EFFECT OF GENOTYPE X ENVIRONMENT INTERACTION ON THE EFFICIENCY OF DIFFERENT METHODS OF SELECTION A COMPUTER SIMULATION STUDY*)

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RINGKASAN

Pengaruh interaksi antara faktor-faktor genotipe x lingkungan terhadap efisiensi beberapa methode pemuliaan tanaman dipelajari melalui simulasi dengan menggunakan komputer IBM 370 model 135. Program komputer yang ditulis dalam bahasa FORTRAN IV dibuat untuk methode-methode seleksi masa, seleksi saudara sekandung, seleksi saudara tiri dan seleksi keturunan saudara tiri. Tehnik simulasi yang digunakan, serupa dengan tehnik yang digunakan dalam penelitian terdahulu (Prajitno, 1979).

Hasil penelitian menunjukkan bahwa estimasi kemajuan genetis dengan menggunakan varians genetik yang bersifat aditif, yang diperoleh dari sistem perkawinan design I dari Comstock dan Robinson (1948), hanya berlaku untuk satu siklus seleksi saja. Hal ini dikarenakan nilai prediksi dari kemajuan genetis yang diperoleh dari estimasi varians genetik aditif dengan menggunakan design I, ternyata jauh lebih tinggi dari nilai kemajuan genetis aktuil yang diperoleh. Besarnya bias ini akan makin meningkat dengan makin bertambahnya siklus seleksi yang dilakukan. Makin besarnya bias ini juga diakibatkan oleh makin berkurangnya variasi phenotipik dengan makin bertambahnya siklus seleksi.

Dalam studi ini, seleksi saudara tiri memperlihatkan keunggulannya sebagai methode seleksi yang terbaik, dalam goncangan lingkungan yang berubah-ubah mengingat :

a. Adanya kemajuan genetis yang cukup besar per siklus seleksi.

b. Diperolehnya kemajuan genetis yang konsisten tanpa memandang besarnya variasi lingkungan yang timbul maupun pengaruh interaksi antara genotipe x lingkungan.

c. Memiliki rate yang cukup tinggi dalam proses pencapaian nilai genotipik maksimum.

Namun demikian, mengingat kompleksnya faktor-faktor yang berpengaruh, pendapat di atas perlu diuji melalui suatu penelitian lapangan jangka panjang, setidak-tidaknya 20 sampai 30 generasi.

INTRODUCTION

There is agreement among plant breeders that the interaction between genotype and environment plays an important role in the development of better varieties. The importance of this interaction is even more pronounced in the tropics where the environments within the same location differ greatly over time by virtue of three growing seasons in a year, namely: wet, dry and summer. Thus the choice of a variety to fit an environment will have to consider not only environmental variability over location, but also changes over season in a location.

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Genotype x environment interaction influences the selection procedure in several ways. First, it affects the estimate of genetic variances in that, a large interaction will result to a corresponding reduction in the variance among genotypes. Consequently the effectiveness of most selection procedures will also be reduced. Second, certain types of population, by virtue of its genetic configuration, maybe more stable over environments than others. Consequently, the magnitude of the genotype x environment interaction may influence the kind of population that a breeder will aim for his selection program.

In this study the use of computer simulation technique is proposed to define the significance of genotype x environment interaction on the relative efficiency of some selection methods.

MATERIALS AND METHODS

A similar simulation procedure (Prajitno, 1979) was used in this study, i.e. through the following :

1. Specification of the phenotype. These rules consist of three major components. First, is specification of the genotypic value which essentially follows the accepted genetic theory. Second, is specification of environmental effect and third, is interaction of genotype by environment.
2. Estimation of variances.
3. Evaluation of the efficiency of different breeding procedures under various condition.

Steps (1) and (2) were discussed in detail in the previous paper (Prajitno, 1979). The succeeding section would be discussed step (3) only.

Predicted and Actual Response to Selection.

Mass Selection. The same individuals from Design I experiment were used for simulating mass selection scheme. The flow chart is shown in figure 1. In each cycle of selection, ten percent top yield individuals were selected from the population. The predicted response to selection was calculated by using the formula :

$$Gs = [\,S\,\delta^2 A] / \delta^2 p \tag{1}$$

Where Gs is the predicted response to selection. $\delta^2 A$ is the estimated additive genetic variance from Design I, $\delta^2 p$ is the phenotypic variance of individual plant and S is the selection differential.

The actual response to selection was calculated through genotypic value data of each individual :

$$Gs = \overline{Yo} - \overline{Yp} \tag{2}$$

where $\overline{Y}o$ is the average genotypic value of the offspring come from top 10% selected parents and $\overline{Y}p$ is the average genotypic value of parental population. A comparison between actual and predicted selection response was made.

Full-Sib Family Selection. The full-sib family selection was simulated by using the same individuals from the Design I experiment. The 100 males were crossed to 100 females. The predicted response of full-sib family selection was calculated by using the formula :

$$GS = [\, S\,(1/2)\delta^2 A] / \delta^2 p_{FS} \tag{3}$$

where $\delta^2 p_{FS}$ is the phenotypic variance of full-sib family means.

The actual response to selection was calculated by using the genotypic value data of each population, i.e.

$$Gs = \overline{Y}o(fs) - \overline{Y}p(fs) \tag{4}$$

where $\overline{Y}o(fs)$ is the average genotypic value of offsprings come from selected parents of 10% top full-sib families. $\overline{Y}p(fs)$ is the average genotypic value of parental population. Flow chart of the program is shown in figure 2.

Half-Sib Family Selection. This is the well known technique commonly called as ear-to-row selection. Individuals of superior half-sib family are the selection unit. In simulating this selection scheme the same individuals from Design I experiment were used. For this type of selection the predicted response to selection is :

$$Gs = [\, S(1/4)\, \delta^2 A] / \delta^2 p_{HS} \tag{5}$$

where $\delta^2 p_{HS}$ is the phenotypic variance of half-sib family means.

The actual response to selection was calculated from genotypic value data :

$$Gs = \overline{Y}o(hs) - \overline{Y}p(hs) \tag{6}$$

where $\overline{Y}o(hs)$ is the average genetic value of the offsprings come from male parents of top 10% selected half-sib families. $\overline{Y}p(hs)$ is the average genetic value of parental population. The flow diagram is shown in figure 3.

Half-Sib Progeny Selection. The selection is the self progeny of the common parent of superior half-sib progenies. Similar to half-sib family selection, the same individuals from Design I experiment were used for simulating this selection scheme. In this case the predicted response to selection :

$$Gs = [\, S(1/2)\, \delta^2 A] / \delta^2 p_{HS} \tag{7}$$

The actual response to selection was calculated directly from the genotypic value data :

$$Gs = \overline{Y}o(s_1) - \overline{Y}p(hs) \tag{8}$$

where $\bar{Y}o\ (s_1)$ is the average genotypic value of the offsprings come from the self progeny of the common (male) parents of 10% superior half-sib progenies. $\bar{Y}p(hs)$ is the average genotypic value of parental population.

RESULTS AND DISCUSSION

Artificial selection changes the population mean through (1) selection of superior parents for the next generation results in a change of gene frequency, (2) the change in gene frequency will bring about a change in mean in the next generation, and finally (3) the product of (1) and (2) is the expected change in the population mean from one generation to the next.

Population improvement methods currently used can be devided into intra-population selection schemes where the objectives is the improvement of the population mean, and inter-population selection schemes where the improvement of the variety cross is the desired goal. This section will describe the role of G x E interaction on genotypic and phenotypic response to selection in four intra-population selection schemes namely, (1) mass selection, (2) full-sib family selection, (3) half-sib family selection and (4) half-sib progeny selection methods. The discussion will be presented in the following manner: first, a discussion of each selection method separately and then secondly, a general evaluation of all selection methods under study.

One of the advantages on using a simulation technique for evaluating a breeding methodology is both genotypic and phenotypic value of each simulated individual known exactly. This means a comparative study between predicted and actual response to selection is possible to be conducted.

For each selection procedure two kind of simulation studies were done. First, simulation of selection procedure under different genetic and environmental models. In this study only three cycles of selection were simulated. The G x E interaction effect was expressed as cases 1, 2, 3 and 4, as mentioned in the previous paper (Prajitno, 1979). The aim of the study was (1) to see the effect of G x E interaction and genetic model on genotypic and phenotypic population means, (2) to compare the actual and predicted selection response under different genetic and environmental model. Secondly, simulation of ten cycles selection program for all selection methods using the additive genetic model under case 1 and 4. This was done to look at the effect of long term selection process on genotypic mean of population, i.e. in what generation the population will reach its genetic fixation.

Mass Selection

When there was no environmental effect (case 1) the phenotypic mean was almost similar to its corresponding genotypic mean, while when seasonal effect was occured (case 2, 3, and 4) those values were different. Although there was an up and down variation in phenotypic mean due to seasonal fluctuation, genetic gain due to selection seem not to be affected by the environmental and genotype x environment interaction variances.

When selection was increased to ten cycles, however the results show that the genotypic mean of population increase steadily up to three cycles. Then there was large fluctuation of genotypic mean after three cycles (Figures 5 and 6).

In two loci model, the ranges of genotypic mean of population after 3 cycles of mass selection was from 49.85 to 58.15 while the phenotypic mean varied from 44.74 to 65.82. In ten loci model, for genotypic mean, the range was 49.95 to 79.42 while its phenotypic mean had a range from 45.13 to 86.36.

