combinations. In this study, nine combinations were selected arbitrarily to create nine different populations (Table 1). Four different methods of selection were applied in each population. For each method of selection, each population was permitted to pass through 9 generations of selection and mating.

The printout of data was not obtained for each generation, but data were stored on magnetic tape for the statistical analyses. Results from the statistical analyses were printed out as means, variances-covariances, and correlations of phenotype and genotype of body weight, egg production and egg weight for the offspring population and for the selected parents in each generation.

Replicated runs were considered unnecessary, as checking on several replicated runs showed essentially the same results, because of the large number of birds per run.

Mean genetic change under mass selection (Method I)

The expected and observed genetic changes of body weight, egg production and egg weight are presented in Table 2. The expected genetic change on body weight was calculated by using the formula

Table 1.--Parameter Combinations Selected for Simulation Study.

Population	h^2_{BW}	h^2_{EP}	$h^2_{EW.}$	$r_{GBW.EP}$	$r_{GBW.EW}$
I	.4	.3	.5	-.6	.5
II				-.4	.3
III				-.2	.2
IV	.3	.2	.3	-.6	.5
V				-.4	.3
VI				-.2	.2
VII	.1	.1	.1	-.6	.5
VIII				-.4	.3
IX				-.2	.2

presented by Falconer (1960): $\Delta G_1 = i\ h_1^2\ \sigma P_1$, where i is selection intensity, h_1^2 is heritability for body weight and σP_1 is phenotypic standard deviation of body weight.

Genetic change on egg production:

$\Delta G_2 = i\ h_1\ h_2\ rG_{12}\ \sigma P_2$, where h_2^2 is the heritability for egg production, rG_{12} is the genetic correlation between body weight and egg production and σP_2 is the standard deviation of egg production.

Genetic change on egg weight:

$\Delta G_3 = i\ h_1\ h_3\ rG_{13}\ \sigma P_3$, where h_3^2 is the heritability for egg weight, rG_{13} is the genetic correlation between body weight and egg weight and σP_3 is the standard deviation of egg weight. From this point subscripts 1, 2 and 3 will be used to indicate body weight, egg production and egg weight respectively.

The selection intensity was obtained from the table presented by Becker (1975). Selection intensity for males and females were

Table 2.--Expected and Observed Mean Genetic Change on Body Weight, Egg Production and Egg Weight Per Generation under Mass Selection.

Population	ΔG_1 (Kg)		ΔG_2 (unit egg)		ΔG_3 (g)	
	Expected	Observed	Expected	Observed	Expected	Observed
I	.1694	.1805	-2.2011	-1.6357	1.8944	1.9577
II	.1694	.1812	-1.4673	-1.8937	1.1366	1.1339
III	.1694	.1883	-.7337	-.9517	.7577	.6632
IV	.1271	.1368	-1.5564	-1.8277	1.2708	1.4041
V	.1271	.1337	-1.0376	-1.0524	.7625	.7755
VI	.1271	.1462	-.5188	-.6566	.5083	.6245
VII	.0424	.0462	-.6354	-.7168	.4236	.3741
VIII	.0424	.0433	-.4236	-.4948	.2542	.3196
IX	.0424	.0452	-.2118	-.1700	.1694	.3567

2.589 and 1.647 respectively, where 1.25% males and 12.5% females were selected for breeding.

The prediction of mean genetic change on body weight as a direct response to selection was more precise than the prediction for egg production and egg weight, both as correlated responses. This probably happened because the correlated responses were affected more by random chance than the direct response.

The prediction of mean genetic change for egg weight as correlated response due to positive genetic correlation was more accurate compared to the prediction of egg production as correlated response due to negative genetic correlation.

Despite a larger random error that seemed to affect data of population IV, when the genetic correlation between body weight and egg weight was low (.2) the accuracy of prediction was somewhat less, a result also indicated by Clayton et al. (1957).

The mean genetic change in egg production was predicted accurately when the heritabilities were low and even more so when genetic correlation was also low. Under high heritabilities the prediction was poor, especially in combination with high negative genetic correlation.

As expected, the mean genetic change in body weight increased as the heritability increased from .1, .3 to .4. Within the same levels of heritabilities of body weight, egg production and egg weight, the observed correlated responses on egg production and egg weight were increased as the magnitude of genetic correlation increased. Under the same level of genetic correlation of body weight and egg production and body weight and egg weight, the correlated responses on egg production and egg weight were increased as the heritability increased.

The effect of the magnitude of the genetic correlation on the correlated responses depends on the level of heritability of the two traits. The effect is greater in combination with higher heritability. Further, combination between the highest heritability and the highest genetic correlation gave the highest mean genetic change on correlated traits as was expected. However, the observed value of mean genetic change on egg production in population I was somewhat deviate, probably due to random chance.

Mean genetic change when selection index was used in females (Method II)

The expected and observed mean genetic change on body weight and egg production are presented in Table 3.

In the offspring population the expected mean genetic change on body weight and egg production was calculated as the average genetic change contributed by male and female parents.

$$\Delta G_0 = \frac{\Delta G_M + \Delta G_F}{2}$$

Where subscripts 0, M and F stand for offspring, male and female respectively, and ΔG is the expected genetic change.

Males were selected based on their own phenotypic value of body weight, where 1.25% of males were saved for parents. The expected genetic change of body weight in males was calculated as

$$\Delta G_{M1} = i\, h_1^2\, \sigma P_1$$

and the mean genetic change of egg production in males was calculated as the correlated response, so

$$\Delta G_{M2} = i\ h_1\ h_2\ rG_{12}\ \sigma P_2$$

Selection on female parents was based on the non restricted index value, which was calculated based on the method presented by Hazel (1943). The expected genetic change on body weight and egg production was then calculated according to VanVleck (1976).

$$\Delta G_{F1} = \frac{\mathrm{Cov}(G_1 ;I)\ i}{\sigma I}$$

$$\Delta G_{F2} = \frac{\mathrm{Cov}(G_2 ,I)\ i}{\sigma I}$$

where, $\mathrm{Cov}(G_1 ,I) = b_1 \sigma^2 G_1 + b_2 \mathrm{Cov}G_{12}$

$$\mathrm{Cov}(G_2 ,I) = b_2 {}^2 G_2 + b_1 \mathrm{Cov}G_{12}$$

and b_1 and b_2 are the index weighting factors. The variance of index is calculated as: $\sigma_I^2 = b_1^2\ \sigma^2 p_1 + b_2^2\ \sigma^2 p_2 + 2\ b_1\ b_2\ \mathrm{Cov}\ P_{12}$

Table 3 shows close agreement between the expected and observed values of genetic change on body weight and egg production, due to the fact that the genetic and phenotypic variances and covariances indicated no trends over times. However, random chance seems to affect more the genetic change in egg production as a trait correlated to body weight, and the prediction for body weight was more accurate.

Within the same heritabilities, the highest mean genetic change on body weight was when the negative genetic correlation was the lowest. But genetic change of egg production was highest but negative when the negative genetic correlation was the highest. And when the genetic correlation was low (-.2), a positive genetic change on egg production was observed. Apparently when a small negative correlation was the case, the selection index was effective in preventing a negative genetic change on one trait but also tended to decrease a positive change on the other trait.

Table 3.--Expected and Observed of Mean Genetic Change on Body Weight and Egg Production per Generation when Selection Index Was Used in Females.

Population	ΔG_1 (Kg)		ΔG_2 (unit egg)	
	Expected	Observed	Expected	Observed
I	.1469	.1721	-1.7083	-1.1053
II	.1362	.1503	-.3875	-.7506
III	.1516	.1766	.0683	.0627
IV	.1141	.1223	-1.1571	-.8502
V	.1140	.1311	-.5710	-.4621
VI	.1160	.1379	-.0408	.1830
VII	.0306	.0312	-.2658	-.2337
VIII	.0330	.0393	-.0790	-.0734
IX	.0353	.0373	.1066	.1979

Mean genetic change when restricted selection index was used in females (Method III)

Restricted selection index was constructed to impose no change in egg production while selecting for body weight.

The expected and observed mean genetic change in body weight and egg production are presented in Table 4. To obtain the expected value of genetic change the same formula as was applied when selection index was used. The b value was the index weighting factor in the restricted selection index equation. The observed and expected values showed a close agreement. Only females were selected based on the restricted index values. Selection on males were based on their own phenotypic value of body weight which caused a correlated response on egg production.

The theoretical expectation showed that the restricted selection index was effective in holding the mean genetic change on egg production in females close to zero (Table 5). An exact zero value was not obtained, although a zero covariance between genetic egg production and index was imposed, probably because of rounding errors. Mean genetic change of egg production contributed by females was trivial but males were selected in a different way. Males contributed half of the genetic value of egg production and this caused the change. The genetic contribution from males was large as the selection intensity was high especially when the heritabilities of two traits and the genetic correlation were high.

Data from the phenotypic mean in Tables (13, 14, 15) showed that the restricted selection index was quite effective when the

Table 4.--Expected and Observed of Mean Genetic Change on Body Weight and Egg Production per Generation When Restricted Selection Index was Used in Females.

Population	ΔG_1 (Kg)		ΔG_2 (unit egg)	
	Expected	Observed	Expected	Observed
I	.1315	.1538	-1.3452	-.8821
II	.1652	.1811	-1.2176	-1.0017
III	.1661	.1858	-.4479	-.6032
IV	.1051	.1292	-.9501	-1.0060
V	.1165	.1298	-.6339	-.4979
VI	.1243	.1506	-.3213	-.5210
VII	.0352	.0374	-.3869	-.0459
VIII	.0383	.0388	-.2579	-.4164
IX	.0415	.0395	-.1278	-.1586

Table 5.--Mean Genetic Change on Egg Production in Females under Restricted Selection Index.

Population	ΔG_2[1]
I	.0000
II	.0000
III	.0010
IV	.0023
V	.0006
VI	.0006
VII	.0028
VIII	.0021
IX	.0034

---

[1] This expected value of ΔG_2 was calculated by the formula

$$\Delta G_2 = \frac{\mathrm{Cov}(G_2, I)\, i}{\sigma_I}$$

heritabilities of both traits were .1, especially when the genetic correlation was -.2.

The values in Table 4 showed that within the same heritabilities, the genetic change on body weight was the highest when combined with the lowest negative genetic correlation. But the highest negative genetic change in egg production was observed with the highest genetic correlation.

Mean genetic change when two stage selection was used in females (Method IV)

The method of two stage selection or independent culling level was used to select females for parents.

The expected and observed values of mean genetic change are presented in Table 6. The observed values were in close agreement with the expected values. This table shows that the genetic change in body weight can be predicted more precisely than the genetic change on egg production. The latter was affected more by random chance as explained before.

The expected genetic changes in females were calculated following the approach of Harvey and Bearden (1962).

$$\Delta G_{F1} = (\alpha_1 h_1^2 + \alpha_2 \; rG_{12} \; h_1 \; h_2) \sigma P_1$$

$$\Delta G_{F2} = (\alpha_2 h_2^2 + \alpha_1 \; rG_{12} \; h_1 \; h_2) \; \sigma P_2 \quad \text{and}$$

$$\alpha_1 = \frac{i_1 - rP_{12} i_2}{1 - r^2 P_{12}} \qquad \alpha_2 = \frac{i_2 - rP_{12} i_1}{1 - r^2 P_{12}}$$

Table 6.--Expected and Observed Genetic Change of Body Weight and Egg Production per Generation when Two Stage Selection was Used in Females.

Population	ΔG_1 (Kg)		ΔG_2 (unit egg)	
	Expected	Observed	Expected	Observed
I	.1555	.1565	-1.7735	-1.0439
II	.1461	.1474	-.6383	-.6015
III	.1507	.1674	-.0099	-.0384
IV	.0955	.1148	-.9529	-.7984
V	.1156	.1204	-.5010	-.6750
VI	.1128	.1241	-.0456	-.2791
VII	.0338	.0405	-.3669	-.4019
VIII	.0355	.0423	-.1729	-.2008
IX	.0371	.0389	-.0126	-.0878

Where, i_1 and i_2 are the selection intensities for body weight and egg production, which are 1.27 and .80 respectively (Becker, 1975). And rP_{12} is the phenotypic correlation between the two traits, calculated according to the formula (Falconer, 1960)

$$rP_{12} = h_1 \ h_2 \ rG_{12} + e_1 \ e_2 \ rE_{12}$$

Assumption was made that the environmental correlation (rE_{12}) was equal to zero. So $rP_{12} = h_1 \ h_2 \ rG_{12}$

The genetic change of males was calculated with the same procedure as already explained.

The values in Table 6 showed that within the same levels of heritabilities the mean genetic changes of body weight were more when the genetic correlation was lowest. The negative change on egg production was small when the correlation was low (-.2).

Harvey and Bearden (1962) also presented the formula to calculate the expected correlated response for the unselected trait. The correlated response on egg weight can be calculated as follows:

$$\Delta G_3 = \alpha_1 \ rG \ \ h_1 \ h_3 + \alpha_3 \ rG_{23} \ h_2 \ h_3$$

However as in this study, the value of rG_{23}, correlation of egg production and egg weight, was not known in the population so the expected values of the correlated response can't be obtained.

Change of the phenotypic mean under different method of selections

The changes of the phenotypic mean in different populations under different method of selections are presented in Table 7 to Table 15. From this point method I, II, III, or IV designates how females were selected: mass selection (method I), selection index (method II), restricted selection index (method III), independent culling level (method IV).

Mass selection in all populations was very effective in increasing the mean of body weight, obviously because selection was on the additive genetic variation. The percent of improvement was nearly double when the heritability of body weight was .4, and was about 75% and 25% when heritability was .3 and .1 respectively. The correlated responses in egg production and egg weight were as expected. Egg production was declining due to negative genetic correlation between body weight and egg production. And the positive genetic correlation between body weight and egg weight caused a positive correlated response on egg weight.

The percent decline of egg production at generation ten was 16.9%, 16.9%, 8.4%, 15.5%, 8.6%, 4.5%, 6.1%, 4.3% and 1.3% in populations 1 to 9 respectively. The corresponding percent increase of egg weight was 45.5%, 26.4%, 15.3%, 33.8%, 21.7%, 15.0%, 8.4%, 7.6% and 7.4%.

In some populations the percent decline in egg production was noticeable when the heritability and the genetic correlation were high, but the response to selection on body weight was also high. For example in population I the average decline of egg production per generation was about 1.7%. At generation 10, the mean body weight was 3.26 kg and it seems that a good marketable size of livebird is around 3 kg. If this method is going to be applied then, should selection be continued after 10 generations on the same direction if egg production continues to decline while body weight continues to increase? Or, should selection be changed by keeping body weight constant while improving egg production? To answer this question, one needs to identify which of these nine simulated populations the native chicken population is most likely to resemble.

Selection using selection index showed that mean body weight was increased and egg production declined. Though egg weight was not subjected to selection, mean egg weight was also increased as a correlated response due to positive genetic correlation with body weight.

The purpose of using selection index is to select body weight and egg production simultaneously to get a maximum total economic

Table 7.--Means of Body Weight, Egg Production and Egg Weight in Population I Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6477	1.6722	1.6081	1.6447	103.6821	103.0085	104.1105	103.9426	38.7295	38.6926	38.6657	38.4579
2	1.8212	1.8395	1.7486	1.8000	101.8830	102.1605	103.9539	102.4498	40.9467	39.8931	40.9052	39.5259
3	2.0527	2.0128	1.9036	1.9817	100.2515	100.4178	101.8246	101.7901	43.6186	42.1898	42.7126	41.4668
4	2.2461	2.1626	2.0243	2.1416	98.4367	100.2051	100.6352	100.2101	45.6980	43.5533	44.1389	43.8009
5	2.3726	2.3410	2.1540	2.3238	96.7228	99.6251	100.1087	98.4739	47.5230	45.8292	46.0088	44.9207
6	2.5801	2.5306	2.3011	2.4940	94.8678	97.8612	98.6788	97.6189	50.1573	47.5705	47.6683	47.7092
7	2.7421	2.7365	2.4856	2.6001	93.5889	96.0445	98.6269	97.2437	52.4060	49.2129	49.3186	48.2302
8	2.9134	2.8850	2.6485	2.7363	92.2974	95.6217	97.6031	96.3286	53.1993	52.4025	51.6443	49.9385
9	3.1254	3.0762	2.8359	2.8984	90.6823	93.5891	96.5833	94.9092	55.0689	53.8173	54.1559	51.0095
10	3.2591	3.2253	3.0013	3.0547	89.0023	93.1304	96.6093	93.4303	56.3611	55.4475	55.8364	53.2321

Method I:	mass selection
Method II:	selection index
Method III:	restricted selection index
Method IV:	independent culling levels

Table 8.--Means Body Weight, Egg Production and Egg Weight in Population II Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6669	1.6193	1.6186	1.6253	103.4406	104.1208	104.7853	102.8339	38.2199	38.7316	36.8657	38.8181
2	1.8686	1.7575	1.7527	1.7702	101.3229	103.2913	103.8796	102.1168	39.3996	39.8057	36.9319	38.6665
3	2.0629	1.8814	1.9283	1.9175	99.0426	102.2529	102.3794	101.2033	40.6193	41.2473	38.2908	40.1997
4	2.2706	2.0271	2.0852	2.0359	97.7022	102.6116	101.5826	101.6429	40.8726	42.3235	40.0104	42.6096
5	2.4387	2.1485	2.2614	2.1767	96.0365	101.8333	100.2709	100.7344	41.8524	42.4827	41.3409	43.7975
6	2.6224	2.3360	2.5077	2.3056	94.0972	101.1632	99.1750	100.6779	43.2731	44.8526	42.1897	44.5342
7	2.8363	2.5388	2.6973	2.4671	92.3604	100.6753	99.1020	99.8821	44.2039	45.9884	43.6681	46.6884
8	2.9534	2.6861	2.8999	2.6212	90.5091	99.5020	97.8003	98.9213	45.3860	47.9523	45.4194	47.6514
9	3.1326	2.8817	3.0899	2.7559	88.2355	97.8870	96.3281	98.5616	47.2706	48.3810	46.0896	49.1360
10	3.2987	3.0409	3.2494	2.9539	86.0132	97.4919	95.7611	97.7782	48.3264	49.0499	47.7190	50.5390

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 9.--Means Body Weight, Egg Production and Egg Weight in Population III Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6461	1.6167	1.6647	1.6322	102.7230	104.8349	104.1806	104.7807	37.8292	37.7177	38.8273	37.5613
2	1.8283	1.7896	1.8759	1.8186	101.2672	104.2903	103.9644	104.4156	38.5570	38.2402	40.6650	38.0706
3	2.0154	1.9554	2.0753	1.9450	101.1970	104.9131	103.2101	104.4605	38.8820	39.1751	42.2678	39.2163
4	2.2264	2.1511	2.2268	2.1463	99.2961	104.3946	102.2423	104.6706	40.1352	40.2397	43.0589	39.4265
5	2.4156	2.3319	2.4008	2.2913	97.7371	104.1319	101.2099	105.1135	40.2028	41.5831	43.8116	40.0068
6	2.5578	2.5258	2.6023	2.4364	97.0522	104.5919	99.6264	105.1558	40.6276	43.1740	44.9397	40.5600
7	2.7419	2.7045	2.7907	2.6052	96.7046	103.7915	98.8684	105.5684	41.4103	43.1612	45.6181	41.3747
8	2.9241	2.8611	3.0305	2.7417	95.9455	104.9262	98.9448	105.2385	42.7289	43.1307	47.0890	41.5584
9	3.1204	3.0502	3.2011	2.9623	95.7059	104.6286	99.3163	104.6299	42.8022	44.4558	47.7897	43.0713
10	3.3428	3.2092	3.3450	3.1386	94.1062	105.5502	98.5911	104.5963	43.6138	44.6875	47.9394	43.0763

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 10.--Means Body Weight, Egg Production and Egg Weight in Population IV Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6298	1.6661	1.6149	1.6213	103.9919	102.6167	104.2302	103.8501	37.5270	39.3058	38.6869	37.7001
2	1.8096	1.8122	1.7648	1.6998	101.7578	101.5467	103.6734	103.9822	39.2344	40.7349	39.9021	39.2846
3	1.9325	1.9341	1.9085	1.8269	100.6507	100.5757	102.7624	103.1835	41.1106	42.2878	41.1157	40.1650
4	2.0712	2.0467	2.0206	1.9488	99.6063	99.7827	101.8218	102.7509	42.9663	43.7720	42.3872	40.7230
5	2.1684	2.1717	2.1311	2.1023	97.8846	99.0824	101.4975	102.1416	43.2615	44.7517	43.4140	42.3216
6	2.3004	2.2897	2.2768	2.2353	96.5114	98.5149	100.1428	100.5227	44.7335	45.3172	44.7718	44.0256
7	2.4526	2.3959	2.3825	2.3683	94.2099	97.8111	99.8633	98.9238	45.6066	46.5900	46.7869	45.0478
8	2.5655	2.5188	2.5146	2.4694	92.6239	97.8341	98.0821	98.4465	46.9770	47.9182	48.3307	45.5207
9	2.7223	2.6534	2.6765	2.5686	90.4313	96.1620	96.6793	97.6832	48.1677	48.9066	50.1260	46.5861
10	2.8640	2.7559	2.7777	2.6569	87.8983	95.6730	95.4589	96.9098	50.2182	50.0130	51.0789	47.4370

