THE UNIVERSITY OF MICHIGAN
COLLEGE OF ENGINEERING
Simulation Center

Technical Report

ARTIFICIAL GENETIC BREEDING PROCEDURES FOR PARAMETER OPTIMIZATION

Roy B. Hollstien

with assistance from:

NATIONAL SCIENCE FOUNDATION
GRANT NO. GJ-36115
WASHINGTON, D.C.

administered through:

OFFICE OF RESEARCH ADMINISTRATION ANN ARBOR

September 1973

ABSTRACT

This report describes a method of applying the breeding procedures of agriculture to optimization problems in computer science and/or engineering. A direct search in parameter space is guided by an artificial breeding program, so mathematical relationships between the parameters and the objective are not required. Artificial organisms are represented by diploid genotypes composed of chromosome-like arrays of binary bits. Each genotype controls the synthesis of a trial point in parameter space, and the phenotypic worth of each individual is determined by a measure of the search objective evaluated at that point. Gene action algorithms employ intra-allelic additivity, intra-allelic interaction with dominance at the gene level controlled by modifier loci, inter-allelic additivity of multiple factors, and epistatic control of different steps in synthetic pathways. Agricultural breeding methods are used to select and mate parents in successive generations, starting with heterozygous populations that simulate wide crosses of genetically dissimilar varieties. Offspring are produced by meiotic division of parental genotypes and the union of two gametic sets of chromosomes. Genetic recombination is induced by independent segregation of chromosomes and crossing-over of nonsister chromatids during gametogenisis; recombination is suppressed by inhibiting crossing-over within inverted or translocated chromosome segments. Background variation is maintained by point mutations that transform the diallelic genes into their opposite conformation. Mathematical functions of numerical parameters are used to test combinations of artificial species and breeding methods for rates and limits of progress on objective surfaces with topological features such as ridges, plateaus, and multiple peaks that are nemeses of general methods of optimization.

FORWARD

This report covers research partially supported by the National Science Foundation Office of Computing Activities under Grant No. GJ-36115. The project, entitled "Artificial Genetic Breeding Procedures for Parameter Optimization," was conducted at the University of Michigan College of Engineering Simulation Center while the author was an Associate Research Engineer in the Department of Aerospace Engineering. The grant was effective from October 1, 1972 to March 31, 1974. National Science Foundation support during this period is greatfully acknowledged.

Basic concepts of the ARTIFICIAL BREEDING method of optimization were developed at the University of Michigan prior to the NSF assisted study. I especially thank Professors Robert M. Howe, Chairman of the Department of Aerospace Engineering, and Laurence E. Fogarty, Director of the Simulation Center, for the opportunity to pursue this study.

I am also very greatful to Dr. R. W. Allard, Department of Genetics, University of California at Davis for his personal critique of the fundamental concepts of ARTIFICIAL BREEDING in simulating the genetic search process involved in agricultural breeding programs and as a method of optimization in computer science and/or engineering. The breeding methods used in this study are based on the techniques lucidly described in his book: Principles of Plant Breeding.

ROY B. HOLLSTIEN

California Polytechnic State University
February 1974

CONTENTS

LIST OF FIGURES

1

INTRODUCTION

1.1 PARAMETER SEARCH PROBLEMS IN COMPUTER SCIENCE

The mathematical programming approach to parameter optimization is based on the mathematical expression of cause-and-effect relationships between the adjustable parameters and a quantitative measure of the objective to be either maximized or minimized. When they are not known, or when the mathematical models are so complex that the programming approach is impractical, direct search methods of optimization may be the only available method of attack.

The direct search approach determines experimentally how parameters are related to the objective. The objective is evaluated at trial points in parameter space and the results are used to deduce what new trials are to be made. If successful, the search progresses surely and rapidly to optimal parameter values. Algorithms for direct search optimization have a wide range of applications and are of great practical interest in computer science.

How objective values of trial points are obtained is not particularly important in developing direct search algorithms; it may be assumed that they are determined by an unknown mathematical function V(X) that is to be maximized by adjusting the components $x_1, x_2, \ldots, x_N$ of the N-dimensional parameter vector X. Minimization problems can always be transformed into an equivalent maximization problem.

In practical search problems, there are always bounds on the range of individual parameter values. There may also be constraints that define admissible domains within the larger space bounded by the individual parameter ranges. These constraints are usually expressed on the form of mathematical relations among the parameters X.

It is usually desireable to find the optimal parameters in as few trials as possible. This may not be particularly important when the effects of parameters are evaluated by computer simulation. However, charges for computing time are

seldom negligible. Minimizing the number of trials required to find optimal parameter values may be very important in on-line control applications where losses are suffered while operating at suboptimal conditions.

Most direct search algorithms move incrementally through parameter space along paths of progressive improvement in the objective value (McMurtry, 1970; Swann, 1972). These algorithms are locally exploratory and may progress very slowly or stall on ridges, or wander aimlessly on plateaus in an objective surface. The possibility of multiple peaks makes search problems insolvable, in general, except by exhaustive trial of all admissible points. Some risk of missing optimal peaks must be accepted. But the risk can be reduced by continuing the search at additional cost; for example, incremental searches can be started at many points throughout the parameter space if the cost of repeatedly returning to suboptimal peaks is not too great. The most useful search procedures are those that minimize the cost of reliability for a broad range of problems.

It appears that general search algorithms should begin with globally random trials and progressively narrow the exploration to the most promising regions of the parameter space. The question is how to infer from previous trials what new trials should be made.

1.2 GENETIC SEARCH PROBLEMS IN AGRICULTURAL PLANT BREEDING

Breeding for improvement in quantitative characteristics of agricultural plants can be viewed as a direct search for genotypic parameters that maximize a phenotypic objective character. The genotypic parameters of the search affect the objective at various levels of gene action, by means of extremely complex biochemical reactions that for practical purposes are unknown to the breeder. The quantitative objective characters of an agricultural breeding program are analogous to continuous functions of parameters in a computer search. Qualitative characters are similar to discontinuous functions of search parameters.

To develop improved plant varieties, explorations of genetic parameter space are first induced by crossing two or more source varieties. If the breeder crosses varieties that are homozygous but differ genetically at loci having a major effect on the objective character, there will be a large phenotypic variation

in the hybrid F_1 generation produced by the cross. The breeder's job is to select and propagate (either by self- or cross-fertilization) specific plants in the F_1 and subsequent F_2, F_3, ... generations until a new, true-breeding variety is developed.

Specialized breeding methods for self- or cross-pollination, for diploid or polyploid genotypes, and for additive or epistatic gene action have been developed by agricultural geneticists. Selecting plants to be propagated entirely on the basis of individual merit will not always produce the best results.

The varietal development methods of agricultural plant breeding are actually random searches in genetic parameter space that start with global explorations and end with incremental explorations in the most promising regions of the parameter space. In the early generations, while there is still a large amount of genetic variation in the population, offspring are apt to have new combinations of genes that are unlike those of their predecessors. In later generations, as the population approaches homozygosity, there is a transition from a global to an incremental random search because the offspring of nearly homozygous parents are less variable.

Trial points in genetic parameter space are only indirectly controlled by the breeder. Once plants have been selected and pollinated, genotypes in the next generation are determined by the random mechanisms of inheritance. Nature, therefore, deserves much of the credit for success in agricultural breeding programs, for it has been through natural selection over countless generations that the remarkably adaptive capability of sexually reproductive populations has evolved (Mettler, 1969).

1.3 AN ARTIFICIAL BREEDING APPROACH TO DIRECT SEARCH OPTIMIZATION

The adaptive mechanisms of sexually reproductive populations and the breeding methods of agriculture can, by means of simulation, be applied to optimization problems in computer science. This report describes a direct search method in which trial points in parameter space are synthesized by artificial gene action and information stored in the genotypes of artificial organisms. Parameter values simulate intermediate products of gene action, and the phenotypic value of an

individual in a population of artificial organisms is represented by the search objective value at the corresponding trial point.

Wide crosses of genetically dissimilar varieties are simulated by assigning heterozygous alleles with random coupling/repulsion phase relationship in the genotypes of F_1 populations of artificial breeding programs. The hybrids are bred for improvement in the simulated character of interest (search objective) using the selection and propagation techniques of agricultural plant breeding. After improved varieties have been developed from completely heterozygous first-cross populations, crosses among the improved varieties can be used to continue the artificial breeding process of parameter optimization.

1.4 BACKGROUND AND OBJECTIVES

The artificial breeding method of direct search optimization was first envisioned as a means of providing adaptive capability in computer-controlled systems (Hollstien, 1971). Prior to this study, emphasis had been placed on the use of cross-fertilizing species and random mating because the ability to store partial descriptions of parameters in recessive form appeared to be genetically best fulfilled by outbreeding.

In late 1971 and early 1972 I began to reconsider methods of plant breeding, having earlier rejected the use of self-fertilizing organisms because latent information can not be stored in homozygotes. Many plants are self-fertilizing and these species rapidly approach homozygosity under almost any breeding plan. I now believe that plant reproductive systems offer a powerful repertoire of adaptive mechanisms, and, in this study, apply the breeding methods described by Allard (1960) to completely self-fertilizing, partially cross-fertilizing, and completely cross-fertilizing populations of artificial species.

Partial support of this study from November 1972 to August 1973 was provided by National Science Foundation Grant No. GJ-36115. This portion of the study was devoted to static and deterministic parameter optimization--where the dynamic performance of the breeding population does not affect the stability of the overall system, and there are no probabilistic phenomena involved in determining the objective value of trial points in parameter space.

The specific objectives of the project were to

(1) Determine the relative effectiveness of additive vs. epistatic gene action

(2) Model and investigate the effects of intra-allelic dominance at the genotypic level

(3) Develop artificial breeding systems (computer programs) for direct search optimization in up to 32-dimensional parameter spaces.

2

METHOD

2.1 ARTIFICIAL BREEDING FOR PARAMETER OPTIMIZATION

Let X represent a parameter vector with components x_1, x_2, ... , x_N and V(X) the scalar measure of an objective to be maximized by finding the optimal parameter values X^*. Only maximization problems are considered because minimization problems can easily be converted to equivalent maximization problems.

Cause-and-effect relationships between the parameters and the objective are represented by a function V(X), but it will be assumed that these relationships are either not known, are not expressible in mathematical form, or are not amenable to the "mathematical programming" approach to parameter optimization.

The ARTIFICIAL BREEDING procedure described here is a "direct search" method based on simulation of agricultural plant-breeding programs. Contrived functions V(X) will be used to test the method, but the mathematical form of these objective functions are not used in any other way.

The method is summarized as follows:

Artificial organisms are represented by diploid genotypes composed of chromosome-like arrays of binary bits. Each bit corresponds to a diallelic locus at which there may reside either a "0" or a "1" allele.

Offspring are produced by the union of gametic sets of chromosomes obtained by meiotic division of parental genotypes. Chromosomes segregate independently during gametogenesis. Crossing-over between nonsister chromatids occurs randomly along the chromosomes.

Random translocations and inversions of chromosome segments occur during interphase. Suppression of recombination is simulated by producing only functional gametes in which there are no duplications or deficiencies of loci due to

crossing-over within inverted or translocated segments.

Background variation is provided by random mutation from one allelic conformation of genes to the other.

Numerical values of parameters are synthesized by gene action algorithms that incorporate a) intra-allelic additivity, b) intra-allelic interaction with dominance at the gene level controlled by modifier loci, c) inter-allelic additivity of multiple factors, and d) epistatic effects of genes that control different steps in synthetic pathways. The parameter values correspond to intermediate effects of gene action, such as concentrations or activity levels of enzymes synthesized by the combined effects of several genes in living organisms.

Quantitative characters of artificial organisms are simulated by evaluating the search problem objective at trial points in parameter space corresponding to the individual genotypes.

Plant breeding methods for varietal or hybrid development are applied to populations of artificial organisms. Initial hybrids formed by wide crosses of genetically dissimilar varieties are simulated by random assignment of heterozygous alleles with random coupling/repulsion phase relationship. Improved varieties developed from random source populations are later crossed to continue long-term searches in the most promising regions of the parameter space.

Achievement of maximum theoretical genetic gain in a simulated breeding program corresponds to the optimal solution of the underlying parameter search problem.

2.2 GENETIC COMPOSITION OF ARTIFICIAL ORGANISMS

The artificial organisms are diploids with genotypes composed of two homologous sets of chromosomes as shown schematically in Fig. 1. A particular artificial species may have from 1 to 32 chromosomes, depending on the number of parameters involved in the search problem and the type of gene action used to synthesize the numerical values of parameters. Genes are located in complexes of 16 adjacent loci and occur in either of two allelic conformations: "0" or "1". The complement of genes in a species does not change during the course of a breeding program,

however, the relative positions of complexes in the chromosomes may be altered by inversions and/or translocations. Up to 4096 genes in 256 complexes segregate in present artificial breeding programs, but the maximum number is limited only by the digital computer memory available.

In Fig. 2, which shows how a typical artificial chromosome might appear under three degrees of magnification, we see that the complexes are on one arm of the chromosomes, and that the positions of complexes within the chromosomes are numbered from left to right, starting with the position nearest a hypothetical centromere. Separation of gene complexes is represented by PCROS, the probability that gametes will be produced with an odd number of cross-overs between any two adjacent complexes, or between the centromere and the first position. Numerals above the left end of each complex identify the function of the complex in the artificial gene action algorithm. Loci within complexes are numbered from left to right, and their separation is represented by PCROL, the probability that an odd number of cross-overs will occur between any two adjacent loci within a complex. The relative positions of loci within gene complexes are fixed, so the function of every locus in the genome is uniquely identified by 1) a number indicating its gene complex, and 2) the position of the locus within the complex. At the bottom of the figure, under the highest magnification, the "0" and "1" alleles at individual loci may be seen.

The basic elements of artificial genotypes are genes, and the binary alleles of each gene simulate two conformations of chromosome segments that in living organisms control the synthesis of either two functionally distinguishable products (enzymes) or one functional and one nonfunctional product. In living organisms, distinguishable effects of alleles are sometimes due to a difference in only one nucleotide base pair, even though a long sequence of nucleotides may be required to specify the amino acid sequence of the polypeptide chains. Based on experiments with the bacterial virus T4, Watson (1970) estimates that the average gene contains from 900 to 1500 nucleotide pairs!

Gene action in artificial organisms then begins with the interaction of intermediate products of individual gene action rather than the primary genetic code that translates DNA base-pair sequences into amino acid sequences of polypeptide chains.

2.3 REPRODUCTION

During the reproduction of artificial organisms, the genotypes of two parents and their offspring are stored in two, 3-dimensional arrays CP(I,J,K) and S(I,J,K). Subscript I identifies a gene complex by its function in the gene action algorithm, J identifies the parental genome, and K identifies one of the two parents or the offspring. The organisms are monoecious, so the order of parent genotypes may be interchanged. They are also capable of self-fertilization, so the parent genotypes may be identical. Numbers indicating the chromosome and position of complexes I are packed into integer locations of array CP. The binary alleles in the complexes are contained in the corresponding elements of array S.

Inversion and translocation of chromosome segments during interphase are programmed by calling subroutines INVER(CP,NSEG,PINV) and TRANS(CP,NSEG,PTRA), where argument NSEG is the number of gene complexes in the genome, PINV is the probability of chromosome breakage between any two adjacent loci and subsequent fusion with a chromosome segment in an inverted position, and PTRA is the probability of chromosome breakage between any two adjacent loci and subsequent fusion with a translocated segment from a different chromosome.

Independent segregation of chromosomes, crossing-over of nonsister chromatids, and the union of gametic sets of chromosomes to form zygote genotypes is programmed by calling subroutine FZYGO(CP,S,NSEG,PCROS,PCROL). Crossing-over occurs with uniform probabilities PCROS and PCROL as defined previously. Crossing-over between complexes is inhibited whenever duplications or deficiencies of loci would occur in the resultant gametic sets of chromosomes. This eliminates the need for time-consuming test for nonfunctional gametes and the repeated matings that would otherwise be required to obtain a chance union of functional gametes. FZYGO returns with the offspring genotype in array locations CP(I,J,3) and S(I,J,3).

Independent mutation of zygote alleles with probability PMUT of transformation from "0" to "1" or "1" to "0" is programmed by calling subroutine MUTAT(S,NSEG, PMUT).

One record of a direct-access file is used to store the genotype of each artificial organism. Parent genotypes are read from the file and offspring genotypes

are written into the file as illustrated in the following sequence of instructions. Artificial organisms with genotypes in records K1 and K2 of file F1 are mated and the offspring genotype is stored in record K3 of the same file.

```
READ(F1'K1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
READ(F1'K2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
CALL INVER(CP,NSEG,PINV)
CALL TRANS(CP,NSEG,PTRA)
CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
CALL MUTAT(S,NSEG,PMUT)
WRITE(F1'K3)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
```

2.4 PARAMETER SYNTHESIS

Agricultural breeders try to anticipate the effects of various breeding methods on the genetic composition of populations when the phenotypic characters of interest exhibit a) intra-allelic additivity, b) dominance interaction, c) cumulative effects of multiple factors, and/or d) epistatic interaction.

These phenomena must also occur at an intermediate level of biochemical products (enzymes) that interact in the final phases of gene action to produce observable effects. In the ARTIFICIAL BREEDING method, the search-problem parameters play the role of the postulated intermediate products of gene action. Numerical values of the parameters are synthesized by artificial gene action algorithms that exhibit each of the properties mentioned above; i.e., additivity, dominance, cumulative effect, and epistasis. The following gene action algorithms have been investigated in artificial breeding programs.

2.4.1 Gene Action 1

Individual parameters are controlled by the cumulative action of four complexes containing a total of 64 genes. The number of "1" alleles in each complex is multiplied by a weighting factor and the results are summed to form the numerical value of the parameter.

The parameter range under this gene action algorithm is [0,65535]. If all loci are homozygous 0/0, the minimum value is synthesized. And if all loci are homozygous 1/1, the maximum value is synthesized; this is obtained by summing the maximum contributions of the four complexes given in the right-hand column below.

complex	weighting factor	
1	15/32	15
2	15/2	240
3	120	3840
4	1920	61440
	maximum value	65535

The algorithm is additive at the intermediate (parameter) level because the effect of heterozygous genotype 0/1 is midway between those of the two homozygous genotypes 0/0 and 1/1.

2.4.2 Gene Action 2

Individual parameters are controlled by the cumulative action of 16 genes in a single complex. Each gene has a different level of effect equal to an integral power of 2: $2^{15} = 32768$, $2^{14} = 16384$, ... , $2^{0} = 1$. The effects of all loci are summed to form the numerical value of the parameter.

The parameter range is [0,65535] since genotypes 0/0 at all loci are equivalent to the binary number $0000000000000000_2 = 0_{10}$ and genotypes 1/1 at all loci are equivalent to $1111111111111111_2 = 65535_{10}$.

This algorithm is also additive at the intermediate (parameter) level because homozygous genotypes 1/1 contribute the full effect of the binary-weighted loci, heterozygous genotypes 0/1 contribute half that amount, and homozygous genotypes 0/0 contribute nothing to the parameter value.

The algorithm can be viewed as though the parameter value is produced by a sequence of reactions that transform a hypothetical substrate into one of 65535 possible intermediate products or activity levels. In Fig. 3, the substrate is shown on the left and alternate pathways at each reaction step appear as branching points. Each gene in the complex controls one step in the reaction sequence: gene 1 controls the first step, gene 2 the second step, etc. Homozygous genotypes 0/0 route the pathway along the lower branches, and homozygous genotypes 1/1 route the pathway along the upper branches at each step in the simulated reaction

sequence. When heterozygous genotypes occur, both of the possible reactions are activated, creating alternate pathways through which two or more numerical products are synthesized. Two are produced if any one of the loci are heterozygous, four if any two loci are heterozygous, etc. The composite value of the parameter is the average of values produced along the alternate pathways. This simulates additive products of intermediate gene action.

A disadvantage of the binary number system as a basis for simulated gene action is that the alleles at many loci must sometimes change simultaneously to produce small changes in the numerical values of parameters. We can see from Fig. 3, for example, that the alleles at every locus must change to transform the genotype for the numerical value 32767 to that for 32768. All but one of the loci must change to transform 16383 to 16384 or 49151 to 49152. To the breeder these genotypes represent barriers in genetic parameter space that are very difficult to transcend by random recombination of genes.

If biochemical pathways have a similar structure, this mechanism could explain the existence of suboptimal limits to selection for quantitative characters in agricultural breeding.

2.4.3 Gene Action 3

Individual parameters are controlled by a single complex of 16 genes that determi the numerical parameter values according to the synthetic pathway model in Fig. 4 Each gene controls one of a sequence of hypothetical reactions that transform a substrate into one of 65535 possible intermediate products. In the group of reaction steps controlled by a particular gene, the directions are reversed for every other branch point as compared with the model in Fig. 3. These directions are based on a permutation of the binary number system (the "Gray" code) in which contiguous numerical values are encoded by changing only one bit in the binary representation.

In Fig. 3, changing the genotype at a locus controlling one of the first few reactions will always have a large effect, whereas, in Fig. 4 the effect may be large or small depending on the genotypes that control subsequent reactions. In this algorithm, therefore, the genes in each complex are epistatic at the intermediate (parameter) level.

The average of values produced along all pathways described by heterozygous genotypes will always be the median of the possible values associated with the branch point corresponding to the first heterozygous locus. To avoid this cancellation of the effects of several heterozygous loci, an additional inter-allelic interaction is introduced to make all heterozygous loci act simultaneously as either 0/0 or 1/1 genotypes. The products of two alternate pathways are then averaged to obtain the final parameter value corresponding to each gene complex. If one locus is heterozygous, this will produce the median value associated with the corresponding branch point. If two or more loci are heterozygous, various end product interactions will be produced depending on the genotypes at the homozygous loci.

2.4.4 Gene Action 4

In Gene Action 1, genotypes containing all "0" or all "1" alleles are required to develop extreme values of parameters. Many genotypes produce intermediate values in the parameter range, but there is no genetic redundancy at the extreme values.

To provide genetic redundancy over the complete range of parameter values, this algorithm uses a subroutine PGA4(S1,S2,M) that returns a primary value M as in Gene Action 1 and a subroutine SGA4(NSEG,S,NPAR,X) that transforms M into a secondary value X as shown in Fig. 5. This increases the number of genotypes that represent parameter values near the extremes of the parameter range.

Resolution is sacrificed to obtain this redundancy. Now only even values of parameters in the range [0,65535] are synthesized.

The transformation from M into X is a discrete mapping of integers into integers and is only represented approximately in Fig. 5 by what appears to be a continuous function.

2.4.5 Gene Action 5

The transformation of Fig. 5 is used in conjunction with the primary algorithm of Gene Action 2. The effect, as shown by the synthetic pathway model in Fig. 6,

is better distribution of genetic redundancy, for there are now alternate pathways to all of the intermediate products represented by numerical parameter values.

2.4.6 Gene Action 6

The transformation of Fig. 5 is used in conjunction with the primary algorithm of Gene Action 3. This is the approach used to obtain Gene Action 4 from 1 and Gene Action 5 from 2. After several experiments had been run, it was discovered that there is in fact no increase in genetic redundancy provided by this scheme. This is a result of the reflected nature of the Gray code (Fig. 7). The folding effect of the secondary transformation very nearly eliminates the influence of gene 2 on the numerical product, because the fold lines of the secondary transformation pass through the pathway branch points associated with gene 2. Gene 2 does have a small residual effect, however, due to the integer arithmatic involved in the folding operation of the secondary transformation. We should expect only slight differences in the average performance of artificial populations that use Gene Actions 3 and 6, even though there may be considerable differences in particular breeding experiments in which the two algorithms are used.

2.4.7 Gene Action 7

Intra-allelic interaction is simulated by associating a dominance modifier locus with each of the functional loci in the genome. Even-numbered complexes contain functional genes whose dominance modifiers are found in corresponding positions within the next, odd-numbered complex. Parameter values are synthesized by the cumulative effect of four complexes containing polygenes weighted as in Gene Action 1. If the functional loci are all homozygous, the modifier loci have no effect and the parameter values will be the same as those determined by Gene Action 1. When functional loci are heterozygous and the associated dominance modifier loci are homozygous, dominance of the alleles present at the modifier loci is imposed at the functional loci. When functional loci and the corresponding modifier loci are both heterozygous, dominance at the functional loci is determined randomly.

This simulated dominance at the gene level is programmed by modification of the primary gene action algorithm of Gene Action 1. Similar modifications of

Gene Actions 2 through 6 are used to obtain additional algorithms as follows:

2.4.8 Gene Action 8

Dominance modifier loci are added to the primary algorithm of Gene Action 2. There is now a single pathway in Fig. 3 along which the parameter values are synthesized; the direction at each reaction branch point is determined by the combined effects of a functional gene and its associated dominance modifier.

2.4.9 Gene Action 9

Dominance modifier loci are added to the primary algorithm of Gene Action 3.

2.4.10 Gene Action 10

Dominance modifier loci are added to the primary algorithm of Gene Action 4.

2.4.11 Gene Action 11

Dominance modifier loci are added to the primary algorithm of Gene Action 5.

2.4.12 Gene Action 12

Dominance modifier loci are added to the primary algorithm of Gene Action 6.

2.4.13 Gene Action 2A

A modification of the binary encoding scheme of Gene Action 2 is used in this algorithm. Each parameter is controlled by a single complex of 16 genes. The left-most gene acts as a regulator that controls the function of all the other genes in the complex. If the regulator is homozygous 0/0, the arrays of alleles in the two homologous chromosome segments are read separately as binary numbers in the range [0,32767] and their values are summed to form the numerical value of the parameter controlled by the complex. If either of the regulatory alleles are "1", the alleles on the same chromosome are complemented before the value is read and used in the parameter computation. For example, the genotypes

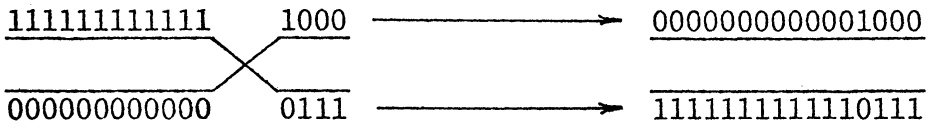
$$\frac{1111111111111000}{0000000000000111} \quad \text{and} \quad \frac{1111111111111000}{1111111111111000}$$

are "equivalent" to the homozygous genotype

$$\frac{0000000000000111}{0000000000000111}$$

which represents the numerical parameter value 14, obtained by summing the two gametic values of 7.

A single crossover between the 12th and 13th loci of the heterozygous genotype above will produce two gametic arrays having numerical value 7 as illustrated below



A synthetic pathway interpretation of the algorithm is illustrated in Fig. 8. As in the previous diagrams, the pathways shown are those determined by a completely homozygous gene complex. In this algorithm, a complex heterozygous at any loci will produce alternate products that are summed (not averaged) to form the final parameter value. This corresponds to a cumulative effect of intermediate products.

This algorithm was developed with two objectives in mind. The first is to reduce the chance of stalling at suboptimal selection limits. To do this, it provides a mechanism by which crossing-over, a "normal" event that occurs frequently in short-term breeding programs, is capable of producing small variations in parameter values throughout the parameter range. This should dimish the effects of the barriers in genetic parameter space that are a result of the cyclic properties of the binary number system.

The second objective is to slow down the approach to homozygosity. There are polymorphic genotypes that encode the same parameter values throughout the parameter range, so the selection intensity for a particular allele at any locus should be reduced. Maintaining genetic variation as long as possible helps avoid premature fixation of undesireable alleles.

The algorithm might also be viewed as a model of multi-allelic gene action with

the arrays of 0's and 1's in the homologous chromosome segments representing different functional conformations of a single gene. Parameter values would then correspond to distinct enzymes with structural compositions controlled by specific genes.

2.4.14 Gene Action 5A

The primary gene action algorithm is the same as that used in Gene Action 2A. A secondary gene action subroutine transforms the primary value M into the parameter value X as in Gene Action 4, but in this case the transformation is discontinuous as shown in Fig. 9. The intent was to increase the genetic redundancy of the algorithm. Fig. 10 shows this transformation also nullifies the effect of gene 2.

2.4.15 Gene Action 8A

Dominance modifier loci are added to the primary algorithm of Gene Action 2A.

2.4.16 Gene Action 11A

Dominance modifier loci are added to the primary algorithm of Gene Action 5A.

2.5 OBJECTIVE CHARACTERS

Objective characters may be any process that transforms trial sets of parameter values into corresponding objective values. The objective characters may be evaluated either within or outside the computer used to simulate the artificial population and breeding program. In the experiments described in this report, objective characters were evaluated internally by subroutines that evaluate mathematical functions of the parameters in simulated direct-search problems.

Two-dimensional contour plots of six objective functions used in the experiments are shown in Fig. 11. These objective characters are identified by names that refer to their main topological feature.

Functions of more than two parameters are obtained by summing evaluations of

2-parameter functions. For example, if a 2-parameter objective character is defined by V(X1,X2), the 8-parameter character of the same type is V(X1,X2,X3, X4,X5,X6,X7,X8) = V(X1,X2) + V(X3,X4) + V(X5,X6) + V(X7,X8).

2.5.1 Plane

A hyperplane is inclined in parameter space in such a way that the maximum phenotypic value of 100 units is achieved at the lower bound (0) of the odd-numbered parameters and the upper bound (65535) of the even-numbered parameters.

2.5.2 Ridge

A curved, knife-edged ridge passes through the origin and upper-right-hand corner of each 2-parameter plane. The phenotypic value increases gradually along the ridge to a maximum value of 100 units at the upper bound (65535) of all parameters. The objective value decreases rapidly in directions away from the ridge line.

2.5.3 Peak NE

Three peaks--the highest of which is located in the North East quadrant--rise out of each 2-parameter plane. The peaks have the form of normal probability density functions and are therefore characterized by the means (locations of peaks), standard deviations (sharpness of the peaks), and the correlation coefficients (interaction of the two parameters) of the three probability density functions. The functions are multiplied by weighting factors and summed to form the phenotypic value of the objective character. When the peaks are sharp (small standard deviations) and widely separated (differences in mean values large compared to the standard deviations), the objective value at each peak is determined primarily by the three weighting factors.

The maximum value of this objective function is achieved when all parameters have the value 49151, corresponding to the location of the North East peak in each 2-parameter plane. The objective value is 60 at the West peak (coordinates 0,32767 in the 2-parameter plane) and 40 at the South peak (coordinates 26214,6553). The parameters interact (correlation coefficient 0.95) in the neighborhood of the

NE peak but do not interact (correlation coefficients 0.0) in the vicinity of the other two peaks.

The standard deviations that characterize the sharpness of the peaks are all equal to 10 percent of the parameter range. The peaks are, therefore, quite sharp and isolated. As may be seen in Fig. 11, the phenotypic objective value is less than 10 units over a large part of the 2-parameter plane.

2.5.4 Peak W

This objective character is similar to Peak NE with the weighting factors of the North Ease and West peaks interchanged to make the West peak the highest-valued of the three peaks in each 2-parameter plane.

2.5.5 Peak S

This objective character is also similar to Peak NE except that the weighting factors of all three functions are interchanged to make the South peak the highest valued, West peak the second, and North East peak the third highest of the three.

2.5.6 Hypersphere

A hyperspherical surface is centered in the range of parameter values so that the objective character has a maximum value of 100 units when all parameters are equal to 32767. The character has a phenotypic value of 0 if all parameters are either 0 or 65535, i.e., they are all at the extemes of the parameter range.

2.6 BREEDING METHODS

There are basically two different approaches to agricultural plant breeding. One is to develop new, improved, true-breeding varieties. The other is to improve the hybrid offspring of two or more established varieties.

To develop improved varieties, two or more source varieties are first crossed

to obtain a hybrid F_1 generation. The breeder then selects and propagates (by self- or cross-pollination) individuals in successive generations of the hybrid population until a new variety is established. If 1) the original varieties are complementary, 2) the variation needed for improvement in the characteristics of interest is present in the F_1 generation, and 3) the necessary recombinations of alleles occur and are not lost by genetic drift or too intense selection, then the breeding program may succeed in producing an improved variety having greater phenotypic value than the source varieties.

The second approach is used when the hybrids produced by the first cross of two varieties are superior to either of the parents, but lose their superiority when propagated in an effort to establish an improved, true-breeding variety. Selection and mating of individuals within the two parental populations according to the phenotypic value of their cross-bred progeny, rather than on the basis of their own characteristics, has become a standard plant-breeding procedure.

Methods of selection and propagation differ for self- and cross-pollinated plant species, but a surprisingly few basic methods are applied successfully to many different species and characteristics. While these agricultural breeding methods do not guarantee success, they often <u>do</u> produce significant improvement in the characters of interest in only a few breeding generations. What makes these relatively simple breeding algorithms for selection and mating as reliable and robust as they are?

One reason is that there is an intrinsically adaptive capability of sexually reproductive populations under artificial or natural selection. Another reason is that the mechanisms of reproduction and gene action are fundamentally the same in all species of plants and animals (Stahl, 1964).

The basic idea of ARTIFICIAL BREEDING is that, if the mechanisms of reproduction and gene action are accurately simulated, the genetic principles of agricultural breeding should also be effective in breeding for improvement in direct-search objective characters of artificial organisms.

The practical value of the method can only be established by experimental investigations using realistic objective functions and specific breeding methods.

The artificial breeding methods used in this study are based on the agricultural methods of plant breeding described by Allard (1960).

Main programs, subroutines, input data and PDP-9 CHAIN/EXECUTE systems for all of the artificial breeding systems are included in the Appendix.

2.6.1 Pedigree Method 1

In pedigree breeding, the procedure most widely used to improve characteristics of self-pollinated species, two or more well established varieties are crossed to form a large, hybrid F_1 generation. Families are started in the F_2 generation by growing several plants from self-pollinated seeds of F_1 individuals selected for general appearance, but without particular regard to the objective of the breeding program. Selection for the objective character is started within families in the F_2 generation. As family differences appear in later generations, selection among families is introduced until finally the entire population is produced by the single, most valuable individual selected from the previous generation.

Pedigree Method 1 (PM1) simulates an ideal F_1 population formed by a cross of parental varieties that differ at all loci contributing to the objective character. F_1 alleles are randomly assigned to one genome and the complement alleles are assigned to the other. Although the virtual F_1 population is large, completely heterozygous, and in gametic phase equilibrium, only a sample of the F_1 generation is used to produce the F_2 generation. Therefore, the original genetic variation needed to optimize the objective character in subsequent generations of pedigree breeding may not be present in the F_2 generation.

Trial points in the direct-search parameter space are first produced in the F_2 generation. The S_2 highest-valued individuals selected from the F_2 generation are selfed N_3/S_2 times to produce N_3 individuals in the F_3 generation. Thereafter, commensurate population sizes N_i and numbers of families S_{i-1} are specified for successive generations in which families are propagated by selfing the single, highest-valued member of the family in the previous generation.

2.6.2 Pedigree Method 2

The pedigree method of PM1 is used to obtain a sequence of improved varieties starting with an initial cross of random, dissimilar varieties. In the second cross, the first improved variety replaces one of the random parental varieties. The third variety is bred from a cross of the first two improved varieties. Subsequent varieties are derived from crosses between the two, highest-valued varieties previously developed.

2.6.3 Bulk Population Breeding 1

Characters positively correlated with natural fitness are sometimes improved by propagating the entire (bulk) population. The breeder assumes (or knows from previous experience with the species) that the fittest plants will also be the most desireable with respect to the character of interest.

In Bulk Population Breeding 1 (BPB1), fitness is made proportional to the direct-search objective value of each individual. The breeder may also impose artificial selection by specifying some number NSEL of the highest-valued individuals in each generation among which the competition for producing offspring occurs. The artificial species may be completely self-fertilizing, partially cross-fertilizing, or completely cross-fertilizing as specified by a probability POUCR of outcrossing in producing each offspring organism.

2.6.4 Mass Selection 1

A procedure used to improve characteristics of outcrossing species is simply to select individuals from each generation entirely on the basis of their own merit and then mate the selected individuals randomly to produce the next generation. Genetic variation in the original population can be produced by crossing two or more varieties, or, as is often the case, there may be enough variation in populations that have not previously been under selection for the character of interest to the breeder.

In Mass Selection 1 (MS1), a completely heterozygous first generation is formed with random alleles in one genome and the complement alleles in the other.

The population size and number of individuals selected in each generation remain fixed throughout the breeding program. The artificial organisms are considered monoecious and have equal probabilities of self-fertilization or cross-fertilization with any other selected individual.

2.6.5 Simple Recurrent Selection 1

Hybrid populations of outcrossing but self-compatible species are sometimes self- and cross-pollinated in alternate generations; two such consecutive generations are called a selection cycle. Simple recurrent selection is started by selecting the most desireable individuals in a hybrid population. These selected individuals are selfed to produce progeny that, on the average, are homozygous at half of the loci contributing to the character of interest to the breeder. The third generation (first generation of the second recurrent selection cycle) is formed by making all possible crosses of offspring from individuals selected in the first generation. This process of selection in alternate generations is continued until a new, true-breeding variety is obtained.

In Simple Recurrent Selection 1 (SRS1), the population size is made an integer multiple of the $N(N - 1)/2$ possible crosses of offspring from N individuals selected in each cross-bred generation. Trial points are evaluated in only the cross-bred generations, so the method is no more costly in terms of trial point evaluations than the mass selection method.

Time is required to simulate the intermediate generations, but, because the progeny of selfed individuals can be produced as they are needed and do not have to be stored in disk memory, the total time required for a recurrent selection cycle is less than twice that of a mass selection generation of equivalent population size. The additional memory required to simulate the intermediate generations is negligible.

2.6.6 Simple Recurrent Selection 2

The simple recurrent selection method of SRS1 is used to obtain a sequence of improved varieties starting with an initial cross of random, dissimilar varieties. The first improved variety replaces one of the random varieties, and the third

is bred from a cross of the first two improved varieties. Subsequent varieties are derived from crosses between the two, highest-valued varieties previously developed.

2.6.7 Reciprocal Recurrent Selection 1

Reciprocal Recurrent Selection 1 (RRS1) improves the hybrid offspring of two parental varieties. Two completely heterozygous source populations, A and B, are formed by randomly assigning alleles and their complements to homologous chromosomes as described earlier. Each individual in population A is crossed with a sample chosen randomly from B, and each individual in B is crossed with a sample chosen randomly from A. The recurrent parents in each population having progeny with highest individual value are selected and selfed to propagate populations A and B.

The objective values of A and B individuals are never required, so trial points in direct-search parameter space are evaluated for only the hybrids in each selection cycle. The entire A and B populations must be stored in disk memory because any particular individual may be required in determining the combining ability of individuals in the opposite population. There is no need to store the hybrid individuals, however, once their objective value has been determined.

In RRS1, populations A and B are the same size and equal numbers of trial crosses are used in determining individual combining abilities. The number of hybrid offspring in each reciprocal recurrent selection cycle is therefore 2Nn, where N is the size of populations A and B, and n is the number of trial crosses of each recurrent parent.

Initially, populations A and B are completely heterozygous. After several selection cycles, the two populations approach homozygosity. Individuals in the final A and B populations may themselves have low phenotypic value, but, if the breeding program is successful, they will have high combining ability with the opposite population. The recurrent selection procedure was originally developed to test simultaneously for general and specific combining ability. General combining ability is measured by an individual's progeny when crossed with a heterozygous population; specific combining ability is measured by an individual's progeny when crossed with a particular homozygous population.