A comparative studies between predicted genetic gain obtained from an equation $Gs = S(\delta^2 A)/\delta^2 p$ and actual genetic gain obtained from genotypic value data was done. The results were presented in table 1 and 2.

It was shown that the predicted values were higher than the actual value, which means that estimate of genetic gain by using $\delta^2 A$ from Design I was an overestimate. The bias was higher in the later generation (after second cycle). The major reason here was the reduction of phenotypic variance $\delta^2 p$, after two cycles of selection process due to reduction in genetic variation. This caused a small $\delta^2 p$, which lead to the high genetic gain (Gs). However, reduction of genetic variation reduced the selection differential S which lead to small value of Gs. This is another reason why in some cases estimate of genetic gain Gs is smaller in advanced generation.

Because Gs is a function of S and $\delta^2 p$, generally speaking it can be said that the ratio of $S/\ \delta^2 p$ has an important role in estimating genetic gain. Relating to the reduction of genetic variation after a selection process, it was obvious that estimate of genetic gain using additive genetic variance come from mating design was good only for one cycle of selection. The upward bias became higher with the increase of a number of cycles of selection process as Comstock and Moll (1963) stated before.

In two loci model, when there was no environmental effect (case 1) the range of actual gain was from 1.62 to 2.31 or 2.82% to 4.42% of population mean. While in ten loci model the range was from —0.60 to 1.37, or —0.79% to 1.75% of population mean.

When there was an environmental effect (cases 2, 3, and 4), for two loci model the range of actual genetic gain was from 0.25 to 2.40 (0.33% to 3.08%). In ten loci model the range of actual genetic gain was from —0.33 to 1.45 (—0,44% to 1.83%). It was obvious here that G x E interaction increased the variation of actual genetic gain.

Variation in predicted genetic gain was higher than that in actual genetic gain. For two loci model with no environmental effect, is varied from 8.90 to 15.58 (15.47% to 27.11% of phenotypic mean of population) while in ten loci model it ranged from 12.95 (16.93%) to 25.77 (32.90%). When there was an environmental fluctuation (cases 2, 3, and 4) the predicted genetic gain ranged from 6.83 to 17.19 (10.40% to 33.55%)\for two loci model, and from 11.63 to 35.00 (14.30% to 51.63%) in ten loci model. Thus the G x E interaction increased the variation of predicted genetic gain. Comparing to actual genetic gain, the variation was higher.

Full-Sib Family Selection

Using the same 400 individuals as the base population, simulation was also done for full-sib family selection. Similar to mass selection, in case 1, i.e. when there was no seasonal fluctuation the phenotypic values almost similar their corresponding genotypic values, while in case 2, 3, and 4 was very different. Until three cycles of selection the genotypic mean of population still increase except in case 3 of two loci, dominant model, although the phenotypic mean fluctuated due to environmental variation. For two loci model, the range of genotypic mean was 49.85 to 65.00. The range of phenotypic mean was 44.74 to 70.33.

Because the genetic model permits a wider range of genotypic values for ten loci comparing to two loci, for ten loci model both ranges of phenotypic and genotypic mean of population are also wider. The range of genotypic mean in ten loci model was 49.95 to 111.10, while for phenotypic mean was 45.13 to 110.81.

A simulation of ten cycles full-sib family selection for additive model under case 1 and case 4 shows that for both two and ten loci model, the genotypic mean of population still increase after three cycles of selection. When there is no environmental effect (case 1) the genotypic mean of population reached its maximum value after five cycles of selection in two loci model (Figure 7). In ten loci model it reached its maximum value after six cycle of selection (Figure 8). Under case 4, where the environmental fluctuation was very high, the genotypic mean moved up and down due to environmental fluctuation. It reached its maximum value after seven cycles for two loci and after eight cycles for ten loci. It was also known that two loci were more influenced by environment than ten loci model. From both figure 7 and 8 it can be concluded that G x E interaction can delay the population in reaching its maximum genotypic mean.

A comparative studies between predicted and actual genetic gain are presented in table 3 and 4. Similar to mass selection, it is shown that most of predicted genetic gain is overestimated. Actual genetic gain from second cycle to third cycle was also less than its corresponding actual genetic gain from first to second cycle. This was also due to reduction of genetic variation in population after selection process. Comparing to mass selection the reduction seemed much higher. This was true in full-sib family selection, the number of selected individuals which were used for random mating were only twenty individuals (from 200 male and female parents) comparing to forty individuals in mass selection. This means that the genetic variation of selected individuals is also smaller.

When there was no environmental effect, the actual genetic gain varies from 1.95 (3.10%) to 7.35 (11.88%) in two loci model, and from 7.52 (8.18%) to 18.16 (19.28%) in ten loci model. However when environmental effect was occured the variation seemed becoming higher, i.e. from —0.06 (—0.10%) to 7.25 (11.74%) in two loci model and from 4.20 (4.77%) to 26.24 (21.79%) in ten loci model. Thus similar to mass selection, the G x E interaction increased variation of actual genetic gain.

Variation in predicted genetic gain was higher than variation in actual genetic gain. When no environmental effect, the predicted genetic gain varied from 53.32 (92.25%) to 129.68 (210.35%) in two loci model, and 52.10 (83.21%) to 87.65 (79.11%) for ten loci model. Similar to actual genetic gain, the variation seemed higher when there was an environmental effect. The range was 32.79 (58.96%) to 116.19 (206.49%) for two loci model and 38.95 (48.03%) to 168.76 (135.19%) in ten loci model. Thus the G x E interaction increased variation of predicted genetic gain. Comparing to actual genetic gain, the variation was wider.

Half-Sib Family Selection

The third simulation was done for half-sib family selection, using the same 400 individuals as the base population. When there was no environmental effect the phenotypic value was similar to its corresponding genotypic value, otherwise, in cases 2, 3, and 4 were very different. Similar to the previous selection scheme, the trend of genotypic mean of population moved upward until the third cycle. However the phenotypic mean of population moved up and down depending on its environmental fluctuation. For two loci model the range of genotypic mean is 49.85 to 67.00 while the range of phenotypic mean was 44.79 to 71.31. In ten loci model, the range was wider, i.e. from 49.95 to 132.15 for genotypic mean and 45.13 to 132.75 for phenotypic mean.

An additional simulation for ten cycles under case 1 and case 4 for additive model gave similar result to that of full-sib family selection. It was shown that the trend of genotypic mean of population moved upward steadily due to selection process, and reached its maximum value after a certain cycle of selection. For two loci model the maximum genotypic value was reached after three cycles of selection in case 1, and after 5 cycles of selection under case 4 (Figure 9). Thus the effect of G x E interaction delayed the population in reaching its maximum genotypic value. In ten loci model, the maximum genotypic value was reached after six cycles of selection under case 1 (no environmental effect) and after seven cycles under case 4. Thus similar to two loci model, the G x E interaction delayed population in reaching its maximum genotypic value. It could be concluded also that the maximum genotypic value was difficult to reach in ten loci rather than in two loci model.

A comparative studies between predicted and actual genetic gain were presented in tables 5 and 6. It was shown in these tables that the prediction was over estimate. The actual genetic gain from second to third cycle was less than its corresponding genetic gain from first to second cycle because of reduction of genetic variation in population after selection process. Comparing to full-sib family selection, it seemed that the reduction was a little bit higher, probably because random mated of fewer selected parents in half-sib family selection (ten male parents comparing to twenty in full-sib) which means a smaller genetic variation for the next generation.

When there was no environmental effect the actual genetic gain varied from 1.09 (1.63%) to 11.42 (17.18%) in two loci model, and from 4.05 (4.42%) to 29.18 (27.52%) in ten loci model. However the variation became wider when environmental fluctuation was presented, such as in cases 2, 3 and 4, i.e. 0.42 (0.67%) to 11.39 (17.29%) in two loci model and 0.35 (0.39%) to 32.07 (29.45%) in ten loci model. Similar to previous selection schemes, the G x E interaction increased variation of genetic gain.

A higher variation was appeared in predicted genetic gain. When there was no environmental effect the range of predicted genetic gain was 196.27 (304.62%) to 429.37 (789.14%) in two loci model, and 54.61 (82.97%) to 466.07 (575.39%) in ten loci model. Under cases 2, 3, and 4 i.e. there was an environmental fluctuation, the range was 52.63 (53.32%) to 549.00 (752.16%) in two loci model and 48.31 (68.89%) to 276.77 (214.77%) for ten loci model. Different to the previous selection methods, it was shown that in ten loci model the range of predicted genetic gain under environmental effect was smaller.

Half-Sib Progeny Selection

In simulating the half-sib progeny selection, the selection unit was the self progeny of the common (male) parent of superior half-sib progenies. Similar to the other family selection it was obvious that the trend of genotypic value moved upward until 3 cycles of selection. However the trend of phenotypic mean was much influenced by its corresponding environmental effect. The phenotypic trend was very different from one case to another, and also different from one genetic model to another.

The range of genotypic value is 49.95 to 109.59 in ten loci model and 49.85 to 67.00 for two loci model. The range of phenotypic value was from 45.13 to 114.62 in ten loci model and 44.74. to 71.04 for two loci model.

Ten cycle of selection was simulated also. The results were shown in figures 11 and 12. It seemed that the genotypic mean of population increased very high during the first cycle of selection. For two loci model it reached the maximum value after 3 cycles of selection under case 1, and after 4 cycles of selection under case 4. Similar with two loci, in ten loci model the first cycle gave the highest increment of genotypic mean. However it took more cycles on reaching its maximum value i.e. it required nine cycles of selection for both case 1 and case 4. It seemed also for both two and ten loci models, the trend under case 1 was similar with the trend under case 4. This means that the half-sib progeny selection was less influenced by environmental condition comparing to the other selection methods.