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 11.--Means Body Weight, Egg Production and Egg Weight in Population V Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6601	1.6093	1.5957	1.6655	104.2268	103.2785	104.1137	104.2928	38.7276	38.5990	37.6041	39.6837
2	1.7761	1.7523	1.7554	1.8030	102.7944	103.1242	103.3991	102.9059	39.4925	39.4372	37.4247	41.0732
3	1.9571	1.8652	1.8932	1.9397	101.3215	102.3611	102.5760	101.5813	41.0539	40.1197	37.5117	42.3787
4	2.0896	1.9823	2.0110	2.0397	101.1820	102.2328	102.7237	101.4941	42.2594	39.6795	38.9246	43.1474
5	2.2376	2.1237	2.1359	2.1588	99.8848	100.7385	102.1288	101.1526	43.7186	41.1233	40.6939	43.9234
6	2.3621	2.2542	2.2682	2.2847	99.7754	99.7111	101.5918	100.6673	44.2192	41.6098	41.2752	45.0528
7	2.4823	2.3876	2.3882	2.4026	99.7712	99.0220	101.5765	99.8531	44.6168	42.4944	41.2651	45.1432
8	2.5895	2.5222	2.5255	2.5191	97.5626	98.9198	100.4011	100.4262	46.3168	43.5901	41.9456	45.5951
9	2.7435	2.6717	2.6400	2.6164	96.2923	98.7116	100.6346	99.9545	46.9282	44.4757	42.0932	45.9759
10	2.8623	2.7939	2.7647	2.7450	95.2261	99.1455	99.6961	98.9248	47.1323	44.4522	42.6525	46.5243

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 12.--Means Body Weight, Egg Production and Egg Weight in Population VI Under Different Methods of Selection

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6582	1.6377	1.6124	1.6522	103.7125	104.4114	104.1251	103.4433	38.5758	38.1492	38.1784	37.8061
2	1.8188	1.7634	1.7301	1.8000	103.3350	105.1172	103.3550	103.7163	39.7299	38.4494	38.3225	38.3051
3	1.9822	1.9249	1.8584	1.9175	103.6967	105.3326	104.0396	103.8707	40.3005	38.2481	39.6999	38.6702
4	2.1134	2.0752	2.0389	2.0538	102.9732	105.7403	102.6466	103.3579	40.0289	37.7247	40.1569	39.0733
5	2.2638	2.2082	2.2419	2.1545	101.8003	106.5686	101.8010	102.9646	40.6783	38.3051	41.1956	39.1372
6	2.4180	2.3649	2.3747	2.2944	102.1478	106.1164	101.5087	102.8265	40.9174	38.6536	41.9071	39.2335
7	2.5570	2.5094	2.5379	2.4186	101.2743	106.4734	101.1918	102.1158	42.2159	38.9385	42.0474	38.9799
8	2.6906	2.6627	2.7153	2.5513	101.0117	106.4616	100.4963	101.7909	42.6598	39.1043	43.2795	39.4132
9	2.8486	2.7868	2.8378	2.6435	100.0218	106.2945	99.9917	101.4680	43.3638	39.3222	42.6159	40.0350
10	2.9748	2.8823	2.9652	2.7679	99.0100	105.9030	99.6029	101.2302	44.3683	39.8859	42.6901	41.7528

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 13.--Means Body Weight, Egg Production and Egg Weight in Population VII Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.5911	1.6293	1.6073	1.5937	104.4935	103.3657	103.5674	103.5286	38.1346	38.7222	37.5561	38.0841
2	1.6319	1.6502	1.6323	1.6262	104.0230	103.5252	103.4719	103.2677	38.2459	39.3004	38.3687	38.5025
3	1.6972	1.6865	1.6442	1.6536	103.5435	103.2221	103.2113	103.0962	38.8593	39.5049	37.6759	39.0290
4	1.7306	1.7365	1.6670	1.6943	102.5900	102.3701	103.1695	103.3159	39.3280	39.7372	37.8138	39.5909
5	1.7600	1.7575	1.6969	1.7423	102.3724	102.9165	102.8187	102.7148	39.0522	39.7864	38.3078	40.0523
6	1.8135	1.7856	1.7708	1.7874	101.5901	102.4246	102.1088	102.3687	39.4886	40.0132	38.7282	40.7382
7	1.8460	1.8222	1.8104	1.8166	100.6177	101.8667	101.6946	101.8206	39.9661	40.4199	38.7300	41.1682
8	1.8971	1.8463	1.8514	1.8550	99.9632	102.4158	100.4725	100.9979	40.0823	40.5945	39.7253	41.6348
9	1.9503	1.8789	1.8836	1.8941	99.2103	101.9582	100.1059	100.6127	40.4252	40.5864	40.8094	41.9798
10	2.0089	1.9105	1.9465	1.9642	98.1066	101.5312	100.0943	100.2552	41.3197	41.0613	41.0497	42.5553

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 14.--Means Body Weight, Egg Production and Egg Weight in Population VIII Under Different Methods of Selection.

Method / Generation	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6246	1.6193	1.6170	1.6044	103.9935	103.9885	103.7267	103.7548	38.1289	38.3131	37.9200	38.2122
2	1.6506	1.6221	1.6221	1.6193	103.1524	104.0212	103.3308	103.3075	38.2967	38.4519	38.3861	38.0807
3	1.6975	1.6793	1.6772	1.6795	103.0916	103.7207	102.8772	103.2081	38.6480	38.3285	38.0387	38.6889
4	1.7463	1.7106	1.7252	1.7175	102.9350	104.1797	102.5638	102.9285	39.0407	38.8028	38.4304	39.0803
5	1.7848	1.7238	1.7606	1.7464	102.3109	104.3346	102.5179	103.0769	39.3804	39.1911	38.2323	39.6269
6	1.8257	1.7536	1.8000	1.7955	102.0463	104.4117	101.9379	103.1560	39.1391	38.9530	38.8049	40.0120
7	1.8783	1.8162	1.8251	1.8298	101.2871	104.7585	101.9319	102.9863	39.5533	39.7301	39.0617	40.0426
8	1.9105	1.8731	1.8726	1.8779	100.9563	104.2114	101.0740	103.0997	40.0148	39.8736	39.6228	40.3807
9	1.9755	1.9285	1.9188	1.9218	99.9019	103.8770	100.8982	102.1896	40.4631	40.3646	39.7444	40.5243
10	2.0047	1.9749	1.9623	1.9622	99.5112	103.8541	100.9888	101.8490	41.0323	40.3497	40.4446	41.1784

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

Table 15.--Means Body Weight, Egg Production and Egg Weight in Population IX Under Different Methods of Selection.

Generation \ Method	Body Weight (Kg)				Egg Production (unit egg)				Egg Weight (g)			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
1	1.6189	1.6381	1.6121	1.6098	104.1820	104.0641	104.5440	103.7660	38.3722	37.8518	37.8637	38.0897
2	1.6856	1.6638	1.6439	1.6258	103.3858	104.2477	104.3713	103.9469	38.8280	38.1028	38.1134	38.2267
3	1.7421	1.7193	1.7072	1.6686	103.2854	104.6214	103.9051	103.6285	39.2655	38.4110	38.2096	38.3626
4	1.7814	1.7755	1.7286	1.7213	103.4437	103.8958	103.8100	103.8575	39.5812	38.5792	38.1847	38.3460
5	1.8019	1.8062	1.7565	1.7586	103.5492	104.2205	104.0162	103.8592	39.9117	38.7950	38.1270	38.5766
6	1.8430	1.8448	1.7966	1.7898	103.8330	104.0593	103.4429	103.8486	40.1115	39.1204	38.4527	38.8393
7	1.9018	1.8768	1.8556	1.8454	103.1719	104.6124	102.6632	103.2479	40.1557	39.0570	38.6330	38.6873
8	1.9422	1.8994	1.8669	1.8829	103.3095	104.8620	102.5432	103.3849	40.6902	39.2309	38.5336	39.1155
9	1.9652	1.9463	1.9157	1.9075	102.8822	105.6470	102.5313	103.6880	41.1386	39.8424	38.3543	39.3086
10	2.0240	1.9745	1.9620	1.9582	102.8632	105.3556	102.6226	103.6365	41.2115	39.4539	38.8251	39.4557

Method I: mass selection
Method II: selection index
Method III: restricted selection index
Method IV: independent culling levels

response, and it was theorized that this method is never inferior compared to other methods (Lush, 1942; Young, 1961; Finney, 1962). Discussion on total economic response will be presented in later part of this section.

At generation ten, the means body weight was improved by 92.9%, 87.8%, 98.5%, 65.4%, 73.6%, 76.0%, 17.3%, 22.0%, 20.5% in populations 1 to 10 respectively, and the corresponding decreased on egg production in the same population was 9.6%, 6.4%, 0.0%, 6.8%, 4.0%, 0.0%, 1.8%, 0.0%, 0.0%. The mean egg weight was increased by 43.3%, 26.6%, 18.5%, 27.2%, 15.2%, 4.6%, 6.0%, 5.3%, 4.2% in populations 1 to 9 respectively.

In all populations the response on body weight was greater under mass selection than selection index. The decline of mean egg production and the increase of mean egg weight also were greater for mass selection. These results were really obvious , as mass selection was concentrated only on body weight but in selection index method egg production was accounted for, which in turn caused less decrease in egg production.

Further the results also indicated that the percent response was dependent on the level of the heritabilities, the higher the heritability the higher the response. The percent decrease and the percent increase in egg production and egg weight, respectively, showed a consistent pattern that within the same levels of heritability the magnitude of percent response was ranked directly with the magnitude of genetic correlation. However this pattern was not clearly observed on percent response on body weight. In populations where the genetic correlation of body weight and egg production was low (-.2) the percent decrease of egg production was equal to zero, although the observed phenotypic means showed slight increase. It seems that the effect of low negative genetic correlation in this study is trivial and even selection using selection index eliminates the effect to some extent.

The results from selection using restricted selection index showed that mean body weight and egg weight were increased although egg weight was not selected directly. Previously it was shown that when the genetic change on egg production was calculated using the theoretical expectation, this method should be successful in preventing genetic change in egg production. However, the observed phenotype showed that mean egg production was declining slightly. The reason for this decline can be explained. Although restricted selection index was successful in imposing no change on the mean genetic egg production in female parents the index was not used in selecting male parents. Thus it may be concluded that the genetic change was contributed by male parents.

The percent decline of mean egg production at generation ten was 7.2%, 8.6%, 5.4%, 8.4%, 4.2%, 4.3%, 3.4%, 2.6%, 1.8% in populations 1 to 9 respectively. The question whether the restricted index selection in this study has been successful can't be answered by experimental evidence.

In restricted selection index studies that have been reported both males and females were selected the same way, as the traits were expressed in both sexes. To improve this study males should also be selected using restricted selection index, where the necessary information may come from family or progeny. All the information used to construct the selection index for females come from individual data but as the information in males did not, another restricted selection index is needed.

The mean of body weight at generation ten was increased by 86.6%, 100.8%, 100.9%, 72.0%, 73.3%, 83.9%, 21.1%, 21.4%, 21.7% in populations 1 to 9 respectively. The percent increase of mean egg weight at generation ten was 44.9%, 29.4%, 23.5%, 32.0%, 13.4%, 11.8%, 9.3%, 6.7%, 2.5% in populations 1 to 9 respectively. Populations with the higher heritability combinations showed more percent increase on either body weight or egg weight. The magnitude of genetic correlation between body and egg weight played a role in determining the percent increase of egg weight. In populations with the same heritability combinations, the higher the genetic correlation the higher the percent increase.

For selection using independent culling levels, the results showed that mean body weight and egg weight were increased, accompanied by a decrease in mean egg production. Mean body weight at generation ten was increased by 85.7%, 81.7%, 92.3%, 63.9%, 64.8%, 67.5%, 23.2%, 22.3%, 21.6% in populations 1 to 9 respectively. The mean egg production was decreased by 10.1%, 4.9%, 0.2%, 6.7%, 5.1%, 2.1%, 3.2%, 1.8%, 0.1% in populations 1 to 9 respectively. The percent increase of mean egg weight was 38.4%, 30.2%, 14.7%, 25.8%, 17.2%, 10.4%, 11.7%, 7.8%, 3.6% in populations 1 to 9 respectively.

The method seems good in reducing the decline of egg production to some extent, as egg production was also subjected to selection. The percent of decline was somewhat less than the percent decline under mass selection. When genetic correlation between body weight and egg production was low the decline was trivial, especially in populations where low genetic correlation was combined with low heritabilities. Obviously the percent increase in mean body weight was a little less compared to what was obtained by mass selection. Mean egg weight was increased due to correlated response.

Figures 1.1 to 1.9 show the changes of mean body weight and egg production in populations 1 to 9 respectively. Figures 2.1 to 2.9 show the changes of egg weight and body weight.

Relative percent efficiencies of different selection methods for total economic response

The relative percent efficiency was calculated followed the approach presented by Young (1961). For each method the total economic response was calculated as: $H_i = a_1 \Delta G_1 + a_2 \Delta G_2$ Where subscript i can be I, II, III, or IV indicated which method of selections is considered. Here a_1 and a_2 are the economic value of body weight and egg production respectively and ΔG_1 and ΔG_2 are genetic change of body weight and egg production.

Table 16 shows the expected and observed total response per generation in economic units, where 1 unit equal to \$.10. There was close agreement between the expected and observed values in most cases. Both the expected and observed value showed that combination of heritabilities and magnitude of genetic correlation affected the total economic response. This was true for all method of selection.

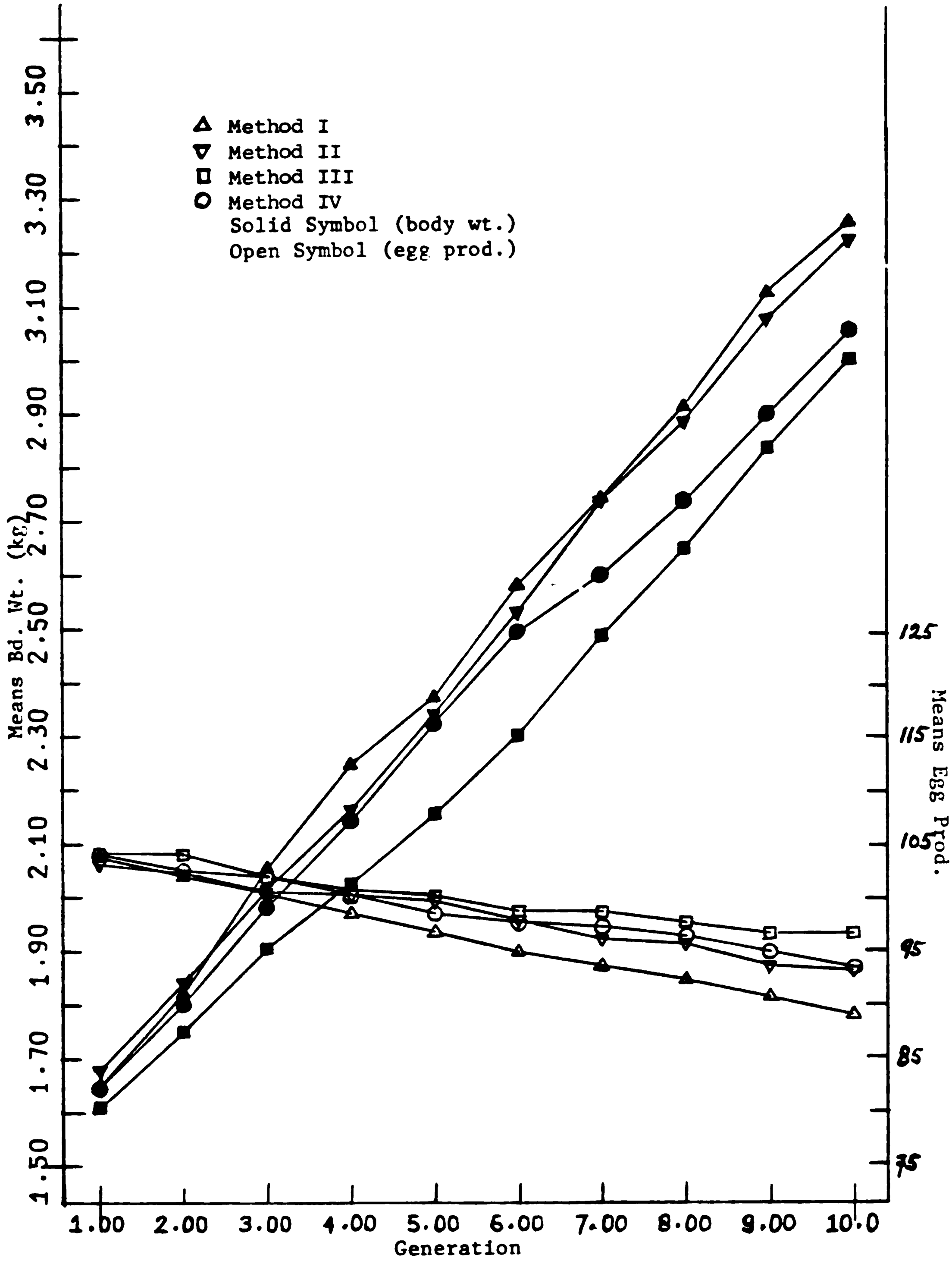

Figure 1.1. Means of Body Weight and Egg Production in Population I Under Different Method of Selections. (h_1^2 = .4, h_2^2 = .3, h_3^2 = .5, rG_{12} = -.6, rG_{13} = .5)

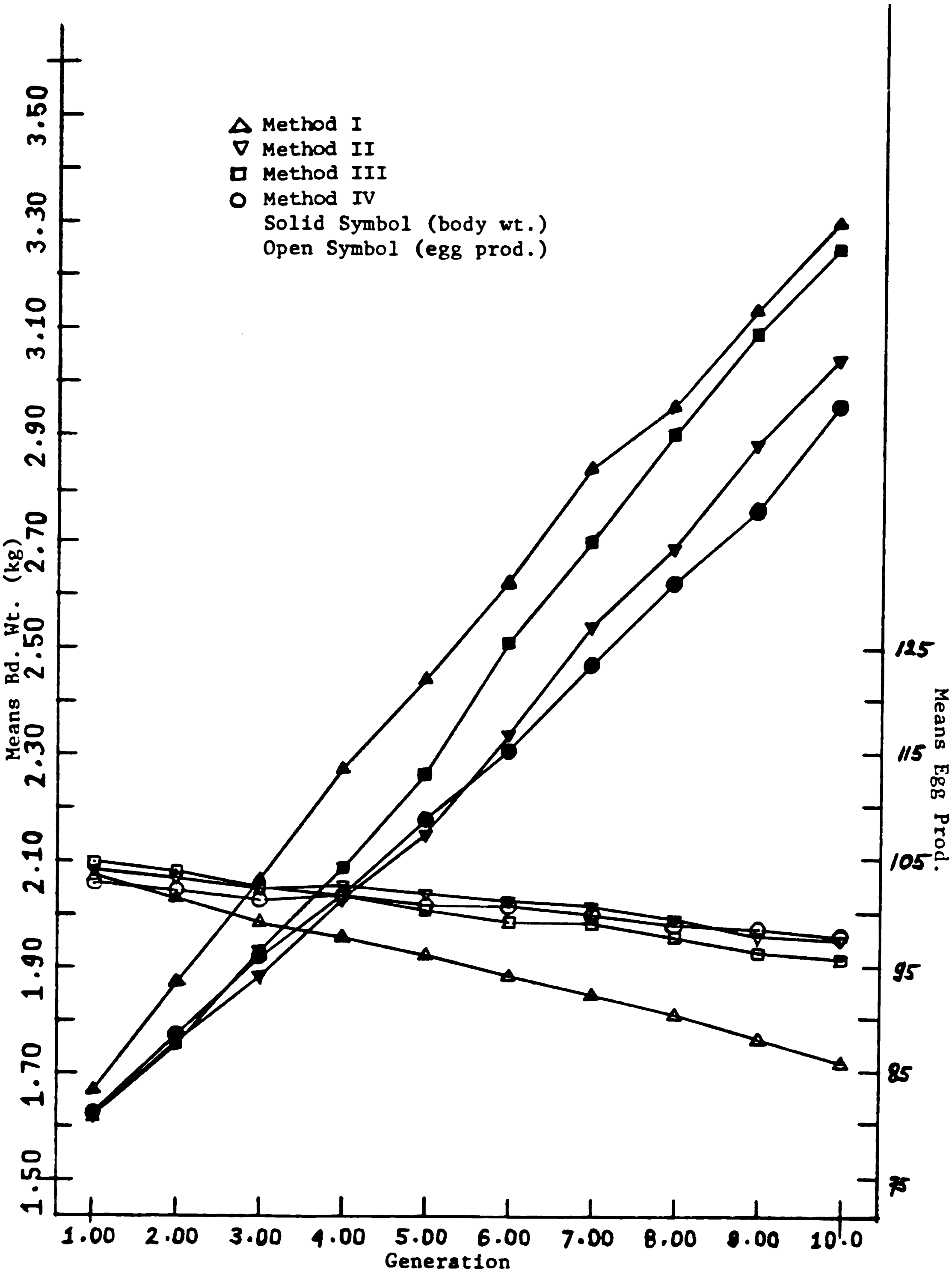

Figure 1.2. Means of Body Weight and Egg Production in Population II Under Different Method of Selections. (h_1^2 = .4, h_2^2 = .3, h_3^2 - .5, rG_{12} = -.4, rG_{13} = .3)

