

THEORETICAL BASIS FOR DETERMINING THE NUMBER OF X_2 -PLANTS REQUIRED FOR IMPROVEMENT OF QUANTITATIVE CHARACTERS OF SELF-POLLINATING CROPS

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Synopsis. Some theoretical equations, by the use of which the approximate size of X_2 -population for quantitative character breeding can be estimated, were offered in this paper.

Introduction

It would be greatly important from practical standpoint to make some yardstick for determining the number of plants to be grown at X_2 -generation when artificial selection is firstly operated in an ordinary mutation breeding. In relation to this problem, YOSHIDA (1962), who has discussed the relative efficiency of the various types of propagation method* such as ear-to-row method, one-plant-one-grain method etc. to find out the most effective propagation method under various conditions of breeding, gave the number of X_2 -plants required for detecting at least one desirable mutant in the respective propagation methods.

Furthermore, taking it into consideration that mutants are more difficult to detect or obtain under a higher heterogeneity of breeding environment, YOSHIDA (1965) proposed that sufficiently numerous plants for detecting at least 'two' desirable mutants should be grown at X_2 -generation, and studied the relative merits of the various propagation methods under such a condition. By this way of thinking, however, the numbers of X_2 -plants required for detecting at least three, at least four or more desirable mutants need to be obtained according as the heterogeneity of breeding environment gets larger. But, no information as to the relation between the number of X_2 -plants and the heterogeneity of breeding environment can be predicted from

* The authors prefer the term 'propagation method' rather than 'screening method' adopted by YOSHIDA, since the former is thought to be more strict and unmistakable expression than the latter.

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YOSHIDA's equations. And therefore, no criterion can be derived for answering the question, by which requisition for the minimum number of desirable mutants to be detected the number of X_2 -plants should be determined under given breeding environment.

The number of X_2 -plants is considered to be influenced not only by the heterogeneity of breeding environment but also by the intensity of artificial selection, phenotypic stability and genotypic superiority of mutants and so on. Also for these respects, YOSHIDA's equations give us no information.

These inconveniences could be ascribed to the point that, strictly speaking, YOSHIDA's equations were made not on the basis of the probability that mutants are 'obtained', but on the basis of the probability that mutants are 'included'. It is only for qualitative characters that the two different types of probability are the same, in other words, that mutants are detected or obtained without fail if included. Another approach for determining the size of X_2 -population would be needed for quantitative characters in which mutants are not always detected even if included, namely, the two types of probability mentioned above are not the same, the former probability being under the control of selection intensity, heterogeneity of breeding environment and so on.

The main purpose of this paper is to offer one of theoretical bases for estimating the approximate number of X_2 -plants to be grown in breeding of quantitative characters.

Principle and Mathematical Procedures

Characters in which genotypic differences

of individuals are obscured by environmental heterogeneity and therefore mutants are not necessarily detected even if contained, are defined as quantitative characters throughout this paper, irrespectively of the number of loci affecting the characters.

In the cases when improvement of such a character is the objective of breeding, it may easily happen that, in addition to the genotypes suitable for breeding aim, much of unsuitable ones are contained in the portion selected from material population. In this paper, the number of X_2 -plants to be grown, say N , will be formulated in accordance with the principle that at least one desirable genotype should be safely obtained. More explicitly speaking, if

it is now assumed that one loci with three different genotypes AA , AA' and $A'A'$ is of breeder's interest, A and A' being undesirable allele and desirable one respectively, N , is determined in such a way that the probability of desirable genotype $A'A'$ being missed in the portion selected from X_2 -population should be some small value, say ϵ .

