

# THE GENETIC IMPROVEMENT IN POULTRY THROUGH CROSSBREEDING DESI WITH RHODE ISLAND RED—THE USE OF DISCRIMINANT FUNCTION IN NON ORTHOGONAL FACTORIAL EXPERIMENT

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## INTRODUCTION

Kumar [4] had a comparative study on the average performance of Desi, Rhode Island Red and their crosses for their growth, age at first egg, rate of lay, egg quality and many other economic characters and found, using univariate comparisons, that for some characters Desi were superior and for others the crossbreds. Since characters associated with growth, egg production and egg quality traits are important in poultry, these must be considered together in making comparisons among different genetic groups or in measuring genetic improvement due to crossbreeding. This can be done by using the technique of discriminant function in factorial experiment following multivariate extension (Tatsuoka, [6] of weighted mean squares ANOVA (Yates, [7]). The present study using such a technique estimates the genetic improvement in poultry, through crossbreeding Desi with Rhode Island Red (Details of the computation procedure are given in the Appendix). The technique used here is more appropriate than that used by Narain [5] in sheep by converting two factor (years and genetic groups) experiment into single factor one by eliminating the effects of other factor (years), which is not proper when the factors may interact, so as to follow Fisher's [3] discriminant function analysis with single factor experiment.

Material and Method—Data for the present study were taken from the project 'Collection and evaluation of native fowl germ plasm' running at Haryana Agricultural University, Hissar during the

year 1966-71. In all 212 sets of records on growth, reproduction and egg quality traits *viz.* day old body weight ( $X_1$ ), 12 week old body weight ( $X_2$ ), age at first egg ( $X_3$ ), rate of lay ( $X_4$ ), egg weight ( $X_5$ ), and egg shape ( $X_6$ ) as defined in Kumar [4] were taken from 99 Desi and 119 RIR  $\times$  Desi ( $F_1$ ) chicks hatched in ten consecutive seasons during the year 1968. The data for rate of lay being in percentage was transformed into arc-sine. The data fell in  $2 \times 10$  classifications based on genetic groups and season of hatching effects with unequal cell frequencies and so genetic improvement in RIR  $\times$  Desi ( $F_1$ ) over Desi was obtained using the technique of modified version of discriminant function in factorial experiment, and the computational procedure developed for this study has been described in Appendix.

*Result.* The discriminant function was obtained as :

$$X = -0.088X_1 + 0.007X_2 - 0.018X_3 + 0.010X_4 + 0.497X_5 + 0.492X_6 \quad \dots(3)$$

and the eigen value for testing the significance of improvement was computed as :  $\lambda = 0.242$ .

The estimated means of traits  $X_1, X_2, X_3, X_4, X_5$  and  $X_6$  for Desi and RIR  $\times$  Desi ( $F_1$ ) crossbreds; and the improvement in crossbreds over Desi along with its test statistic- $F$  value were computed following Yates [7] and are shown in Table 1.

TABLE 1

Estimated means for different characters along with compound value and improvement in crossbreds over Desi

Trait	Mean values		Improvement	Calculated value	
	Desi	RIR $\times$ Desi		F	$\chi^2$
Day old body weight (g) : $X_1$	32.51	32.70	0.17	<1	—
12 week old body weight (g) : $X_2$	533.16	589.23	56.07	10.684**	—
Age at first egg (days) : $X_3$	209.76	203.66	- 6.10	1.746	—
Per cent rate of lay (arc sine) : $X_4$	34.41	36.06	1.65	1.704	—
Egg weight (g) : $X_5$	47.16	50.23	3.07	26.348**	—
Egg shape : $X_6$	72.59	74.24	1.65	9.602**	—
Compound value : Y	56.59	59.53	2.84 (5%)	—	269.04**

\*\* P &lt; 0.01

The compound values for Desi and crossbreds computed from discriminant function (3) and mean values of traits ; and so improvement in compound value along with its test statistic- $\chi^2$  value obtained from equation (2) (see Appendix) are also shown in the same table.

It is apparent from the table that crossbreeding with Rhode Island Red caused significant improvement in growth trait, 12 week body weight and egg quality traits, egg weight and egg shape ; and the improvement in overall performance was 2.84 (5%) which is highly significant.

