Effect of Family Size and Genetic Correlation between Purebred and Crossbred Halfsisters on Response in Crossbred and Purebred Chickens under Modified Reciprocal Recurrent Selection

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ABSTRACT : Response in a modified reciprocal recurrent selection scheme for egg production was evaluated considering variable family sizes and genetic correlation between purebred and crossbred half sisters. The criteria of selection of purebred breeders included pullet's own performance, purebred full and half sisters and crossbred half sister's performance. Heritability of egg production of crossbreds (aggregate genotype) and purebred's was assumed to be 0.2 and genetic correlation between purebred and crossbred half sisters (r_{pc}) as 0.1, 0.2, 0.3, 0.4, 0.5, 1.0, -0.1, -0.2, -0.3, -0.4, -0.5 and -1.0. Number of dams per sire to produce purebred and crossbred progenies assumed to be 5, 6, 7, 8, while number of purebred female progeny (N_p) and crossbred progeny (N_c) per dam were considered to be 3, 4, 5 and 6 in each case. Considering phenotypic variance as unity, selection indices were constructed for different combinations of dams and progeny for each value of r_{pc}. Following selection index theory, response in crossbred and purebred for egg production was computed. Results indicated that response in crossbreds depended mainly on crossbred family size and also on magnitude of r_{pc} irrespective of its direction, and response was greater with large crossbred family size than the purebred families. Correlated response in purebreds depends both on magnitude and direction of r_{pc} and was expected to be greater with large purebred family size only. Inclusion of purebred information increased the accuracy of selection for crossbred response for higher magnitude of r_{pc} irrespective of its direction. Present results indicate that desirable response in both crossbred and purebred performance is a function of r_{pc} and family sizes. The ratio of crossbred and purebred family sizes can be optimized depending on the objective of improving the performance of crossbreds and/ or of purebreds. *(Asian-Aust. J. Anim. Sci. 2005. Vol 18, No. 1 : 8-12)*

Key Words : Response, Genetic Gain, M-RRS, Genetic Correlation

INTRODUCTION

Reciprocal recurrent selection (RRS) exploits not only non-additive genetic variance but also additive variance (Cress, 1966; Hill, 1971; Bell and moore, 1972) and is suitable for low heritable trait like egg production in poultry. Arthur (1986) pointed out the modern layer breeding systems generally use RRS or some modification of it to improve performance of the cross. A vast literature has accumulated on the theoretical and experimental comparison of within line selection (WLS) and RRS systems for improving the crossbred performance of poultry, pig and lab animals, but the results are inconclusive (Wie and van der Steen, 1991). Bell (1982) emphasized that genetic correlation between the means of purebred and crossbred half sibs (r_{pc}) is a reliable indicator of the relative emphasis to give to purebred versus crossbred informations when selecting for crossbred performance For low or negative r_{pc} RRS is advantageous over WLS for improving crossbred performance (Vinson et al., 1969; Bell, 1982; Wie

and van der Werf, 1994).

There are several modified reciprocal recurrent selection (M-RRS) schemes, each of which has its own advantages. Especially, the M-RRS experiments in which both purebred and crossbred performances were considered all showed higher response than RRS and/or WLS (Krehbiel et al., 1971; Hetzer et al., 1977; Brown and Bell, 1980; Singh and Dempfle, 1989). Following selection index theory, Singh and Kumar (1994) and Wie and van der Werf (1994) have detailed the methodology to combine different sources of informations for a trait considering as two traits for purebreds and crossbreds simultaneously to maximize the genetic response in crossbreds under M-RRS. The question that what should be the family structure for producing crossbred and purebred progeny for a particular value of r_{pc} for M-RRS programme? This is necessary in terms of cost of testing the selection programme. So, the objective of this investigation is to study the impact of varying family sizes of purebreds and crossbreds with variable values of r_{pc} on the expected genetic response in crossbreds and correlated response in purebreds.

MATERIALS AND METHODS

Selection programme to be followed for layers, two purebred populations are required to produce reciprocal crossbreds. In each generation, purebreds are reproduced by

mating S males each female provide N female progeny. Simultaneously, the crossbred half sisters are produced by mating the same S males of a line with the D females of another line. The purebred male progenies are retained for selection and the crossbred male progenies are to be discarded at hatching as not required for breeding. Both purebred and crossbred progenies are identified for their parents. The egg production is recorded on purebred and crossbred females. The selection of purebreds is to be based on an index combining informations on purebred and crossbred individuals with the aim to maximize crossbred performance. Four types of informations for selection assumed to be available i.e. pullet's own performance (X_1), purebred full sisters average (X_{FS}), purebred half sisters average (X_{HS}), and average of crossbred half sisters (Y_{HS}) considering egg production of purebreds (X) and crossbreds (Y) as two different traits.