This probability and therefore N are expected to be differently formulated according to the mode of artificial selection. Three different types of selection model, say A, B_1 and B_2 models, will be taken up in this paper, which are diagrammatically shown in Fig. 1. Model A is the one in which X_2 -plants of C or more phenotypic superiority (standardized

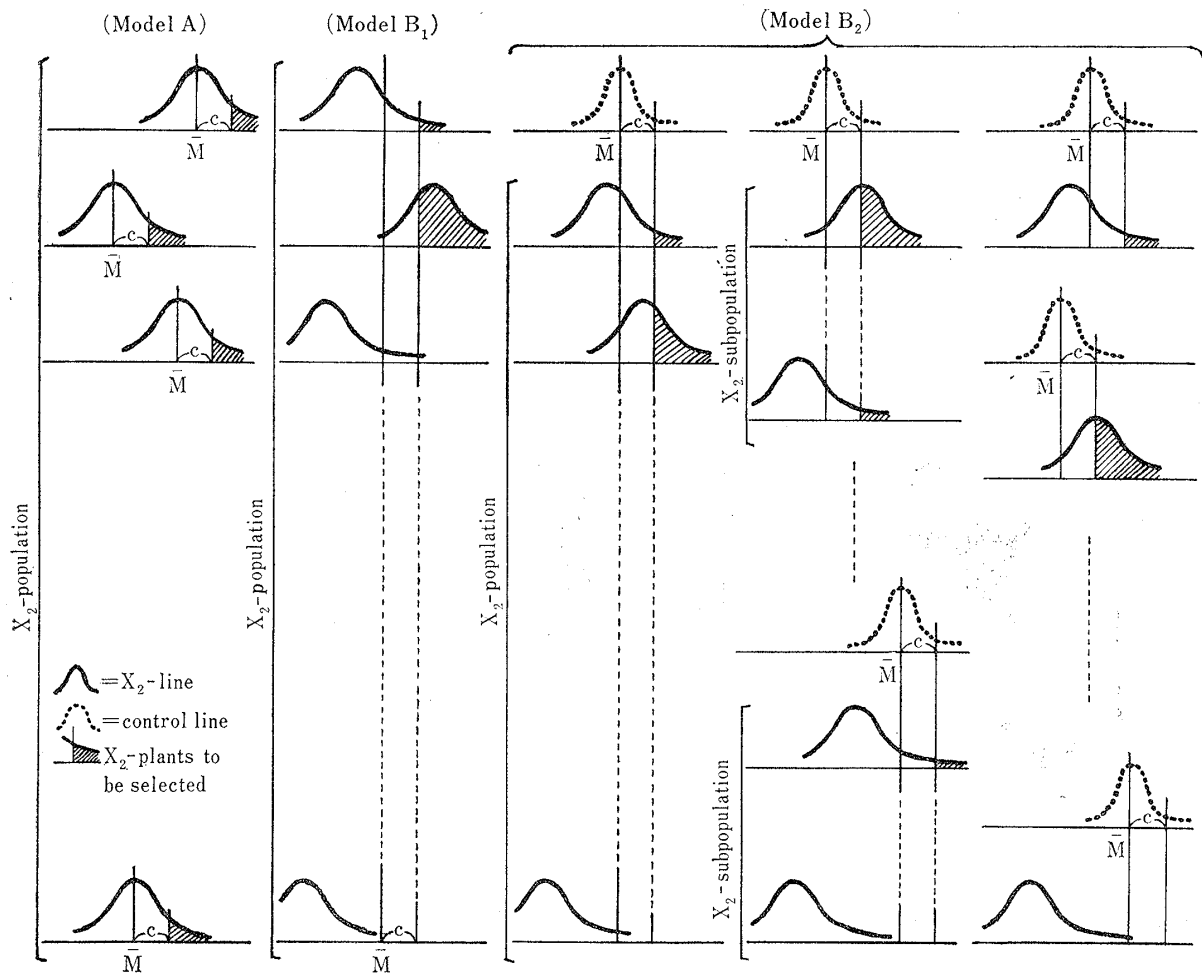


Fig. 1. Diagrammatical explanation of selection models.

