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Efficiency of Selection in Layer-type Chickens by Using Supplementary Information on Feed Consumption

II. Application to Net Income *

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Summary. The value of individual feed consumption records to improve net income through genetic gain was investigated in an egg-type breeding operation. Genetic and phenotype parameters were estimated for body weight, egg mass and feed consumption on 788 layers from two pure lines and 1120 reciprocal crosses. Individual feed records were obtained on all birds over an 8-week test period and on 303 birds over a 24-week period. From the parameter estimates, selection indexes with and without feed consumption records were compared. Also, in lieu of feed records, selection indexes were constructed, which included genetic correlations and phenotypic regressions involving feed records. Although the heritability estimate for the efficiency of feed consumption, independent of body size and egg size, could not be accurately estimated because of the limited amount of data, the results showed that the addition of feed consumption records increased the efficiency of the selection index by 9 %.

Introduction

Feed represents about two-thirds of the cost of egg production. The question is whether breeders can lower feed costs by breeding for higher efficiency. A hen that lays 60 gram eggs at the rate of 80 % using just 100 grams of a balanced 17 % protein diet per day converts only about 1/4 of the dietary energy and 1/3 of the dietary protein into egg mass. Hence, at best, a high producing laying hen is an inefficient converter of feed into human food. On the other hand, because part of the individual variation in efficiency has a genetic basis, it is reasonable to believe that genetic efficiency can be improved.

The feed consumed by a laying hen is used mainly for the production of egg mass and for body maintenance. In general, hens which lay at the highest rate with the smallest body size are the most efficient feed converters. Hence, body size and egg mass output should determine most of the genetic variation in feed consumption.

If hens differ genetically in their ability to digest and metabolize feed and(or) if they differ in the amount of feed wasted at the hopper, a third genetic component of feed consumption can be defined, which we call the residual component, i.e., the difference between the total feed consumed and that used for egg mass output and body maintenance.

The main experimental problem is to estimate the degree of heritability of the residual component (h_U^2). If h_U^2 is much greater than zero then breeders should profit greatly by keeping individual feed consumption records. On the other hand, if $h_U^2 = 0$ this would not necessarily mean that records on feed consumption would have no value. Rather such records could enhance efficiency as an "indicator trait" (Rendel 1954) by making selection for egg mass and body size more effective.

Arboleda et al. (1976) approached the problem of egg production efficiency by comparing the genetic gain in a selection index with and without information on feed consumption. They developed 4 selection indexes.

Selection index Y_1 is designed to maximize income over feed costs (IF) from individual hen information on body size (W), egg mass output (M) and feed consumption (F). In index Y_2 feed consumption is evaluated by the genetic correlations of F with W and F with M. In Y_3 independently estimated regressions of F on W and F on M are used without feed consumption records. Y_4 maximizes income (I) when information is used only on W and M.

To aid the reader in distinguishing the 4 indexes, a shorthand description is used for each. See the footnote of Table 11 or Table 1 of the companion paper (Arboleda et al. 1976).

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Materials and Methods

From an experiment in which feed consumption on individual birds was recorded, parameters were estimated and then applied to the 4 selection indexes described.

The experimental population[1] included two pure White Leghorn lines, A and B, and their reciprocal crosses, AB and BA, where the male line is designated by the first letter of the cross. Both pure lines had been maintained by inbreeding and selection in earlier generations, but more recently as closed flocks with selection for several generations. Lines A and B differed in adult body size, production rate and age at first egg. Both of these lines originated through three generations of full and half-sibbing. With some additional inbreeding due to being maintained as closed populations for several years, the coefficient of inbreeding would be somewhere in the range of 0.6 to 0.75 for each of the lines.

In general, the same males sired both the pure line and the F_1 cross line pullets except that five more males per line were used for producing pure than the cross-line pullets. These additional five males were selected from those used in producing the cross-line progeny the previous generation. Cross-line progenies came from a single hatch of eggs saved over 21 days but the pure line progenies came from three hatches of 14 day saves each. All matings were random except that full or half-sib matings were avoided in the pure line matings.

