

## SELECTION METHODS USING PUREBRED AND CROSSBRED PERFORMANCE

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### ABSTRACT

Comparisons of crossbred selection (e.g. Reciprocal Recurrent Selection, RRS) with pure-line selection (PLS) methods were summarized in theory and experiments. Neither of the methods is an optimal selection strategy to obtain the best crosses, because PLS is better than RRS to exploit additive variance whereas RRS, which makes use of both non-additive and additive gene effects, is more efficient to exploit non-additive variance. Selection methods combining both purebred and crossbred performance are discussed. It is expected that the optimal crossbred response may be obtained by optimally weighing information from purebred and crossbred performance in a selection index to aim at the best hybrids. Some theoretical problems that have to be resolved will be addressed.

### INTRODUCTION

Nowadays, crossbreeding is becoming important in almost all commercial livestock species (Arthur, 1986; Legates, 1988; Siegel, 1988). Reviews on animal crossbreeding have been made by Bowman (1959), King (1971), Bell and Moore (1972), Bell (1982) and Sellier (1970 and 1982). The choice of the selection scheme to obtain the optimal selection response in crossbreds has not been completely resolved (Bell, 1982). Recurrent selection (Hull, 1945) and Reciprocal recurrent selection procedure (RRS) (Comstock et al., 1949) were once considered as an effective way to achieve this goal. Experiments to compare RRS with pure-line selection (PLS) methods in animals have shown that neither RRS nor PLS is an optimal method to exploit additive as well as non-additive genetic variance (see review by Wei and Van der Steen, 1990). These experiments also revealed the fact that both additive and non-additive variance are important to improve crossbreds. The present paper is to evaluate the merits of purebred and crossbred selection schemes and to examine a selection strategy using both purebred and crossbred performance for optimal crossbred response.

### THEORETICAL AND EXPERIMENTAL COMPARISON OF RRS WITH PLS

1. Theory. A formula to compare RRS with PLS was described by Sellier (1982) as,

$$PLS/RRS = r_{pc}(i_p/i_c)(t_c/t_p)[(r_{IA}\sigma_A)_p/(r_{IA}\sigma_A)_c] \text{-----}(1),$$

where PLS/RRS is the ratio of correlated response in crossbred from PLS to direct response from RRS; subscript p and c refer to PLS and RRS, respectively;  $r_{pc}$  is the genetic correlation between purebred and crossbred performance;  $i$  is the selection intensity;  $t$  is the generation interval;  $\sigma_A$  is the additive genetic standard deviation and  $r_{IA}$  is the accuracy of selection. If assuming  $i_p = i_c$ ,  $t_c/t_p = 2$  and  $\sigma_{Ap} = \sigma_{Ac}$ ,  $PLS/RRS = 2r_{pc}(r_{IA})_p/(r_{IA})_c$ . Obviously, PLS/RRS depends on  $r_{pc}$ . When  $r_{pc}$  is near 1, PLS usually is better than RRS. When  $r_{pc}$  is low or even negative RRS will be more efficient.

Hill (1970) used the genetic model on the locus level to compare RRS with PLS, and concluded (1) with partial dominance RRS and PLS have similar

efficiency; (2) with complete dominance RRS is better than PLS and (3) with overdominance PLS is not useful and RRS is more efficient than PLS.

**2. Experiments.** Experimental results on the comparison of RRS with PLS has been conflicting (Bowman, 1959; Sellier, 1970 and 1982; Bell, 1982). Slightly more experiments were favorable to PLS. Experiments designed to compare RRS with PLS in commercial animal are reviewed by Wei and Van der Steen (1990).

The effectiveness of RRS and PLS greatly depends on the trait selected. For highly heritable traits primarily governed by additive genes, such as body weight, PLS generally leads to higher performance than RRS (Bell and Moore, 1958; Vinson et al., 1969; Dickerson et al., 1974). For lowly heritable and heterotic traits, such as litter size or egg production, PLS loses its superiority over RRS (Bowman, 1959; Krehbiel et al., 1971; Bell and Moore, 1972; Brown and Bell, 1980). This has been explained by RRS exploiting non-additive variance more efficiently than PLS, especially over-dominant gene effects (Comstock et al., 1949), whereas PLS is better to use additive variance (Bowman, 1959; Vinson et al., 1969; Bell and Moore, 1972; Orozco, 1974; Bell, 1982).

#### SELECTION METHODS USING PUREBRED AND CROSSBRED PERFORMANCE

While the selection combining information from individual and family performance provides maximum genetic gain in purebreds, there is no agreement about the most effective method to achieve genetic gain in crossbreds. Crossing PLS-selected lines is a commonly-used breeding scheme. However, it is not an optimum strategy to exploit non-additive variance, which is not considered in PLS. Valuable non-additive gene pairs or combinations could be lost during PLS. RRS and PLS are not necessarily contradictory methods to improve crosses (Wei and Van der Steen, 1989), and selection methods using purebred and crossbred performance have been considered to exploit both between- and within-line variation (Hill, 1971; Sellier, 1982; Richard, et al., 1986).