- c : Critical phenotypic superiority (over the point \bar{M}) for artificial selection, standardized by phenotypic standard deviation of X_2 -line for model A, by that of the whole X_2 -population for model B_1 and by that of control line, X_2 -line, X_2 -subpopulation or X_2 -population for model B_2 .
- \bar{M} : Starting-point for measuring the phenotypic superiority of X_2 -plants, namely, mean of X_2 -line for model A, that of X_2 -population for model B_1 and that of control line for model B_2

by the phenotypic standard deviation of an X_2 -line, say σ_L) over the mean of the respective X_2 -line are selected. Model B_1 is the one in which X_2 -plants of C or more phenotypic superiority (standardized by the phenotypic standard deviation of X_2 -population, say σ_T) over the mean of X_2 -population are chosen. In model B_2 , X_2 -plants of C or more phenotypic superiority (standardized by the standard deviation denoted by σ_X) over the mean of the respective control line are selected. Standard deviation σ_X can be arbitrarily determined by the will of breeders and may be equalized to the phenotypic standard deviation of a control line, σ_E , that of an X_2 -line, σ_L , that of X_2 -subpopulation, σ_B , or that of X_2 -population, σ_T .

As predicted from Fig. 1, there is a substantial difference between models A and B_i ($i=1, 2$). That is to say, in model A, the adoption or rejection of X_2 -plants is decided every X_2 -line, more fully speaking, on the basis of the rank in phenotypic superiority X_2 -plants assume not in X_2 -population as a whole but in the very X_2 -line to which they belong. On the other hand, in models B_1 and B_2 , it is of no consequence which phenotypic rank X_2 -plants assume in the X_2 -line they are in. Models B_1 and B_2 differ just in the point that control lines are used in the latter model but not in the former one. Mathematical formulations of N will be carried out for these three types of selection model.

1. Selection by model A

Suppose that all X_2 -plants in an X_2 -line are derived from one and the same X_1 -ear, and let p and q be respectively the probability that X_2 -line is derived from an X_1 -ear generated from an ear primordium with desirable mutant alleles and the probability that desirable mutant is not obtained from such an X_2 -line under given selection intensity. Then, the probability that no desirable mutant is 'obtained' from X_2 -population, say **Pro.** (A), is presented by

$$\begin{aligned} P_{ro.(A)} &= (1-p)^{n_1} + \binom{n_1}{1} (1-p)^{n_1-1} p q^{n_2'} \\ &+ \binom{n_1}{2} (1-p)^{n_1-2} p^2 q^{2n_2'} + \dots \\ &= \{(1-p) + p q^{n_2'}\}^{n_1} \end{aligned} \quad (1)$$

where n_1 and n_2' stand for the number of X_2 -lines and that of X_2 -plants to be selected from

an X_2 -line. Equation (1) is of the same form as the one which can be immediately derived from equation (9) of YOSHIDA (1962), but of different import. Parameters p and q in equation (1) will be formulated below by the use of more elementary parameters such as selection intensity, induced mutation rate, the number of loci concerned and so on.

If the expected frequency of desirable mutant in the X_2 -line it belongs to and the average phenotypic deviation (standardized by σ_L) of desirable mutant from mean of the X_2 -line are denoted by f_A and d_A respectively, the probability of desirable mutant being included in the portion selected from such an X_2 -line, namely, the probability of desirable mutant being obtained from such an X_2 -line is presented by

$$\begin{aligned} P_A &= \frac{f_A}{\sqrt{2\pi} S_A \sigma_E} \int_{(C-d_A)\sigma_L}^{\infty} \exp\left(-\frac{t'^2\sigma}{2\sigma_{E'}^2}\right) \sigma_L dt' \\ &= \frac{f_A}{\sqrt{2\pi} S_A} \int_{(C-d_A)\sigma_L/\sigma_{E'}}^{\infty} e^{-t'^2/2} dt'; C < d_A \end{aligned} \quad (2)$$

Hence, $q=1-P_A$. In this equation, parameter S_A stands for the ratio of X_2 -plants to be selected, to the whole of the X_2 -line they are in and is presented by

$$S_A = \frac{1}{\sqrt{2\pi}} \int_C^{\infty} e^{-t'^2/2} dt \quad (3)$$

and $\sigma_{E'}$, means phenotypic standard deviation of the mutant in the X_2 -line it belongs to. Symbols t' and t are variable of integration. For a character with so high phenotypic stability that mutants are easily detected by phenotypical observation, the absolute value of $(C-d_A)\sigma_L/\sigma_{E'}$ in equation (2) would be very large. It is noted that P_A increases toward unity and S_A decreases toward f_A as the phenotypic stability of the mutant to be obtained gets larger.