Only pullets surviving to the end of the feeding test were included in the statistical analyses. The total numbers were: Line A 573, Line B 215, Cross AB 471 and Cross BA 649 for a total of 1838. These numbers are less than hoped for because of excessive Marek's Disease mortality.

Housing Scheme and Feeding Procedure

At 5 months of age, the cross-line pullets were randomly assigned to 10 adjoining rows of 150 individual cages each. After housing, in addition to production records, egg quality traits were recorded on eggs collected over a 5-day period of the 35th week of age; also individual body weights were then taken. The cross-line pullets were fed a 19 % protein ration during the test period. The pure-line pullets, being about 2 months younger than the cross-lines, were housed 2 months after the cross-line pullets in a separate cage house. Each dam family was divided into two with one group fed a 14 % protein diet and the other a 19 % protein diet. All pullets were fed individually for two 4-week feeding periods separated by an 8-week interval. In addition, 303 of the 573 layers in line A, were individually fed for a 24-week test period.

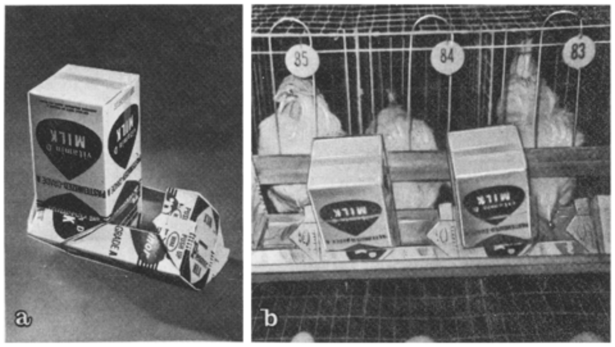

Fig. 1. a) Feed hooper constructed from 2 milk cartons b) Hoppers placed in front of individually caged layers

Measurement of Individual Feed Consumption

The routine for obtaining individual feed records was developed in a preliminary experiment. The aim was to permit a single worker to handle all experimental birds with minimum effort. A special individual feeder, designed to control spillage, consisted of a hopper and a trough fashioned from two half-gallon milk cartons (Fig. 1). Each feeder, properly identified, was filled with 1200 grams of feed weighed out on an automatic scale used by the packaging industry.[2] From 6 to 8 feed rations could be weighed per minute with a minimum error of ±4 grams. The uneaten feed was "weighed back" on a balance with readings rounded to the nearest gram.

Feeders showing cage spillage in the metal trough were adjusted and the spilled feed was returned to the feed hopper. Most feeders required no adjustment. Six days after the start of the test, nearly empty feeders were replaced with a full hopper of 1200 g. On the final day of the test, the leftover feed was collected and stored until weighed back. Individual feeders were then removed, and the birds were returned to a mass feeding regime.

Statistical Procedures

The significance of the regression of feed consumption on each trait was tested sequentially by fitting the variables, body weight, egg mass, age at maturity, albumen height and specific gravity (Kempthorne 1952).

Also a test of significance for the homogeneity of partial regression coefficients of feed consumption on either egg mass of body weight was performed sequentially by fitting first a full model and then a reduced model, restricted by the hypothesis of homogeneity, and finally testing the significance of the sum of squares of this difference (Brown 1970).

The estimates of phenotypic and genetic variances of each trait were derived from an hierarchical analysis of variance. For the pure lines, the traits were adjusted for hatch and ration effects. Heritabilities were estimated from both sire and dam components of variance. Approximate standard errors of the heritability estimates were based on formulas given by Dickerson (1969). Genetic correlations also were computed from sire and from dam components of co-

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[1] Stocks were made available for this study through the courtesy of DeKalb AgResearch, Inc., DeKalb, Illinois.

[2] "Net Weigher Model 610N" manufactured by the Exact Weight Scale Co., Columbus, Ohio.

variance. Phenotypic correlations were computed by the usual product-moment method.