Heritability of egg production of crossbreds (aggregate genotype) and purebreds was taken as 0.2. Genetic correlations between purebred and crossbred half sisters (r_{pc}) were taken as 0.1, 0.2, 0.3, 0.4, 0.5, 1.0, 0, -0.1, -0.2, -0.3, -0.4, -0.5 and -1.0. The number of dams per sire (D) to produce purebred and crossbred progenies were assumed to be 5, 6, 7 and 8. Number of purebred female progenies (N_P) and crossbred female progenies (N_c) per dam were considered to be 3, 4, 5 and 6 in each case, respectively. Assuming phenotypic variance of egg production as unity and thus additive genetic variance equal to heritability, selection indices were constructed considering different combinations of dams and progenies for purebreds and crossbreds for each value of r_{pc}.

The index for the selection of females is

$$I = b_1 X_1 + b_2 X_{FS} + b_3 X_{HS} + b_4 Y_{HS}$$

The index for males excluded the individual information (X_1) since egg production is a sex-limited trait.

The phenotypic matrix (V_P) considering N progeny per dam and D dams per sire has the following form:

$$V_P = \begin{bmatrix} \sigma^2_{Px} & 0.5\,\sigma^2_{Ax} & 0.25\,\sigma^2_{Ax} & 0.25\,\sigma_{Apc} \\ & P_1 & 0.25\,\sigma^2_{Ax} & 0.25\,\sigma_{Apc} \\ & \text{Symm.} & P_2 & 0.25\,\sigma_{Apc} \\ & & & P_3 \end{bmatrix}$$

Where, $P_1 = 0.50\sigma^2_{Ax} - (\sigma^2_{Px} - 0.5\sigma^2_{Ax})/(N_{P-1})$
$P_2 = 0.25\sigma^2_{Ax} - (0.25\sigma^2_{Ax}/(D-1) + (\sigma^2_{Px} - 0.5\sigma^2_{Ax})/N_P(D-1)$
$P_3 = 0.25\sigma^2_{Ay} + (0.25\sigma^2_{Ay}/(D-1) + (\sigma^2_{Py} - 0.5\sigma^2_{Ay})/N_c(D-1)$

P and A stand for phenotypic and additive genetic variances, respectively, and the subscripts p and c for purebreds and crossbreds, and, X and Y are the egg production of purebreds and crossbreds, respectively.

Additive genetic covariance between purebred and crossbred half sisters is

$$\sigma_{Apc} = r_{pc} h_c h_p$$

Where, r_{pc} is genetic correlation between purebred and crossbred half sisters for egg production, h_c and h_p are the square root of heritability of egg production of crossbreds and purebreds, respectively.

Vector of genetic covariances of Y with the phenotypic values of the index

$$V_G' = [\sigma_{Apc} \quad 0.5\,\sigma_{Apc} \quad 0.25\,\sigma_{Apc} \quad 0.25\,\sigma^2_{Ay}]$$

The selection index weights, $b = V_P^{-1} V_G$, and Standard deviation of index, $\sigma_1 = (b'Pb)^{0.5}$

The expected genetic response in crossbreds due to selection of Jth purebred sex is

$$RC_j = 0.5 \; i_j \; \sigma_{ij}$$

Where, i_j is the selection intensity for J^{th} sex and σ_{ij} is the standard deviation of the index. Because of different criterion of selection for males (M) and females (F), total expected response in crossbreds from the selection of both the sexes is

$$R_C = 0.5 \; [i_M \, \sigma_{IM} + i_F \, \sigma_{1F}]$$

Expected genetic correlated response in purebreds due to selection of Jth sex was estimated as under

$$CR_p = 0.5 \; C_j \; b_j \; (i_j/\sigma_{ij})$$

Where, C_j is the row vector of the genetic covariances between breeding value of purebred j^{th} sex with phenotypic values of the index, and computed as under

$$C_j = [\sigma_{2Ax} \quad 0.5 \; \sigma_{2Ax} \quad 0.2 \; \sigma_{2Ax} \quad 0.2 \; \sigma_{Apc}]$$

Total correlated response in purebreds from selection of both sexes is

$$CR_p = 0.5[(C_M \, b_M \, (i_M/\sigma_{1M}) + (C_F \, b_F \, (i_F/\sigma_{IF})]$$

Assuming selection proportion of 0.2 and 0.05 for females and males, respectively, effect of family size and r_{pc} was interpreted in terms of total expected response in crossbreds and purebreds.