Next, parameters p and f_A are formulated. Under the circumstances, firstly, that breeding material is of undesirable genotype for L_1 independent loci and of desirable genotype for L_2 independent loci and j or more loci among the L_1 are to be improved together, keeping the genetic composition of the originally desirable L_2 loci unchanged, and secondly, that mutagenic treatment is operated at the growth stage when ear primordia consist of a single cell, and thirdly, that the effect of natural selection against mutant alleles is

negligibly small, we get

$$p \doteq \sum_{i=j}^{L_1} \binom{L_1}{i} (2m)^i (1-2m)^{L_1-i} \\ \doteq \binom{L_1}{j} (2m)^j (1-2m)^{L_1-j} \quad (4)$$

and

$$f_A \doteq \sum_{i=j}^{L_1} \binom{\bar{l}_1}{i} \left(\frac{1}{4}\right)^i \left(\frac{3}{4}\right)^{\bar{l}_1-i} \times \left(\frac{1}{4}\right)^{\bar{l}_2} \quad (5)$$

where

$$\bar{l}_1 = \sum_{i=j}^{L_1} i \binom{L_1}{i} (2m)^i (1-2m)^{L_1-i} / p \\ \bar{l}_2 = \sum_{i=0}^{L_2} i \binom{L_2}{i} (2m)^i (1-2m)^{L_2-i} = 2mL_2$$

m being induced mutation rate per allele. Especially, if j is decided to be L_1 , that is, if all of undesirable L_1 loci of breeding material are to be improved together, equations (4) and (5) take the form $p = (2m)^{L_1}$ and $f_A = \left(\frac{1}{4}\right)^{L_1+2mL_2}$, respectively.

Now, equalizing the right-hand side of equation (1) to ϵ , the total number of X_2 -plants to be selected is formulated as

$$n_A = n_1 \cdot n_2' \doteq n_2' \cdot \log \epsilon \\ / \log \{1-p+p(1-P_A)^{n_2'}\} \quad (6)$$

and using the relation that the number of X_2 -plants to be grown per X_2 -line equals n_2'/S_A , the total number of X_2 -plants is formulated as

$$N_A = n_1 \cdot n_2 \doteq n_2' \cdot \log \epsilon \\ / S_A \log \{1-p+p(1-P_A)^{n_2'}\} \quad (7)$$

which is approximated by

$$N_A \doteq n_2' \cdot \log \epsilon^{-1} / S_A p \{1-(1-P_A)^{n_2'}\} \\ = n_2' \cdot \log \epsilon^{-1} / S_A p \sum_{i=1}^{n_2'} \binom{n_2'}{i} (-1)^{i-1} P_A^i \quad (8)$$

since $|p|$ is in general considered to be sufficiently small.

2. Selection by models B₁ and B₂

For these models, such probability as $q (=1-P_A)$ which was similarly formulated for every X_2 -line and can be commonly applied to all X_2 -lines derived from the X_1 -ear with the competency for leaving desirable mutants, cannot be defined. This is because selection in models B₁ and B₂ is carried out on the basis of the phenotypic deviation of X_2 -plants from mean of the whole X_2 -population and from mean of their control line, respectively, and therefore selection intensity in each individual X_2 -line cannot be the same. So, the probability of mutants being obtained

should be otherwise defined and formulated, namely, not with respect to X_2 -line individually as in model A but with respect to X_2 -population as a whole.