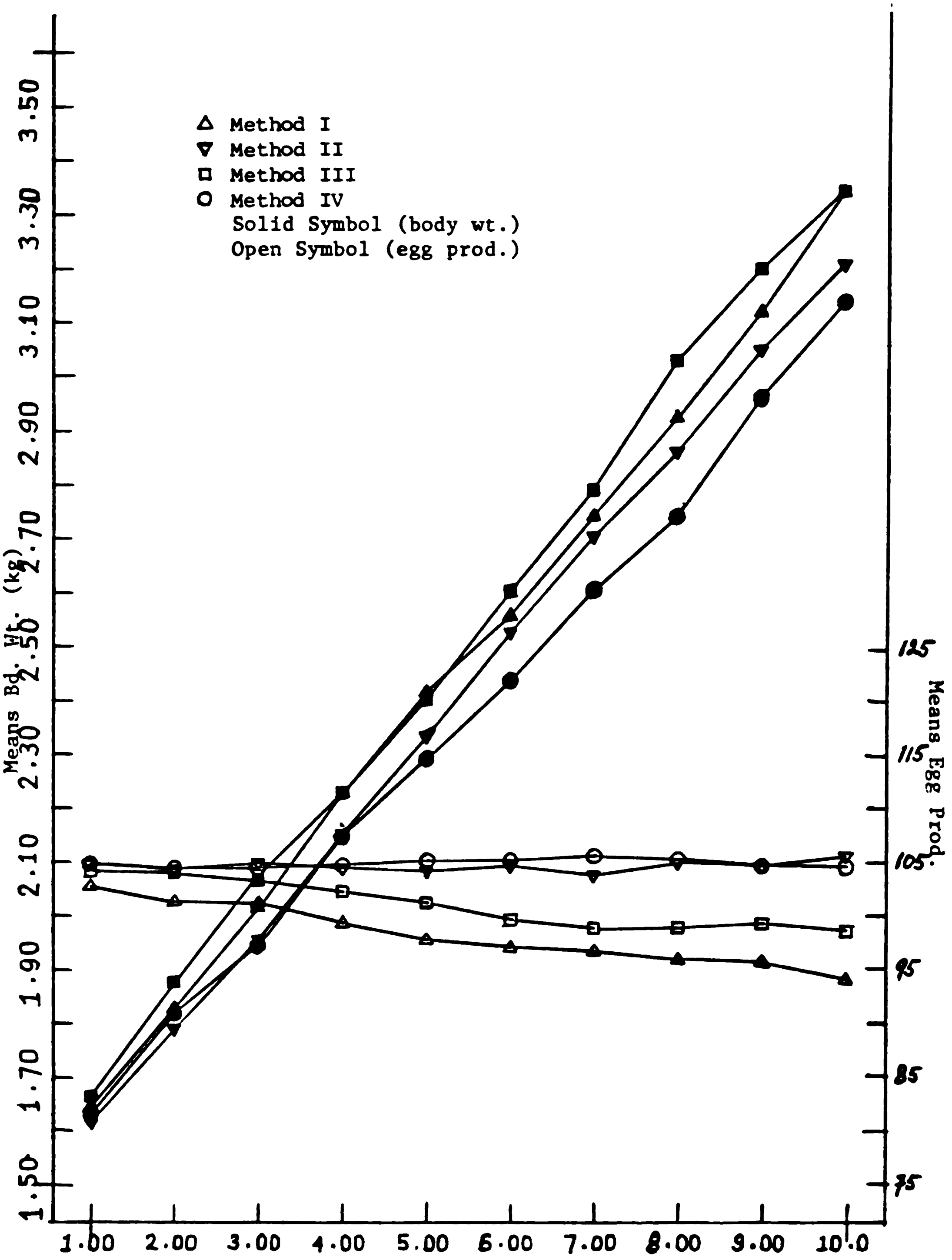

Figure 1.3. Means of Body Weight and Egg Production in Population III Under Different Method of Selections. (h_1^2 = .4, h_2^2 = .3, h_3^2 = .5, rG_{12} = -.2, rG_{13} = .1)

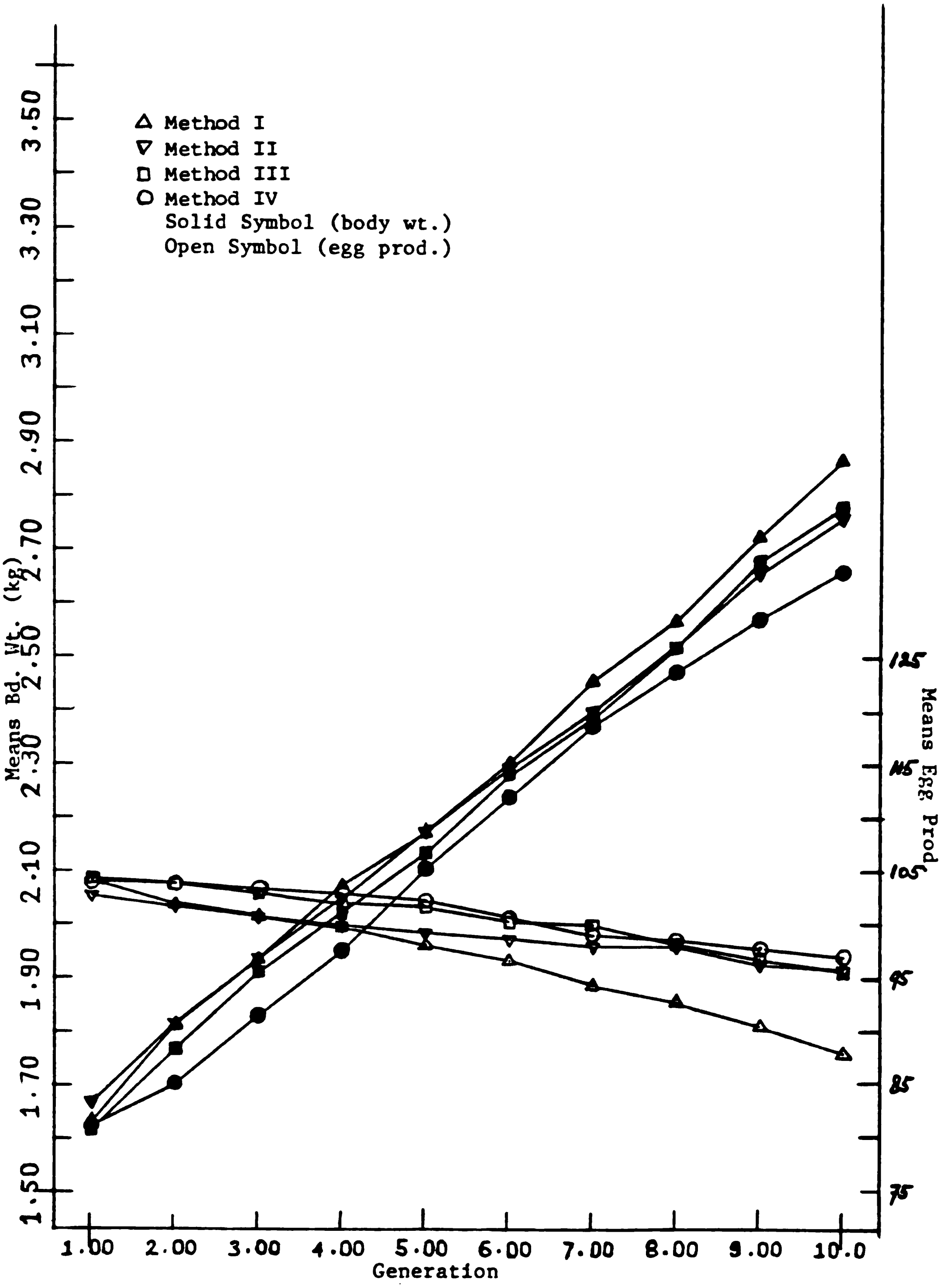

Figure 1.4. Means body Weight and Egg Production in Population IV Under Different Method of Selections. (h_1^2 = .3, h_2^2 = .2, h_3^2 = .3, rG_{12} = -.6, rG_{13} = .5)

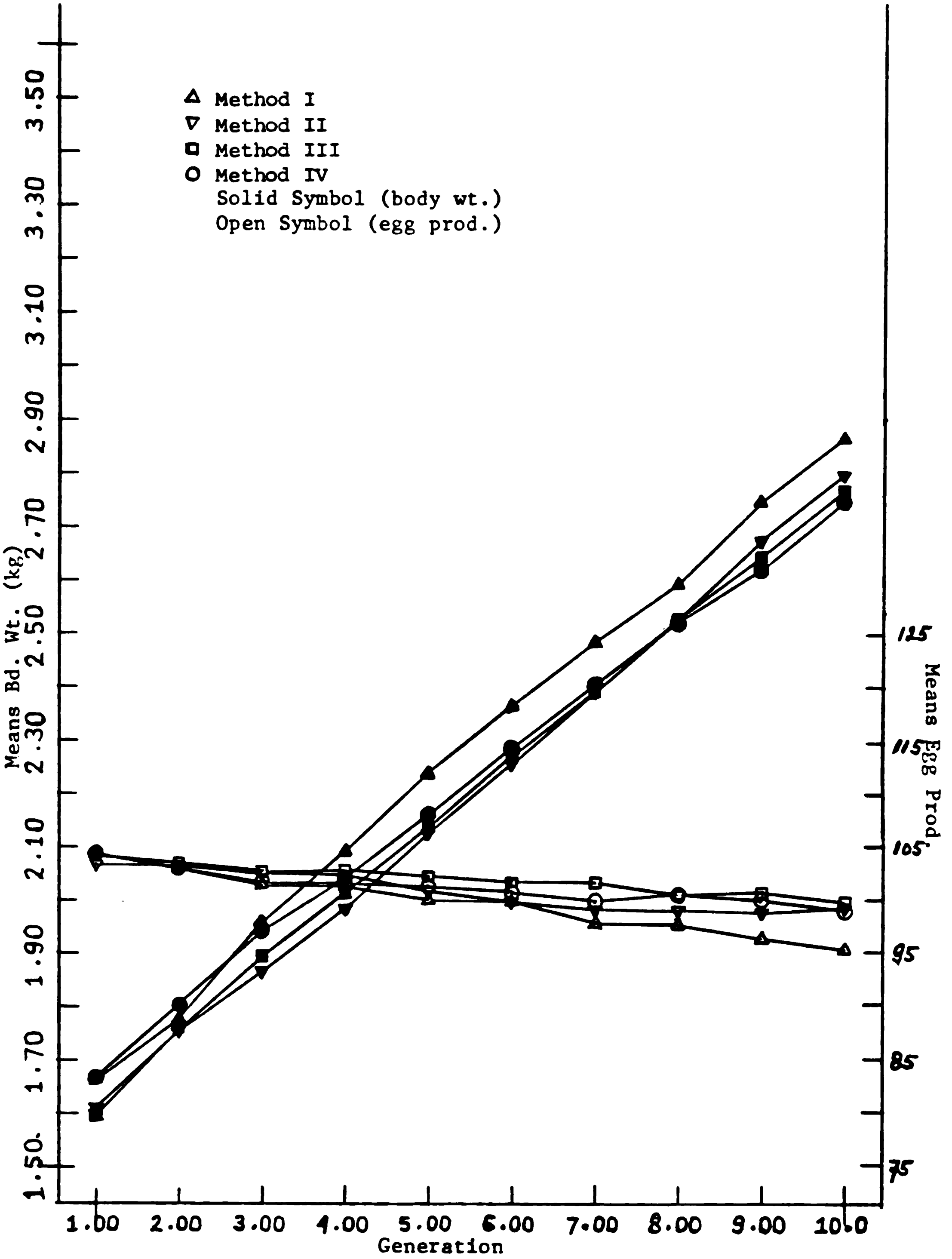

Figure 1.5. Means Body Weight and Egg Production in Population $_2$V Under Different Method of Selections. ($h_1^2 = .3$, $h_2^2 = .2$, $h_3^2 = .3$, $rG_{12} = -.4$, $rG_{13} = .3$)

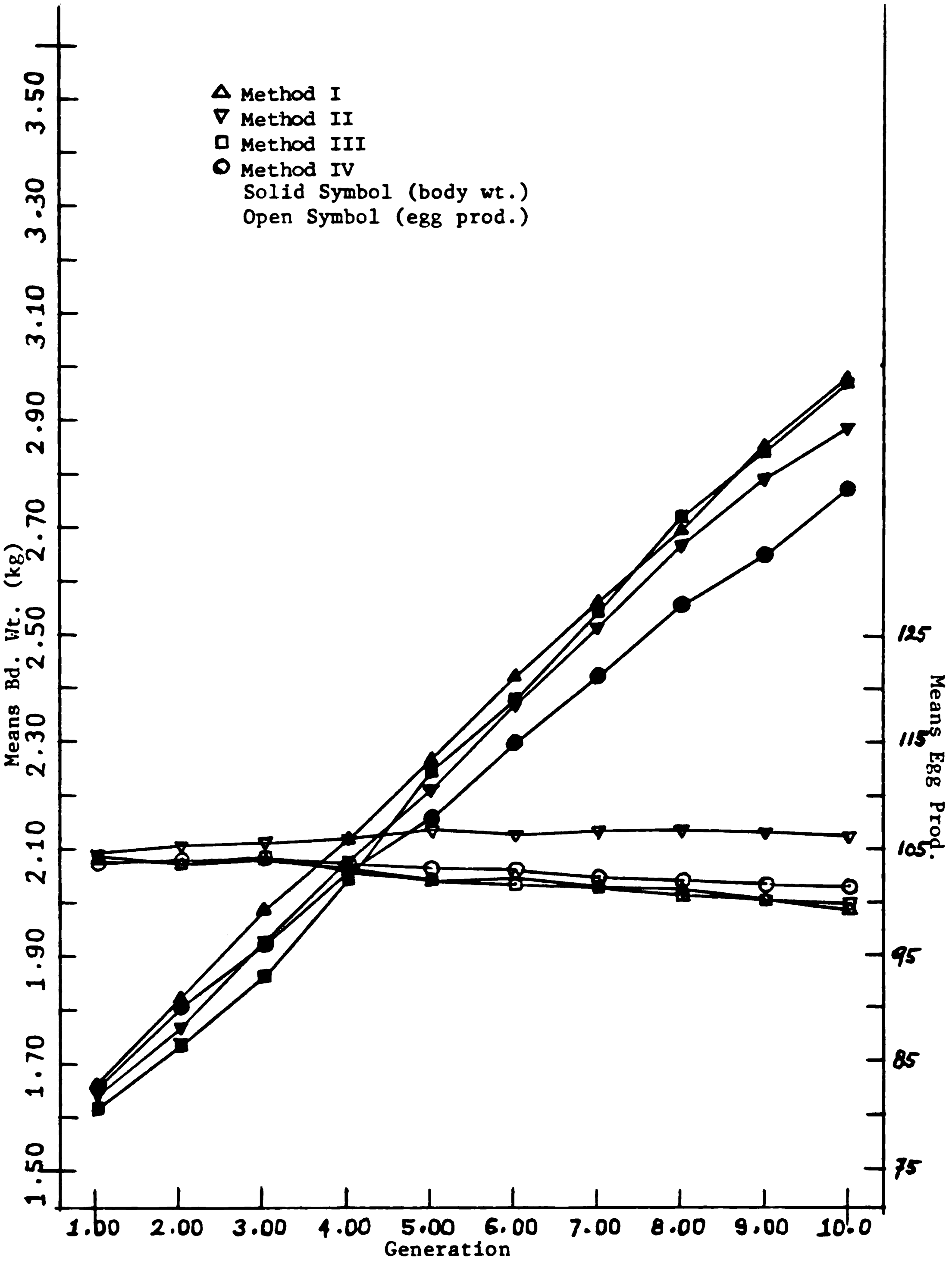

Figure 1.6. Means Body Weight and Egg Production in Population$_2$VI Under Different Method of Selections. (h_1^2 = .3, h_2^2 = .2, h_3^2 = .3, rG_{12} = -.2, rG_{13} = .2)

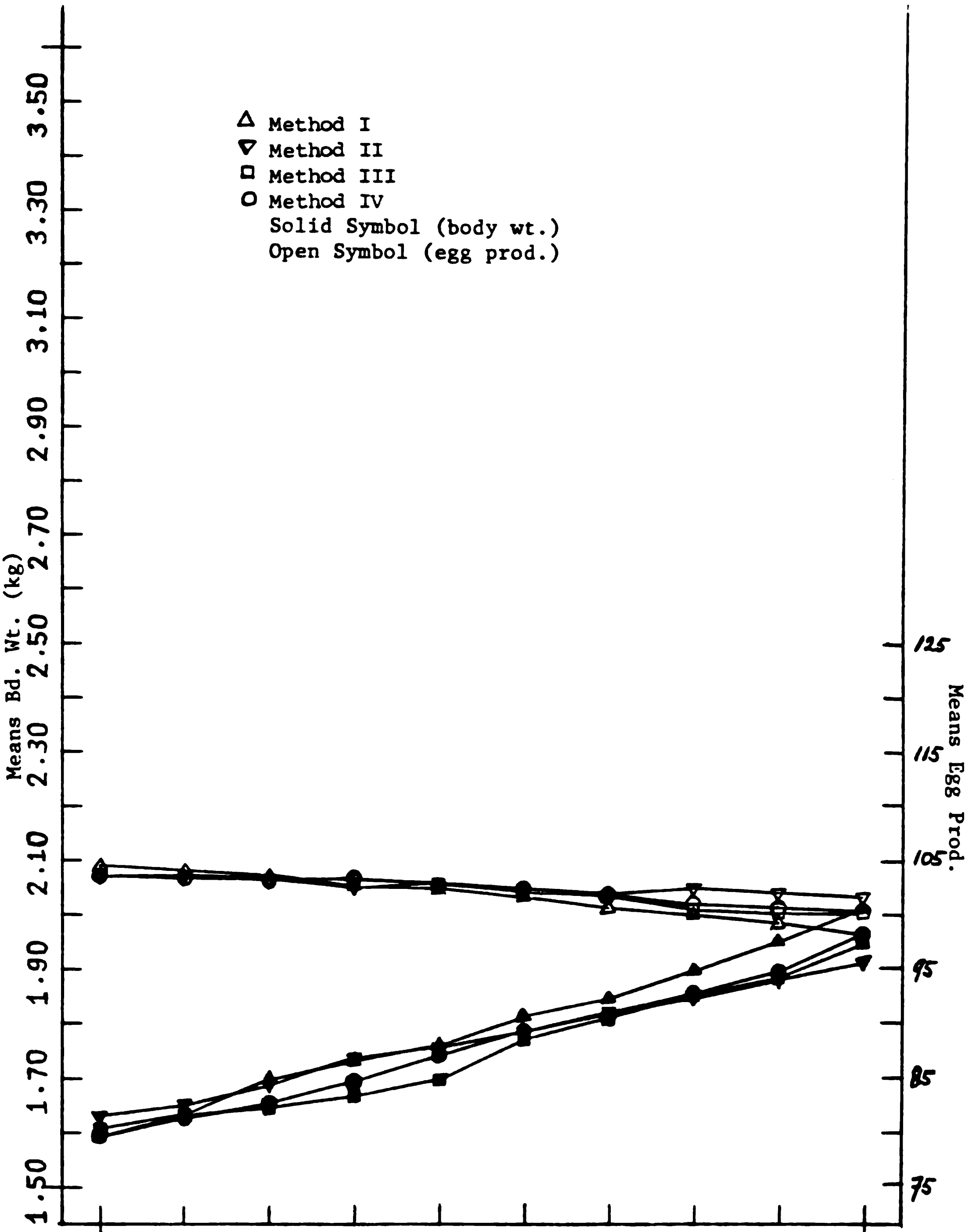

Figure 1.7. Means Body Weight and Egg Production in Population VII Under Different Method of Selections. ($h_1^2 = .1$, $h_2^2 = .1$, $h_3^2 = .1$, $rG_{12} = -.6$, $rG_{13} = .5$)