The component of residual feed consumption was estimated as

$$r_i = F_i - \hat{F}_i$$

where:

F_i = feed-consumption record of the i^{th} individual,

$\hat{F}_i = \hat{F}_m + \hat{\beta}_1(W_i - \overline{w}) + \hat{\beta}_2(M_i - \overline{m})$, the predicted feed consumption of the i-th individual from the least squares regression equation

$\hat{F}_m$ = estimated mean feed consumption

$\hat{\beta}_1$ = estimate of the partial regression of feed consumption on body weight (W) with mean $\overline{w}$

$\hat{\beta}_2$ = estimate of the partial regression of feed consumption on egg mass (M) with mean $\overline{m}$.

To test for genetic variation the residuals (r_i) were subjected to an analysis of variance using the same sire and dam hierarchical model already described.

Results

Cost of Individual Feed Consumption Records

The approximate number of pullets individually feed per month and the corresponding cost of labor for individual feeding and for the construction of the feed hopper are shown in Table 1.

Most of the cost of the individual feeding hoppers was labor. The cost of the automatic weighing machine, being a fixed cost, was excluded. At the conclusion of the feeding test, we believed that a larger number of birds could have been tested. Also the cost of assembling the feeders could have been lowered if certain precautions (e.g., debeaking and proper trough placement) were taken before the feeding test. By taking these factors into consideration, the estimated cost of the individual feed consumption record was modified as shown in Table 1.

The means and standard deviations of the traits measured and the number of survivors in the lines and crosses fed individually for 8 weeks are presented in Table 2. The means of lines A and B differed significantly for all traits observed. Line A was heavier in body weight, produced larger and more eggs and consumed more feed than line B within the 8-week feeding test period. Line A commenced laying about 18 days earlier than line B. Albumen height and specific gravity were slightly higher in line B than line A indicating substantial genetic diversity between the lines.

The crosses also differed significantly. AB was smaller, started laying eggs 7 days earlier, produced more egg mass and consumed more feed than BA. AB also had higher mean albumen height but lower mean specific gravity.

Because the pure lines were hatched later and housed separately from the crosses, a strictly valid comparison between them was not possible. As expected, however, the crosses were heavier, produced more egg mass and consumed only 94 g more feed than the pure lines. Line A, although lighter in weight and producing less egg mass than either cross, consumed 224 g more feed than the average of the two crosses. The higher performance of the crosses is presumably a consequence of the hybrid vigor.

The means and standard deviations of body weight, egg mass and feed consumption of the 303 pullets in line A individually fed for 24 weeks are presented in Table 3.

The partial regressions of feed consumption on the different traits are shown in Table 4. Regressions on body weight and on egg mass were highly significant as expected. Age at first egg had little effect on variation of feed consumption. The regression on albumen height was significant at $P < 0.01$ in AB. The regression on specific gravity was also highly significant in both B and AB.

Table 5 gives the percentage contribution of each trait to the sum of squares of feed consumption when included as an independent variable in the regression model. In general, the joint contribution of the five independent variables accounted for 40 to 51 % of the total sum of squares of feed consumption.

Table 6 gives the analyses of covariance of feed consumption for the different lines and crosses. The joint contribution of body weight and egg mass as independent covariables and the additional contribution of age at first egg and the egg quality traits to the sum of squares of feed consumption are also shown in the tables. The quantity R(W and M) represents the reduction in the sum of squares of feed consumption accounted for jointly by regression on body weight and egg mass as independent variables in the regression equation; R(A,H,S) represents the reduction in sum of squares accounted for by age at first egg, albumen height and specific gravity. Age at first egg and the egg quality traits together accounted for a significant

Table 1. Cost of an individual feed consumption record (1969)

Item	Actual	Modified
Approximate number of individuals fed per month	1700	2000
Cost of labor for feeding	$ 600	$ 600
Assembly cost of individual feeders	$ 100	$ 50
Total cost of individual feed consumption per month	$ 700	$ 650
Cost of individual feed consumption record per bird per month	$ 0.41	$ 0.32

Table 2. Means and standard deviations of traits and number of pullets in the 8-week feeding test