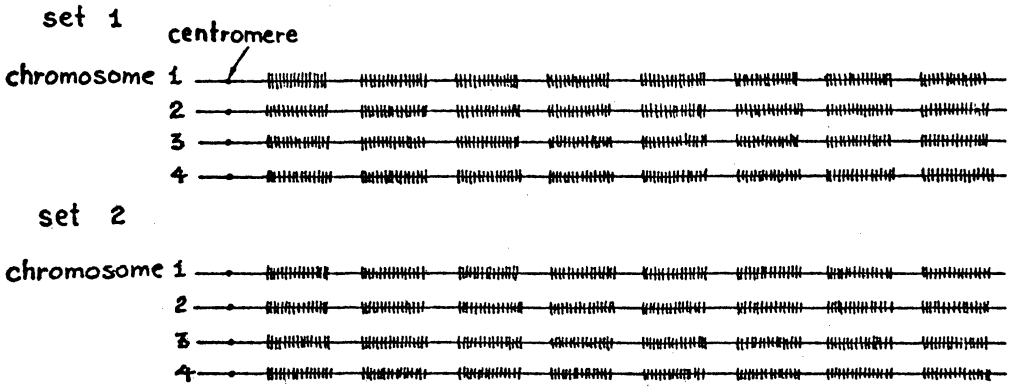


Figure 1 Genotype of an artificial organism

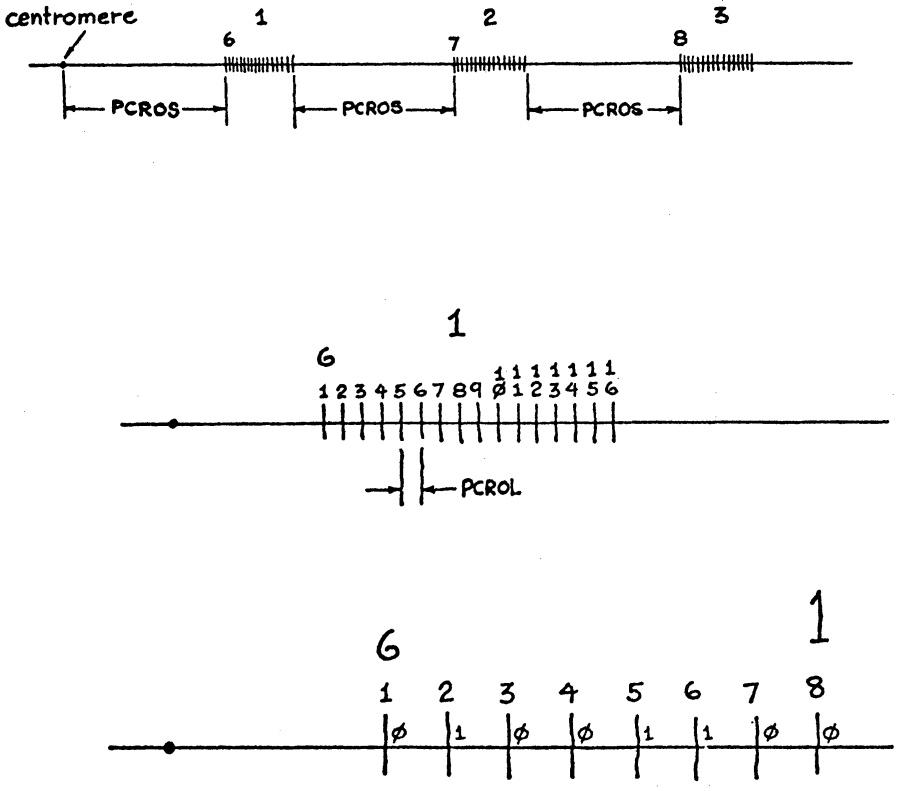


Figure 2 Close-up views of an artificial chromosome

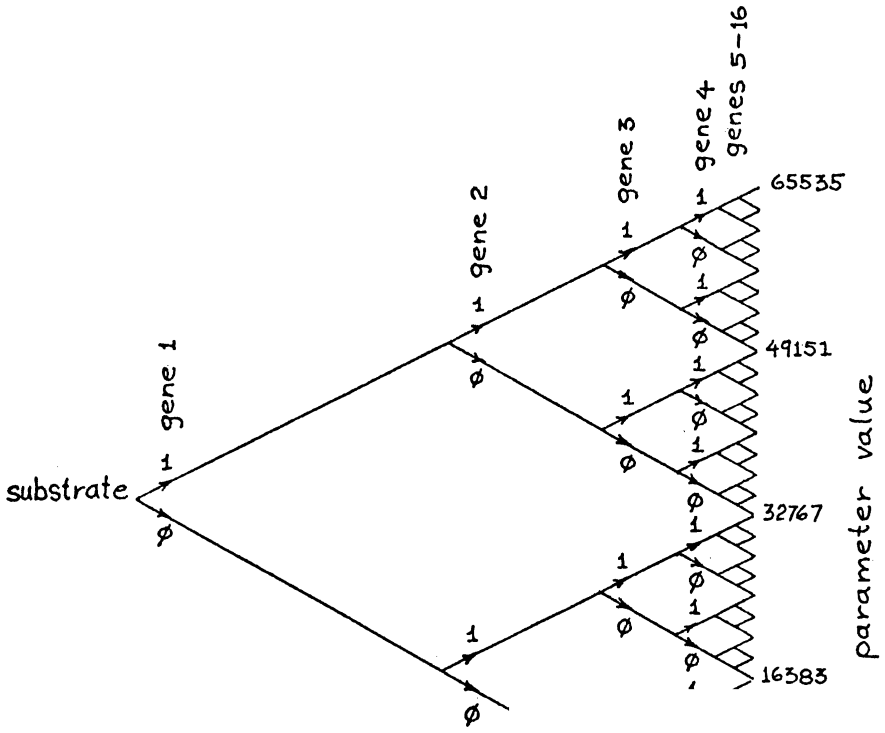


Figure 3 Synthetic pathway model of Gene Action 2

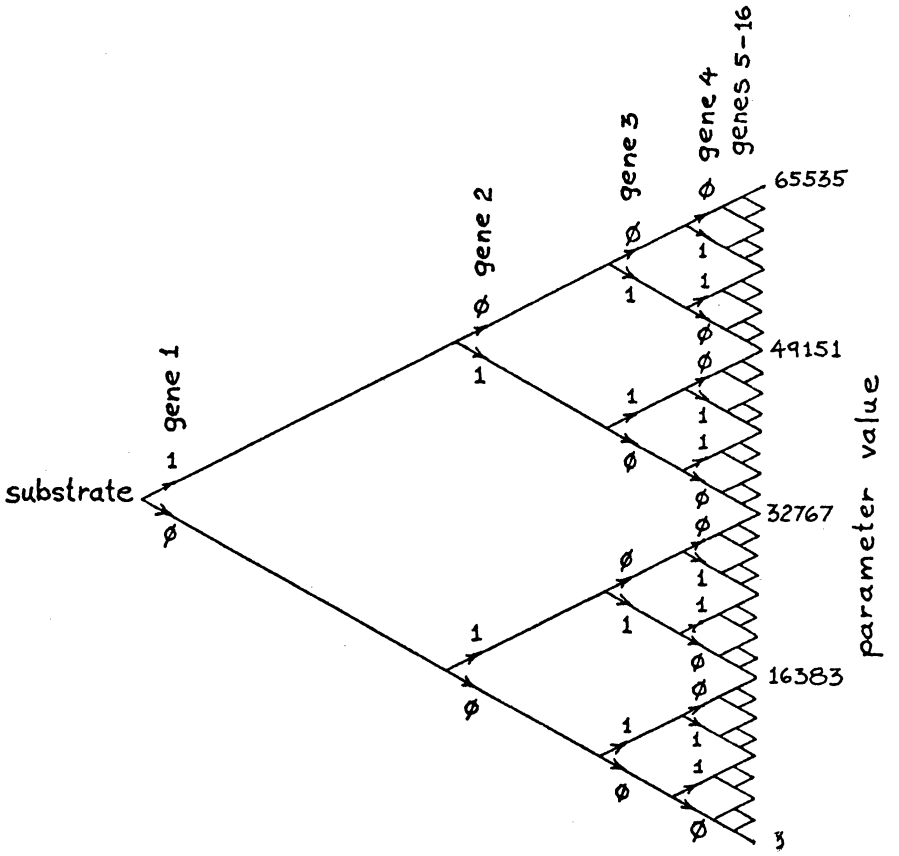


Figure 4 Synthetic pathway model of Gene Action 3

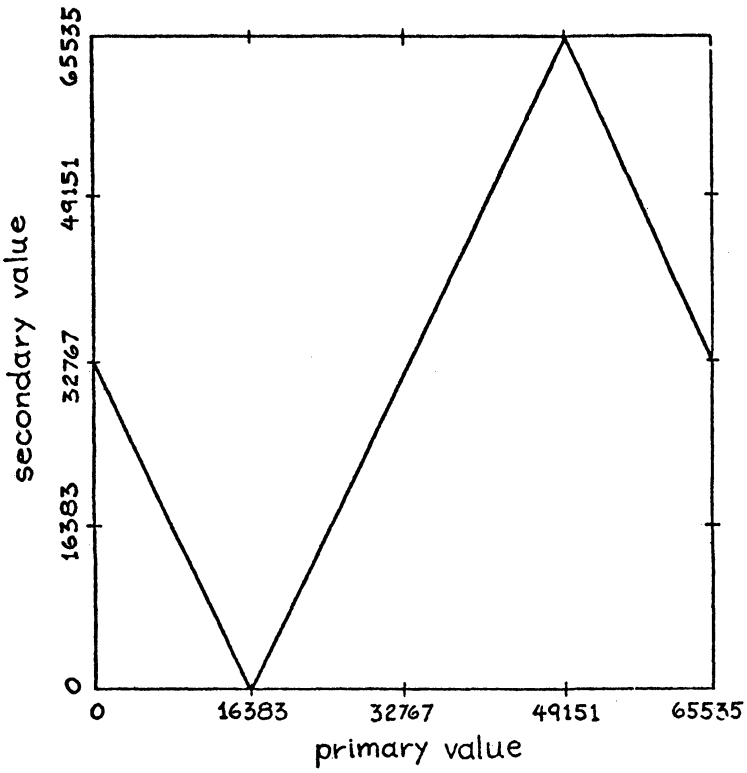


Figure 5 Secondary transformation of Gene Action 4, 5 and 6

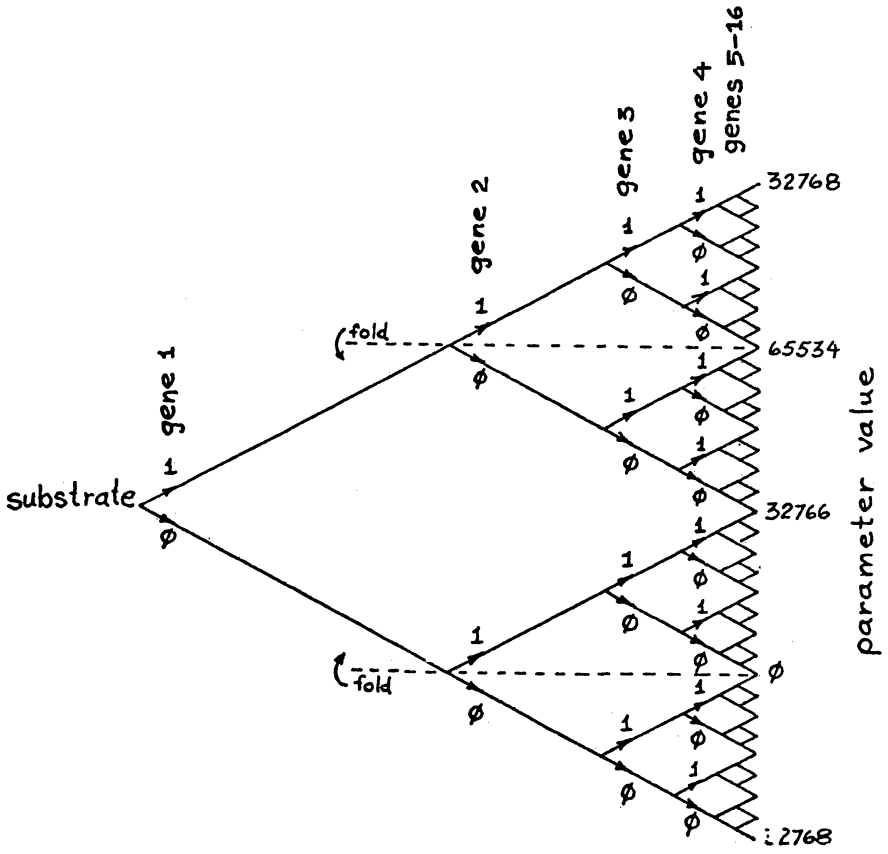


Figure 6 Synthetic pathway model of Gene Action 5

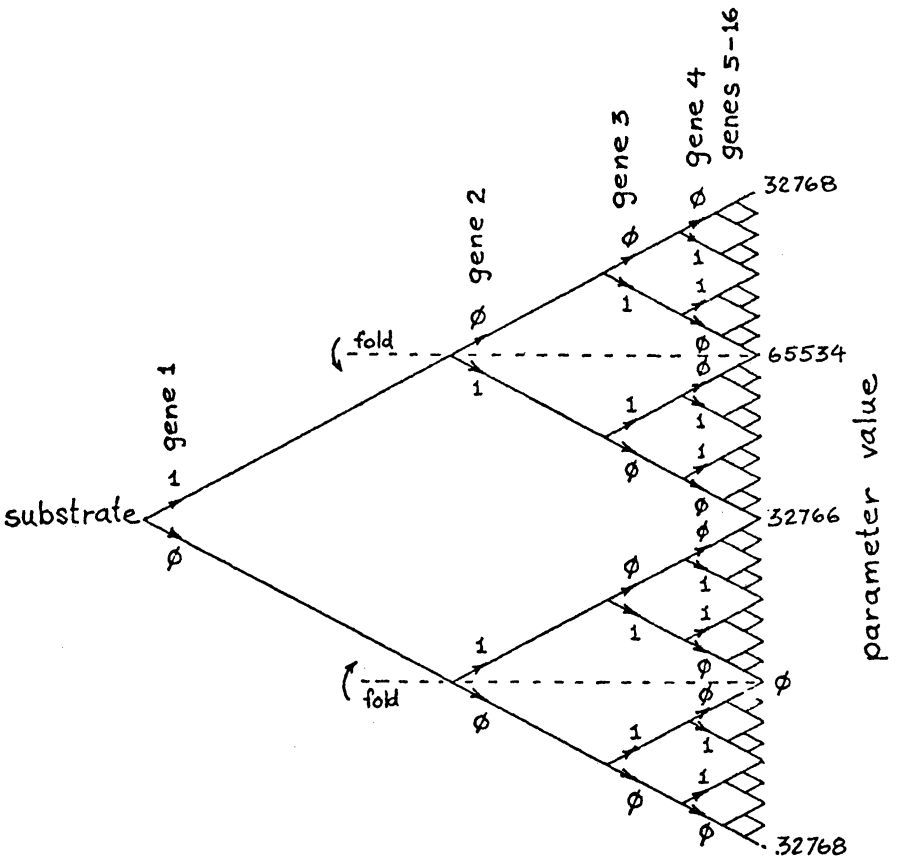


Figure 7 Synthetic pathway model of Gene Action 6

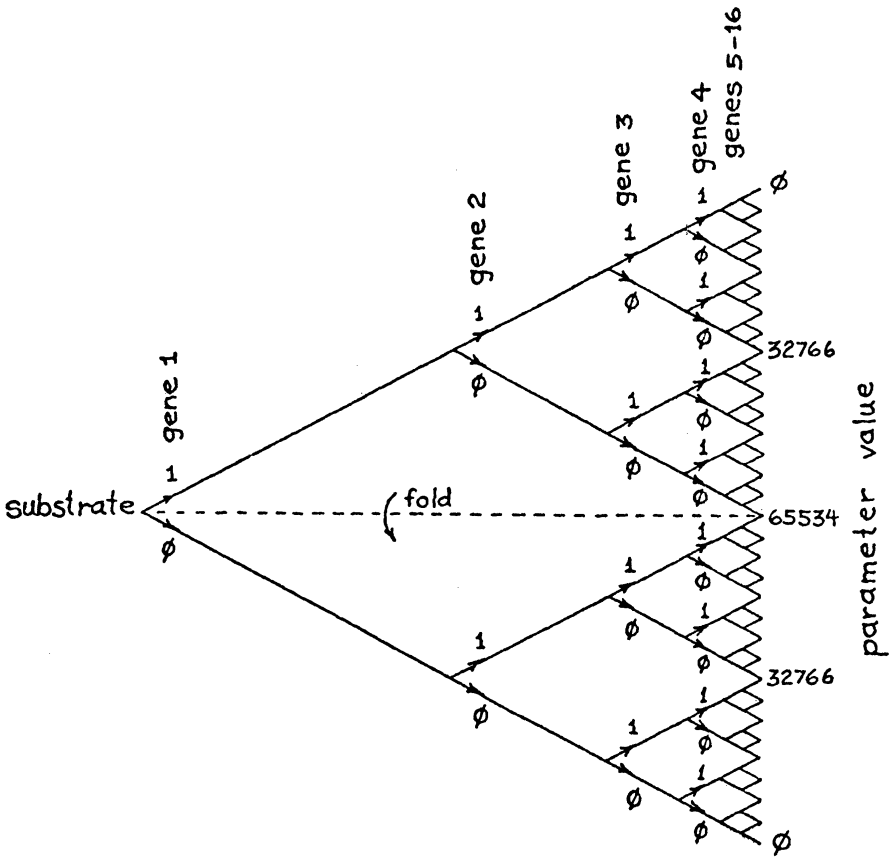


Figure 8 Synthetic pathway model of Gene Action 2A

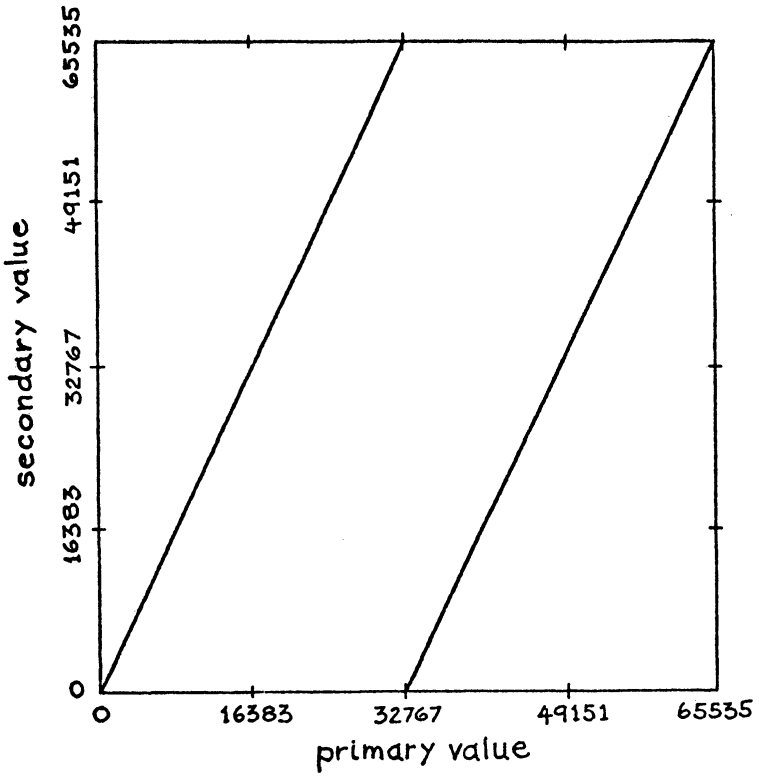


Figure 9 Secondary transformation of Gene Action 5A and 11A

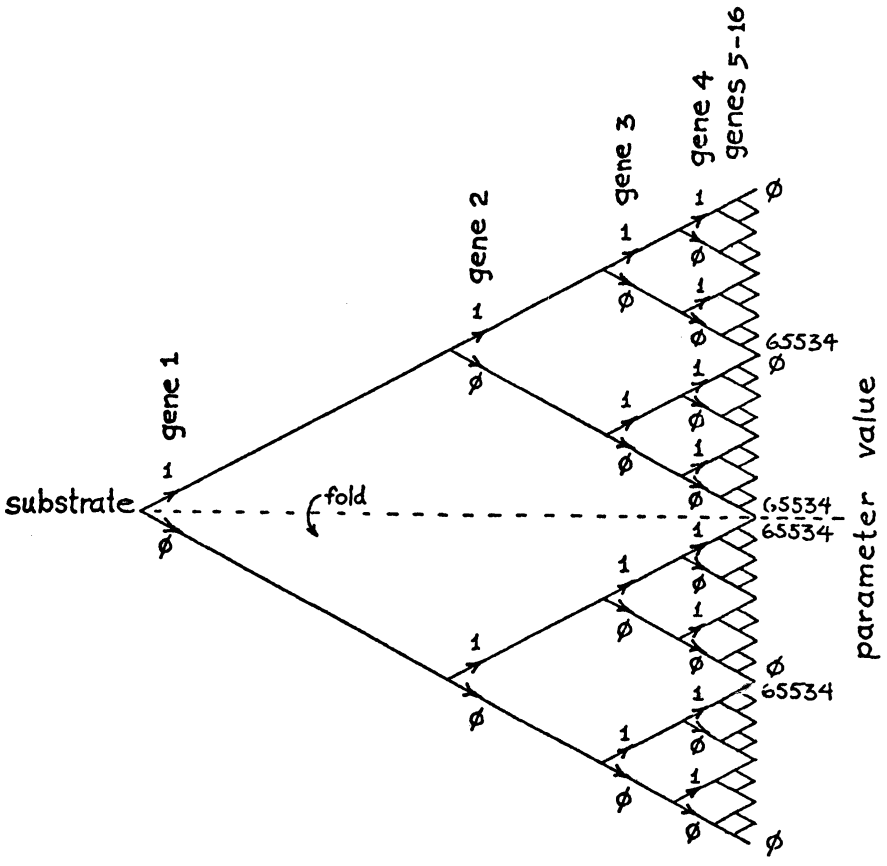


Figure 10 Synthetic pathway model of Gene Action 5A

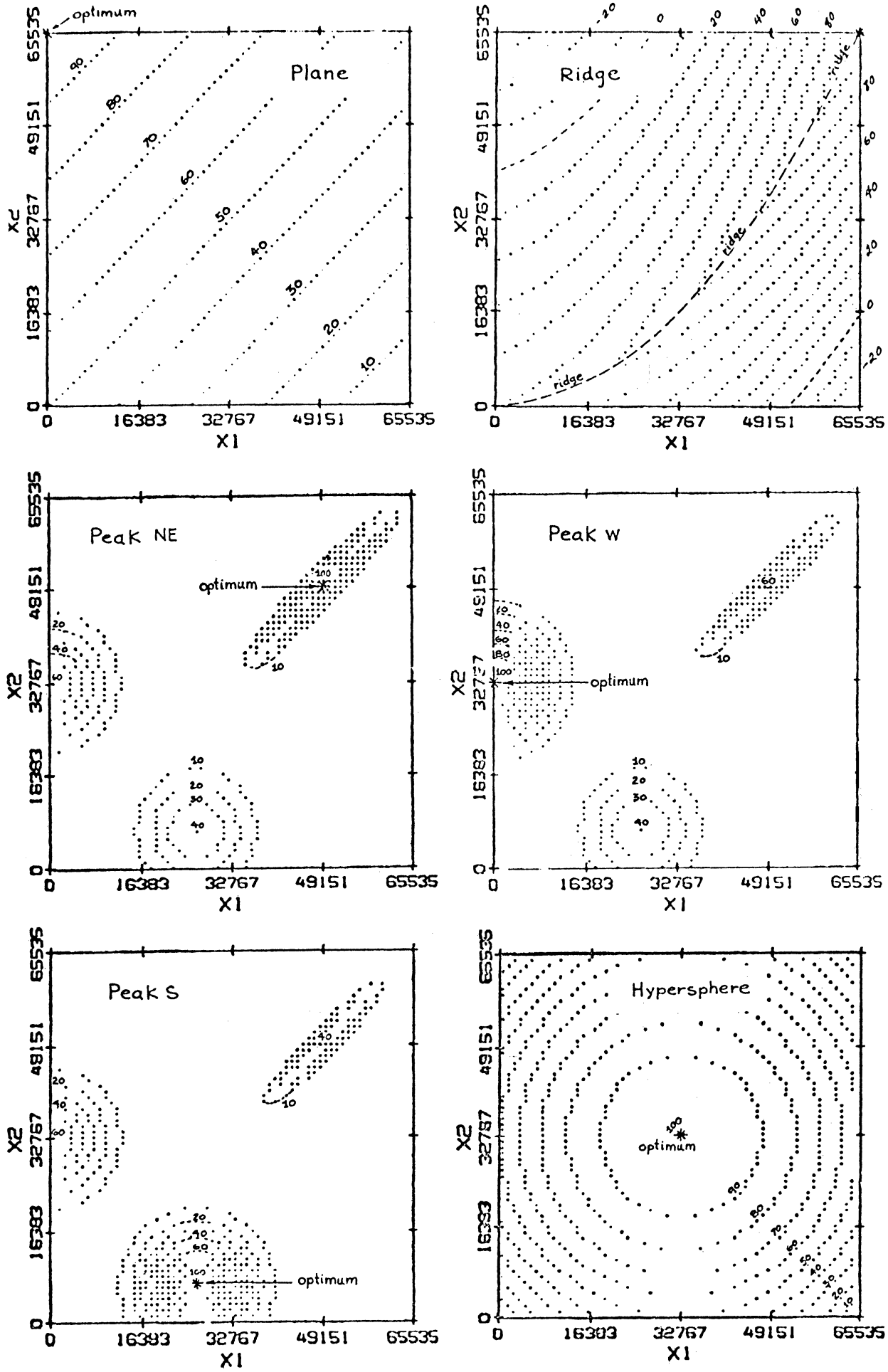


Figure 11 Objective characters Plane, Ridge, Peak NE, Peak W, Peak S and Hypersphere plotted in 2-dimensional parameter space

3

RESULTS

Experimental studies of ARTIFICIAL BREEDING for parameter optimization were run on a Digital Equipment Corporation PDP-9 computer at the University of Michigan Simulation Center. The programs are documented in the Appendix.

3.1 COMPARISON OF GENE ACTION/BREEDING METHOD COMBINATIONS

All combinations of 16 gene action algorithms and five breeding methods were first compared for general performance using an 8-parameter version of objective character Plane.

Genotypes with eight complexes per chromosome were used in each case. Polygenic complexes were arranged in descending order of effect and in normal order of parameter indeces. When using Gene Action 1, for example, each chromosome contained two sets of four complexes and controlled the synthesis of one odd- and one even-numbered parameter. When using Gene Action 2, the genome consisted of one chromosome containing the eight complexes for all of the parameters.

This structural arrangement of genes on the chromosomes was fixed by setting the probabilities of inversion and translocation to zero. Free recombination was simulated by setting crossover probabilities PCROS and PCROL to 0.5, so the genes were effectively unlinked and the structural arrangement is immaterial.

The probability of mutation was also set to zero.

Initial populations were completely heterozygous, simulating an ideal cross of source varieties that differ genetically at all loci contributing to the character of interest to the breeder. Alleles in one genome were chosen randomly and the complementary alleles were assigned to the homologous genome.

The solution of the underlying direct-search problem is at the lower bound (0) of the odd parameters X1, X3, X5 and X7, and at the upper bound (65535) of the

even parameters X2, X4, X6 and X8. Notice that the parameters do not interact in the objective character Plane; the optimal value of each parameter can be determined with the others fixed at any value.

Even though the parameters do not interact, the search problem is somewhat more difficult than it might appear at first glance. Consider a very crude exhaustive search. Suppose we divide each parameter range into ten equal intervals and make trial evaluations at the centers of the 100 million subdivisions of the parameter space. At a rate of one trial evaluation per second, this would require more than 30,000 hours.

Let us obtain a rough estimate of the number of trials required for a sequential search of the parameter space. This will of course depend on the starting point and increment step size used. Starting at the midpoint of each parameter range and incrementing by say five percent (10 steps to either extreme parameter value) will require 80 trial points. This is the average number for randomly chosen starting points. If five replications of the sequential search are made to be reasonably sure a global optimum is found, 400 trial points are required.

The populations for each breeding method were sized to obtain approximately the same number of trial points in each experiment--about 300--which is somewhat less than the estimated number of trials required to make a sequential search of the 8-dimensional space. The objective of this preliminary comparison of gene action/breeding method combinations was to determine whether marked differences in performance could be used to narrow the study to those most promising combinations. It seemed essential to base this decision on ARTIFICIAL BREEDING experiments that use an encouraging number of trials.

Pedigree Method 1. An F_2 population was formed by selfing completely heterozygous individuals drawn from a large, virtual F_1 population. In the following generations the highest-valued individuals in each family were compared, and the highest-valued individuals among these family representatives were selected and selfed to propagate their families into the next generation. The population size was held constant after the F_3 generation by increasing the family size as the number of selected families was reduced according to the following schedule:

Generation	Population size	Families selected	Family size
2	64	32	
3	32	16	1
4	32	16	2
5	32	8	2
6	32	4	4
7	32	2	8
8	32	1	16
9	32	1	32
10	32	1	32

Bulk Population Breeding 1. Populations of 32 self-fertilized individuals were propagated in bulk for ten generations with simulated artificial selection of the highest-valued half of each generation. The probability of outcrossing, POUCR, was set to zero.

Mass Selection 1. Populations of 32 cross-fertilized individuals were bred for ten generations with mass selection of the highest-valued half of each generation. The selected individuals were mated randomly to produce each individual in the next generation.

Simple Recurrent Selection 1. Populations were bred for ten simple recurrent selection cycles. The eight, highest-valued individuals in each cross-bred generation were selected and selfed to produce the intermediate generations. A diallel cross of eight individuals in each intermediate generation was used to produce (8)(7)/2 = 28 individuals in each cross-bred generation. The diallel cross of eight individuals numbered 1 to 8 is illustrated by the following diagram:

	1	2	3	4	5	6	7	8
1		x	x	x	x	x	x	x
2			x	x	x	x	x	x
3				x	x	x	x	x
4					x	x	x	x
5						x	x	x
6							x	x
7								x
8								

Reciprocal Recurrent Selection 1. Two populations of eight individuals were bred for ten reciprocal recurrent selection cycles. Four individuals were selected from each population on the basis of the highest-valued offspring produced by crossing each individual with a random sample of two individuals from the opposite population. There were, therefore, (4)(2)(2) = 32 individuals in the hybrid generation of each selection cycle. The selected individuals were selfed to propagate the two parental lines.

A single breeding experiment was run for each gene action/breeding method combination. Graphical results of the experiments are shown in Fig. 12a-h. In each part of the figure the phenotypic values of all individuals are shown in the order that they are produced in the simulated breeding program. The sequential order of individuals within a particular generation is not significant from the genetic or breeding viewpoint, but the progressive improvement of the objective character is of principal interest in evaluating the direct-search algorithm performance.

The best overall performance was obtained using Gene Actions 4 and 6 in combination with simple recurrent selection. These combinations achieved approximately 90 percent of the maximum theoretical genetic gain within 280 trials. In each experiment, however, there was evidence that major genes reached fixation prematurely. Without mutation, there was no way to break through the resulting selection limits.

Gene action/breeding method combinations that reached at least 80 percent of the maximum theoretical genetic gain were considered promising for use in ARTIFICIAL BREEDING. A list of these prospects is given below in descending order of phenotypic value achieved by the end of a single breeding experiment:

Gene Action 4/simple recurrent selection
Gene Action 6/simple recurrent selection
Gene Action 3/simple recurrent selection
Gene Action 9/simple recurrent selection
Gene Action 6/mass selection
Gene Action 6/pedigree method
Gene Action 8/simple recurrent selection
Gene Action 8/mass selection

Gene Action 2A/pedigree method

Gene Action 11A/simple recurrent selection

Gene Action 4/mass selection

It was of course impossible to draw firm conclusions on the basis of single experiments with each gene action/breeding method combination. Therefore, several of the most promising gene action models and breeding methods were investigated in further experiments.

3.2 PEDIGREE METHOD 1 EXPERIMENTS

Definite progress was observed in pedigree breeding for the 8-parameter objective character Plane during the preliminary comparison of gene action/ breeding method combinations described in Section 3.1. However, in every case fixation of undesireable alleles prevented genetic advance beyond suboptimal selection limits of approximately 75 to 85 phenotypic units. The maximum possible objective value for Plane is 100 phenotypic units.

3.2.1 Breeding for 2-Parameter Plane

To verify that this problem is related to the number of segregating loci, the Gene Action 3/Pedigree Method 1 combination was used in ARTIFICIAL BREEDING for a 2-parameter version of Plane. The results of this experiment are shown in Figs. 13a-c. The population reached a limit of 96.77 in the 8th generation with final parameter values of X1 = 2078 and X2 = 63379. This is greater than the genetic advance observed in any of the experiments using the 8-parameter version; it shows that the chances of finding optimal values are greatest when there are fewer loci (parameters) affecting the objective character.

The results of ARTIFICIAL BREEDING experiments are averaged over replications of the experiment. The AVERAGE VALUES are printed at the bottom of the output as shown in Fig. 13c. When the experiment is not replicated, the AVERAGE VALUES are the actual values of the single experiment, as in the case of Fig. 13c. The column headings for the AVERAGE VALUES are defined as follows:

EFF — Efficiency of the breeding program; the ratio of the total phenotypic value of all individuals to the maximum possible total value

AVG	Average phenotypic value of the population in the current generation
STD	Standard deviation of phenotypic values for the population in the current generation
AVGS	Average phenotypic value of selected individuals in the current generation
STDS	Standard deviation of phenotypic values of selected individuals in the current generation
NIZ	Number of inviable zygotes in the current generation
NTR	Number of trial evaluations of the objective function in the current generation

PM1A in the input data of Fig. 13c indicates that Gene Actions 2A, 5A, 8A and 11A had been compiled on disk at the time the experiment was run.

3.2.2 No Selection Among Families After the F_3 Generation

If fixation of undesireable alleles was caused by too intense a selection among families in the early generations of the last experiment, reducing that pressure might improve the breeding performance. So the experiment was repeated with 32 individuals selected from the F_2 generation as before, but 16 families were kept in the remaining generations. There were two members in each family. These results are shown in Fig. 14a,b. The average value of the late generations decreased, but the maximum individual value remained about the same as in the previous experiment--96.201 compared with the previous value of 96.770. The population did not reach genetic fixation, but the average value changed very slowly after the 7th generation.

Other experiments, in which no selection among families was practiced after the F_3 generation, were also run using Gene Action 3 and Gene Action 4 in conjunction with the 8-parameter Plane. The results were similar to those of Fig. 14.

Eliminating selection among families, therefore, did not have an appreciable effect on the pedigree method performance.

3.3 BULK POPULATION BREEDING 1 EXPERIMENTS

In the preliminary experiments of Section 3.1, bulk population breeding also produced definite genetic advance in the 8-parameter objective character Plane. Several populations reached phenotypic values of 75 to 80 units, but in all cases progress was limited by fixation of undesireable alleles.

The following additional experiments were run using Gene Action 4/Bulk Population Breeding 1.

3.3.1 Effect of Selection Intensity

Figure 15 shows the results of three experiments in which 4,8 and 16 individuals were artificially selected from populations of 32. Increasing the artificial selection intensity increased the initial rate of response with little effect on the final selection limit.

3.3.2 Effect of Population Size

Bulk population breeding of these extremely small populations can not be compared with agricultural programs where hundreds or thousands of individual plants are bulked in each generation. However, large populations can not be used in ARTIFICIAL BREEDING for parameter optimization if it is important to keep the number of trials at a minimum. We must be concerned with the performance of the bulk population method when applied to very small populations even though the results will be subject to "small sample errors."

Effects of population size were explored briefly in experiments using populations of 16 and 64 individuals. These results are shown in Fig. 16. In each case one-fourth of the population was artificially selected. The small population reached fixation in approximately five generations (after 160 trials). The larger population did not reach fixation during the 10-generation breeding program, but the total genetic advance was only slightly greater than the selection limit of the smaller population.

There appeared to be no reason to use populations of more than 32 individuals in ARTIFICIAL BREEDING by the bulk population method.

3.3.3 Effect of Cross-fertilization

Performance improved when the probability of outcrossing, POUCR, was increased from zero to 0.5 and 1.0. Results obtained using Gene Action 4/ Bulk Population Breeding 1 and artificially selecting four individuals from a population of 16 are shown in Fig. 17. A greater initial rate of response and a higher final selection limit were observed when using the completely outcrossing species. The eight parameter values of each individual produced during that experiment are shown in Fig. 18. The selection limit is clearly due to fixation of genes that control parameters X3 and X8.

Increasing the population size to 32 with artificial selection of eight individuals in each generation produced further improvement in the parameter optimization performance. These results are shown in Fig. 19a,b. Progress was steady over the ten generations, and genetic variation remained in the population throughout the breeding program. The selection limit was increased to above 90 phenotypic units.

3.3.4 Effect of Linkage

In the last experiment all eight of the parameters approached the optimal values individually, but the performance would have been greatly improved if the values nearest the optimal values had occurred in the same individuals. This raises a question as to whether linkage would improve the parameter optimization performance of the ARTIFICIAL BREEDING program.

The experiment was repeated with 0.05 probability of crossover between adjacent loci within complexes (PCROL) and 0.1 probability of crossover between adjacent complexes (PCROS). Results are shown in Fig. 20a,b. The rate of response is slightly lower, but steady. Genetic variation is maintained, but there is now evidence of fixation of many genes that control parameters X2 and X4. The other parameters also exhibited slower convergence.

It appears that linkage impedes the performance of bulk population breeding of cross-fertilized species.

3.3.5 Replicated Breeding for 8-Parameter Plane

Five replications of a bulk population breeding program for 8-parameter Plane were run using Gene Action 4, no linkage, completely cross-fertilizing organisms, populations of 32 individuals, artificial selection of eight individuals and 20 generations.

In Fig. 21a are plotted the generation mean and standard deviation when averaged over the five replications. The printed results of the replicated experiment are shown in Fig. 21b. With the print control IPBP set to 1, only parameter values with corresponding objective values that exceed the values at previous trial points are printed. The AVERAGE, MAXIMUM, and MINIMUM VALUES of "generation" information are printed following the parameter values for the five experiments. The lowest mean phenotypic value for the 20th generation in the five replications was 93.259, so the bulk population breeding method appears to be reliable.

The maximum individual phenotypic values that occurred in each of the five replications of the breeding program are listed below:

Experiment	Maximum value	Trial
1	97.871	611
2	97.870	586
3	96.684	575
4	97.037	457
5	97.606	589

3.3.6 Breeding for 8-Parameter Ridge

The same bulk population breeding program was applied to the 8-parameter objective character Ridge with the results shown in Fig. 22a,b. Genetic progress was slow but steady over the 20 generations. Parameters X1 and X2 became stalled along the ridge line in the 2-dimensional subspace, but the other parameters were driven close to the optimal values at the upper bound of the parameter range, 65535.

3.3.7 Replicated Breeding for 8-Parameter Ridge

Five replications of the same experiment were run with the results shown in Fig. 23a,b. The population mean of the 20th generation, averaged over the five replications, was 80.795 phenotypic units.

Robustness of the ARTIFICIAL BREEDING system should not be judged on the basis of averaged phenotypic values, since these values may vary widely depending on the features of the objective character. A distance measure of how close trial points come to the optimal point would be more appropriate. A numerical measure of this sort was not computed, however, Fig. 22 gives an indication of the parameter "miss distance" in one particular experiment.

The 605th trial of the first replication came closest to the optimal parameters for Ridge during the replicated experiments. The parameter values for this individual are 55388, 48452, 64206, 62950, 63086, 61146, 63160, and 63564 for X1 to X8 respectively. The phenotypic value is 94.023 phenotypic units, quite close to the maximum theoretical gain considering the complexity and degree of interaction among the parameters in this objective character.

3.4 MASS SELECTION 1 EXPERIMENTS

Bulk population breeding of cross-fertilized species with artificial selection is actually a form of mass selection with random matings biased in favor of mating the highest-valued individuals among those selected artificially. Mass selection with uniform random mating was also investigated in experiments described here.

3.4.1 Effect of Selection Intensity

Half of the population was selected for random mating in the preliminary comparison of gene action/breeding method combinations described in Section 3.1. Increasing the selection intensity by selecting eight of the 32 individuals in each generation produced the results shown in Fig. 24a,b. The objective

character is 8-parameter Plane with parameter synthesis by Gene Action 4. Progress was steady during the first ten generations (320 trials). Considerable genetic variation was maintained throughout the breeding program even though there was no mutation of individual genes. All parameters approached the optimal values at about the same rate. The final selection limit was at approximately 90 to 95 phenotypic units.

3.4.2 Effect of Dominance in Polygene Action

Repeating the experiment in breeding for 8-parameter Plane using Gene Action 10 instead of Gene Action 4 produced the results shown in Fig. 25a,b. Recall that Gene Action 10 has functional polygenes as in Gene Action 4, and also dominance modifier loci that determine intra-allelic interaction at the level of parameter synthesis.

The most noticeable effect of the dominance is an increase in phenotypic variation during the early generations. The overall performance is about the same as in the previous experiment using Gene Action 4. Parameters X6 and X8 show loss of genetic variation in the later generations.

3.4.3 Effect of Epistatic Gene Action

Using Gene Action 3 in the mass selection program for 8-parameter Plane produced rapid convergence of some parameters with nearly complete elimination of genetic variation in later generations. These results are shown in Fig. 26a,b. Parameters X1, X5, X6 and X7 are driven very close to the optimal values, but the others are stalled by premature fixation of genes having major effect in the parameter synthesis.

3.4.4 Effect of Dominance in Epistatic Gene Action

The results in Fig. 27a,b were obtained by repeating the experiment using Gene Action 9, which incorporates dominance modifier loci in the primary algorithm of Gene Action 3. The most noticeable effect here too was a marked increase in parameter variation, especially during the early generations.

Sustained variation at the most significant locus controlling parameter X8 caused X8 excursions from one extreme of the parameter range to the other even during the later generations when the less significant loci had become fixed.

3.4.5 Breeding for 8-Parameter Ridge

Experiments in ARTIFICIAL BREEDING for 8-parameter Ridge using Gene Actions 4, 10, 3 and 9 were also run. Slow progress was observed in all cases. Greater variation in parameters occurred when using Gene Actions 10 and 9, which employ intra-allelic dominance.

3.4.6 Effect of Gene Number

Rapid convergence to within a small neighborhood of the optimum was observed in breeding by mass selection for 2-parameter Ridge using Gene Action 3. When Gene Action 9 was used, however, the population converged rapidly to a point along the ridge line below the optimum.

3.4.7 Effect of Population Size

Only slight differences in averaged performance were observed in five replications of mass selection for 8-parameter Ridge using populations of 16, 32 and 64 individuals. The results are shown in Fig. 28a,d. The initial rate of average response is the same for all three cases, but the larger populations reached slightly higher average phenotypic values.

The highest-valued individual in the replicated experiments was the 1004th trial in the second replication of the largest population. Its parameter values are 56623, 49183, 61423, 55421, 56850, 52249, 49951 and 38511 for X1 to X8 respectively, and its phenotypic value is 87.508.

3.5 SIMPLE RECURRENT SELECTION 1 EXPERIMENTS

In the experiments of Section 3.1, populations bred by simple recurrent selection had not reached a definite selection limit by the tenth cycle.

The method was continued for 20 cycles in the experiments described here, with results that indicate species capable of self- and cross-fertilization are probably the most versatile organisms for use in ARTIFICIAL BREEDING.

3.5.1 Effects of Selection Intensity and Population Size

Figure 29a,c shows the results of a single experiment in breeding by simple recurrent selection for 8-parameter Plane using Gene Action 4 with free recombination, no inversion or translocation and no mutation of alleles. Eight individuals were selected from 32 in each cross-bred generation, the selected individuals were selfed, and their offspring were crossed in all possible combinations to complete a selection cycle. The breeding program was run for 20 cycles.

The mean phenotypic value increased from 50.00 in the first cycle to 93.169 in the last cycle. Genetic variation was maintained throughout the 20 cycles, and individual parameter converged to the neighborhood of optimal values more rapidly than in previous experiments using other breeding methods.

The initial rate of response increased when higher selection intensity and smaller populations were used, but fixation of alleles caused selection limits below the total genetic advance indicated in Fig. 29.

3.5.2 Effect of Epistatic Gene Action

The use of Gene Action 9 instead of Gene Action 4 caused even greater variation of parameter values than that shown in Fig. 29b. Fixation of undesireable alleles also caused lower selection limits.

3.5.3 Effect of Gene Number

Experiments were also run using Gene Action 4 and simple recurrent selection for 8- and 2-parameter Ridge. These results show less dependence on the number of interacting genes than had previously been observed using Gene Action 3 and mass selection. This can not be definitely attributed to 1) differences in the epistatic effects of the two gene action algorithms,

or to 2) differences in the effectiveness in breeding for epistatic characters by the two methods.

3.5.4 Effect of Linkage

Additional experiments were run using Gene Action 9 and simple recurrent selection for 8-parameter Plane, first with free recombination and then with gene linkage defined by probabilities 0.1 of crossing-over between adjacent segments and 0.05 of crossing-over between loci within complexes. A large amount of parameter variation was observed in the experiment using free recombination, as had been the experience using other breeding methods with this gene action algorithm. Parameter values converged more rapidly when gene linkage was introduced, and there was evidence that the linkage inhibited the dismantling of desireable complexes. But the linkage also had the effect of accelerating the fixation of undesireable alleles, so the population with linked genes stalled at a selection limit below that of the population with unlinked genes.

3.6 PEDIGREE METHOD 2 EXPERIMENTS

So far, initial populations have been either completely heterozygous or they have been formed by selfing completely heterozygous individuals. This can be viewed as simulating either of two situations in plant breeding: 1) the development of new varieties from wild populations in which there is a large amount of genetic variation, or 2) the development of improved varieties from a cross of parental lines that differ genetically at all loci contributing to the character of interest to the breeder. In either case, these ARTIFICIAL BREEDING experiments have simulated only the first step of what in agricultural plant development may require a protracted series of breeding programs.

The results of extended ARTIFICIAL BREEDING for 8-parameter Plane using Gene Action 4 and the pedigree method are described here. The "extended" means that after two varieties have been developed from completely heterozygous source populations, further search of the genetic parameter space is based on simulating the development of improved varieties. There are, of course, many ways varieties could be crossed to obtain the hybrids. In this case,

the two previous varieties that produced the highest individual phenotypic value were used.

Six varieties were developed in all, including the first two derived from completely heterozygous source populations. Ten generations of pedigree breeding were used to develop each new variety. The population size was decreased in the later generations of each varietal development program to avoid repeated trials as the populations reached homozygosity. A total of 102 individuals were produced during each varietal development program.

Inversion, translocation and mutation were prevented by setting the probabilities of occurrence to zero. Free recombination was simulated by using 0.5 probability of crossover between adjacent loci.

The results in Fig. 30a,c illustrate the importance of the extended breeding program. The first two varieties reached phenotypic values of 72.929 and 76.489 respectively; the third variety, developed from a cross of the first two, reached 85.371. The succeeding varieties improved steadily as shown in the following list:

Variety	Highest individual value
1	72.929
2	76.489
3	85.371
4	87.262
5	90.066
6	93.219

The highest phenotypic value of the sixth variety exceeds that of the fifth by 2.804 units. This improvement exceeds the standard deviation of the F_1 population from which the sixth variety was derived, indicating that the fourth and fifth varieties have complementary genotypes even though they are descendents of the same parental lines. Moreover, the pedigree method is capable of fixing favorable combinations of the complementary genes in an improved, true-breeding variety.

The standard deviations of phenotypic value in the first two F_1 generations are 7.366 and 7.518 respectively. The last four F_1 generations have either zero or very small variance, since they are obtained by crossing parental lines that are homozygous at nearly all loci.

The effect of each varietal cross and the ensuing pedigree breeding process can be followed closely in Fig. 30b. The complementary effects of crossing previously improved varieties are strongest in the synthesis of parameter X7 and weakest in the synthesis of parameter X8.

3.7 SIMPLE RECURRENT SELECTION 2 EXPERIMENTS

Extended breeding experiments were also run using simple recurrent selection for 8-parameter Plane, Ridge, Peak NE, Peak W, Peak S and Hypersphere. Five varieties were developed in each composite breeding program. The first two were developed from completely heterozygous source populations, the third from a cross of the first two, the fourth and fifth from crosses of the two previous varieties that produced the highest individual phenotypic values.

Ten selection cycles were used in each varietal development program. In each cycle, eight individuals were selected from 32 members of a cross-bred generation and their self-bred offspring were crossed in all possible combinations to produce the cross-bred generation of the next cycle. The intermediate, self-bred individuals were not evaluated phenotypically, so the number of trial points in parameter space was equal to the number of cross-bred individuals.

Free recombination was simulated by setting the probability of crossing over between any adjacent loci to 0.5.

Inversions, translocations and mutations were first inhibited by setting their probabilities to zero. In later experiments random chromosome aberrations were simulated and were found to have a surprisingly advantageous effect on the performance of the ARTIFICIAL BREEDING system.

Gene Action 4 was used in the first sequence of experiments described below. The epistatic Gene Action 6 was also tried but did not perform as well as

Gene Action 4, which was then used again in the final experiments.

3.7.1 Breeding for 8-parameter Objective Characters Using Gene Action 4 Without Inversion, Translocation or Mutation

Plane. The phenotypic values and parameters for each individual are shown in parts a and b of Fig. 31a,c. Each tic mark on the horizontal axis represents the beginning or end of a varietal development program. The generation statistics for the five varieties are shown in part c of the figure.

The first two varieties reached phenotypic values of 80.967 and 86.886 respectively. Further improvement to a value of 93.798 was obtained in the third variety. The mean value of the crossbred generations reached a limit of approximately 94.5 during the fourth variety and, thereafter, remained nearly constant.

The improvement obtained in the third variety of the extended breeding program illustrates the importance of crossing "improved" varieties rather than starting from completely heterozygous source populations. In this case, the improvement was due primarily to complementary effects in the synthesis of parameter X6 (Fig. 31b).

Ridge. The results of this experiment (Fig. 32a,c) also exhibit the advantage of extending the ARTIFICIAL BREEDING program. The first two varieties reached mean phenotypic values of 67.914 and 70.632 with only one individual phenotypic value greater than 80 units. The population means reached 74.877, 79.078 and 89.683 in the last three varietal development programs, with maximum phenotypic values exceeding 93 units during the last program.

In this case the complementary effects that produced the improvement during the development of the last three varieties are most evident in the plots of parameters X5, X6 and X8 (Fig. 32b). The 2-dimensional Ridge functions V(X1,X2), V(X5,X6) and V(X7,X8) are nearly optimized by the end of the sequence of five varieties. However, the function V(X3,X4) was further from its optimal value at the end of the fifth varietal development than at the end of the first.

Peak NE. Each of the four, 2-dimensional Peak NE functions have three local peaks at parameter-pair values: (49151,49151), (0,32767) and (26214,6553). The North East peak at (49151,49151) is the optimum. There are three locally optimal values of the four pairs of parameters, so there are $3^4 = 81$ local peaks.

The results of the experiment are shown in Fig. 33a,c. The first two varieties reached mean phenotypic values of 17.988 and 10.502 with only two individual phenotypic values greater than 40 units. Definite improvement was obtained in the last three varieties, but the mean values reached only 18.173, 22.134 and 27.146. Several individuals in the fifth varietal development program had phenotypic values just under 60 units.

The extended breeding program converged in parameter values toward the suboptimal peak with (X1,X2) and (X5,X6) at (0,32767) and (X3,X4) and (X7,X8) at the optimal values (49151,49151). The optimal values of (X3,X4) were determined as a result of complementary effects of crossing the first two varieties (Fig. 33b). The optimal values of (X7,X8) were determined during the first two varietal development programs. Parameters (X5,X6) converged toward (0,32767) in both of the first two programs and remained in the neighborhood of these values throughout the last three programs. Parameters (X1,X2) converged rapidly to the same values in the first program, but failed to converge to any of the local peak values during the second, third or fourth development programs. Finally, during the last program, (X1,X2) were drawn again to the false peak at (0,32767).

The breeding program determined the optimal values of four of the eight parameters, but converged to a false peak. It seems unlikely that the system would be able to move off the false peak in the development of additional varieties.

Peak W. This objective function has local peaks at the same parameter-pair values as Peak NE: (49151,49151), (0,32767) and (26214,6553), but the optimum is at West peak values (0,32767).

Results of the experiment are shown in Fig. 34a,c. Mean phenotypic values of 24.274 and 17.176 were reached in the first two varietal development

programs. Means of 42.989, 46.315 and 56.491 were reached in the last three. From Fig. 34a, complementary effects in crossing the first two varieties were obtained in the starting population for the third. However, the cross used to develop the fourth variety was a poor one and no further improvement was obtained in the fourth or fifth variety as compared with the third.

The breeding program found the optimal values of parameters X1-X6, but failed to find the optimal values for X7 and X8. At the end of the fifth varietal development program, parameters X7 and X8 are near but are not precisely at values corresponding to the false peak at (26214,6553). So there is some possibility that the system would find the optimal values of X7 and X8 if the program had been continued.

Hypersphere. This objective function has a smooth, hyperspherical peak at parameter-pair values (32767,32767). When using additive Gene Action 4, the parameters of every individual in the completely heterozygous F_1 populations used to develop the first two improved varieties are precisely at the optimal values. The amount that the F_2 mean value drops below the optimal value of 100.00 units is a measure of the average parameter error at the beginning of the breeding program, and may be used to compare the parameter dispersion produced by the use of completely heterozygous source populations with various gene action algorithms.

Results of the experiment are shown in Fig. 35a,c. For the reasons explained above, the mean values of the F_1 generations in the first two varietal development programs are 100.00 units. The means drop to 88.182 and 88.132 in the F_2 generations but increase to 94.475 and 94.929 by the end of the first two programs. Mean values of 97.053, 97.236 and 98.940 are achieved in the last three varieties. By the end of the fifth program, the average value of individuals selected from the cross-bred generations reached 99.515.

3.7.2 Effect of Epistatic Gene Action

Similar experiments in breeding for 2- and 8-parameter versions of the objective characters were also run using Gene Action 6.

Rapid convergence to the optimal parameter values was observed in breeding for 2-parameter Plane and Ridge. The system converged rapidly but to false peaks in breeding for 2-parameter Peak NE and Peak W. Optimum parameter values were found in the third and fourth varieties while breeding for 2-parameter Peak S; but the fifth variety reverted to lower mean phenotypic values, as had been observed in earlier experiments. Rapid convergence was also observed in breeding for 2-parameter Hypersphere.

Gene Action 6 was effective in breeding for 8-parameter Plane. However, poor performance was observed in breeding for 8-parameter Ridge; some parameters failed to converge, and some became prematurely fixed with undesireable alleles at loci having major effect.

Further experiments using Gene Action 6 were then suspended in order to explore the effects of chromosomal aberrations while using Gene Action 4.

3.7.3 Effect of Inversions, Translocations and Mutations in Breeding for 8-Parameter Objective Characters Using Gene Action 4

The experiments described in Section 3.7.1 were repeated with the probabilities of inversion (PINV), translocation (PTRA) and mutation (PMUT) all set at 0.0010. This means that, on the average, one chromosome in a thousand will rupture between any two specific, adjacent loci and then re-fuse with a chromosome segment in either an inverted or translocated configuration. It means also that, on the average, one zygote in a thousand will have an allele at a specific locus that is a mutant of the one transmitted by the normal processes of inheritance.

Plane. Results are shown in Fig. 36a,c. The differences in parts a and b of Figs. 31 and 36 are not pronounced, however, an improvement in performance can be seen by comparing part c. The random aberrations of chromosome structure and gene conformation increased the mean phenotypic value of the fifth variety from 94.551 to 97.201. Many individuals in the last generation of the fifth varietal development program (Fig. 36c) have phenotypic values greater than 97.0, while only one individual in the last generation exceeds this value in the previous experiment. One individual in this experiment

reached a phenotypic value of 98.082 units. The parameter values X1 to X8 of this individual are respectively: 416, 64156, 1082, 64774, 1096, 63724, 2182 and 64206.

Ridge. Results are shown in Fig. 37a-c. In the previous experiment (Fig.32), a mean phenotypic value of 89.683 was reached in the last generation of the fifth varietial development program; the corresponding value in this case was 87.407. The final phenotypic values in Fig. 32c are higher than those of Fig. 37c. The general performance was, however, quite similar, and the small differences observed in these two experiments do not indicate a decrease in performance due to the use of simulated inversion, translocation and mutation; performance variations of this amount would be expected in replicated tests.

Peak NE. Results are shown in Fig. 38a-c. In this experiment, parameter pairs (X1,X2), (X5,X6) and (X7,X8) converged toward the optimal values (49151,49151) of the 2-parameter Peak NE objective function. The parameters (X3,X4) converged to false peak values (26214,6553). Although the system again converged to a false peak, six of the eight parameters were optimized here compared to four in the previous experiment where inversion, translocation and mutation were inhibited.

Peak W. Results are shown in Fig. 39a-c. Mean phenotypic values of 18.865 and 16.769 were reached in the first two varietal development programs with only three individuals exceeding phenotypic values of 40 units. In the last three programs, mean values reached 41.403, 50.990 and 78.063 units with many individual values in the fifth variety exceeding 80 units; one individual in the fifth variety reached a phenotypic value of 94.855 units.

All four of the parameter-pairs (X1,X2), (X3,X4), (X5,X6) and (X7,X8) converged toward the optimal values (0,32767). Individuals with desireable combinations of alleles at loci controlling parameter-pairs (X3,X4), (X5,X6) and (X7,X8) were produced in the first varietal development (see Fig. 39b), and it appears that some of these combinations were preserved in the cross of the first and second varieties used to develop the third. Crossing the first and third varieties to develop the fourth must have produced many homozygous loci that control (X3,X4), (X5,X6) and (X7,X8) because these parameter-pairs were near

the optimal values in the earliest generations and remained there throughout the fourth varietal development. Parameter-pairs (X1,X2), on the other hand, moved toward the false peak at (26214,6553) during the fourth program. In the fifth program (X1,X2) too were driven rapidly to the optimal values (0,32767).

By the end of the fifth varietal development, the system had definitely found the optimal peak among the 81 local peaks of the objective function. Continued breeding would have undoubtedly refined the adjustment of the parameters.

Peak S. Results are shown in Fig. 40a-c. The first two varieties reached mean phenotypic values of 35.802 and 34.721 units; the third, fourth and fifth varieties reached means of 71.129, 64.784 and 76.083 respectively. The third variety reached a higher mean value than the fourth, and the highest-valued individual was in fact produced in at the end of the third program. The setback in the fourth variety was overcome in the fifth variety which reached the highest mean phenotypic value.

From Fig. 40b, it appears that desireable combinations of alleles for parameter-pairs (X1,X2), (X3,X4) and (X5,X6) were found in the first varietal development program. The pair (X7,X8) converged to the optimal values (26214,6553) in the third program, but the cross used to develop the fourth variety appears to have been heterozygous at many of the loci controlling this pair of parameters. This would explain the setback at the beginning of the fourth program observed in Fig. 40a.

The populations had not reached complete homozygosity by the en breeding program, so, strictly speaking, they should not have been referred to as "varieties". However, the genetic variance does decrease within and over successive programs, and it is incorrect to infer from the increasing phenotypic variance that the genetic variance also increased. Increasing phenotypic variance is brought about by the greater steepness of the objective function in the vicinity of the optimal parameter values. A population with small genetic variance but nearly optimal genotype may, therefore, have larger phenotypic variance than a population with large genetic variance but far from optimal genotypes.

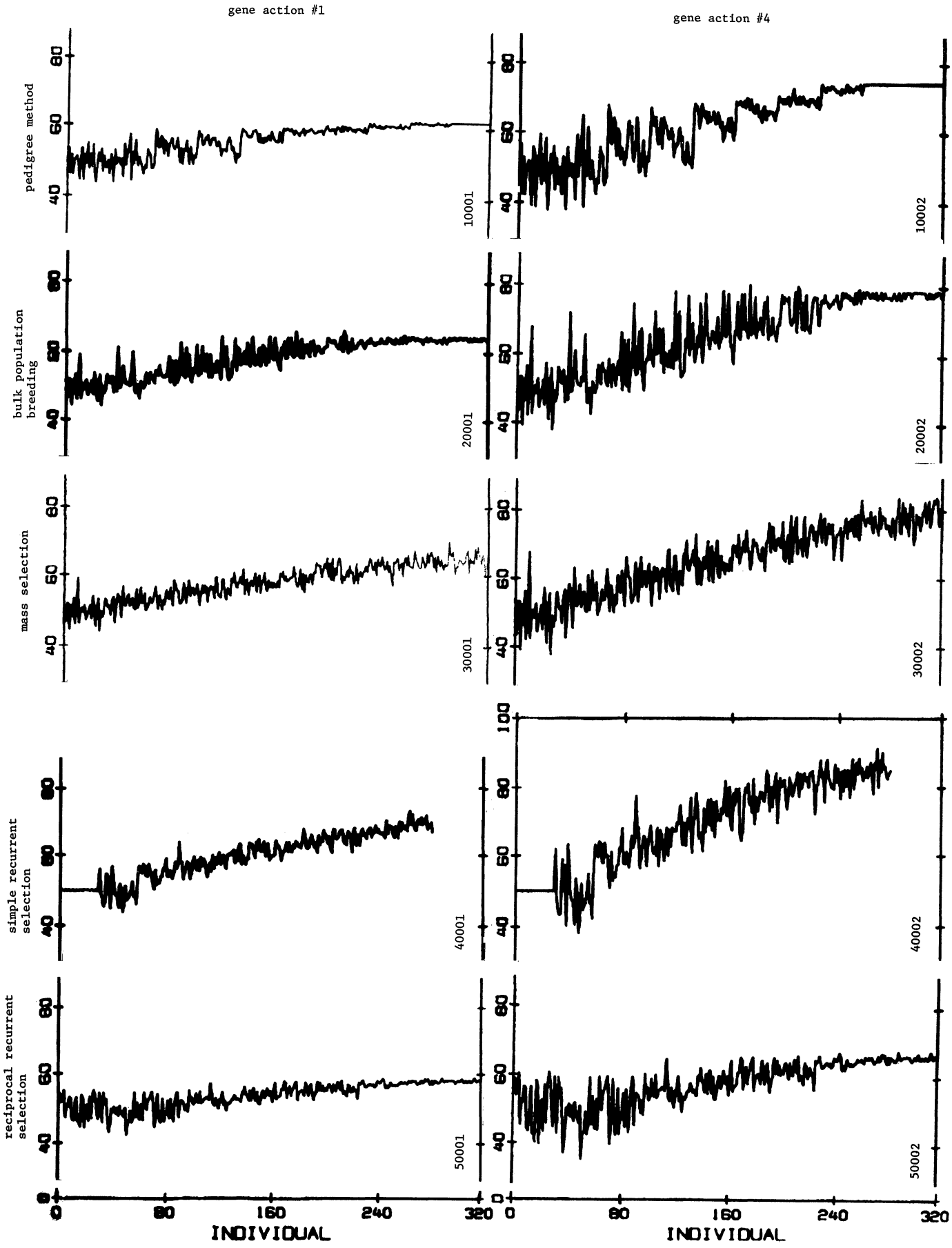


Figure 12a Comparison of gene action/breeding method combinations: Gene Action 1 and Gene Action 4 in combination with five breeding methods

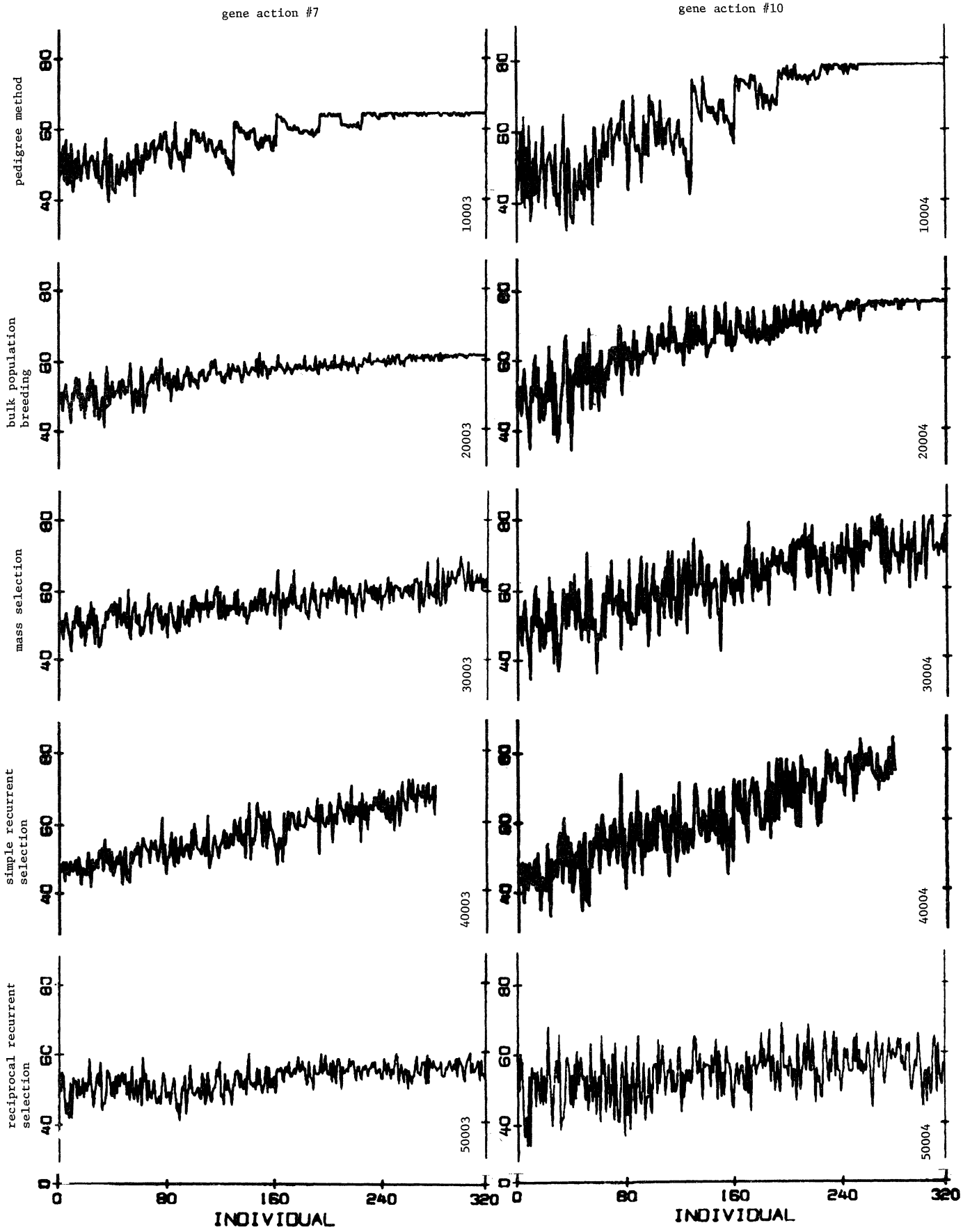


Figure 12b Comparison of gene action/breeding method combinations: Gene Action 7 and Gene Action 10 in combination with five breeding methods