A results of comparison between actual and predicted genetic gain were shown in tables 7 and 8. Similar to the previous selection schemes, it was shown that the predicted values biased upward comparing to actual values. For two loci model, when there was no environmental effect the range of actual genetic gain was 0.85 (1.27%) to 11.66 (17.62%) while when there was an environmental effect the range was 0.07 (0.11%) to 10.86 (16.62%). In ten loci model the range was —1.59 (—1.60%) to 24.29 (24.02%) for no environmental effect, and 3.13 (3.50%) to 22.72 (22.82%) when there was an environmental fluctuation (cases 2, 3, and 4).

The predicted genetic gain was very high comparing to actual value. This was because of the high additive genetic variance from Design I, high selection differential and small phenotypic variance of half-sib family means. The range of predicted value for two loci model was 466.73 (736.98%) to 1013.48 (1530.94%) under no environmental effect (case 1) and 97.43 (187.33%) to 1445.12 (2442.41%) when there is an environmental effect (case 2, 3 and 4). In ten loci model, under no environmental effect, the range was 144.57 (237.12%) to 389.57 (391.49%) and 110.79 (163.7%) to 581.70 (615.88%) when there was an environmental effect.

Evaluation of Selection Methods

The relative efficiency of the four selection methods maybe evaluated on the following basis :

1. Actual and theoritical genetic advance per cycle.
2. Number of generation per cycle.
3. Magnitude of genotype x environment interaction.

An effective selection methods is a method that will give the highest genetic advance per unit of time. Furthermore a selection procedure that minimized the magnitude of G x E interaction would be most desirable.

Theoritically, mass selection will have the highest genetic gain (Gs) since it includes all of additive genetic variance. Full-sib family selection and half-sib progeny selection will be the second choice, because they include $\frac{1}{2}\,\delta^2A$, and half-sib family selection is the last choice because of only having $\frac{1}{4}\,\delta^2A$.

However, in most breeding program for cross pollinated crops, mass selection usually gives a low genetic gain. This discrepancy is due to the fact that in theoritical genetic gain it was assumed that the phenotypic variance of selection methods were the same, while in actual experiments they differed from one selection to the other. It must be considered that mass selection usually has the highest δ^2 p which causes a small genetic gain. This is true in this study as it is shown in table 9. If the maximum genetic gain was preferred as consideration in choosing the best selection method, it seemed that for both conditions, half-sib family selection would give the best result. The reason here was that in half-sib, a fewer selected individuals (parents) were randomized, which also means a high selection pressure comparing to other methods. This lead to high selection differential (S) which finally give a high genetic gain (Gs). Furthermore, the phenotypic variance of half-sib family selection was lowered compared to that of other selection methods. Half-sib family selection had more plants per family which influenced phenotypic variance. It might be recalled that every male used as half-sib family, had three females and these were all included in the calculation of phenotypic variance.

However for a long term program, in how many cycles or generations the population can reach maximum genotypic value must be considered. This was shown in table 10. It seemed that half-sib family selection also gave the best choice.

The third criterium for an effective selection procedure is response to genotype x environment interaction. A selection method was effective only if a high degree of assurance that the best lines or entries in one planting season would also be the best one in the next planting season. This consistency in performance among entries from one planting season to another was measured by entry x season interaction. Other things being equal, therefore a selection scheme that has a lower expected entry x season interaction would be more preferable (Hakim, 1969).

In this simulation study, consistency of performance could be shown by computing the difference between actual genetic gain under no environmental effect and when there was an environmental effect as shown in table 11. A selection method which had the smallest value means least influenced by genotype x environment interaction. Table 11 shows that half-sib family selection was the least affected by genotype x environment interaction.

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Table 1. **A comparison between actual and predicted genetic gain in mass selection. Two loci model.**

Genetic model and cycles			**Case 1**	**Case 2**	**Case 3**	**Case 4**
Additive						
	1 - 2	actual	2.31	1.78	1.95	1.50
		predicted	10.10	9.08	8.78	12.47
	2 - 3	actual	0.50	0.73	0.62	1.00
		predicted	11.68	8.46	10.17	17.19
Dominant						
	1 - 2	actual	1.62	1.59	1.82	1.10
		predicted	8.90	8.04	8.40	6.83
	2 - 3	actual	0.68	0.30	0.25	0.74
		predicted	11.14	6.95	10.57	8.30
Epistasis						
	1 - 2	actual	1.82	2.27	2.40	1.81
		predicted	13.57	13.65	13.19	11.89
	2 - 3	actual	1.47	0.67	0.74	1.30
		predicted	15.58	13.02	14.66	13.38

Table 2. **A comparison between actual and predicted genetic gain in mass selection. Ten loci model.**

Genetic model and cycles			**Case 1**	**Case 2**	**Case 3**	**Case 4**
Additive						
	1 - 2	actual	1.04	0.64	0.91	0.69
		predicted	14.74	17.47	13.02	15.51
	2 - 3	actual	0.22	0.80	0.60	0.35
		predicted	15.21	15.46	14.26	15.96
Dominant						
	1 - 2	actual	1.07	0.80	0.60	0.35
		predicted	12.95	13.65	13.72	14.29
	2 - 3	actual	-0.60	–0.33	0.32	0.50
		predicted	11.23	11.63	12.94	12.75
Epistasis						
	1 - 2	actual	1.37	1.15	1.17	1.03
		predicted	25.77	29.36	27.35	35.00
	2 - 3	actual	0.97	1.45	1.09	0.73
		predicted	23.69	27.57	25.96	33.17

Table 3. **A comparison between actual and predicted genetic gain in full-sib family selection. Two loci model.**

Genetic model and cycles		Case 1	Case 2	Case 3	Case 4
Additive					
1 - 2	actual	5.69	5.39	6.14	4.09
	predicted	91.62	80.81	67.68	39.17
2 - 3	actual	2.02	3.30	2.43	2.33
	predicted	53.32	37.78	42.14	116.19
Dominant					
1 - 2	actual	5.19	4.99	5.05	4.72
	predicted	80.98	64.94	77.22	29.05
2 - 3	actual	1.95	1.42	−0.06	0.65
	predicted	57.11	39.76	32.79	51.44
Epistasis					
1 - 2	actual	7.35	7.11	7.25	6.34
	predicted	129.68	103.74	94.39	65.44
2 - 3	actual	2.78	3.40	2.50	1.45
	predicted	101.15	59.0[illegible]	69.56	109.41

Table 4. **A comparison between actual and predicted genetic gain in full-sib family selection. Ten loci model.**

Genetic model and cycles		Case 1	Case 2	Case 3	Case 4
Additive					
1 - 2	actual	12.32	11.66	12.37	12.43
	predicted	52.10	63.55	56.59	43.16
2 - 3	actual	14.63	10.99	9.57	8.98
	predicted	60.43	73.96	42.05	56.44
Dominant					
1 - 2	actual	8.40	6.06	6.86	8.61
	predicted	53.54	38.95	60.87	40.33
2 - 3	actual	7.52	9.30	7.64	4.20
	predicted	85.71	82.91	93.77	102.39
Epistasis					
1 - 2	actual	18.16	17.35	16.26	18.84
	predicted	79.61	80.27	69.98	90.17
2 - 3	actual	16.12	26.24	19.09	15.44
	predicted	87.65	168.76	93.57	136.63

Table 5. **A comparison between actual and predicted genetic gain in half-sib family selection. Two loci model.**

Genetic model and cycles			Case 1	Case 2	Case 3	Case 4
Additive						
	1 - 2	actual	8.49	7.78	8.12	7.53
		predicted	290.19	254.00	175.21	77.48
	2 - 3	actual	1.66	2.37	1.09	2.07
		predicted	211.78	58.41	70.30	549.00
Dominant						
	1 - 2	actual	7.80	7.14	7.99	6.30
		predicted	272.59	212.19	247.31	54.71
	2 - 3	actual	1.35	2.01	1.16	0.42
		predicted	196.27	52.63	60.15	125.02
Epistasis						
	1 - 2	actual	11.42	9.62	11.39	9.82
		predicted	429.37	389.03	425.24	107.97
	2 - 3	actual	1.09	2.89	0.46	1.95
		predicted	356.80	108.42	79.70	476.11

Table 6. **A comparison between actual and predicted genetic gain in half-sib family selection. Ten loci model.**

Genetic model and cycles			Case 1	Case 2	Case 3	Case 4
Additive :						
	1 - 2	actual	16.05	17.36	17.52	11.56
		predicted	54.61	83.29	48.31	53.96
	2 - 3	actual	14.64	16.00	14.80	11.15
		predicted	466.07	175.07	131.14	137.26
Dominant :						
	1 - 2	actual	12.31	13.01	12.35	9.27
		predicted	80.27	121.96	97.85	78.88
	2 - 3	actual	4.05	5.09	0.35	3.02
		predicted	118.04	178.05	86.91	97.66
Epistasis :						
	1 - 2	actual	29.18	32.07	28.01	28.76
		predicted	89.78	144.89	90.70	137.02
	2 - 3	actual	11.81	14.48	23.85	26.57
		predicted	195.91	276.77	245.06	266.47

Table 7. **A comparison between actual and predicted genetic gain under half-sib progeny selection. Two loci model.**