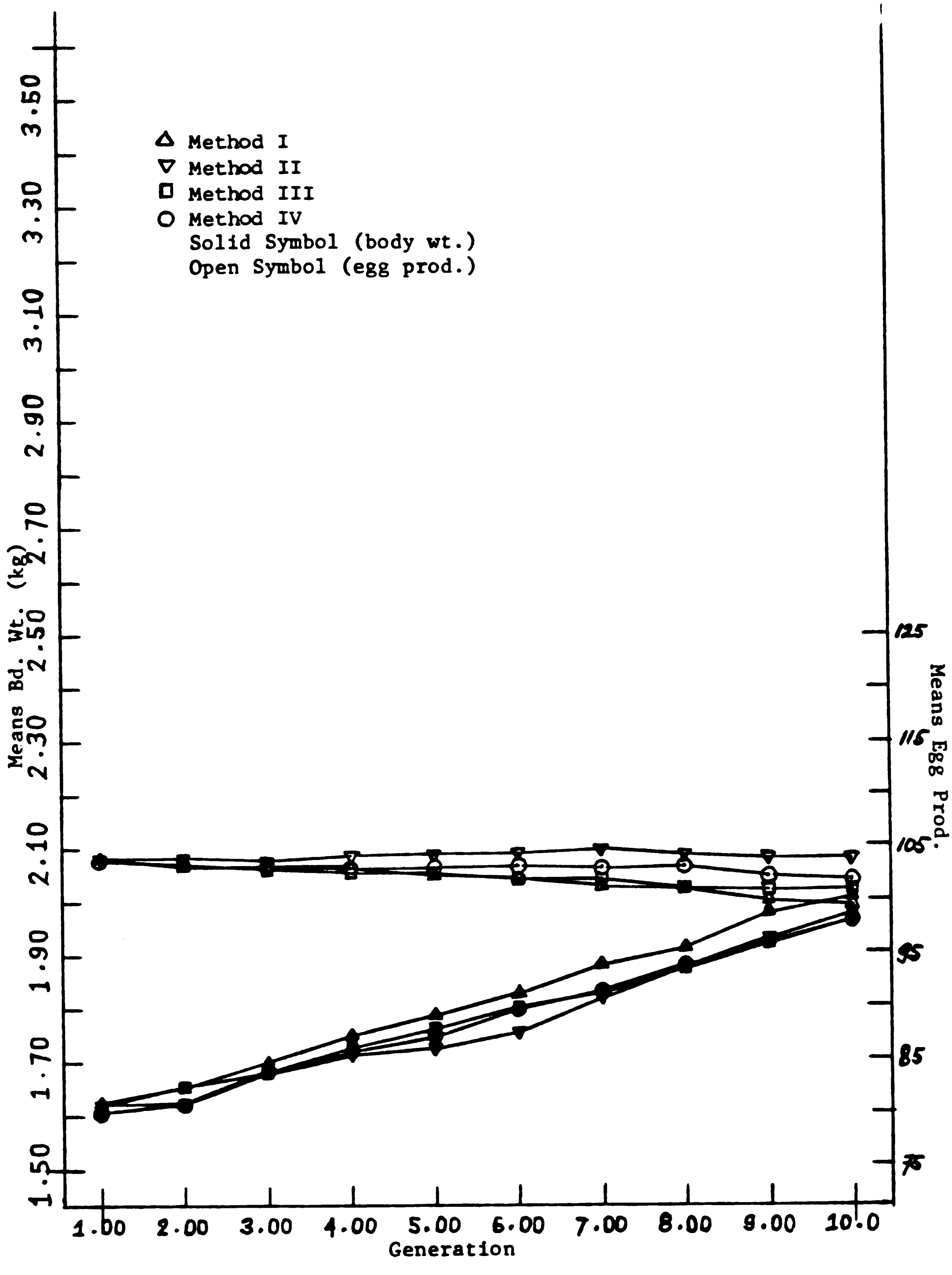

Figure 1.8. Means of Body Weight and Egg Production in Population VIII Under Different Method of Selections. (h_1^2 = .1, h_2^2 = .1, h_3^2 = .1, rG_{12} = -.4, rG_{13} = .3)

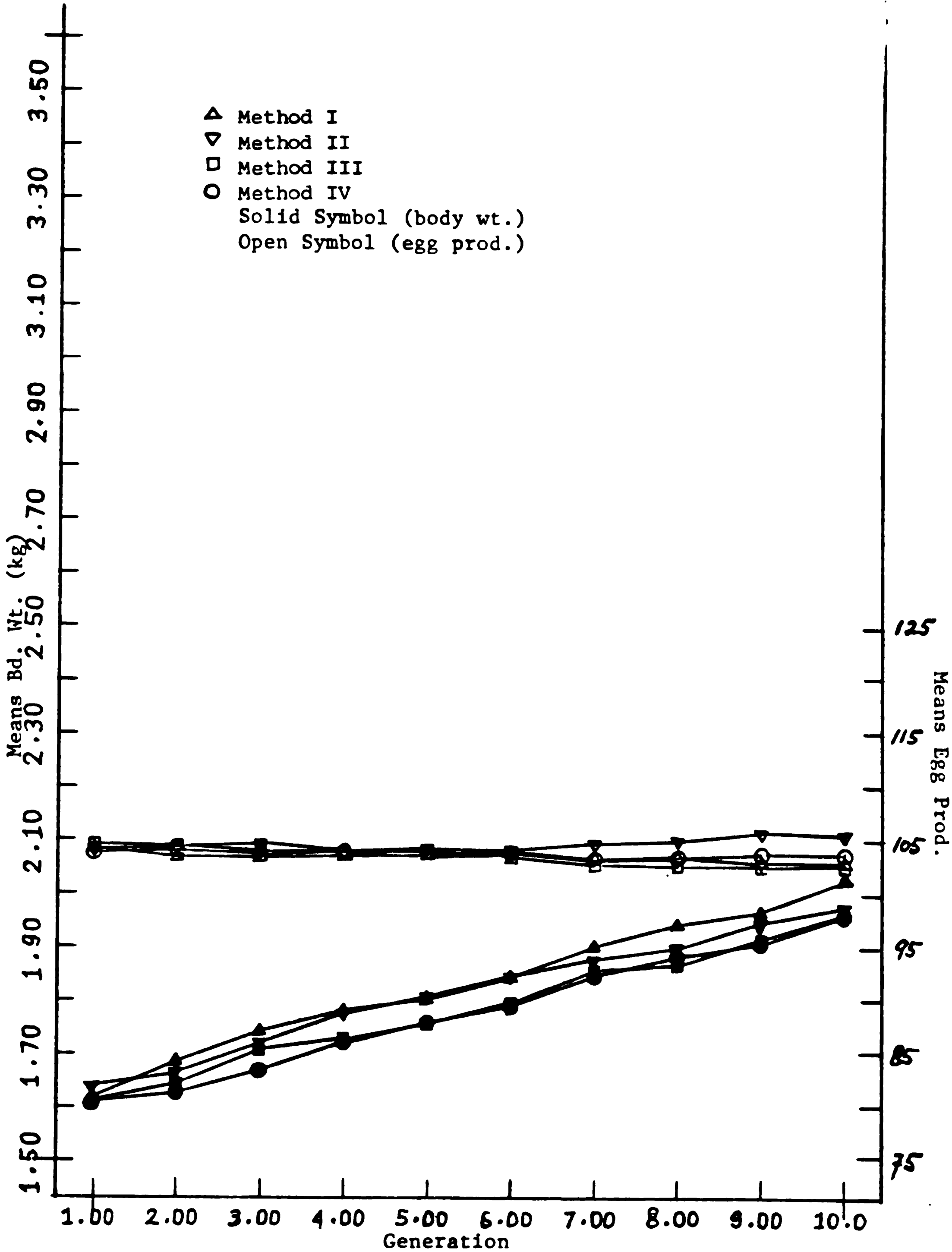

Figure 1.9. Means of Body Weight and Egg Production in Population IX Under Different Method of Selections. ($h_1^2 = .1$, $h_2^2 = .1$, $h_3^2 = .1$, $rG_{12} = -.2$, $rG_{13} = .2$)

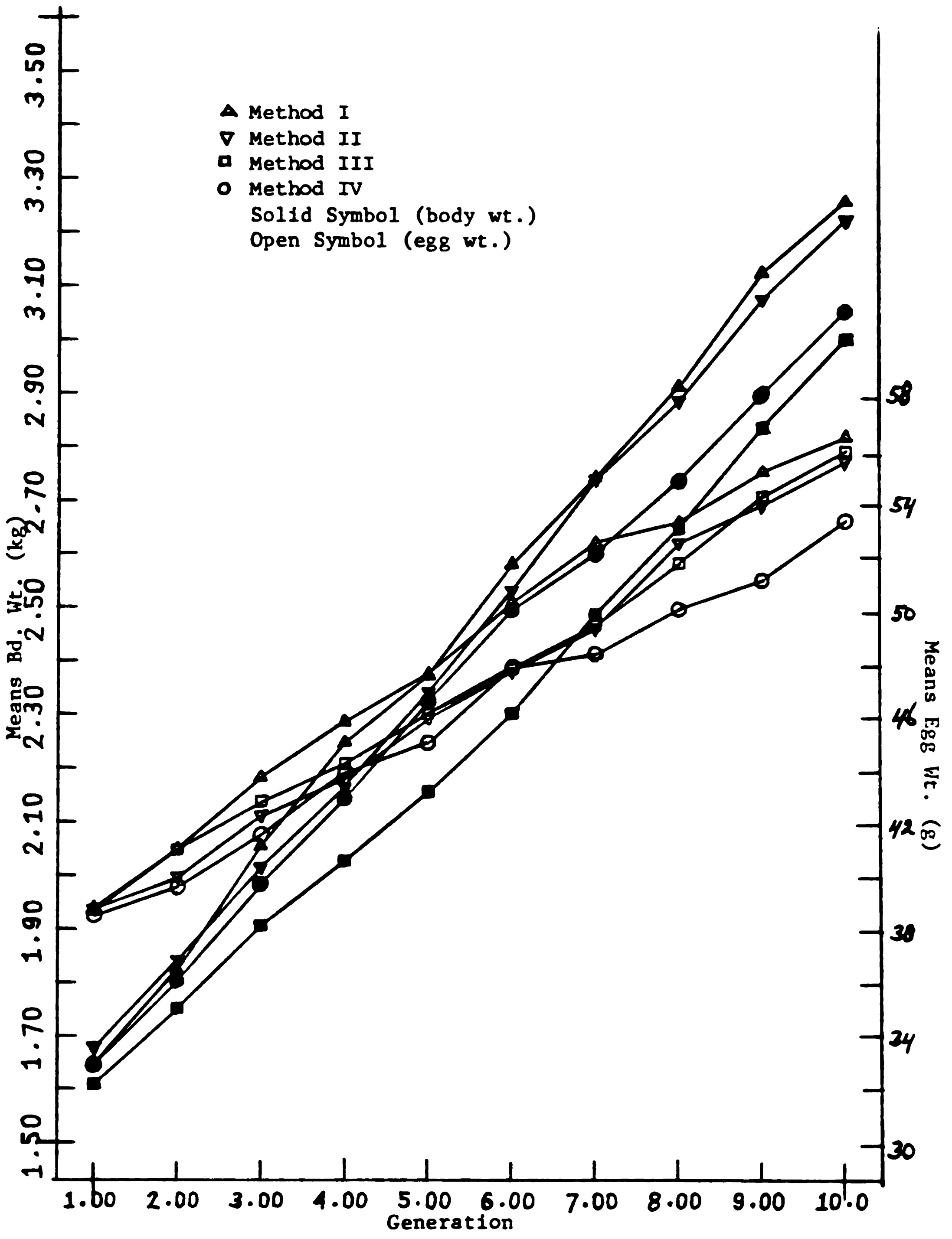

Figure 2.1. Means of Body Weight and Egg Weight in Population I Under Different Method of Selections. ($h_1^2 = .4$, $h_2^2 = .3$, $h_3^2 = .5$, $rG_{12} = -.6$, $rG_{13} = .5$)

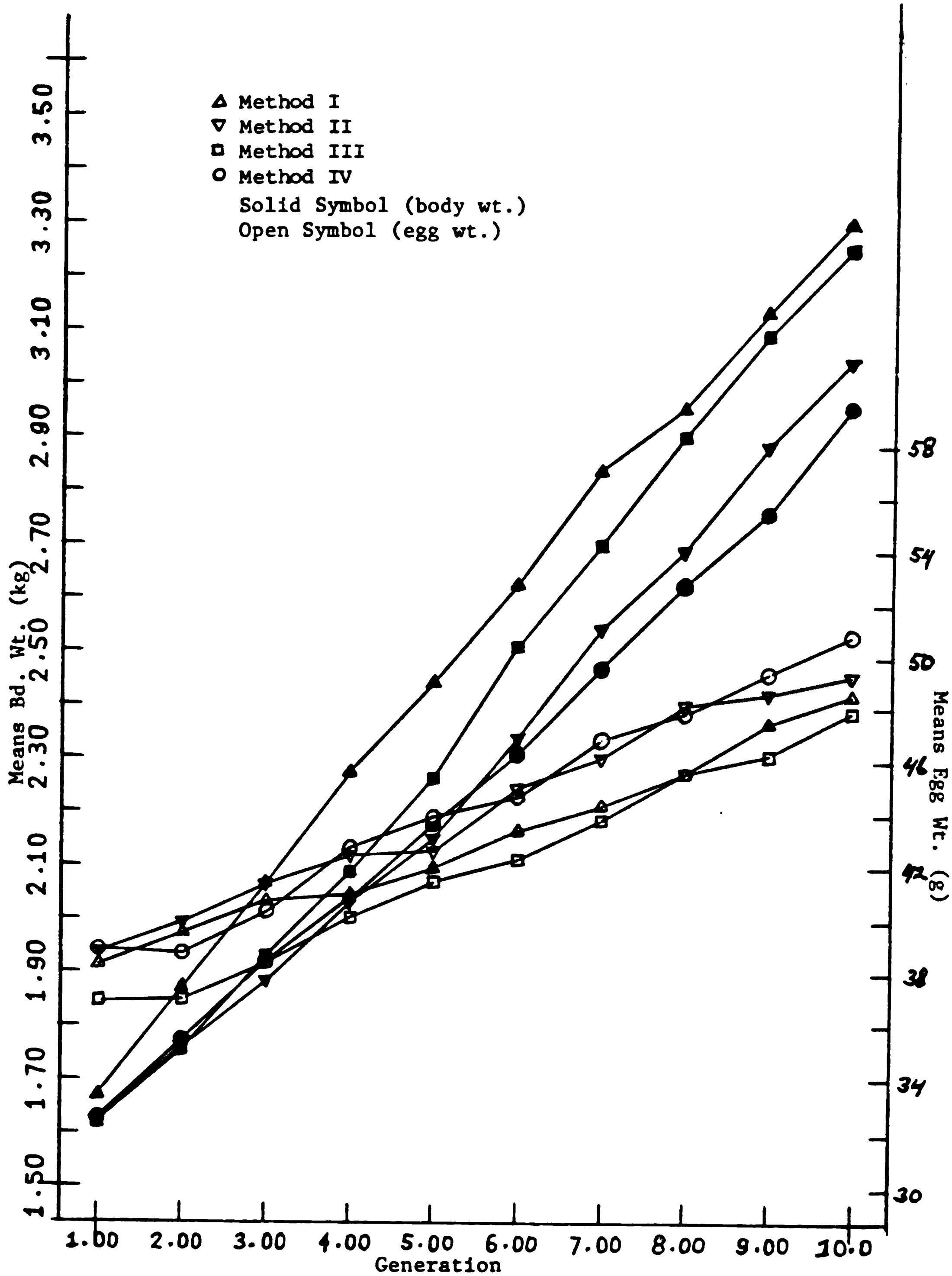

Figure 2.2. Means of Body Weight and Egg Weight in Population II Under Different Method of Selections. ($h_1^2 = .4$, $h_2^2 = .3$, $h_3^2 = .5$, $rG_{12} = -.4$, $rG_{13} = .3$)

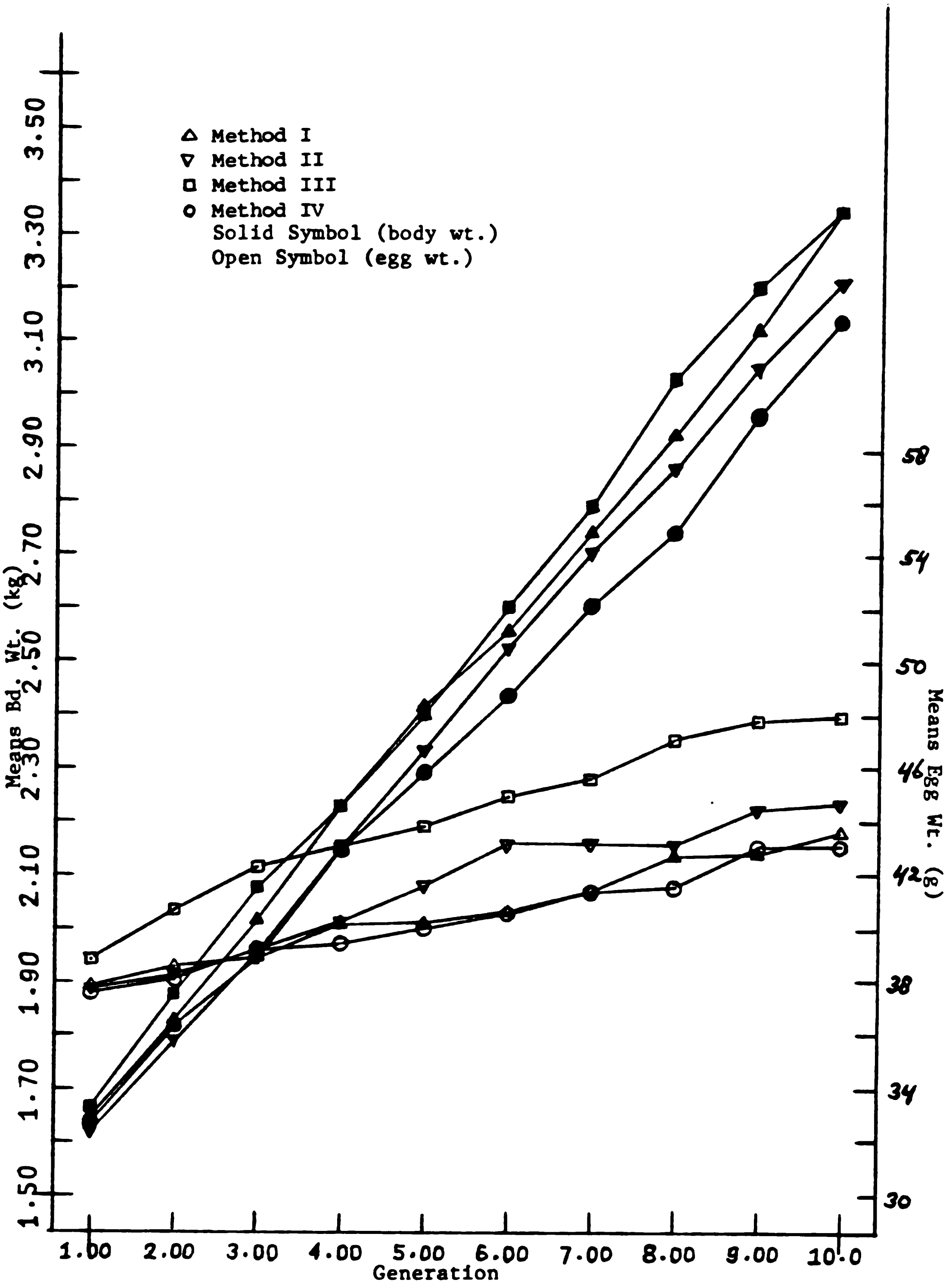

Figure 2.3. Means of Body Weight and Egg Weight in Population III Under Different Method of Selections. (h_1^2 = .4, h_2^2 = .3, h_3^2 = .5, rG_{12} = −.2, rG_{13} = .2)