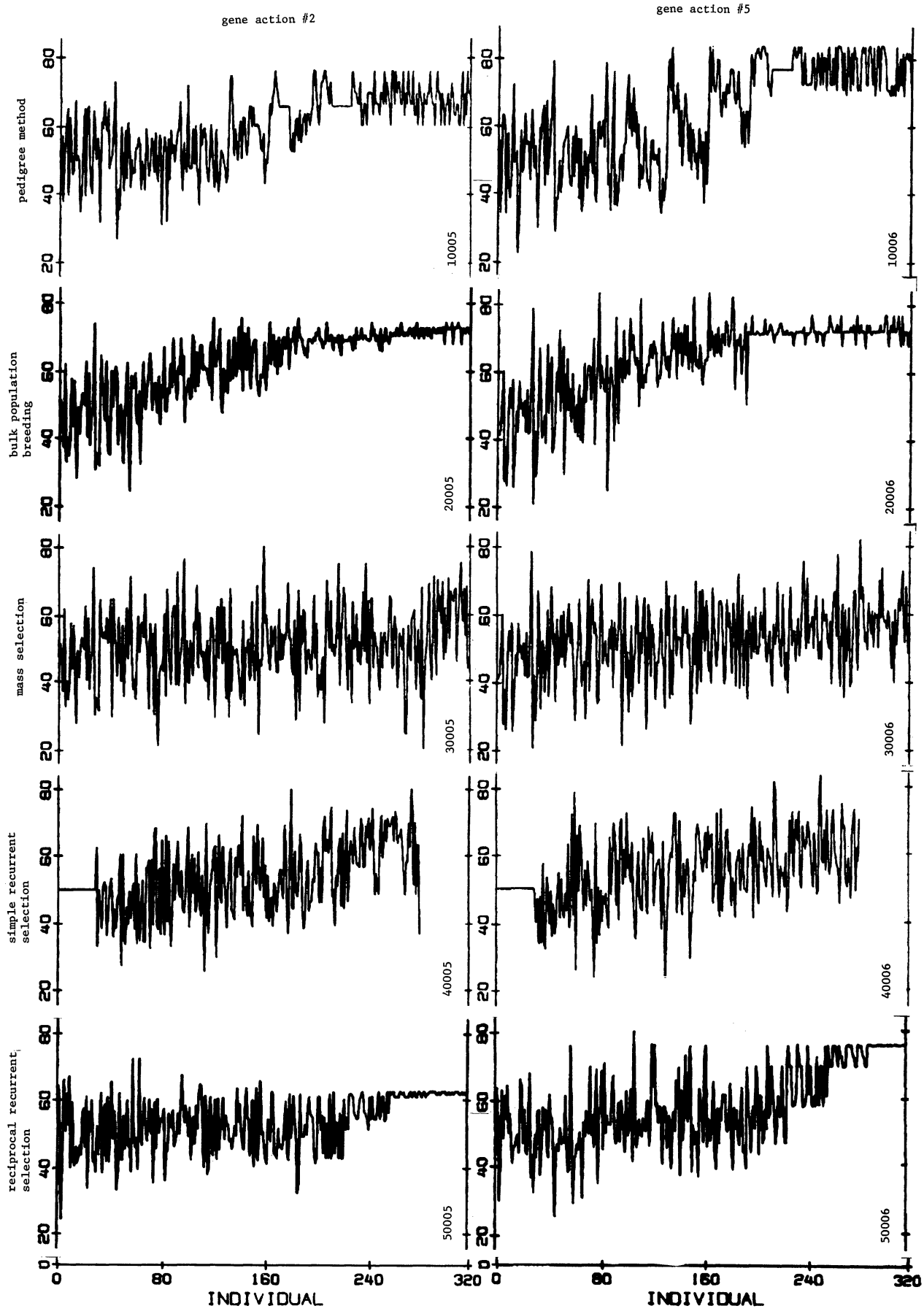


Figure 12c Comparison of gene action/breeding method combinations: Gene Action 2 and Gene Action 5 in combination with five breeding methods

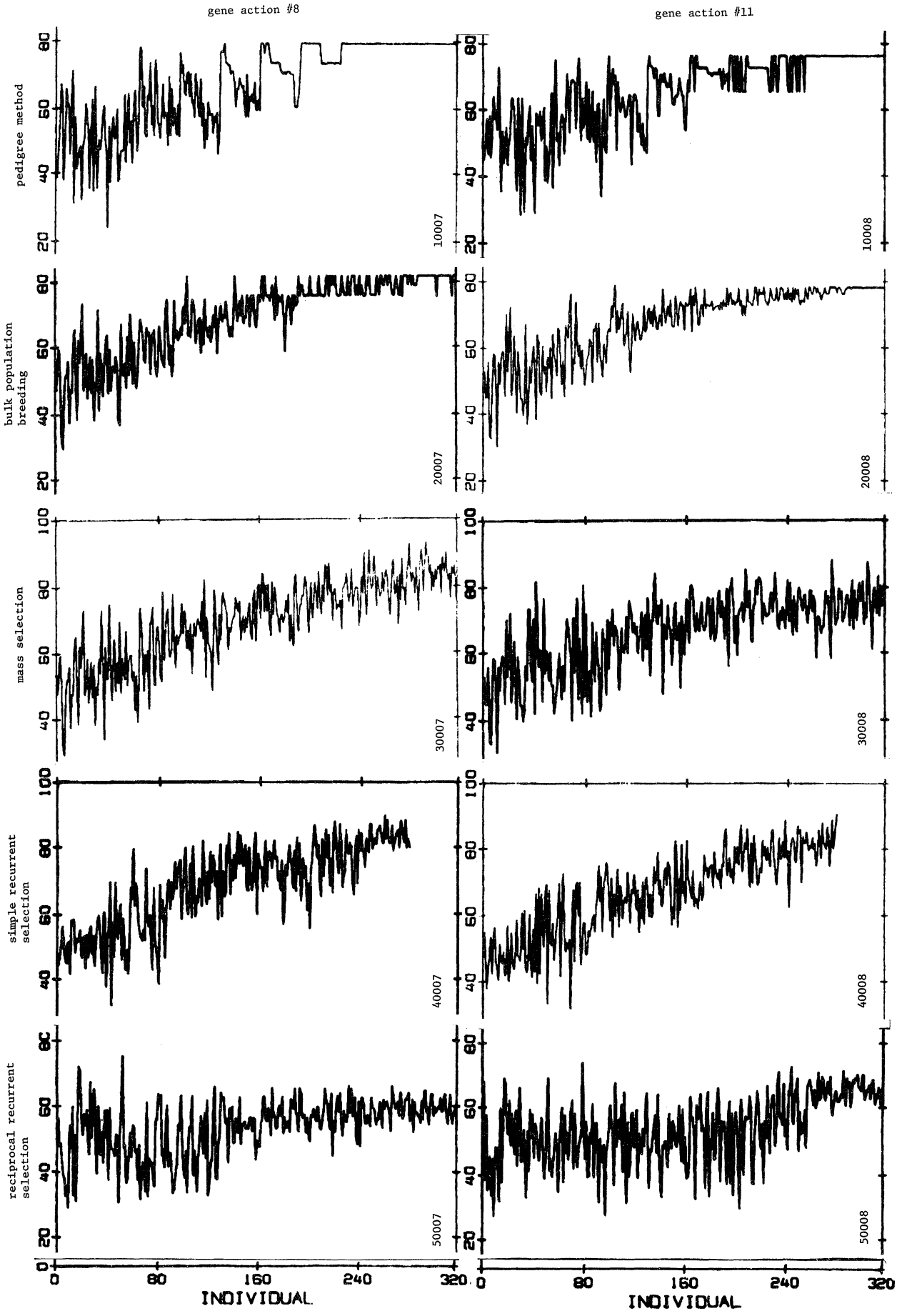


Figure 12d Comparison of gene action/breeding method combinations: Gene Action 8 and Gene Action 11 in combination with five breeding methods

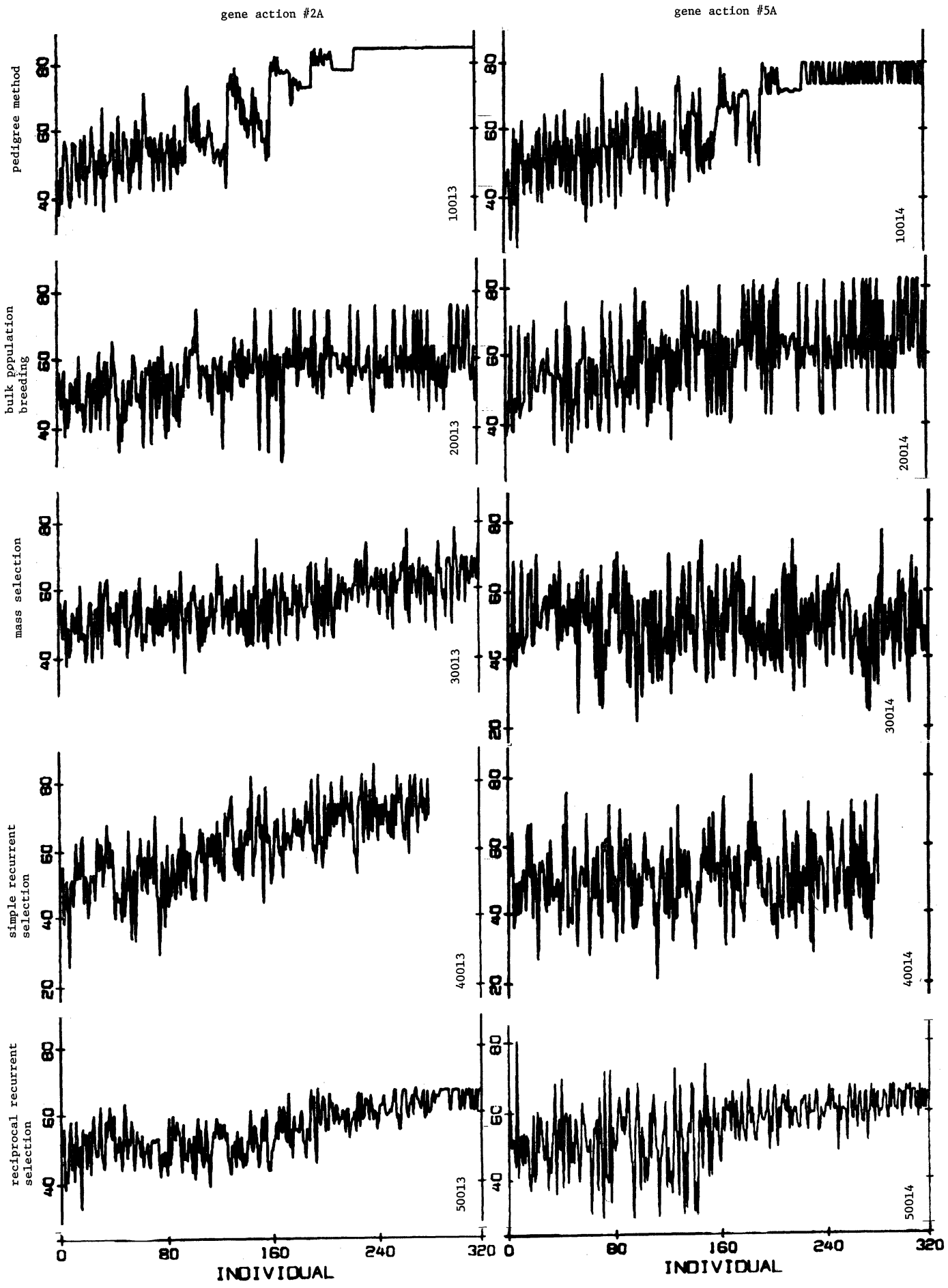


Figure 12e Comparison of gene action/breeding method combinations: Gene Action 2A and Gene Action 5A in combination with five breeding methods

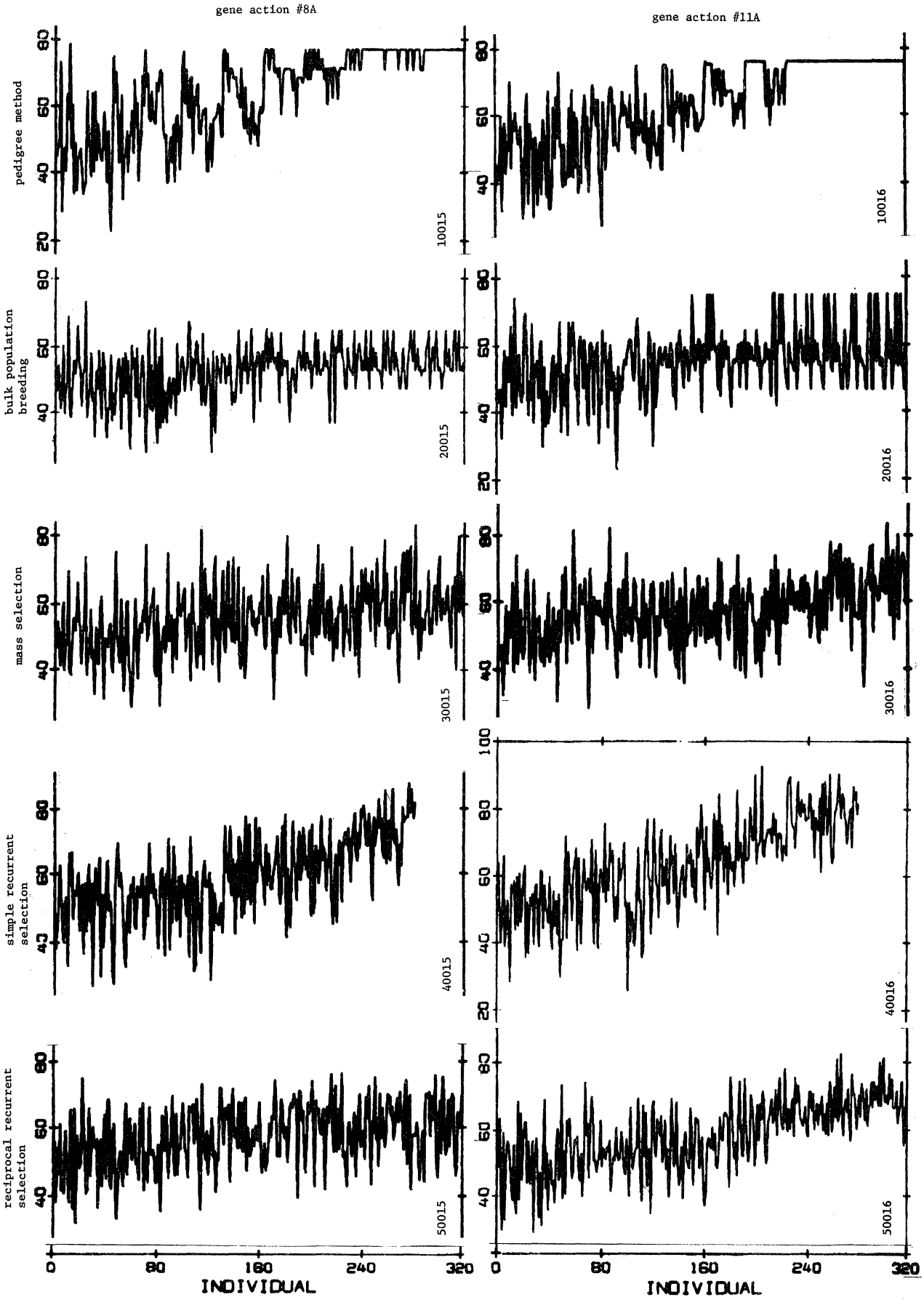


Figure 12f Comparison of Gene action/breeding method combinations: Gene Action 8A and Gene Action 11A in combination with five breeding method

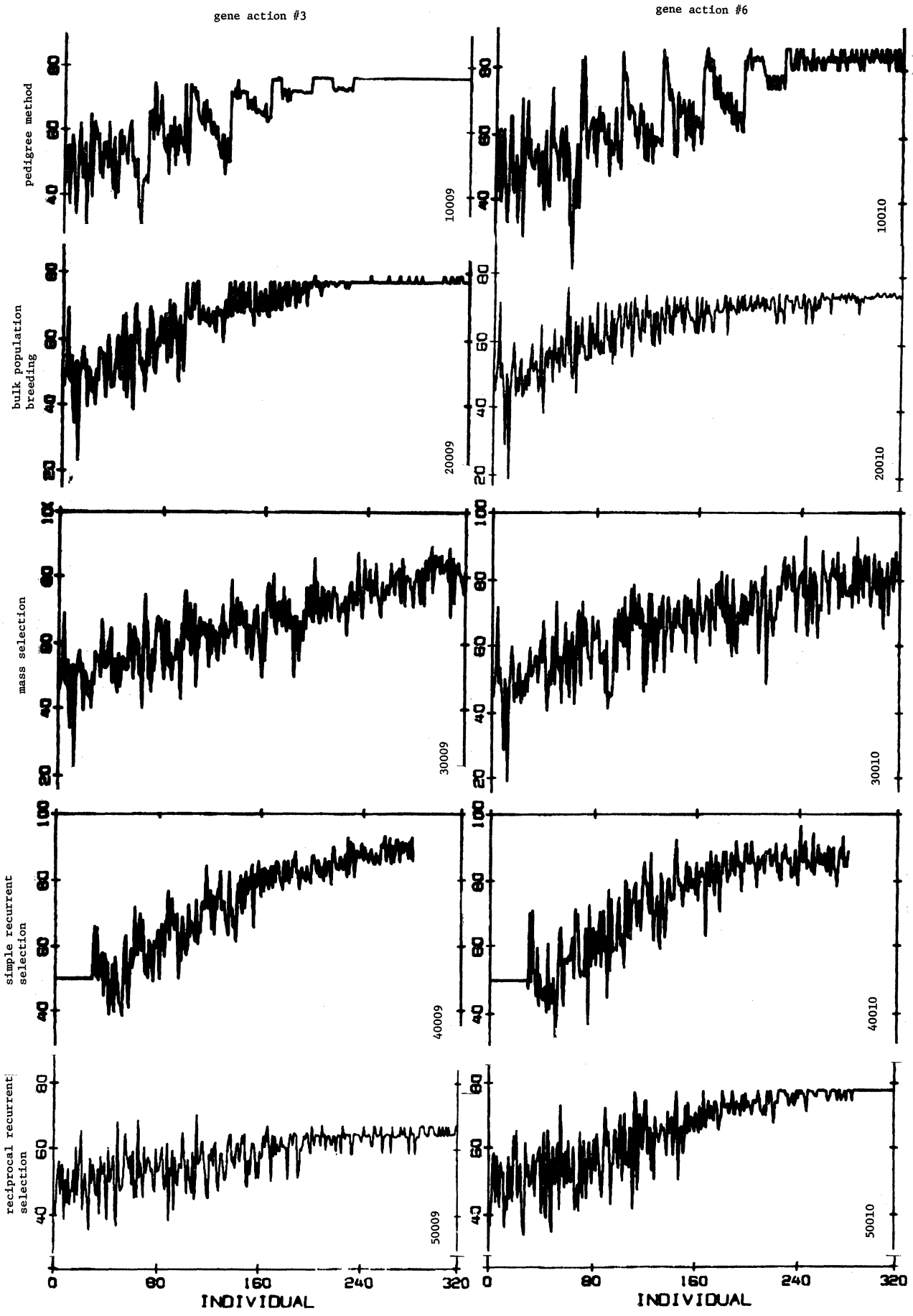


Figure 12g Comparison of gene action/breeding method combinations: Gene Action 3 and Gene Action 6 in combination with five breeding methods

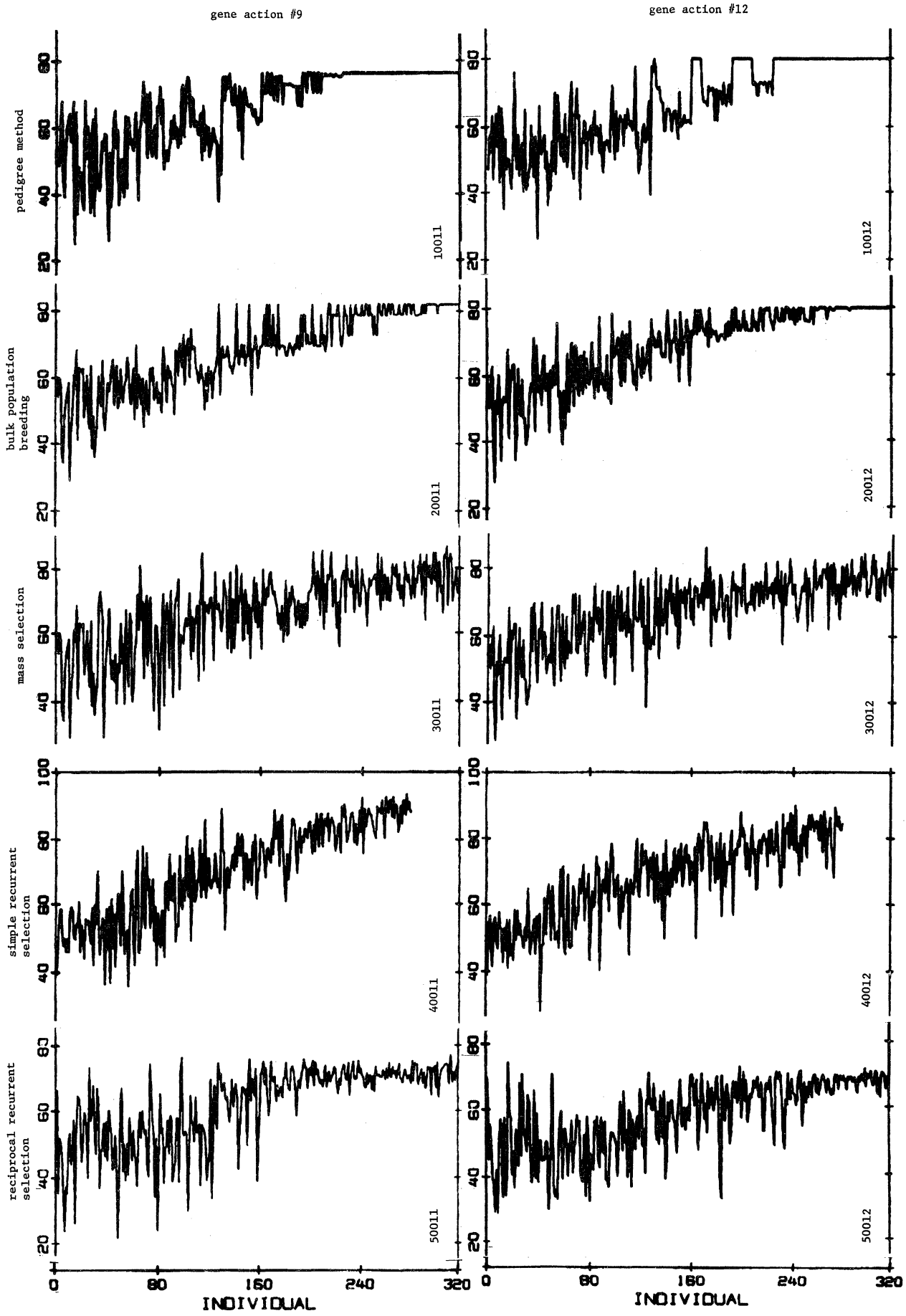


Figure 12h Comparison of gene action/breeding method combinations: Gene Action 9 and Gene Action 12 in combination with five breeding methods

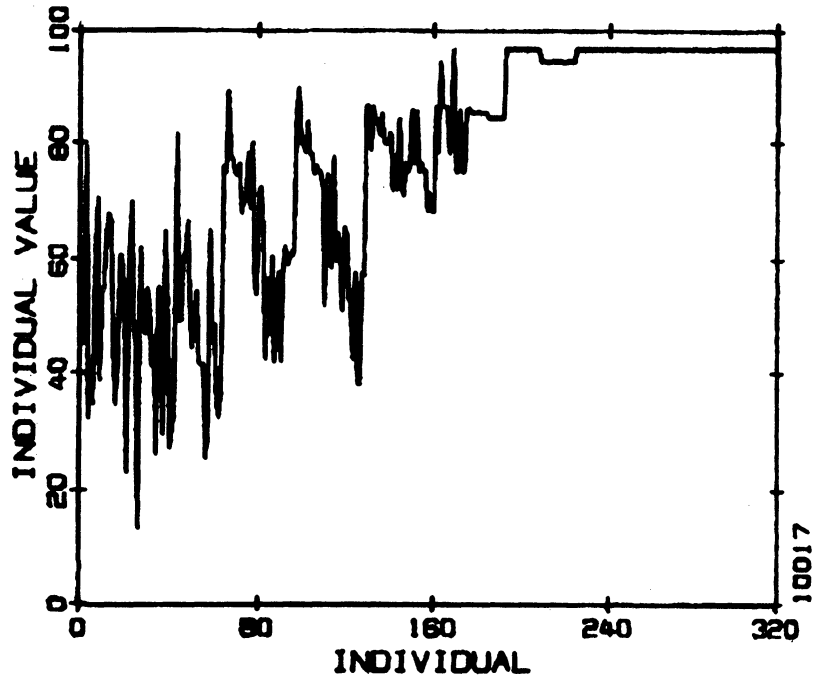


Figure 13a Phenotypic value of individuals during pedigree breeding for 2-parameter Plane using Gene Action 3 and the schedule of selection described in Section 3.1

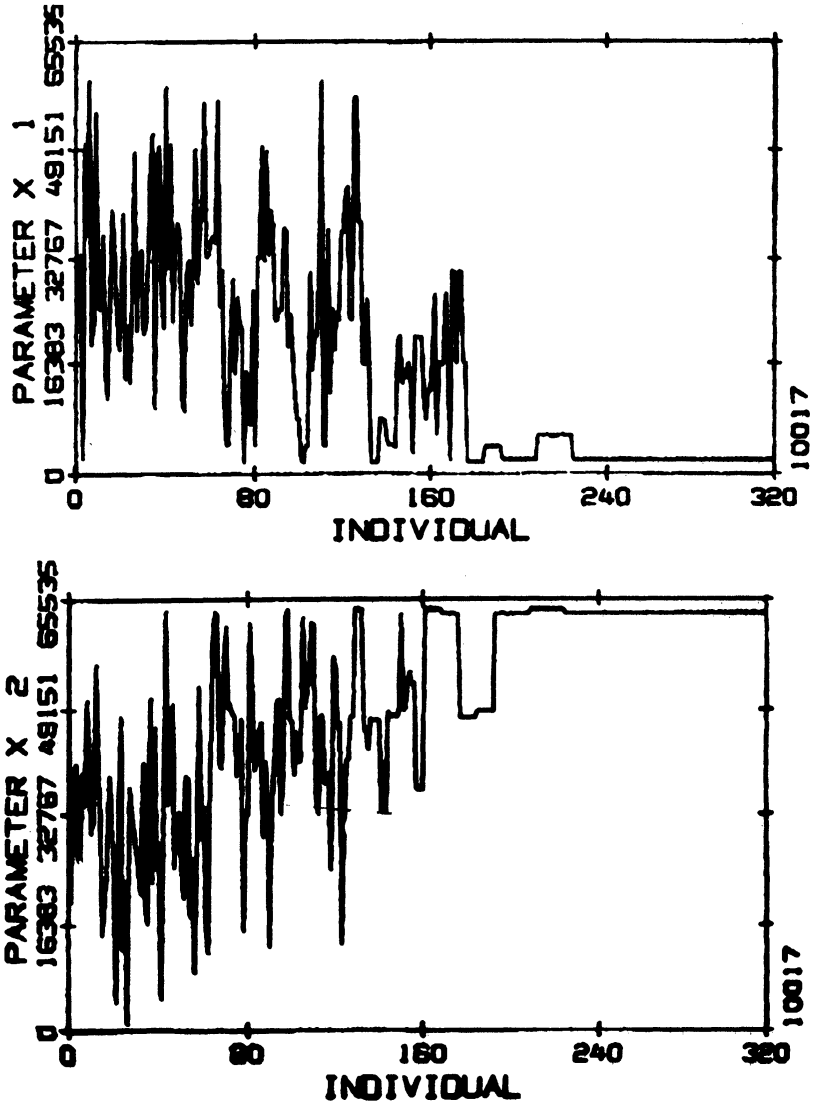
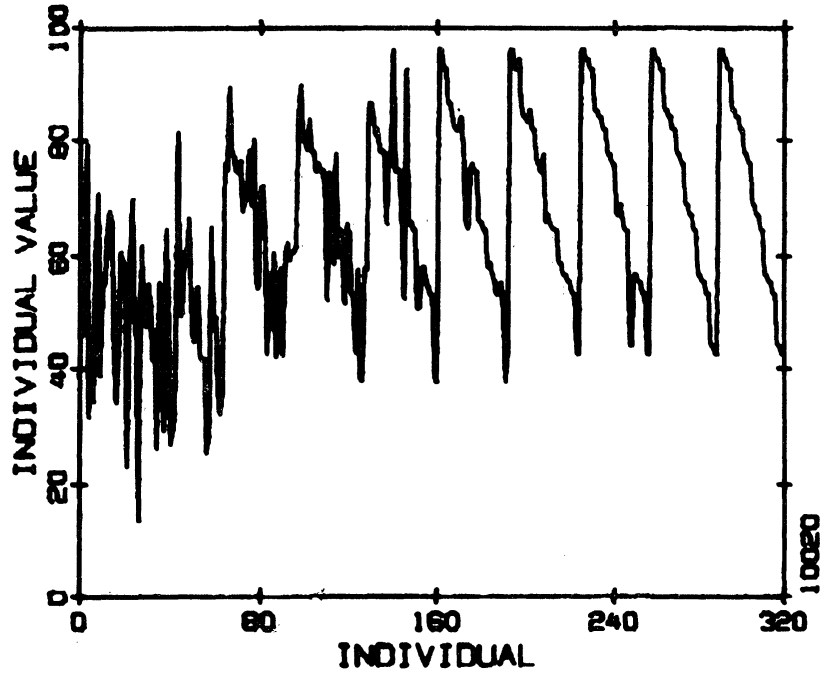


Figure 13b Parameter values of individuals during pedigree breeding for 2 parameter Plane using Gene Action 3 and the schedule of selection described in Section 3.1

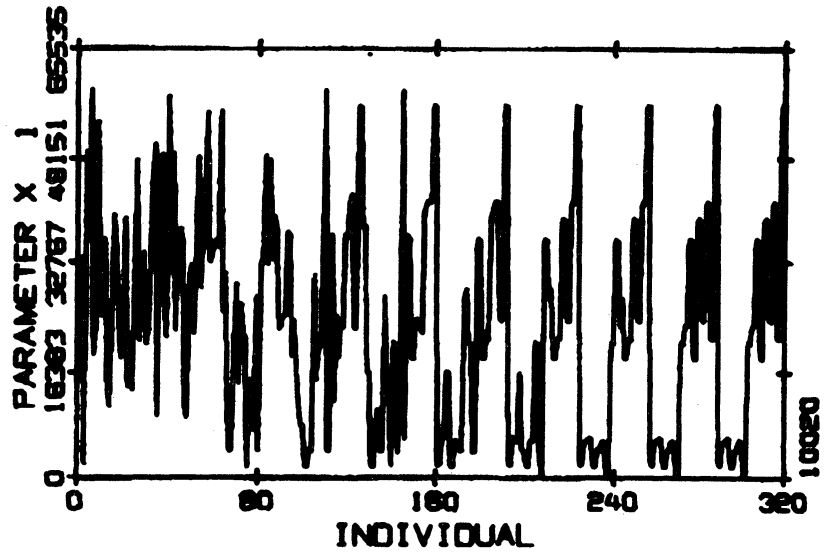
```
        10017
PM1A 6/26/73/
NDVLP          3
NVALU          1
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      0.0000
CV        0.0000
NPOP           64      32      32      32      32      32      32      32      32
NSEL           32      16      16       8       4       2       1       1       1
NPAR            2
NSEG            2
NREP            1
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
        STOP
    1    45.447   25901   19933
    2    53.536   33570   38204
    3    79.265    2191   40549
    4    31.885   50151   26408
    5    42.112   36403   26064
    6    34.483   59436   39098
    7    61.425   19132   34107
    8    70.900   23159   50553
    9    38.698   54686   39873
   10    53.925   24839   29984
   11    55.456   24674   31[illegible]
   12    64.913   36[illegible]
   13    67.[illegible]
   14
         [illegible]  2078   63379
         96.770   2078   63379
  312    96.770   2078   63379
  313    96.770   2078   63379
  314    96.770   2078   63379
  315    96.770   2078   63379
  316    96.770   2078   63379
  317    96.770   2078   63379
  318    96.770   2078   63379
  319    96.770   2078   63379
  320    96.770   2078   63379

AVERAGE VALUES
 GEN       EFF       AVG       STD      AVGS      STDS       NIZ       NTR
   1     0.000     0.000     0.000     0.000     0.000     0.000     0.000
   2    48.855    48.855    14.537    60.387     8.732     0.000    64.000
   3    54.054    64.453    11.930    68.926    10.311     0.000    32.000
   4    57.125    66.338    13.786    69.037    13.189     0.000    32.000
   5    61.312    78.058     5.813    81.003     5.523     0.000    32.000
   6    65.118    84.148     4.816    90.181     6.369     0.000    32.000
   7    69.476    95.627     1.162    95.667     1.560     0.000    32.000
   8    72.888    96.770     0.000    96.770     0.000     0.000    32.000
   9    75.542    96.770     0.000    96.770     0.000     0.000    32.000
  10    77.664    96.770     0.000    96.770     0.000     0.000    32.000
```

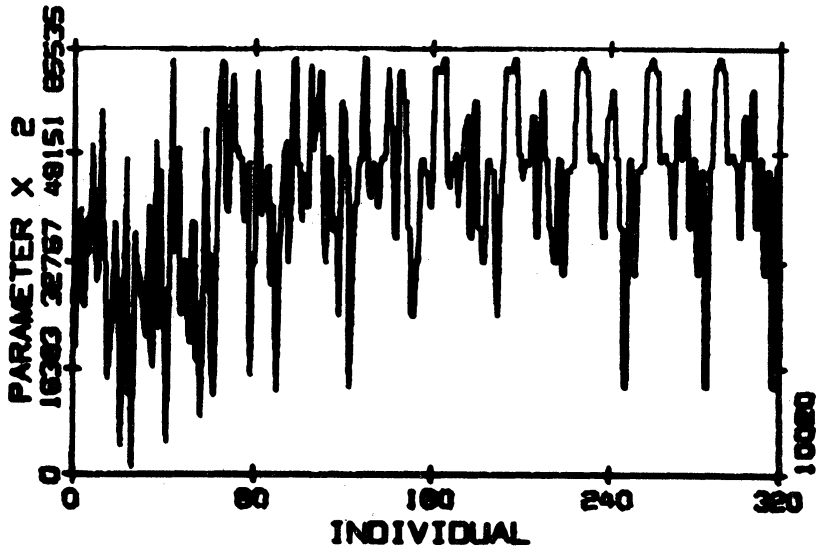
Figure 13c Input data, parameter values and generation statistics during pedigree breeding for 2-parameter Plane using Gene Action 3 and the schedule of selection described in Section 3.1



(a)

Figure 14a Phenotypic value of individuals during pedigree breeding for 2-parameter Plane using Gene Action 3





(b)

Figure 14b Parameter values of individuals during pedigree breeding for 2-parameter Plane using Gene Action 3

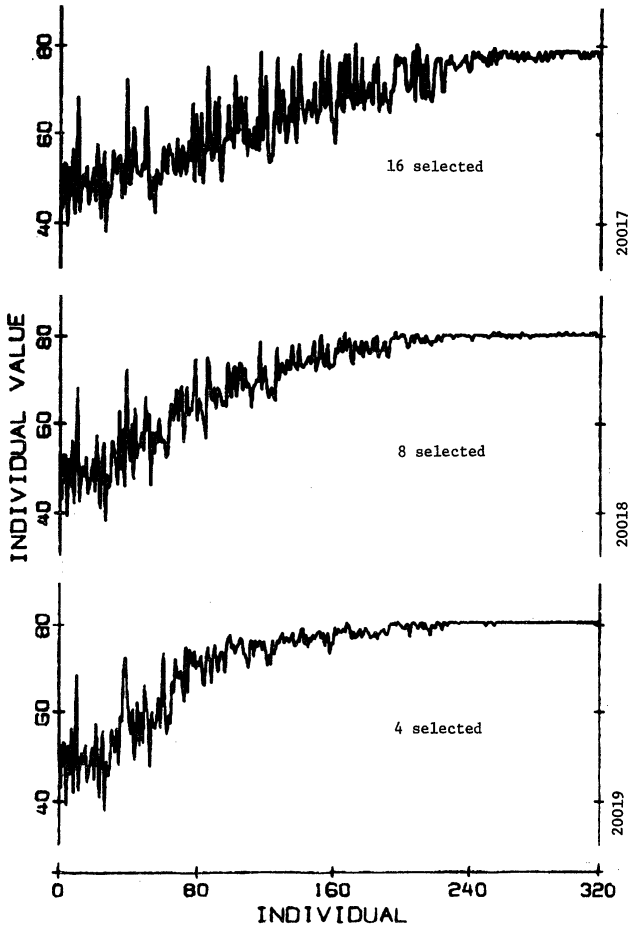


Figure 15 Effect of artificial selection intensity in bulk population breeding for 8-parameter Plane using Gene Action 4

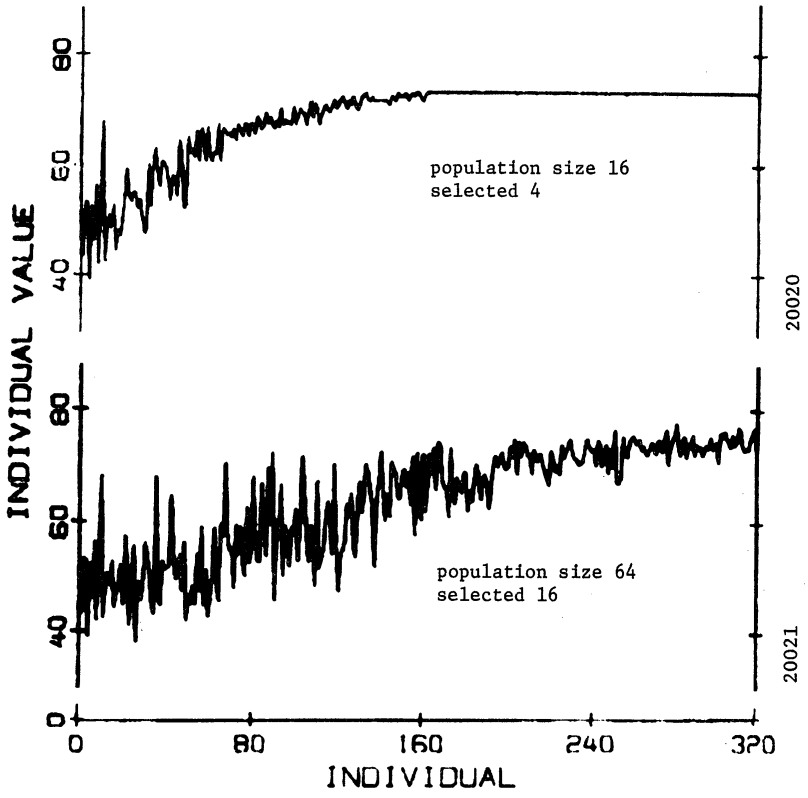
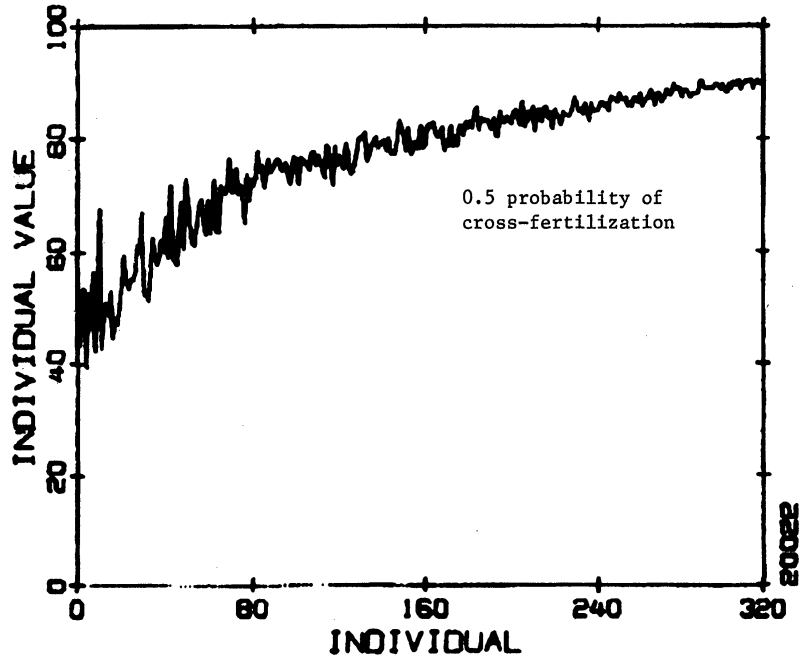


Figure 16 Effect of population size in bulk population breeding for 8-parameter Plane using Gene Action 4



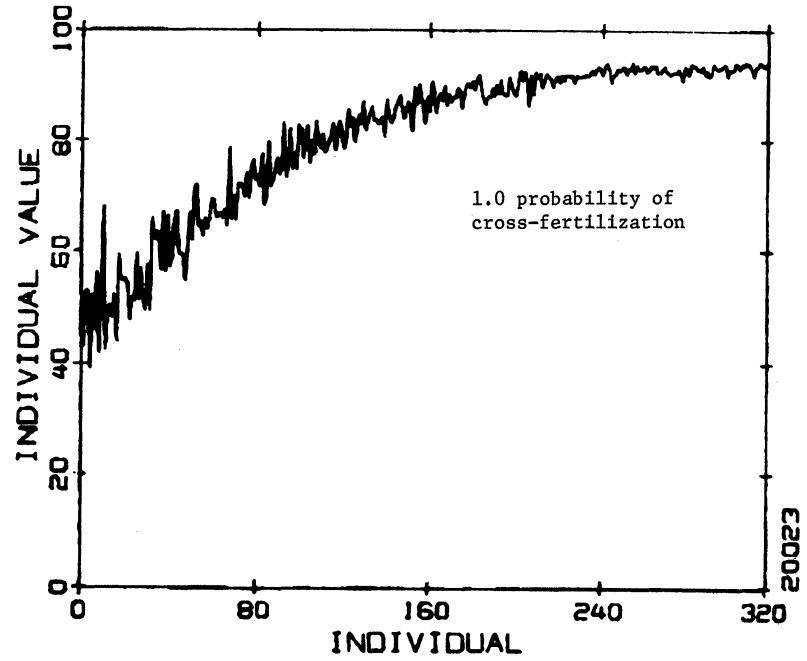


Figure 17 Effect of cross-fertilization in bulk population breeding for 8-parameter Plane using Gene Action 4

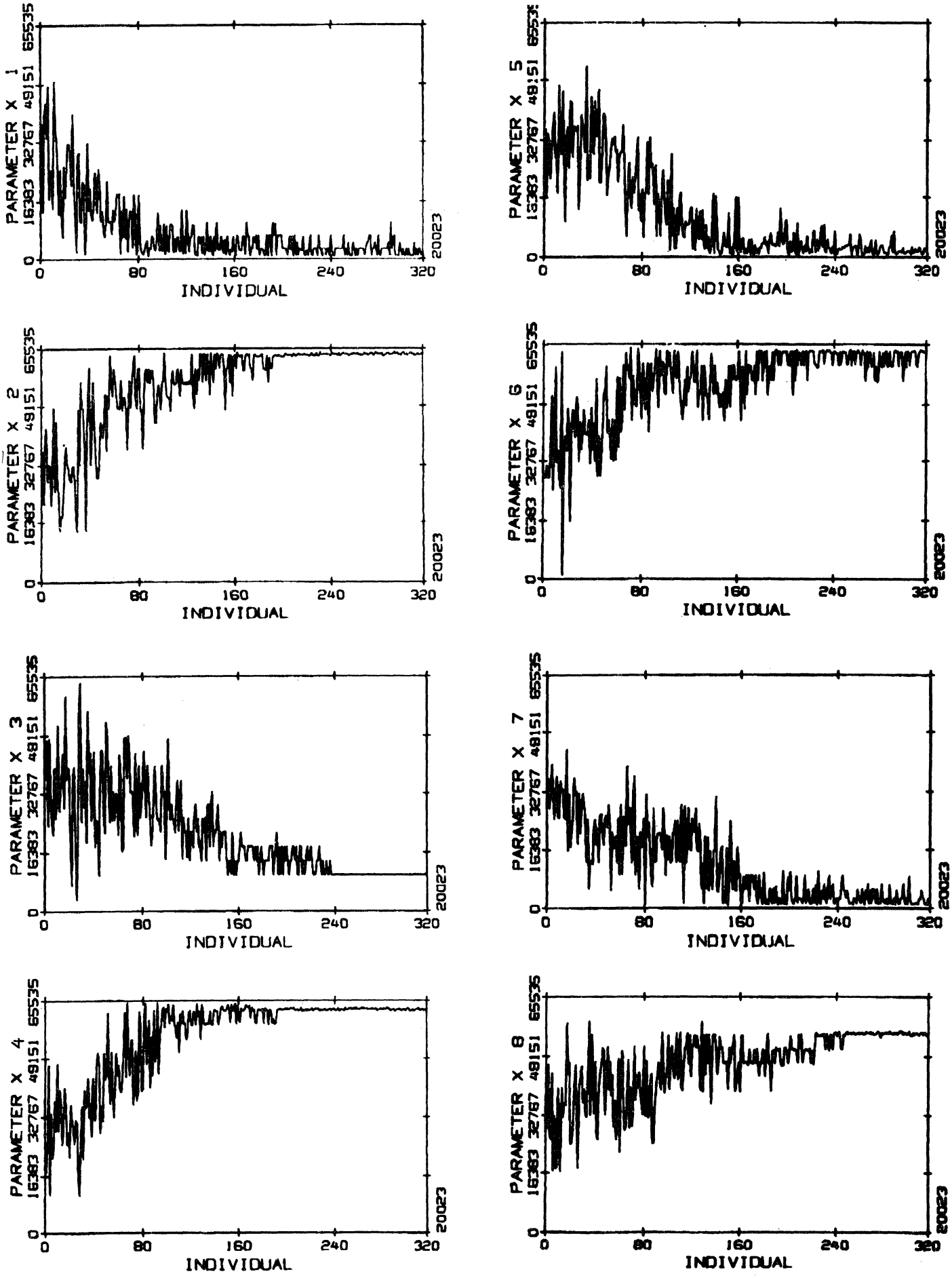


Figure 18 Parameter values of individuals produced in bulk population breeding for 8-parameter Plane using Gene Action 4

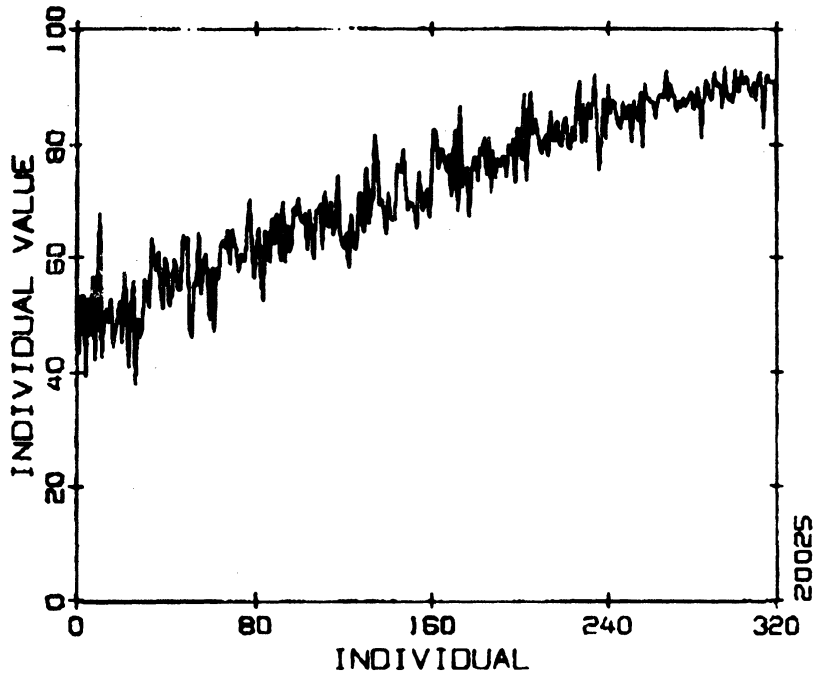


Figure 19a Phenotypic value of individuals during bulk population breeding for 8-parameter Plane using Gene Action 4

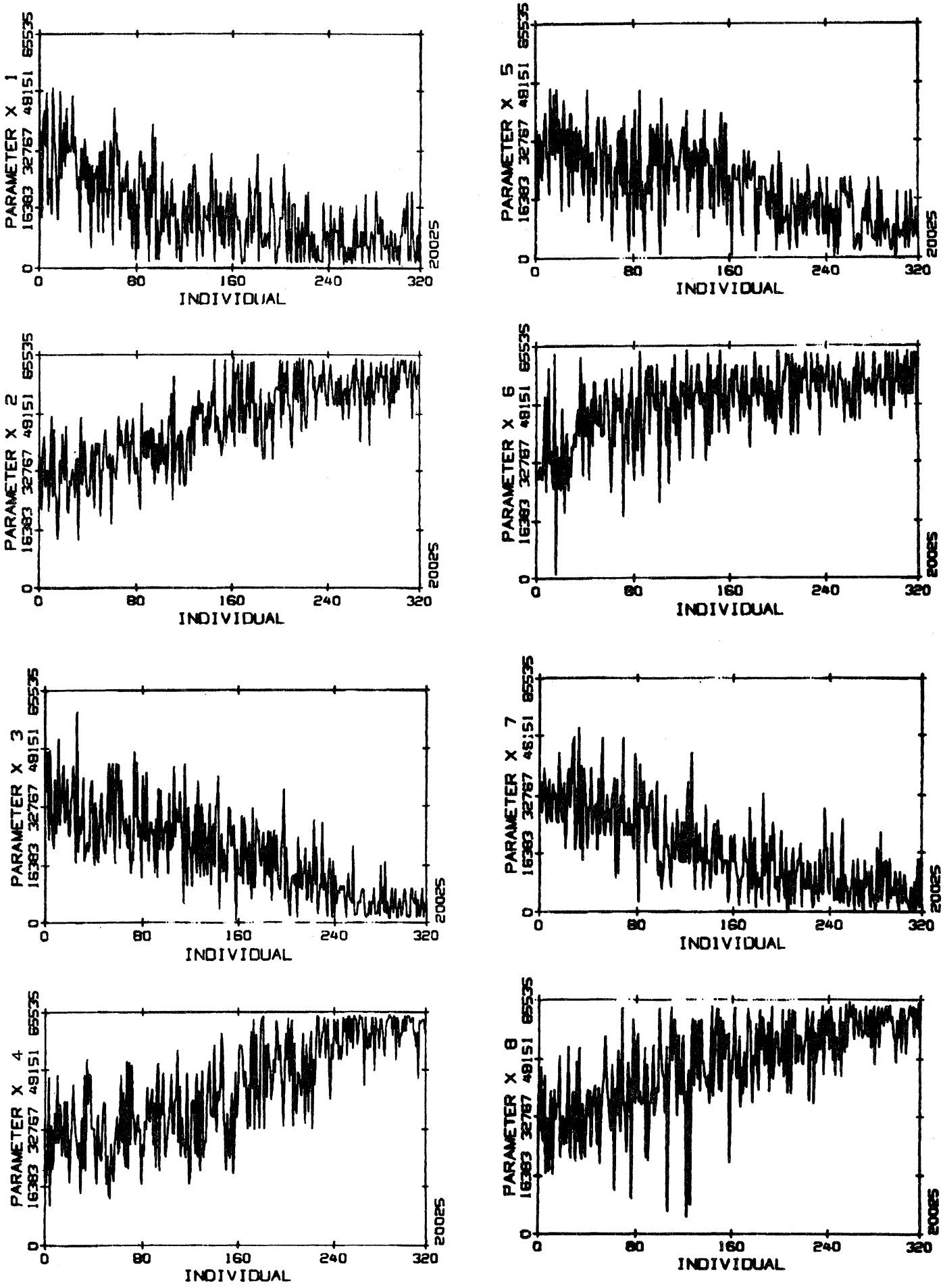


Figure 19b Parameter values of individuals during bulk population breeding for 8-parameter Plane using Gene Action 4

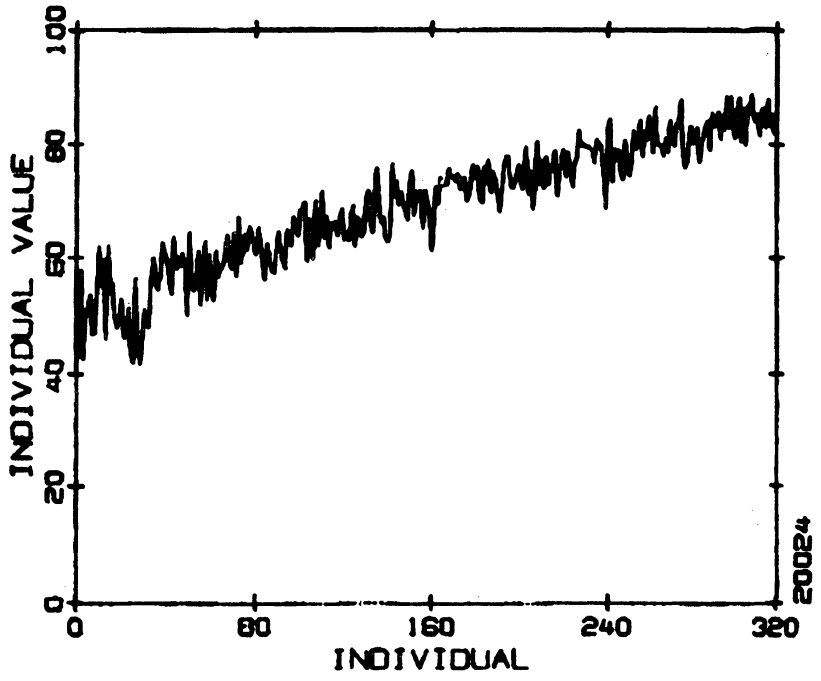


Figure 20a Phenotypic value of individuals during bulk population breeding for 8-parameter Plane using Gene Action 4 with linkage