Several types of the combined strategy were considered. King (1961) suggested to select for specific combining ability for egg production and viability, and select other traits within lines. Krehbiel et al. (1971) and Hetzer et al. (1977) made their experiments by selecting animals based on the mean of purebred and crossbred progeny performance. Brown and Bell (1980) used a selection scheme based on purebred and crossbred performance in two-stage selection with independent culling levels for purebred and crossbred progeny performance. However, none of these methods were optimal in the sense of maximum genetic gain assuming a certain variance and covariance structure.

Some authors have considered combining purebred and crossbred performance into a selection index (Henderson, 1963; Jakubec et al., 1974). Singh and Dempfle (1989) used, in an experiment, a selection index including the information from purebred and crossbred. However, they all used the classic method described by Hazel (1943). It is disputable whether the method is still suitable for the case with crossbred performance.

How should the selection index combine purebred and crossbred information? The present theory on crossbred selection is based on an additive effect model, and the selection theory with crossbred response as a breeding goal has not very well been worked out, especially for long-term selection (Wei and Van der Steen, 1990). Moreover, some basic genetic parameters involved in crossbred selection, such as the genetic correlation between purebred and crossbred performance ( $r_{pc}$ ) and the additive genetic variance (or heritability,  $h^2_c$ ) in crossbreds, are not well understood theoretically.

For example, the parameter,  $r_{pc}$ , is generally used as an indicator for the

correlation between performance in the purebred and the crossbred population. Many authors explained a high positive  $r_{pc}$  due to a high additive genetic variance and a low  $r_{pc}$  was assumed to be due to a large non-additive variance. A negative  $r_{pc}$  was probably attributed to overdominance. A study on the one-locus model (Wei et al., 1990) shows that partial dominance does not affect  $r_{pc}$ , and only with overdominance the  $r_{pc}$  becomes negative at certain gene frequencies (Table 1). Hence, for an one-locus model the value of  $r_{pc}$  is equal to 1 or -1. Without overdominance,  $r_{pc}$  is always 1. Crossbred selection could therefore still be useful, because with large dominance effects the value of  $r_{pc}$  could be highly positive. Thus,  $r_{pc}$  is not a very reliable indicator to reflect the usefulness of crossbred selection like RRS.

Another problem has been found in the estimation and use of the additive genetic variance in crossbreds (or  $h^2_c$ ). The sire component of variance has been used to estimate it. Table 1 shows that on a one-locus level the sire component of variance is not an estimate of additive variance in crossbreds, and the sire and dam line contribute different amount of additive variance to the crossbreds, when the two purebred lines have different gene frequencies. The sire component could be used to indicate covariance between the sire line and the crossbred population, and therefore, to predict response from selection of sires. But, the additive genetic variance in crossbred (or  $h^2_c$ ) can not generally be estimated as four times the sire component of variance. For example, in case of selection within the crossbred population or selection on both sires and dams based on crossbred performance, the  $h^2_c$  can not be used to predict crossbred selection response. The proper estimate of the variance would be twice the sum of sire and dam component of variance in crossbreds (Wei et al., 1990).

It is concluded that the methods to optimize crossbred selection response should combine purebred and crossbred information. The genetic parameters to be used in crossbred selection need more theoretical study.

Table 1. Genetic parameters under one-locus model in case of partial dominance ( $d = 0.5$ ) and overdominance ( $d = 1.5$ ).

$f_1$	$f_2^a$	$d = 0.5$					$d = 1.5$				
		$V_{Ac}^b$	$V_{Ap}$	$V_{Am}$	$V_{hsc}$	$r_{pc}$	$V_{Ac}$	$V_{Ap}$	$V_{Am}$	$V_{hsc}$	$r_{pc}$
.1	.3	.541	.130	.412	.065	1	1.247	.230	1.016	.115	1
.1	.9	.209	.032	.176	.016	1	.439	.004	.436	.002	-1
.3	.1	.541	.412	.130	.206	1	1.247	1.016	.230	.508	1
.3	.7	.437	.134	.302	.067	1	.573	.034	.538	.017	1
.7	.3	.437	.302	.134	.151	1	.571	.538	.034	.269	1
.7	.9	.133	.076	.058	.038	1	.023	.008	.014	.004	-1
.9	.1	.209	.176	.032	.088	1	.439	.436	.004	.218	-1
.9	.7	.133	.058	.076	.029	1	.023	.014	.008	.007	-1

<sup>a</sup> frequency of gene  $A_1$  in sires ( $f_1$ ) and dams ( $f_2$ ).

<sup>b</sup>  $V_{Ac}$  - additive variance in crossbreds.  $V_{Ai}$  - additive variance in crossbred population contributed by paternal ( $i=1$ ) and maternal line ( $i=2$ ).  $V_{hsc}$  - sire component of variance in crossbreds.  $r_{pc}$  - genetic correlation between purebred and crossbred progeny.

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