#### SUMMARY

Advantage of crossbreeding Desi with Rhode Island Red has been assessed here by estimating the measure of genetic improvement based on economic characters: (1) day old body weight, (2) 12 week old body weight, (3) age at first egg, (4) rate of lay, (5) egg weight, and (6) egg shape, using the technique of discriminant function in non-orthogonal factorial experiment. The genetic improvement obtained was highly significant. The study indicates that crossbreeding Desi chicken with exotic Rhode Island Red is quite advantageous.

#### REFERENCES

- [1] Bertlett, M.S. (1947) : Multivariate Analysis. *J. Roy. Statis Soc. Series B*, 9, 176.
- [2] Federer, W.T. and Zelen, M. (1966) : Analysis of multifactor classifications with unequal number of observations. *Biometrics* 22 : 525.
- [3] Fisher, R.A. (1936) : The use of multiple measurements in taxonomic problems. *Ann. Eugen.* 7 : 178.
- [4] Kumar, Jitendra (1973) : Genetic studies on the performance of Desi chickens and their crosses with exotic breeds. Ph.D. Dissertation. Haryana Agricultural University.
- [5] Narain, P. (1974) : Techniques for measuring genetic improvement in livestock breeding. *Indian J. Genet.* 34A : 966.
- [6] Tatsuoaka, M.M. (1971) : Multivariate analysis. New York Wiley.
- [7] Yates, F. (1934) : The analysis of multiple classifications with unequal numbers in different classes. *J. Amer. Statis. Assoc.* 29 : 51.

## APPENDIX

### *Computational Procedure for Estimating Improvement in $r(=2) \times c$ non-orthogonal factorial experiment with $p$ traits*

The problem of estimating the genetic improvement based on  $p$  traits is to estimate the difference in the average compound values of two groups, and the average compound value of each group is obtained by substituting the least square mean of each trait in the discriminant function

$$Y = a_1X_1 + a_2X_2 + \dots + a_pX_p \quad \dots(1)$$

where  $Y$  is a compound value and  $X_1, X_2, \dots, X_p$  are known  $p$  variables and  $a_1, a_2, \dots, a_p$  are unknown coefficients and can be determined by estimating the eigen vector of  $W^{-1}B$ , where  $W^{-1}$  is the inverse of within groups SSCP matrix and  $B$  is the between groups SSCP matrix each of order  $p$ .

To derive the requisite quantities in such a study for a  $r(=2) \times c$  factorial experiment with unequal cell frequencies, we suppose that  $n_{ij}$  is the number of individuals in  $(i, j)$ th cell and  $X_{hjk}$  ( $h=1, 2, \dots, p, i=1, 2, \dots, r, j=1, 2, \dots, c$ ; and  $k=1, 2, \dots, n_{ij}$ ) is the observation on  $h$ th trait for the  $k$ th individual in the  $(i, j)$ th cell. Let  $\bar{X}_{hi}$  be the mean of the  $h$ th trait for  $n_{ij}$  individuals in  $(i, j)$ th cell.

The computation for estimating the group means for each trait and the unknown coefficient vector  $a=(a_1, a_2, \dots, a_p)$  of (1) can be carried out as follows:

*Step 1.* Compute the least square group means of  $h$ th trait, following Federer & Zelen (1966), as:

$$\bar{X}_{hi} = \frac{1}{c} \sum_j \bar{X}_{hij}, \text{ with average number of}$$

$$\text{observations, } n_i = c \sum_j \frac{1}{n_{ij}}$$

*Step 2.* Compute the  $W$ , the within cell SSCP matrix as:

$$W = \sum_i \sum_j \begin{bmatrix} SSW_{11(ij)} & SPW_{12(ij)} & \dots & SPW_{1p(ij)} \\ & SSW_{22(ij)} & \dots & SPW_{2p(ij)} \\ & & & SSW_{pp(ij)} \end{bmatrix}^*_{p \times p}$$

where,  $SSW_{hh(ij)}$  and  $SPW_{hm(ij)}$  ( $h \neq m = 1, 2, \dots, p$ ) are corrected sum of squares and corrected sum of products of  $p$  traits respectively in each  $(i, j)$ th cell and given as :

$$SSW_{hh(ij)} = \left[ \sum_{k=1}^{nij} X_{hijk}^2 - \frac{(\sum_k X_{hijk})^2}{n_{ij}} \right]$$

and  $SPW_{hm(ij)} = \left[ \sum_k X_{hijk} X_{mijk} - \frac{\sum_k X_{hijk} \sum_k X_{mijk}}{n_{ij}} \right]$