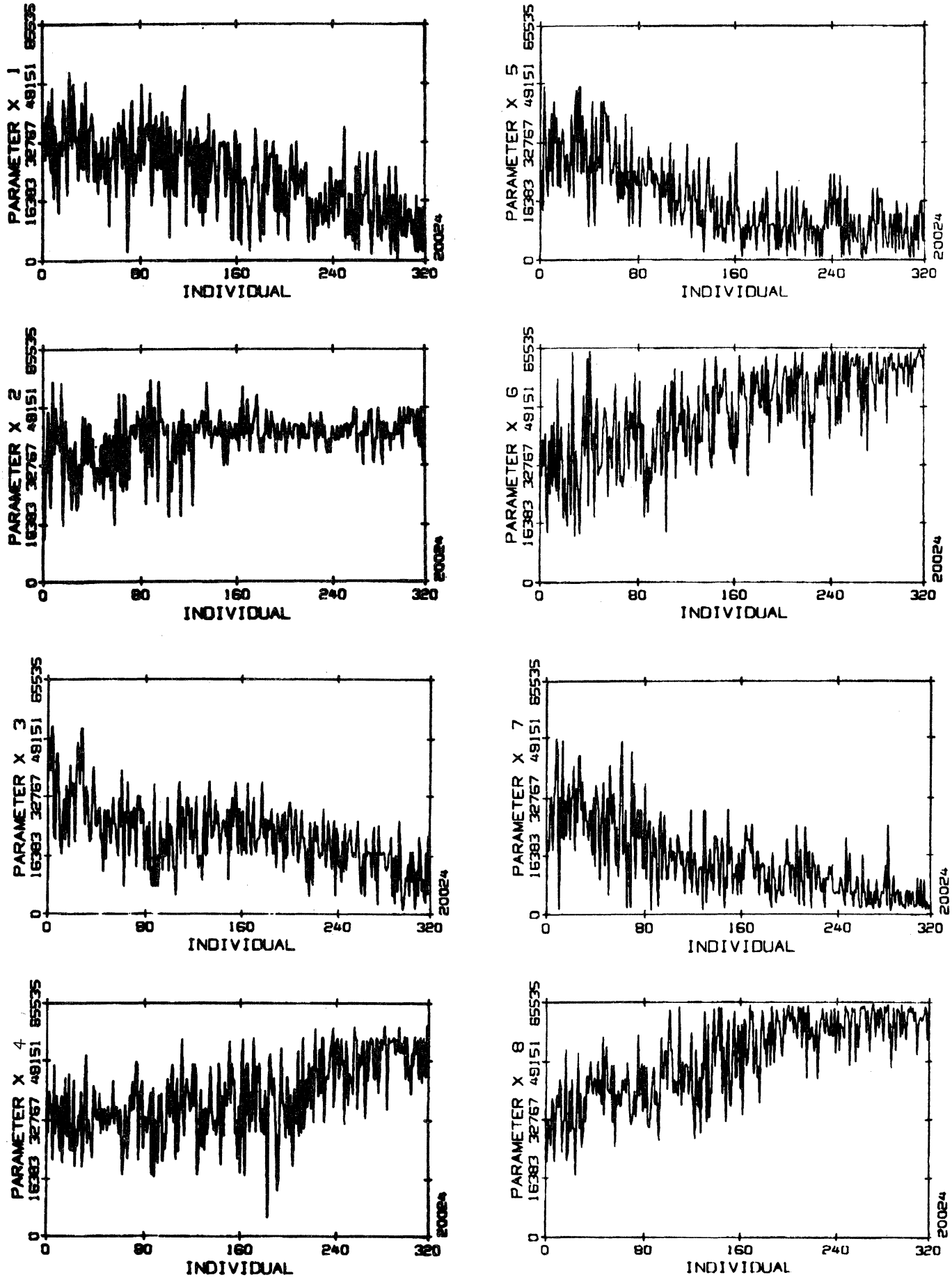


Figure 20b Parameter values of individuals during bulk population breeding for 8-parameter Plane using Gene Action 4 with linkage

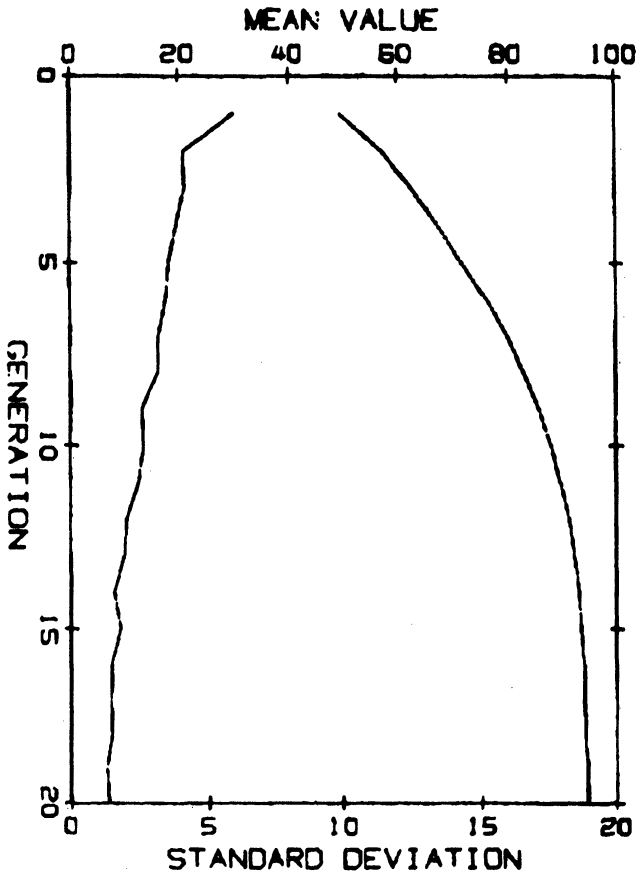


Figure 21a Averaged results of five replications of bulk population breeding for 8-parameter Plane

```
        20026
BPB1A 6/26/73
NDVLP          4
NVALU          1
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      0.0000
POUCR     1.0000
CV        0.0000
NPOP           32
NSEL            8
LGEN           20
NPAR            8
NSEG           32
NREP            5
IX              1
IPAP            0
IPBP            1
IPAF            0
PCS             0
        STOP
```

1	43.275	37836	36646	37100	17678	35828	28564	36598	29214
2	53.071	13514	21984	48080	25490	16928	28204	27996	46942
3	53.112	40220	39766	23660	47122	34610	31548	32796	29166
7	56.377	17106	32556	21262	24382	36546	51484	32572	32496
10	67.922	14468	48560	32766	47644	29446	59602	25368	40202
77	70.348	17348	47888	28686	32074	18126	48394	17450	59936
99	70.621	8436	43790	27970	24860	33680	60366	13840	63024
111	71.822	17030	59662	36878	44570	32962	51976	14618	59690
117	74.593	1984	44464	10718	48108	13382	48290	25100	39258
130	76.032	1728	48048	29660	48904	21966	51696	13612	54798
134	81.681	9632	51950	13838	40720	5868	60532	17680	59914
161	82.508	2194	64910	13852	56066	17614	53120	21520	51516
173	86.757	5528	62946	10068	63486	26356	47616	2394	63006
202	88.677	12966	63698	6288	63712	6440	47824	9534	62770
205	89.178	5510	55040	12960	63038	11236	58626	982	59388
227	91.063	2634	63020	5832	63742	10756	47572	2064	62238
234	92.064	1742	59946	1686	60622	6422	56224	4882	58474
267	92.663	5776	56076	1478	64010	6648	63632	8470	62326
295	93.414	9390	61868	1272	63710	4916	63454	6500	60656
321	95.218	5736	63730	2184	63800	3002	63550	6862	63774
324	95.731	5764	64748	1596	62990	1588	63182	2390	60178
342	96.177	1190	60670	890	62780	2806	63438	4884	64978
391	97.113	1904	62720	1894	62768	1734	63586	970	64434
470	97.503	2126	64030	1878	63500	1876	63392	728	64736
611	97.871	1460	63710	996	64012	1092	63358	772	64216
1	44.831	37322	20872	40280	56002	24556	12352	35624	21458
2	52.697	32344	24616	32060	25050	32252	49596	26046	37578
6	64.473	40536	25336	25110	59650	9440	47648	37550	55880
66	64.515	25148	25360	18408	56556	35858	46686	28732	55644
69	64.969	27724	25264	18348	52448	21650	51994	25342	41840
70	66.310	37386	28718	17154	64238	23862	39964	33438	64432
75	67.855	20780	58006	20778	28580	6786	48320	33786	40834
78	70.009	14812	14316	13836	56558	24636	47642	24120	63792
99	72.352	12602	49596	13896	32482	6500	47858	32838	53086
126	73.027	6424	64060	13820	56318	10382	44750	35692	21918
133	77.202	14032	25622	13582	51972	1338	59406	25562	60128
161	78.152	9998	33796	13416	59924	9526	44060	17868	60622
162	78.959	9996	36650	5898	51746	14018	58160	28950	64130
169	80.643	3546	30366	13820	59168	14256	63186	21048	60606

Figure 21b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Plane (Sheet 1 of 4)

195	82.586	18368	51464	1816	56936	10206	60832	20818	52714
196	83.540	11466	40940	2230	44022	2352	64494	9978	52412
235	83.666	14828	40670	1670	43828	1964	59122	9484	60830
239	86.583	6680	48156	2184	63746	6126	44032	13606	64460
265	87.807	1584	40156	5672	63446	2000	63054	16530	56298
271	88.312	2736	62744	6084	64658	12636	63518	25124	56522
297	91.452	860	62940	1596	62570	5180	63472	21042	57020
309	93.411	594	59614	1944	55526	6740	62990	5946	64688
353	93.905	7372	63648	5962	63672	10144	63022	1368	64688
366	95.801	400	63436	1464	59814	864	64462	9034	64178
424	95.970	6396	62956	998	63546	2764	63486	3206	64386
444	96.438	2780	62522	1900	63544	1318	63714	2684	62366
457	97.602	1284	62958	1192	63544	342	63984	2982	64880
476	97.781	280	63468	2350	63928	2220	64192	902	64670
586	97.870	520	63694	1464	63914	1334	63982	372	63072
1	47.238	56348	56270	32078	28850	36354	25270	36876	36786
2	54.746	35226	37598	16896	36888	20780	37564	40292	26028
11	55.908	25070	29392	40956	42860	25522	26030	20768	45008
14	58.080	48368	28372	20738	35650	25056	41362	25820	56960
33	60.272	20976	35870	36650	51770	16820	40402	36366	36624
43	60.827	33250	33416	25292	39908	21726	33260	13582	44028
44	61.299	25356	37782	23394	40176	25326	25116	13594	43836
52	62.384	43582	55748	20918	44532	32060	42064	36394	55536
67	67.279	20998	31972	17480	53842	5348	39966	36384	45020
76	71.279	19838	51428	9216	59920	17318	49748	47690	44528
100	72.208	31806	52386	5584	59632	24322	50000	39982	56106
120	73.427	21008	47796	8718	51712	5110	45170	27946	40926
131	73.959	40238	56468	6544	56314	13266	49506	32720	56090
132	75.500	32510	51878	1924	55822	12864	53358	36084	56016
139	75.943	14260	55432	12784	48356	9666	41530	27426	54830
159	77.932	22492	47856	2194	56498	6096	42110	28192	58952
168	78.561	24160	55460	9170	30894	5942	59870	16944	59732
182	79.184	32960	48262	8930	59860	21230	60764	9010	56252
191	82.112	26272	47736	5298	52630	1284	57618	19760	62986
193	82.615	10988	58372	6050	44494	1310	42052	16386	60812
197	84.033	33758	51620	6502	59586	5168	49816	1088	63920
198	84.276	28894	51348	17300	60098	8736	64114	5200	64274
203	84.526	29676	55190	8630	50994	2316	60770	8764	63446
212	85.159	17182	63980	9908	63934	4990	52924	28146	63720
240	85.623	22012	55448	7940	59604	1806	56228	15934	63178
241	87.870	17678	59930	5378	63716	2018	49266	9426	60132
257	89.135	13042	64432	9456	59884	4942	64834	20736	64202
267	90.932	14544	55750	9638	63938	1056	61490	5108	63764
290	91.366	6862	55416	12486	59478	1402	65106	2318	59944
295	91.499	16930	55006	1430	63092	4626	60020	1296	63736
306	91.705	22926	64810	4776	60174	2500	62154	2060	63774
307	91.869	14316	62436	1492	60098	2224	53108	2524	64426
325	92.252	17410	55728	1942	63176	830	60558	1506	63746
335	92.971	7068	63592	5256	63200	4940	58588	6100	63274
366	93.937	2766	55490	2124	59140	2602	65346	5390	63258
400	94.283	5210	63850	1476	62998	10438	60754	1750	63438
401	94.702	4674	64340	2168	59602	802	64356	1598	55306
405	96.135	2766	64344	1970	63684	800	65090	1056	55348
575	96.684	1386	62748	1646	63414	4430	64596	2528	63988
1	55.425	21290	37098	40420	41346	35930	55764	44282	36154
9	55.953	21920	25416	33096	44226	27756	29632	44260	58970
21	59.474	24622	39490	14060	36532	32738	10494	9936	44510
22	59.987	40248	40182	21724	44268	26076	36530	35798	55224
32	65.712	8766	43596	6786	36290	17378	28776	37176	43820
34	68.275	23900	54864	22714	35826	7358	36592	21262	43762
67	71.382	5166	47166	14716	39680	8780	36218	29722	47422
68	74.479	5406	59488	22936	40386	25566	51680	21248	51938
102	74.790	9470	47232	15228	27918	10656	40492	13598	63278

Figure 21b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Plane (Sheet 2 of 4)

112	75.932	12876	47934	14278	40894	15470	48218	13792	55328
125	76.004	13610	53590	17360	43366	17946	51534	22408	59168
132	77.610	11676	63924	19054	51080	15260	39728	12610	48620
138	78.340	13186	53380	29320	55114	14552	47408	13496	63232
143	78.670	8540	63038	9930	32986	4896	44074	25796	59376
159	80.346	9050	63940	29646	43130	14732	55536	14018	63936
162	80.452	1128	64194	26496	62810	18378	43572	20728	55806
174	81.659	1340	59124	10626	47928	14062	44798	22124	62286
179	82.526	6182	60130	25268	55116	17866	59166	17592	63022
198	83.885	1722	55090	24982	59434	22186	62506	13528	63040
203	83.891	2086	63472	21664	47418	15018	51968	10676	64270
210	85.019	5928	60356	18112	39500	1046	59450	14052	63428
220	85.337	1098	63038	14450	59192	11390	47934	21192	63230
223	87.003	9244	59226	6048	51662	3708	52432	14512	64192
242	87.691	9710	55356	5090	52114	3730	52418	6800	63050
259	88.243	2146	62528	13492	52186	11116	58700	6060	59902
265	88.786	9978	64388	2958	55082	8028	44766	3506	63582
266	89.139	2298	59168	1492	63690	11406	52446	18368	63458
270	90.940	1832	64928	6290	51230	6588	58928	6106	60368
286	92.027	1548	59198	13986	63200	7098	63440	5874	63008
322	93.069	2006	63758	9156	55310	7356	64748	2742	63248
347	93.087	9182	59628	9936	58938	598	64208	828	63666
359	93.100	5920	64432	5826	64044	3226	55790	6832	63502
361	94.244	2296	63696	9618	54364	552	62750	606	64222
384	94.270	1766	59122	6068	63456	3004	64452	664	56572
385	94.593	1552	63514	5724	59616	4882	60878	1590	63530
429	94.602	1586	60400	2420	63504	3424	56574	2738	63530
435	95.494	1774	63500	1462	59868	4660	64462	1338	59918
436	95.777	1794	64688	1390	64254	170	60428	1596	55582
457	97.037	2018	63982	1642	63482	3038	64272	1848	63414
1	54.433	25548	44256	36770	29108	24876	37794	33504	32782
5	55.051	16698	36816	32540	51080	51666	40654	40866	39702
9	56.165	28700	36878	44330	37104	28510	36874	25610	48618
12	60.275	27708	44238	36918	28326	9992	28506	21936	49356
27	60.624	24622	51970	16926	40686	9936	20046	43326	37806
31	61.350	29404	59138	21426	40432	32288	36412	32588	39230
44	62.356	21020	45488	37582	32556	17916	45044	21800	40012
54	63.479	8736	56958	39548	47196	37536	48588	32378	36124
57	63.904	21188	47172	13340	32544	13612	36338	38808	43790
67	72.856	2258	55492	29210	40612	3220	35200	18162	41376
106	73.494	3240	51706	21064	31012	5676	51758	25820	44496
109	81.826	5628	55522	21316	44198	2724	50544	10464	56724
187	81.974	1344	63186	18374	47860	13818	38782	13570	64912
190	82.552	6850	55836	1370	28390	1286	47436	7086	55596
198	90.270	1596	64272	2330	54762	2762	54880	18176	62076
257	90.755	6882	63732	1288	58088	11012	59166	11424	63290
263	91.634	1266	63740	666	55568	5942	62270	10738	55314
293	91.971	13296	56756	2100	64120	790	59436	4416	60338
294	93.032	8928	60610	2524	63190	2024	58700	7596	64178
308	95.476	800	63732	2074	65032	3288	63050	10976	63744
380	95.830	1712	59864	2360	63670	1542	63980	1506	59886
391	96.570	2350	64708	1876	59800	2468	62750	588	64182
455	97.496	1884	62624	504	64086	1722	63730	1064	63744
506	97.599	1374	64184	264	63590	2214	63936	2786	64478
589	97.606	1358	63256	1302	63736	1718	62784	544	64734

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	49.680	49.680	5.903	57.092	3.285	0.000	32.000
2	53.497	57.313	4.163	62.140	1.467	0.000	32.000
3	56.460	62.387	4.187	67.704	2.258	0.000	32.000
4	59.141	67.181	3.886	71.850	1.960	0.000	32.000
5	61.592	71.397	3.636	76.097	1.666	0.000	32.000

Figure 21b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Plane (Sheet 3 of 4)

6	64.005	76.069	3.522	80.271	1.388	0.000	32.000
7	66.277	79.911	3.229	83.892	1.714	0.000	32.000
8	68.352	82.875	3.213	86.511	1.102	0.000	32.000
9	70.286	85.762	2.606	89.040	1.336	0.000	32.000
10	72.052	87.945	2.671	91.247	1.041	0.000	32.000
11	73.655	89.684	2.490	92.652	0.908	0.000	32.000
12	75.127	91.318	2.031	93.666	0.772	0.000	32.000
13	76.453	92.362	1.956	94.757	0.741	0.000	32.000
14	77.646	93.165	1.564	95.044	0.637	0.000	32.000
15	78.708	93.566	1.815	95.748	0.803	0.000	32.000
16	79.668	94.077	1.469	95.749	0.549	0.000	32.000
17	80.520	94.154	1.446	95.907	0.464	0.000	32.000
18	81.288	94.334	1.484	96.071	0.579	0.000	32.000
19	81.995	94.727	1.301	96.106	0.494	0.000	32.000
20	82.633	94.756	1.379	96.397	0.429	0.000	32.000

MAXIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.513	50.513	6.637	57.918	4.814	0	32
2	54.344	58.460	5.286	63.793	2.740	0	32
3	57.234	64.281	4.801	70.044	2.926	0	32
4	60.218	69.169	4.851	74.337	3.778	0	32
5	63.021	74.232	4.457	77.710	2.233	0	32
6	65.371	77.120	4.228	81.939	2.348	0	32
7	67.540	81.017	3.668	85.542	2.992	0	32
8	69.488	85.109	3.795	89.286	1.668	0	32
9	71.376	87.956	3.252	90.411	1.687	0	32
10	72.956	89.801	3.181	92.514	1.797	0	32
11	74.480	91.480	2.965	94.735	1.306	0	32
12	75.843	92.373	2.274	94.656	1.269	0	32
13	77.139	93.473	2.564	95.594	1.156	0	32
14	78.333	94.011	1.911	95.530	0.969	0	32
15	79.409	94.484	2.058	96.428	0.930	0	32
16	80.350	94.664	1.678	96.319	0.730	0	32
17	81.182	94.931	1.692	96.783	0.710	0	32
18	81.924	95.535	1.790	96.951	0.749	0	32
19	82.624	95.749	1.648	97.103	0.680	0	32
20	83.260	95.904	1.833	97.075	0.661	0	32

MINIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	48.961	48.961	5.191	56.406	1.287	0	32
2	53.018	56.394	3.278	60.553	0.993	0	32
3	55.427	60.244	3.718	65.885	1.553	0	32
4	57.987	65.668	2.669	70.049	1.071	0	32
5	60.247	69.286	2.925	74.429	1.263	0	32
6	62.692	74.918	2.844	78.688	0.924	0	32
7	65.179	77.640	2.805	81.241	0.464	0	32
8	67.331	80.599	2.661	83.876	0.788	0	32
9	69.384	83.353	2.077	86.612	1.100	0	32
10	71.132	85.824	2.312	89.900	0.568	0	32
11	72.645	87.781	2.131	91.557	0.653	0	32
12	74.167	90.371	1.777	92.963	0.486	0	32
13	75.552	91.143	1.581	94.126	0.416	0	32
14	76.802	92.443	1.101	94.567	0.461	0	32
15	77.864	92.297	1.439	94.423	0.626	0	32
16	78.812	93.046	1.232	94.831	0.420	0	32
17	79.657	93.174	1.213	94.981	0.359	0	32
18	80.417	93.339	1.136	95.086	0.347	0	32
19	81.122	93.804	1.081	95.414	0.317	0	32
20	81.729	93.259	0.967	95.409	0.275	0	32

Figure 21b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Plane (Sheet 4 of 4)

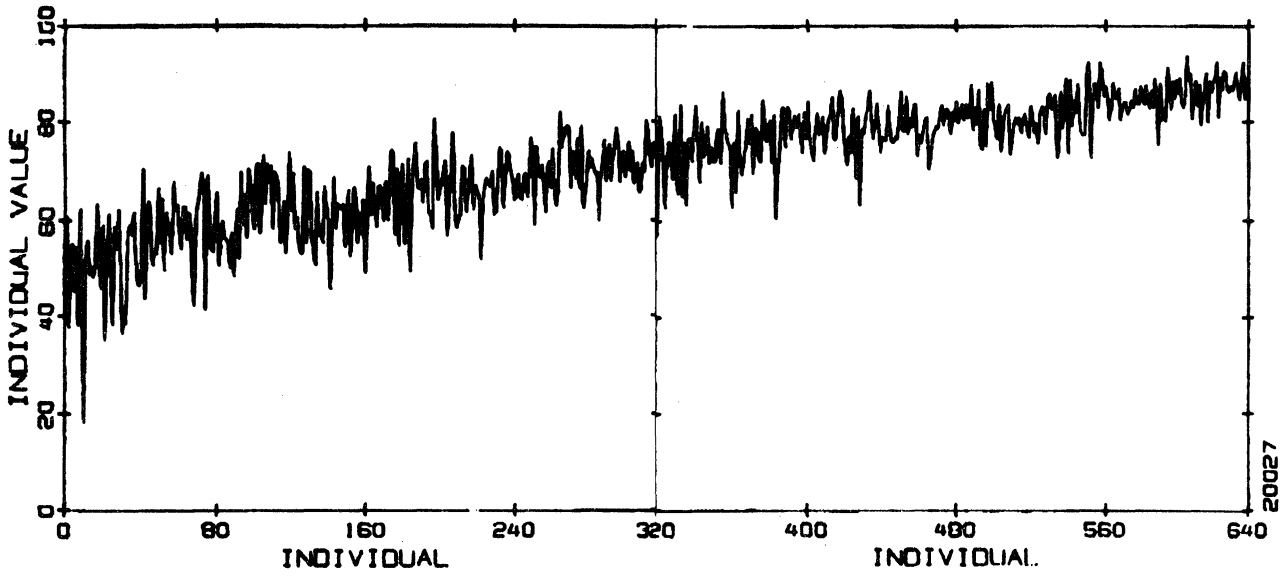


Figure 22a Phenotypic value of individuals during bulk population breeding for 8-parameter Ridge using Gene Action 4

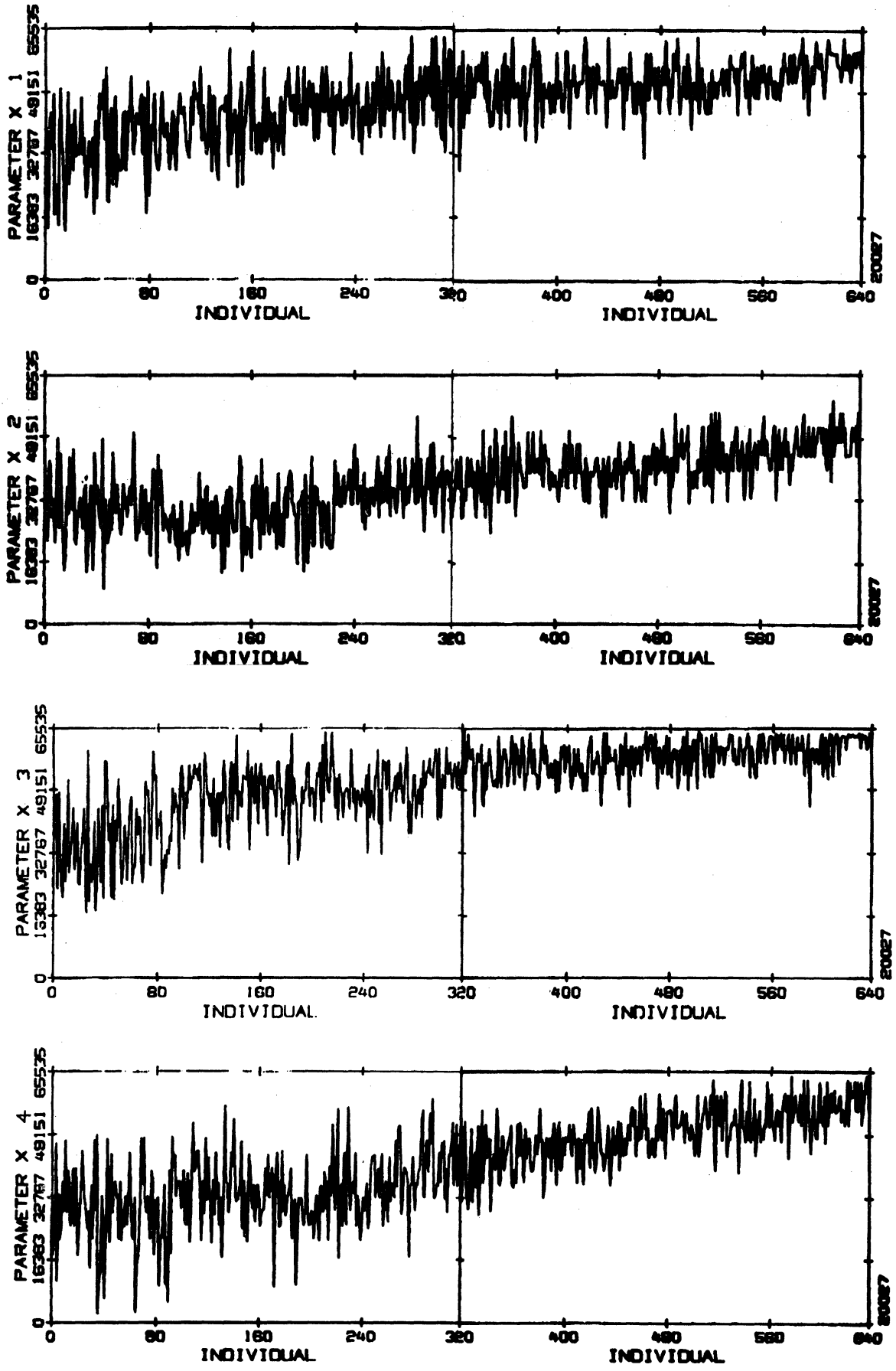


Figure 22b Parameter values of individuals during bulk population breeding for 8-parameter ridge using Gene Action 4 (Sheet 1 of 2)

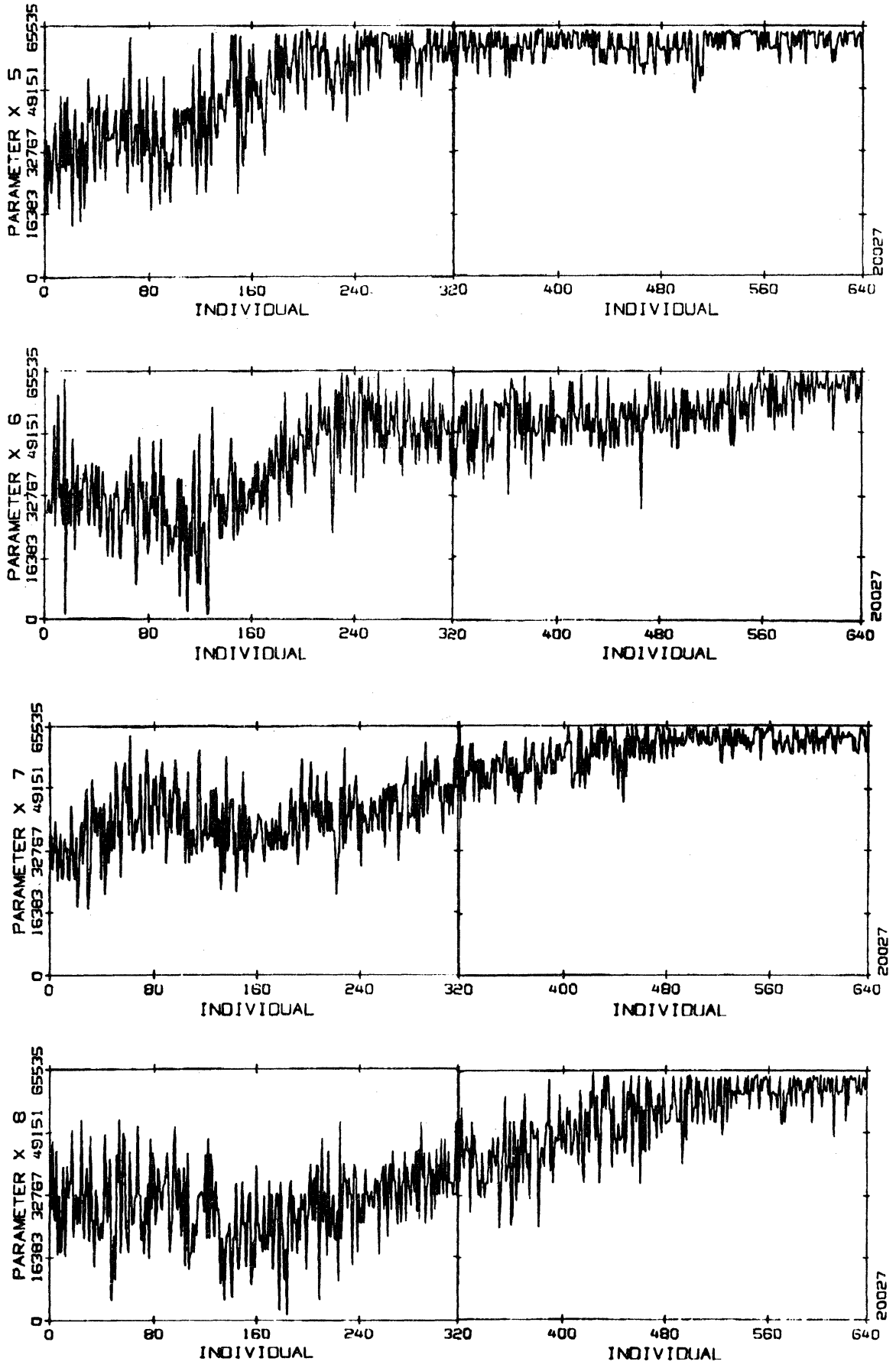


Figure 22b Parameter values of individuals during bulk population breeding for 8-parameter Ridge using Gene Action 4 (Sheet 2 of 2)

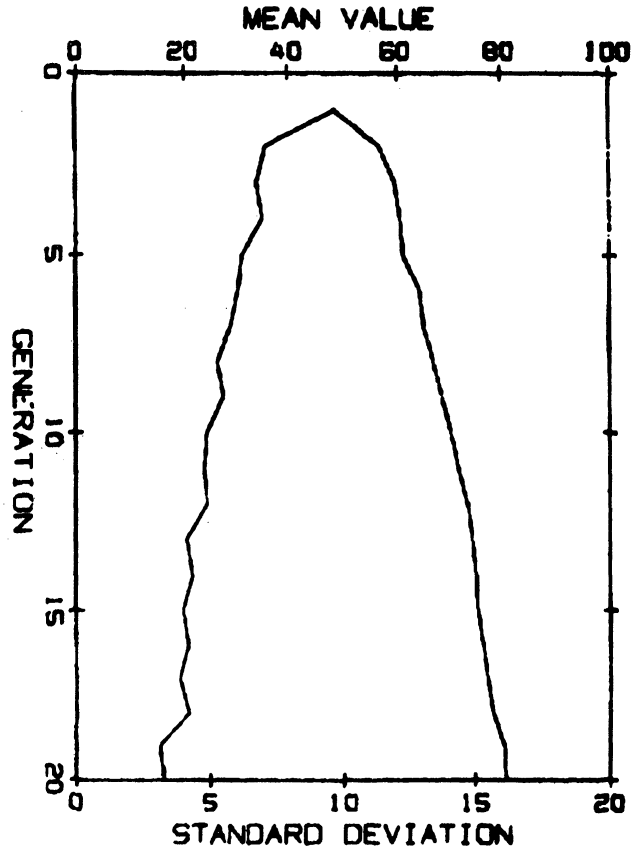


Figure 23a Averaged results of five replications of bulk population breeding for 8-parameter Ridge

```
        20031
BPB1A 6/26/73
NDVLP          4
NVALU          2
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      0.0000
POUCR     1.0000
CV        0.0000
NPOP           32
NSEL            8
LGEN           20
NPAR            8
NSEG           32
NREP            5
IX              1
IPAP            0
IPBP            1
IPAF            0
PCS             0
        STOP
```

1	60.860	37836	36646	37100	17678	35828	28564	36598	29214
8	62.091	24606	21518	40238	37106	40476	24756	37116	17588
17	63.083	49100	36110	32236	25026	47256	37026	36140	49954
41	70.135	48836	31458	45948	21978	47828	40160	44812	28714
102	71.118	45066	27588	44298	25572	44200	36398	41616	25354
105	72.844	43854	32180	49116	33534	43734	36876	41406	28712
119	73.452	55776	39574	48396	32062	59514	49128	36798	27962
174	73.728	43564	23506	56598	44620	59062	45246	37786	21214
187	75.377	48146	35778	46026	28436	58842	40474	48798	36376
197	80.589	44076	31622	56300	44094	59540	53178	42392	28626
265	82.054	47932	35942	52776	36384	63384	60920	49098	40906
333	83.626	55356	36408	56782	51520	64312	60874	53942	43518
355	86.436	51486	40234	52716	44800	59286	49610	61384	58864
417	86.650	51576	39782	61070	48852	59996	56556	60182	55730
433	86.661	51516	39512	56782	51700	59230	52686	57576	55506
488	87.850	51546	39556	59840	51208	59468	52206	60198	56226
497	88.370	48158	44790	56586	47892	63564	60860	65016	64016
499	88.514	51308	43846	57036	50980	59472	60394	64760	64284
539	89.346	55356	47474	60592	51220	63340	59900	64504	59358
550	91.088	51530	40756	56316	52422	63114	60874	65270	64044
551	92.762	58716	51796	63710	55512	63610	62274	64760	64400
605	94.023	55388	48452	64206	62950	63086	61146	63160	63564
1	59.048	37322	20872	40280	56002	24556	12352	35624	21456
17	62.520	35380	24606	26046	24878	43564	29680	43790	43116
23	65.366	25312	21230	44272	35888	44296	37146	47904	29404
36	66.097	39662	25336	40898	25298	33272	25086	37088	33340
53	69.636	40012	28958	48400	39460	48156	37146	35628	35690
91	75.873	44064	33072	44560	27698	54180	44872	35854	19116
195	79.075	56736	47978	39996	24100	46500	33562	47898	39682
292	80.306	44976	40478	51216	38488	61112	56108	49176	39968
463	83.070	60638	55692	52222	36850	57992	48670	48410	39982
549	83.085	56768	48172	52206	44484	64756	57344	48154	39714
565	85.330	59890	55374	48110	36324	57914	49452	52234	39250
1	63.389	56348	56270	32078	28850	36354	25270	36876	36786
4	66.333	51968	32596	47916	28220	39486	32028	44106	40732
41	68.434	48588	29538	48138	32764	35946	24602	45012	44510
42	69.285	52192	47690	47872	36380	44240	36108	38946	45546
45	70.515	36576	21214	52204	44296	44268	25356	44226	45260
57	71.957	56720	56014	40958	32494	39684	25778	37070	26014

Figure 23b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Ridge (Sheet 1 of 3)

86	71.986	52448	40934	48350	37296	50990	20764	51494	45774
95	73.118	28896	16624	52908	47420	43656	28236	44526	33210
102	75.957	56960	52652	45286	28154	35844	19098	41648	26234
159	76.038	51888	36812	53388	40442	39892	21528	51248	37386
232	79.543	60336	53462	51966	39932	38946	28026	48848	34456
275	81.973	63966	62852	57260	45000	44420	33082	48352	41630
326	82.675	63754	60824	53210	44804	39654	29180	52446	44800
394	82.694	63476	61326	56522	48842	43446	20780	56258	45020
436	83.304	59838	55094	57980	48632	39158	25276	52026	40266
441	85.504	64466	64414	57756	52216	50690	36336	51730	48394
541	86.451	63048	58722	56782	52174	43460	31114	59618	56044
545	87.308	64722	62292	59930	52444	47316	38962	59078	56222
578	89.151	64678	64668	56092	47898	50960	43310	56240	48378
638	89.391	64662	64430	60170	56106	50706	43266	59588	59834
1	45.288	21290	37098	40420	41346	35930	55764	44282	36154
2	56.226	40130	28898	33022	44736	41000	40282	37598	32316
3	64.661	47140	47210	25296	28504	45260	32838	44508	28220
31	76.403	40730	24698	52656	39574	48786	37338	37180	20810
184	76.824	48152	35484	56286	51542	45496	28370	36248	23166
310	77.036	55754	47048	63804	58906	33092	16610	32094	11902
363	77.230	56010	46822	59838	51268	33046	16150	32124	15710
389	77.398	55772	46808	59598	54854	36694	16134	31642	15726
390	77.814	56282	46824	59650	51508	36932	20212	32124	15292
418	77.969	49292	38862	60124	55574	32820	16132	35680	19372
451	78.621	53146	43168	64188	59386	36614	20210	31136	15534
509	78.884	55534	46808	63264	58934	32852	16120	32618	15488
582	80.130	55548	47048	63506	58980	37156	20168	35242	18652
1	41.820	25548	44256	38770	29108	24876	37794	33504	32782
3	46.837	28906	36846	36816	26270	21770	39526	51678	28656
4	52.471	28178	28418	40156	35890	44510	25082	20046	29166
11	65.159	33440	21230	39968	35466	32706	17632	51892	32498
17	65.453	44784	28442	36828	43582	52206	29930	49352	39022
26	67.939	37100	28032	47808	33740	40910	20994	28926	14778
70	69.944	45262	22066	36850	17110	48528	37360	44522	28850
102	70.892	48096	33784	32962	26694	52172	40732	39932	33166
116	71.217	59388	43186	33888	19262	40358	25326	48766	44962
147	71.840	52402	41720	32044	26062	44016	26048	48408	32690
160	72.708	55036	43934	36992	15694	44480	36668	55980	60334
162	72.969	62972	51108	37474	19024	40416	28690	51904	48832
168	74.456	47824	37662	28384	16910	48548	36638	63722	52610
220	75.011	51422	51794	29598	16144	49056	32796	59628	56466
239	77.740	51962	44390	40848	27436	49040	44526	55746	44466
292	81.070	51660	36694	33228	24540	56420	48232	64414	63188
336	82.805	55322	44118	33212	20460	56418	48426	63436	59600
373	83.030	59776	48198	37072	20672	55712	48170	63720	59332
419	83.338	51228	43906	41104	24046	52610	44030	63918	62510
439	84.833	52412	47956	40656	27646	60528	55850	63694	60174
489	85.206	55516	47688	32960	16610	55926	48140	63342	62762
527	88.267	59146	54900	36290	20194	60274	55610	64030	63244

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	48.186	48.186	9.728	60.176	4.760	0.000	32.000
2	52.393	56.599	7.143	65.110	2.632	0.000	32.000
3	54.751	59.468	6.801	67.683	2.216	0.000	32.000
4	56.206	60.572	7.023	69.013	2.367	0.000	32.000
5	57.183	61.089	6.245	68.589	2.258	0.000	32.000
6	58.377	64.347	6.079	71.384	2.044	0.000	32.000
7	59.346	65.163	5.777	72.032	2.448	0.000	32.000
8	60.309	67.044	5.262	73.380	1.959	0.000	32.000
9	61.249	68.771	5.502	75.410	2.101	0.000	32.000
10	62.174	70.497	4.850	76.373	1.937	0.000	32.000
11	63.062	71.949	4.756	77.739	1.718	0.000	32.000

Figure 23b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Ridge (Sheet 2 of 3)

12	63.951	73.725	4.860	79.245	1.624	0.000	32.000
13	64.766	74.553	4.059	79.421	1.348	0.000	32.000
14	65.512	75.209	4.275	80.507	1.477	0.000	32.000
15	66.182	75.553	3.926	80.275	1.491	0.000	32.000
16	66.831	76.577	4.124	81.620	1.626	0.000	32.000
17	67.454	77.407	3.789	82.111	1.622	0.000	32.000
18	68.061	78.389	4.154	83.132	1.509	0.000	32.000
19	68.721	80.603	3.028	84.054	1.188	0.000	32.000
20	69.325	80.795	3.209	84.456	1.320	0.000	32.000

MAXIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	49.311	49.311	10.808	60.466	7.200	0	32
2	53.599	58.850	8.250	68.884	3.175	0	32
3	56.255	61.568	7.462	69.595	3.313	0	32
4	58.123	63.728	8.092	71.162	3.050	0	32
5	59.104	63.026	8.406	72.328	2.487	0	32
6	59.984	65.286	7.213	72.343	2.952	0	32
7	60.736	66.474	6.961	73.718	3.681	0	32
8	61.783	69.110	5.753	74.820	2.366	0	32
9	62.538	70.574	7.216	78.131	2.523	0	32
10	63.291	72.314	5.839	77.533	2.753	0	32
11	64.150	74.239	6.329	80.649	2.144	0	32
12	65.157	76.229	5.983	82.081	2.278	0	32
13	65.888	78.678	4.753	83.032	1.428	0	32
14	66.693	77.891	5.063	84.035	2.023	0	32
15	67.544	79.453	4.483	83.985	1.874	0	32
16	68.359	80.587	5.632	85.782	2.308	0	32
17	69.111	81.144	4.642	86.522	2.072	0	32
18	69.960	84.384	4.894	90.067	2.416	0	32
19	70.785	85.641	3.865	90.180	1.795	0	32
20	71.607	87.231	3.671	90.872	1.705	0	32

MINIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	46.517	46.517	8.966	59.804	2.417	0	32
2	50.978	55.298	6.359	63.684	1.859	0	32
3	53.711	57.727	6.249	66.574	1.236	0	32
4	54.912	58.130	5.664	67.473	1.348	0	32
5	56.248	59.950	5.133	66.960	2.080	0	32
6	57.489	62.303	5.091	68.948	1.523	0	32
7	58.421	64.012	4.774	70.374	1.404	0	32
8	59.496	63.228	4.244	70.526	1.673	0	32
9	60.570	67.650	4.512	73.441	1.563	0	32
10	61.477	69.636	3.718	75.127	1.487	0	32
11	62.266	69.283	3.974	73.808	0.956	0	32
12	62.975	70.666	3.422	75.618	1.074	0	32
13	63.643	71.661	3.563	76.177	1.226	0	32
14	64.278	72.155	3.724	76.728	0.621	0	32
15	64.863	72.067	3.073	76.007	1.313	0	32
16	65.407	72.872	2.076	76.904	0.846	0	32
17	65.928	73.516	2.697	76.776	1.085	0	32
18	66.382	74.101	3.111	77.182	0.713	0	32
19	66.889	76.018	2.497	78.538	0.647	0	32
20	67.361	76.333	2.062	78.743	0.729	0	32

Figure 23b Parameter values of individuals with increasing phenotypic values during five replications of bulk population breeding for 8-parameter Ridge (Sheet 3 of 3)

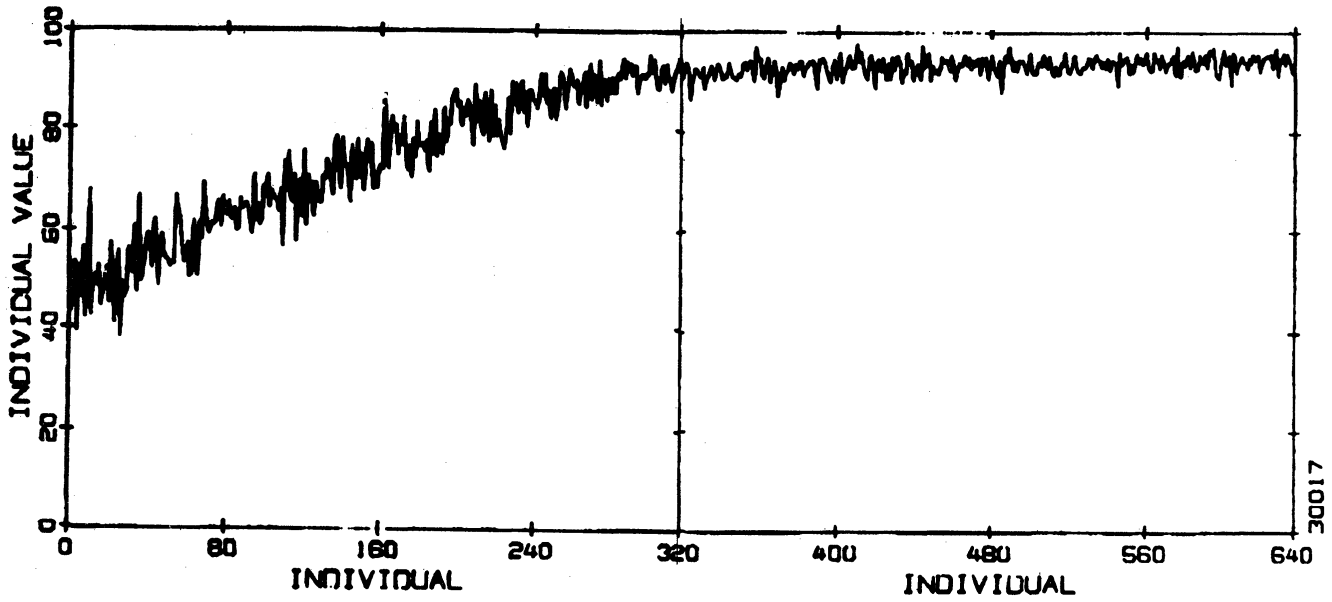


Figure 24a Phenotypic value of individuals during mass selection for 8-parameter Plane using Gene Action 4

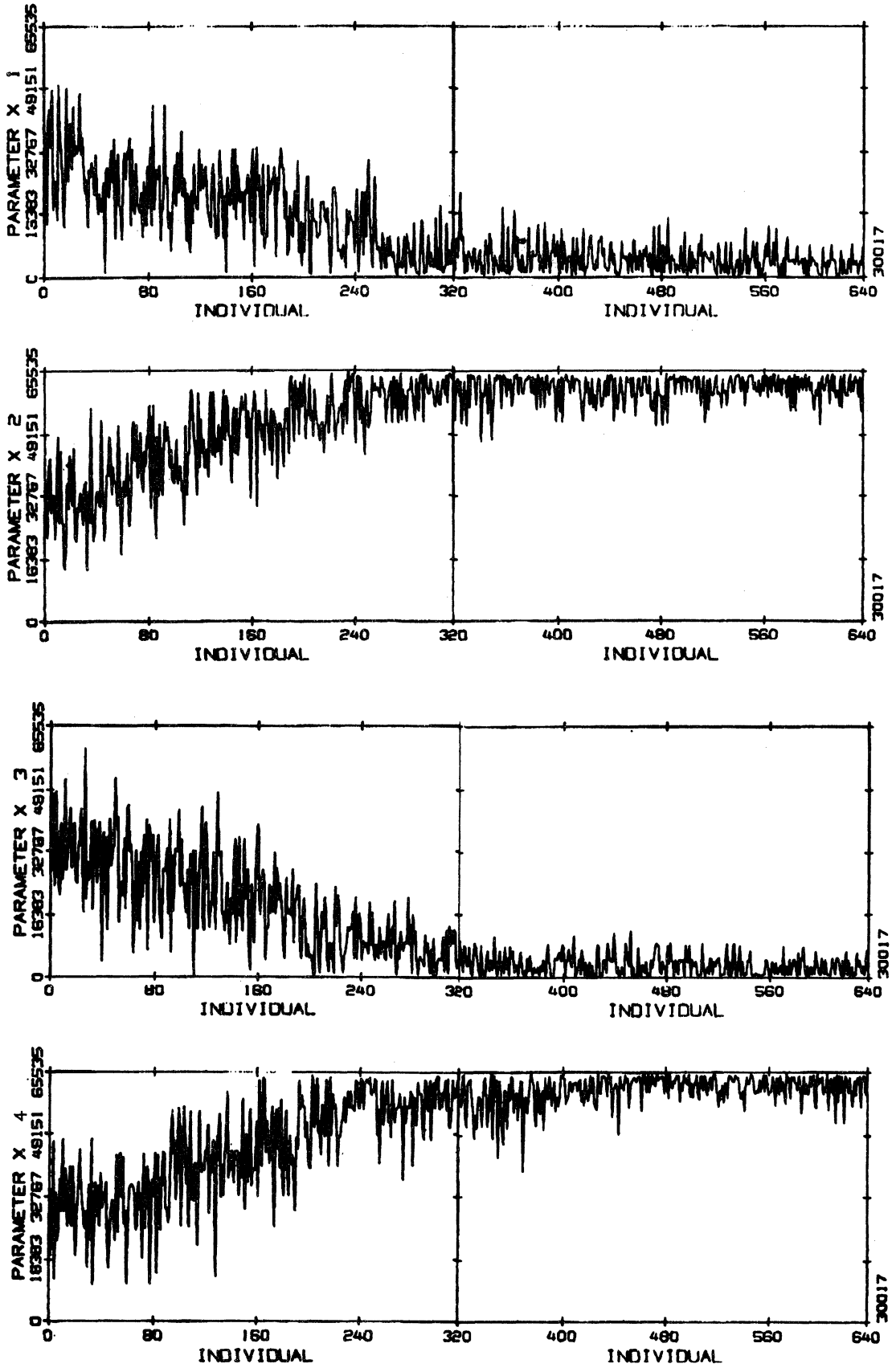


Figure 24b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 4 (Sheet 1 of 2)

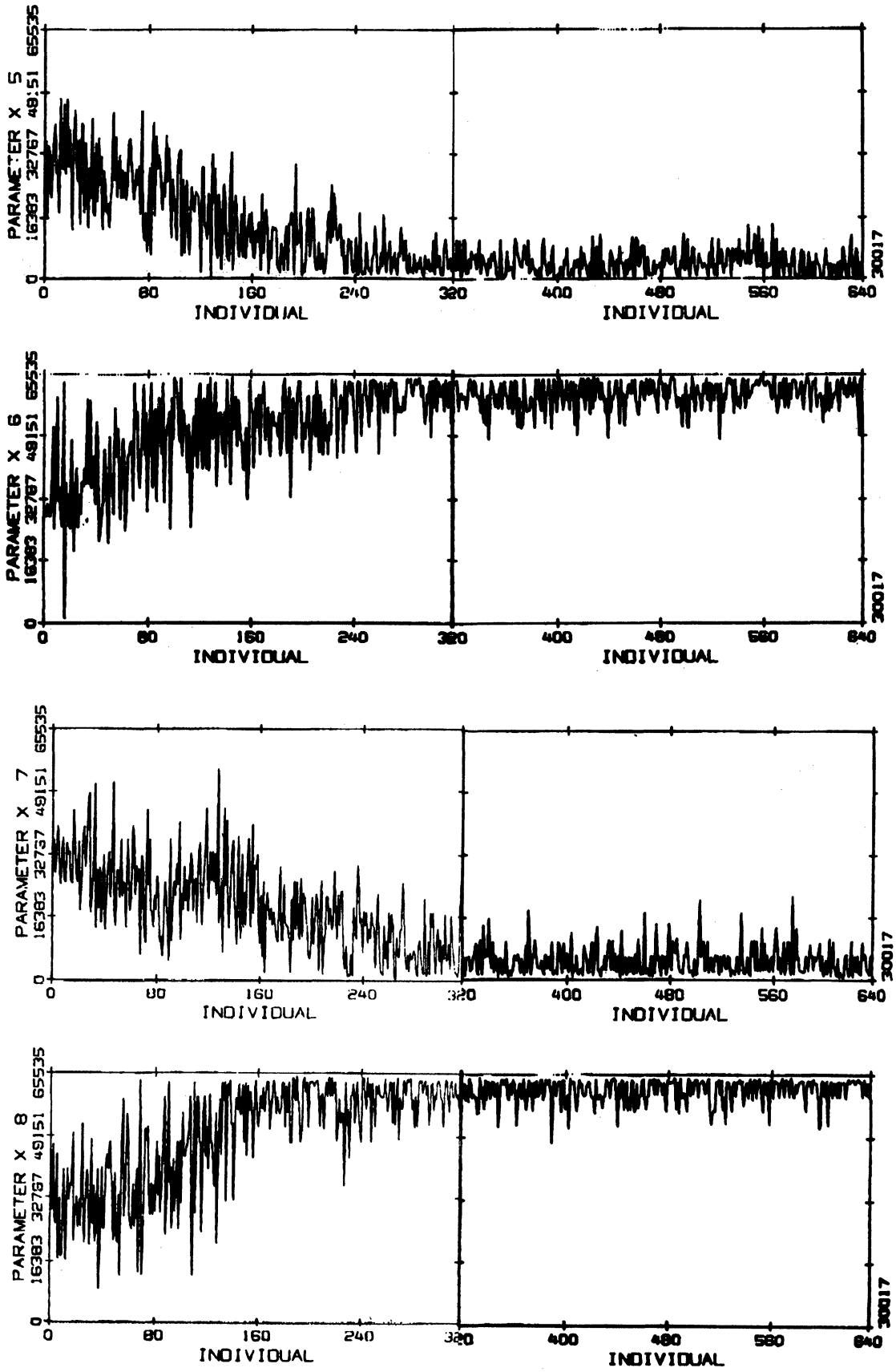


Figure 24b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 4 (Sheet 2 of 2)