Genetic model and cycles		**Case 1**	**Case 2**	**Case 3**	**Case 4**
Additive :					
1 - 2	actual	8.87	7.76	7.79	7.20
	predicted	484.59	561.70	359.03	160.65
2 - 3	actual	1.28	2.39	1.38	2.24
	predicted	1848.28	471.34	264.61	1445.42
Dominant :					
1 - 2	actual	7.44	6.58	8.32	6.44
	predicted	466.73	302.70	382.60	97.43
2 - 3	actual	1.66	1.83	0.07	0.38
	predicted	589.32	342.77	126.27	343.97
Epistasis :					
1 - 2	actual	11.66	9.95	10.86	9.06
	predicted	1013.48	969.60	724.33	213.21
2 - 3	actual	0.85	1.99	1.65	3.03
	predicted	837.71	254.05	289.56	1399.70

Table 8. **A comparison between actual and predicted genetic gain under, half-sib progeny selection. Ten loci model.**

Genetic model and cycle		**Case 1**	**Case 2**	**Case 3**	**Case 4**
Additive :					
1 - 2	actual	11.22	14.34	12.70	7.37
	predicted	144.57	320.03	215.75	127.69
2 - 3	actual	15.46	7.11	5.09	9.20
	predicted	366.98	379.26	218.08	229.81
Dominant :					
1 - 2	actual	8.38	11.04	8.84	3.10
	predicted	265.04	360.87	178.64	110.79
2 - 3	actual	3.07	3.13	4.90	11.28
	predicted	243.39	501.70	201.82	981.62
Epistasis :					
1 - 2	actual	24.29	22.72	22.32	21.65
	predicted	389.57	306.63	307.54	447.80
2 - 3	actual	—1.59	10.05	10.04	7.99
	predicted	329.45	410.28	302.22	376.78

Table 9. **Range of actual genetic gain of four selection methods under different environmental condition. (Percentage to genotypic mean of population).**

Method of selection	No environmental effect (Case 1)	Under environmental effect (Cases 2, 3, 4)
Mass	2.82 — 4.42	0.44 — 3.08
Full-sib family	3.10 — 19.28	0.10 — 21.79
Half-sib family	1.63 — 27.52	0.67 — 29.45
Half-sib progeny	1.60 — 24.02	0.85 — 22.82

Table 10. **Number of cycles and generations needed for reaching the maximum genotypic value.**

Selection method	number of cycle		Number of generation	
	2 loci	10 loci	2 loci	10 loci
No environmental effect (case 1) :				
Mass	>10	>10	>10	>10
Full-sib family	5	6	10	12
Half-sib family	3	7	6	14
Half-sib progeny	3	9	9	27
Environmental effect (case 4) :				
Mass	>10	>10	>10	>10
Full-sib family	7	8	14	16
Half-sib family	5	7	10	14
Half-sib progeny	4	9	12	27

Table 11. **The difference between actual genetic gain under no environmental effect and when there was an environmental effect (cases 2, 3 and 4).**

Selection method	Difference	
Mass	2.30	
Full-sib family	2.85	
Half-sib family	1.44	
Half-sib progeny	1.82	