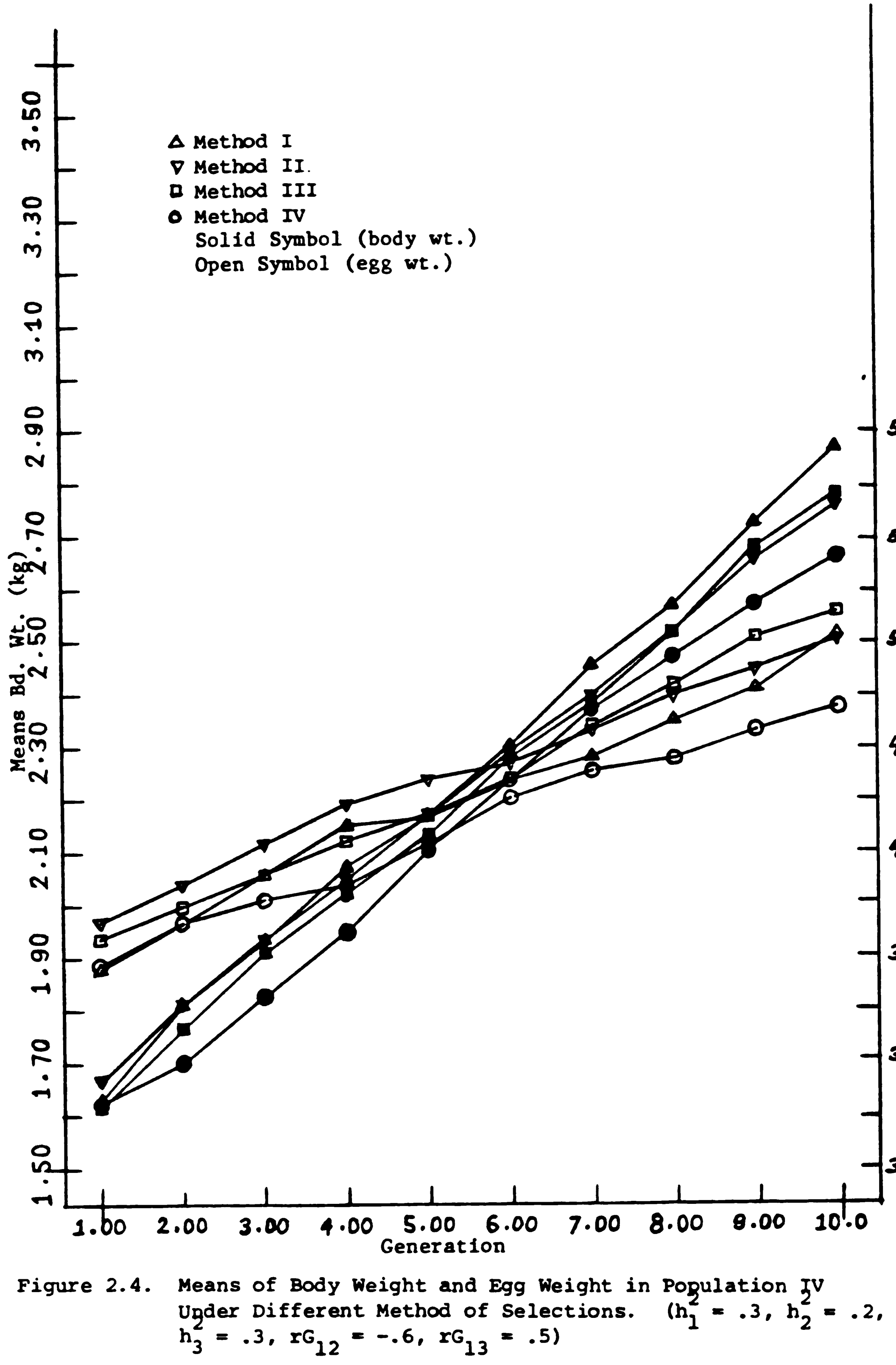

Figure 2.4. Means of Body Weight and Egg Weight in Population IV Under Different Method of Selections. ($h_1^2 = .3$, $h_2^2 = .2$, $h_3^2 = .3$, $rG_{12} = -.6$, $rG_{13} = .5$)

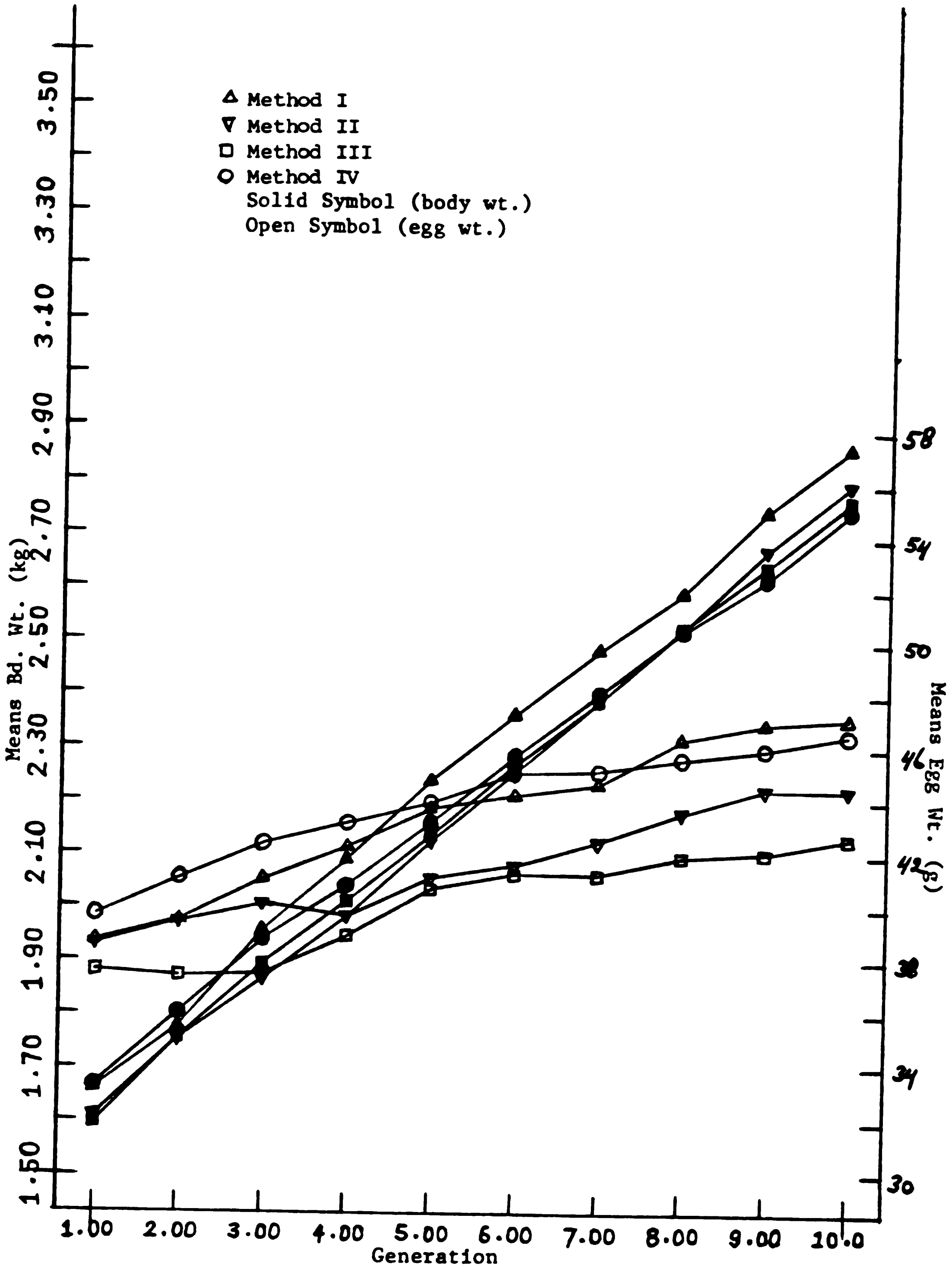

Figure 2.5. Means of Body Weight and Egg Weight in Population Y_2 Under Different Method of Selections. ($h_1^2 = .3$, $h_2^2 = .2$, $h_3^2 = .3$, $rG_{12} = -.4$, $rG_{13} = .3$)

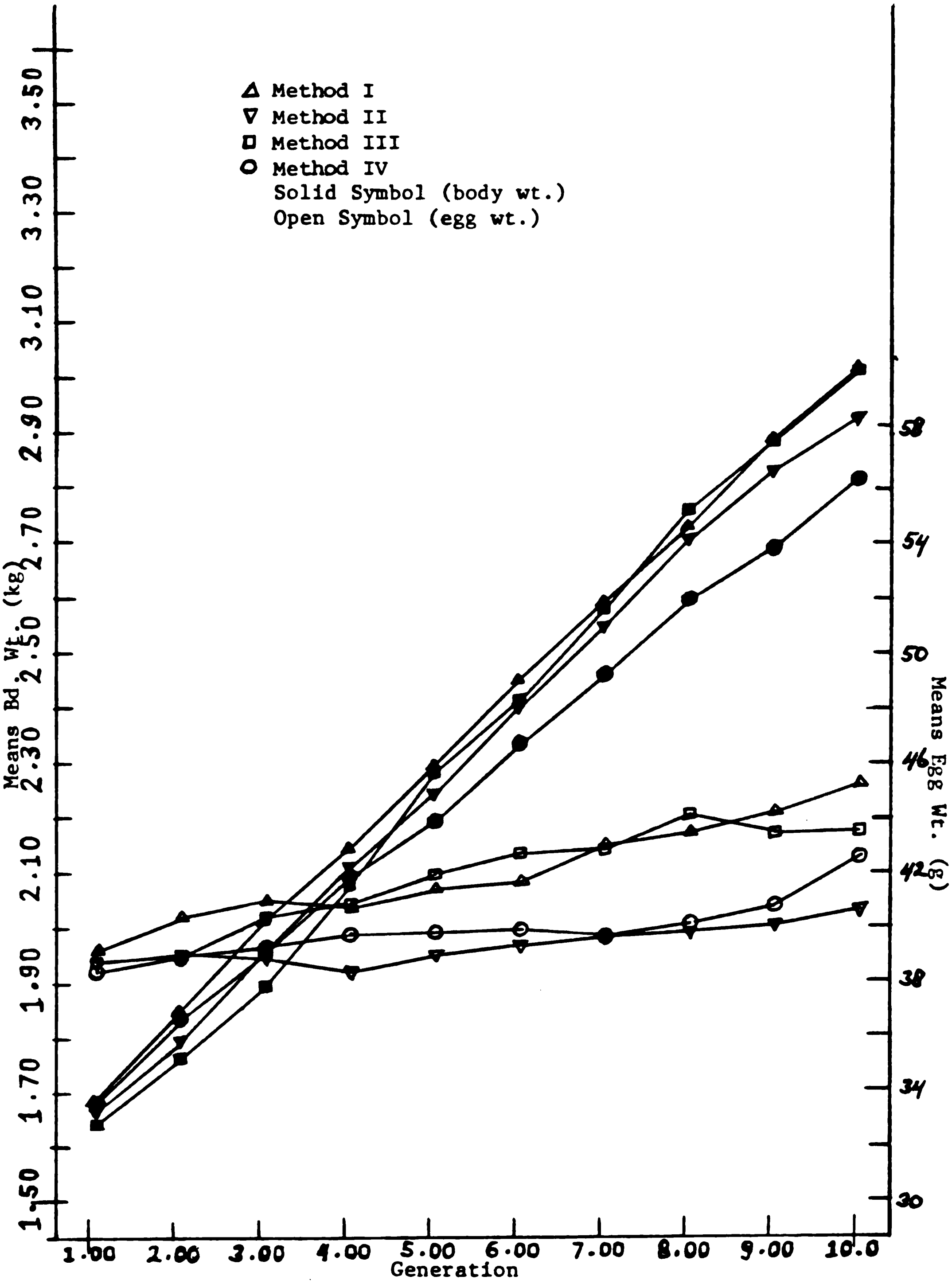

Figure 2.6. Means of Body Weight and Egg Weight in Population VI Under Different Method of Selections. (h_1^2 = .3, h_2^2 = .2, h_3^2 = .3, rG_{12} = -.2, rG_{13} = .2)

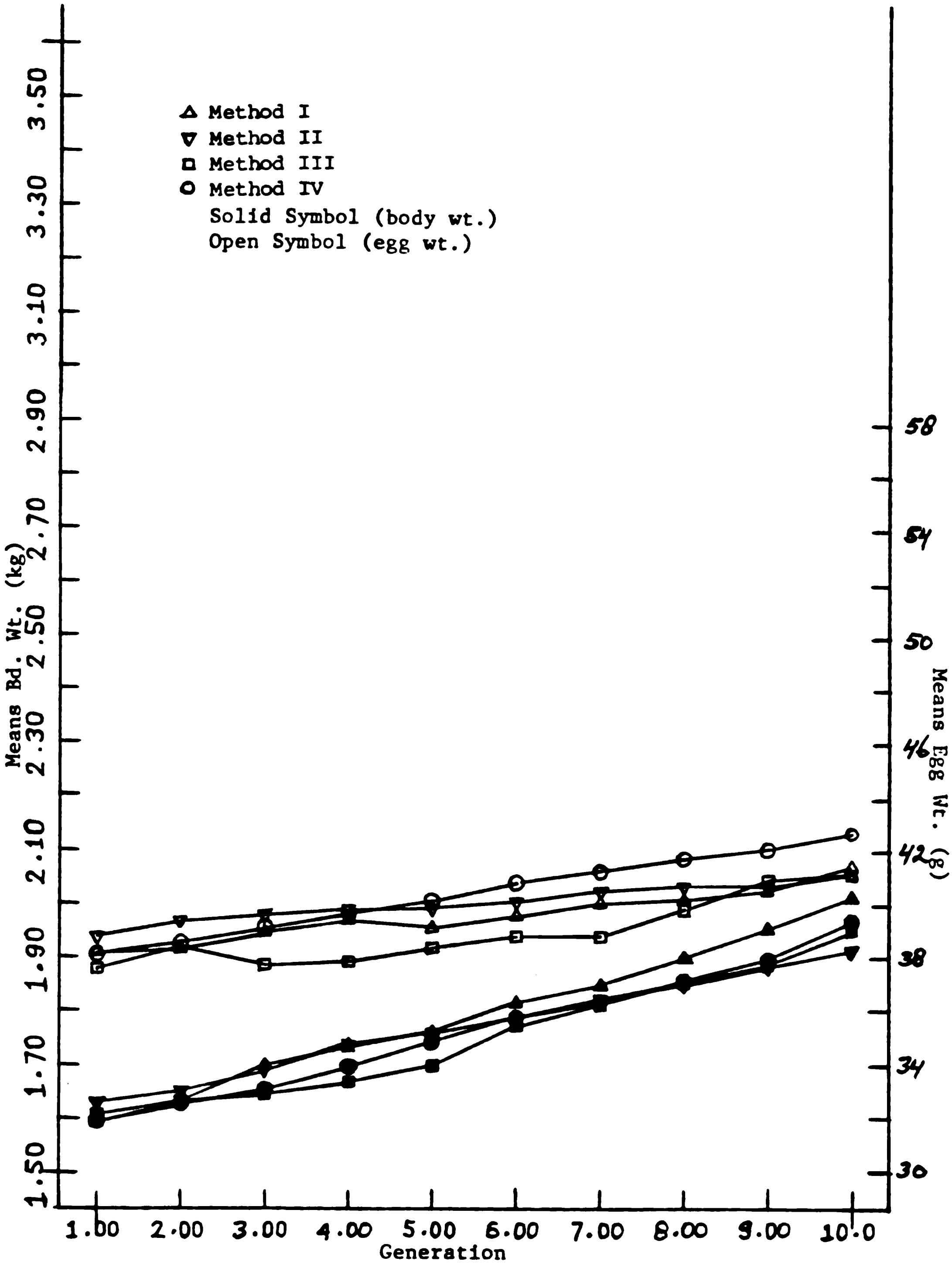

Figure 2.7. Means of Body Weight and Egg Weight in Population VII Under Different Method of Selections. (h_1^2 = .1, h_2^2 = .1, h_3^2 = .1, rG_{12} = −.6, rG_{13} = .5)

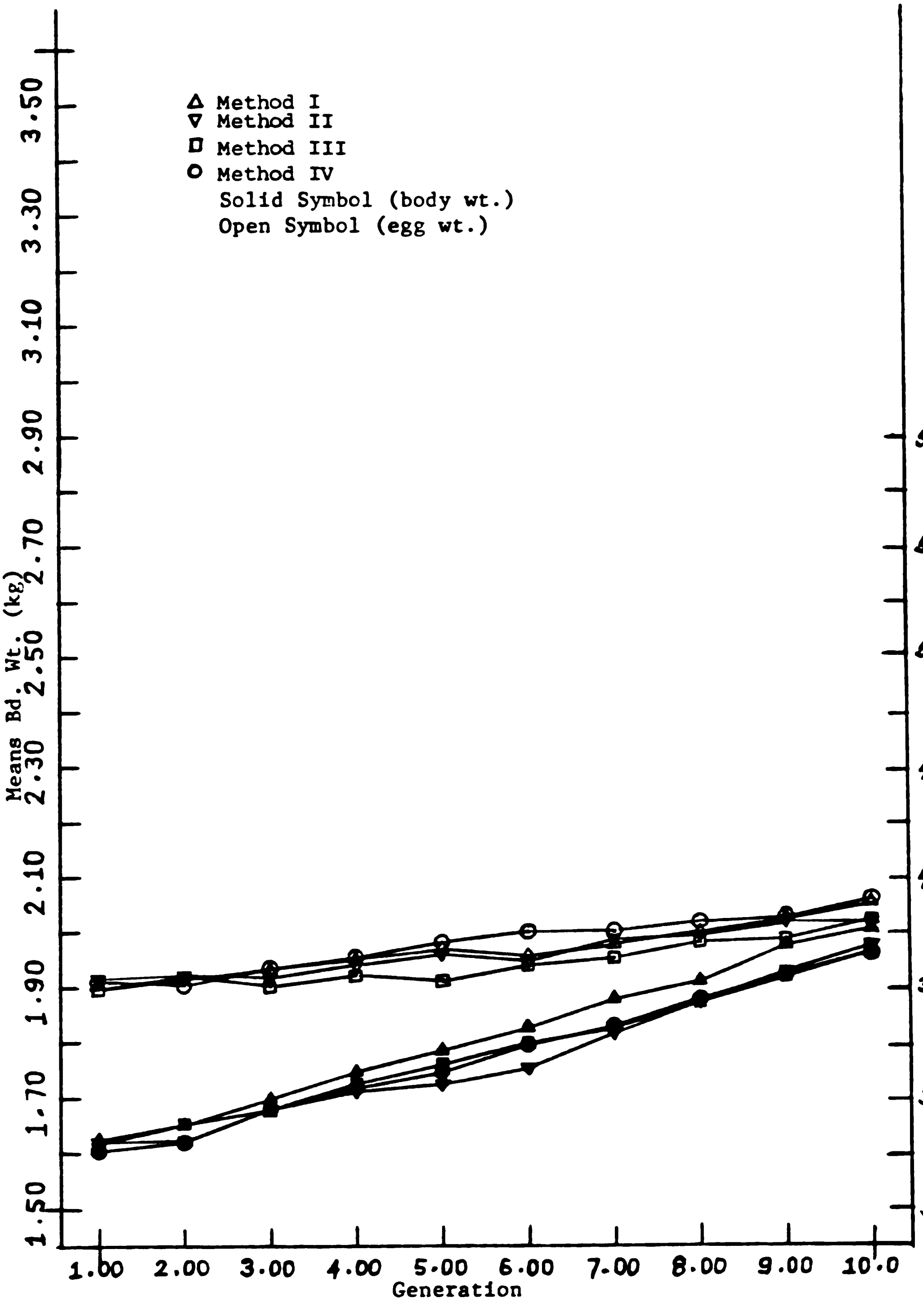

Figure 2.8. Means of Body Weight and Egg Weight in Population VIII Under Different Method of Selections. (h_1^2 = .1, h_2^2 = .1, h_3^2 = .1, rG_{12} = -.4, rG_{13} = .3)

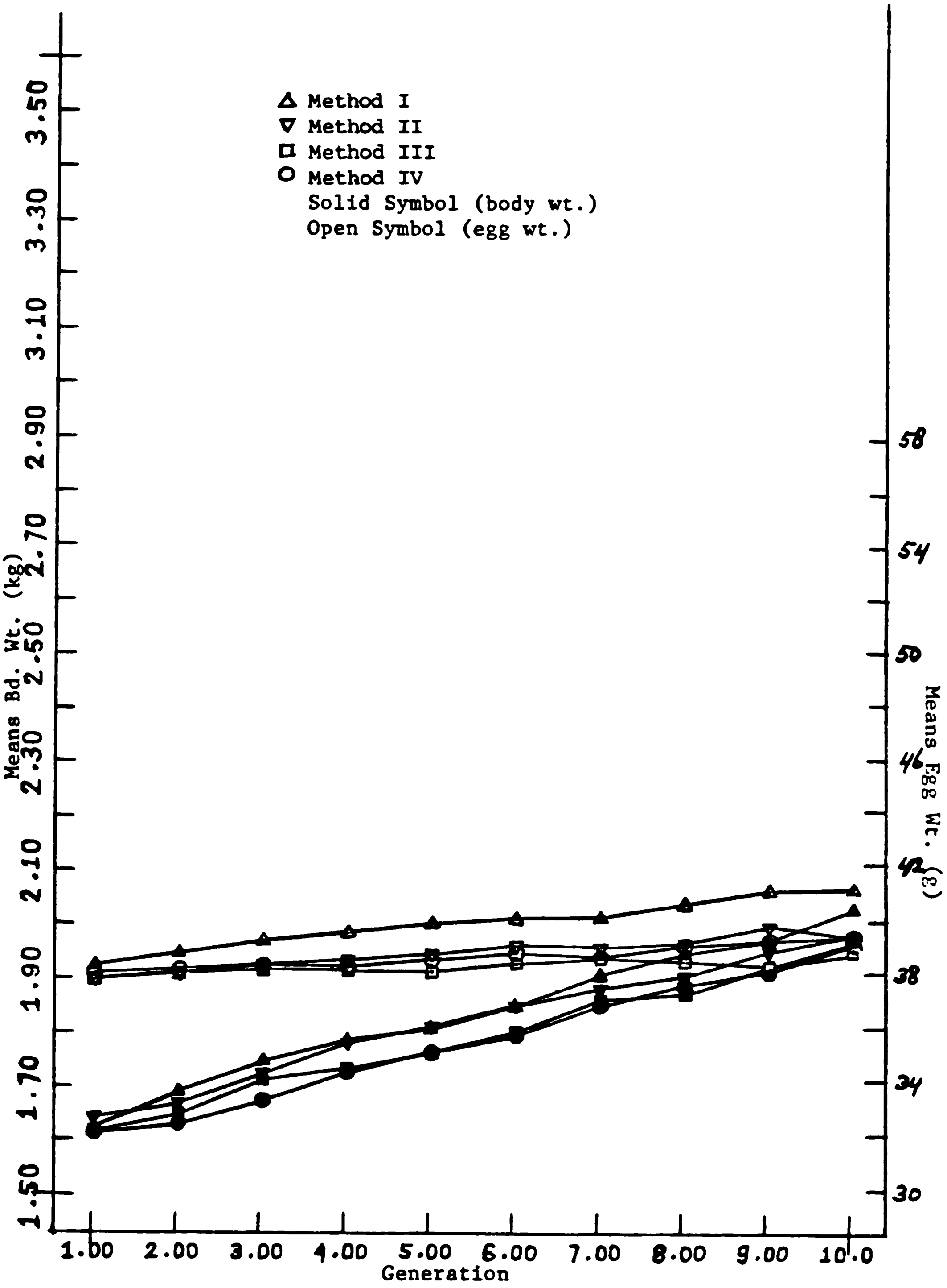

Figure 2.9. Means of Body Weight and Egg Weight in Population IX Under Different Method of Selections. ($h_1^2 = .1$, $h_2^2 = .1$, $h_3^2 = .1$, $rG_{12} = -.2$, $rG_{13} = .2$)

Table 16.--The Expected and Observed of Total Response Per Generation in Economic Unit. (1 unit = $.10)

Method / Population		I	II	III	IV
I	E	2.0339	1.9642	1.9423	2.114
	O	2.8768	3.1972	2.9629	2.8686
II	E	2.7677	3.0175	2.1874	3.0142
	O	2.6363	3.0069	3.5258	3.0835
III	E	3.5013	3.7217	3.5493	3.7576
	O	3.7558	4.3523	4.0418	4.1466
IV	E	1.6211	1.6954	1.6774	1.4346
	O	1.5923	2.2073	2.2240	2.0716
V	E	2.1399	2.2790	2.2786	2.3890
	O	2.2901	2.8154	2.7471	2.3350
VI	E	2.6587	2.8592	2.7862	2.7744
	O	2.9984	2.8592	3.4437	2.8234
VII	E	.4246	.4992	.4931	.4781
	O	.4382	.5463	.8891	.6106
VIII	E	.6364	.7460	.6996	.7146
	O	.5877	.9091	.5536	.8567
IX	E	.8482	.9891	.9097	.9401
	O	.9600	1.1304	.8289	.8847

METHOD I : Mass Selection

METHOD II : Selection Index

METHOD III : Restricted Selection Index

METHOD IV : Independent Culling Levels

Within the same levels of heritabilities, the larger the genetic correlation, the less the total economic response.