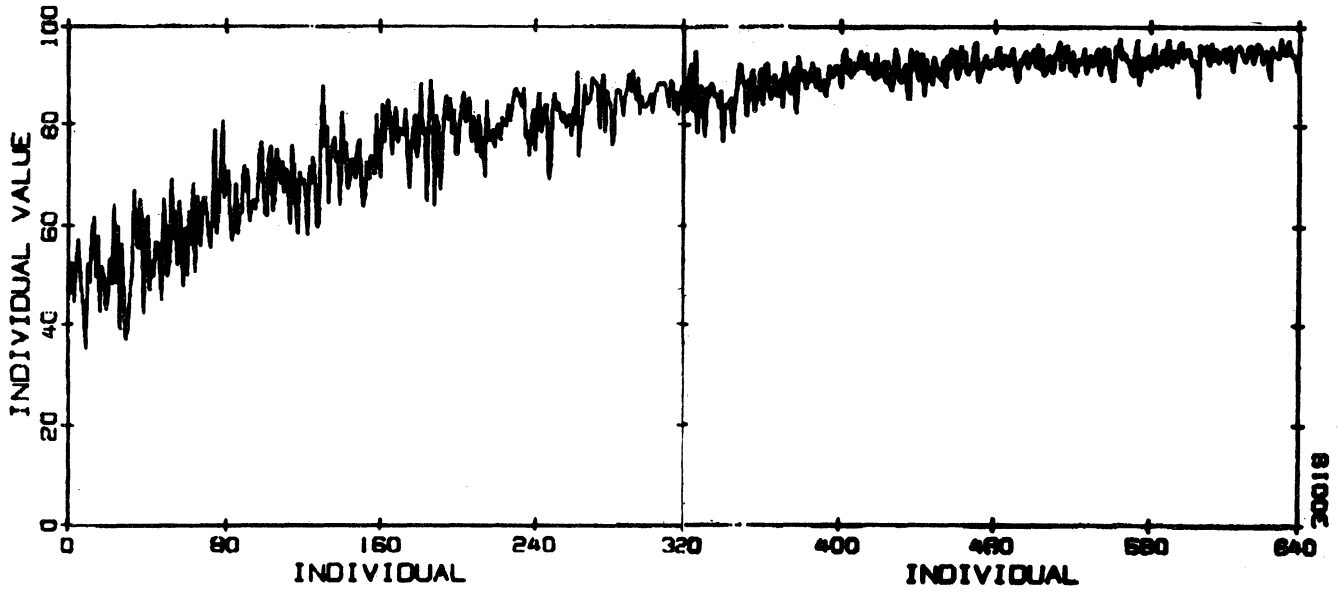


Figure 25a Phenotypic value of individuals during mass selection for 8-parameter Plane using Gene Action 10

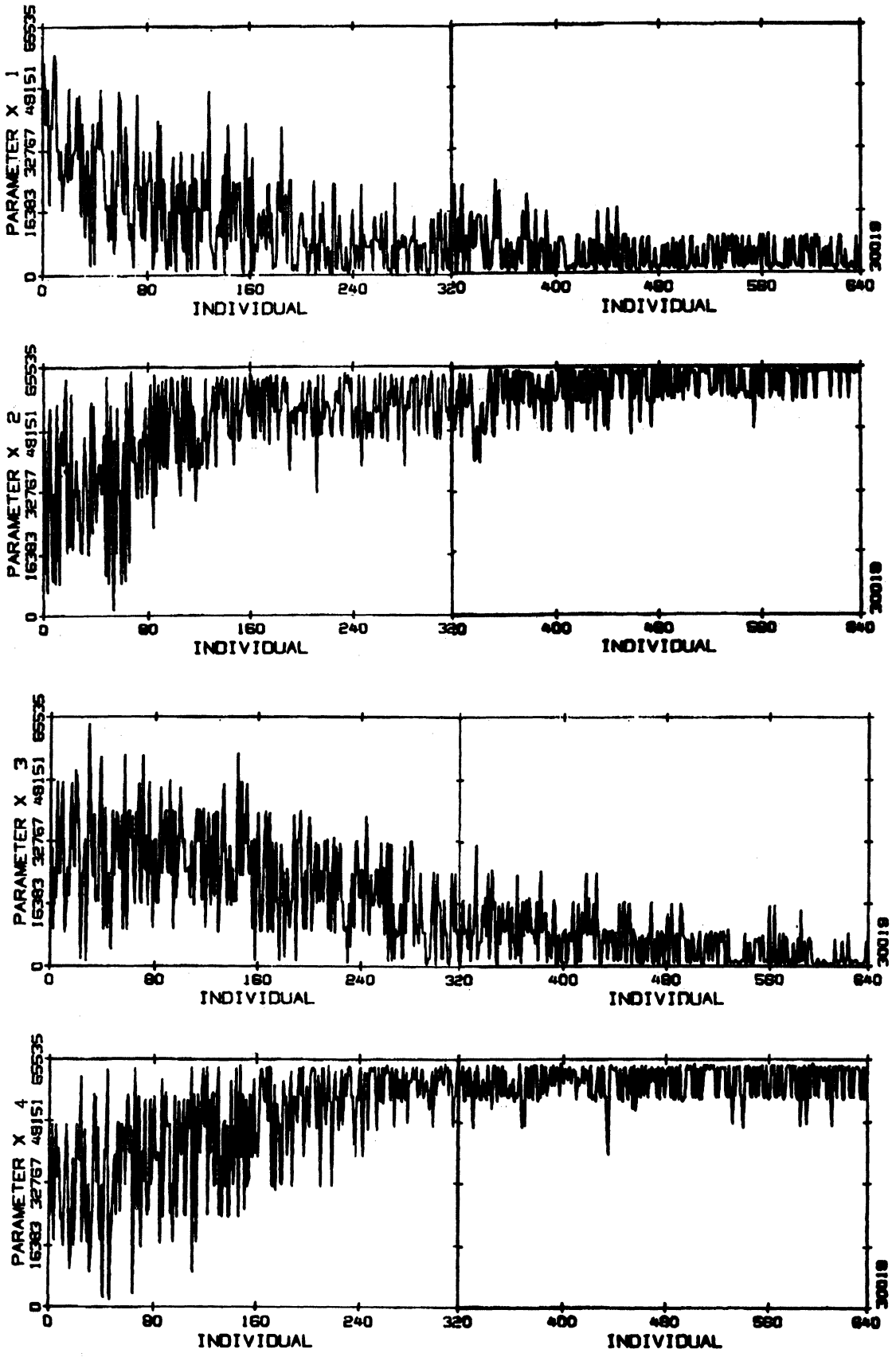


Figure 25b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 10 (Sheet 1 of 2)

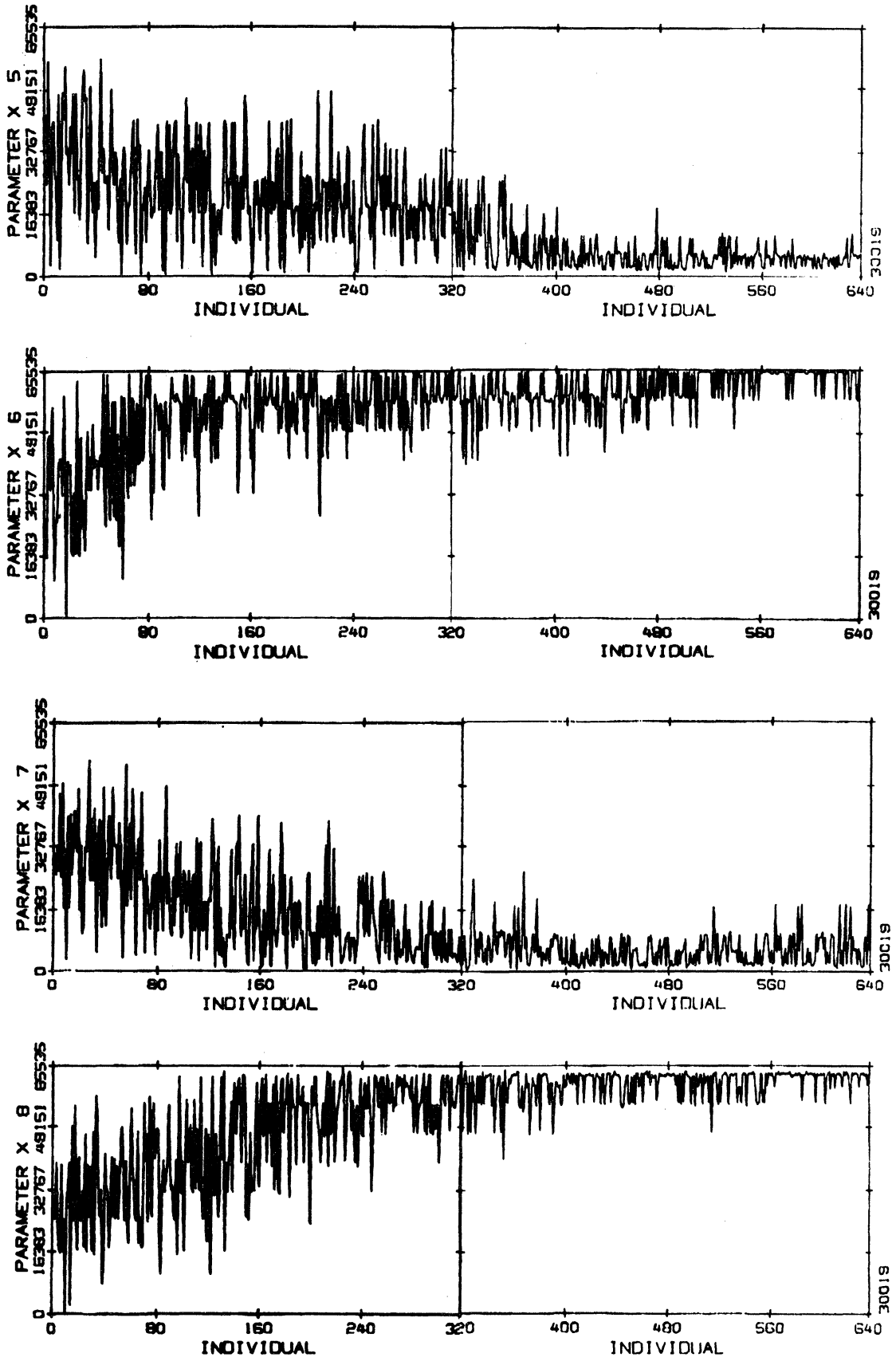


Figure 25b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 10 (Sheet 2 of 2)

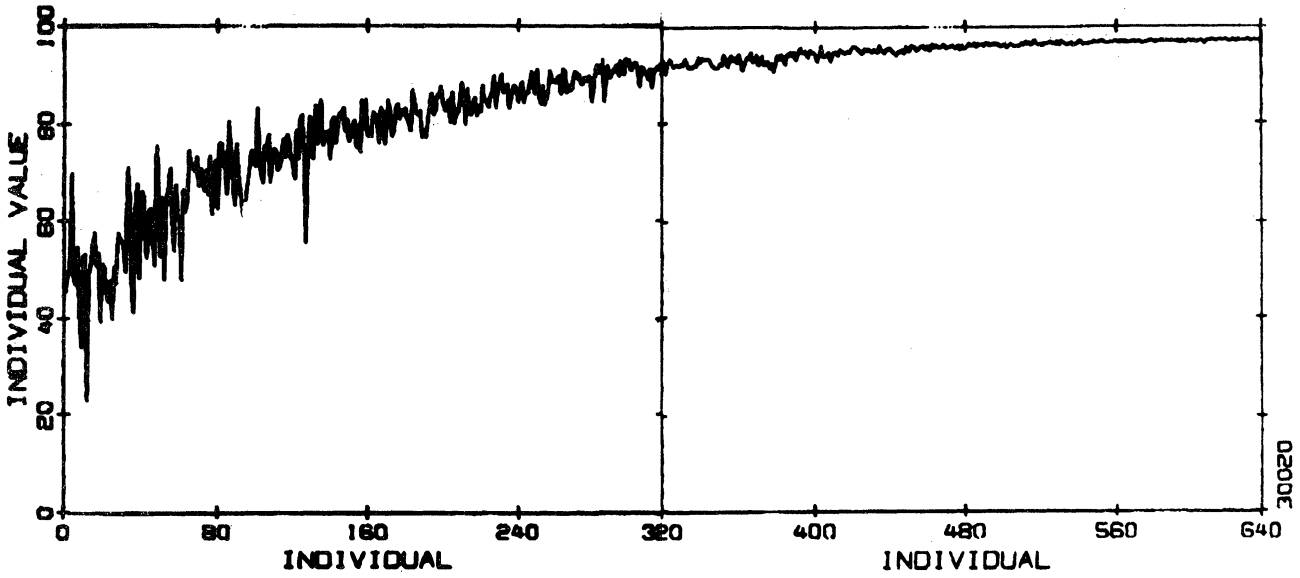


Figure 26a Phenotypic value of individuals during mass selection for 8-parameter Plane using Gene Action 3

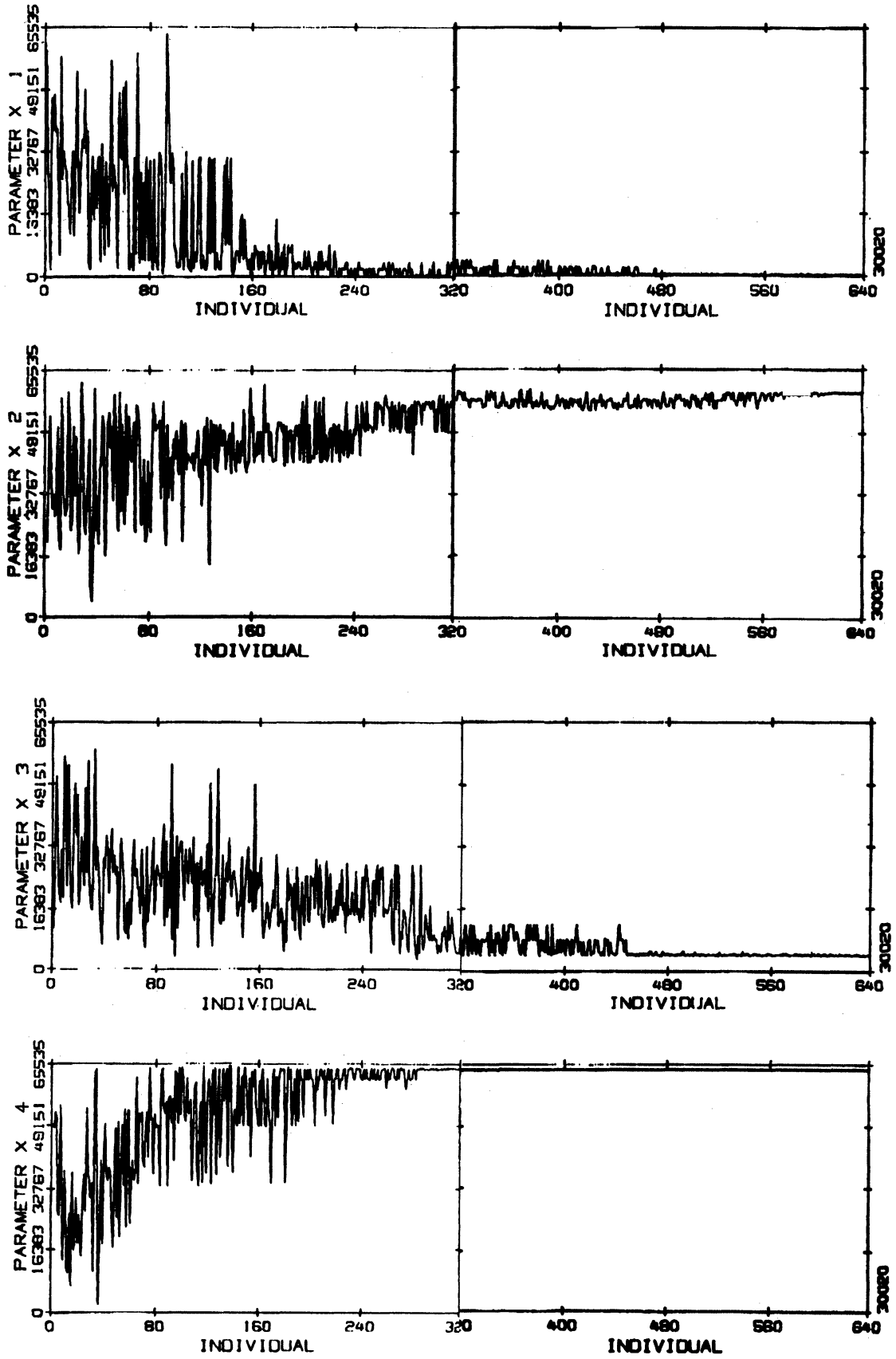


Figure 26b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 3 (Sheet 1 of 2)

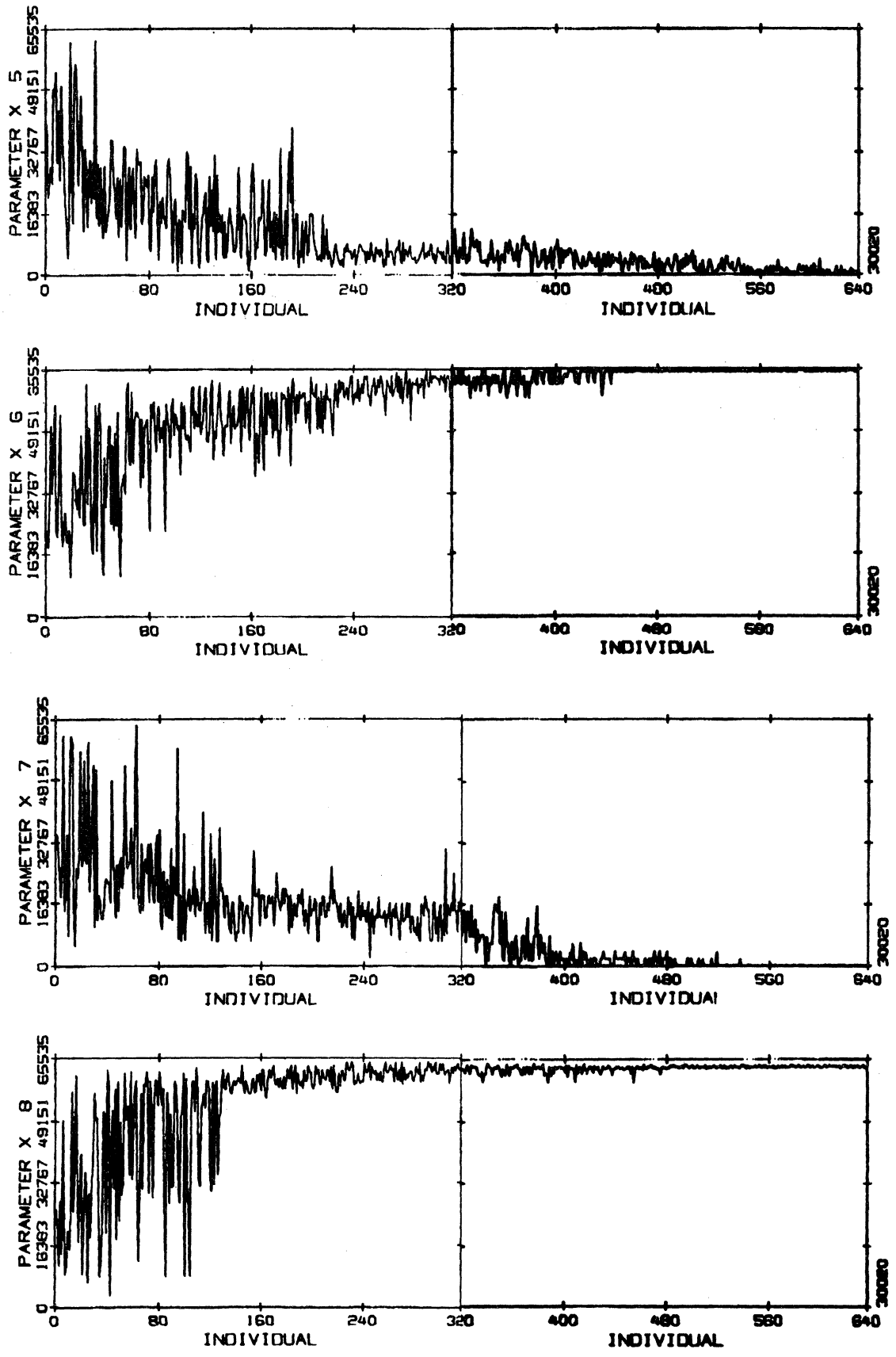


Figure 26b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 3 (Sheet 2 of 2)

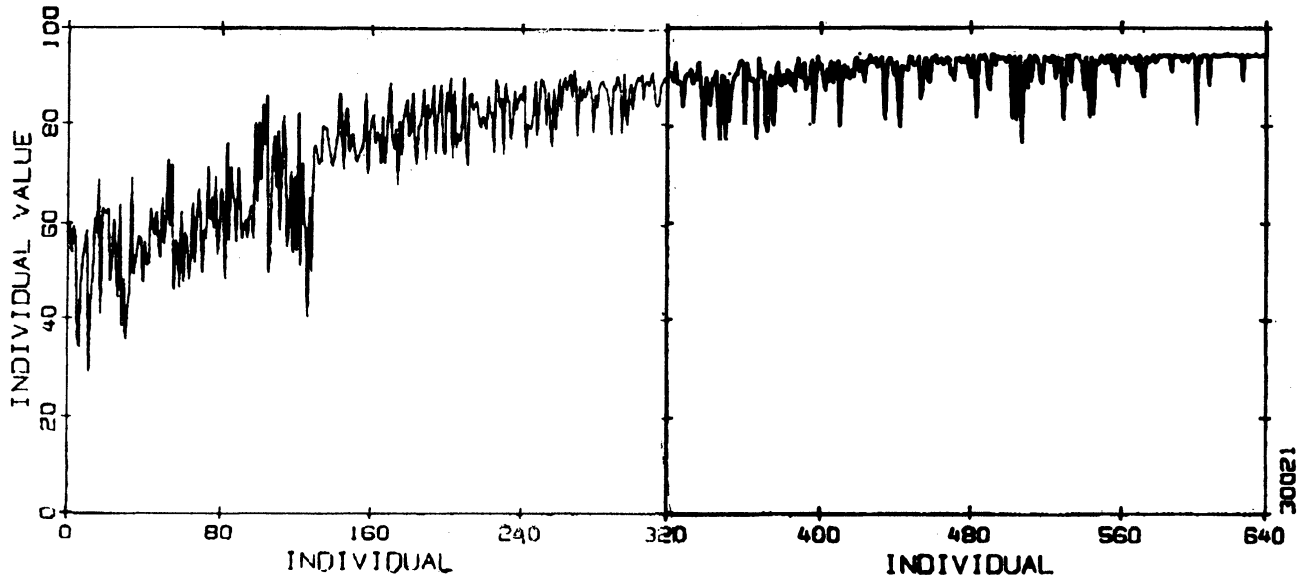


Figure 27a Phenotypic value of individuals during mass selection for 8-parameter Plane using Gene Action 9

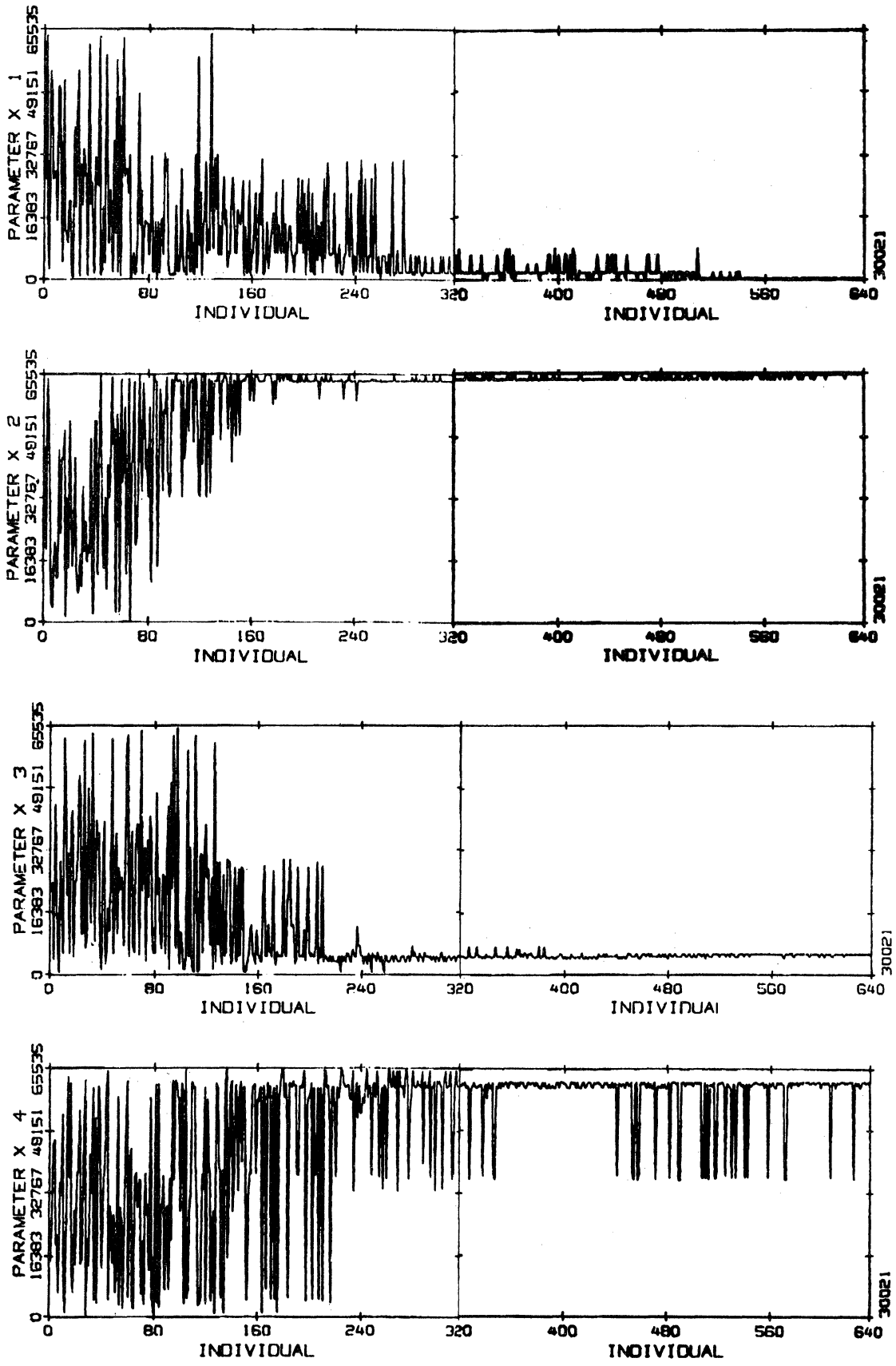


Figure 27b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 9 (Sheet 1 of 2)

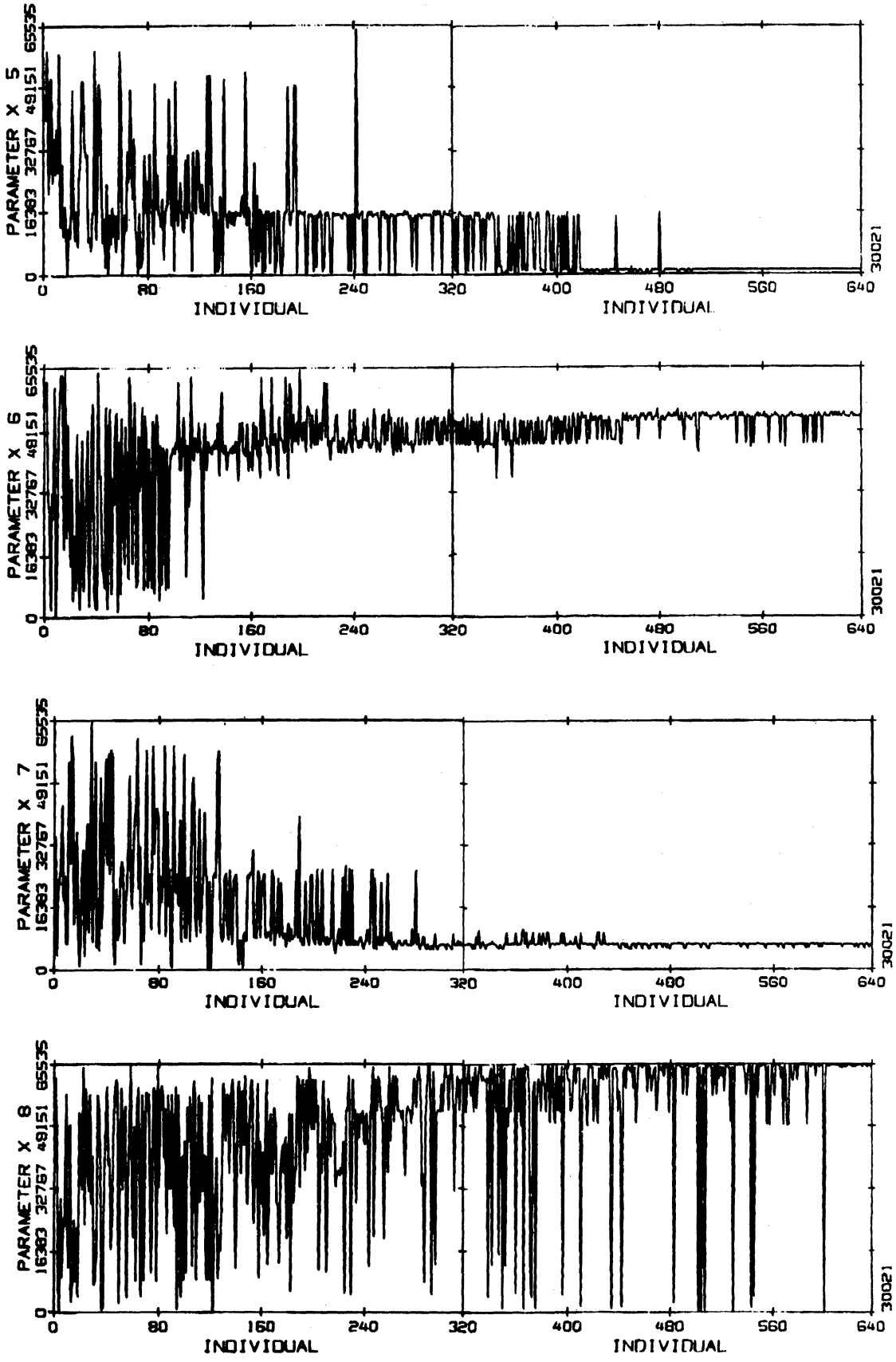


Figure 27b Parameter values of individuals during mass selection for 8-parameter Plane using Gene Action 9 (Sheet 2 of 2)

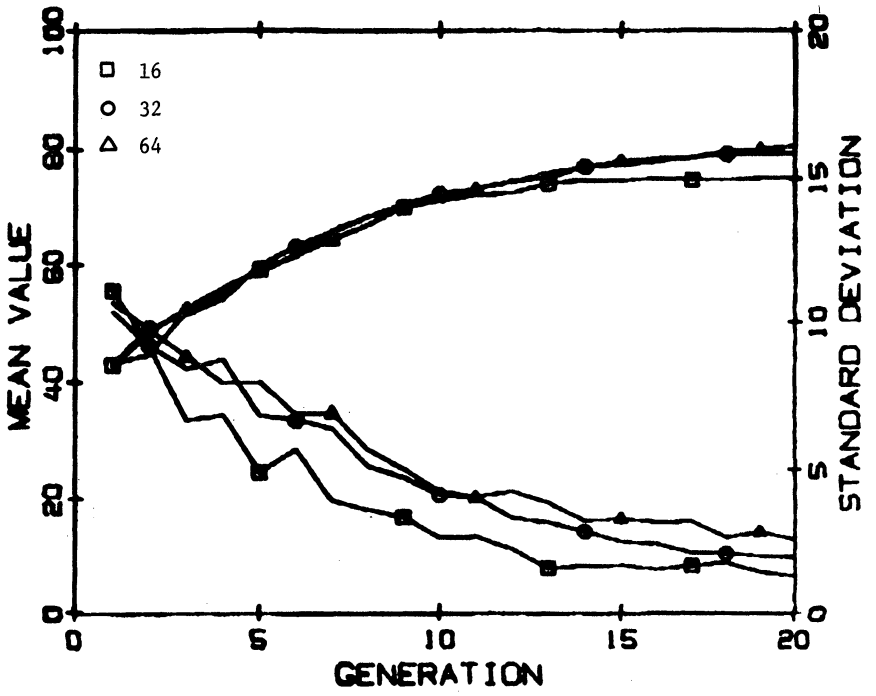


Figure 28a Averaged population mean and standard deviation of phenotypic values for five replications of mass selection for 8-parameter Ridge using Gene Action 3 and three population sizes: 16, 32 and 64

30028

MS1A 6/26/73

NDVLP	3
NVALU	2
PINV	0.0000
PTRA	0.0000
PCROS	0.5000
PCROL	0.5000
PMUT	0.0000
CV	0.0000
NPOP	16
NSEL	4
LGEN	20
NPAR	8
NSEG	8
NREP	5
IX	1
IPAP	0
IPBP	1
IPAF	0
IPCS	0

30029

1	41.606	58976	25258	11077	49266	39450	22494	34951	25403
2	47.945	28104	20386	32387	48630	20589	18130	30506	21491
3	50.046	21952	34525	51038	52512	26394	30198	24330	11162
5	52.362	47053	38976	21429	26844	24417	32671	26971	14206
6	62.901	38445	28951	18120	25380	49353	48225	60994	49458
36	63.909	49274	54280	12364	18247	32220	22586	63294	59740
49	67.431	52518	51827	12303	12221	32239	24395	63936	59267
69	77.965	52646	50162	36592	19335	40911	24425	63487	59263
159	79.048	52519	36863	57054	51085	32767	24503	63487	59160
166	81.638	52741	37253	57038	51079	40908	24495	63487	57599
207	81.671	52735	37253	57101	51077	40959	24503	63487	57599
213	81.731	52525	37252	57089	52351	40959	24503	62994	57496
229	81.972	52525	37252	57024	50170	40959	24503	63487	57599
247	82.076	52525	37252	57024	51077	40959	24503	62994	57599
249	82.194	52525	37252	57024	51077	40959	24503	62994	57831
281	82.263	52525	37252	57089	51077	40908	24503	62994	57831
316	82.286	52525	37252	57149	51077	40959	24503	62994	57831
320	82.308	52525	37252	57151	51077	40909	24503	62994	57831
1	55.200	31338	10644	42964	20148	37819	28407	16201	22554
4	62.266	35302	20052	30522	19292	33938	29241	30800	18433
6	64.733	35567	31372	48981	29467	33549	10691	56648	59655
20	65.067	35583	29711	30463	32737	43519	27644	50173	40727
37	66.769	34687	39413	53410	52347	53441	31189	53248	46908
49	70.978	35068	41226	60834	54079	48319	33276	53212	55549
97	74.221	34306	33807	60671	53222	54016	59951	57311	53506
127	74.818	34974	34314	56738	53055	54527	59951	60289	53375
130	75.091	34812	34314	57506	53029	54377	60031	60416	53375
141	75.725	34815	34314	56738	53082	54527	59951	60290	55679
144	78.532	35169	17914	56738	53247	54271	59903	57373	50939
1	38.726	31741	29120	1403	36938	55908	22438	22450	6464
3	43.135	47263	25113	2750	21257	17706	28854	20769	13399
4	43.547	17931	31034	37977	50492	42263	23201	16948	21982
10	50.836	51773	31453	31411	27905	34391	19374	50036	5272
26	55.270	36417	31821	32255	20883	34455	19489	41980	5230
34	62.859	30191	4056	61052	49937	32331	28558	35830	20350
55	64.077	37695	18425	56807	44652	38915	32578	49151	19388
87	65.859	45368	14321	51074	43505	41535	32347	42623	24611
98	67.493	33080	16349	50811	43423	33191	25376	49263	27551
109	67.683	37119	16343	50433	43411	42627	26500	32767	27584
117	68.398	45055	20161	56559	43519	41383	32767	42735	24511

Figure 28b Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 16 (Sheet 1 of 3)

118	71.404	35071	16343	50413	44032	40995	26432	46831	27696
143	74.273	34808	18721	51408	43409	42584	32580	42735	28767
153	74.798	33272	18173	52482	43409	40999	26683	45055	28799
171	75.396	34815	18109	55550	43885	40956	25600	42735	28751
200	76.280	34815	18110	53709	43885	42584	26564	42735	28671
216	76.391	34815	18110	52735	43885	40995	25530	45055	31743
228	76.391	34823	18110	53487	43885	40956	25530	42735	28671
243	76.453	34823	18110	53694	43885	40956	25599	42735	28784
261	76.492	34823	18110	53679	43885	40956	25599	42735	28671
295	76.493	34823	18110	53680	43885	40959	25599	42735	28671
1	38.742	21478	53862	11192	29068	29511	22112	50475	50131
2	42.915	16597	32135	49089	22887	26290	34517	15164	5125
3	56.518	11712	5082	61786	63612	26683	39982	38608	13268
10	57.485	25633	22082	28169	15173	29259	25683	34761	21395
36	60.132	7891	5301	30683	19360	50270	32830	31309	22668
65	64.469	5612	12159	60319	65019	45636	39424	40262	20304
86	66.077	5564	12178	60319	64941	43003	39458	47103	32767
107	66.564	5624	8978	60308	64945	45124	39458	46406	28671
114	68.853	5705	8831	60331	65099	46719	39457	47103	31919
122	69.282	5695	8831	60331	65099	46591	39457	47103	32943
131	69.411	5631	8831	60331	65097	46380	39457	46406	32943
132	69.869	5708	8850	60319	65019	46508	39457	47103	33791
148	69.691	5705	8813	60331	65099	46803	39457	46406	32943
153	69.835	5708	8850	60331	65099	46803	39457	47103	33967
169	69.839	5708	8831	60331	65099	46803	39457	47103	33791
179	69.870	5705	8831	60331	65019	46803	39457	47103	33967
193	69.895	5705	8831	60331	64950	46803	39457	47103	33967
246	69.898	5705	8831	60331	64943	46803	39457	47103	33967
269	69.900	5705	8831	60331	64937	46803	39457	47103	33967
277	69.905	5705	8813	60331	64937	46803	39457	47103	33967
1	33.315	19113	33189	27041	30923	14952	45929	22429	10839
3	57.815	53338	22094	33516	10064	29792	22521	49197	41923
4	58.534	24631	17167	28929	13546	26173	20267	50486	57250
24	59.919	44274	48829	32807	1867	49121	45057	46290	41167
48	61.699	48806	32804	26482	7344	38598	31651	27794	23692
51	63.301	50451	60801	15140	2971	45549	41974	38373	23543
52	63.320	50340	62556	8283	1087	45295	38507	52065	35581
55	65.337	50522	53361	15286	1994	47107	39636	38598	29495
85	68.239	50417	53189	15363	1168	45543	40414	54491	49095
87	70.742	55206	57393	15391	1199	47091	40960	54471	42239
92	71.192	56674	54143	15329	2954	47106	37887	40959	31542
98	74.364	56674	54143	15333	2954	48665	37195	46726	31542
124	74.964	56674	54111	15332	2955	48665	37195	46726	32767
135	75.562	55295	54111	15237	2939	48665	37908	54975	45055
136	76.848	56674	54143	15230	2954	48665	38580	54918	46281
146	76.848	56674	54321	15236	2960	48665	37908	55041	47103
160	77.245	56674	54143	15233	2944	48665	37215	54975	46281
171	77.264	56674	54111	15233	2954	48665	37195	54975	46281

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	42.813	42.813	11.093	55.003	3.532	0.000	16.000
2	43.593	44.373	9.137	54.739	2.885	0.000	16.000
3	46.290	51.666	6.676	59.269	3.254	0.000	16.000
4	48.477	55.039	6.877	63.090	1.816	0.000	16.000
5	50.616	59.171	4.902	64.855	2.693	0.000	16.000
6	52.383	61.218	5.694	67.751	1.488	0.000	16.000
7	54.313	65.896	3.893	70.486	1.162	0.000	16.000
8	56.062	68.299	3.560	72.431	0.789	0.000	16.000
9	57.618	70.067	3.297	73.550	1.265	0.000	16.000
10	58.986	71.301	2.547	74.244	0.906	0.000	16.000
11	60.179	72.107	2.590	74.802	1.017	0.000	16.000
12	61.211	72.560	2.148	75.113	0.710	0.000	16.000

Figure 28b Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 16 (Sheet 2 of 3)

13	62.210	74.205	1.483	75.909	0.464	0.000	16.000
14	63.103	74.712	1.565	76.349	0.204	0.000	16.000
15	63.875	74.676	1.584	76.296	0.236	0.000	16.000
16	64.574	75.055	1.445	76.466	0.175	0.000	16.000
17	65.179	74.869	1.574	76.520	0.117	0.000	16.000
18	65.713	74.785	1.685	76.462	0.145	0.000	16.000
19	66.202	75.014	1.341	76.380	0.259	0.000	16.000
20	66.649	75.145	1.209	76.402	0.173	0.000	16.000

MAXIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	46.454	46.454	13.616	61.899	5.670	0	16
2	47.041	47.676	11.066	61.320	4.447	0	16
3	50.381	57.768	9.094	64.282	5.862	0	16
4	53.266	61.919	7.847	69.100	2.316	0	16
5	55.517	64.521	10.027	69.635	5.717	0	16
6	56.397	63.966	7.441	72.349	1.866	0	16
7	57.968	69.218	4.331	74.271	2.189	0	16
8	59.343	70.856	4.920	75.178	1.195	0	16
9	60.783	72.304	4.275	75.756	2.039	0	16
10	61.986	72.857	5.197	76.888	1.914	0	16
11	63.058	73.772	4.683	77.750	3.073	0	16
12	64.098	75.547	4.127	77.951	2.245	0	16
13	64.984	78.122	2.670	80.530	1.104	0	16
14	65.713	80.293	3.154	81.558	0.403	0	16
15	66.314	80.812	2.453	81.846	0.535	0	16
16	66.857	80.609	2.120	82.027	0.329	0	16
17	67.408	80.453	3.450	82.082	0.267	0	16
18	68.159	80.925	4.427	82.175	0.322	0	16
19	68.823	80.769	2.804	82.235	0.764	0	16
20	69.422	80.811	2.184	82.269	0.662	0	16

MINIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	36.790	36.790	8.472	46.665	1.239	0	16
2	38.908	38.908	6.356	50.468	1.099	0	16
3	41.460	46.566	5.496	55.613	1.566	0	16
4	43.886	48.756	5.799	57.025	1.478	0	16
5	46.562	56.117	3.213	60.735	1.225	0	16
6	48.776	58.369	3.031	63.375	1.172	0	16
7	50.628	61.740	3.488	65.881	0.159	0	16
8	52.601	65.392	1.777	68.890	0.295	0	16
9	54.418	68.577	0.551	69.543	0.105	0	16
10	55.917	69.402	0.276	69.744	0.042	0	16
11	57.158	69.573	0.201	69.827	0.014	0	16
12	58.198	69.641	0.215	69.855	0.013	0	16
13	59.076	69.611	0.180	69.863	0.033	0	16
14	59.837	69.726	0.178	69.875	0.024	0	16
15	60.489	69.617	0.173	69.875	0.023	0	16
16	61.065	69.709	0.194	69.884	0.015	0	16
17	61.576	69.749	0.148	69.897	0.002	0	16
18	62.031	69.759	0.190	69.900	0.003	0	16
19	62.432	69.665	0.198	69.900	0.000	0	16
20	62.794	69.669	0.213	69.901	0.005	0	16

Figure 28b Parameter values of individuals with increasing phenoty. ues during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 16 (Sheet 3 of 3)

```
        30029
MS1A 6/26/73
NOVLP          3
NVALU          2
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP           32
NSEL            8
LGEN           20
NPAR            8
NSEG            8
NREP            5
IX              1
IPAP            0
IPBP            1
IPAF            0
IPCS            0
        30030
     1  41.606  58976  25258  11077  49266  39450  22494  34951  25403
     2  47.945  28104  20386  32387  48630  20589  18130  30506  21491
     3  50.046  21952  34525  51038  52512  25394  30198  24330  11162
     5  52.362  47053  38976  21429  26844  24417  32671  26971  14206
     6  62.901  38446  26951  18120  25380  49353  48225  60994  49458
    27  64.163  29092  30010  55414  53587  47350  48246  31374  18334
    43  68.162  42477  28139  31769  33150  56855  49600  21966   8649
    54  71.535  32742  16668  51236  51918  55835  47008  24655  12587
    72  74.405  32663  16961  59415  56861  53786  48917  24588  12830
   164  74.873  32556  26879  53247  59647  57670  49151  55695  46709
   168  77.206  36378  36376  63807  57295  52413  46831  55026  47012
   200  78.870  36762  23443  57623  49263  57091  48367  49086  46713
   233  79.403  33645  16319  59378  49201  57595  46079  55070  49151
   240  84.785  36223  19451  63883  59676  56837  48390  57150  48761
   428  85.233  32772  16383  61439  59648  59391  53247  55136  46759
   480  85.369  32016  16447  61439  59679  60415  55529  57342  48818
   560  85.629  32766  16384  63495  59789  59073  53247  55039  46767
     1  38.726  31741  29120   1403  36938  55908  22438  22450   6464
     3  43.135  47263  25113   2750  21257  17706  28854  20769  13399
     4  43.547  17931  31034  37977  50492  42263  23201  16948  21982
    10  50.836  51773  31453  31411  27905  34391  19374  50036   5272
    21  55.425  52005  50622   7073  25982  47818  33681  22252  22332
    22  57.678  26067  24934  34401  12327  37818  37638  48080  45199
    27  63.132  52869  38935  53366  26586  25414  18336  36189  22763
    43  64.301  50039  34259  22498  35015  31421  19300  57991  50281
    86  64.575  47961  35807  32735  16791  24707  24323  37384  17454
   129  69.512  48779  38911  48957  58517  32445  18432  45156  32904
   164  72.480  57983  44274  33945  21656  37628  24837  46280  32636
   202  72.540  49716  36915  55489  61929  33224  27074  46944  33712
   213  76.501  53314  40146  59383  46846  37664  19507  48320  34600
   216  78.392  49167  34816  56326  53760  37899  24323  49137  36686
   245  78.417  49103  34816  55281  52053  49138  37843  49697  32085
   260  78.970  48144  32831  60609  55061  37682  17541  51214  40783
   371  78.990  50116  47564  57345  49408  37902  24786  51592  40783
   385  79.713  56324  48063  53255  41449  37651  25643  49141  39376
   420  80.152  57343  47116  53255  42241  37600  24786  52153  40522
   475  80.181  56324  48127  51208  41493  37855  18477  51493  39936
   477  80.563  56324  48063  50368  42241  38639  25363  52113  42927
   499  81.066  57343  49074  52431  42239  37864  25601  51664  42927
   552  81.672  56324  48140  52023  42241  37916  24319  52207  42934
```

Figure 28c Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 32 (Sheet 1 of 4)

603	82.009	57343	49087	52431	41727	38620	24766	51640	41551
1	33.315	19113	33189	27041	30923	14952	45929	22429	10839
3	57.815	53338	22094	33516	10064	29792	22521	49197	41923
4	58.534	24631	17167	28929	13546	26173	20267	50486	57250
19	66.134	17512	12985	48001	36632	50080	47517	30034	11953
53	67.505	26855	15021	42121	24550	60859	48240	23404	8319
98	67.536	46526	24029	53244	28591	47609	31139	48090	38531
143	69.091	42138	29308	55742	51327	36511	34404	42630	20819
178	70.582	34638	16966	47035	50537	57743	55265	41968	22803
193	74.602	33945	17151	57855	49408	40893	27941	40555	22889
209	77.564	40096	26715	54968	60381	61909	57040	42928	30678
353	77.973	32443	15330	55869	49151	55359	44933	38911	23211
365	79.166	31587	15612	63671	61056	52418	46843	40951	26495
421	80.758	32399	15490	61438	57513	59134	49151	44275	30671
447	81.423	32407	15384	61885	57344	57553	49151	44275	29728
548	81.719	32408	15366	63487	61014	57343	49247	40970	25599
1	40.291	30168	6779	51811	19459	19523	32435	24028	29811
3	50.279	32476	12491	22918	26284	28170	25592	21675	17647
5	51.981	12251	31276	39251	21576	52634	51754	28287	33397
8	52.012	45252	29174	21759	28514	26961	32342	32187	26048
20	57.998	38195	21410	53430	31944	33290	29350	18115	18888
29	60.843	55359	53767	11189	18757	33204	17871	33423	25827
88	63.216	51008	38460	25088	26597	40886	24702	35667	34188
96	66.903	28974	13653	51873	37704	34915	19805	31999	26147
140	66.985	52225	49086	27023	30717	32790	18495	55103	43422
146	70.623	53299	38661	32832	24459	41471	25343	60479	44960
198	71.633	52479	40608	33727	24719	42492	18895	56287	45587
199	73.924	49865	34561	32095	16391	41987	25327	57453	44964
254	76.921	53249	41055	33563	16439	41987	25357	57261	47635
296	77.115	54587	39420	40326	24000	41987	24927	56109	47607
305	77.796	53201	40650	39999	24064	41831	24271	55473	45599
312	78.368	51981	41087	40351	24062	41979	24316	55295	45119
353	78.485	53250	40951	40764	23985	41984	29919	55391	47488
355	78.725	53359	41303	40515	23999	42335	30172	55244	47519
386	78.765	51969	40578	39932	24049	42343	24383	55374	47487
403	79.186	54417	48247	39931	24051	42343	29919	57119	47488
435	79.266	54415	48250	40447	23795	42496	30195	55281	47615
457	79.274	54637	45498	40575	24177	42496	24883	57132	47599
465	79.484	54526	47173	40195	24000	42343	29935	57152	47663
476	80.042	54591	45253	40966	24255	42344	29935	55314	47615
486	80.354	54639	45253	40194	24255	42495	29916	55295	47799
498	80.546	54589	45567	40194	24191	42495	29916	55314	47431
553	80.605	54529	45509	40192	24205	42643	29887	55295	47432
598	80.764	54642	45567	40067	24383	42647	29884	55295	47607
1	45.172	33200	18813	24161	6269	24529	34132	9872	28466
2	56.217	47919	54023	21818	5944	32246	36291	50176	27749
17	59.736	54506	38018	30417	15775	40936	22540	23725	34495
19	65.318	51500	22938	26853	16915	53848	39043	48148	38470
22	66.196	61279	55171	31414	35058	50877	24002	48312	33103
34	68.463	52459	43583	34418	17748	30994	24575	50736	55987
73	75.954	48638	38031	32101	15934	40097	24387	54049	42376
118	76.579	57439	46884	33151	16367	45162	28284	53551	41380
166	77.568	59194	53683	30760	15362	48516	33303	48135	40671
223	78.223	61532	55054	32369	16268	46053	36803	53991	41343
231	78.681	60441	54235	31238	14207	47114	37191	53729	41191
259	78.735	59364	59315	32160	15810	54378	40963	51677	38948
263	78.965	60442	56484	30047	15756	49015	33212	51485	41743
323	79.146	57849	54059	30582	10236	53095	44483	52255	41751
326	79.310	57375	54047	33654	16463	48274	36607	51498	41940
337	79.435	59390	53268	42889	22479	54362	40959	53301	40867
350	80.924	59040	53017	33193	15362	52232	44540	52191	40731
423	82.651	61567	57360	32672	16303	53359	44543	52255	44099
470	83.225	61951	58127	32886	16447	54275	44732	52223	43991

Figure 28c Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 32 (Sheet 2 of 4)

520	83.348	63615	59628	41920	22925	53481	44287	54005	44031
597	83.442	63460	59346	42015	23154	54047	44799	53215	44095
602	83.603	63015	60602	41887	22530	54340	44731	52277	42004
607	83.780	63615	61663	42068	22335	54043	44551	52223	40956

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	43.088	43.088	10.370	55.720	4.775	0.000	32.000
2	45.995	48.902	9.180	59.700	3.762	0.000	32.000
3	47.744	51.244	8.421	61.251	4.167	0.000	32.000
4	49.303	53.980	8.707	63.533	2.379	0.000	32.000
5	51.402	59.797	6.852	67.871	2.424	0.000	32.000
6	53.360	63.152	6.693	70.733	1.762	0.000	32.000
7	55.112	65.623	5.387	73.073	2.385	0.000	32.000
8	56.756	68.205	5.084	74.597	2.408	0.000	32.000
9	58.225	70.431	4.693	75.999	1.635	0.000	32.000
10	59.665	72.364	4.100	77.005	1.288	0.000	32.000
11	60.914	73.212	4.018	77.711	1.093	0.000	32.000
12	62.052	74.568	3.256	78.503	1.071	0.000	32.000
13	63.055	76.092	3.086	78.597	0.868	0.000	32.000
14	64.062	77.153	2.769	80.313	0.957	0.000	32.000
15	64.948	77.349	2.402	80.178	1.064	0.000	32.000
16	65.702	77.981	2.331	80.717	0.677	0.000	32.000
17	66.517	78.562	2.021	80.959	0.749	0.000	32.000
18	67.222	79.206	2.003	81.375	0.569	0.000	32.000
19	67.853	79.223	1.917	81.551	0.594	0.000	32.000
20	68.423	79.258	1.883	81.643	0.569	0.000	32.000

MAXIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	47.094	47.094	11.159	58.818	5.565	0	32
2	47.856	52.089	10.030	64.100	4.565	0	32
3	50.415	55.533	9.732	66.162	5.003	0	32
4	52.078	57.770	12.128	70.196	3.239	0	32
5	54.736	65.370	7.586	73.062	3.880	0	32
6	56.903	67.734	8.715	74.944	2.560	0	32
7	58.664	70.071	10.608	76.323	3.874	0	32
8	60.064	71.759	6.131	77.639	3.283	0	32
9	61.404	75.104	6.376	80.000	2.656	0	32
10	62.705	77.217	6.119	81.426	2.085	0	32
11	63.963	76.538	5.425	81.982	1.369	0	32
12	65.227	79.126	4.893	82.874	1.560	0	32
13	66.302	79.201	4.713	82.132	1.337	0	32
14	67.331	80.706	3.841	83.712	1.562	0	32
15	68.171	79.936	2.897	83.134	1.324	0	32
16	68.965	80.882	3.020	83.631	0.884	0	32
17	69.655	80.684	2.835	83.822	1.267	0	32
18	70.321	81.642	2.855	84.616	1.131	0	32
19	70.929	81.868	2.618	84.490	1.091	0	32
20	71.429	82.150	2.975	84.520	0.946	0	32

MINIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	40.660	40.660	9.670	53.215	3.250	0	32
2	43.416	45.665	8.217	53.337	2.880	0	32
3	44.779	47.505	5.626	58.266	2.514	0	32
4	46.289	50.118	7.297	59.489	1.719	0	32
5	48.929	55.045	6.277	62.698	1.749	0	32
6	50.491	57.994	4.146	67.269	0.532	0	32
7	52.341	59.011	4.449	71.430	1.414	0	32
8	54.132	64.264	3.507	72.047	1.711	0	32
9	55.808	64.922	2.583	71.448	0.880	0	32
10	56.930	66.080	2.700	73.054	0.565	0	32