For model B₁, the propability or desirable mutant being obtained is formulated by

$$P_{B_1} \doteq \frac{f_{B_1}}{\sqrt{2\pi} S_{B_1}} \int_{(C-d_{B_1})\sigma_T/\sigma_{E''}}^{\infty} e^{-t^2/2} dt; C < d_{B_1} \quad (9)$$

where d_B , f_{B_1} and $\sigma_{E''}$ stand for the genotypic superiority of desirable mutant defined by the average phenotypic deviation (in the unit of σ_T) of the mutant from mean of X_2 -population, the expected frequency of the mutant and the phenotypic standard deviation of the mutant in the whole X_2 -population, respectively. S_{B_1} is presented by the same equation as (3). If j or more loci among originally undesirable L_1 loci are to be improved together, maintaining other desirable L_2 loci unchanged, and no linkage exists among all of these L_1+L_2 loci, the expected frequency of desirable mutant, f_{B_1} , in other words, the probability of the mutant being included is represented by

$$f_{B_1} \doteq \sum_{i=j}^{L_1} \binom{L_1}{i} \left(\frac{1}{2}m\right)^i \left(1-\frac{1}{2}m\right)^{L_1-i} \\ \cdot \left(1-\frac{3}{2}m\right)^{L_2} \\ \doteq \binom{L_1}{j} \left(\frac{1}{2}m\right)^j \left(1-\frac{1}{2}m\right)^{L_1-j} \\ \cdot \left(1-\frac{3}{2}m\right)^{L_2} \quad (10)$$

which holds true whichever method of propagation is adopted for making X_2 -population if mutagenic treatment is operated at some vegetative growth stage of material plants. Equation (10) takes the form

$$f_{B_1} \doteq \left(\frac{1}{2}m\right)^{L_1} \left(1-\frac{3}{2}m\right)^{L_2}$$

when all of the L_1 loci are to be improved.

For B₂ model, the probability of desirable mutant being obtained is formulated by

$$P_{B_2} \doteq \frac{f_{B_2}}{\sqrt{2\pi} S_{B_2}} \int_{(C-d_{B_2})\sigma_X/\sigma_Y}^{\infty} e^{-t^2/2} dt; C < d_{B_2} \quad (11)$$

where

$$S_{B_2} = \left(\frac{1}{\sqrt{2\pi}} \int_{(C-D)\sigma_X/\sigma_Y}^{\infty} e^{-t^2/2} dt\right) \quad (12)$$

and f_{B_2} is similarly defined and formulated as f_{B_1} , d_{B_2} standing for the genotypic superiority

of desirable mutant defined by the average phenotypic deviation (standardized by σ_X) of the mutant from mean of respective control line. Standard deviation $\sigma_{E''}$ means phenotypic standard deviation of desirable mutant in X_2 -population as a whole, in X_2 -subpopulation or in X_2 -line according as only one, some or as numerous control lines as X_2 -line are planted. Standard deviation σ_Y equals σ_T , σ_B or σ_L according to the number of control lines planted (see Fig. 1). Parameter D in equation (12) shows mean of phenotypic deviations standardized by σ_X of all X_2 -plants from mean of the respective control line. It may be preferred for model B_2 where control lines are used to discriminate mutants, that σ_X would be equalized to phenotypic standard deviation of control line, σ_B .

From the foregoing, the probability that no desirable mutant is obtained can be formulated by

$$\text{Pro. } (B_i) = (1 - P_{B_i})^n; \quad i=1, 2 \quad (13)$$

for models B_1 and B_2 collectively. Parameter n stands for the number of X_2 -plants to be selected under some given selection intensity. Letting the right-hand side of this equation equal to ϵ , we get

$$n_{B_i} = \log \epsilon / \log(1 - P_{B_i}) \quad (14)$$

and using the relation $N = n/S$

$$N_{B_i} = \log \epsilon / S_{B_i} \log(1 - P_{B_i}) \quad (15)$$

which can be approximated by

$$\begin{aligned} N_{B_i} &= \log \epsilon^{-1} / S_{B_i} P_{B_i} \\ &= \sqrt{2\pi} \log \epsilon^{-1} / f_{B_i} \int_{(C-d_{B_i})k_i}^{\infty} e^{-t^2/2} dt \quad (16) \\ &; \quad i=1, 2. \quad k_1 = \sigma_T / \sigma_{E''}, \quad k_2 = \sigma_X / \sigma_{E''} \end{aligned}$$

if P_{B_i} is very small as compared to unity, which is considered not to be a rare case in quantitative character breeding.