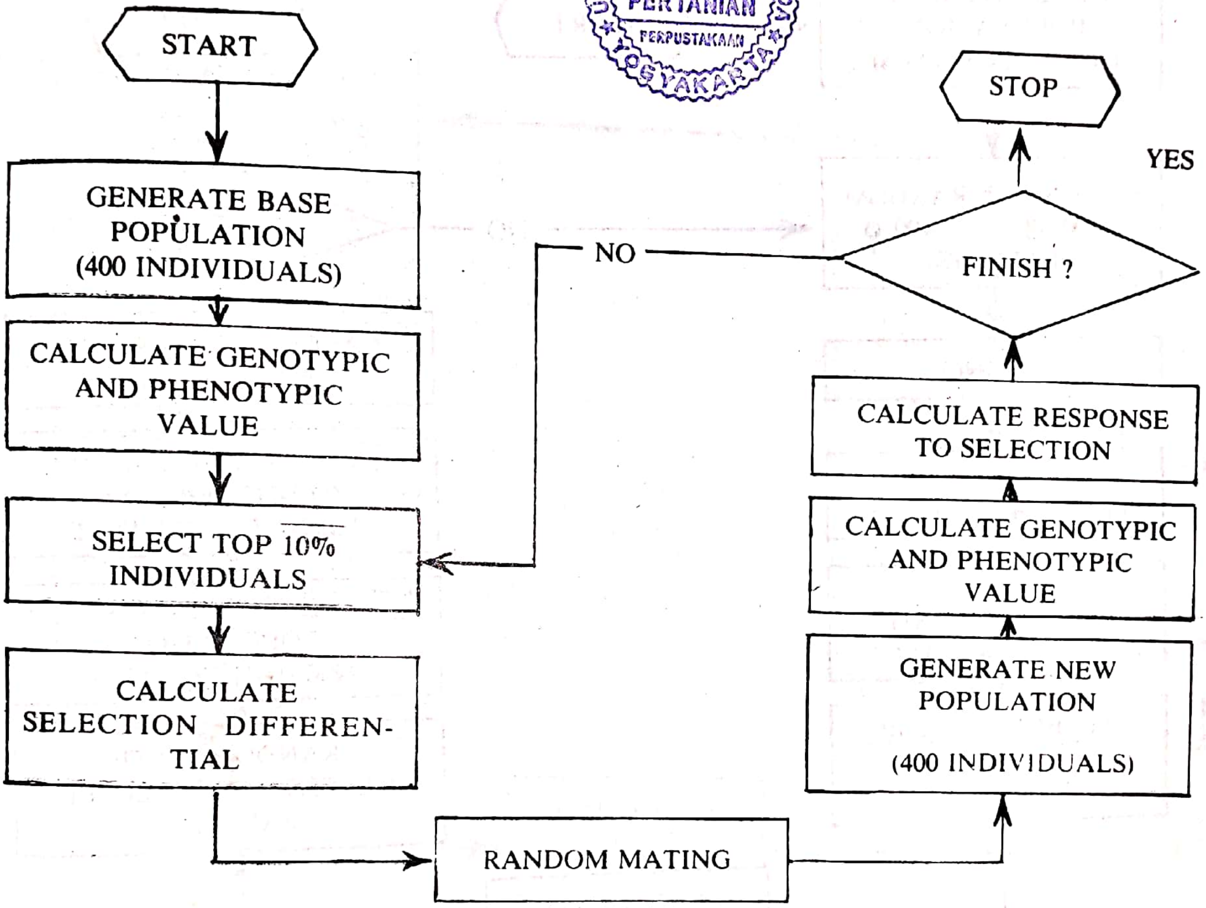

Figure 1. **Flow chart of mass selection scheme.**

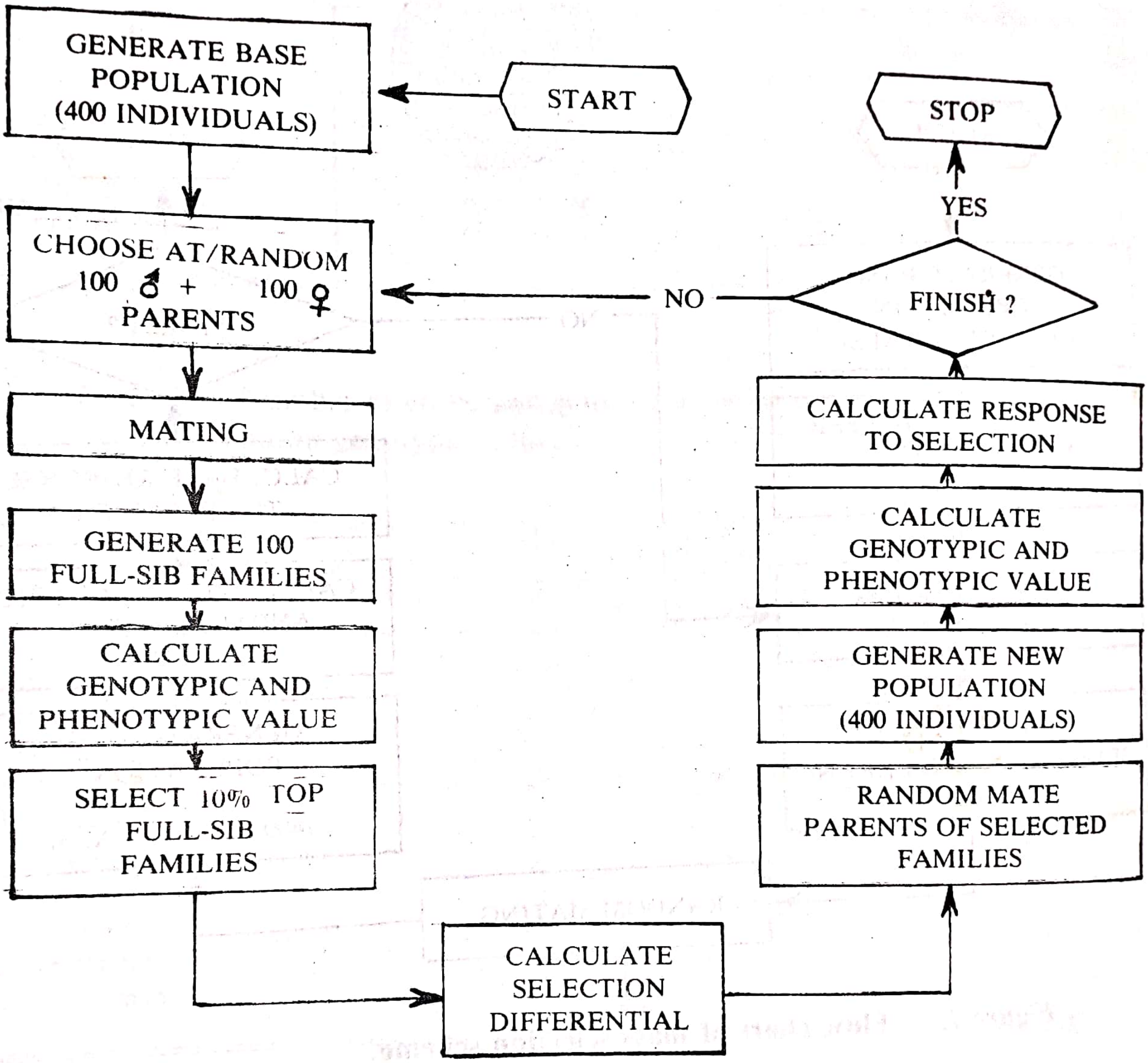

Figure 2. **Flow chart of full-sib family selection scheme.**

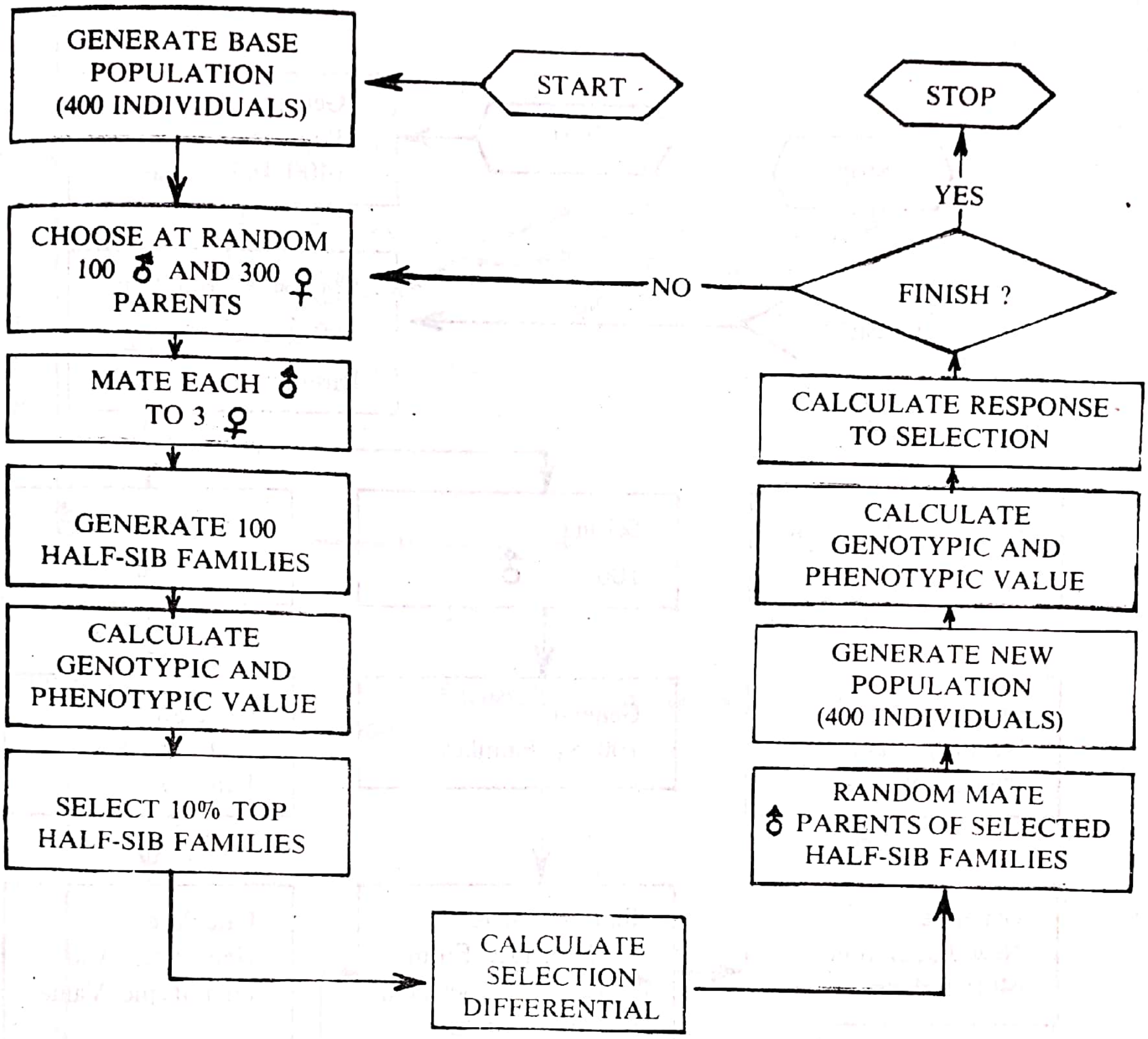

Figure 3. **Flow chart of half-sib family selection scheme.**

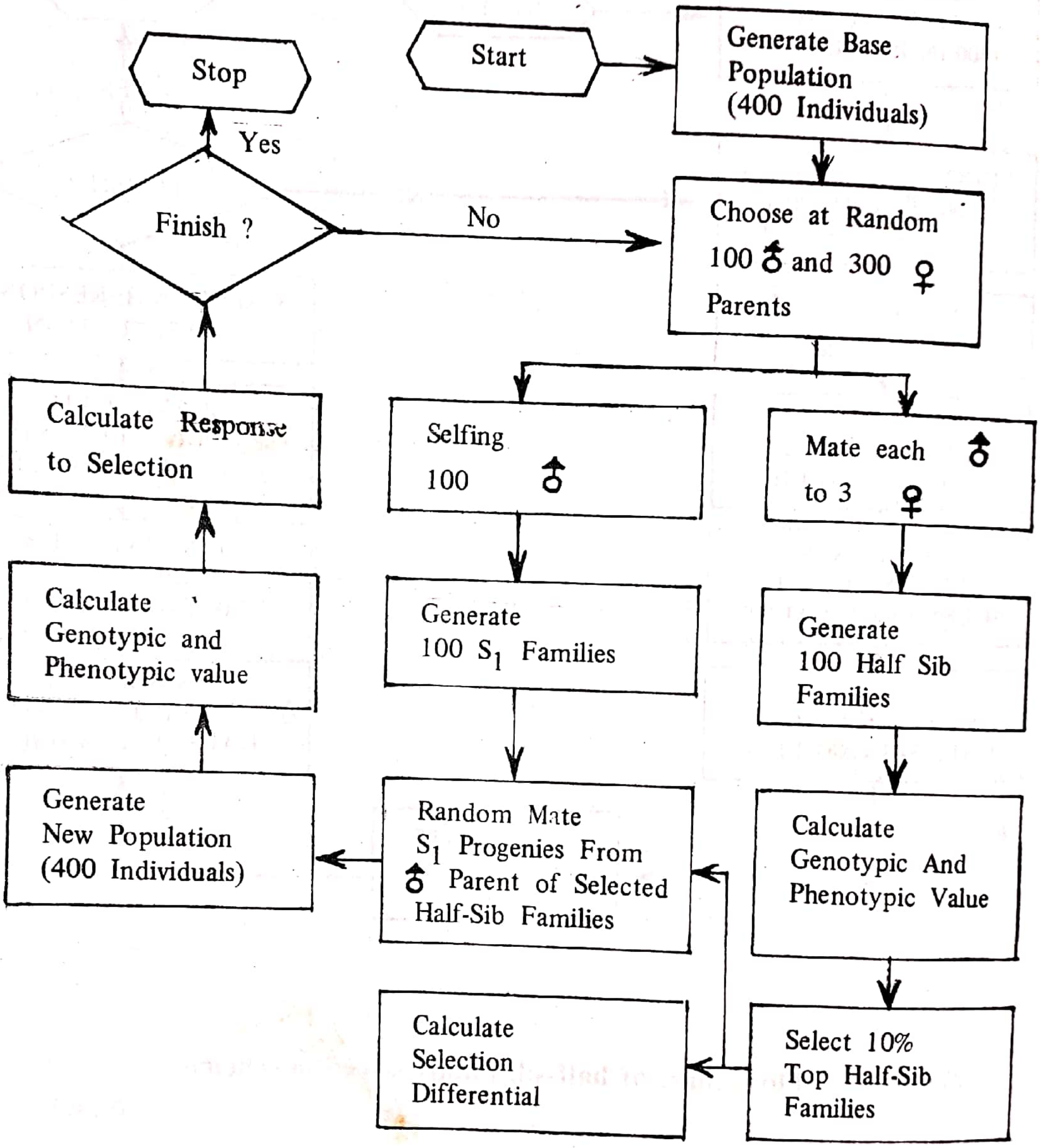

Figure 4. **Flow chart of half-sib progeny selection scheme.**