Figure 28c Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 32 (Sheet 3 of 4)

11	58.070	69.478	2.376	74.733	0.911	0	32
12	59.242	72.102	1.674	77.227	0.669	0	32
13	60.169	71.293	1.356	76.215	0.388	0	32
14	61.183	74.359	1.504	78.664	0.333	0	32
15	62.154	75.750	1.343	78.845	0.413	0	32
16	62.972	75.234	1.106	78.780	0.400	0	32
17	63.756	76.305	0.889	79.232	0.381	0	32
18	64.475	76.697	0.871	79.448	0.181	0	32
19	65.079	75.957	0.934	79.284	0.247	0	32
20	65.627	76.043	0.831	79.978	0.098	0	32

Figure 28c Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 32 (Sheet 4 of 4)

```
        30029
MS1A 6/26/73
NOVLP           3
NVALU           2
PINV        0.0000
PTRA        0.0000
PCROS       0.5000
PCROL       0.5000
PMUT        0.0000
CV          0.0000
NPOP            32
NSEL             8
LGEN            29
NPAR             8
NSEG             8
NREP             5
IX               1
IPAP             0
IPBP             1
IPAF             0
IPCS             0
        30030
     1  41.606  58976  25258  11077  49266  39450  22494  34951  25403
     2  47.945  28104  20586  32387  48630  20589  18130  30506  21491
     3  50.046  21952  34525  51038  52512  25394  30198  24330  11162
     5  52.362  47053  38976  21429  26844  24417  32671  26971  14206
     6  62.901  38445  26951  18120  25380  49353  48225  60994  49458
    27  64.163  29092  30010  55414  53587  47350  48246  31374  18334
    43  68.162  42477  28139  31769  33150  56855  49600  21966   8649
    54  71.535  32742  16668  51236  51918  55835  47008  24655  12587
    72  74.405  32663  16961  59415  56861  53786  48917  24588  12830
   164  74.873  32556  26879  53247  59647  57670  49151  55695  46709
   168  77.206  36376  36376  63807  57295  52413  46831  55026  47012
   200  78.870  36752  23443  57623  49263  57091  48367  49086  46713
   233  79.403  33645  16319  59378  49201  57595  46079  55070  49151
   240  84.785  36223  19451  63883  59676  56837  48390  57150  48761
   428  85.233  32772  16583  61439  59648  59391  53247  55136  46759
   480  85.369  32016  16447  61439  59679  60415  55529  57342  48818
   560  85.629  32760  16384  63495  59789  59073  53247  55039  46767
     1  38.726  31741  29120   1403  36938  55908  22438  22450   6464
     3  43.135  47263  25113   2750  21257  17706  28854  20769  13399
     4  43.547  17931  31034  37977  50492  42263  23201  16948  21982
    10  50.836  51773  31453  31411  27905  34391  19374  50036   5272
    21  55.425  52005  50622   7073  25982  47818  33681  22252  22332
    22  57.678  26067  24934  34401  12327  37818  37638  48080  45199
    27  63.132  52669  38935  53366  26586  25414  18336  36189  22763
    43  64.301  50039  34259  22498  35015  31421  19300  57991  50281
    86  64.575  47961  35607  32735  16791  24707  24323  37364  17454
   129  69.512  48779  38911  48957  58517  32445  18432  45156  32904
   164  72.480  57983  44274  33945  21656  37628  24837  46280  32636
   202  72.540  49716  36915  55489  61929  33224  27074  46944  33712
   213  76.501  53314  40146  59383  46846  37664  19507  48320  34600
   216  78.392  49167  34816  56326  53760  37899  24323  49137  36686
   245  78.417  49103  34816  55281  52053  49138  37843  49697  32085
   260  78.970  48144  32831  60609  55061  37682  17541  51214  40783
   371  78.990  50116  47564  57345  49408  37902  24786  51592  40783
   385  79.713  56324  48063  53255  41449  37651  25643  49141  39376
   420  80.152  57343  47116  53255  42241  37600  24786  52153  40522
   475  80.181  56324  48127  51208  41493  37855  18477  51493  39936
   477  80.563  56324  48063  50368  42241  38639  25363  52113  42927
   499  81.066  57343  49074  52431  42239  37864  25601  51664  42927
   552  81.672  56324  48140  52023  42241  37916  24319  52207  42934
```

Figure 28d Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 64 (Sheet 1 of 3)

208	73.813	35199	15090	55134	57772	49151	41015	48505	38179
269	75.302	35839	15438	57718	55735	47047	40089	54207	40974
300	76.312	33163	8130	61342	57158	48987	39159	53999	51206
353	76.550	35059	14900	57744	54143	51328	33271	53322	44035
355	79.801	40307	33445	59401	57491	53251	40296	53438	42782
396	82.589	45251	31627	59005	53352	46233	37185	53598	43149
576	83.100	45633	32639	60428	55404	50059	35376	54089	42801
787	83.306	45823	31997	59914	53247	48143	34067	53792	45879
800	84.440	45766	31777	58303	53575	52200	41173	53739	42993
816	84.926	45824	34503	58395	54298	55440	46743	53246	42847
1044	85.553	47155	32762	58942	53226	56162	45527	55348	47388
1	49.928	33731	34169	33876	15224	26257	26081	22787	28334
3	50.834	35623	22555	35096	42242	14599	12898	26962	2279
6	55.283	25934	17619	33533	28061	29883	31670	46547	24571
27	64.015	54453	38528	46266	13968	53647	58931	37821	23597
86	70.829	44841	32541	35986	27000	48113	37662	33541	20330
153	72.395	38589	25038	43261	37610	52845	49561	40747	26114
243	73.882	43936	34017	38701	22591	54242	42905	36278	23540
262	77.642	25107	13066	45075	32473	58479	52527	54285	49090
539	77.881	41023	26111	42971	33032	57119	49038	52128	49183
698	79.467	42931	28044	42031	26438	57858	49052	48368	37438
840	79.504	45055	33692	42799	26877	54057	44945	49175	36469
843	79.764	46323	33248	43455	27078	53556	44155	48522	37269
866	79.829	46592	33055	42815	32216	58363	49151	53226	40908
998	80.368	46779	32912	43275	32366	58092	50995	54249	40830
1021	80.689	46523	33279	43799	26431	58659	51091	49374	37305
1039	80.927	46079	33021	42042	26575	58087	51133	51069	37372
1101	80.999	46079	33280	42975	26408	60126	55381	48127	37441
1126	81.152	46147	33135	43956	32446	58346	51005	53238	40959
1204	82.085	47872	37475	42981	26633	61160	57201	49188	37443
1235	82.137	46007	32991	43986	33071	61142	57235	49129	37370
1258	82.260	49083	37903	43002	27392	59710	55298	50427	37446
1	44.458	21285	31651	35793	30942	9977	22015	59483	36111
4	49.631	37234	25648	25556	21046	18286	20449	22792	27691
7	58.927	58291	29940	52733	24788	57890	29872	61505	55377
8	66.463	55094	37278	49085	53617	40994	24702	25161	7879
129	67.289	35831	14924	39812	22591	59156	49116	59928	35001
147	67.609	58336	54272	46121	34261	52295	38051	59864	21595
169	74.140	56423	32845	39645	29227	57647	49904	55996	55062
202	74.251	57960	49660	33279	13437	50079	27853	52773	41998
361	77.007	61391	49229	32342	13977	58159	47100	59883	49652
394	78.232	58384	52955	19659	4672	48332	33315	56076	47396
409	79.301	57387	49189	39019	24674	53355	52676	56714	57617
630	80.382	49280	36599	40640	26785	51425	45503	56642	48123
757	80.516	46345	32775	39222	26880	55359	46631	60167	50653
794	81.122	46294	36656	40959	24207	53420	42701	59638	55115
848	81.287	46338	33560	40833	26717	52833	45057	58562	51221
855	82.191	46336	32767	40905	26993	53408	42544	59615	55855
901	83.702	46335	32751	40831	26878	55252	48127	61692	58276
1194	83.918	46372	32791	40450	24451	55319	47135	61427	57333

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	42.536	42.536	10.667	55.382	5.099	0.000	64.000
2	45.379	48.222	9.736	60.004	4.038	0.000	64.000
3	47.688	52.307	8.835	63.021	3.531	0.000	64.000
4	49.744	55.912	7.951	65.272	3.204	0.000	64.000
5	51.529	58.668	7.980	68.393	2.989	0.000	64.000
6	53.200	61.556	6.894	70.050	2.538	0.000	64.000
7	54.784	64.288	6.933	72.371	2.400	0.000	64.000
8	56.294	66.860	5.661	73.571	1.931	0.000	64.000
9	57.841	70.224	4.984	76.302	1.986	0.000	64.000
10	59.225	71.679	4.230	76.750	1.707	0.000	64.000

Figure 28d Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 64 (Sheet 2 of 3)

11	60.507	73.323	4.020	78.053	1.316	0.000	64.000
12	61.669	74.458	4.221	79.156	1.277	0.000	64.000
13	62.777	76.072	3.807	80.352	1.100	0.000	64.000
14	63.791	76.975	3.137	80.745	1.215	0.000	64.000
15	64.744	78.075	3.227	81.661	1.062	0.000	64.000
16	65.601	78.457	3.109	82.118	1.055	0.000	64.000
17	66.374	78.746	3.151	82.415	0.950	0.000	64.000
18	67.105	79.532	2.573	82.574	0.804	0.000	64.000
19	67.778	79.898	2.766	83.088	0.948	0.000	64.000
20	68.415	80.511	2.502	83.422	0.674	0.000	64.000

MAXIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	43.695	43.695	11.959	56.793	6.432	0	64
2	46.371	49.422	10.265	60.576	5.322	0	64
3	48.665	53.359	9.361	64.391	4.218	0	64
4	51.061	58.416	9.008	68.651	3.513	0	64
5	53.286	62.182	9.629	72.321	4.080	0	64
6	55.574	67.015	8.691	74.200	3.938	0	64
7	57.744	70.766	9.063	77.051	2.818	0	64
8	59.627	72.805	6.270	77.585	2.913	0	64
9	61.223	73.996	6.919	78.960	2.091	0	64
10	62.620	75.193	4.735	79.686	2.697	0	64
11	63.819	75.809	4.965	80.956	1.691	0	64
12	64.872	76.753	6.965	81.275	2.145	0	64
13	65.893	78.138	4.941	82.643	1.655	0	64
14	66.781	78.334	4.142	82.792	1.718	0	64
15	67.634	79.572	4.558	83.505	1.965	0	64
16	68.340	79.348	4.139	83.731	1.951	0	64
17	68.967	79.773	4.492	83.535	1.513	0	64
18	69.539	81.319	3.945	83.781	1.105	0	64
19	70.092	81.455	3.792	84.600	1.663	0	64
20	70.622	82.532	3.164	85.338	0.805	0	64

MINIMUM VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	TR
1	40.315	40.315	9.695	52.788	4.497	0	64
2	43.454	46.593	9.354	59.181	2.707	0	64
3	46.178	50.112	8.487	60.753	1.986	0	64
4	48.226	53.784	6.583	62.990	2.789	0	64
5	50.267	55.273	6.458	65.005	2.478	0	64
6	51.412	57.136	5.477	67.629	1.464	0	64
7	52.692	60.376	5.576	69.841	2.050	0	64
8	54.071	63.725	3.974	71.272	1.498	0	64
9	55.576	67.392	4.095	73.413	1.814	0	64
10	56.953	69.346	3.462	74.553	1.206	0	64
11	58.153	70.159	3.418	75.890	1.102	0	64
12	59.195	70.650	2.973	77.355	0.914	0	64
13	60.368	74.143	2.697	77.493	0.644	0	64
14	61.381	74.537	2.164	78.426	0.812	0	64
15	62.410	76.356	2.122	78.811	0.604	0	64
16	63.429	76.577	1.905	78.863	0.521	0	64
17	64.309	77.373	1.918	79.873	0.631	0	64
18	65.254	77.186	1.619	79.701	0.678	0	64
19	66.106	78.157	1.726	80.419	0.565	0	64
20	66.928	78.285	1.682	80.864	0.556	0	64

Figure 28d Parameter values of individuals with increasing phenotypic values during five replications of mass selection for 8-parameter Ridge using Gene Action 3 and population size 64 (Sheet 3 of 3)

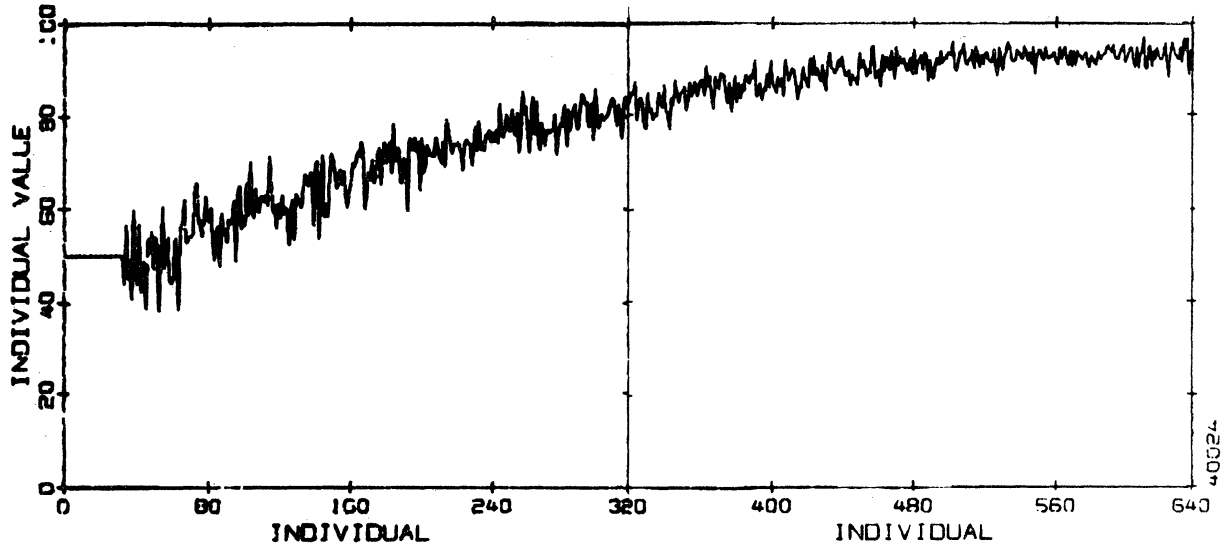


Figure 29a Phenotypic value of individuals during simple recurrent selection for 8-parameter Plane using Gene Action 4

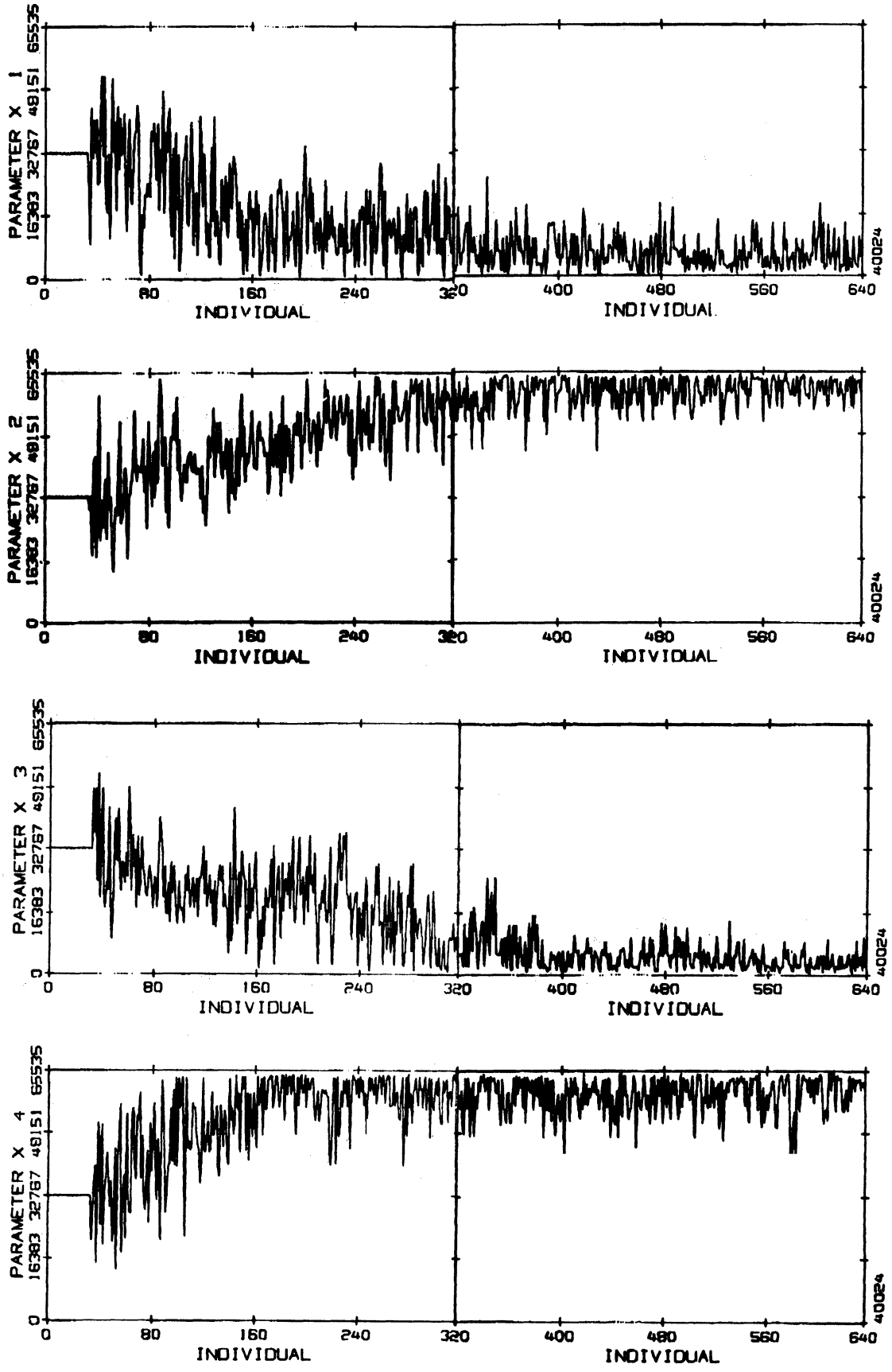


Figure 29b Parameter values of individuals during simple recurrent selection for 8-parameter Plane using Gene Action 4 (Sheet 1 of 2)

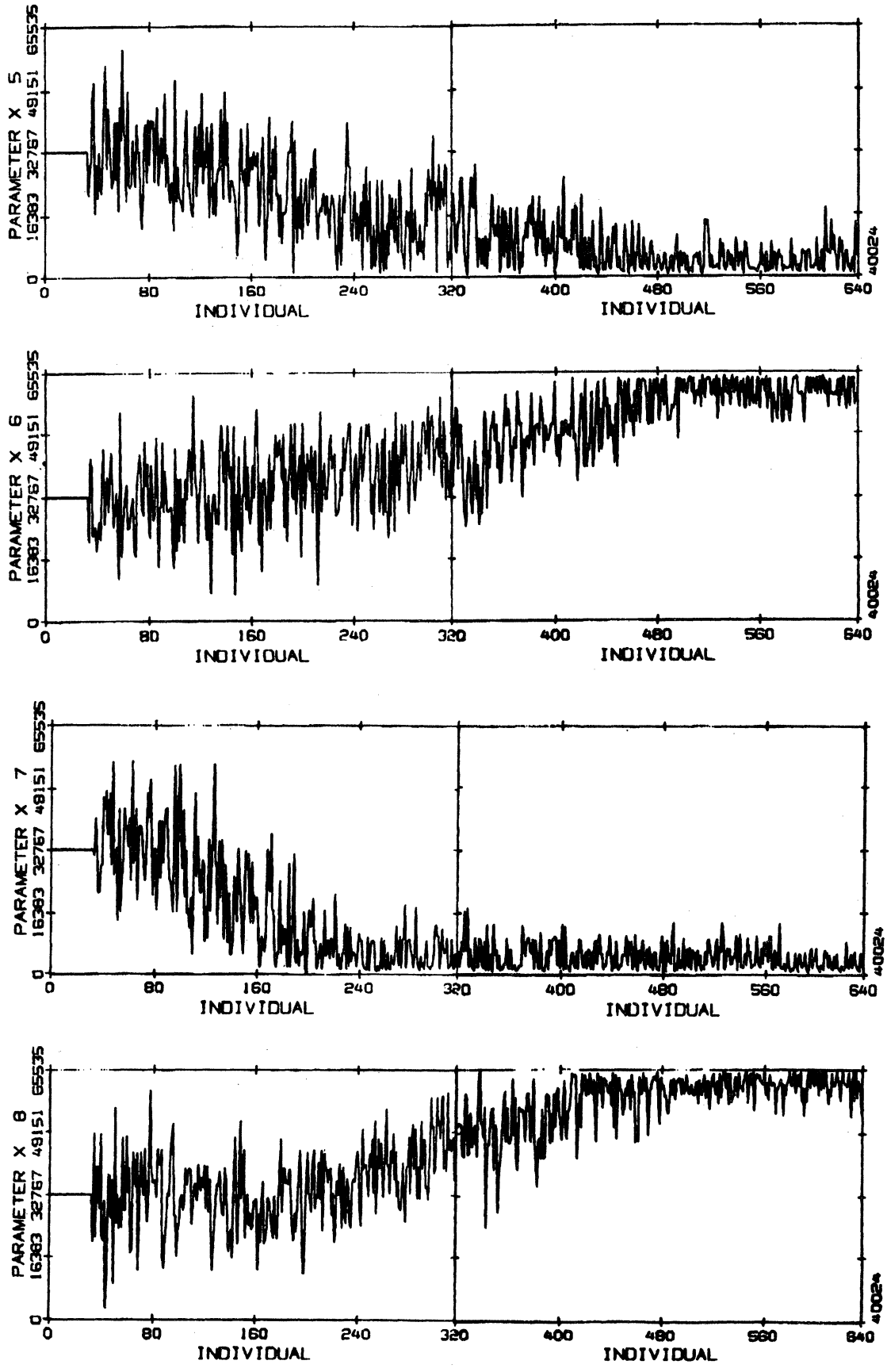


Figure 29b Parameter values of individuals during simple recurrent selection for 8-parameter Plane using Gene Action 4 (Sheet 2 of 2)

```
        40024
SRS1A 7/4/73
NDVLP           4
NVALU           1
PINV        0.0000
PTRA        0.0000
PCROS       0.5000
PCROL       0.5000
PMUT        0.0000
CV          0.0000
NPOP            32
NSEL             8
LCYC            20
NPAR             8
NSEG            32
NREP             1
IX               1
IPAP             1
IPBP             0
IPAF             0
IPCS             0
```

STOP

1	50,000	32766	32766	32766	32766	32766	32766	32766	32766
2	50,000	32766	32766	32766	32766	32766	32766	32766	32766
3	50,000	32766	32766	32766	32766	32766	32766	32766	32766
4	50,000	32766	32766	32766	32766	32766	32766	32766	
5	50,000	32766	32766	32766	32766	32766			64642
6	50,000	32766	32766	32766	32766			5306	62330
7	50,000	32766	32766	32766			55442	1840	53350
8	50,000	32766			60374	2328	59834	2826	60756
9	50,000			2328	63254	3256	63854	5900	65154
10			55566	4958	62804	1034	56130	2680	57414
	60,033	3008	63486	2964	63240	3258	63614	2096	64948
636	94,127	2738	59888	5238	63512	4934	63796	1208	58270
637	96,677	2020	62994	1384	60626	804	63778	1030	62556
638	88,664	10702	62752	10360	62340	14316	56686	5560	61866
639	94,011	5166	63276	2424	62796	5690	59402	2316	60864
640	90,212	9246	59888	5382	60824	6860	59252	1782	54130

AVERAGE VALUES

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50,000	50,000	0,000	50,000	0,000	0,000	32,000
2	49,491	48,983	6,034	56,483	2,401	0,000	32,000
3	51,858	56,592	4,260	62,227	2,088	0,000	32,000
4	54,055	60,646	4,081	65,732	3,106	0,000	32,000
5	56,155	64,554	4,377	69,564	1,579	0,000	32,000
6	58,348	69,314	4,107	73,841	1,969	0,000	32,000
7	60,383	72,592	2,961	75,671	1,634	0,000	32,000
8	62,314	75,835	2,989	79,618	2,081	0,000	32,000
9	64,096	78,350	3,632	82,987	1,482	0,000	32,000
10	65,783	80,967	2,832	84,267	0,937	0,000	32,000
11	67,308	82,561	2,951	86,033	1,141	0,000	32,000
12	68,858	85,893	2,472	88,861	0,907	0,000	32,000
13	70,288	87,457	2,474	90,678	1,284	0,000	32,000
14	71,659	89,479	2,102	92,212	1,045	0,000	32,000
15	72,963	91,212	2,259	94,065	0,776	0,000	32,000
16	74,148	91,933	2,012	94,245	0,974	0,000	32,000
17	75,242	92,740	1,726	94,747	0,500	0,000	32,000
18	76,219	92,831	1,398	94,464	0,363	0,000	32,000
19	77,103	93,013	1,499	94,850	0,333	0,000	32,000
20	77,906	93,169	2,232	95,769	0,832	0,000	32,000

Figure 29c Input data, parameter values and generation statistics during simple recurrent selection for 8-parameter Plane using Gene Action 4

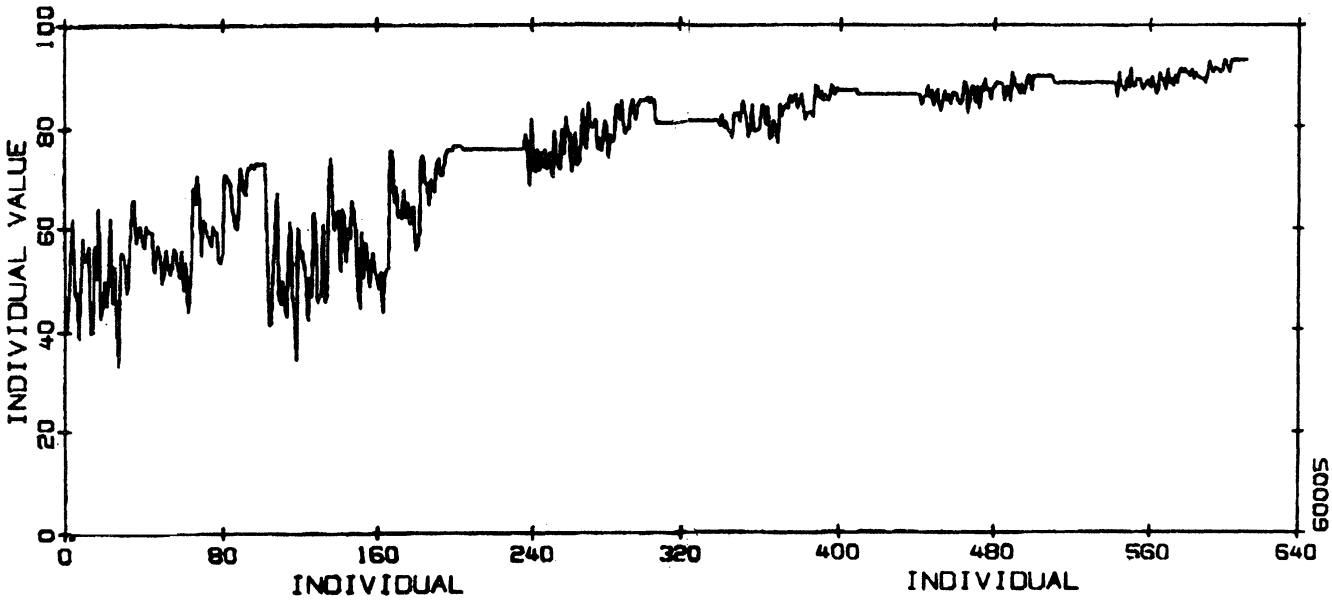


Figure 30a Phenotypic value of individuals during extended pedigree breeding for 8-parameter Plane using Gene Action 4

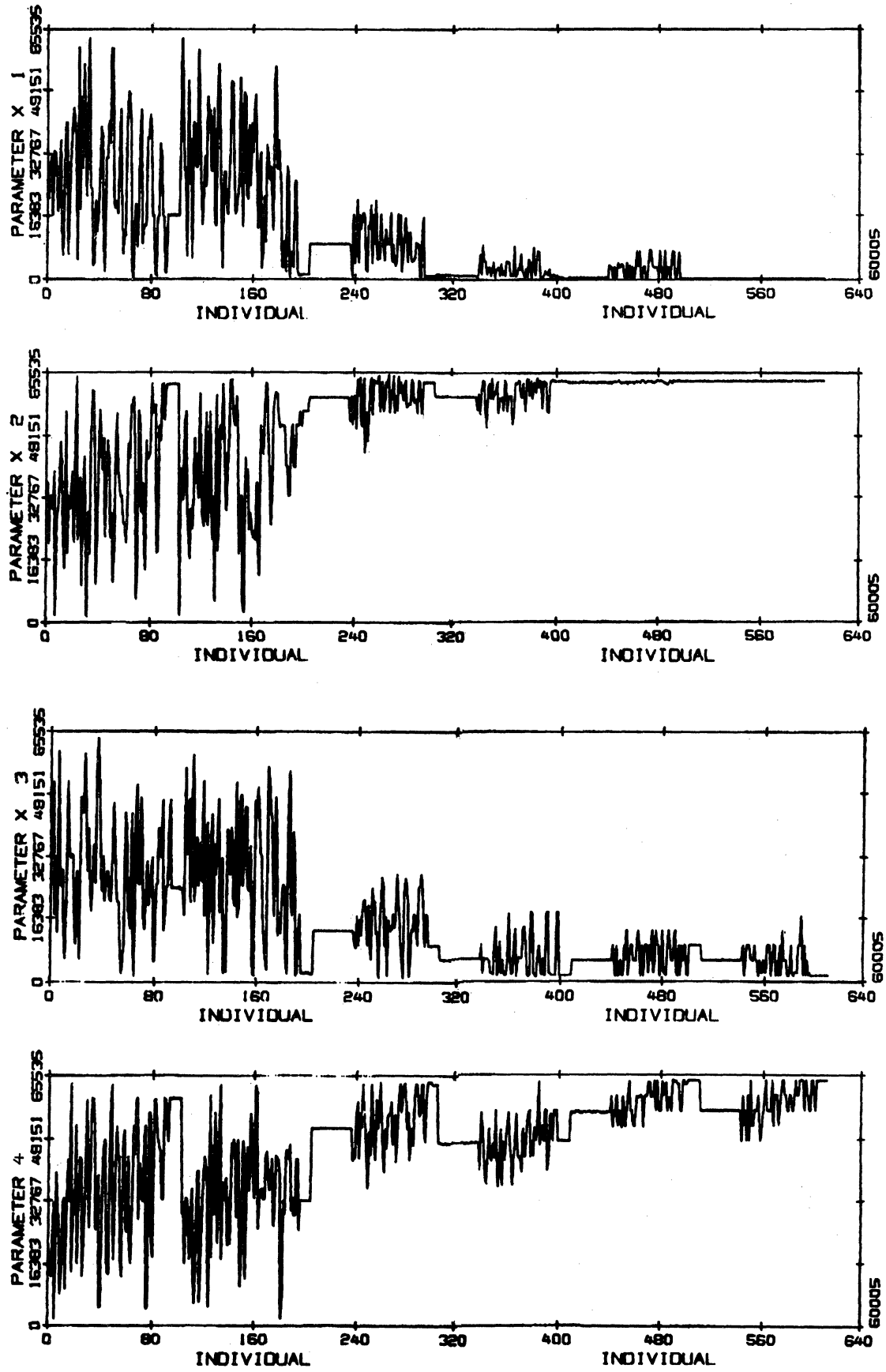


Figure 30b Parameter values of individuals during extended pedigree breeding for 8-parameter Plane using Gene Action 4 (Sheet 1 of 2)

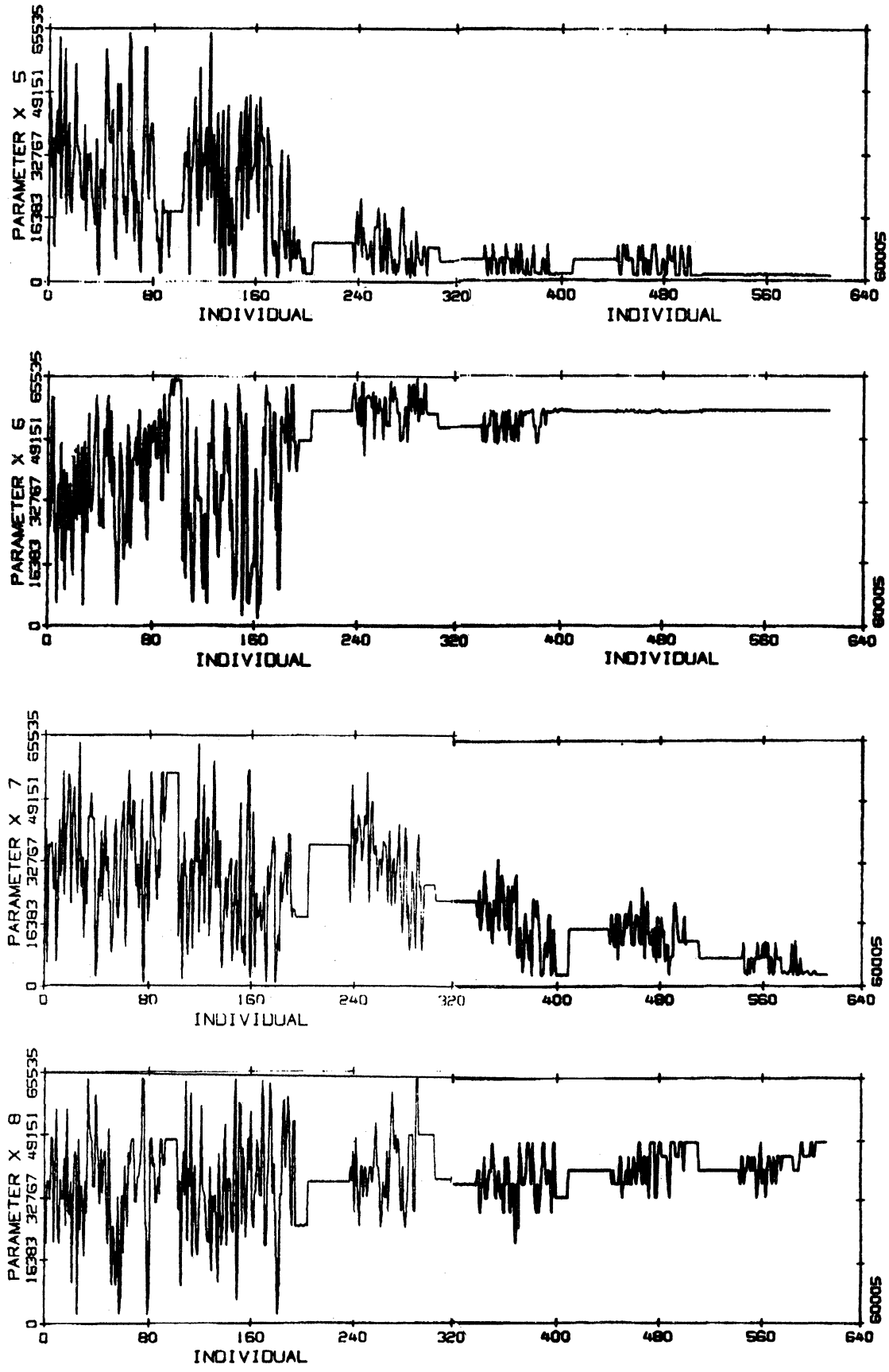


Figure 30b Parameter values of individuals during extended pedigree breeding for 8-parameter Plane using Gene Action 4 (Sheet 2 of 2)

```
        60005
PM2 7/9/73
NDVLP          4
NVALU          1
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP           32    32    16     8     4     2     2     2     2     2
NSEL           16    16     8     4     2     1     1     1     1     1
LGEN           10
NPAR            8
NSEG           32
NVAR            6
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
        STOP
     1  39.958  21262  36816  44348  17360  47416  26316  41136  21020
     2  46.610  29138  20522  52146  13310  29516  28790   6384  36888
     3  55.195  32302  33022  17330  21040  37086  60190  37096  36800
     4  61.984  16686  33408  32736  32196   9200  60122  36590  32316
     5  47.010  33498  29658  12666   1790  36558  24846  37626  48380
     6  47.461  33002  39920  60138  40460  44468  28942  39[illegible]
     7  38.946  29300   2002  28910  29406  33214  [illegible]
     8  48.164  17628  28206  25056  28524  [illegible]  3730  44848
     9  57.799  21454  29434  29[illegible]  [illegible]  56338  3250  44850
    10  53.301  36130  [illegible]  [illegible]  1654  56338  3250  44850
    11  53.812  [illegible]  [illegible]  60214  1174  56336  3970  44850
    12          [illegible]  63410  2286  60184  1174  56336  3970  44850
                  162  63410  1556  56344  1654  56338  10930  44850
        90.832    162  63396  2284  56344  1414  56352  3010  44850
    75  90.011    162  63396  2268  60198  1174  56338  7570  41010
    76  89.924    132  63408  2284  64038  1414  56338  11650  41012
    77  89.508    132  63426  9250  60184  1414  56320  3010  41010
    78  89.512    132  63426  9250  60184  1414  56338  3010  41012
    79  88.730    162  63396  16930  64054  1174  56352  3490  41010
    80  90.192    162  63396  9252  64054  1174  56338  7330  44848
    81  93.130    132  63426  1556  64024  1174  56336  3490  48688
    82  91.662    132  63426  9252  64024  1414  56336  3250  48688
    83  90.873    162  63396  1572  56374  1174  56308  3730  44848
    84  91.559    162  63396  5412  64054  1414  56308  3730  44848
    85  91.566    146  63396  1554  60184  1174  56336  3970  44850
    86  91.432    162  63426  2270  60184  1174  56338  3970  44850
    87  90.930    132  63396  1542  56344  1414  56338  3250  44850
    88  90.976    132  63396  1542  56344  1414  56338  3010  44850
    89  93.219    132  63426  1572  64024  1174  56336  3010  48688
    90  93.130    132  63426  1556  64024  1174  56336  3490  48688
    91  91.563    146  63396  1570  60184  1174  56336  3970  44850
    92  90.834    146  63396  1554  56344  1174  56336  3970  44850
    93  93.219    132  63426  1572  64024  1174  56336  3010  48688
    94  93.219    132  63426  1572  64024  1174  56336  3010  48688
    95  93.219    132  63426  1572  64024  1174  56336  3010  48688
    96  93.219    132  63426  1572  64024  1174  56336  3010  48688
    97  93.219    132  63426  1572  64024  1174  56336  3010  48688
```

Figure 30c Input data, initial and final parameter values, and generation statistics for six varieties in extended pedigree breeding for 8-parameter Plane using Gene Action 4 (Sheet 1 of 3)

98	93.219	132	63426	1572	64024	1174	56336	3010	48688
99	93.219	132	63425	1572	64024	1174	56336	3010	48688
100	93.219	132	63425	1572	64024	1174	56336	3010	48688
101	93.219	132	63426	1572	64024	1174	56336	3010	48688
102	93.219	132	63426	1572	64024	1174	56336	3010	48688

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	49.425	49.425	7.366	55.303	4.388	0	32
2	52.176	54.926	4.991	56.687	4.497	0	32
3	53.717	59.881	5.307	61.672	5.211	0	16
4	54.809	65.729	4.793	66.096	4.970	0	8
5	55.437	69.272	2.526	69.807	3.232	0	4
6	55.793	72.145	0.065	72.191	0.000	0	2
7	56.142	72.535	0.552	72.926	0.000	0	2
8	56.484	72.924	0.002	72.926	0.000	0	2
9	56.813	72.903	0.101	72.974	0.000	0	2
10	57.129	72.929	0.000	72.929	0.000	0	2

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.374	50.374	7.518	56.453	5.196	0	32
2	53.214	56.055	7.187	58.868	6.522	0	32
3	55.387	64.076	5.653	65.853	4.784	0	16
4	56.683	69.646	3.220	70.611	2.675	0	8
5	57.350	72.026	1.650	72.280	2.201	0	4
6	57.705	74.048	1.279	74.952	0.000	0	2
7	58.079	75.662	0.032	75.685	0.000	0	2
8	58.446	76.052	0.520	76.420	0.000	0	2
9	58.805	76.397	0.097	76.466	0.000	0	2
10	59.152	76.489	0.032	76.512	0.000	0	2

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	75.811	75.811	0.000	75.811	0.000	0	32
2	75.568	75.324	3.775	77.621	3.351	0	32
3	76.217	78.815	2.766	80.173	2.469	0	16
4	76.732	81.877	2.503	82.575	2.688	0	8
5	77.034	83.686	1.589	84.557	1.248	0	4
6	77.206	85.102	0.494	85.452	0.000	0	2
7	77.378	85.476	0.035	85.501	0.000	0	2
8	77.543	85.447	0.076	85.501	0.000	0	2
9	77.699	85.371	0.033	85.394	0.000	0	2
10	77.850	85.371	0.033	85.394	0.000	0	2

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	80.956	80.956	0.023	80.977	0.000	0	32
2	80.857	80.758	2.383	82.162	2.147	0	32
3	81.471	83.928	1.602	84.732	1.539	0	16
4	81.899	86.181	1.241	86.505	1.182	0	8
5	82.139	87.421	0.843	87.805	0.272	0	4
6	82.247	87.215	0.067	87.262	0.000	0	2
7	82.351	87.216	0.000	87.216	0.000	0	2
8	82.450	87.193	0.032	87.216	0.000	0	2
9	82.545	87.239	0.032	87.262	0.000	0	2
10	82.638	87.262	0.000	87.262	0.000	0	2

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	86.326	86.326	0.023	86.346	0.016	0	32
2	86.080	85.835	1.622	86.938	1.296	0	32
3	86.370	87.529	1.325	88.202	0.626	0	16
4	86.538	88.215	1.448	88.894	1.294	0	8
5	86.658	89.301	1.454	90.033	0.048	0	4
6	86.730	90.066	0.000	90.066	0.000	0	2
7	86.800	90.066	0.000	90.066	0.000	0	2
8	86.867	90.066	0.000	90.066	0.000	0	2

Figure 30c Input data, initial and final parameter values, and generation statistics for six varieties in extended pedigree breeding for 8-parameter Plane using Gene Action 4 (Sheet 2 of 3)

9	86.930	90.066	0.000	90.066	0.000	0	2
10	86.992	90.066	0.065	90.112	0.000	0	2

VARIETY 6

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	88.687	88.687	0.000	88.687	0.000	0	32
2	88.709	88.732	1.402	89.585	1.265	0	32
3	89.044	90.384	0.843	90.761	0.784	0	16
4	89.269	91.516	0.726	91.808	0.924	0	8
5	89.396	92.186	1.180	92.391	1.171	0	4
6	89.477	93.219	0.000	93.219	0.000	0	2
7	89.555	93.219	0.000	93.219	0.000	0	2
8	89.630	93.219	0.000	93.219	0.000	0	2
9	89.702	93.219	0.000	93.219	0.000	0	2
10	89.771	93.219	0.000	93.219	0.000	0	2

Figure 30c Input data, initial and final parameter values, and generation statistics for six varieties in extended pedigree breeding for 8-parameter Plane using Gene Action 4 (Sheet 3 of 3)

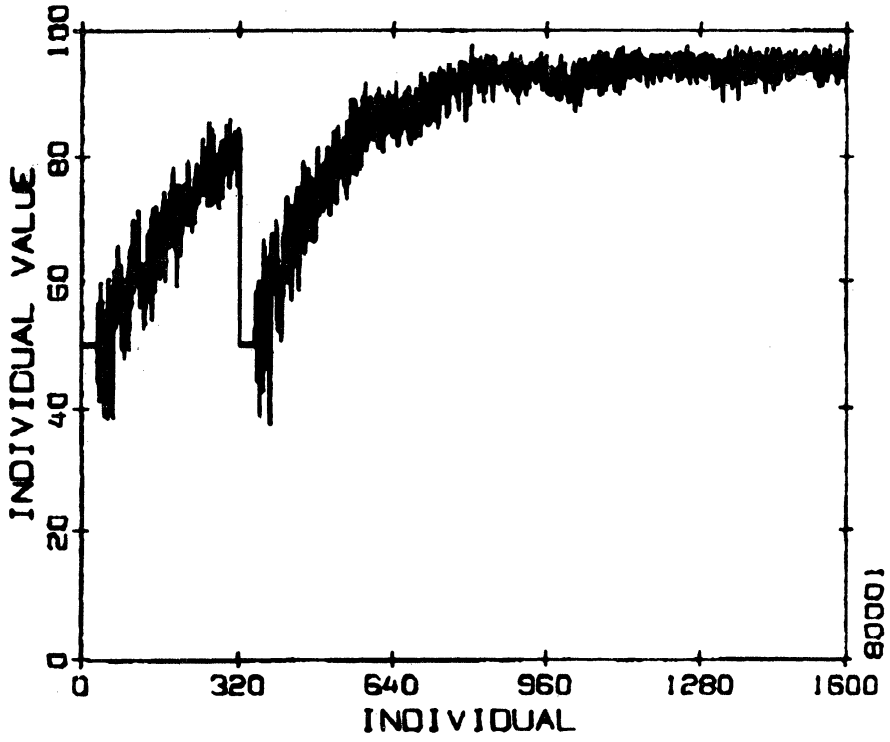


Figure 31a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Plane using Gene Action 4

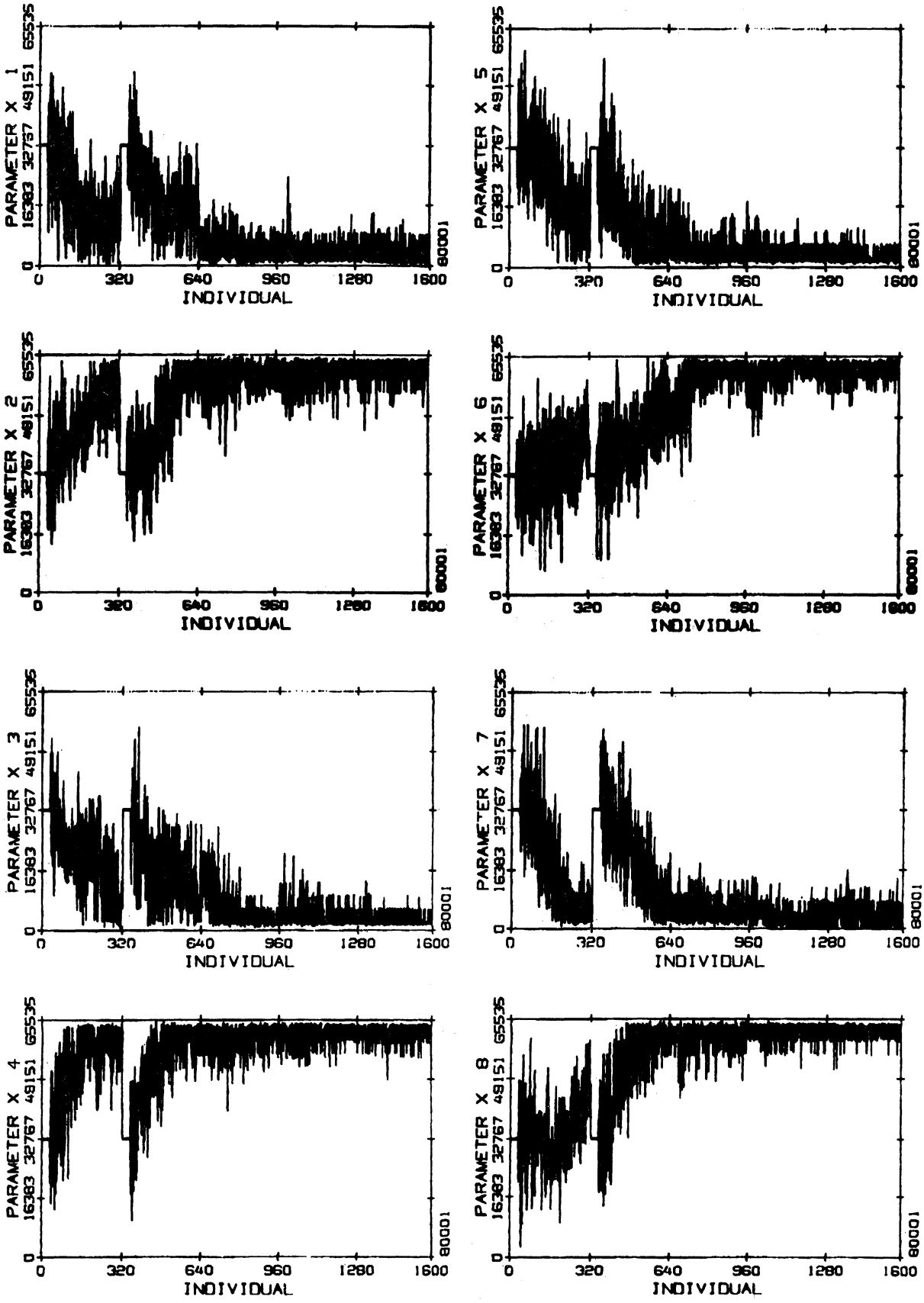


Figure 31b Parameter values of individuals during extended simple recurrent selection for 8-parameter Plane using Gene Action 4

```
        80001
SRS2 7/12/73
NOVLP          4
NVALU          1
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP           32
NSEL            8
LCYC           10
NPAR            8
NSEG           32
NVAR            5
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
```

	STOP								
1	50.000	32766	32766	32766	32766	32766	32766	32766	32766
2	50.000	32766	32766	32766	32766	32766	32766	32766	32766
3	50.000	32766	32766	32766	32766	32766	32766	32766	32766
4	50.000	32766	32766	32766	32766	32766	32766	32766	32766
5	50.000	32766	32766	32766	32766	32766	32766		
6	50.000	32766	32766	32766	32766	32766			63226
7	50.000	32766	32766	32766				7442	63182
8	50.000	32766	32766				924	62776	3348	64048
9	50.000					59408	4720	63016	4572	64016
10					1876	60142	4960	63974	3586	63482
			8320	56306	5900	64236	1794	63332	7186	62956
	92.817	3186	60146	2050	63040	1520	55622	3108	55546
309	92.698	442	56320	1780	59184	5664	63544	6694	59388
310	95.467	4494	60130	5660	53262	1760	64648.	974	63224
311	95.200	4752	64242	5900	62784	1520	59448	506	63180
312	93.480	7236	64212	2286	59184	5810	63914	7172	63152
313	92.736	8560	59166	5630	63980	5586	63704	6946	63930
314	93.385	7012	60594	1794	62784	1840	59448	4586	59866
315	95.502	922	60370	5900	60352	2350	64454	1196	63750
316	93.363	652	59180	1794	60338	6110	64184	6948	59144
317	95.512	8304	64224	1794	60396	2240	63332	492	63486
318	97.527	2722	64448	1836	63010	1404	64408	746	64016
319	94.381	6810	60130	2060	59140	5140	64196	12	63244
320	94.909	8334	63006	5676	64222	1790	63332	3362	64050

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.000	50.000	0.000	50.000	0.000	0	32
2	49.491	48.983	6.034	56.483	2.401	0	32
3	51.858	56.592	4.260	62.227	2.088	0	32
4	54.055	60.646	4.081	65.732	3.106	0	32
5	56.155	64.554	4.377	69.564	1.579	0	32
6	58.348	69.314	4.107	73.841	1.969	0	32
7	60.383	72.592	2.961	75.671	1.634	0	32
8	62.314	75.835	2.989	79.618	2.081	0	32
9	64.096	78.350	3.632	82.987	1.482	0	32
10	65.783	80.967	2.832	84.267	0.937	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.000	50.000	0.000	50.000	0.000	0	32

Figure 31c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Plane using Gene Action 4 (Sheet 1 of 2)

2	50.918	51.836	7.101	60.980	3.882	0	32
3	54.404	61.375	4.692	67.966	1.748	0	32
4	57.521	66.872	4.356	72.165	1.823	0	32
5	60.369	71.764	3.890	76.729	1.726	0	32
6	62.984	76.956	3.124	79.779	1.503	0	32
7	65.376	79.729	3.180	83.667	1.341	0	32
8	67.525	82.569	3.988	87.945	1.554	0	32
9	69.568	85.909	2.580	88.979	1.503	0	32
10	71.300	86.886	2.381	89.563	0.859	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	87.237	87.237	2.641	90.276	1.140	0	32
2	87.140	87.044	2.736	90.626	1.590	0	32
3	87.869	89.325	2.693	92.535	0.891	0	32
4	88.674	91.090	1.972	93.566	1.001	0	32
5	89.220	91.405	2.214	94.166	1.032	0	32
6	89.907	93.341	1.832	95.638	0.992	0	32
7	90.439	93.632	1.635	95.630	0.532	0	32
8	90.773	93.114	1.640	94.902	0.676	0	32
9	91.002	92.832	1.689	94.810	0.776	0	32
10	91.282	93.798	1.269	95.408	0.612	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	91.936	91.936	1.749	94.300	0.836	0	32
2	91.640	91.343	1.843	93.734	0.881	0	32
3	92.115	93.067	1.756	95.105	0.480	0	32
4	92.467	93.522	1.970	96.138	0.618	0	32
5	92.782	94.042	1.795	96.185	0.853	0	32
6	93.094	94.656	1.356	96.311	0.561	0	32
7	93.287	94.446	1.375	95.872	0.225	0	32
8	93.467	94.721	1.237	96.167	0.292	0	32
9	93.594	94.610	1.318	96.172	0.249	0	32
10	93.696	94.615	1.358	96.295	0.577	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	94.390	94.390	1.331	95.944	0.413	0	32
2	93.811	93.233	1.710	95.378	0.870	0	32
3	93.893	94.055	1.825	96.267	0.721	0	32
4	93.972	94.209	1.616	96.174	0.676	0	32
5	94.070	94.463	1.777	96.339	0.609	0	32
6	94.133	94.448	1.486	96.354	0.545	0	32
7	94.201	94.612	1.262	96.293	0.427	0	32
8	94.302	95.003	1.130	96.453	0.639	0	32
9	94.316	94.430	1.627	96.598	0.692	0	32
10	94.339	94.551	1.473	96.294	0.670	0	32

