OPTIMUM REPLICATION IN PEDIGREE SELECTION UNDER RESTRICTIONS OF FIELD SIZE

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Synopsis. Under the restriction of field size, the optimum replication was determined to maximize (1) genetic gain and (2) the lower α percent point of genetic value at the point of truncation by phenotypic value, assuming that genotypic and environmental value of a given trait are random variates having normal density function independent of each other, and phenotypic value is given by the sum of these two variates.

Introduction

Various economical and technical conditions impose restrictions upon breeding programs. One of such restrictions arises from a field size available. And an appropriate design within a limited field capacity may markedly improve efficiency of the programs, though yet little attention has been drawn to it. FINNEY (1957) indicated that a relation between environmental variance ϵ^2 , and genetic variance σ^2 , depends upon the number of line to be tested and the area available, and he estimated the optimum selection intensity for a given relation between ϵ^2 , σ^2 and final selection intensity, *i. e.* the product of selection intensities at successive generations. While HANSON (1963) emphasized that heritability statement is affected by the choice of selection unit particularly in plant breeding. He called attention to the fact that heritability estimate on a given material varies depending upon the design of experiment.

Under a limited field capacity, when the change of plot size is ignored, an increase of replication elevates the level of heritability to some extent, but this will reduce selection intensity, since replication can be increased in inverse proportion to the number of line. Consequently we may assume the existence of the optimum replication which maximize genetic gain, because the latter is the product of selection intensity and heritability.

It is the purpose of this paper to determine the optimum replication in pedigree selection.

The result obtained here may be valid only when the field size is sufficiently large for the selection to be regarded as that of a portion in population with normal distribution. However, it will likely give indications that are at least qualitatively useful even when the field size is not so large enough as to allow the assumption of normal distribution for a sample population. In this paper, the effect of segregation is not taken into account. Though this gives rise to some limitation for general application, the supposition provided here will be actual more or less, in later generation, especially in the first pedigree selection which is subsequent to bulk population.

Assumptions

For a given quantitative trait, frequency distributions of genetic value, x_g and environmental value, x_e are respectively defined as normal distribution as follows:

$$\left. \begin{array}{l} N(0, \sigma_g^2) \\ N(0, \sigma_e^2) \end{array} \right\} \quad (1)$$

And let us assume that x_g distributes independently of x_e .

On the other hand, the relation between field size, S , replication, r and number of line to be tested, l is given by

$$r_l = S. \quad (2)$$

Let us select l_0 lines of the highest values of population. Actually l_0 may be determined considering the possibility of the partial elimination of the selected lines due to defects in another trait.

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Effect of replication on genetic gain

Genetic gain, ΔG in standard unit is expressed by

$$\Delta G = ih^2, \quad (3)$$

where i is selection differential and h^2 is heritability.

Assuming normality, i can be replaced by z/v , where z is the ordinate of a unit normal distribution at the point of truncation, v is the portion selected. Then i can be expressed as a function of r , corresponding to given l_0 and S , since z and v is determined by r , l_0 and S .

While heritability with r resplication test is given by

$$h^2(r) = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/r} = \frac{r}{r + (1-h^2)/h^2}, \quad (4)$$

where h^2 is a value derived from components of variance in variance analysis.

Thus, the genetic gain in the case of r -replication becomes,

$$\begin{aligned} \Delta G(r) &= i(r)h^2(r) \\ &= \frac{1}{\sqrt{2\pi}} e^{-\frac{t_0^2}{2}} / \frac{1}{\sqrt{2\pi}} \int_{t_0}^{\infty} e^{-\frac{t^2}{2}} dt \cdot \frac{r}{r + (1-h^2)/h^2} \end{aligned} \quad (5)$$

where t_0 is fixed by following equation,

$$l_0/l = r l_0/S = \frac{1}{\sqrt{2\pi}} \int_{t_0}^{\infty} \frac{1}{\sqrt{2\pi}} e^{-\frac{t^2}{2}} dt. \quad (6)$$

By equation (5), r maximizing $\Delta G(r)$ can be calculated for given h^2 , l_0 and S .

Effect of replication on the lower α percent point of genetic value at the point of truncation

In pedigree selection greater stress is occasionally placed on the performance of individual line selected, rather than on the mean of the selected part as whole, since in practice the selected lines which are estimated superior as for quantitative traits under consideration, are sometimes discarded because of their inadequacy in another characters.

Under the following additive assumption of the phenotypic values (x_p),

$$x_p = x_g + x_e, \quad (7)$$

the simultaneous probability density function of x_g and x_p is

$$P(x_g, x_p) = \frac{1}{\sqrt{\sigma_p^2} 2\pi} \exp \left[-\frac{1}{2} \left(\frac{x_p}{\sigma_p} \right)^2 \right] \cdot \frac{1}{\sqrt{2\pi} \sigma_p h \sqrt{1-h^2}} \exp \left[-\frac{1}{2} \left(\frac{x_g - h^2 x_p}{\sigma_p h \sqrt{1-h^2}} \right)^2 \right]. \quad (8)$$

The derivation and the related problem with this bi-variables distribution function have already been discussed in detail by ROBSON, D. S., LE ROY POWERS and N. S. URQUHART (1967) and HASHIGUCHI (1968). Therefore, only the conclusion necessary for further consideration is cited here. From formula (8), when a fixed value x_{p_0} is taken as one of x_p , then the conditional probability density function will become,

$$N\{h^2 x_{p_0}, \sigma_p^2 h^2 (1-h^2)\}. \quad (9)$$

Consequently, for a given x_{p_0} , the lower α percent point of genetic value x_g , E is given by

$$E = h^2 x_{p_0} - t_\alpha \sigma_p h \sqrt{1-h^2}, \quad (10)$$

where t_α is given as a definite value corresponding to α .