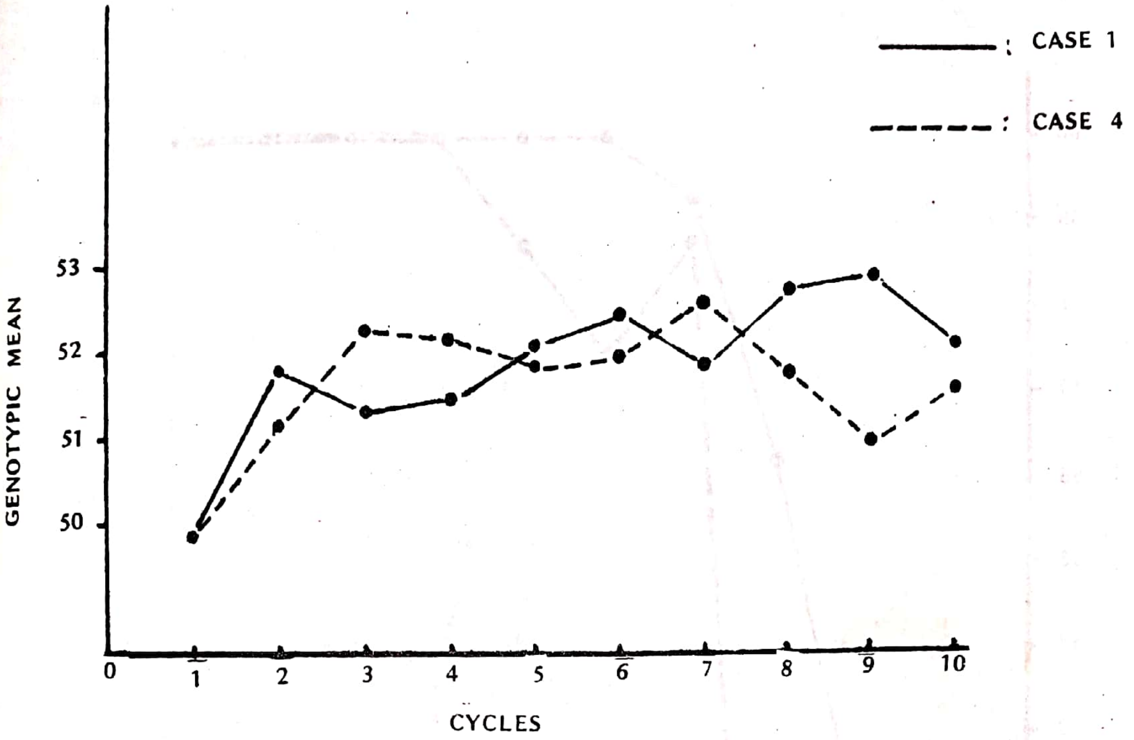

Figure 5. **Genotypic mean of population in ten cycles of mass selection. Two loci model.**

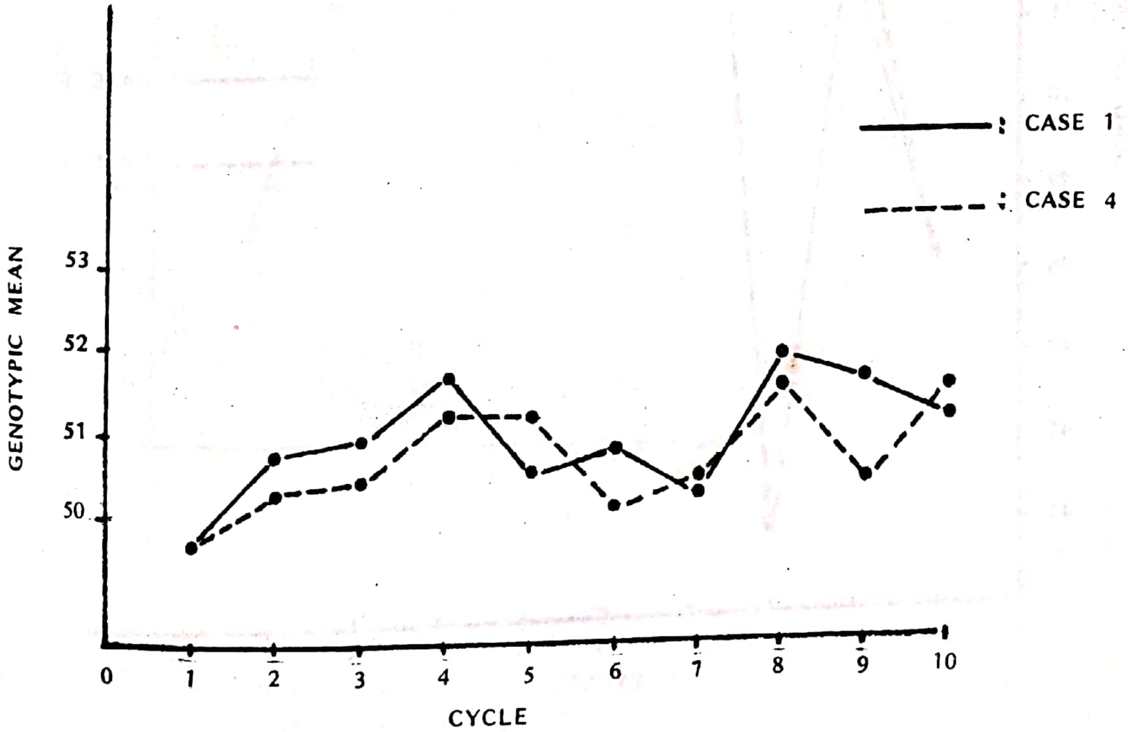

Figure 6. **Genotypic mean of population in ten cycles of mass selection. Ten loci model.**

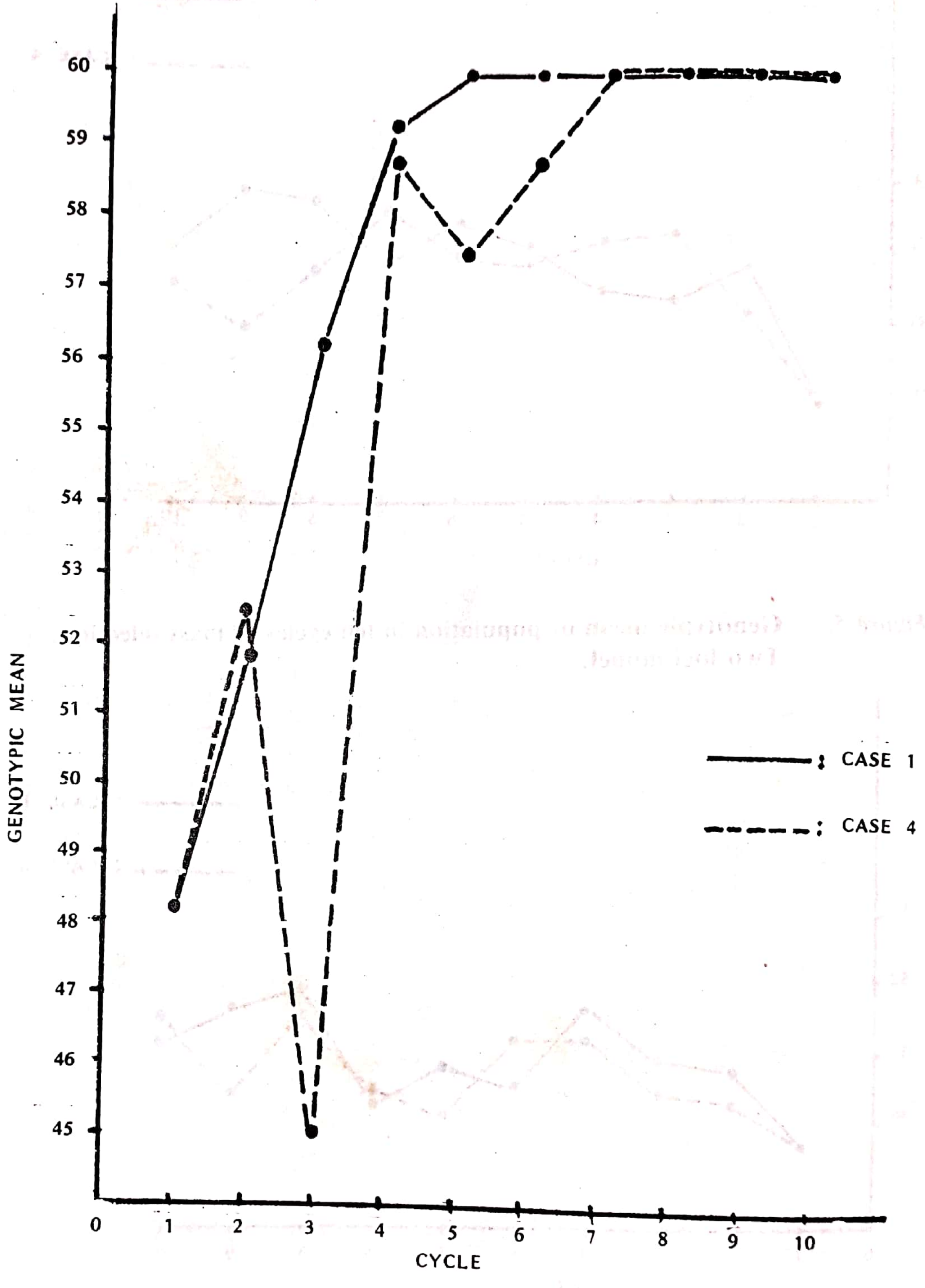

Figure 7. **Genotypic mean of population in ten cycles of full-sib family selection. Two loci model.**