Figure 31c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Plane using Gene Action 4 (Sheet 2 of 2)

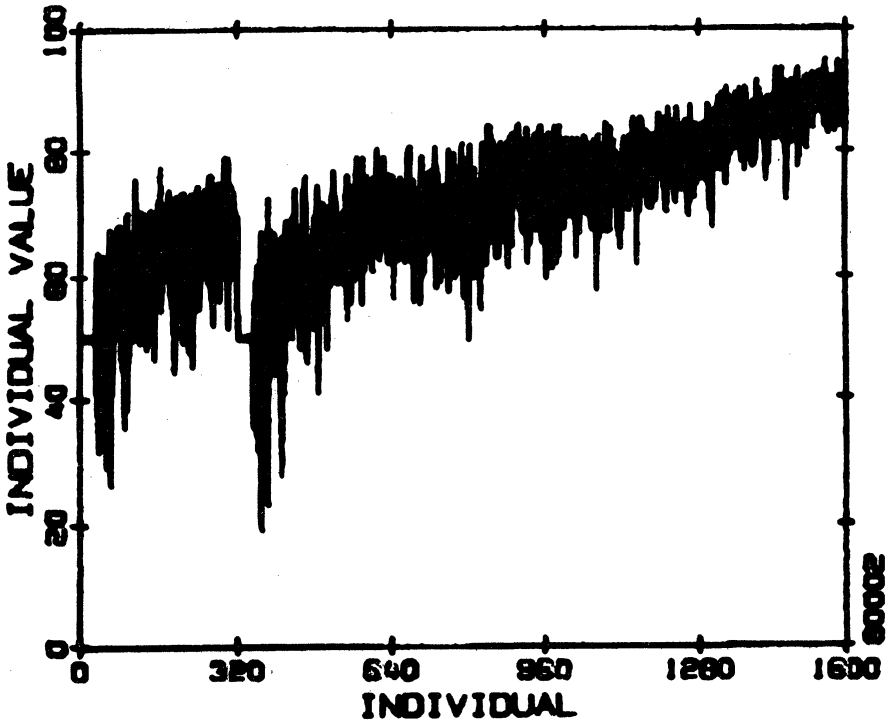


Figure 32a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Ridge using Gene Action 4

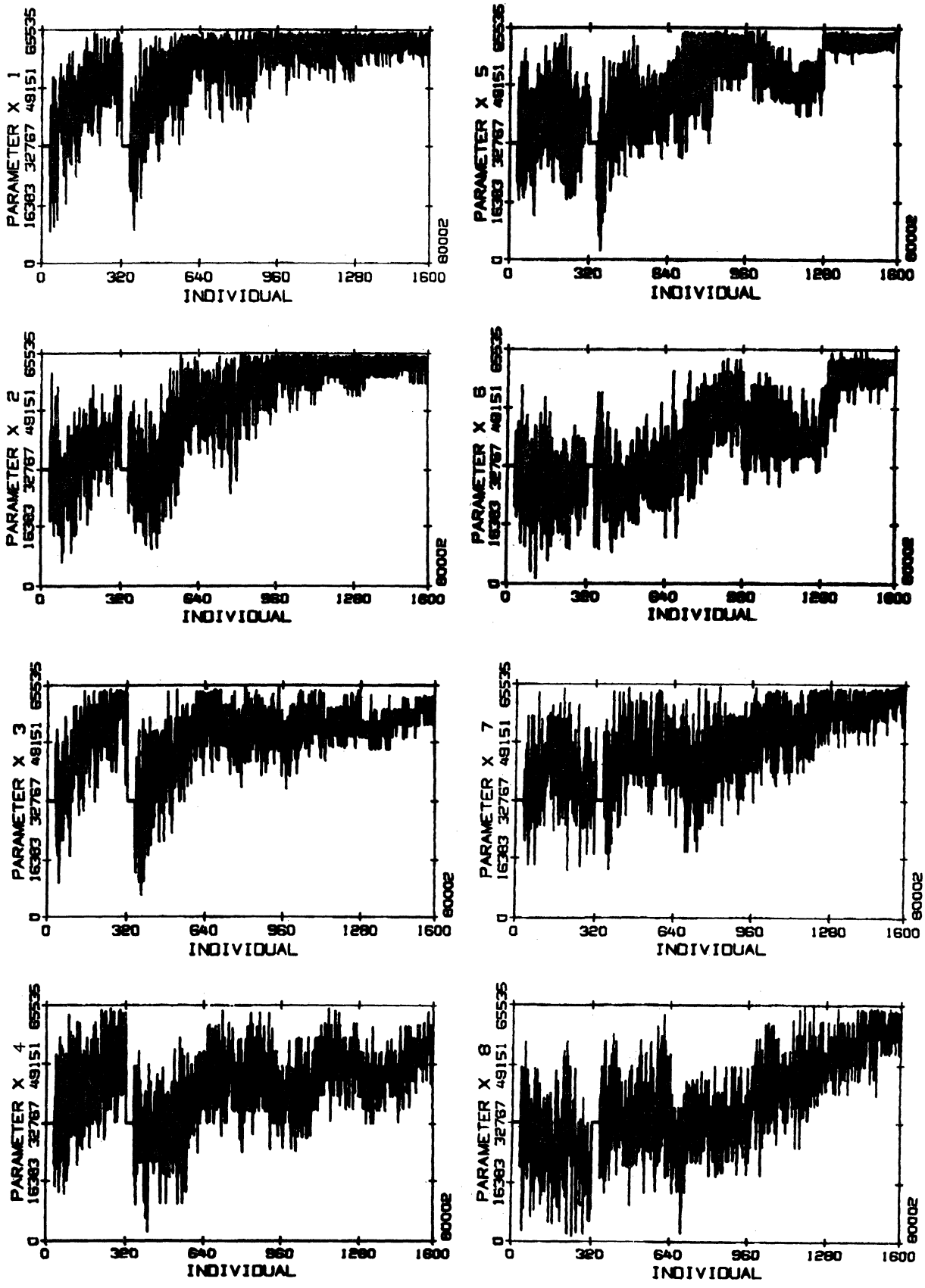


Figure 32b Parameter values of individuals during extended simple recurrent selection for 8-parameter Ridge using Gene Action 4

```
          80002
SRS2 7/12/73
NOVLP          4
NVALU          2
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
          80003
     1    50.109  32766  32766  32766  32766  32766  32766  32766  32766
     2    50.109  32766  32766  32766  32766  32766  32766  32766  32766
     3    50.109  32766  32766  32766  32766  32766  32766  32766  32766
     4    50.109  32766  32766  32766  32766  32766  32766  32766  32766
     5    50.109  32766  32766  32766  32766  32766  32766  32766
     6    50.109  32766  32766  32766  32766  32766                  03562
     7    50.109  32766  32766  32766                        64430  59962
     8    50.109  32766  32766                  03872  62030  61088  63800
     9    50.109                        59678  62608  62298  57502  59226
    10                        60020  54616  56300  63902  58686  60578  63562
                    04720  64430  62294  59690  63330  62048  62980  56362
    84.658  58730  64686  62054  51980  63572  62030  59378  63818
   309  93.124  64180  64430  62042  56106  63328  62044  62542  55882
   310  91.962  62808  64446  58230  52206  63346  58670  63998  59736
   311  88.774  58714  64432  62026  56076  63904  62016  60398  60442
   312  87.992  64706  60606  62536  60170  64656  62270  53436  59948
   313  91.349  62778  64430  58458  59404  63902  62526  64238  59706
   314  92.518  63048  56766  62266  59646  63316  61806  60142  59960
   315  93.064  62328  60590  57960  48140  63328  62270  63230  60440
   316  92.798  63018  56766  58682  55850  63086  62046  64942  63546
   317  89.501  62810  60830  54168  43820  64050  58416  60368  52040
   318  87.592  59464  60590  54858  55610  63328  62286  60848  59706
   319  93.224  59196  56990  57976  52206  63808  62268  62992  59960
   320  83.672  54872  64670  58216  55342  63794  62510  64464  56120
VARIETY   1
GEN       EFF       AVG       STD      AVGS      STDS      NIZ      NTR
  1    50.109    50.109     0.000    50.109     0.000        0       32
  2    47.923    45.736    10.522    59.952     4.859        0       32
  3    50.636    56.063     8.461    65.465     3.144        0       32
  4    52.766    59.154     7.257    68.502     3.362        0       32
  5    54.458    61.227     6.644    68.814     1.902        0       32
  6    55.852    62.822     6.931    71.224     3.243        0       32
  7    57.034    64.126     6.138    70.511     2.256        0       32
  8    58.059    65.237     6.509    71.776     1.735        0       32
  9    58.952    66.090     6.189    73.955     1.738        0       32
 10    59.848    67.914     6.111    75.368     2.863        0       32
VARIETY   2
GEN       EFF       AVG       STD      AVGS      STDS      NIZ      NTR
  1    50.109    50.109     0.000    50.109     0.000        0       32
```

Figure 32c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 (Sheet 1 of 2)

2	47.743	45.377	12.266	60.446	6.373	0	32
3	49.911	54.246	9.027	65.355	1.870	0	32
4	52.498	60.259	5.572	67.514	3.431	0	32
5	53.551	57.706	6.999	67.275	4.830	0	32
6	55.043	62.502	7.365	70.976	2.015	0	32
7	56.484	65.128	4.385	70.691	3.121	0	32
8	57.825	67.216	6.376	75.024	1.955	0	32
9	59.095	69.249	4.867	74.835	1.836	0	32
10	60.248	70.632	4.843	76.565	2.467	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	68.837	68.837	4.811	74.556	0.853	0	32
2	67.237	65.637	6.555	74.543	3.926	0	32
3	67.998	69.520	5.591	76.568	2.349	0	32
4	68.258	69.041	4.905	74.692	2.546	0	32
5	68.405	68.993	6.467	76.980	2.542	0	32
6	68.349	68.068	7.196	76.974	2.650	0	32
7	69.004	72.932	5.753	80.407	2.921	0	32
8	69.822	75.552	6.037	81.435	0.773	0	32
9	70.524	76.133	5.282	81.986	1.984	0	32
10	70.959	74.877	5.336	82.213	2.000	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	71.205	71.205	6.947	80.770	2.967	0	32
2	72.941	74.677	4.247	80.162	1.405	0	32
3	73.610	74.948	4.611	80.553	1.710	0	32
4	73.866	74.634	6.651	81.517	1.467	0	32
5	74.144	75.258	5.185	81.354	1.723	0	32
6	74.512	76.348	4.799	82.275	1.937	0	32
7	75.080	78.493	4.372	83.800	1.399	0	32
8	75.548	78.824	3.892	83.605	1.945	0	32
9	76.047	80.034	3.996	84.755	1.667	0	32
10	76.350	79.078	4.588	84.462	1.336	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	78.922	78.922	4.701	84.840	1.366	0	32
2	80.959	82.995	4.424	88.304	1.295	0	32
3	82.192	84.660	3.173	88.695	0.999	0	32
4	82.573	83.715	3.761	88.164	1.339	0	32
5	83.069	85.053	3.659	89.229	1.118	0	32
6	83.688	86.785	3.512	90.965	1.736	0	32
7	84.089	86.491	4.636	91.202	1.210	0	32
8	84.645	88.539	2.968	91.785	0.731	0	32
9	85.146	89.151	2.872	92.917	0.911	0	32
10	85.599	89.683	3.027	92.966	0.860	0	32

Figure 32c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 (Sheet 2 of 2)

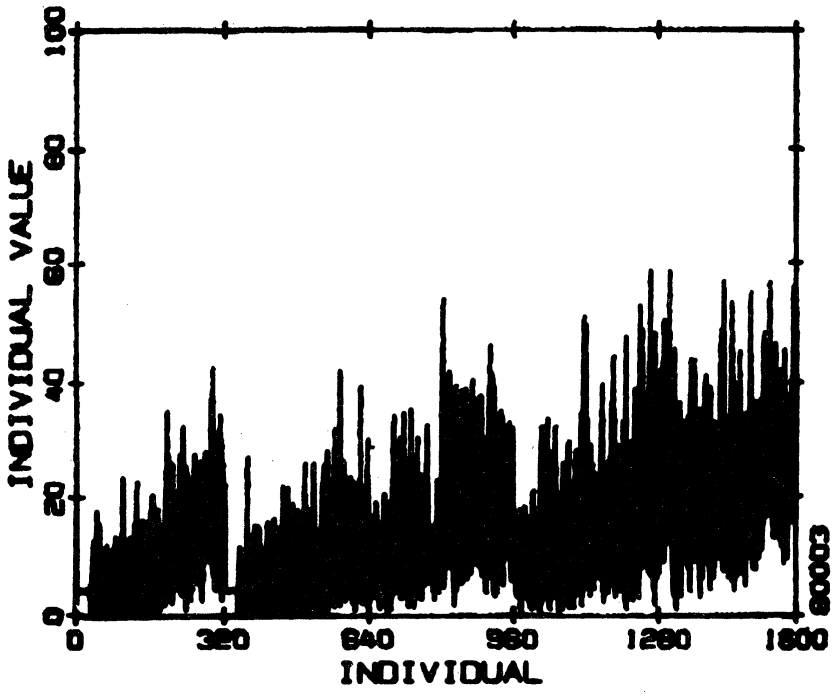


Figure 33a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4

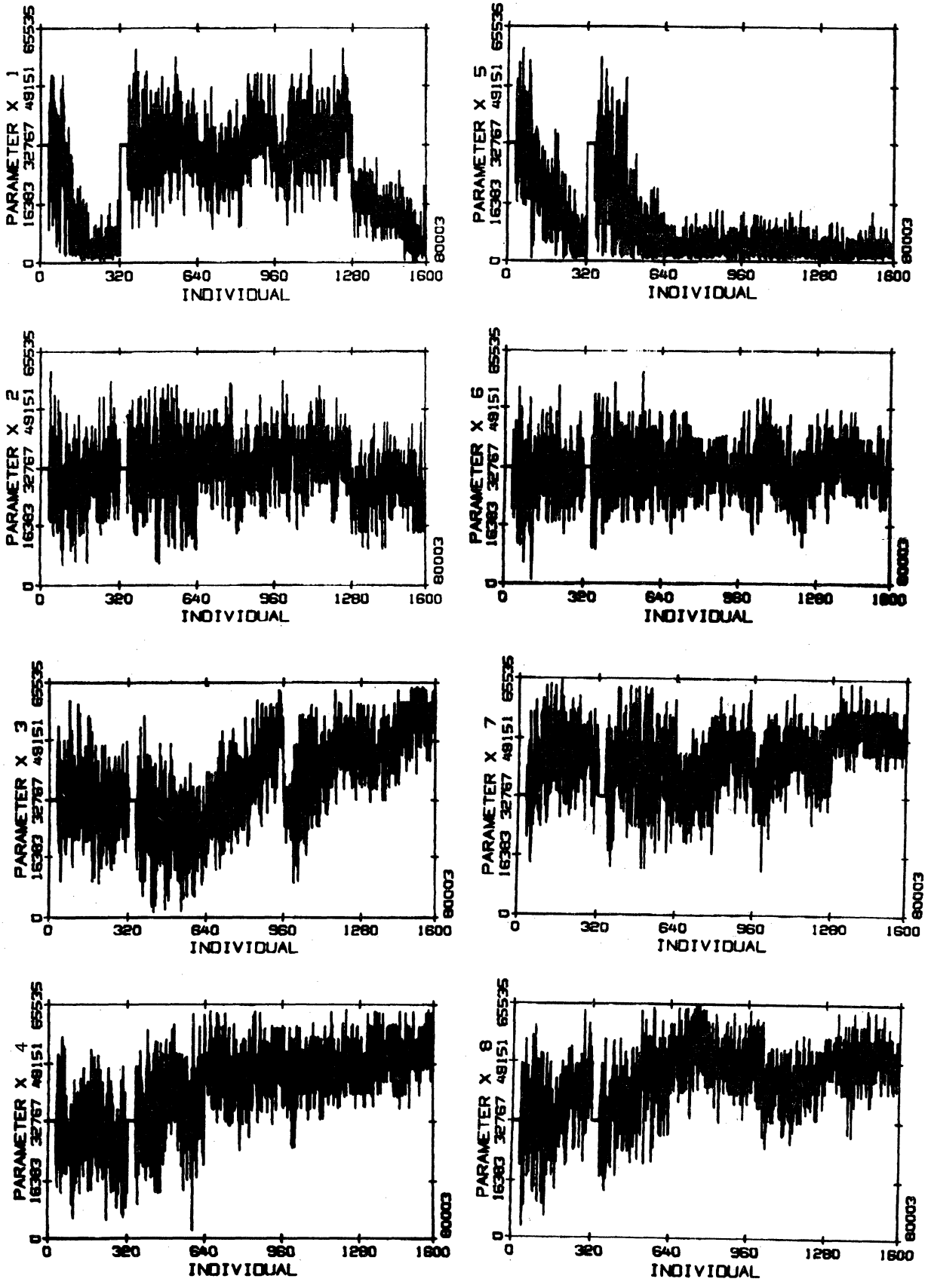


Figure 33b Parameter values of individuals during extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4

```
          80003
 SRS2 7/12/73
  NOVLP          4
  NVALU          3
  PINV      0.0000
  PTRA      0.0000
  PCROS     0.5000
  PCROL     0.5000
  PMUT      0.0000
  CV        0.0000
  NPOP          32
  NSEL           8
  LCYC          10
  NPAR           8
  NSEG          32
  NVAR           5
  IX             1
  IPAP           1
  IPBP           0
  IPAF           0
  IPCS           0
          80004
      1     4.061  32766  32766  32766  32766  32766  32766  32766  32766
      2     4.061  32766  32766  32766  32766  32766  32766  32766  32766
      3     4.061  32766  32766  32766  32766  32766  32766  32766  32766
      4     4.061  32766  32766  32766  32766  32766  32766  32766  32766
      5     4.061  32766  32766  32766  32766  32766  32766  [illegible]  47956
      6     4.061  32766  32766  32766  32766  32766  [illegible]  49298  52068
      7     4.061  32766  32766  32766  [illegible]  0858  32786  48610  44164
      8     4.061  32766  32766  [illegible]  63396  1340  28706  48342  51768
      9     4.061  32766  [illegible]  59452  48800  2062  28934  45472  48726
     10     [illegible]  6530  13982  52014  52372  2078  28210  42130  51576
            9.422   926  41640  55120  59360  5678  21012  52450  43426
    308    23.191  2018  45452  51772  48110  2270  32788  52974  48168
    309    36.093  6766  26234  51522  59600  1764  24852  48862  48228
    310    34.516  2238  29852  59470  59600  1568  33042  45534  51824
    311    22.021  2524  37742  55854  59360  5394  28964  56770  47448
    312    37.903  7246  29838  63038  56000  2512  28916  45026  44376
    313    26.796  6816  29625  55360  52400  2286  28706  45744  51602
    314    15.375  6348  29582  55360  63200  1550  40692  49090  40984
    315    16.650  21696  25982  59438  55476  1508  32022  49118  55366
    316    28.973  6798  29102  55360  44240  4912  36144  45504  47958
    317    22.892  10160  14250  55614  51652  2482  36654  48866  52022
    318    41.620  1700  25996  63502  60306  2046  25362  48848  48454
    319    56.383  9398  22382  51492  52162  1358  37614  52450  52052
    320    25.679  6034  22184  55782  59330  2992  29684  45010  47944
 VARIETY   1
 GEN       EFF       AVG       STD       AVGS      STDS      NIZ       NTR
   1     4.061     4.061     0.000     4.061     0.000        0        32
   2     3.513     2.964     4.501     9.069     5.571        0        32
   3     3.521     3.538     4.200    10.071     2.781        0        32
   4     4.118     5.910     5.074    12.967     4.897        0        32
   5     4.716     7.109     5.687    15.278     3.161        0        32
   6     5.216     7.715     5.733    15.797     2.333        0        32
   7     6.372    13.307     8.214    25.480     5.102        0        32
   8     7.337    14.093     8.527    25.510     3.280        0        32
   9     8.255    15.594     6.901    24.191     2.364        0        32
  10     9.228    17.988     9.647    30.519     7.139        0        32
 VARIETY   2
 GEN       EFF       AVG       STD       AVGS      STDS      NIZ       NTR
   1     4.061     4.061     0.000     4.061     0.000        0        32
```

Figure 33c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 (Sheet 1 of 2)

2	4.036	4.018	5.285	10.742	6.800	0	32
3	4.338	4.942	5.150	13.158	2.197	0	32
4	4.427	4.693	4.631	11.945	2.530	0	32
5	4.881	6.701	6.740	17.007	3.544	0	32
6	5.433	8.191	6.135	16.539	4.125	0	32
7	5.735	7.546	7.819	18.954	5.145	0	32
8	6.543	12.199	9.912	25.343	8.213	0	32
9	7.218	12.616	7.581	22.281	1.966	0	32
10	7.546	10.502	8.862	22.395	8.562	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	9.395	9.395	4.603	14.971	1.837	0	32
2	10.362	11.329	7.907	21.481	7.718	0	32
3	11.158	12.750	8.503	23.933	8.640	0	32
4	11.236	11.472	6.930	20.605	6.025	0	32
5	11.174	10.923	6.257	18.980	6.383	0	32
6	12.203	17.352	11.926	34.237	10.028	0	32
7	13.667	22.452	11.754	36.756	2.252	0	32
8	14.281	18.573	10.179	33.715	4.851	0	32
9	14.600	17.158	12.251	35.356	7.624	0	32
10	14.958	18.173	9.401	31.789	2.284	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	10.445	10.445	4.619	15.625	1.602	0	32
2	9.603	8.761	6.849	17.233	6.590	0	32
3	10.787	13.154	10.319	28.171	4.093	0	32
4	10.976	11.544	7.782	21.395	4.524	0	32
5	11.665	14.421	10.709	28.920	10.129	0	32
6	12.333	15.671	9.630	28.635	9.470	0	32
7	13.052	17.368	11.389	33.447	6.944	0	32
8	13.073	13.221	11.079	29.146	9.629	0	32
9	13.565	17.504	13.470	36.846	10.062	0	32
10	14.422	22.134	14.713	42.062	8.938	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	23.850	23.850	12.041	39.938	9.949	0	32
2	20.976	18.102	11.879	34.533	5.191	0	32
3	20.959	20.924	11.627	37.526	4.654	0	32
4	21.118	21.594	12.339	38.315	1.679	0	32
5	21.027	20.667	12.100	37.177	10.375	0	32
6	21.023	20.999	13.063	39.275	7.410	0	32
7	20.915	20.267	10.723	34.699	8.892	0	32
8	21.114	22.510	10.944	37.386	4.738	0	32
9	21.748	26.818	10.046	39.096	8.759	0	32
10	22.288	27.146	11.700	42.441	6.372	0	32

Figure 33c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 (Sheet 2 of 2)

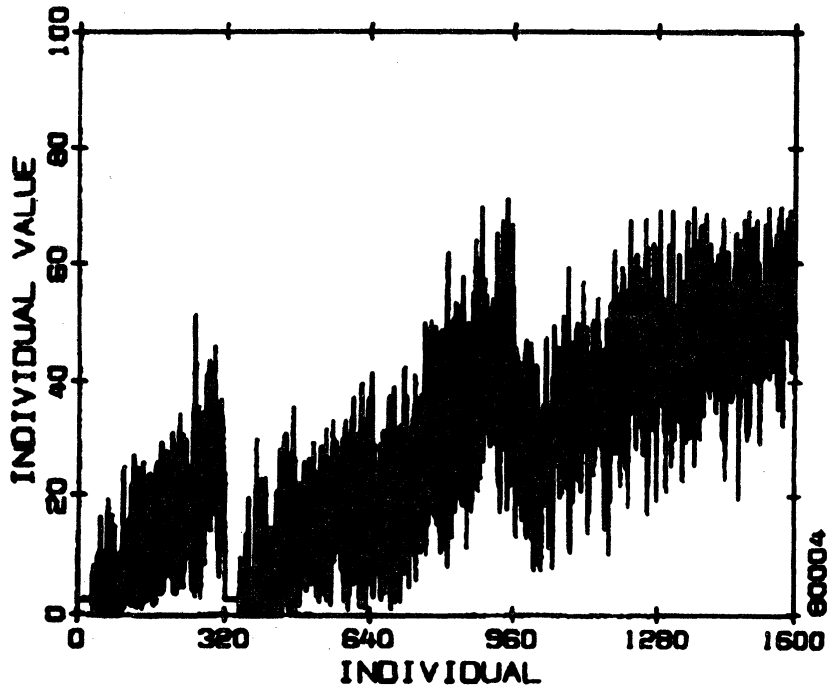


Figure 34a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Peak W using Gene Action 4

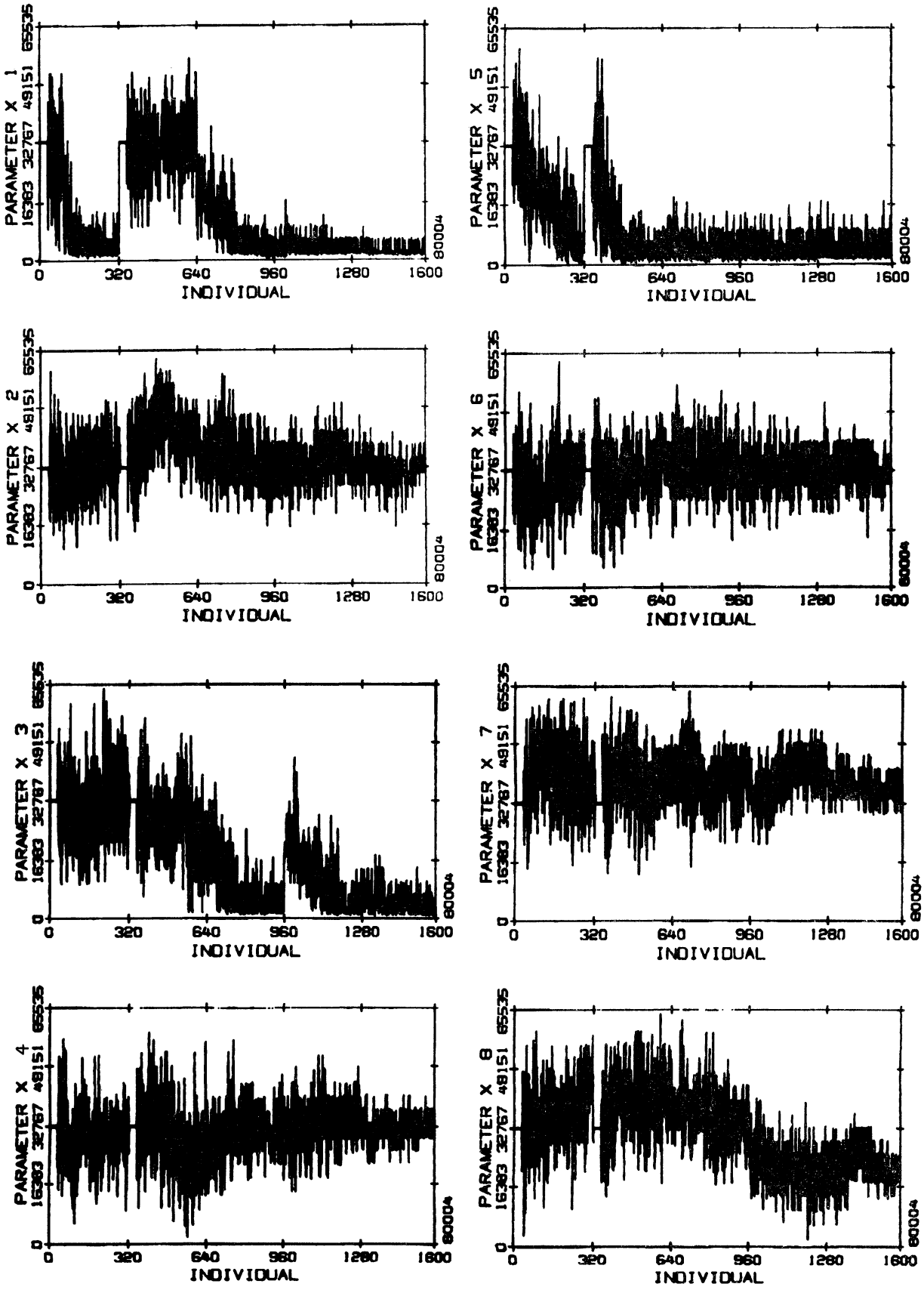


Figure 34b Parameter values of individuals during extended simple recurrent selection for 8-parameter Peak W using Gene Action 4

```
        80004
SRS2 7/12/73
NOVLP          4
NVALU          4
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      0.0000
CV        0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
        80005
     1    2.440  32766  32766  32766  32766  32766  32766  32766  32766
     2    2.440  32766  32766  32766  32766  32766  32766  32766  32766
     3    2.440  32766  32766  32766  32766  32766  32766  32766  32766
     4    2.440  32766  32766  32766  32766  32766  32766  32766  32766
     5    2.440  32766  32766  32766  32766  32766  32766  32766  17604
     6    2.440  32766  32766  32766  32766  32766  28432  42110  17350
     7    2.440  32766  32766  32766  32766   1798  28982  42142  17112
     8    2.440  32766  32766  32766   1026  29658   9496  32552  41650  17634
     9    2.440  32766  32766   8720   1612  37322   5892  29192  38062  17636
    10    2.440   2032  34640   2726  29384   2056  29192  42128  25284
VARIETY   1
GEN        EFF        AVG        STD        AVGS       STDS       NIZ        NTR
     1    2.440      2.440      0.000      2.440      0.000      0          32
     2    2.640      2.840      3.851      8.427      3.988      0          32
     3    3.081      3.962      5.157     11.560      4.801      0          32
     4    4.639      9.315      7.749     20.401      4.501      0          32
     5    6.019     11.539      7.640     22.312      2.191      0          32
     6    7.265     13.492      8.357     24.893      2.261      0          32
     7    8.341     14.798      8.727     27.152      3.822      0          32
     8    9.796     19.981     10.414     32.649      9.730      0          32
     9   11.167     22.133     10.264     35.638      5.553      0          32
    10   12.477     24.274     10.168     37.990      4.653      0          32
VARIETY   2
GEN        EFF        AVG        STD        AVGS       STDS       NIZ        NTR
     1    2.440      2.440      0.000      2.440      0.000      0          32
```

Figure 34c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak W using Gene Action 4 (Sheet 1 of 2)

2	3.063	3.665	4.273	9.380	4.826	0	32
3	4.344	6.907	7.990	18.976	6.206	0	32
4	5.160	7.606	7.340	18.005	4.647	0	32
5	6.725	12.985	9.771	26.695	5.154	0	32
6	7.937	13.996	7.354	23.778	2.209	0	32
7	8.883	14.502	8.015	24.813	4.108	0	32
8	9.830	16.457	7.350	25.694	3.879	0	32
9	10.670	17.395	9.757	29.743	4.669	0	32
10	11.321	17.176	10.296	31.310	4.808	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	16.803	16.803	8.843	28.264	6.033	0	32
2	15.553	14.304	11.384	30.792	5.755	0	32
3	17.677	21.925	9.253	33.101	4.920	0	32
4	18.874	22.463	10.476	37.279	6.449	0	32
5	21.326	31.135	11.370	45.304	3.680	0	32
6	23.434	33.976	14.180	51.839	5.375	0	32
7	25.338	36.757	12.829	52.607	2.496	0	32
8	27.340	41.357	12.636	56.734	7.202	0	32
9	29.023	42.483	10.630	55.720	4.279	0	32
10	30.419	42.989	14.558	63.186	4.982	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	30.621	30.621	10.168	43.822	2.434	0	32
2	28.276	25.931	11.235	39.182	4.429	0	32
3	28.912	30.184	9.451	41.797	5.130	0	32
4	30.215	34.126	11.226	46.971	5.863	0	32
5	31.386	36.067	10.482	48.924	3.582	0	32
6	32.109	35.723	9.761	47.847	3.429	0	32
7	32.532	35.076	10.001	47.339	4.150	0	32
8	33.666	41.599	12.779	57.027	2.623	0	32
9	35.204	47.508	9.689	59.741	3.669	0	32
10	36.315	46.315	12.305	60.097	4.702	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	44.861	44.861	11.392	59.039	5.733	0	32
2	44.127	43.394	10.754	56.175	6.282	0	32
3	44.716	45.894	11.375	61.221	5.919	0	32
4	46.355	51.269	9.730	63.772	3.298	0	32
5	46.648	47.820	9.695	60.632	3.945	0	32
6	46.948	48.448	9.580	59.619	3.045	0	32
7	47.169	48.495	11.614	62.527	4.645	0	32
8	47.630	50.857	9.569	61.911	4.418	0	32
9	48.299	53.650	8.342	63.508	3.021	0	32
10	49.118	56.491	9.214	67.101	2.236	0	32

Figure 34c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak W using Gene Action 4 (Sheet 2 of 2)

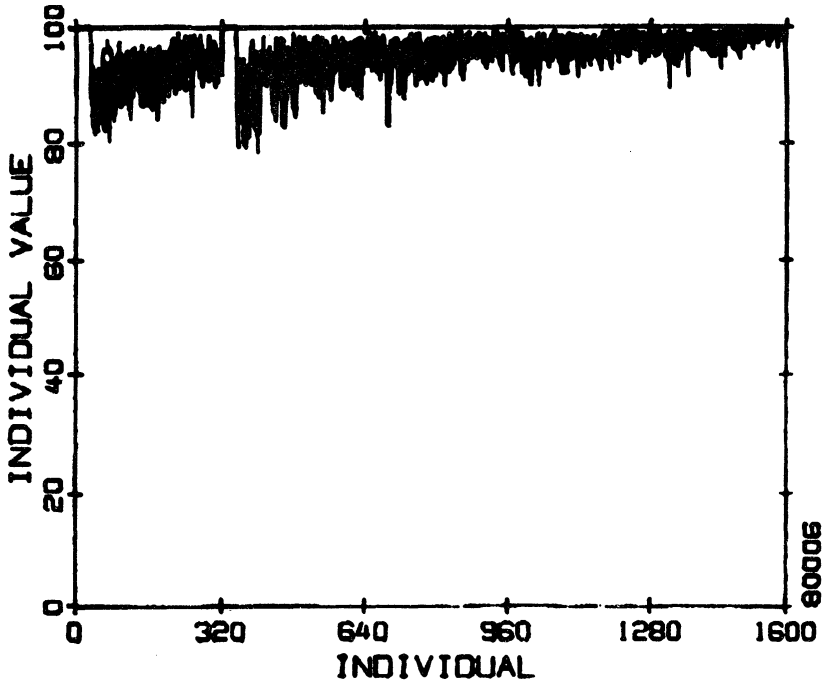


Figure 35a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Hypersphere using Gene Action 4

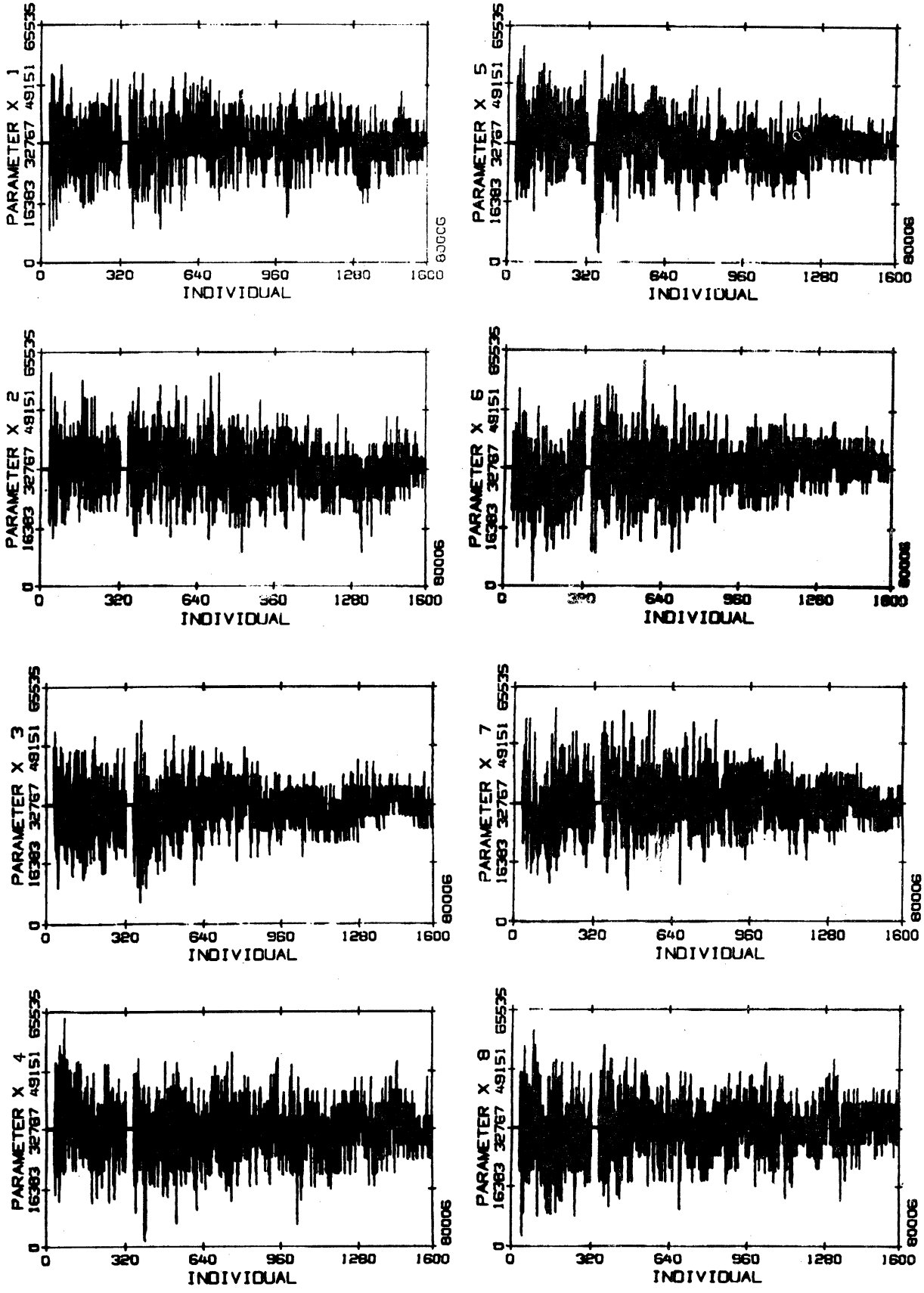


Figure 35b Parameter values of individuals during extended simple recurrent selection for 8-parameter Hypersphere using Gene Action 4

80006

SRS2 7/12/73

NDVLP	4
NVALU	6
PINV	0.0000
PTRA	0.0000
PCROS	0.5000
PCROL	0.5000
PMUT	0.0000
CV	0.0000
NPOP	32
NSEL	8
LCYC	10
NPAR	8
NSEG	32
NVAR	5
IX	1
IPAP	1
IPBP	0
IPAF	0
IPCS	0

80007

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	100.000	100.000	0.000	100.000	0.000	0	32
2	94.091	88.182	3.830	92.913	2.005	0	32
3	93.111	91.152	4.245	95.961	1.051	0	32
4	92.935	92.406	3.513	95.541	0.510	0	32
5	92.792	92.222	2.894	95.537	0.684	0	32
6	92.657	91.979	3.060	95.416	0.722	0	32
7	92.815	93.764	3.118	97.242	0.939	0	32
8	92.929	93.725	3.128	97.267	0.820	0	32
9	93.105	94.513	2.353	97.500	0.815	0	32
10	93.242	94.475	2.237	97.009	0.767	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	100.000	100.000	0.000	100.000	0.000	0	32
2	94.066	88.132	4.897	93.325	0.874	0	32
3	93.140	91.286	4.841	96.275	1.183	0	32
4	93.029	92.697	3.410	96.234	1.092	0	32
5	92.962	92.696	4.136	97.407	1.036	0	32
6	93.107	93.832	3.421	97.369	0.738	0	32
7	93.163	93.500	3.496	97.458	0.718	0	32
8	93.274	94.046	2.938	97.117	0.775	0	32
9	93.353	93.983	2.791	97.288	0.302	0	32
10	93.510	94.929	2.760	97.557	0.311	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	95.760	95.760	1.766	97.991	0.741	0	32
2	94.516	93.272	3.434	96.625	1.127	0	32
3	94.653	94.927	2.903	97.528	0.245	0	32
4	94.834	95.379	2.344	98.097	0.734	0	32
5	94.862	94.973	2.376	97.587	0.275	0	32
6	94.973	95.524	2.151	97.857	0.592	0	32
7	95.128	96.058	2.357	98.528	0.512	0	32
8	95.325	96.704	1.263	98.167	0.536	0	32
9	95.452	96.473	1.599	98.310	0.417	0	32
10	95.612	97.053	1.639	98.716	0.564	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	96.841	96.841	1.797	98.692	0.405	0	32
2	95.964	95.086	2.392	97.380	0.387	0	32

Figure 35c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Hypersphere using Gene Action 4 (Sheet 1 of 2)

3	95.923	95.841	2.083	97.930	0.563	0	32
4	96.048	96.423	1.829	98.304	0.501	0	32
5	96.084	96.231	1.899	98.135	0.433	0	32
6	96.067	95.982	1.465	97.809	0.580	0	32
7	96.128	96.491	1.623	98.376	0.461	0	32
8	96.272	97.282	1.518	98.871	0.317	0	32
9	96.393	97.364	1.273	98.948	0.331	0	32
10	96.478	97.236	1.272	98.552	0.392	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	97.109	97.109	1.303	98.685	0.527	0	32
2	96.882	96.654	2.123	98.618	0.388	0	32
3	96.908	96.959	1.614	98.604	0.548	0	32
4	97.127	97.785	0.841	98.876	0.277	0	32
5	97.245	97.716	1.286	99.065	0.346	0	32
6	97.323	97.713	1.478	99.163	0.339	0	32
7	97.416	97.973	1.185	99.050	0.254	0	32
8	97.529	98.324	0.770	99.252	0.341	0	32
9	97.659	98.692	0.700	99.460	0.151	0	32
10	97.787	98.940	0.683	99.515	0.173	0	32

Figure 35c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Hypersphere using Gene Action 4 (Sheet 2 of 2)

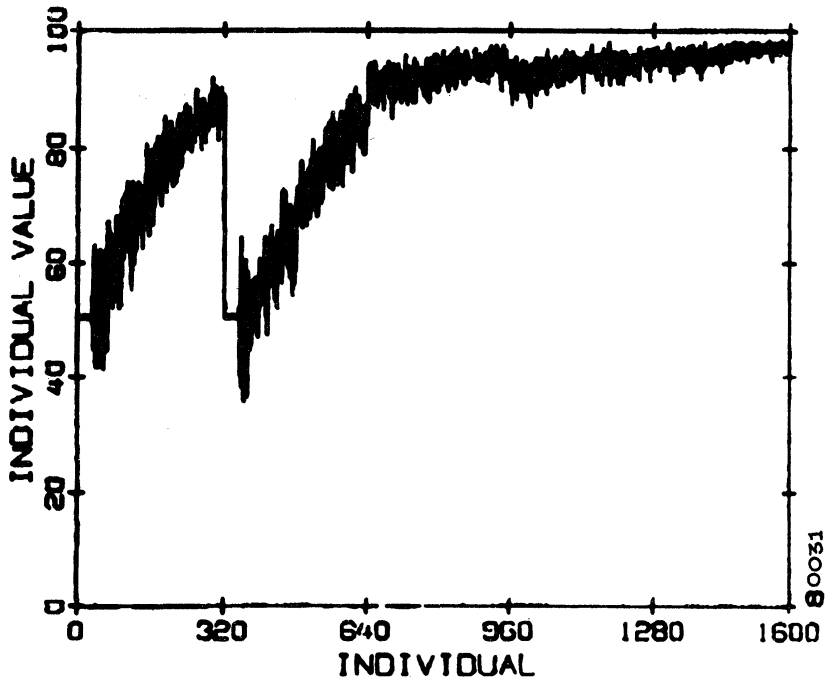


Figure 36a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Plane using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

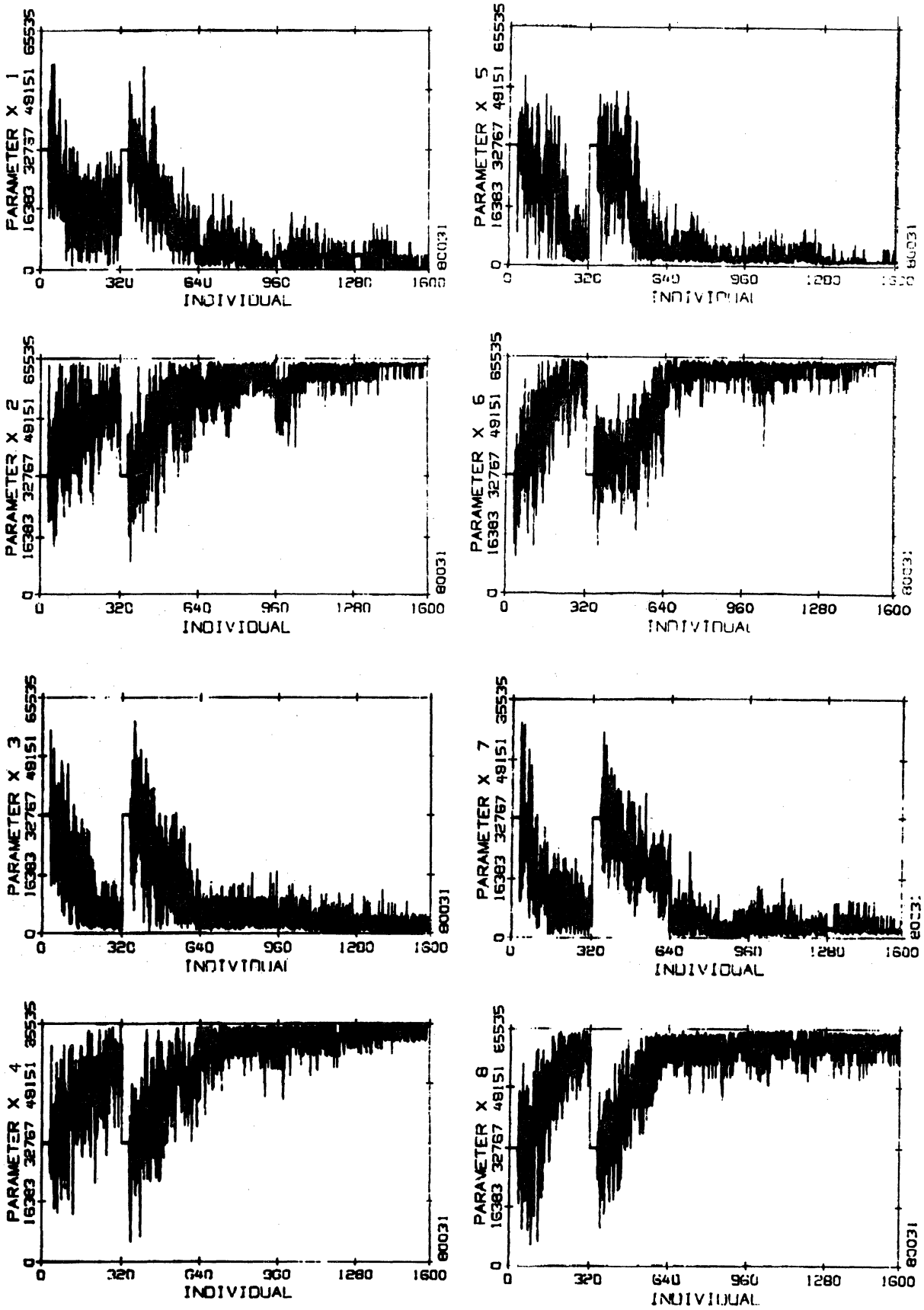


Figure 36b Parameter values of individuals during extended simple recurrent selection for 8-parameter Plane using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

80031

SRS2 7/20/73

NOVLP	4
NVALU	1
PINV	0.0010
PTRA	0.0010
PCROS	0.5000
PCROL	0.5000
PMUT	0.0010
CV	0.0000
NPOP	32
NSEL	8
LCYC	10
NPAR	8
NSEG	32
NVAR	5
IX	1
IPAP	1
IPBP	0
IPAF	0
IPCS	0

80032

1	50.000	32766	32766	32766	32766	32766	32766	32766	32766
2	50.000	32766	32766	32766	32766	32766	32766	32766	32766
3	50.000	32766	32766	32766	32766	32766	32766	32766	32766
4	50.000	32766	32766	32766	32766	32766	32766	32766	32766
5	50.000	32766	32766	32766	32766	32766	32766		
6	50.000	32766	32766	32766	32766	32766			63964
7	50.000	32766	32766	32766				1448	59156
8	50.000	32766	32766			1114	64446	1672	64186
9	50.000				64562	4952	64460	1420	62996
10			00076	1052	60692	1352	64218	2180	63072
		3720	63904	826	65026	1624	64444	1690	64414
307	97.942	150	63888	1070	64534	1112	64458	2438	63250
308	97.929	402	64302	3282	60932	1096	64458	2422	63996
309	97.478	162	63904	380	64292	1096	64444	2180	60096
310	96.863	4170	64144	604	61114	1096	64428	1164	63040
311	95.895	388	63888	3012	64564	2994	64444	2180	56296
312	97.107	388	63904	1054	64324	4936	64218	2406	63312
313	96.711	660	63888	812	64804	1112	64204	1926	56508
314	96.126	150	63904	4398	64786	4938	64458	1926	60094
315	96.918	3930	64144	1052	64996	1354	64458	1956	60678
316	96.734	3930	63902	4186	64532	1354	64444	1674	63284
317	98.082	416	64156	1082	64774	1096	63724	2182	64206
318	97.941	640	63904	828	64804	1368	63964	2408	63918
319	96.623	418	64144	576	64998	1110	64428	2648	55616
320	97.535	162	63888	816	64776	1112	63966	5290	63964

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.000	50.000	0.000	50.000	0.000	0	32
2	50.024	50.048	6.275	58.835	3.608	0	32
3	52.087	58.914	5.067	65.859	1.683	0	32
4	56.350	66.438	4.571	72.264	1.424	0	32
5	59.402	71.611	3.902	76.230	2.563	0	32
6	62.215	76.276	3.878	80.964	2.644	0	32
7	64.684	79.500	3.188	83.731	1.240	0	32
8	66.971	82.984	2.397	86.121	0.846	0	32
9	68.981	85.656	2.244	87.863	0.981	0	32
10	70.820	87.309	2.395	89.978	0.904	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.000	50.000	0.000	50.000	0.000	0	32

Figure 36c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Plane using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 1 of 2)

2	49.886	49.772	5.938	56.313	4.607	0	32
3	51.556	54.696	4.194	59.665	2.593	0	32
4	53.468	59.203	3.546	63.965	1.768	0	32
5	55.694	64.641	4.509	70.038	2.078	0	32
6	58.190	70.670	2.983	74.634	1.918	0	32
7	60.536	74.960	3.599	79.297	1.359	0	32
8	62.903	79.127	3.469	83.295	1.634	0	32
9	64.892	80.799	3.425	85.149	2.355	0	32
10	66.894	84.910	2.337	88.195	1.098	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	90.841	90.841	2.155	93.627	0.961	0	32
2	90.881	90.922	2.304	93.632	0.568	0	32
3	91.102	91.545	1.773	93.624	0.983	0	32
4	91.142	91.259	1.870	93.455	1.002	0	32
5	91.379	92.329	2.097	95.005	0.638	0	32
6	91.675	93.152	1.764	95.320	0.589	0	32
7	91.976	93.766	1.374	96.084	0.538	0	32
8	92.209	93.843	1.279	95.442	0.794	0	32
9	92.453	94.399	1.628	96.437	0.454	0	32
10	92.628	94.208	1.798	96.561	0.683	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	91.873	91.873	1.895	94.197	0.882	0	32
2	91.723	91.567	2.002	94.332	0.583	0	32
3	92.106	92.877	1.914	95.240	0.604	0	32
4	92.423	93.376	1.567	95.273	0.727	0	32
5	92.760	94.107	1.371	95.752	0.361	0	32
6	93.017	94.301	1.473	95.975	0.700	0	32
7	93.176	94.127	1.664	96.052	1.038	0	32
8	93.283	94.035	1.705	96.013	0.279	0	32
9	93.406	94.387	1.065	95.611	0.252	0	32
10	93.581	95.164	1.194	96.510	0.326	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	95.443	95.443	0.970	96.542	0.324	0	32
2	95.245	95.047	1.426	96.762	0.561	0	32
3	95.311	95.444	1.212	96.943	0.419	0	32
4	95.223	94.960	1.417	96.798	0.698	0	32
5	95.321	95.713	1.005	96.952	0.409	0	32
6	95.436	96.011	1.248	97.599	0.324	0	32
7	95.592	96.527	0.944	97.612	0.212	0	32
8	95.750	96.859	0.735	97.762	0.249	0	32
9	95.885	96.961	0.794	97.908	0.243	0	32
10	96.016	97.201	0.729	98.072	0.133	0	32

Figure 36c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Plane using Gene Action 4 with random inverstion and translocation of chromosome segments and random mutation of gene conformation (Sheet 2 of 2)

