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ON THE VALIDITY OF THE THEORY OF GENETIC CORRELATION IN THE FOWL SELECTION EXPERIMENTS WITH TWO STRAINS OF FAYOUMI CHICKENS

By

M. A. El-Hossari,

Individual selection was carried out for seven generations to increase body weight at eight weeks of age in a strain of Fayoumi chicken, and family selection was practiced for five generations to increase egg number in another strain. An unselected population was used for genetic analysis and to estimate direct and correlation responses to selection more accurately. The genetic correlations were estimated from the selected and unselected populations in order to test the validity of the theory of genetic correlation.

In both selection experiments there were insignificant differences between the realised genetic correlation estimates obtained from the two selected strains and the expected estimates obtained from analysis of covariance. This supports the validity of quantiiative genetic theory. However, in some cases the agreement in the magnitude of genetic correlations were lacking for traits of low heritabilities. This indicates that the assumption underlining the theory of genetic correlation needs more explanation, although the theory has been valid in the general argument of these seletcion experimets.

The theory of genetic corrlation was developed, on a purely qualitative basis, by Mather (Wigan and Mather, 1942; Mather and Harrison 1949), and on quantitative basis by Smith (1936) and by Hazel (1943) from the respective fundamental formulation of biometrical genetics of Fisher and Wright. The explanation of the subject was discussed by lerner (1958) and by Falconer (1960) in terms of correlated responses to selection.

There several different genetic mechanisms underlying correlated responses. The most obvious are pleiotropy and linkage (Lerner, 1958).

The theory was tested by many workers, but the complete understanding and the precision of the validity of the theory is still lacking. Unfortunately, in the literature, the genetic correlation is given without standard errors. There have not yet been enough studies dealing with correlated response, and to what extent the observed correlated response to selection agrees with the theoretical one.

Close agreement between observed and predicted correlated responses was shown by Reeve and Robertson (1953) when studying the genetic correlation between the thorax length and wing length in Drosophila melanogaster. They found that the genetic corrleations based on selection for large

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Poultry Research Dept., Ministry of Agriculture.

and small size were in close agreement as 0.71 and 0.73. They found also agreement between the estimates from selected and unselected population which showed that the correlated responses were very close to what would have been predicted from the genetic analysis of the unselected population.

Falconer (1954) selected for body weight and for tail length in two different lines of mice. He found agreement between the realized genetic correlations between these traits in both lines (.62 vs .57). He concluded that the theory upon which the estimate of correlations is based, accounts fully for the correlated response in his experiments. However, Clyton et al. (1957) did not find such agreement and showed that the expected response was small and was liable to be obscured by random drift.

On chicken, Jaap et al. (1962) did not find agreement between expected (predicted and observed correlated response in low heritable traits (egg production, broodiness and height of albumin), when they selected for body weight at 8 weeks of age. Similarly, Ideta and Siegel (1966) selecting on the same trait, found agreement only in the traits of high heritabilities (body weight and egg weight), but the agreement was lacking in traits of low h^2 (age at sexual maturity, and egg number).

These results showed that, in some cases, although the agreement in sign was found, it was not close with regard to the size of genetic correlation. Additional selection experiments are needed to throw more light on the magnitude of genetic correlation in breeding under the ordinaty farm conditions. In this paper, the theory of genetic correlation was tested in two different selection experiments on Fayoumi chicken to increase body weight and to increase egg number.

Material and Methods

Selection experiments were carried out in two strains of Fayoumi chicken in Fayoum Poultry Experimental Station. One to increase body weight at 8 weeks of age (the growth strain), and the other to increase egg number to the first of January (the production strain). Seven generations of individual selection were practised in the former strain, and five generations of family selection in the latter. Since the beginning of selection experiments a randombred control (unselected population) was established for comparison and to estimate the genetic changes in the characters more accurately. The samples analysed to estimate the genetic correlations were taken from the pedigree unselected population.