Table 17 shows the expected and observed relative percent efficiency for total economic response for different selection methods. Each value in the table was calculated as: $(H_i/H_{II}) \times 100\%$ Where subscript i can be either I, II, III, or IV. Thus, selection index was considered to be 100% efficient.

On the average the expected values and observed values indicated that selection index method was better than the other three methods. When the results from mass selection and selection index were compared, the observed values showed that except in population VI mass selection was about 20% less efficient. Here, in comparing percent efficiency there was no indication of the effect of different parameter combinations. Random error might be the cause for observed value in population VI a little over 100%.

Is 20% less efficiency for mass selection too much to pay for the simplicity and conveniences of the method? Selection index requires genetic parameters such as heritabilities, genetic and phenotypic correlations, and economic value of traits which have to be made available before the index can be constructed. Further, experts suggested that the index should be recalculated each cycle of selection as the required genetic parameters might change due to selection. Another thing to note is characteristic of selection index, i.e., it has its greatest value only for a particular population with particular economic values of traits which the index is intended for.

Table 17.--Relative Percent Efficiency of Different Selection Methods.

Population \ Method		I	II	III	IV
I	E*	103.55	100	98.88	107.63
	O*	89.98	100	92.67	89.72
II	E	91.72	100	72.49	99.89
	O	87.68	100	117.25	102.55
III	E	94.08	100	95.37	100.96
	O	86.29	100	92.86	95.27
IV	E	95.62	100	98.94	84.62
	O	72.14	100	100.75	93.85
V	E	93.89	100	99.98	104.83
	O	81.34	100	97.57	82.93
VI	E	92.99	100	97.45	97.03
	O	104.87	100	120.44	98.75
VII	E	85.06	100	98.78	95.77
	O	80.21	100	162.75	111.77
VIII	E	85.31	100	93.78	95.79
	O	64.65	100	60.89	94.24
IX	E	85.75	100	91.97	95.05
	O	84.92	100	73.33	78.26

*E = Expected

*O = Observed

METHOD I : Mass Selection

METHOD II : Selection Index

METHOD III : Restricted Selection Index

METHOD IV : Independent Culling Levels

The observed percent efficiency of restricted selection index showed that this method was almost as efficient as when selection index was used. However, in the populations where genetic correlation was low the observed value seems subjected to larger random error which made further interpretation difficult.

Independent culling method was somewhat less efficient than selection index method. On the average this method was about 10% less efficient. Using independent culling method the population size was reduced after the first stage of selection where females were selected for body weight at sexual maturity. At this stage only 25% females were saved until the second stage where females were then selected for egg production. From the number of females that entered the second stage selection, 50% were saved for parents producing the same size of breeding flock as when other methods were used. This means that with this method the cost to maintain the flock was reduced 75% compared to when selection index was used. The reduction of cost and avoidance of the known complexity of constructing a selection index seems more than enough to pay for the 10% loss in efficiency from use of this method. In practice independent culling is as simple as mass selection but the results in this study also indicated it's more efficient than mass selection.

Genetic correlations during selection study

The required genetic correlations, rG_{12} and rG_{13} (subscript 1, 2 and 3 is for body weight, egg production and egg weight, respectively) were first introduced when the base populations were generated, according to the simulation method presented in a previous section. A separate run was made to check the sample values of rG_{12} and rG_{13} for different parametric values of rG_{12} and rG_{13} required. Table 18 shows the range of rG_{12} and rG_{13} for 30 sample populations with sample size equal 132 individuals. These values indicated that the simulation technique used to build up the required correlation was successful, as the parametric values fall within the range of values observed.

The second time the required genetic correlations were forced in when the offspring populations were generated, with the procedure already explained.

The genetic correlations in unselected offspring and selected offspring in each generation were calculated as the product moment correlation of genotypic values. For different selection methods the genetic correlations in the unselected and selected offspring were plotted together for every two generations and are presented in figures 3.1 to 6.3. In all populations the genetic correlation was maintained regardless of the method of selection, because the genotypic and phenotypic variances and covariances did not change substantially.

Results from mass selection indicated that in all levels of heritability used in this study truncation selection decreased the genetic correlations in the selected offspring, except when the genetic correlations were low ($rG_{12} = -.2$ and $rG_{13} = .2$). Thus both the positive or negative genetic correlation showed the same results. The decrease of rG_{12} and rG_{13} in the selected offspring were observed more clearly when heritability of body weight = .4, $rG_{12} = -.6$ and

Table 18.--Range of Sample Values of Genetic Correlation of Body Weight and Egg Production and Body Weight and Egg Weight in Base Population.*

h_1^2	h_2^2	h_3^2	Parametric Values		Range of Sample Values	
			rG_{12}	rG_{13}	rG_{12}	rG_{13}
.4	.3	.5	-.6	.5	-.67 to -.41	.27 to .53
			-.4	.3	-.55 to -.25	.16 to .43
			-.2	.2	-.31 to .01	.04 to .40
.3	.2	.3	-.6	.5	-.69 to -.42	.31 to .66
			-.4	.3	-.58 to -.26	.12 to .44
			-.2	.2	-.39 to -.08	.03 to .38
.1	.1	.1	-.6	.5	-.71 to -.52	.34 to .64
			-.4	.3	-.49 to -.23	.16 to .43
			-.2	.2	-.36 to -.02	.08 to .37

* Range of 30 samples and sample size = 132 individuals

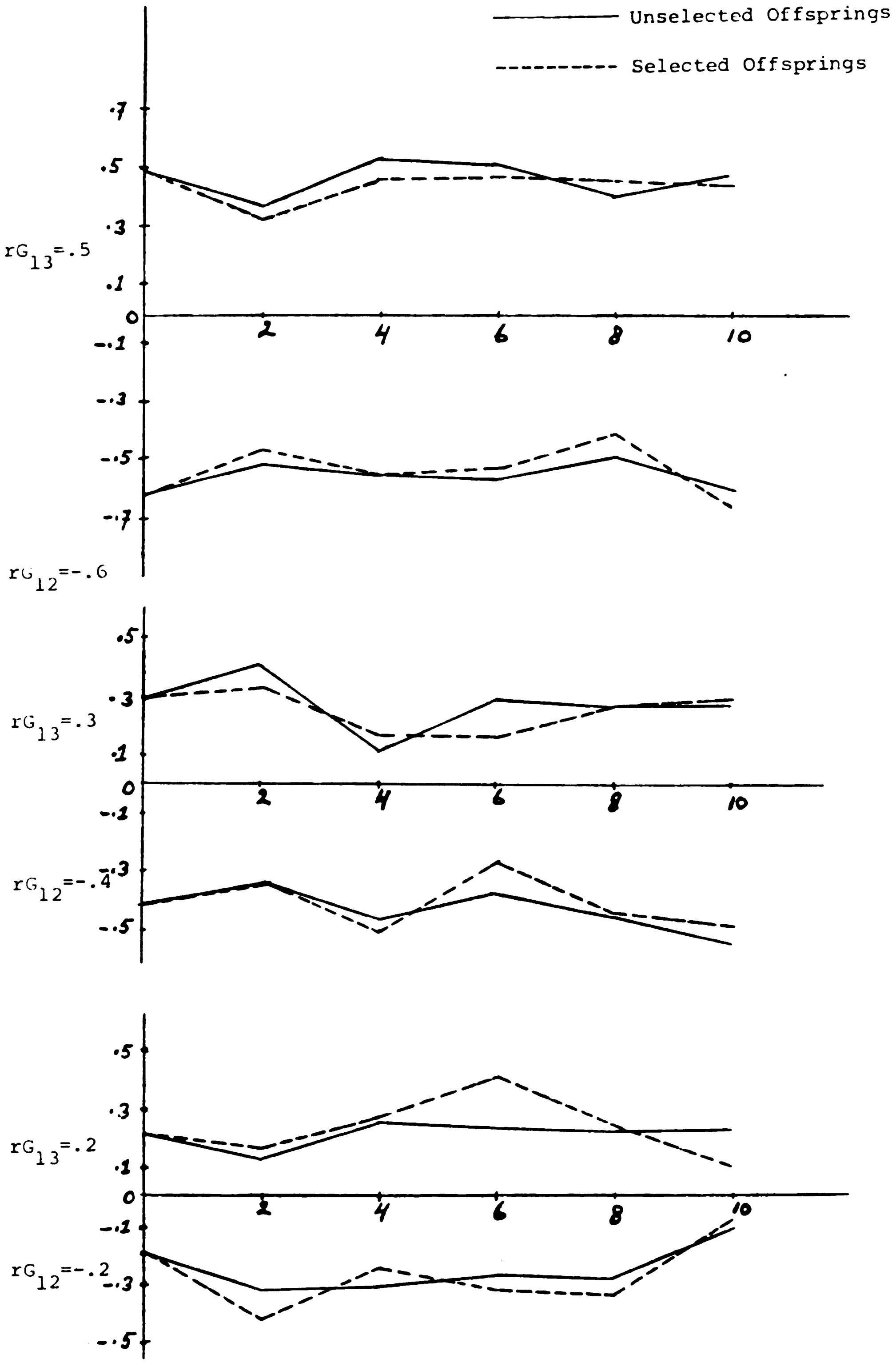

Figure 3.1. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Mass Selection. ($h_1^2 = .4$, $h_2^2 = .3$, $h_3^2 = .5$)

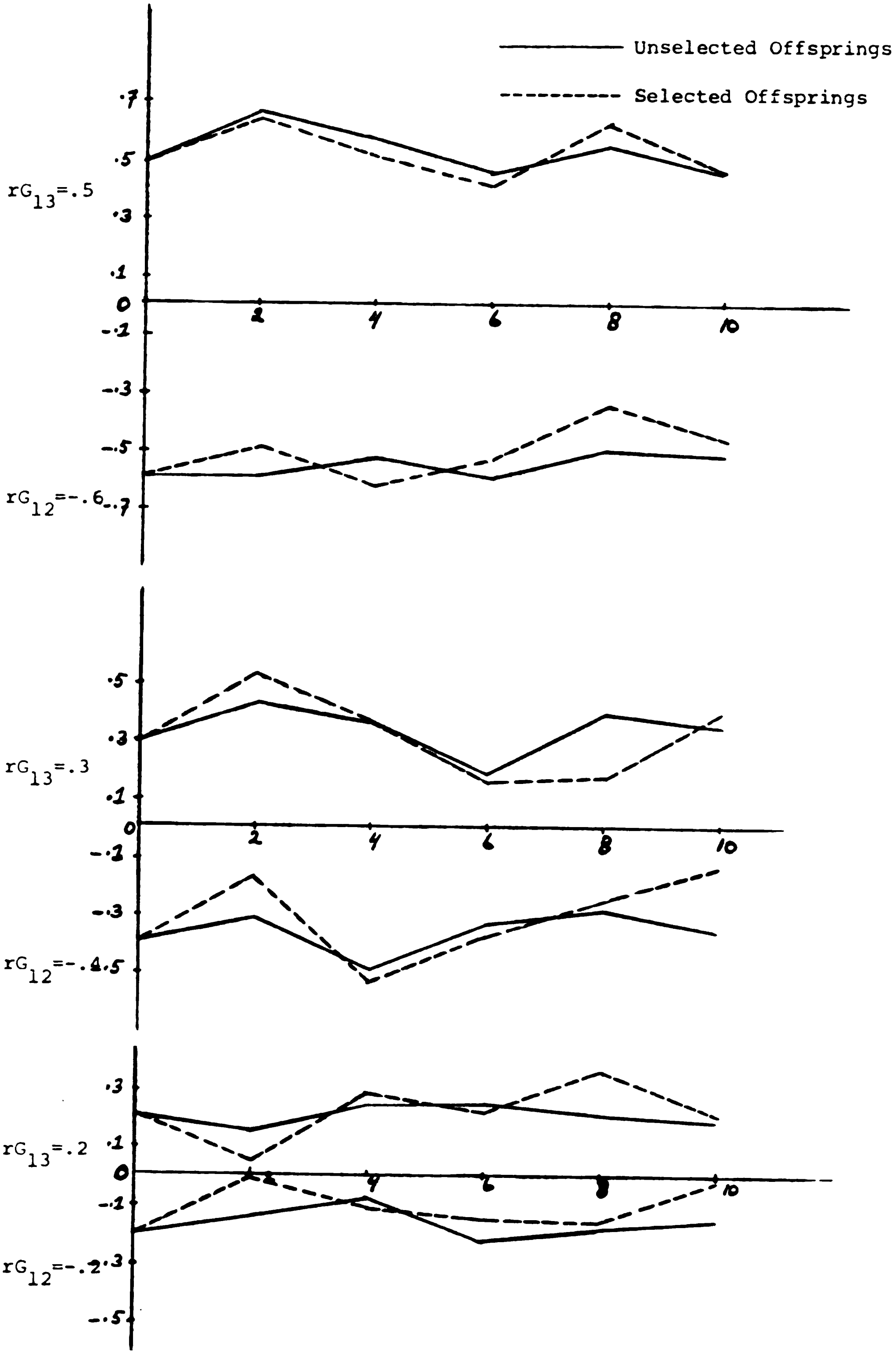

Figure 3.2. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Mass Selection. (h_1^2 = .3, h_2^2 = .2, h_3^2 =.3)

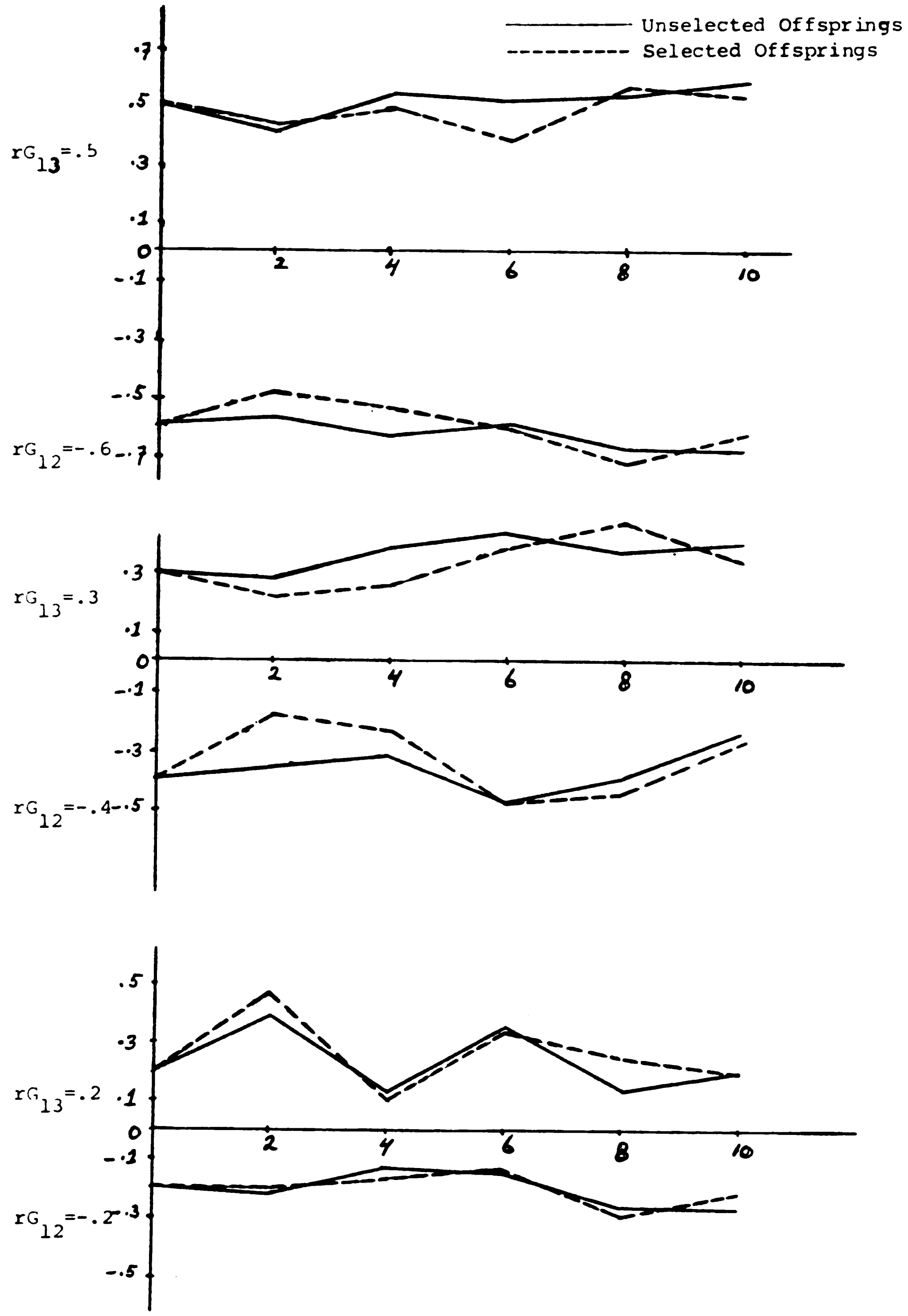

Figure 3.3. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Mass Selection (h_1^2 = .1, h_2^2 = .1, h_3^2 = .1)