A considerable number of experiments showed that population mean for many quantitative characters is not or just a little, if any, changed by mutagenic treatment if mutants with too terribly changed form or appearance to be practically utilized are set aside (OKA *et al.*, 1958. RAWLINGS *et al.*, 1958. YAMAGATA *et al.*, 1960. KRULL *et al.*, 1961. MATSUO *et al.*, 1961. WILLIAMS *et al.*, 1961. YAMAGUCHI, 1962. KAWAI, 1963 etc.). This suggests that parameter D in equation (12) can in general be ignored.

Conclusions and Discussions

Some general conclusions which could be read from the theoretical equations will be mentioned.

Equations (8) and (16) shows that the number of X_2 -plants is roughly in inverse proportion to pP_A in model A and to P_{B_i} in models B_i ($i=1, 2$). So, it may be said that, under given selection intensity, the approximate number of X_2 -plants is inversely proportional to $\left(\frac{L_1}{j}\right)\left(\frac{1}{2}m\right)^j$. This means that induced mutation rate and the number of loci to be improved have a great influence on the number of X_2 -plants, in other words, on the efficiency of mutation breeding. An extraordinarily large number of X_2 -plants would be required to be grown if induced mutation rate is very low, and/or if material plants are undesirable for some multiple loci and all or most of these loci are to be improved together, maintaining other originally desirable loci unchanged. Not mutation breeding but hybridization breeding should be preferred in such a case (TORIYAMA *et al.*, 1962. YONEZAWA *et al.*, 1969)

It can be seen from equations (6) and (14) that the number of X_2 -plants to be selected decreases asymptotically as selection intensity increases, but equations (7) and (15) show that the number of X_2 -plants to be planted, N , increases sharply as selection intensity gets larger since the decrease rate of n due to the increase of selection intensity is much smaller than that of S , as expected from the feature of normal distribution. This leads us to the general conclusion that a larger number of X_2 -plants need to be grown if a higher selection intensity is to be adopted, by which genetic advance by artificial selection can be raised and consequently the time required for attaining breeding aim can be economized.

As understood from the definition of the various parameters in this paper, $\sigma_X / \sigma_{E''}$ and σ_X / σ_Y in equations (11) and (12) respectively are expected to get larger as the number of control lines does. This means that, under given selection intensity, the probability of mutant being obtained gets larger as the number of control lines or plants does, in

other words, that the number of X_2 -plants required for obtaining at least one desirable mutant with given probability $(1-\varepsilon)$ can be decreased as the number control lines or plants is increased. It may be of practical consequence that the relation between the number of X_2 -plants and that of control lines should be clarified. This relation, however, is considered to vary with breeding environment and character and would be too complicated to be settled into a simple formula. As a proof of this, the smaller the homogeneity of breeding environment and/or the phenotypic stability of breeding character are, the more strongly the number of X_2 -plants would be influenced by the number of control lines.

It has been assumed in the previous sections that X_2 -line and X_2 -population obey normal distribution. Theoretically speaking, this assumption is thought not to be unreasonable unless the total number of loci affecting breeding character is small and breeding material per se is of so unusual and extreme phenotype concerning the character at issue. Conditions for normality of X_2 -line and X_2 -population are considered to be fulfilled in most, if not all, cases of mutation breeding for quantitative characters.

Divergences from normal distribution, which often take place in practical breeding for quantitative characters, could in most cases be ascribed not to the intrinsic and inevitable cause that X_2 -line or X_2 -population are really apart from normality, but just to the accidental and avoidable cause that the number of X_2 -plants grown is too small for the normality of X_2 -population to be secured. Of course, the divergence from normality due to the latter cause does not need to be taken into account for making the equations presented in this paper. Even though X_2 -population happen to be diverse, but not so much, from normal distribution owing to the former cause, the present theory is thought to meet our necessities fairly well. About this respect, KRULL *et al.* (1961) reported that no consistent positive or negative shift in skewness was detected for the three biometric characters of oats.