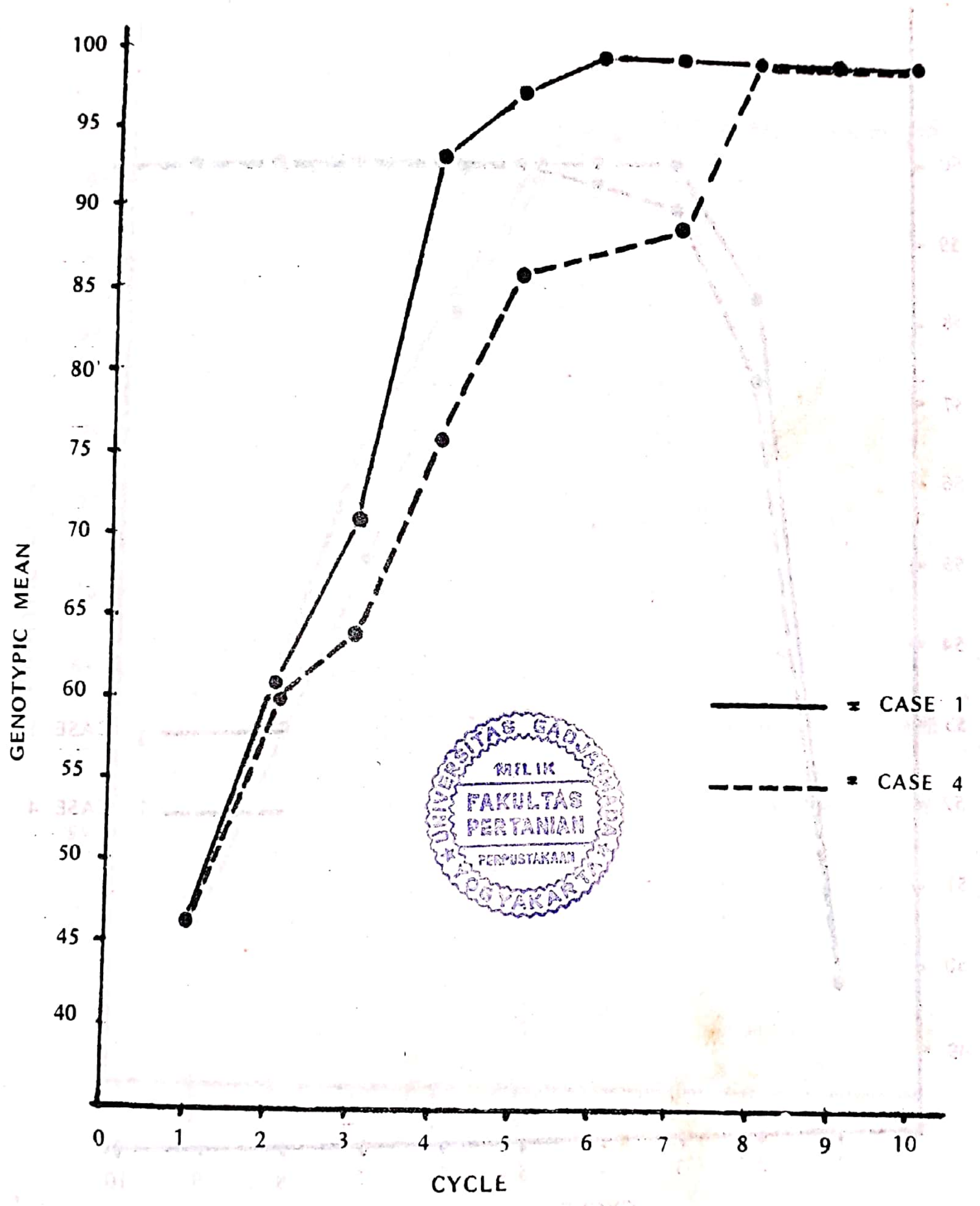

Figure 8. **Genotypic mean of population in ten cycles of full-sib family selection. Ten loci model.**

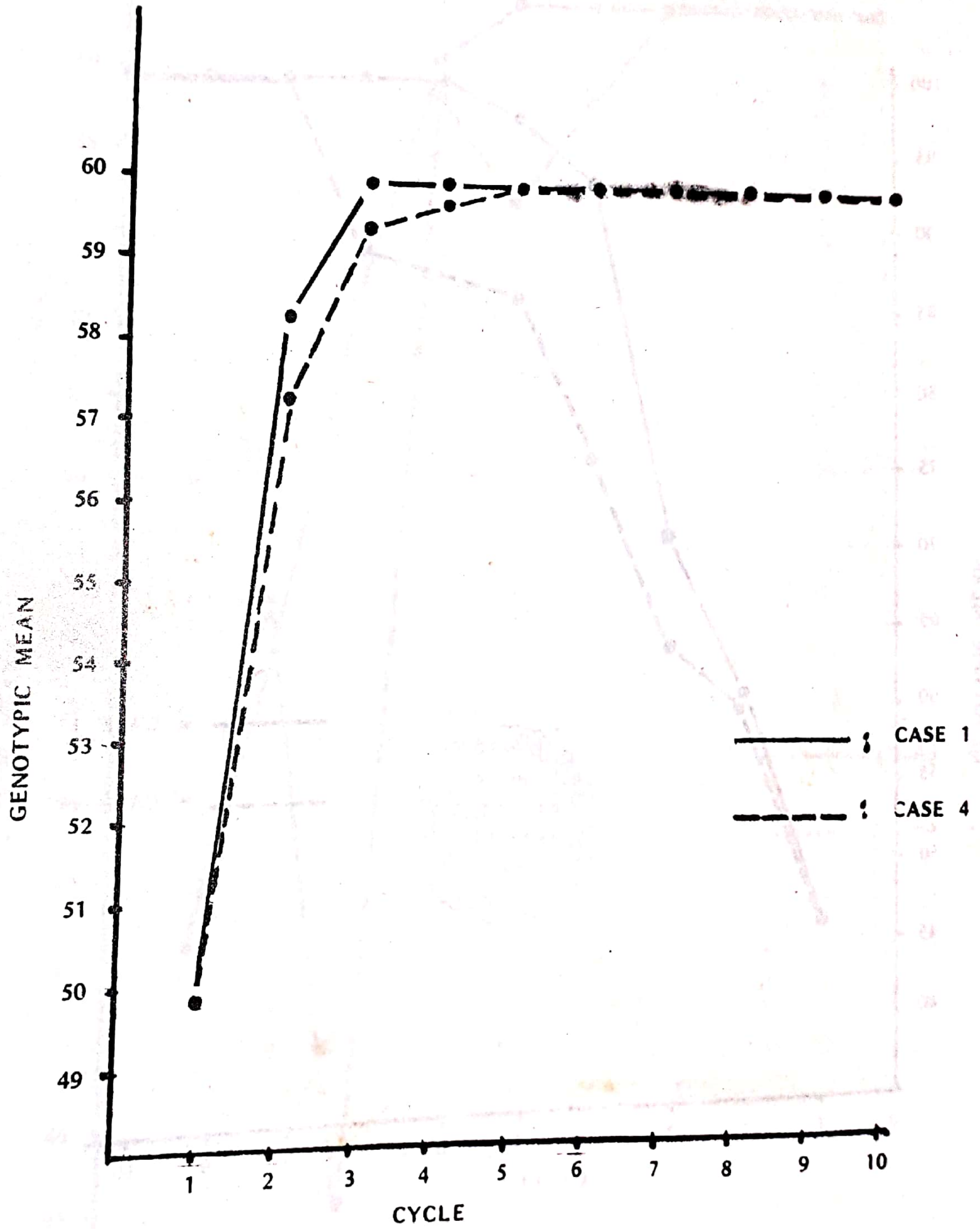

Figure 9. **Genotypic mean of population in ten cycles of half-sib family selection. Two loci model.**