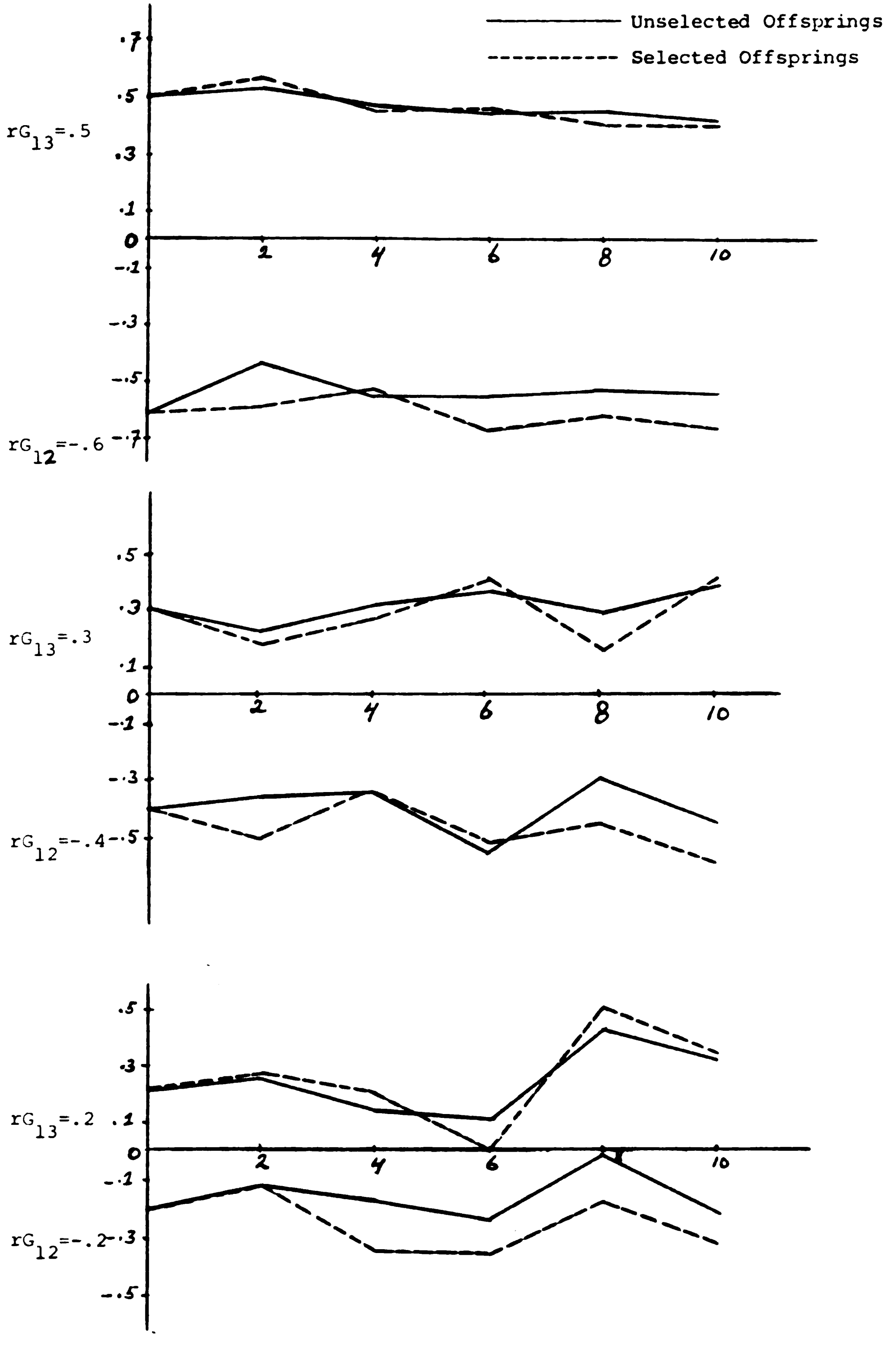

Figure 4.1. rG$_{12}$ and rG$_{13}$ in the Unselected and Selected Offsprings Under Selection Index. (h_1^2 = .4, h_2^2 = .3, h_3^2 = .5)

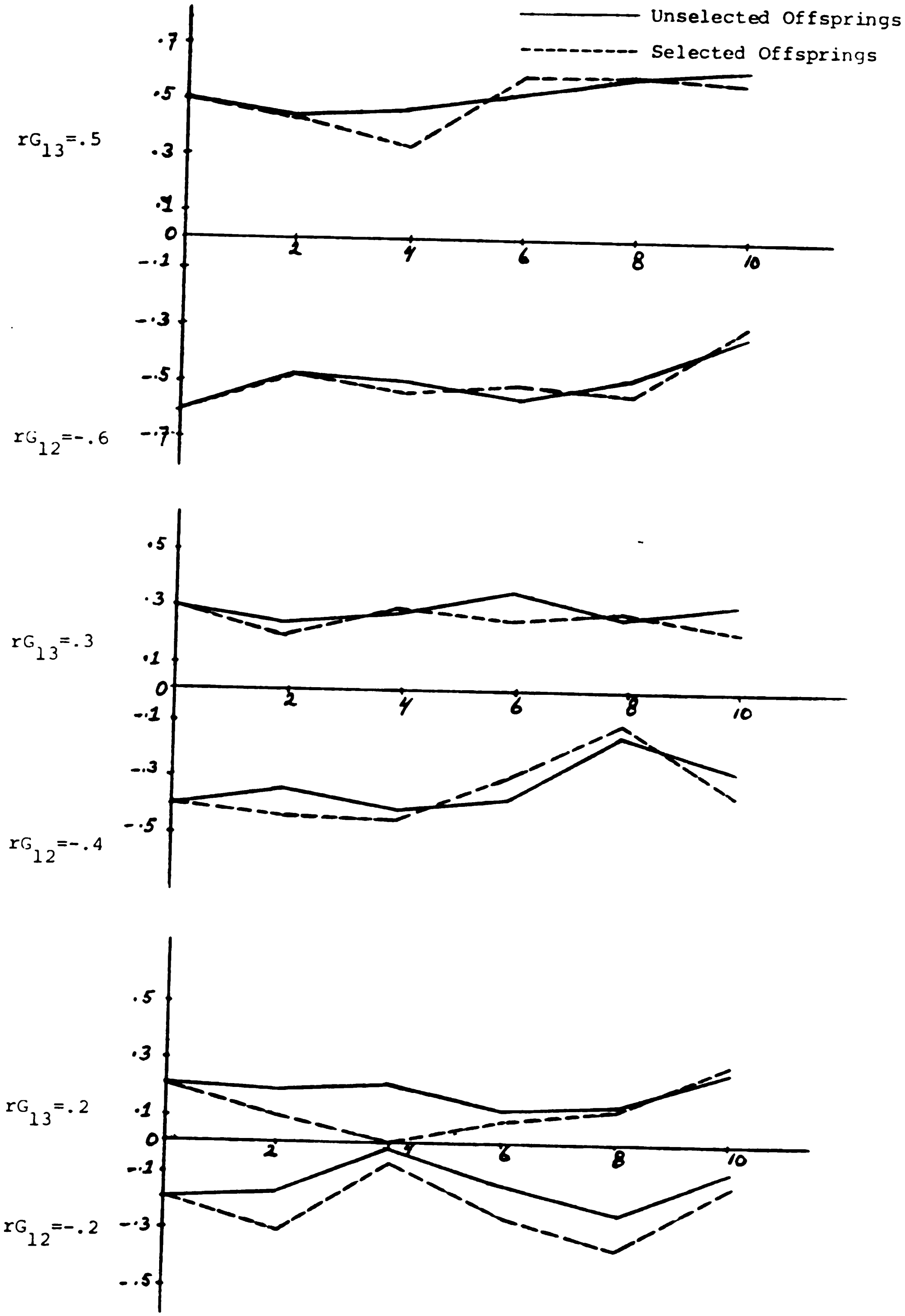

Figure 4.2. rG$_{12}$ and rG$_{13}$ in the Unselected and Selected Offsprings Under Selection Index. ($h_1^2 = .3$, $h_2^2 = .2$, $h_3^2 = .3$)

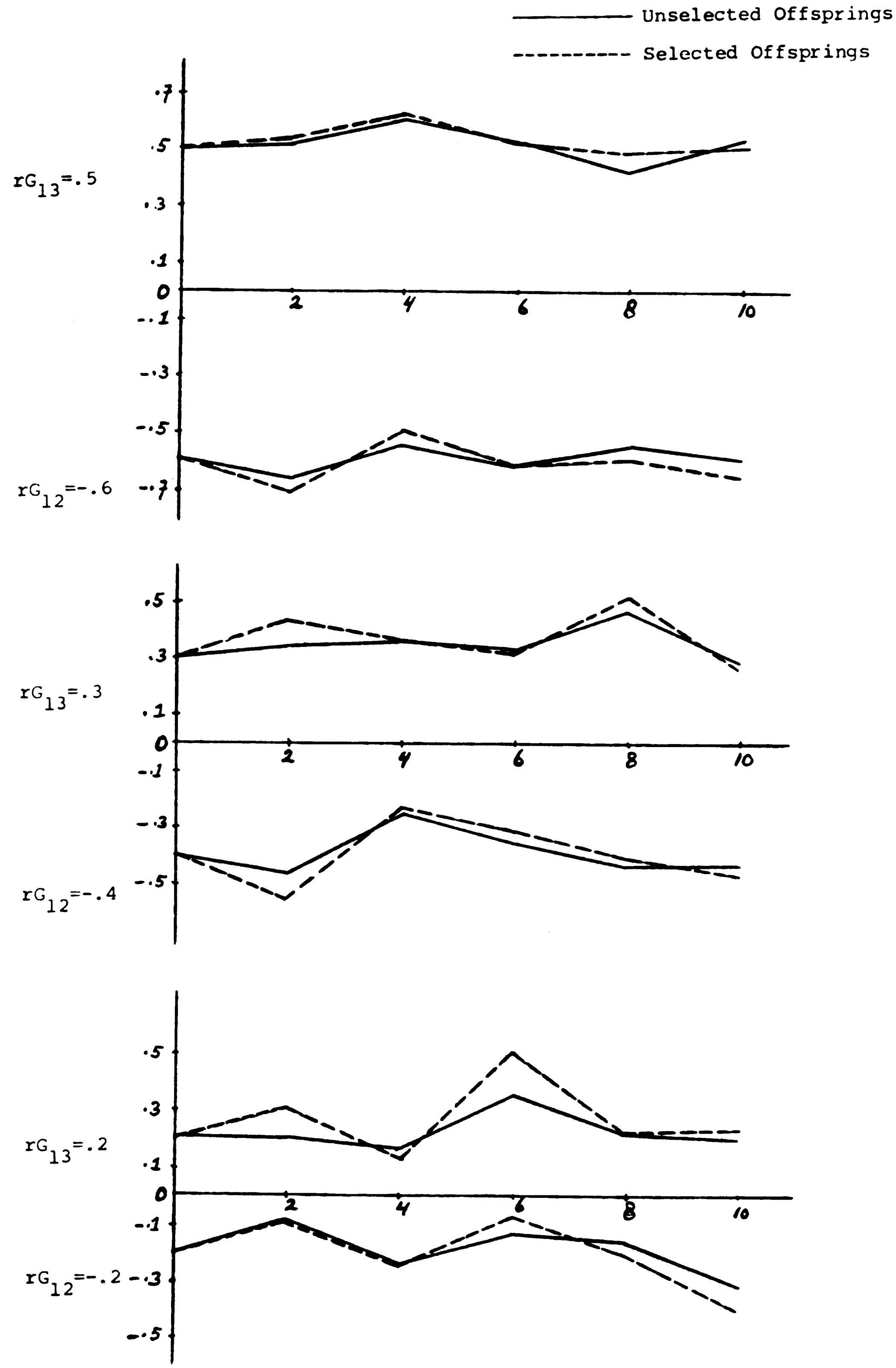

Figure 4.3. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Selection Index. ($h_1^2 = .1$, $h_2^2 = .1$, $h_3^2 = .1$)

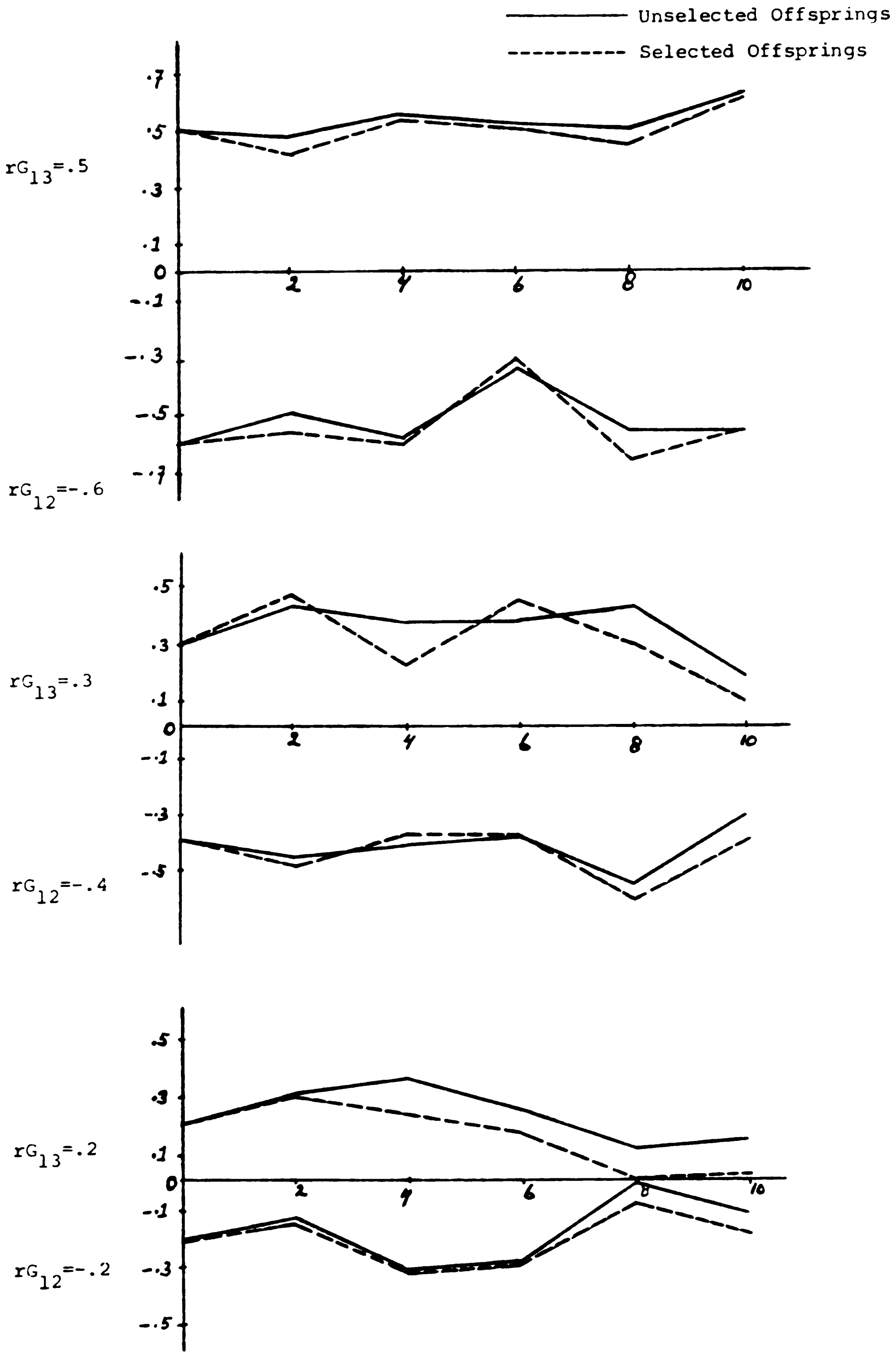

Figure 5.1 rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Restricted Selection Index. ($h_1^2 = .4$, $h_2^2 = .3$, $h_3^2 = .5$)

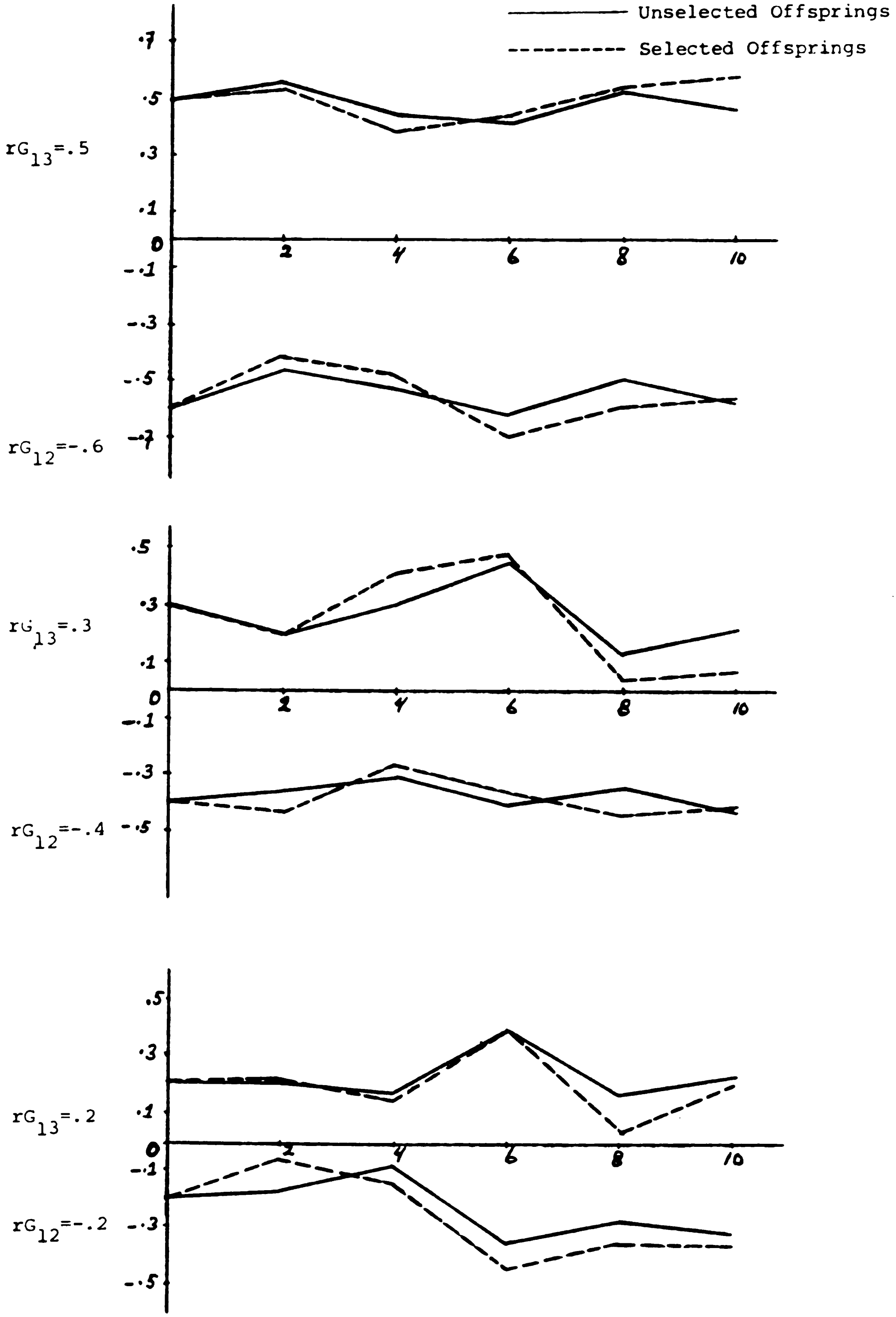

Figure 5.2. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Restricted Selection Index. ($h_1^2 = .3$, $h_2^2 = .2$, $h_3^2 = .3$)

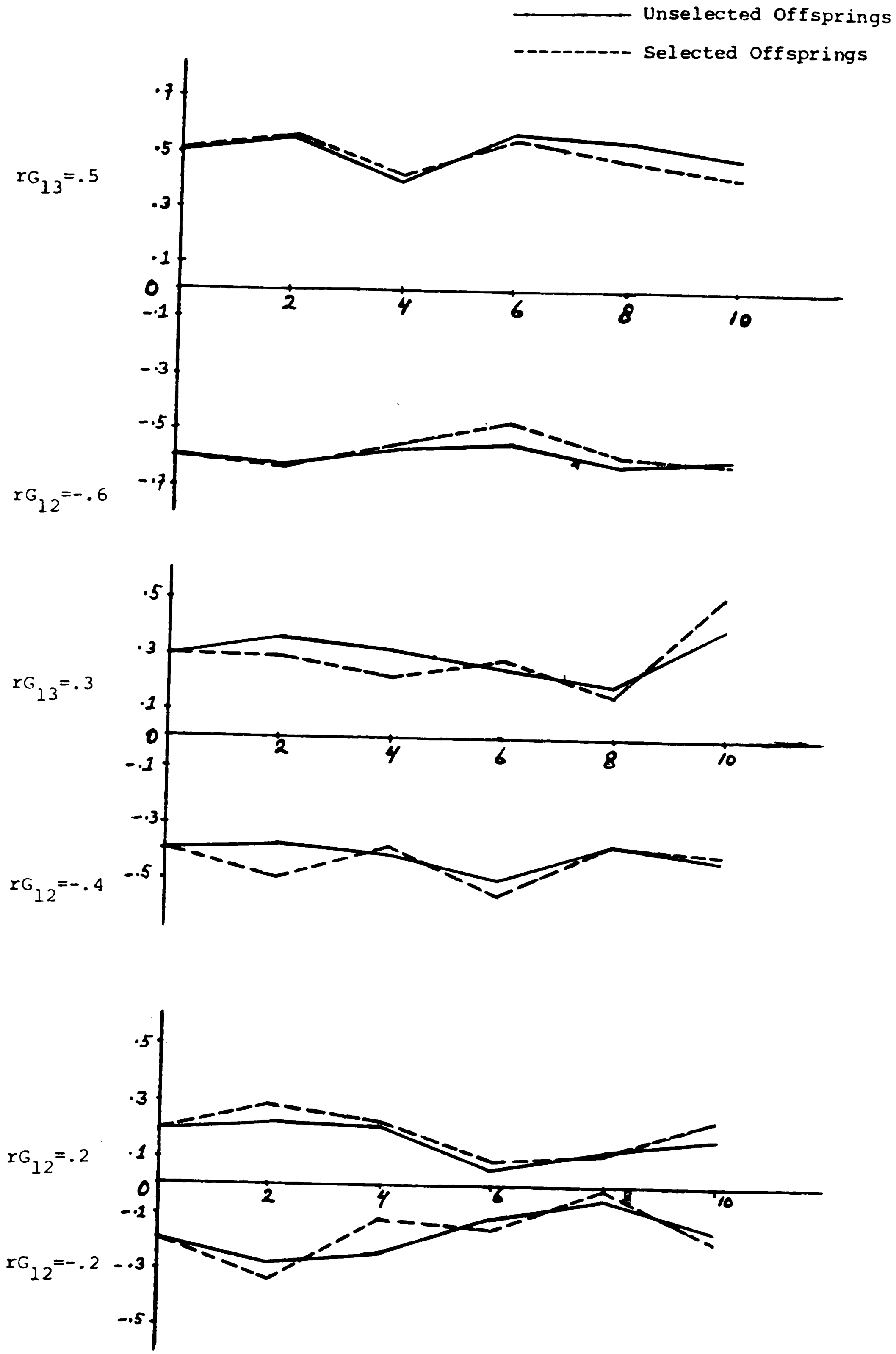

Figure 5.3. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Restricted Selection Index. (h_1^2 = .1, h_2^2 = .1, h_3^2 = .1)