Step 3. Compute the between groups SSCP matrix as :

$$B = \begin{bmatrix} SS_{11} & SP_{12} & \dots & SP_{1p} \\ & SS_{22} & \dots & SP_{2p} \\ & & & SS_{pp} \end{bmatrix}_{p \times p}$$

where,  $SS_{hh}$  and  $SP_{hm}$  ( $h \neq m = 1, 2, \dots, p$ ) are between groups sum of squares and sum of sum of products respectively of  $p$  traits which can be estimated using Federer and Zelen (1966) as :

$$SS_{hh} = C \left[ \sum_i n_i \bar{X}_{ht}^2 - \frac{(\sum_i n_i \bar{X}_{ht})^2}{\sum_i n_i} \right]$$

and  $SP_{hm} = C \left[ \sum_i n_i \bar{X}_{ht} \bar{X}_{mt} - \frac{(\sum_i n_i \bar{X}_{ht} \sum_i n_i \bar{X}_{mt})}{\sum_i n_i} \right]$

where,

$\bar{X}_{ht}$  and  $n_i$  being available from step 1.

Step 4. Compute inverse of  $W$  matrix and postmultiply it by  $B$  matrix so as to have  $W^{-1}B$ . Find its non-zero eigen value  $\lambda$  and vector  $a$  by following steps 5-7 if there are three or less traits, otherwise compute it following iterative method given in steps 8-14.

Step 5. Find the non-zero eigen value from the characteristic equation  $|W^{-1}B - \lambda I| = 0$ ,  $I$  being  $p$  order unit matrix.

Step 6. Substitute the value of  $\lambda$  in  $(W^{-1}B - \lambda I)$  and find its adjoint  $\text{Adj}(W^{-1}B - \lambda I)$ . Note that all columns of this adjoint matrix are proportional to one other which offers a partial check on the computations.

Step 7. Divide the elements of any column of adjoint matrix by the square root of the sum of squares of these elements. The resulting elements are the elements of the vector  $a$ .

*Step 8.* Take any  $p$  dimensional  $a_0$ , say, as initial trial vector.

*Step 9.* Form the product  $W^{-1}B \cdot a_{(0)} = b_{(1)}$  vector, say.

*Step 10.* Divide  $b_{(1)}$  vector by its largest (in absolute value) element and denote the result by  $a_{(1)}$  vector.

*Step 11.* Use  $a_{(1)}$  as the second trial vector and repeat steps 9 and 10 to obtain  $a_{(2)}$  which then becomes the third trial vector.

*Step 12.* The foregoing cycle is repeated (iterated) until two successive trial vectors, say  $a_{(k)}$  and  $a_{(k+1)}$ , are identical with a specified number of decimal places.

*Step 13.* The number by which  $b_{(k+1)}$  was divided in order to get  $a_{(k+1)}$ , is the required eigen value  $\lambda$ .

*Step 14.* Normalise the terminal trial vector  $a_{(k)}$  to unity by dividing it by the sum of squares of its elements. The result is the required eigen vector  $a$ . Thus the discriminant function is determined.

The compound values for each group can then be estimated by substituting in equation (1) the estimates of group means for each character which can be obtained from step 1. The improvement thus can be obtained as the difference in the compound values.

The test statistic for significance of improvement can be taken as:

$$V = -2.3026 \left[ N - rc + r - 1 - \frac{p+r-1}{2} \right] \log \lambda_{10} \quad \dots(2)$$

where  $N = \sum_i \sum_j n_{ij}$  and  $V$  is distributed approximately as a chi-square

with  $p(r-1)$  d.f., provided  $N - rc + r - 1 - \frac{p+r-1}{2}$  is large (Bartlett, 1947).