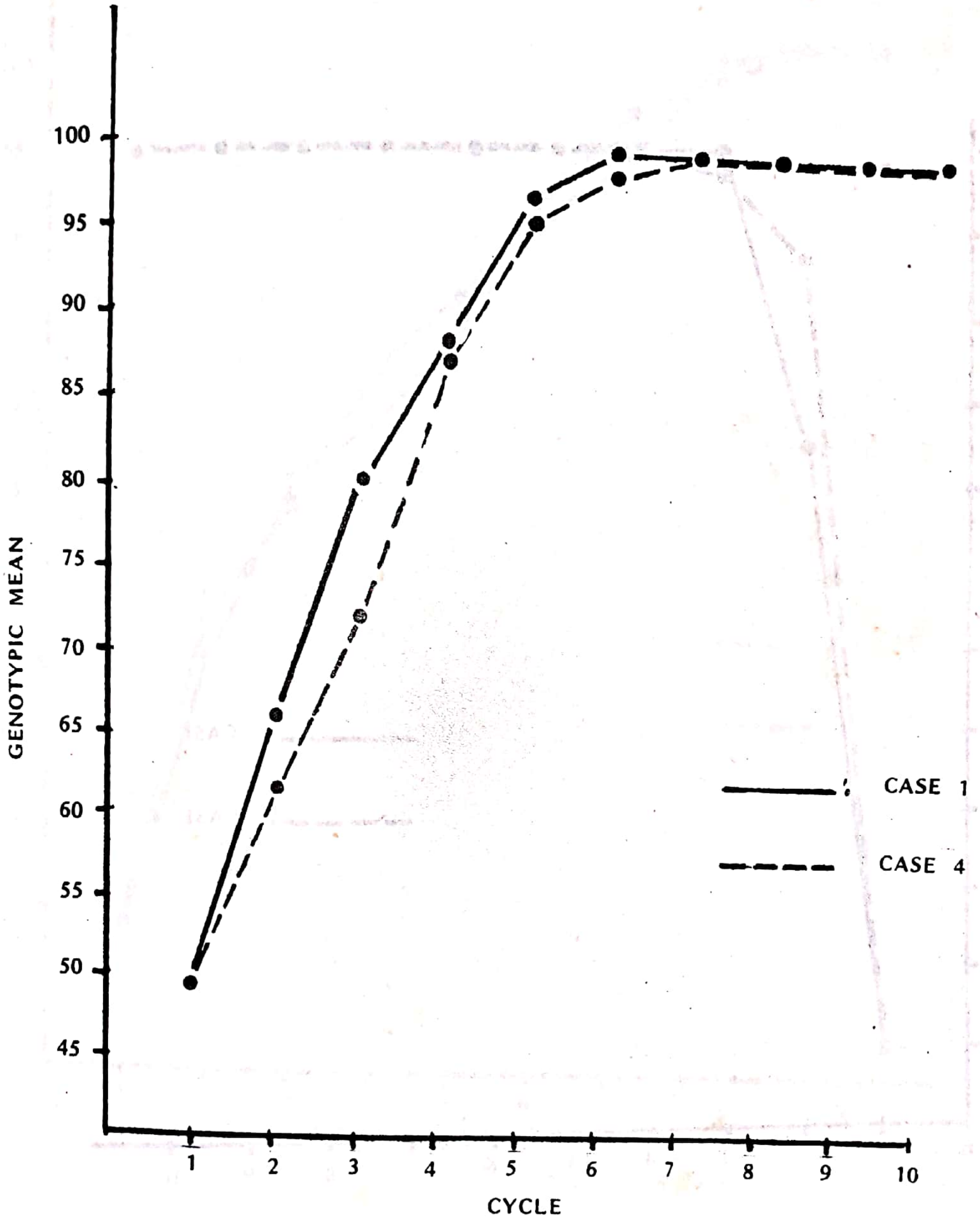

Figure 10. **Genotypic mean of population in ten cycles of half-sib family selection. Ten loci model.**

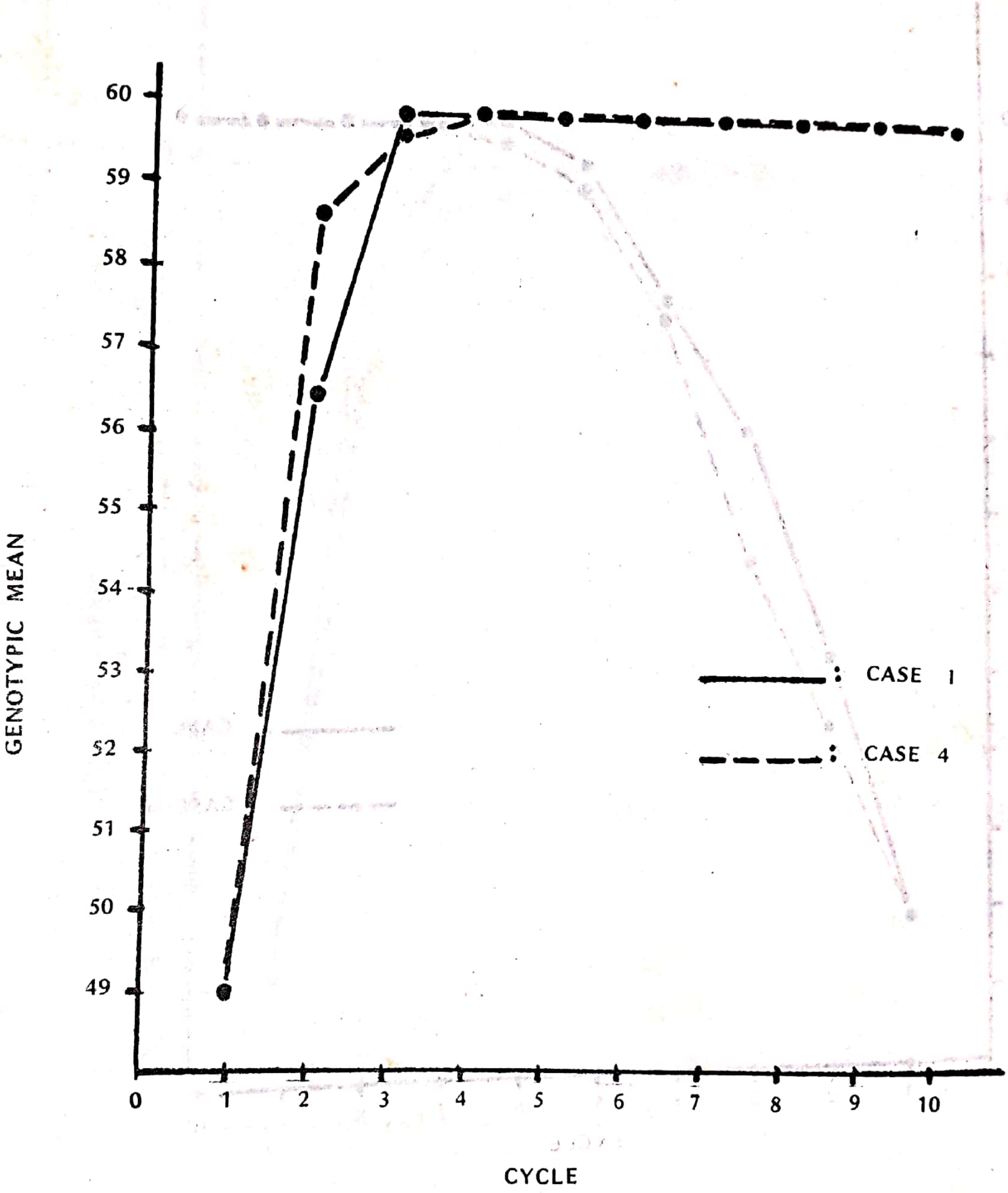

Figure 11. **Genotypic mean of population in ten cycles of half-sib progeny selection. Two loci model.**

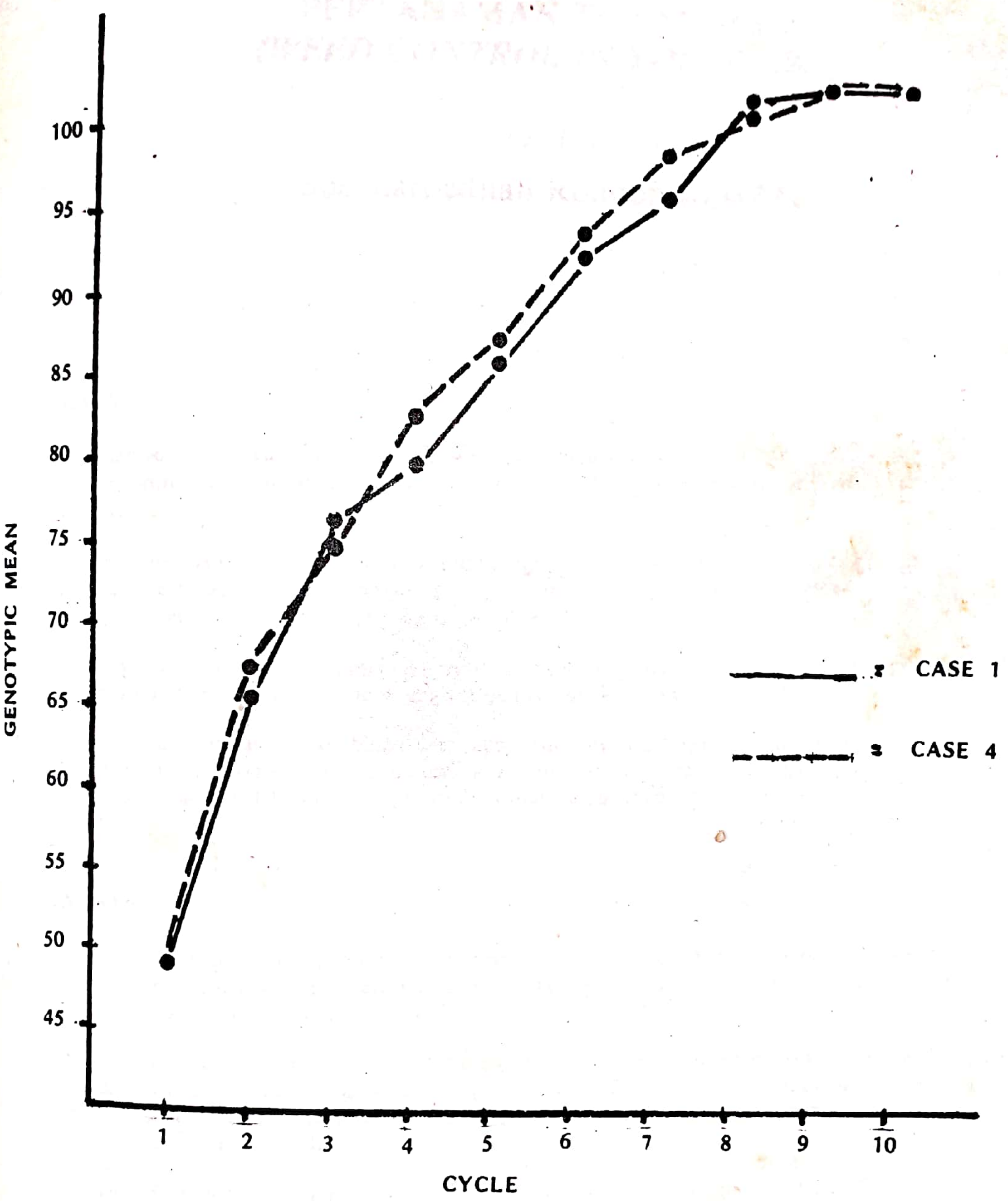

Figure 12. **Genotypic mean of population in ten cycles of half-sib progeny selection. Ten loci model.**