	Lines and Crosses			
Traits	A	B	AB	BA
Body weight (gm)	1551 ± 176	1441 ± 167	1570 ± 163	1590 ± 168
Egg mass (gm)	1974 ± 559	1550 ± 582	2562 ± 347	2412 ± 443
Feed consumption (gm)	5986 ± 720	5330 ± 632	5838 ± 645	5667 ± 676
Age at first egg (days)	152.46 ± 13.54	170.44 ± 12.85	153.71 ± 13.48	160.72 ± 16.88
Albumen height (mm)	47.16 ± 6.99	48.73 ± 6.94	45.02 ± 5.22	41.42 ± 4.78
Specific gravity (%)	74.10 ± 5.09	77.99 ± 4.83	74.09 ± 4.76	76.81 ± 4.38
Number of pullets	573	215	471	649

Table 3. Means and standard deviations of the traits observed in line A pullets in the 24-week test

Traits	Mean ± standard deviation (gm)
Body weight	1520 ± 168
Egg mass	5704 ± 1757
Feed consumption	17160 ± 2385
No. of pullets	303

component of variance in feed consumption in line B and in cross AB.

The joint contribution of body weight and egg mass to the total sum of squares of feed consumption ranged from 38.7 to 46.7 % so that other factors, including residual, accounted for 53 to 61 % of the total sum of squares. Because age at first egg and the two egg quality traits accounted for only a small portion of the variance of feed consumption, only body weight and egg mass were retained as the independent variables in further regression analyses of feed consumption.

Other factors possibly influencing the regression of feed consumption on body weight and egg mass also were studied but to save space only a brief statement will be given here. Differences in the regression between the 2 pure lines or between the 2 cross lines were nonsignificant. On the other hand, the difference in regressions between the average of the pure lines and the average of the 2 crosses was significant ($P < 0.01$), but this could be a house effect since the pure lines and crosses were in different houses.

The two rations (14 % vs. 19 % protein) were compared in the pure lines only. The regression of feed consumed on body weight was significant ($P < 0.01$) in line A but not in line B.

Because of the rather small number of birds in line B and the possibility that they may have been more severely affected by Marek's disease, only line A and the two reciprocal crosses, AB and BA, were used to obtain pooled estimates of the parameters.

The coefficients of variation and phenotypic correlations for W, M and F are presented in Table 7. Egg mass was consistently the most variable trait. Also line A was more variable than the crosses as expected because the performance of crosses is usually more uniform. The phenotypic correlations between body

Table 4. Partial regression coefficients of 8-week feed consumption on different traits as independent variables of a multiple regression equation

Variable	Lines and crosses			
	A	B	AB	BA
Body weight (g)	1.92 **	1.72 **	1.82 **	1.60 **
Egg mass (g)	0.51 **	0.53 **	0.70 **	0.81 **
Age at first egg (days)	0.97	- 3.43	0.39	-0.92
Albumen height (mm)	-1.59	1.15	-12.16	-6.92
Specific gravity (%)	-6.36	-19.92 *	-17.55 **	-0.33

** $P < 0.01$
* $P < 0.05$

Table 5. Percent sum of squares of 8-week feed consumption due to regression on the different independent variables in the multiple regression equation

Variable	Lines and crosses			
	A	B	AB	BA
Body weight	20.65	19.18	20.46	15.85
Egg mass	11.93	11.41	13.75	25.68
Age at first egg	0.02	0.28	0.06	0.05
Albumen height	0.02	0.00	0.93	0.23
Specific gravity	0.16	1.88	1.61	0.00
All variables	39.77	50.68	43.49	46.46

Table 6. Sources of variation contributing to the reduction (R) in total sums of squares in feed consumption from regression (percent)

Source of variation	Lines and crosses			
	A	B	AB	BA
Total	100.-	100.-	100.-	100.-
R (all variables)	40.7 **	52.0 **	43.5 **	46.5 **
R (W and M)	38.7	46.7 **	-	-
R (A,H,S)	0.2	2.6 *	2.3 *	0.3
R (residual)	59.3	48.0	56.5	53.5

W = Body wt. M = Egg mass A = age at 1st egg H = albumen height
S = specific gravity of eggs

weight and egg mass, ranging from 0.04 to 0.15, were consistently lower than those between feed consumption and body weight or between feed consumption and egg mass.