Table 1. Effect of r_{pc} and dams per sire on expected response in crossbreds and purebred assuming number of progenies ($N_C=N_p=6$)

	Response in crossbreds (R_c)					Response in purebreds (CR_p)			
r_{pc} Dam →	5	6	7	8	Dams →	5	6	7	8
0.1	0.275	0.290	0.301	0.310		0.071	0.069	0.067	0.066
0.2	0.280	0.294	0.305	0.316		0.139	0.135	0.132	0.129
0.3	0.288	0.301	0.312	0.320		0.202	0.197	0.193	0.190
0.4	0.299	0.311	0.321	0.328		0.258	0.253	0.249	0.245
0.5	0.313	0.324	0.332	0.340		0.306	0.302	0.298	0.295
1.0	0.425	0.429	0.432	0.434		0.425	0.429	0.432	0.434
-0.1	0.275	0.290	0.301	0.310		-0.071	-0.069	-0.067	-0.066
-0.2	0.280	0.294	0.305	0.316		-0.139	-0.135	-0.132	-0.129
-0.3	0.288	0.301	0.312	0.320		-0.202	-0.197	-0.193	-0.190
-0.4	0.299	0.311	0.321	0.328		-0.258	-0.253	-0.249	-0.245
-0.5	0.313	0.324	0.332	0.340		-0.306	-0.302	-0.298	-0.295
-1.0	0.425	0.429	0.432	0.434		-0.425	-0.429	-0.432	-0.434
0	0.274	0.288	0.300	0.309		0	0	0	

RESULTS AND DICUSSION

Effect of r_{pc} on response in crossbreds and purebreds

Expected genetic response in crossbreds and correlated response in purebreds considering equal number of progenies ($N_P=N_C=6$) per dam and different numbers of dams mated to sire for different values of r_{pc} is presented in Table 1. The results indicated that with the increase in magnitude of r_{pc}, there is increase in crossbred response irrespective of the direction of r_{pc}. The response in purebreds is also expected to increase with the increase in magnitude of r_{pc}, but the direction of response depends on the direction of r_{pc}. For r_{pc}, equal to zero, response in purebreds was expected to be zero which is similar to the correlated response that is expected in an uncorrelated trait in a selection programme. For equal number of dams per sire to produce both purebreds and crossbreds, crossbred response was expected to increase and purebred response was expected to decrease with increasing number of dams per sire for all values of r_{pc} (except unity). Per cent rate of increase in crossbred response is more for low r_{pc} than for higher r_{pc} value when number of dams per sire is increased. This indicates that for low r_{pc}, number of dams per sire to produce crossbred progenies is more important for higher crossbred response.

From the results, it may be inferred that to improve crossbred performance through M-RRS, magnitude of r_{pc} irrespective of its direction is important while for response in purebreds, both magnitude and direction of r_{pc} is important. Inclusion of purebred informations in the index add to the accuracy of selection if there exist some amount of covariance between purebreds and crossbreds. Weightage to crossbred information will be more than to purebred information for selection as the crossbred performance measures the breeding goal directly. Many workers have indicated that crossbred selection schemes are not necessary when r_{pc} is positive and high, and WLS followed by crossing is a better scheme (Biswas and Craig, 1969;

Robertson, 1971; Bell, 1982; Sellier, 1982) which is contrary to the present findings. Depending upon the magnitude and direction of r_{pc}, the decision on use of number of dams per sire for producing crossbred and purebred progenies may be taken keeping in view the expected correlated response in the purebreds. This is because; a minimum level of performance is reasonably required in purebred populations.

Effect of variable purebred family size versus constant crossbred family size ($N_C=6$)

Expected response in crossbreds and correlated response in purebreds considering equal numbers of dams (D=6) and fixed number of crossbred progeny per dam ($N_C=6$) but different number of purebred progenies for different values of r_{pc} is tabulated in Table 2. For each value of r_{pc}, results indicated that response in crossbreds is marginally increased with the increase in number of purebred progenies, while response in purebreds was expected to be higher with the increasing purebred progenies per dam. However, rate of increase in crossbred response was more with the increasing number of purebred progenies for higher values of r_{pc}.

High value of r_{pc} is the indicative of the fact that additive genetic variance of purebreds and crossbreds is approaching to be similar. Wong et al. (1971) indicated that if all genetic effects for a trait were completely additive the sire component of variances in purebreds and crossbreds and sire component of covariance between purebreds and crossbreds should be equal. The relative size of these quantities depends on the kind of gene action controlling the expression of a trait (Comstock, 1961). Improvement of crossbred performance based on purebred performance is the function of genetic covariance between purebred and crossbred performance. It is interesting to note that for $r_{pc}=0$, response in crossbreds is independent of the number of purebred progenies (Table 2) which is in conformity to the

Table 2. Expected response in crossbreds and purebreds considering equal dams (D=6) and crossbred progenies (N_c= 6) but variable purebred progenies