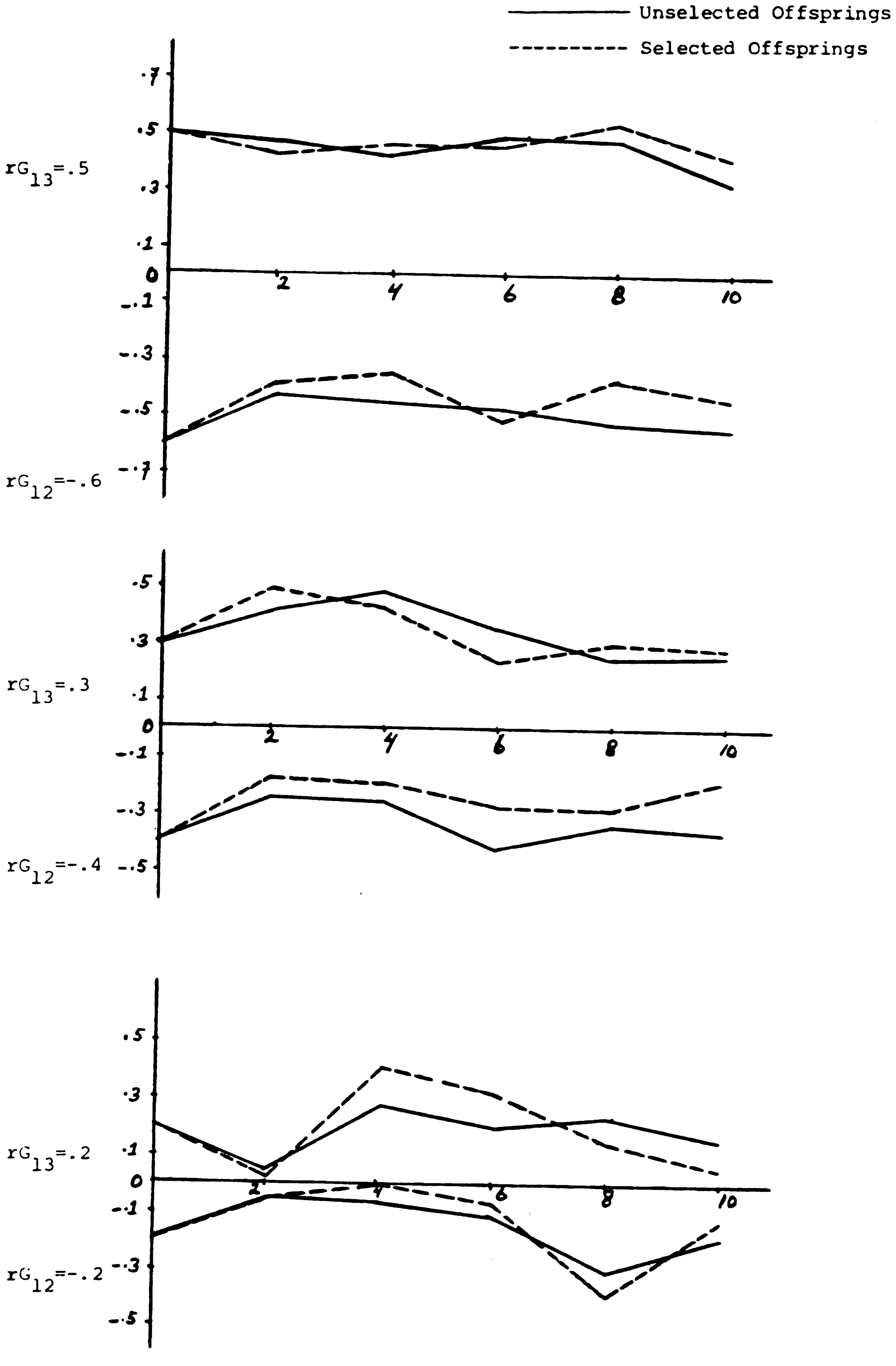

Figure 6.1. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Independent Culling Levels. (h_1^2 = .4, h_2^2 = .3, h_3^2 = .5)

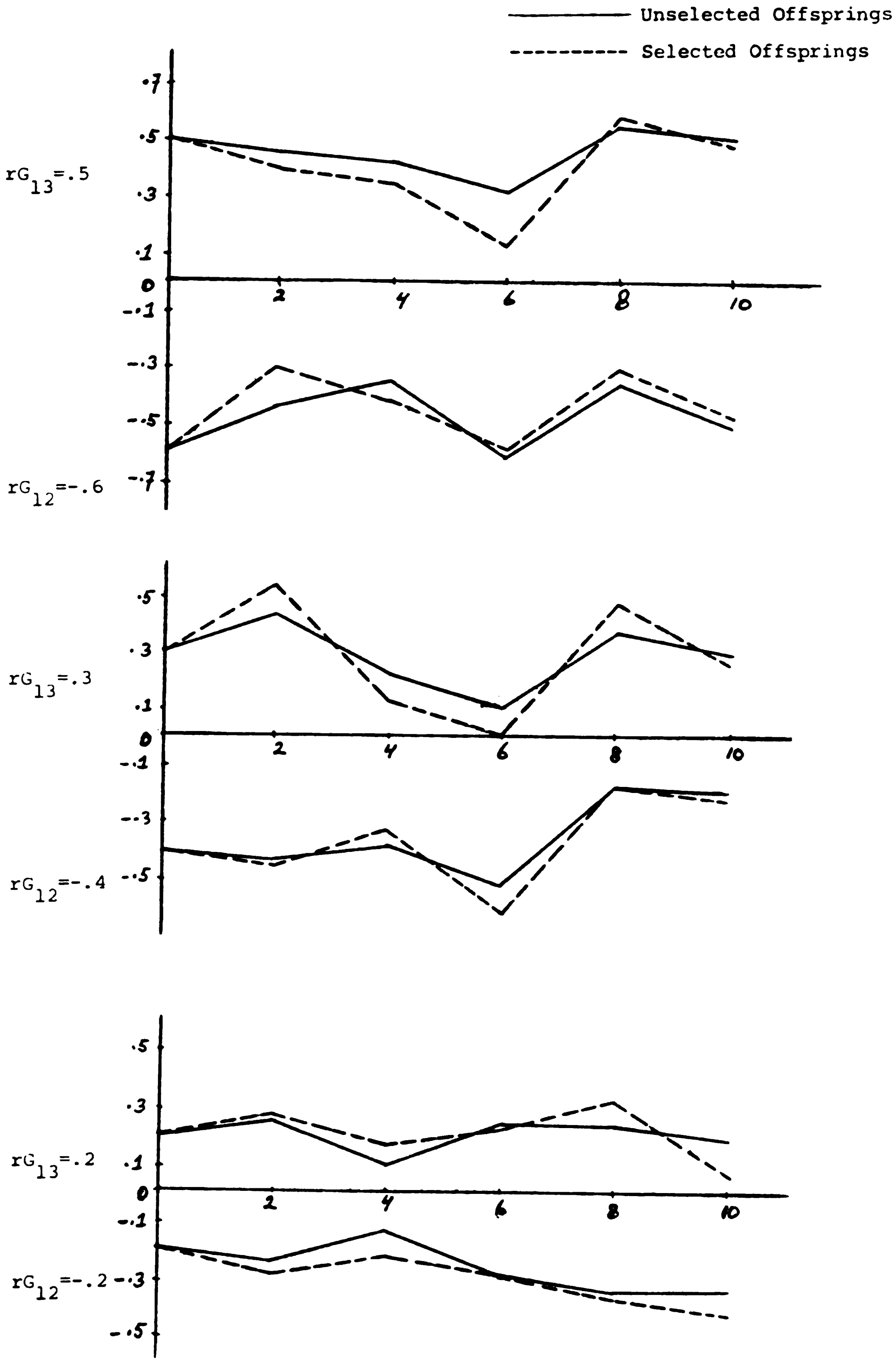

Figure 6.2. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Independent Culling Levels. (h_1^2 = .3, h_2^2 = .2, h_3^2 = .3)

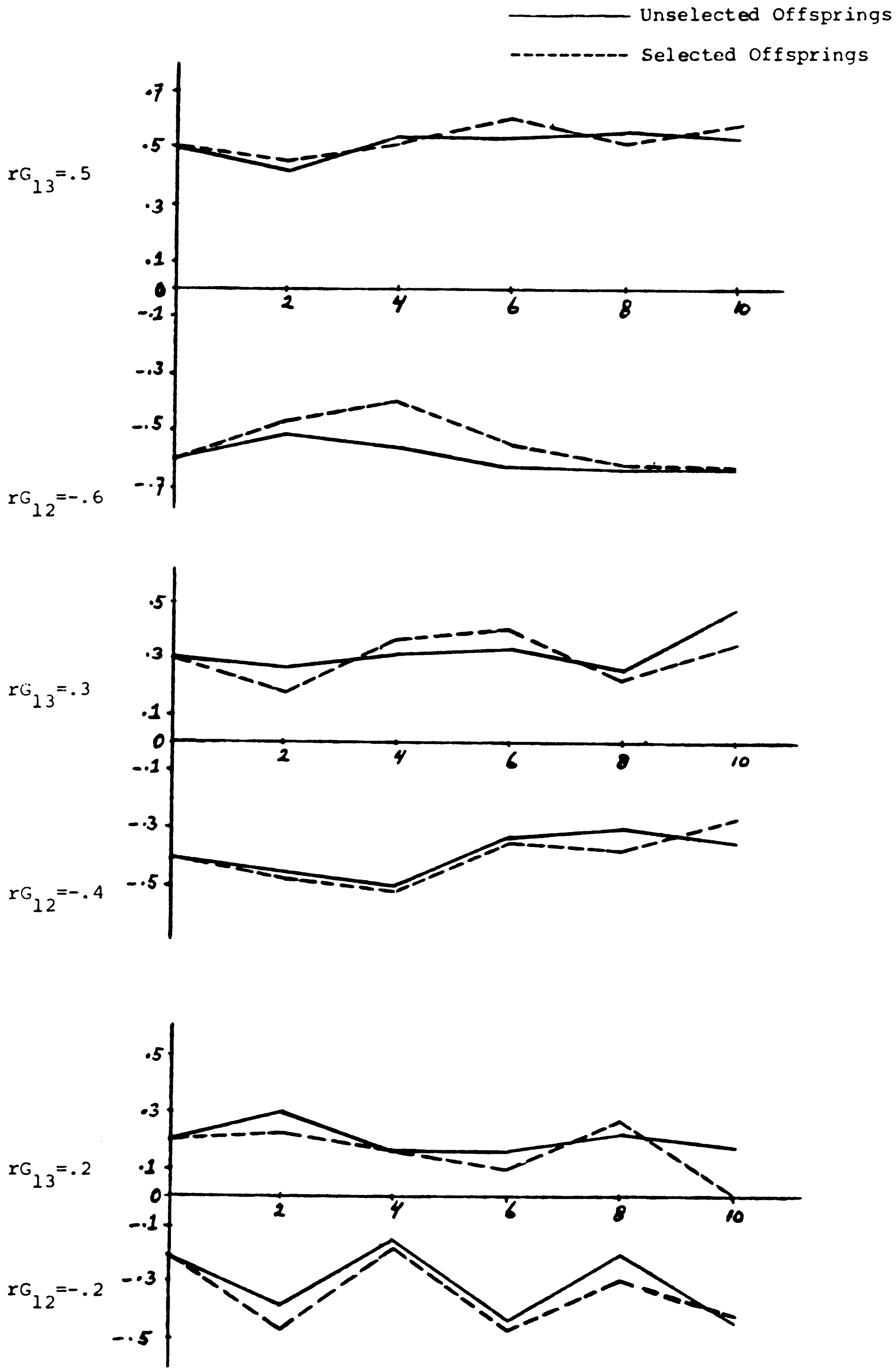

Figure 6.3. rG_{12} and rG_{13} in the Unselected and Selected Offsprings Under Independent Culling Levels. $(h_1^2 = .1,\ h_2^2 = .1,\ h_3^2 = .1)$

$rG_{13} = .5$. Further, examination on the genetic variances and covariances indicated that the covariances were decreased slightly more than the variances. The same evidence was reported by Parker et al. (1969) and Cheung and Parker (1974).

When either selection index or restricted selection index was used, the results didn't indicate that the genetic correlations in the selected offspring were decreased but it appeared that the genetic correlations in the unselected offspring were maintained after truncation (Figures 4.1 to 4.3 and figures 5.1 to 5.3). This evidence was seen more clearly when the genetic correlations were high. Probably this can be explained by the fact that when the index was used, the truncation was applied not directly on the phenotypic distribution of traits but rather on the index values.

Results from independent culling seem to indicate that the genetic correlations in the selected offspring were reduced only when the genetic correlations were high ($rG_{12} = -.6$ to $-.4$ and $rG_{13} = .5$ or $.3$), and this applied for all levels of heritabilities used in this study (Figures 6.1 to 6.3). When the genetic correlations were low, the interpretation of results became difficult.

Possibly if more generations were added, the effect of truncation on the genetic correlations in the selected offspring could be examined more clearly as was done by Parker et al. (1969) who carried the selection for 30 generations.

IMPLICATIONS FOR THE NATIVE CHICKEN POPULATION IN INDONESIA

The results from this simulation study indicate that improvement of body weight in native chicken populations is possible by selection within the populations. Although the exact genetic parameters are unknown, it seems reasonable to assume that the parameters are within the range of parameter values used in this study.

Selection index showed the best result but the method can't be recommended at this time because of its complexity and impracticality.

Mass selection and independent culling levels are simple and practical and have proved effective in improving body weight in other populations. The applications of these two methods are straightforward, understandable, and little difficulty should be encountered in beginning and continuing such selection for several generations. However, egg production may be decreased as much as 1.7% per generation by mass selection and somewhat less by independent culling levels. If one may not worry for a while about the decrease in egg production and if mass selection should be the first choice, then the operational cost should be reduced even more than when independent culling levels are used. Although in this study mass selection was simulated for a designed breeding experiment, extensive application of this method in the native chicken populations in the rural areas is not impractical. The method may be combined with random mating, then progress per generation will depend primarily on the selection intensity. The selection intensity to be practiced should be based on judgments about each local area regarding acceptable culling percentages.

Some have suggested improving the native chicken populations by crossbreeding because of the promising results from heterosis in the first generation following the crossing. But, after the first generation, there is confusion about planning for further improvement. It is not justifiable to continue to breed the first cross as the effect of heterosis will disappear. Furthermore in a crossbreeding program there is uncertainty about which breeds will be appropriate for crossing with the native chickens. Also, it is questionable if the chosen breed will adapt well to the local conditions.

Others may think to replace the native chicken populations with imported broiler strains as they see the results in developed countries. However, one should not forget the conditions of the rural areas and how those differ from environments that the broiler strains have been developed in and intended for.

The broiler industry is growing in Indonesian urban areas. Urbanization might make possible changes in existing conditions for poultry husbandry, leading to a decision to discard the native chicken populations, which at present still provide nearly 90% of chicken meat for the nation. But, again urbanization is a relatively slow process, affecting only minor portions of the land, and decisions concerning ways to improve poultry production are urgently needed.

Given the results of this study concerning the near optimal efficiency of mass selection and its practicality compared to other selection schemes, it appears to be the method of choice for short-term progress in native chickens. Modifications may be required in the future if egg production declines to unacceptable levels.

SUMMARY AND CONCLUSIONS

A simulation study was performed to examine the effectiveness of four different methods of selection: mass selection, selection index, restricted selection index, and independent culling levels (two stage selection). These methods were compared for each of nine simulated native chicken populations. The populations were distinguished by different genetic parameter values of heritabilities of body weight, egg production, and egg weight, and genetic correlations of body weight with egg production and egg weight. Respective values for the nine populations are: I: .4, .3, .5, -.6, .5

II: .4, .3, .5, -.4, .3
III: .4, .3, .5, -.2, .2
IV: .3, .2, .3, -.6, .5
V: .3, .2, .3, -.4, .3
VI: .3, .2, .3, -.2, .2
VII: .1, .1, .1, -.6, .5
VIII: .1, .1, .1, -.4, .3
IX: .1, .1, .1, -.2, .2

Simulation continued for ten generations with selection beginning at generation one. Size of breeding flock was kept constant through generations (12 males and 120 females) by saving the upper 1.25% males and 12.5% females to become parents for the next generation. The economic value per unit of body weight was 25 times the economic value per unit of egg production.

Method of selection differed for females but the same selection was applied to all males, phenotypic mass selection for high body weight.

Examination of mean genotypic values showed that in all methods, selection theory was relatively accurate in predicting the response. For mass selection, predictions of direct response were more precise than those for correlated responses, and prediction was more accurate for positively than for negatively correlated responses. When the negative genetic correlation and heritabilities were low, the correlated responses were predicted more precisely than when both were high. Direct responses increased as heritability increased and the amount of correlated response depended on the magnitude of genetic correlation, as expected.

For the selection index method, within the same combination of heritabilities, mean genetic change of body weight was highest when genetic correlation between body weight and egg production was lowest, but on the contrary the smallest negative genetic change in egg production occurred. In populations with negative genetic correlation equal -.2, this method prevented negative genetic change on one trait but also tended to decrease positive change on the other trait.

Restricted selection index showed much the same results as for selection index: that the magnitude of negative genetic correlation affected the mean genetic change of the two traits in opposite ways.

The same evidence also was found when independent culling levels were used.

Mean body weight response was largest when mass selection was used. At generation ten, mean body weight had almost doubled, or increased 75% and 25% when heritability was .4, .3 and .1 respectively. This was accompanied by decrease of egg production and increase of egg weight, the magnitudes depending on the heritabilities and genetic correlations. Populations with the combination of highest heritabilities and genetic correlation showed that egg production was decreased 1.7% per generation.

In most populations selection index and restricted selection index showed comparable responses of mean body weight. Independent culling levels produced slightly smaller responses. Selection index showed no decrease in egg production in populations with genetic correlation equal to -.2.

Restricted selection index produced decreases in egg production 40-50% less than mass selection when the genetic correlation between body weight and egg production was either -.6 or -.4, regardless of the heritabilities.

The relative efficiency for total economic response showed that in all populations when the selection index was considered 100% efficient then, mass selection was about 20% less efficient, independent culling levels was 10% less efficient and restricted selection index was almost as efficient, especially when genetic correlation was high.

During the selection process, in all populations and for all methods of selection, the initial genetic correlations were maintained and the genetic and phenotypic variances and covariances did not change more than trivially. Mass selection and independent culling levels reduced genetic correlations in selected offspring but those differences were clear only when the genetic correlation was high. Selection index and restricted selection index maintained genetic correlations in all cases.

Selection index method showed higher total economic response than either mass selection or independent culling levels, but because of the complexity and impracticality of the index for Indonesian conditions, it shouldn't be the first choice. Genetic parameters needed to construct an index should be made available from the population where the selection is going to be applied, but values of the genetic parameters are still unknown for the native chickens. Furthermore selection index requires identification of individuals along with the record for each measurement used in the index. Present conditions would not permit such identification without major changes in current practices. However, mass selection and independent culling levels are simple and could easily be practiced under present conditions.

If selection is for the improvement of body weight per se then mass selection gives the highest response, but when total economic response is considered, then independent culling levels provide better results. But when independent culling levels are used, after the first stage of selection, at sexual maturity, 25% of the offspring are saved to enter the second stage of selection and later only half of them will be selected for breeding. In mass selection at sexual maturity only 12.5% of individuals are saved for breeding. It is questionable if the additional cost of keeping 12½% more individuals would be paid for by the additional economic return from independent culling. The decrease in egg production is somewhat smaller for independent culling than for mass selection. If the decrease in egg production is considered to be an important problem then, it is questionable if as much as 1.7% decrease per generation by mass selection could be accepted.

When a negative genetic correlation exists and effort is made to prevent negative change of a secondary trait (but not to obtain positive change), then results of this study indicate that application of restricted index selection is not effective when practiced on only one sex.

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