Next, the number of X_2 -plants required for qualitative character breeding will be briefly

discussed in relation to the present theory.

For a character in which genotypic differences are easily distinguished through phenotypic observation, the probability of mutant being obtained is equal to the probability of mutant being included in X_2 -population. So, the number of X_2 -plants can be formulated on the basis of the latter probability, which is of course given by letting the selection intensity C in equations (2), (9) and (11) be negative infinity for the respective selection models. Then, the probability that no desirable mutant is obtained is presented by

$$\begin{aligned} \text{Pro.}(A) &= \lim_{c \rightarrow -\infty} \{1 - p + p(1 - P_A)^{n_2'}\}^{n_1} \\ &= \{1 - p + p(1 - f_A)^{n_2}\}^{n_1} \end{aligned} \quad (17)$$

for model A, and

$$\begin{aligned} \text{Pro.}(B_i) &= \lim_{c \rightarrow -\infty} (1 - P_{B_i})^n \\ &= (1 - f_{B_i})^N; \quad i=1, 2 \end{aligned} \quad (18)$$

for models B_i . The relations $\lim_{c \rightarrow -\infty} n_2' = n_2$ and

$\lim_{c \rightarrow -\infty} n = N$ were used for deriving these equations. Straightward, equalizing the last side of these equations to ε , we get

$$\begin{aligned} N_A &= n_1 \cdot n_2 = n_2 \cdot \log \varepsilon / \log \{1 - p + p(1 - f_A)^{n_2}\} \\ &= \begin{cases} \log \varepsilon^{-1} / p f_A & \dots \dots n_2 = 1 \\ n_2 \cdot \log \varepsilon^{-1} / p \{1 - (1 - f_A)^{n_2}\} & \dots \dots n_2 \geq 2 \end{cases} \end{aligned} \quad (19)$$

and

$$N_{B_i} = \log \varepsilon / \log(1 - f_{B_i}) = \log \varepsilon^{-1} / f_{B_i} \quad (20)$$

for the respective selection models. It is noted that the last side of equation (17) and the middle side of equation (19) are the same form and import as those given by YOSHIDA (1962), though different symbols were used in this paper.

Lastly, theoretical relations between the three selection models are briefly mentioned.

In models B_i ($i=1, 2$), artificial selection is operated in such a way that X_2 -plants are chosen independently of what rank in phenotypic superiority they assume in the X_2 -line they belong to. This holds true also for model A if the one-plant-one-grain method of propagation is adopted. Hence, under the condition that n_2 is unity, namely, one-plant-one-grain method of propagation is adopted, N_A is to be formulated similarly as N_{B_1} or N_{B_2} according as no or some control lines are used for detecting mutants.

Noticing that the average number of X_2 -plants to be selected from a X_2 -line, n_2' , is in

this case equal to the ratio of selected X_2 -plants to the whole of X_2 -population, S_A , and that $(1-P_A)^{n_2}$ can be approximated by $1-n_2'P_A$, we get from equation (8)

$$N_A|_{n_2=1} = \log \varepsilon^{-1} / p S_A P_A \\ = \sqrt{2\pi} \log \varepsilon^{-1} / p f_A \int_{(C-d_A)\sigma_L/\sigma_B}^{\infty} \frac{e^{-t^2/2} dt}{\sigma_B} \quad (21)$$

where of course σ_L cannot but be σ_T or σ_X in the absence or presence of control lines, respectively. Besides, by the definition of parameters, $p f_A$ in equation (21) equals f_{B_1} when $n_2=1$. As a proof, under the circumstances that the premises adopted in making equations (4), (5) and (10) are fulfilled and that all of undesirable L_1 loci of breeding material are to be improved together,

$$p f_A = (2m)^{L_1} \left(\frac{1}{4}\right)^{L_1+2mL_2} = \left(\frac{1}{2}m\right)^{L_1} \left(1-\frac{3}{4}\right)^{2mL_2} \\ \doteq \left(\frac{1}{2}m\right)^{L_1} \left(1-\frac{3}{2}m\right)^{L_2} = f_{B_1}$$