Thus, if we select the section of the population upper (lower) than x_{p_0} by phenotypic value, the advance in genetic value is expected to be at least larger than E point. So let us define the lower limit of $\bar{x}_g$ as "the least significant selection difference".

If we divide E by $\sigma_g = h\sigma_p$, we have

$$e = E/\sigma_g = h t_0 - t_\alpha \sqrt{1-h^2}, \quad (11)$$

where t_0 is x_{p_0}/σ_p .

In r replication test, heritability must be replaced by (4). Therefore, e with r -replication test is,

$$e(r) = \frac{t_0 h \sqrt{r} - t_\alpha \sqrt{1-h^2}}{\sqrt{h^2(r-1)+1}}. \quad (12)$$

And if we select l_0 lines taking upper portion than x_{p_0} from l line, t_0 is determined by (6), then we can calculate $e(r)$ by (12), when h^2 and r are provided. After all, for given S , l_0 and h^2 , the r value can be determined to get maximum $e(r)$.

Numerical Results

It is assumed here for numerical calculation that l_0 is equal to 10. The results will be applicable to another value of l_0 . When r is given, the value of l_0/S determine t_0 , as shown in equation (6). Therefore, when l_0/S is equal to l'_0/S' , the same $\Delta G(r)$ and $e(r)$ will be given.

Fig. 1. Relation between replication and genetic gain under the restriction of field size S , provided the selection of 10 lines of highest value of population.

Fig. 2. Effect of replication on the lower limit of genetic value at the point of truncation by phenotypic value under the restriction of field size.

Note: $\alpha=0.05$, $l_0=10$

For instance, $\Delta G(r)$ as well as $e(r)$ corresponding to $l_0=20$ and S_0 are equal to those corresponding to $l_0=10$ and $1/2 S_0$.

Some numerical results of practical importance are shown in Fig. 1 and Fig. 2. It is noteworthy from the result that when h^2 exceeds about 0.6, an increased replication diminish $\Delta G(r)$ and especially $e(r)$ under limited field size. And it is also evident that when S is restricted within a range from 100 to 400, and h^2 is less than 0.6, as usual in actual cases, 2 to 3 replications will be more

efficient than the single replication, compensating the decreases of the number of lines to be tested.

Discussion

In application of the result given here, there still remain several difficulties besides the problem mentioned above. First of all, the value of h^2 should be provided as a given constant independent of r . Furthermore, the h^2 estimate have a considerably wide confidence interval as shown by Nei (1956) and

HASHIGUCHI (1958). However, fortunately, heritability value have been estimated for many traits in recent years, though approximately. In connection with this, heritability estimate obtained from experiments with r replications should be converted into the value independent of r before the application of principle proposed here.

While, particular attention will be drawn to the fact that the value of $G(r)$ greatly varies depending upon h^2 and r . This suggests that replication is also an important factor affecting the efficiency of indirect selection, *i. e.*, the selection of aimed traits with low heritability value through indirect selection of characters with high heritability and close genetic correlation with the former. Generally speaking, a design with reduced replications increases the efficiency of indirect selection under a strong restriction in field size.

Finally, it should be briefly referred to the effect of change of plot size. In the selection of a trait with low heritability, sufficiently large S and r are found to be necessary. Under the limit of field capacity, the reduction of plot size may be efficient procedure to enlarge S . In relation to this the utilization of hill plot has been proposed in rice breeding (Ito *et al.*, 1965).

Summary

Under the assumption that genotypic and environmental values of a given quantitative trait are the random variates having normal density function independent of each other and phenotypic value is given by the sum of these two variates, when the restriction of field size is given as the product of replication and number of lines to be tested, an increase

in replications elevates heritability estimate as an indicator of a selection effect. However, this decreases the selection intensity, provided the number of selected lines necessary for further stages is definite. Therefore, the optimum numbers of replication maximizing (1) genetic gain and (2) the lower α percent point of genetic value at the point of truncation by phenotypic value are able to be determined. Some numerical results of practical importance are given in Figure 1 and Figure 2. And some limitations in the application of the result as well as related problems were discussed briefly.

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一定圃場内の系統選抜における最適反復回数

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供試系統数×反復数が限られる際に、上位一定系統数を選抜するとき、所与の形質の環境変動と遺伝値が、それぞれ独立に正規分布に従い、かつ表現型値がそれらの

和であると仮定して、(1) 遺伝獲得量および (2) 最下位選抜系統の遺伝値の信頼区間の下限を、それぞれ最大とする反復数を求めた。