Methods of analysis

The genetic correlation was estimated by two methods :

1. *Covariance analysis*: The estimates obtained according to the model shown by Lerner (1950). The formula used is

$$r_{Gxy} = \frac{(\mathrm{Cov}_s\ .xy + \mathrm{Cov}_d\ .axy)}{\sqrt{(\sigma^2_s\ .x + \sigma^2_d\ .x)\ (\sigma^2_x .y + \sigma^2_d\ .y)}}$$

where :

r_{Gxy} is the genetic correlation between selected trait x, and correlated trait y,

Cov_S . xy and Cov_d , xy are the covariance component due to dams and sires respectively,

σ^2_S .x, σ^2_d .x, σ^2_S .y, and σ^2_d ,y are the variance components due to sires and dams for traits x and y in respective order.

The standard errors were estimated according to the method shown by Robertson (1959).

2. *Realised genetic correlation* : The estimates are obtained from the direct response to selection in trait x, using the method shown by Nordskog and Festing (1962).

The equation derived as :

(*a*) For mass selection,

$$r_G = \frac{\Delta \bar{G}y}{\Delta \bar{G}x} = \frac{h^2x}{h^2y} = \frac{\sigma x}{\sigma v}$$

(*b*) For family selection,a

$$r_G = \frac{\Delta \bar{G}y}{\Delta \bar{G}x} = \frac{h^2}{h^2y} = \frac{\sigma x}{\sigma y} \sqrt{\frac{2 + (n - 1)\, h^2y}{2 + (n - 1)\, h^5x}}$$

where $\Delta\ \bar{G}x$ and $\Delta\ \bar{G}y$ are the direct and correlated responses, estimated from the difference between the performance of the selected strain and the randombred control.

h^2_x and h^2_x are the realised heritabilities estimated from correlated responses to selection (Falconer, 1960 ; Ideta and Siegel, 1966).

σ x and σ y are the standard deviations of traits x and y, and (n) is the size of the dam family.

The traits measured :

4 Wk.	: Body weight of 4 weeks of age·
8 Wk.	: Body weight at 8 weeks of age.
12 Wk.	: Body weight at 12 weeks of age.
S.M.	: Age at sexual maturity (at first egg).
M.B.W.	: Body weight at sexual maturity.
M.E.W.	: Egg weight at sexual maturity.
12.E.W.	: Egg weight at 12 months of age.
Pause 5	: Unproductive days during five months (Dec. to April).
P_1	: Egg number in the first 21 weeks production.
P_2	: Egg number to 12 months of age.
P_3	: Egg number to the first of January.
P_4	: Egg number to the first of June.

Results and Discussion

The theory of genetic correlation was tested in this study by comparing the genetic correlation estimates obtained from the two selected strains with those obtained from the genetic analysis of the unselected population. That is to say, the validity of the theory in breeding depends on the agreement between the theoretical estimates obtained from the analyses of covariance and those obtained from selection responses.

The following table shows the estimates of the genetic correlations obtained from the two methods discussed :

(*a*) from direct and correlated responses (realiezed genetic correlation $r_G 1$ to selection for high body weight a 8 weeks of age and to selection for high egg number to January the first.

(*b*) from the analysis of covariance (the theoretical estimate $r_G 2$).

GENETIC CORRELATION ESTIMATES

Traits	(x) 8-week Body Weight (8 Wk.)		(x) Egg Number to January the first (P_3)	
(y)	Expected	Observed	Expected	Observed
4 Wk.	0.923 ± .024	1.117	—	—
12 Wk.	0.900 ± .025	0.868	—	—
S.M.	0.150 ± .070	0.282	—0.800 ± .084	—0.530
M.B.W.	0.370 ± .094	0.426	—0.328 ± .105	—0.540
M.E.W.	0.115 ± .074	0.214	—0.570 ± .134	—0.588
12.E.W.	0.155 ± .069	0.198	0.073 ± .021	—0.269
Pause 5	—0.053 ± .021	—0.009	—0.460 ± .112	—0.696
P_1	0.664 ± .070	0.189	1.000 ± .000	1.000
P_2	—0.063 ± .021	—0.037	1.000 ± .000	.969
P_3	0.418 ± .081	0.128	—	—
P_4	0.160 ± .068	—0.133	1.000 ± .000	1.000

(x) : Selected trait.

(y) : Correlated traits (for symbols see "the traits measured").