So, it could now be proved that equation (21) is the same as (16) when $n_2=1$, and therefore $N_A|_{n_2=1} = N_{B_1}$. This holds true also for qualitative characters as can be readily seen from equations (19) and (20), both of which are exactly the same if $n_2=1$ and $p f_A = f_{B_1}$. It is added here that one-plant-one-grain method of propagation has been proved to be most preferable as compared to other propagation methods if the number of X_2 -plants but not that of X_1 -plants is taken into account (YOSHIDA, 1962).

Summary

Theoretical equations for estimating the number of X_2 -plants to be grown for quantitative character breeding were presented in this paper. From these equations, some general conclusions could be derived, which will be mentioned below.

1). Under the assumption of no linkage among the loci concerned and with given selection intensity, the number of X_2 -plant is roughly in inverse proportion to $\binom{L_1}{j} \cdot \left(\frac{1}{2}m\right)^j$, where m stands for induced mutation rate per allele, L_1 and j being the number of undesirable loci of breeding material and that of loci to be improved together, respectively. This means that the number of X_2 -plants is greatly

influenced by induced mutation rate and the number of loci to be improved. An extraordinarily large number of X_2 -plants would be required if induced mutation rate is very low, and/or if material plants are undesirable for some multiple loci and all or most of these loci are to be improved together, keeping the genetic composition of other originally desirable loci unchanged. 2). A larger number of X_2 -plants need to be grown if a higher selection intensity is to be adopted. This leads us to the conclusion that the number of X_2 -plants can be decreased only at the sacrifice of genetic advance from X_2 -to X_3 -generation. 3). The number of X_2 -plants can be economized by increasing the number of control lines to be applied for discriminating mutants. The relation between the number of X_2 -plants and that of control lines, however, is considered to be greatly affected by the homogeneity of breeding environment and/or the phenotypic stability of breeding character and therefore would be too complicated to be formulated by a simple formula.

More definite knowledges could be drawn from some numerical computations calculated by the use of the equations in this paper, which will be presented in the next paper.

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自殖性作物の量的形質に関する突然変異育種 2 世代目における
栽植個体数推定のための理論的基礎

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量的形質が育種対象であるときの X_2 -個体数を推定するための諸式を、3つの異なる選抜モデルについて、理論的に求めた。これらの理論式から、以下に述べるような一般的な知見が得られた。

1) 育種形質に関与する遺伝子座間に連鎖がなければ、ある選抜強度のもとで、 X_2 -個体数は大まかにいって $\binom{L_1}{j} \left(\frac{1}{2m}\right)^j$ に反比例すると言える。ここに、 m は遺伝子あたりの人為突然変異率を、また L_1 および j はそれぞれ、育種素材の劣悪遺伝子座の総数およびそのうちで突然変異処理によつて一挙に改良すべき遺伝子座の数を示す。このことは、 X_2 -個体数が人為突然変異率および改良すべき遺伝子座数に強く影響されることを意味

する。特に、劣悪遺伝子の突然変異率が極めて低かつたり、いくつかの遺伝子座を同時に改良しようとする場合には、法外に多くの X_2 -個体数が必要であろう。2) 選抜強度を高めて選抜効果をあげようとするれば、それだけ多くの X_2 -個体が必要である。3) 突然変異個体を識別するための対象個体あるいは区の数を増すほど、 X_2 -個体は少なくて済む。しかしながら、両者の関係は、育種環境の均一度や育種形質の形質発現安定度など表わすて大きく変わることが考えられ、簡明な理論式によつことは困難なようである。

本報中の諸式を用いて数値計算を行なつた結果、より具体的な知見がいくつか得られた。それらは次報で述べることにする。