Estimates of genetic parameters from the sire and dam components of variance are given in Table 8. These estimates were obtained from sire and dam components pooled over genetic groups to reduce sampling variance even though it is realized that the true population parameters might be different for the different genetic groups. The heritabilities for W were highest and for the residual consistently the lowest. Except for body weight the heritability estimates from the dam component were consistently higher than those from the sire component suggesting possible importance of dominance. The estimates of the heritability of body weight and egg mass are well within the range of those published in the literature (Kinney 1969, Waring et al. 1962, Nordskog et al. 1974).

Estimates of genetic correlations between F and W were higher than those between F and M. Genetic correlations between the residual and M differed widely.

Table 7. Coefficients of variation and phenotypic correlations

	Line and crosses				
	A		AB	BA	Mean
Coefficients of variation	8-week test	24-week test			
Body weight (W)	0.11	0.11	0.10	0.10	.10
Egg mass (M)	0.28	0.31	0.13	0.18	.22
Feed consumption (F)	0.12	0.14	0.11	0.11	.12
Phenotypic correlations					
WM	0.11 **	0.04	0.15 **	0.09 **	0.10 **
WF	0.49 **	0.60 **	0.52 **	0.44 **	0.51 **
MF	0.43 **	0.46 **	0.46 **	0.55 **	0.48 **

** $P < 0.01$

Table 8. Genetic parameters as estimated from the sire plus dam components pooled over genetic groups A, AB and BA

	From Sire component (80) *	From Dam component (558) *
Heritabilities		
Body weight (W)	0.68 ± 0.18	0.66 ± 0.18
Egg mass (M)	0.06 ± 0.05	0.28 ± 0.12
Feed (F)	0.20 ± 0.10	0.47 ± 0.15
Residual (R)	0.01 ± 0.00	0.29 ± 0.21
Genetic correlations		
WM	0.60	0.11
WF	0.94	0.71
MF	0.60	0.43
WR	0.27	0.27
MR	-0.41	0.22

* Pooled degrees of freedom for error are 1052

The low heritability estimated for the sire component residual, however, suggests that the true genetic correlations with the residual are also close to zero with large sampling errors.

As yet, there does not seem to be any formally published work on genetic studies of feed consumption of adult laying hens. Von Krosigk and Pirchner (1964) presented such a study at the British Poultry Breeders' Roundtable in England. From data on 545 cross line pullets from two White Leghorn lines, they estimated that the heritability of F was 0.15 and the respective genetic correlations with W and M were 0.62 and 0.24, slightly lower than those obtained in this study.

The phenotypic standard deviations and partial regressions used in constructing the different selection indexes are given in Table 9. These are pooled averages of line A and crosses AB and BA. The σ for M and F are adjusted to a standard 56-week production period obtained by multiplying the 8-week test values by 7. The test values for the 24-week period were similarly adjusted to a standard period by multiplying by 2.33. Likewise, the partial regression of feed consumption on body weight estimated from the 8-week test was multiplied by 7 to adjust to a standard. Thus, the partial regressions specify the grams of feed required to maintain a gram of body weight for the entire 56-week test.

It should be pointed out that these adjustments to 56 weeks are only approximate because these were arrived at by extrapolation from two 4-week periods. To measure feed consumption for the full 56 days did not seem feasible.

Table 9. Phenotypic standard deviations and partial regressions used in constructing the different selection indexes

Trait	Standard deviation	Partial regression of F
W (g)	172	12.01
M (g)	3354	0.69
F (g)	4917	----

Table 10. Annual average prices of cull hens, eggs and feed in 1969[a]

Item	Unit	Value per unit (cents)	Relative economic value
Cull hens	lb	9.70	
	gm	0.019	2.38
Eggs	doz	40.00	
	egg	3.33	
	gm	0.058[b]	7.25
Layer feed	lb	4.00	
	gm	0.008	1.00

[a] Based on 1969 prices of eggs, feed and cull hens reported by the U.S. Department of Agriculture, Economic Research Service (1970).

[b] Assumes one dozen eggs = 24 ounces.