	Response in purebreds (CR_p)					Response in crossbreds (R_c)			
r_{pc} $N_p\rightarrow$	3	4	5	6	$N_p\rightarrow$	3	4	5	6
0.1	0.289	0.290	0.290	0.290		0.060	0.063	0.066	0.069
0.2	0.293	0.293	0.294	0.294		0.117	0.124	0.130	0.135
0.3	0.298	0.300	0.301	0.301		0.171	0.181	0.190	0.197
0.4	0.306	0.308	0.309	0.311		0.220	0.233	0.244	0.253
0.5	0.315	0.319	0.322	0.324		0.265	0.280	0.292	0.302
1.0	0.393	0.407	0.419	0.429		0.393	0.407	0.419	0.429
-0.1	0.289	0.290	0.290	0.290		-0.060	-0.063	-0.066	-0.069
-0.2	0.293	0.293	0.294	0.294		-0.117	-0.124	-0.130	-0.135
-0.3	0.298	0.300	0.301	0.301		-0.171	-0.181	-0.190	-0.197
-0.4	0.306	0.308	0.309	0.311		-0.220	-0.233	-0.244	-0.253
-0.5	0.315	0.319	0.322	0.324		-0.265	-0.280	-0.292	-0.302
-1.0	0.393	0.407	0.419	0.429		-0.393	-0.407	-0.419	-0.429
0	0.288	0.288	0.288	0.288		0	0	0	

Table 3. Expected response in crossbreds (R_c) and purebreds (CR_p) with different number of crossbred (N_c) and purebred (N_p) progenies for r_{pc}=0.5

		No. of purebred progenies/dam (N_p)			
N_C	Response	3	4	5	6
3	R_C	0.286	0.291	0.295	0.298
	CR_p	0.275	0.293	0.307	0.318
4	R_C	0.299	0.303	0.306	0.309
	CR_p	0.270	0.287	0.300	0.311
5	R_C	0.308	0.312	0.315	0.318
	CR_p	0.267	0.283	0.295	0.305
6	R_C	0.315	0.319	0.322	0.324
	CR_p	0.265	0.280	0.292	0.302

In case of r_{pc}=-0.5, response in purebreds will be negative.

views of Wong et al. (1971). Response of equal magnitude in crossbreds and purebreds was observed for r_{pc}=1, but the direction of response in purebreds was as per the direction of r_{pc} (Tables 1 and 2).

Effect of variable family size of both crossbreds and purebreds

For a fixed value of r_{pc} (0.5) and equal number of dams in each case (D=6), expected response in crossbreds and purebreds is given in Table 3. The results indicated that response in crossbreds is expected to be more with the increase in number of crossbred progenies than the purebred progenies; however, the gain was expected to be higher with the increase in the number of crossbred and purebred progenies. On the other hand, the correlated response in the purebreds is a function of number of purebred progenies only. For a fixed number of purebred progenies, the correlated response in purebreds is expected to decrease with the increasing crossbred progenies. This phenomenon hold good for all values of r_{pc}, expect when r_{pc} is zero, where, the response in purebreds will be zero. This indicated that response in crossbreds dependent mainly on the crossbred information. However, efficiency of selection increased with the increase in the informations like that of the purebreds. Response in purebreds depends only on the information on purebreds included in the index and the direction of response in the purebreds included in the index and the direction of response in the purebreds is the consequence of the direction of r_{pc}. Similar to the present results, experiments have shown that purebred performance was improved more slowly than crossbred performance or sometimes even showed a negative response under crossbred selection as reviewed by Wei and van der Steen (1991).

Present results revealed that desirable response in both crossbred and purebred performance is the function of r_{pc}, and family sizes. The ratio of crossbred and purebred family sizes can be optimized depending on the objective of improving the performance of crossbreds and/or of purebreds. These findings are of practical nature which can be helpful in designing the M-RRS program. For species with high reproductivity (poultry and pig), the performance of commercial crossbreds is much more important than of purebreds. A change in r_{pc} due to selection was observed in some experiments (Comstock and Robinson, 1957; Pirchner and von Krosigk, 1973; Pirchner and Mergl, 1977). Such a change in r_{pc} over long time of selection is likely to affect purebred response only under M-RRS system as observed in this study.

M-RRS is suggested to replace the commonly used WLS for all values of r_{pc} for increasing the crossbred performance. The response in the purebreds will be positive when r_{pc} is positive and it will be negative when r_{pc} is negative. Magnitude of r_{pc} is more important than its direction for expecting response in crossbreds. Purebred informations contribute considerably to selection accuracy if r_{pc} is not very small. Therefore, to improve crossbred performance, selection criteria should include informations from both crossbreds and purebreds.

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