Selection on the growth strain indicates that there is no difference in sign between the two estimates. Better agreement in magnitude between the realised genetic correlation and the theoretical one can be noticed with regard to S.M., M.B.W., and M.E.W. which showed high h^2, than with egg production measurements which showed low h^2 (Hossari, 1966). This supports the work of Jaap et al. (1962) and Ideta and Siegel (1966), on chicken, who found that the agreement was lacking in characters of low h^2.

Selection on the production strain shows that thare is also agreement between the realised genetic correlation estimates of egg number with the other egg number measurements, and those estimates obtained from genetic analysis. However, this agreement was not close in magnitude with some traits, S.M., M.B.W. and 12.E.W. Ideta and Siegel (1966), found also differences in the size of some genetic correlation estimates although there were agreements with regards to the sign of the genetic correlations.

Over all the estimates in the both selection experiments, there is insignificant difference, as tested by Chi square method, between the genetic correlation estimates obtained from direct and correlated responses to selection (observed) and the estimates obtained from genetic analysis of covariance (expected). This supports the work of Falcener (1954) on mice who found agreement between the realised genetic correlations obtained from the two selected lines, and Reeve and Robertson (1953) on Drosophila who found close agreement between the genetic correlation estimates obtained from selected and unsetected populations. These support the validity of the theory of genetic correlations.

The genetic correlations of both methods between the selected measurement and the other measurements of early body-weight and egg number are very large (about unity). Therefore the genetic correlations are likely to be due to pleiotropy at least to a degree. This supports the suggestion of Lerner (1958) who reported that pleiotropic effect was important for the genetic correlation between the different parts of a character. In the other cases particutarly with respect to egg number trait where the realzed genetic correlations are small, the cause of linkage would be a possible explanation. Lerner (1958) reported that genetic correlation, which is cauced by linkage, is likely to decrease in magnitude through recombination with a consequent diminution of the correlated response.

It would be fair to conclude that in general, the evidence in this study supports the validity of quantitative genetic theory. However the lack of the agreement with respect to the magnitude of some genetic correlative indicates that the assumption underlining the theory of genetic correlation needs more explanation although the theory has been valid in the general argument of the study.

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صحة نظرية التلازم الوراثى فى الدجاج
تجارب الانتخاب على سلالتين من الدجاج الفيومى

للدكتور محمد على فتح الباب الحصرى *

الملخص

أجرى الانتخاب الفردى لمدة سبعة اجيال لزيادة وزن الجسم فى عمر ٨ اسابيع فى سلالة من الدجاج الفيومى ، كما أجرى الانتخاب العائلى لمدة خمسة اجيال لزيادة عدد البيض حتى أول يناير من موسم الانتاج فى سلالة أخرى من هذا الدجاج . كما استخدم قطيع مقارنة بدون انتخاب للقيام بالتحليلات الوراثية والتقدير التغيرات الوراثية فى الصفات المختلفة نتيجة لهذا الانتخاب . وقد قدر التلازم الوراثى بين الصفات فى السلالتين المنتخبتين ، وكذلك فى السلالة الغير منتخبة ، وقورنت النتائج لمعرفة مدى صحة نظرية التلازم الوراثى .

وقد لوحظ عدم وجود فرق معنوى بين تقديرات الارتباط الوراثى بين الصفات الناتجة من السلالتين المنتخبتين (نتيجة التغيرات الوراثية) وبين نظائرها الناتجة من السلالة الغير منتخبة(نتيجة للتحليلات الوراثية)، ويبرهن ذلك على صحة تطبيق نظرية « الوراثة الكمية » ، ولكن هناك بعض الحالات لم ينطبق فيها حجم التلازم الوراثى فى السلالات المنتخبة وغير المنتخبة خصوصا بين الصفات ذات المعامل الوراثى الصغير ، وهذا يدل على أن صحة نظرية « التلازم الوراثى » لا زال يلزمها بعض التفسيرات عند تطبيقها أثناء عمليات الانتخاب ، رغم ان هذه النظرية تتفق بوجه عام مع نتائج تجربتى الانتخاب السابقتين . فى هذا القطيع .

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