Table 11. Expected gain from different selection indexes

	Selection indexes *			
Criteria	$Y_1 \sim$ Y(IF:W,M,F)	$Y_2 \sim$ Y(IF:W,M,r)	$Y_3 \sim$ Y(IF:W,M,b)	$Y_4 \sim$ Y(I:W,M)
Expected gain (cents)	21.78	20.62	20.61	20.00
Expected gain relative to Y(I:W,M) (%)	109	103	103	100

* A shorthand description of each index is given in parenthesis. Thus, $Y_1 \sim$ Y(IF:W,M,F) means that income over feed costs is maximized and selection is based on W, M and F. In Y_2 and Y_3, r and b are substituted for F. In Y_4, income, I, is maximized and selection is based solely on W and M.

From the pooled estimates of the parameters (Tables 7, 8 and 9) and the relative economic values (Table 11) selection indexes were computed.

Table 10 gives the prices of eggs, cull hens and feed for 1969 from which relative economic values were computed.

Table 11 gives the expected gain in IF or I from mass selection with the different selection indexes. The expected gains relative to $Y_4 \sim$ Y(I:W,M) also are given.

The highest expected gain in income over feed cost was on index, $Y_1 \sim$ Y(IF:W,M,F); expected gains from $Y_2 \sim$ Y(IF:W,M,r) were essentially the same as those expected from $Y_3 \sim$ Y(IF:W,M,b). This indicates that predicting the breeding value of feed consumption from phenotypic regression information on body weight and egg mass (as in Y_3) is equivalent to using feed data to estimate genetic correlations. However, the estimated from Y_2 or Y_3 over Y_4 was only 3 %.

Discussion

Because the genetic variance of feed consumption is a function of the genetic effects of body weight, egg mass and a residual, the intrinsic value of including feed consumption as a variable in a selection index is reflected by the amount of genetic variation in the residual component. To study the residual component, records of feed consumption are required.

In this study, the estimated heritability of the residual was low but the standard error was high. Hence, it is tempting but premature to conclude that most, if not all, of the residual variance is due to random environmental error.

Results of studies on the regression of income over feed cost on economic traits of entries from random sample egg production tests also offer some evidence on the contribution of residual feed consumption. Nordskog (1960) reported that 93 % of the variation in income over feed cost could be accounted for by differences in body weight, egg production and egg size. McNally and Foster (1969) reported that 99 % could be accounted for on this basis. Since other traits of economic importance (e.g., egg quality) may contribute to the variation in income over feed cost but were not included as independent variables in the regression model, it seems that differences in feed consumption can account for only a small part of the remaining unexplained variation in net income.

The failure of this study to demonstrate positive evidence for genetic differences in the residual, however, does not wholly rule out the possibility of true genetic differences in digestive and metabolic efficiency independent of body weight and egg mass. Admittedly, owing to the high mortality from Marek's Disease, the populations studied were probably too small to expect consistent estimates of genetic parameters involving the residual component of feed. It would seem worthwhile to repeat the experiment with a large, and perhaps more typical, population of layer type breeders.

Nesheim (1966) reviewed the results of experiments showing that breeds, strains and individual birds may vary in the utilization of nutrients. He pointed out that the efficiency of the utilization of protein or energy in a diet depends on the metabolism of many individual compounds involving a large number of enzyme-controlled reactions which in turn, are probably under genetic control. Because of the highly complicated metabolic reactions, however, he predicted that selection for better protein utilization is not likely to meet with success.

Wilson's (1969) study on genetic aspects of feed efficiency for weight gains in broilers suggested that genetic factors, in addition to body weight, may be important. He reported that selection for gain in body weight was only 75 % as efficient in improving feed efficiency as direct selection for a low feed/gain conversion ratio. In beef cattle, Koch et al. (1963) estimated the heritability for feed consumption, adjusted for differences in gain, to be 0.28. They conluded that selecting for feed efficiency would increase feed efficiency and increase daily gain without increasing feed consumption.

The present study leaves open the possibility that even a relatively small amount of residual genetic variation may be sufficient to justify measuring feed consumption. With family or sib selection the value of feed consumption records would be enhanced because such records would increase the accuracy of identifying superior genotypes and at the same time, the cost of measurement would be lowered.

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