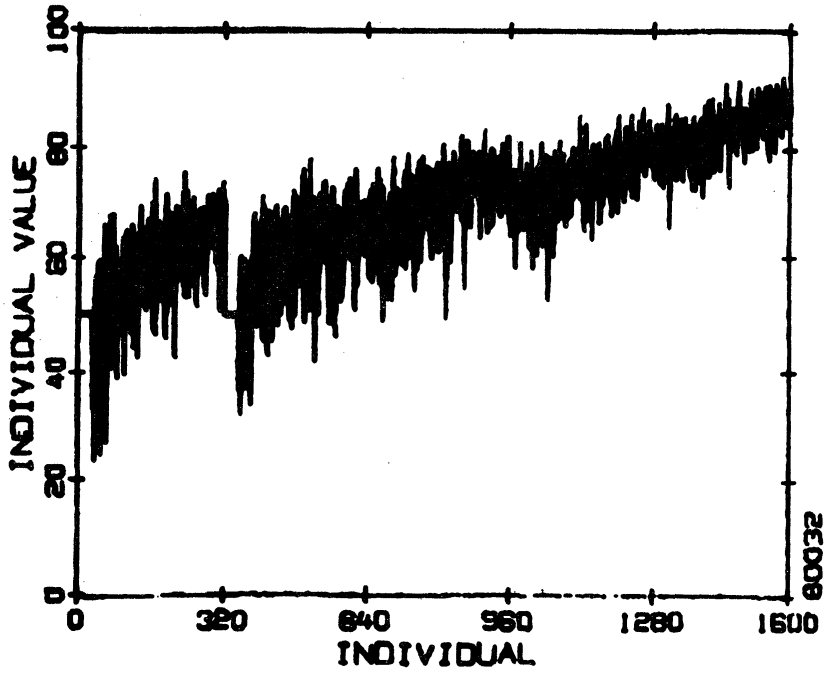


Figure 37a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

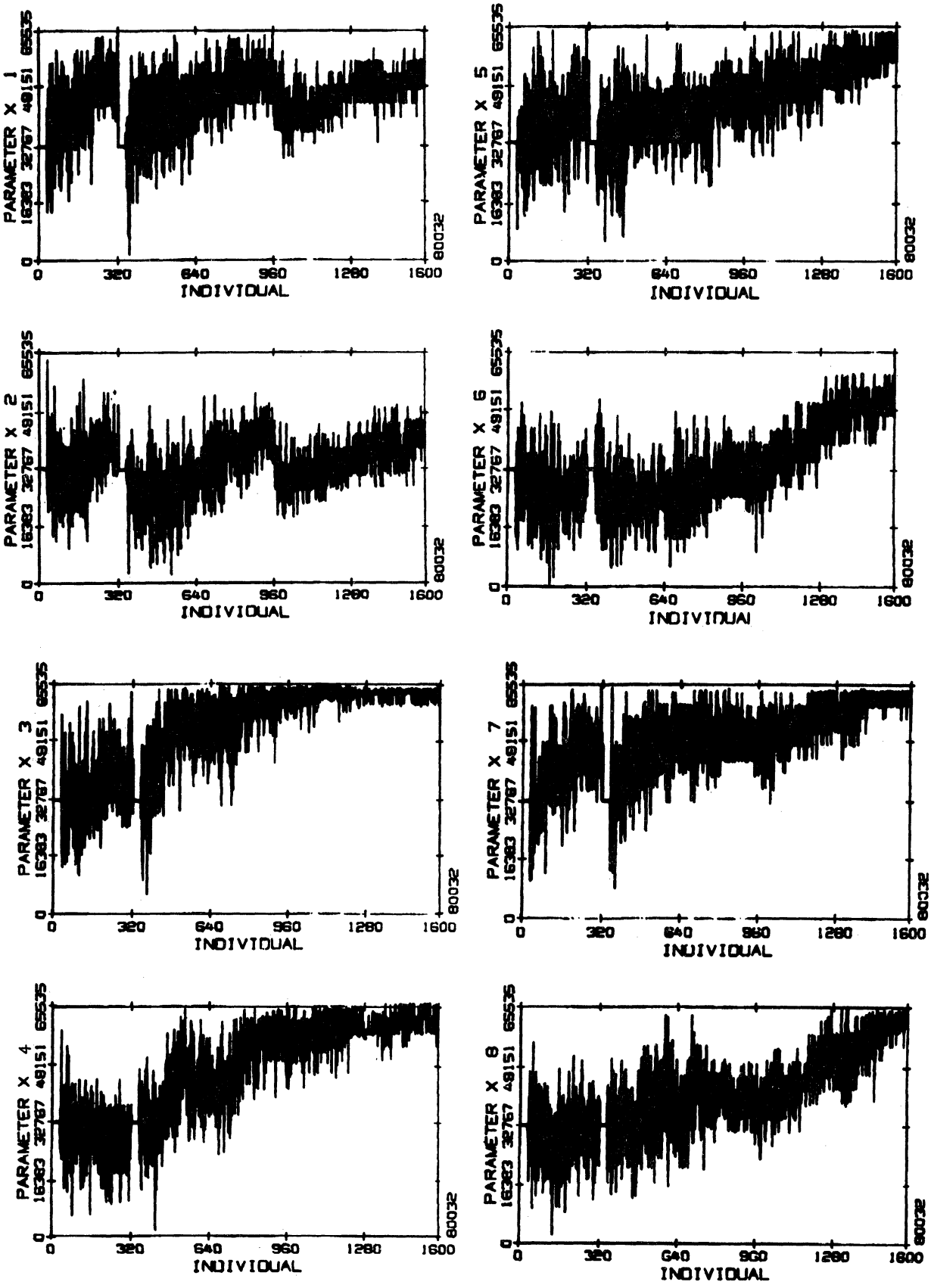


Figure 37b Parameter values of individuals during extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

```
        80032
SRS2 7/2w/73
NOVLP          4
NVALU          2
PINV       0.0010
PTRA       0.0010
PCROS      3.5000
PCROL      0.5000
PMUT       0.0010
CV         0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
        80033
```

1	50.109	32766	32766	32766	32766	32766	32766	32766	32766
2	50.109	32766	32766	32766	32766	32766	32766	32766	32766
3	50.109	32766	32766	32766	32766	32766	32766	32766	32766
4	50.109	32766	32766	32766	32766	32766	32766	32766	32766
5	50.109	32766	32766	32766	32766	32766	32766	[illegible]	[illegible]
6	50.109	32766	32766	32766	32766	32766	[illegible]	[illegible]	60370
7	50.109	32766	32766	32766	[illegible]	[illegible]	[illegible]	63512	62798
8	50.109	32766	32766	[illegible]	[illegible]	[illegible]	63984	55356	55844	59136
9	50.109	[illegible]	[illegible]	[illegible]	57334	55820	51434	63976	64974
10	[illegible]	[illegible]	59304	62720	61428	59916	55104	63224	62766
[illegible]	[illegible]	52402	42440	62526	61650	59902	55328	60134	60640
307	92.874	57230	51080	64270	61628	60144	54846	59926	54846
306	88.139	52896	46970	64044	61638	59902	47394	63494	62750
309	91.968	56978	47226	63804	57816	60130	55100	63542	63230
310	85.439	52696	34986	64704	61652	56304	55130	63736	60370
311	87.046	52910	39530	63170	65214	56064	55330	63254	63020
312	85.206	52882	39290	64030	57550	56320	51490	59640	59602
313	90.597	56736	43626	62750	61656	59906	55314	63702	64014
314	88.099	52642	47226	63804	65242	64030	55114	63060	62960
315	84.347	48560	46506	59136	61414	59918	59170	63480	64014
316	85.680	56948	43160	60190	53720	59922	47408	63254	60430
317	87.082	48788	42906	64390	65346	55820	55304	63720	62722
318	86.521	49086	39306	62720	61176	63996	51756	63978	65198
319	87.174	56750	43366	63804	61882	59808	47392	63484	64480
320	86.741	52928	39500	63170	64974	60156	55356	59160	63216

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.109	50.109	0.000	50.109	0.000	0	32
2	47.949	45.796	10.738	58.334	3.685	0	32
3	49.967	54.002	6.485	61.362	4.325	0	32
4	51.503	56.110	5.859	64.127	1.176	0	32
5	53.003	59.004	5.570	65.226	2.196	0	32
6	54.064	59.371	7.180	68.398	3.614	0	32
7	54.954	60.290	6.039	66.797	1.930	0	32
8	55.990	63.242	6.296	71.004	2.576	0	32
9	56.658	62.003	4.841	68.182	1.953	0	32
10	57.406	64.141	5.547	70.931	1.676	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	50.109	50.109	0.000	50.109	0.000	0	32

Figure 37c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 1 of 2)

2	49.203	48.292	8.135	58.449	1.842	0	32
3	51.652	57.156	7.126	66.474	3.174	0	32
4	53.459	58.261	6.925	67.369	1.696	0	32
5	54.802	60.572	6.197	68.654	2.780	0	32
6	56.430	64.168	7.685	72.955	3.243	0	32
7	57.429	63.426	7.114	71.427	1.867	0	32
8	57.900	61.638	7.004	70.253	1.380	0	32
9	58.741	64.829	5.955	72.112	1.561	0	32
10	59.359	64.918	5.422	71.097	2.264	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	66.305	66.305	5.760	73.238	1.784	0	32
2	65.061	63.817	6.280	71.051	3.711	0	32
3	65.887	67.540	5.193	73.741	2.697	0	32
4	66.937	70.087	5.983	76.575	1.431	0	32
5	67.534	69.923	4.675	75.654	1.921	0	32
6	67.867	69.533	6.592	76.248	2.449	0	32
7	68.751	74.053	5.669	80.305	1.697	0	32
8	69.417	74.077	3.913	78.988	1.518	0	32
9	69.973	74.427	4.301	79.656	1.833	0	32
10	70.503	75.271	4.033	80.267	1.679	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	70.819	70.819	4.803	76.258	2.302	0	32
2	70.897	70.975	5.139	76.833	1.633	0	32
3	71.453	72.563	6.037	79.240	0.987	0	32
4	71.704	72.459	4.597	78.444	2.107	0	32
5	72.474	75.551	3.858	80.273	2.630	0	32
6	72.949	75.327	5.287	81.248	2.147	0	32
7	73.401	76.533	4.275	81.224	1.260	0	32
8	73.902	76.985	4.259	81.895	2.237	0	32
9	74.539	79.634	3.915	84.147	1.037	0	32
10	75.209	81.245	2.828	84.829	1.499	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	79.839	79.839	3.213	83.734	1.149	0	32
2	80.046	80.253	4.251	84.843	1.934	0	32
3	80.453	81.268	3.456	85.150	0.763	0	32
4	80.385	80.180	4.127	85.433	1.303	0	32
5	80.865	82.787	3.847	87.086	1.685	0	32
6	81.412	84.144	3.373	88.023	1.719	0	32
7	81.889	84.755	2.906	88.456	1.715	0	32
8	82.360	85.655	2.871	88.951	1.243	0	32
9	82.745	85.826	3.434	90.101	0.944	0	32
10	83.211	87.407	2.327	90.504	1.442	0	32

Figure 37c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Ridge using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 2 of 2)

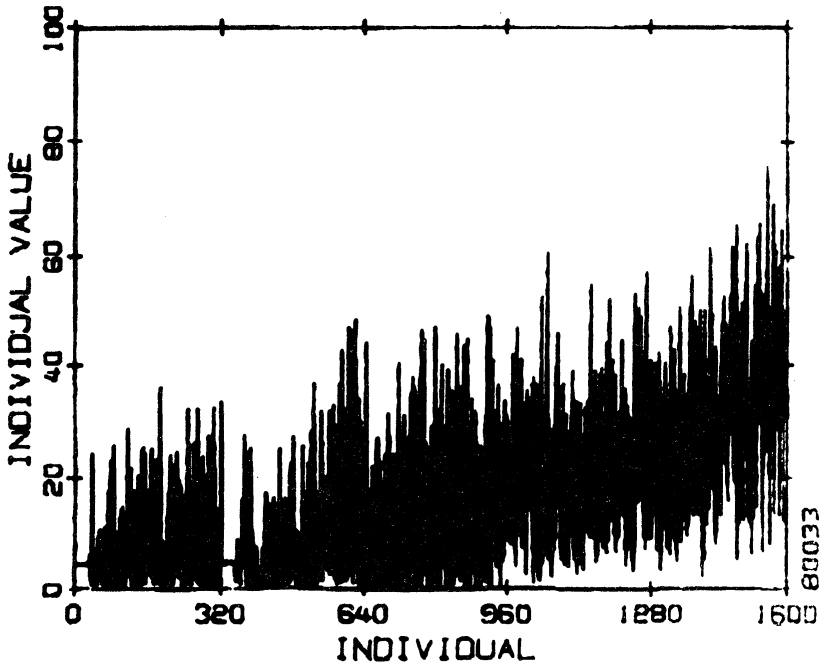


Figure 38a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

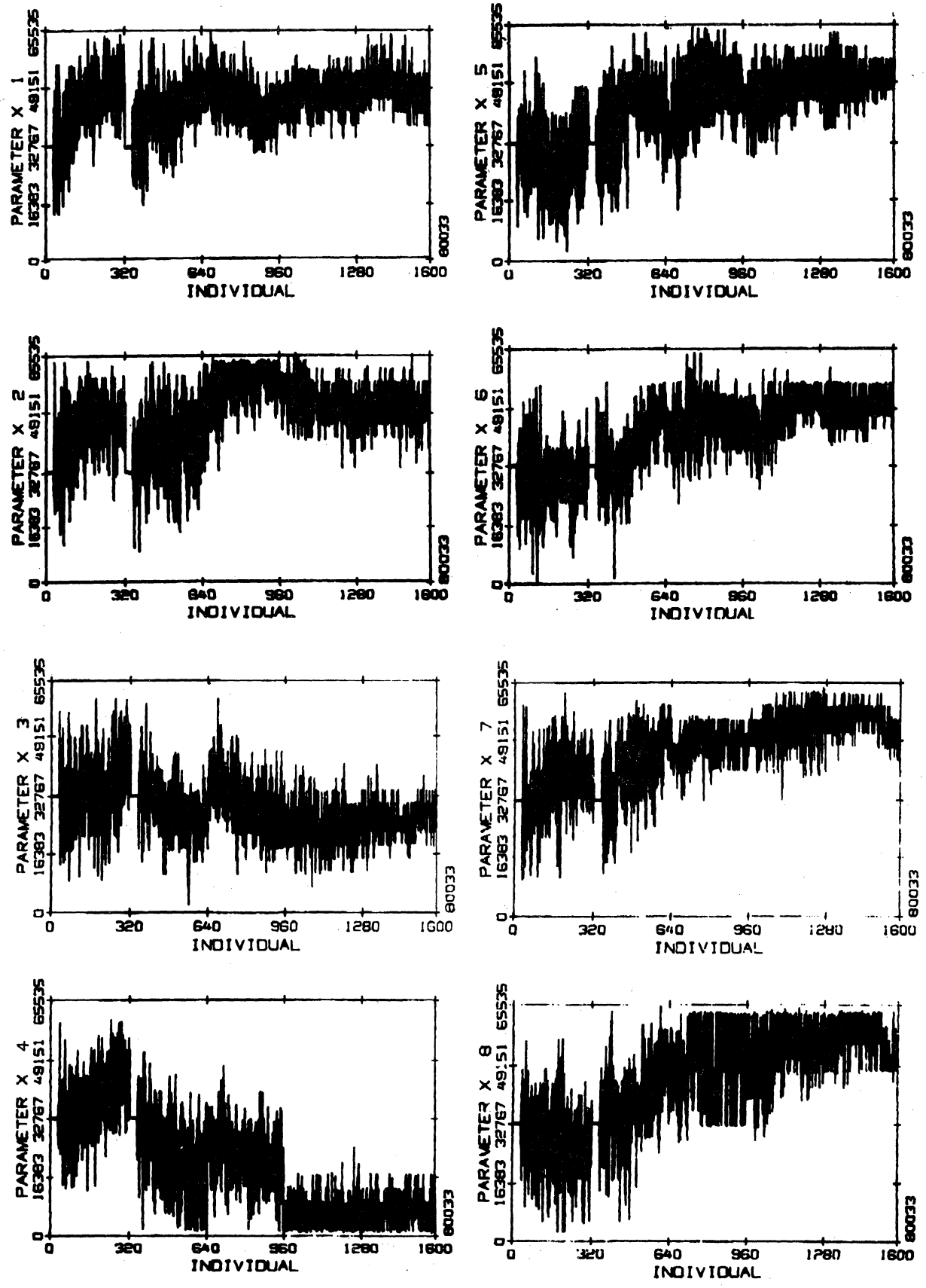


Figure 38b Parameter values of individuals during extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

```
        80033
SRS2 7/20/73
NOVLP          4
NVALU          3
PINV      0.0010
PTRA      0.0010
PCROS     0.5000
PCROL     0.5000
PMUT      0.0010
CV        0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
```

	STOP								
1	4.061	32766	32766	32766	32766	32766	32766	32766	32766
2	4.061	32766	32766	32766	32766	32766	32766	32766	32766
3	4.061	32766	32766	32766	32766	32766	32766	32766	32766
4	4.061	32766	32766	32766	32766	32766	32766	32766	32766
5	4.061	32766	32766	32766	32766	32766	32766	[illegible]	
6	4.061	32766	32766	32766	32766	32766	[illegible]	[illegible]	48066
7	4.061	32766	32766	32766	[illegible]	[illegible]	[illegible]	51754	52146
8	4.061	32766	32766	[illegible]	[illegible]	51470	51726	55100	56228
9	4.061	[illegible]	[illegible]	[illegible]	13114	47704	47360	50538	63682
10	[illegible]	[illegible]	45294	26618	8554	47196	47150	51260	55760
[illegible]	[illegible]	46626	52266	26588	4956	51260	51470	47660	44720
307	58.156	46674	48666	34478	5420	55730	56048	48604	48080
308	27.399	46656	56550	26874	16966	51948	51936	51498	56016
309	13.212	38976	52506	22776	634	51020	47164	47898	52160
310	47.475	50480	52490	26588	1596	51260	51726	43818	48320
311	41.794	54338	48878	26588	9018	51978	51950	51006	48050
312	64.672	50510	52986	30218	4936	51456	51726	51596	52160
313	35.121	50736	48650	18442	4920	55536	56062	46686	51920
314	49.250	46656	48620	26122	9034	47688	47150	54846	59360
315	41.466	50526	52714	22794	16710	47916	51696	47164	48336
316	37.525	43956	48906	26362	856	47180	47404	51708	48320
317	31.611	46448	52986	30216	1590	51470	51726	43596	48080
318	49.939	50706	56588	34540	4938	47196	47164	51036	51920
319	18.790	38752	52746	30922	5192	47196	43324	51276	48080
320	11.915	50526	37868	34538	1574	55746	52448	55566	51650

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	4.061	4.061	0.000	4.061	0.000	0	32
2	3.939	3.816	4.682	9.364	6.427	0	32
3	4.338	5.137	6.743	14.670	6.819	0	32
4	4.837	6.332	6.795	15.776	6.413	0	32
5	5.333	7.316	7.187	18.025	5.107	0	32
6	5.738	7.766	8.379	19.681	8.323	0	32
7	5.842	6.468	7.201	17.201	5.807	0	32
8	6.129	8.136	8.848	20.789	5.969	0	32
9	6.635	10.682	9.281	23.279	4.593	0	32
10	6.780	8.086	9.520	21.760	8.305	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	4.061	4.061	0.000	4.061	0.000	0	32

Figure 38c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 1 of 2)

2	4.629	5.179	6.587	13.902	7.815	0	32
3	4.868	2.964	5.628	9.916	8.123	0	32
4	4.297	4.985	5.208	12.864	3.726	0	32
5	5.075	8.186	7.615	19.363	4.221	0	32
6	5.224	5.971	6.912	15.238	7.251	0	32
7	5.992	10.594	9.469	24.242	7.497	0	32
8	6.855	12.902	9.614	26.241	5.004	0	32
9	7.607	13.622	12.832	32.001	9.404	0	32
10	8.602	17.557	14.269	36.625	7.918	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	10.270	10.270	11.078	26.278	7.778	0	32
2	9.352	8.434	9.104	22.149	5.321	0	32
3	9.785	10.649	11.716	27.200	6.869	0	32
4	10.583	12.978	13.509	32.476	5.451	0	32
5	11.491	15.122	14.337	33.514	10.511	0	32
6	12.249	16.941	12.992	31.786	5.417	0	32
7	13.039	17.782	13.353	34.746	5.137	0	32
8	13.503	16.746	13.140	32.780	7.716	0	32
9	13.994	17.926	15.399	36.924	9.844	0	32
10	14.596	20.012	11.519	32.722	4.079	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	19.664	19.664	10.533	33.592	7.170	0	32
2	20.764	21.863	10.887	35.165	3.488	0	32
3	19.678	17.505	14.804	37.633	12.069	0	32
4	20.084	21.302	11.816	35.852	6.177	0	32
5	19.668	18.007	10.619	32.115	3.369	0	32
6	19.974	21.505	10.539	35.055	9.684	0	32
7	20.205	21.590	11.149	36.640	5.070	0	32
8	20.464	22.435	11.774	37.334	7.036	0	32
9	20.293	18.810	12.699	35.659	8.838	0	32
10	21.957	27.893	14.822	47.505	5.084	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	21.700	21.700	11.356	37.236	4.713	0	32
2	22.302	22.903	11.952	38.304	5.313	0	32
3	22.572	23.113	11.782	38.933	7.943	0	32
4	23.282	25.412	14.264	45.472	6.374	0	32
5	24.117	27.459	13.155	44.806	8.933	0	32
6	25.715	33.703	11.255	47.515	3.928	0	32
7	26.892	33.939	14.445	51.982	7.818	0	32
8	27.565	32.287	16.474	54.249	6.592	0	32
9	28.673	37.537	15.746	58.002	8.817	0	32
10	30.003	41.981	14.739	59.747	5.851	0	32

Figure 38c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 2 of 2)

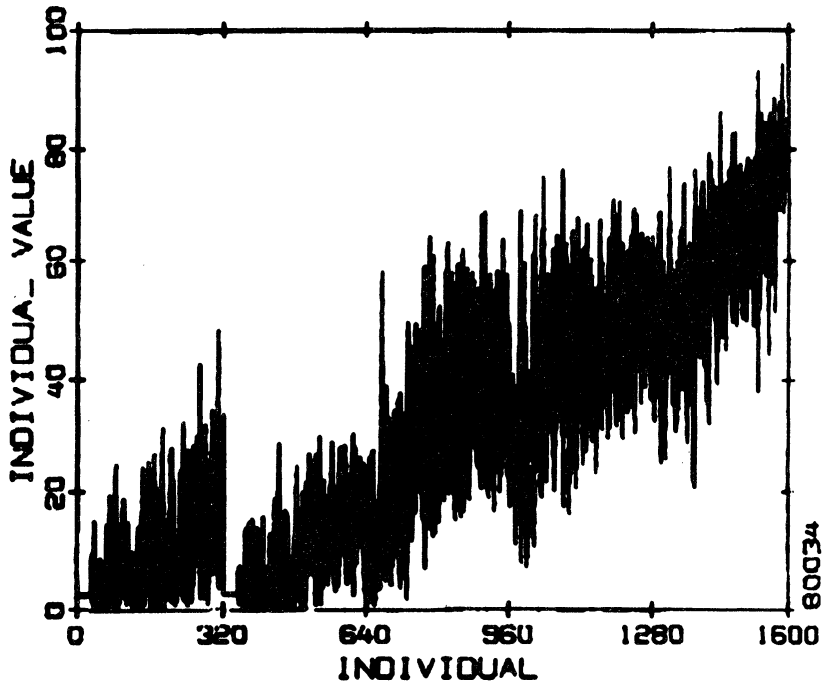


Figure 39a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Peak W using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

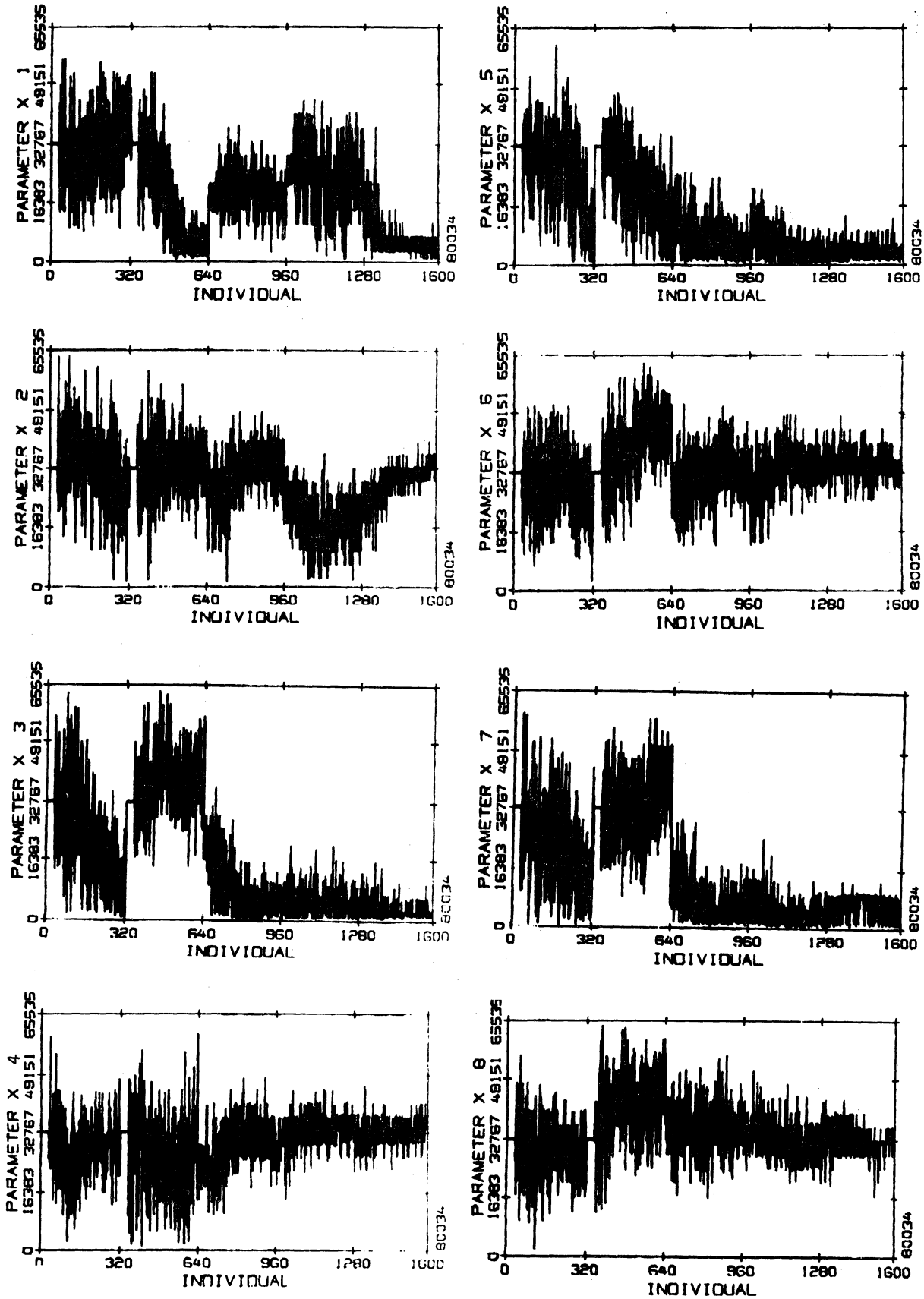


Figure 39b Parameter values of individuals during extended simple recurrent selection for 8-parameter Peak W using Gene Action 4 with random inverstion and translocation of chromosome segments and random mutation of gene conformation

```
        80034
SRS2 7/20/73
NOVLP          4
NVALU          4
PINV       0.0010
PTRA       0.0010
PCROS      0.5000
PCROL      0.5000
PMUT       0.0010
CV         0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
        80035
```

1	2.440	32766	32766	32766	32766	32766	32766	32766	32766
2	2.440	32766	32766	32766	32766	32766	32766	32766	32766
3	2.440	32766	32766	32766	32766	32766	32766	32766	32766
4	2.440	32766	32766	32766	32766	32766	32766	32766	32766
5	2.440	32766	32766	32766	32766	32766	32766	[illegible]	
6	2.440	32766	32766	32766	32766	32766		[illegible]	32164
7	2.440	32766	32766	32766	[illegible]		[illegible]078	5974	32178
8	2.440	32766	32766			1594	32572	10008	28338
9	2.440	[illegible]		[illegible]610	33854	1868	32570	2090	32178
10			32958	1392	33556	1626	35680	5928	32178
[illegible]	[illegible]996	3036	32705	1394	33810	1624	32080	9528	36002
[illegible]	80.885	3036	32764	2718	30002	1400	28492	5416	32162
308	83.676	3436	32944	1316	37442	5436	32330	1114	32192
309	77.728	6876	32718	1348	33362	1372	35920	5658	32164
310	78.144	3036	33184	1392	34096	844	35438	8808	36002
311	94.855	1060	32944	2944	33600	1866	32826	2006	32192
312	78.947	3034	36028	2660	33570	2486	35692	5944	32162
313	73.641	804	36844	2464	30000	2246	31866	9048	36002
314	68.740	6034	36784	1156	41294	1990	35930	1144	32176
315	82.234	3034	37054	1632	37664	1610	32078	1354	36016
316	70.198	6876	32990	1184	33570	6056	32080	5704	36002
317	82.530	2794	33200	2478	37664	2202	28238	2202	32192
318	85.700	2798	29106	2704	33540	1592	32574	1894	28354
319	73.202	2794	36768	1332	37170	5196	35694	5194	32176
320	75.139	1060	32974	2464	37184	2232	39800	4984	32190

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	2.440	2.440	0.000	2.440	0.000	0	32
2	2.938	3.435	3.343	8.088	2.940	0	32
3	3.622	4.991	5.144	13.949	5.765	0	32
4	4.050	5.333	4.694	11.496	4.854	0	32
5	4.589	6.744	6.028	15.253	6.243	0	32
6	5.090	7.596	8.255	19.416	7.983	0	32
7	5.456	7.657	6.879	17.394	6.246	0	32
8	6.188	11.310	9.254	25.232	5.123	0	32
9	7.114	14.516	9.795	27.384	7.423	0	32
10	8.289	18.965	9.646	31.290	8.036	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	2.440	2.440	0.000	2.440	0.000	0	32

Figure 39c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak W using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 1 of 2)

2	4.629	5.179	6.587	13.912	7.815	0	32
3	4.068	2.964	5.628	9.916	8.123	0	32
4	4.297	4.985	5.268	12.864	3.726	0	32
5	5.975	8.186	7.618	19.363	4.221	0	32
6	5.224	5.971	6.912	15.238	7.251	0	32
7	5.992	10.594	9.469	24.242	7.497	0	32
8	6.855	12.902	9.614	26.241	5.004	0	32
9	7.607	13.622	12.832	32.001	9.404	0	32
10	8.602	17.557	14.269	36.625	7.918	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	10.270	10.270	11.078	26.278	7.778	0	32
2	9.352	8.434	9.104	22.149	5.321	0	32
3	9.785	10.649	11.716	27.260	6.069	0	32
4	10.583	12.978	13.509	32.476	5.451	0	32
5	11.491	15.122	14.337	33.514	10.511	0	32
6	12.249	16.941	12.992	31.786	5.417	0	32
7	13.039	17.782	13.353	34.746	5.137	0	32
8	13.503	16.746	13.140	32.780	7.716	0	32
9	13.994	17.926	15.399	36.924	9.844	0	32
10	14.596	20.012	11.519	32.722	4.079	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	19.664	19.664	10.533	33.592	7.170	0	32
2	20.764	21.863	10.887	35.165	3.488	0	32
3	19.678	17.505	14.804	37.633	12.069	0	32
4	20.084	21.302	11.816	35.852	6.177	0	32
5	19.668	18.007	10.619	32.115	3.369	0	32
6	19.974	21.505	10.539	35.055	9.684	0	32
7	20.205	21.590	11.149	36.640	5.070	0	32
8	20.464	22.435	11.774	37.334	7.036	0	32
9	20.298	18.810	12.699	35.659	8.838	0	32
10	21.957	27.893	14.822	47.505	5.084	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	21.700	21.700	11.356	37.236	4.713	0	32
2	22.302	22.903	11.952	38.304	5.313	0	32
3	22.572	23.113	11.782	38.933	7.943	0	32
4	23.282	25.412	14.264	46.472	6.374	0	32
5	24.117	27.459	13.155	44.806	8.933	0	32
6	25.715	33.703	11.255	47.515	3.928	0	32
7	26.890	33.939	14.445	51.982	7.818	0	32
8	27.565	32.287	16.474	54.249	6.592	0	32
9	28.673	37.537	15.746	58.002	8.817	0	32
10	30.003	41.981	14.739	59.747	5.851	0	32

Figure 38c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak NE using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 2 of 2)

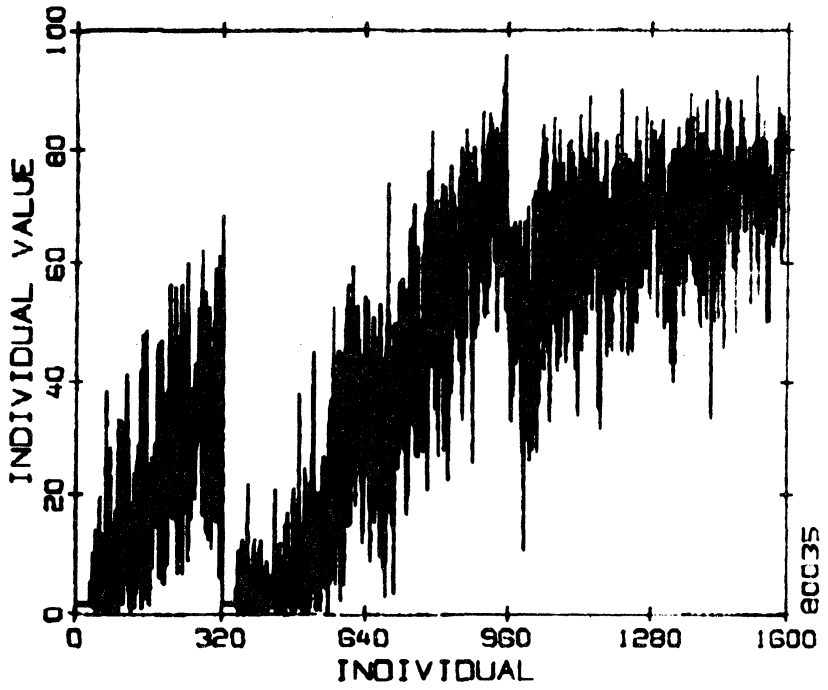


Figure 40a Phenotypic value of individuals during extended simple recurrent selection for 8-parameter Peak S using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

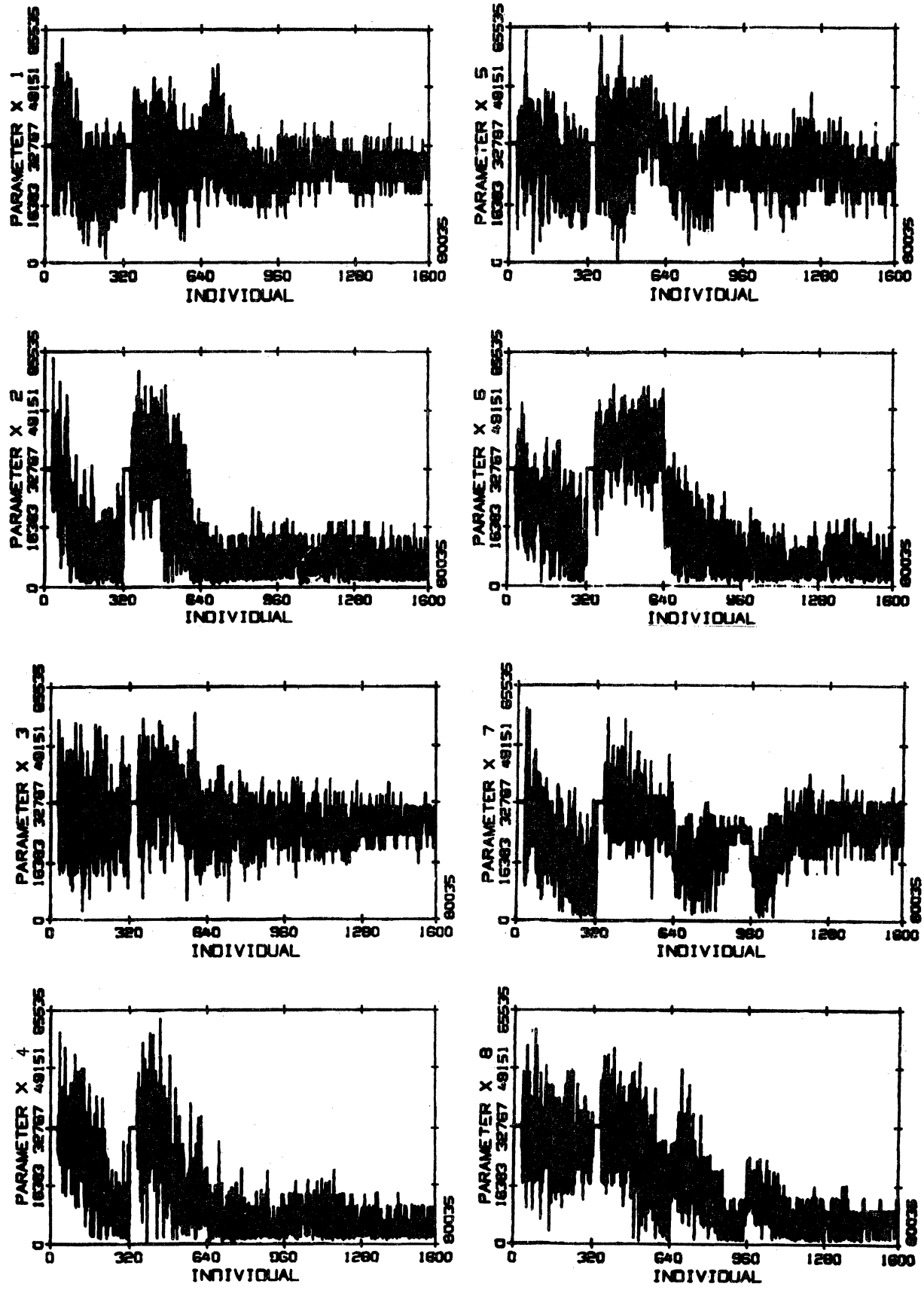


Figure 40b Parameter values of individuals during extended simple recurrent selection for 8-parameter Peak S using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation

```
        80035
SRS2 7/20/73
NOVLP          4
NVALU          5
PINV       0.0010
PTRA       0.0010
PCROS      0.5000
PCROL      0.5000
PMUT       0.0010
CV         0.0000
NPOP          32
NSEL           8
LCYC          10
NPAR           8
NSEG          32
NVAR           5
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
        STOP
```

1	1.642	32766	32766	32766	32766	32766	32766	32766	32766
2	1.642	32766	32766	32766	32766	32766	32766	32766	32766
3	1.642	32766	32766	32766	32766	32766	32766	32766	32766
4	1.642	32766	32766	32766	32766	32766	32766	32766	32766
5	1.642	32766	32766	32766	32766	32766	32766	[illegible]	
6	1.642	32766	32766	32766	32766	32766	[illegible]	[illegible]	5002
7	1.642	32766	32766	32766	[illegible]	[illegible]	[illegible]	25608	9126
8	1.642	32766	32766	[illegible]	[illegible]	28474	2976	29654	8588
9	1.642	[illegible]	[illegible]	[illegible]	2030	24138	5486	25560	9110
10	[illegible]	[illegible]	[illegible]	9810	27678	2016	20778	6770	29102	5272
[illegible]	[illegible]	27486	9694	23598	1568	24632	5360	33210	8870
[illegible]	86.373	30846	1995	28142	5918	28714	6514	24888	5242
308	69.400	27486	9692	27915	1598	32088	1646	21048	9354
309	80.989	27498	9676	24076	5410	24424	9906	21496	1672
310	85.760	26782	5824	27452	9954	20810	2914	25324	5286
311	85.956	27740	9678	27916	5680	28220	1984	29132	8590
312	60.309	27018	1984	20236	5888	26236	14480	33496	4732
313	64.338	30660	13504	27902	2062	24424	10850	32718	4748
314	86.267	23900	9678	24076	2286	24168	6034	28864	4988
315	74.995	27260	1985	31306	1822	20598	5682	25520	5062
316	84.583	23646	5598	24076	5168	20824	6318	29372	9068
317	81.179	27246	5600	31546	2500	24394	1856	25340	8842
318	62.750	27486	5616	31084	2032	16458	6050	25052	12950
319	83.393	27742	9438	27692	2048	28234	6034	21724	9128
320	82.930	27980	5598	27692	1810	28218	2208	29388	8604

VARIETY 1

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	1.642	1.642	0.000	1.642	0.000	0	32
2	3.052	4.463	4.617	11.050	4.276	0	32
3	4.972	8.611	9.871	22.847	9.195	0	32
4	6.911	12.727	11.282	28.622	6.902	0	32
5	9.207	18.395	12.863	34.463	10.047	0	32
6	11.120	20.685	10.853	34.794	8.224	0	32
7	13.453	27.448	13.163	46.070	7.408	0	32
8	15.600	30.633	13.634	48.379	7.813	0	32
9	17.634	33.901	12.534	49.017	7.184	0	32
10	19.451	35.802	14.899	54.661	7.601	0	32

VARIETY 2

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	1.642	1.642	0.000	1.642	0.000	0	32

Figure 40c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak S using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 1 of 2)

2	2.810	3.978	4.668	10.193	5.148	0	32
3	3.211	4.012	3.865	9.467	2.040	0	32
4	3.418	4.042	4.562	10.522	4.651	0	32
5	3.837	5.509	5.703	13.978	4.634	0	32
6	4.382	7.106	8.344	18.959	8.501	0	32
7	5.537	12.469	9.669	25.424	8.567	0	32
8	7.485	21.122	11.366	34.425	8.645	0	32
9	9.717	27.571	12.682	43.759	7.982	0	32
10	12.217	34.721	11.271	48.830	6.091	0	32

VARIETY 3

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	31.810	31.810	10.915	45.902	5.348	0	32
2	31.356	30.903	15.192	49.480	10.726	0	32
3	33.901	38.990	11.315	53.730	3.397	0	32
4	36.709	45.133	12.051	61.315	5.184	0	32
5	39.385	50.091	14.481	69.897	7.784	0	32
6	41.628	52.841	13.981	68.916	3.361	0	32
7	44.359	60.748	12.435	75.923	3.598	0	32
8	46.561	61.970	12.894	76.875	4.116	0	32
9	49.248	70.742	9.770	83.252	3.618	0	32
10	51.436	71.129	11.073	85.562	5.533	0	32

VARIETY 4

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	51.776	51.776	9.528	64.092	2.647	0	32
2	48.159	44.542	15.422	65.118	5.868	0	32
3	50.959	56.558	14.925	76.338	5.093	0	32
4	53.994	63.099	11.475	77.123	5.411	0	32
5	55.478	61.417	12.168	76.450	4.167	0	32
6	57.352	66.720	11.201	80.978	4.420	0	32
7	58.128	62.785	13.141	78.689	3.979	0	32
8	58.836	63.789	10.547	77.061	7.026	0	32
9	59.444	64.307	11.482	78.514	3.362	0	32
10	59.978	64.784	8.305	75.935	5.847	0	32

VARIETY 5

GEN	EFF	AVG	STD	AVGS	STDS	NIZ	NTR
1	72.519	72.519	8.322	83.248	1.731	0	32
2	67.571	62.623	10.491	75.063	4.398	0	32
3	68.402	70.064	10.262	82.977	3.525	0	32
4	68.324	68.089	10.166	81.583	4.374	0	32
5	68.557	69.488	12.985	83.811	4.863	0	32
6	69.624	74.964	10.013	85.159	2.810	0	32
7	70.265	74.110	8.642	82.930	3.151	0	32
8	70.553	72.569	8.499	82.512	5.019	0	32
9	70.476	69.857	8.583	80.185	3.017	0	32
10	71.037	76.083	8.055	85.359	1.592	0	32

Figure 40c Input data, initial and final parameter values, and generation statistics for five varieties in extended simple recurrent selection for 8-parameter Peak S using Gene Action 4 with random inversion and translocation of chromosome segments and random mutation of gene conformation (Sheet 2 of 2)

4

CONCLUSIONS

One objective of this study was to determine the relative effectiveness of additive vs. epistatic gene action algorithms for numerical parameter synthesis. Four additive and twelve epistatic algorithms were investigated in conjunction with five ARTIFICIAL BREEDING procedures. Six mathematical functions were used to test the direct-search performance of the method.

Additive Gene Action 4 exhibited superior performance in a majority of the experiments. In this algorithm, four, 16-gene complexes control the synthesis of each numerical parameter. Four levels of effect are used to obtain a parameter range of [0,65535], but, within each complex, the genes contribute additively and with equal effect. Redundancy of encoding extreme parameter values is provided by a transformation of the primary, cummulative effect of the individual loci.

Of the epistatic models, Gene Action 6 was judged most effective. This algorithm avoids a basic problem of the binary number system as a basis for artificial genetic encoding--the requirement that the conformation of genes at many loci change in order to produce a small change in the encoded parameter value. It too provides redundancy of encoding extreme parameter values by a transformation of the value determined by the primary algorithm.

Another objective was to model and investigate the effects of intra-allelic dominance at the genotypic level. Eight of the sixteen gene action algorithms developed in the study incorporate dominance modifier loci that act in conjunction with the functional loci.

There appears to be no advantage to dominance modification in parameter optimization where storage of latent information is not essential. The most noticeable effect is an increase in parameter variance during the early generations of a breeding program. Dominance would be more important in adaptive system applications of ARTIFICIAL BREEDING.

A third objective of the project was to develop specific ARTIFICIAL BREEDING systems for direct-search optimization in up to 32 dimensional parameter spaces. Seven such systems were developed and investigated in many different experiments. Five are single-breeding-program systems that begin with completely heterozygous source populations of artificial organisms. Two are extended-breeding-program systems that generate a sequence of varieties, starting with two derived from completely heterozygous source populations; improved varieties are bred from crosses of the most valuable of previously developed lines.

The breeding methods used in these systems simulate the following techniques of agricultural plant breeding: 1) pedigree method, 2) bulk population breeding, 3) mass selection, 4) simple recurrent selection and 5) reciprocal recurrent selection. The most effective results were obtained by an extended-breeding-program system using additive, polygenic control of parameter synthesis and simple recurrent selection for the objective character.

The most versatile artificial organisms appear to be those capable--as many plant species are--of both self- and cross-fertilization. They can be crossed to create and systain genetic variation required for exploration of the genetic parameter space; and they can be selfed to rapidly fix desireable combinations of alleles.

Linkage seems to inhibit the dismantling of desireable gene combinations, but it also accelerates fixation of undesireable alleles. The net effect is to impede the progress of short-term breeding programs.

Random inversion and translocation of chromosome segments during simulated interphase and the random mutation of alleles in zygote genotypes appears to significantly improve the performance of extended-breeding by simple recurrent selection. This is based on a sequence of ten experiments in breeding for five different objective characters, with, and without random aberrations of chromosome structure and gene conformation. These experiments were conducted at the end of the study. They are not considered conclusive, but they do indicate the potential of the ARTIFICIAL BREEDING method and will be investigated in further studies.

REFERENCES

R. W. Allard, Principles of Plant Breeding, Wiley, 1960

R. B. Hollstien, "Artificial Genetic Adaptation in Computer Control Systems," University of Michigan Technical Report 032960-14-T, April, 1971

G. J. McMurtry, "Adaptive Optimization Procedures," Adaptive, Learning and Pattern Recognition Systems, J. M. Mendel and K. S. Fu, eds., Academic Press, 1970

L. E. Mettler and T. G. Gregg, Population Genetics and Evolution, Prentice-Hall, 1969

F. W. Stahl, The Mechanics of Inheritance, Prentice-Hall, 1969

W. H. Swann, "Direct Search Methods," Numerical Methods for Unconstrained Optimization, W. Murray, ed., Academic Press, 1972

J. D. Watson, Molecular Biology of the Gene, W. A. Benjamin, Inc., 1970

APPENDIX

COMPUTER PROGRAMS USED IN EXPERIMENTAL INVESTIGATIONS OF ARTIFICIAL GENETIC BREEDING PROCEDURES

Artificial breeding experiments were run on a Digital Equipment Corporation PDP-9 computer at the University of Michigan's Simulation Center. The PDP-9 CHAIN/EXECUTE system structure, format of input data, and listings of all programs used in these experiments are included in this Appendix. The input variables are defined as follows:

NDVLP	integer from 1 to 12 specifying the gene action
NVALU	integer from 1 to 6 specifying the objective character
PINV	probability of chromosome rupture between adjacent gene complexes and refusion with a chromosome segment in an inverted position
PTRA	probability of chromosome rupture between adjacent gene complexes and refusion with segments of two chromosomes translocated
PCROS	probability of crossing over between adjacent gene complexes
PCROL	probability of crossing over between adjacent loci within gene complexes
PMUT	probability of independent mutation of zygote alleles
POUCR	probability of outcrossing in Bulk Population Breeding
CV	lower bound of objective character values for parameters within the admissible domain
NPOP	population size (sequence of values for Pedigree Breeding)
NSEL	number selected (sequence of values for Pedigree Breeding)
LGEN	last generation
NVAR	number of varieties
LCYC	last cycle of recurrent selection
NSAMP	size of half-sib families in Reciprocal Recurrent Selection
NPAR	number of parameters
NSEG	number of gene complexes

NREP	number of replications
IX	initial (odd integer) value of the pseudorandom number generator
IPAP	parameter print control (1 specifies all trial points are to be printed)
IPBP	parameter print control (1 specifies only trial points having objective value greater than previous trials are to be printed)
IPAF	allele frequency print control (1 specifies frequencies are to be printed for each generation)
IPCS	chromosome structure print control (1 specifies locations of gene complexes in each chromosome are to be printed in the last generation)

Graphical results of the experiments were generated by the computer on a storage-type CRT and hard-copy unit.

Input Data

```
          10001
PM1 6/7/73/
NDVLP           1
NVALU           6
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP            64     64     32     16      8      4      4      4      4
NSEL            32     16      8      4      2      1      1      1      1
NPAR             2
NSEG             8
NREP             5
IX               1
IPAP             0
IPBP             1
IPAF             0
IPCS             0
          STOP
```

Main Program (MPM1)

```
001       C MPM1 V1
002       C PEDIGREE METHOD 1
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM PM1
004             INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005             LOGICAL EVENT,VIAB
006             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
007             1,V(100),VS(100),NP(10),NS(10)
008             COMMON /CPS/CP,S
009             DATA F1(1),F2(1),F3(1)/5HF1    ,5HF2    ,5HF3    /
010             1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
011             1,STOP/5HSTOP /,PFILE(1)/5HPM1   /
012       C READ PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,
013       C CV,NP,NS,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,
014       C CDATA FROM DISK FILE
015             IF(ITOG(2).EQ.0)GO TO 6
016             WRITE(6,1)
017       1     FORMAT(1X,'DATA FILE')
018             READ(5,5)PFILE(1)
019       5     FORMAT(A5)
020       6     CALL SEEK(1,PFILE)
```

```
021     10      READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
022             1,PCROS,PCROL,PMUT,CV
023     15      FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
024             READ(1,20)(NP(I),I=2,10),(NS(J),J=2,10)
025     20      FORMAT(9X,916/9X,9I6)
026             READ(1,25)NPAR,NSEG,NREP,IX
027     25      FORMAT(9X,I6,3(/9X,I6))
028             READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
029     30      FORMAT(9X,I6,3(/9X,I6)/9X,A5)
030             CALL CLOSE(1)
031     C DELETE AND RECREATE PRINT FILE
032             CALL DLETE(7,PFILE,I)
033             CALL ENTER(7,PFILE)
034     C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,
035     C CV,NP,NS,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,
036     C CDATA INTO PRINT FILE PFILE
037             WRITE(7,35)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
038             1,PCROS,PCROL,PMUT,CV
039     35      FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
040             1/' PINV',F11.4/' PTRA',F11.4
041             1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
042             1/' CV',F13.4)
043             WRITE(7,40)(NP(I),I=2,10),(NS(J),J=2,10)
044     40      FORMAT(' NPOP',I11,8I6/' NSEL',I11,8I6)
045             WRITE(7,45)NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
046     45      FORMAT(' NPAR',I11/' NSEG',I11/' NREP',I11
047             1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
048             1/' IPCS',I11/10X,A5)
049     C ASSIGN LAST GENERATION
050             LGEN=10
051     C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
052     C UP TO 100 CHROMOSOME ARRAYS
053             CALL DLETE(1,F1,I)
054             CALL DEFINE(1,4*NSEG,100,F1,IV1,0,0,0)
055     C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
056     C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH GENERATION
057             CALL DLETE(2,F2,I)
058             CALL DEFINE(2,80,(NREP+3)*LGEN,F2,IV2,1,0,0)
059     C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
060     C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
061     C AND GENERATION
062             CALL DLETE(3,F3,I)
063             CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
064     C START RANDOM NUMBER GENERATOR AT IX
065             IX=-IX
066             CALL URN(IX,U)
067     C INITIALIZE RUN COUNTER AND BEGIN RUN IRUN
068             IRUN=1
069     50      INDIV=0
070             NTRT=0
071             VSUM=0.
072             E=0.
073             IGEN=2
```

```
074               HIV=0.
075               ISTOR=0
076               IDRAW=50
077       C BEGIN GENERATION IGEN
078       60      IND=1
079               NIZ=0
080               NTR=0
081               NPOP=NP(IGEN)
082               NSEL=NS(IGEN)
083       C FAMILY SIZE
084               NFSZ=NPOP/NSEL
085       C SELECT PARENTAL GENOTYPES AND LOAD INTO CORE
086       C ARRAYS CP AND S
087       70      IF(IGEN.GT.2)GO TO 72
088       C FORM RANDOM HETEROZYGOUS PARENT GENOTYPE
089       C FROM VIRTUAL F1 POPULATION
090               DO 71 I=1,NSEG
091               CALL URN(IX,U)
092               DO 71 K=1,2
093               DO 71 J=1,2
094               N=(I-1)/8+1
095               M=I-(N-1)*8
096               CP(I,J,K)=IPAC(N,M)
097               IF(J.EQ.1)S(I,J,K)=IX
098               IF(J.EQ.2)S(I,J,K)=-IX-1
099       71      CONTINUE
100               GO TO 76
101       C FETCH PARENT
102       72      IFAM=(IND-1)/NFSZ+1
103               IF(IND.EQ.1)GO TO 75
104       73      IFM=IFM+1
105               IF(IFAM.NE.IFAMO)GO TO 75
106               IF(ITOG(1).EQ.1)WRITE(6,74)IFAM,IFM,I1
107       74      FORMAT(29X,3I6)
108               GO TO 76
109       75      I1=R(IFAM)+IDRAW
110               I2=I1
111               READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
112               READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
113               IFAMO=IFAM
114               IFM=0
115               GO TO 73
116       C FORM ZYGOTE GENOTYPE BY UNION OF GAMETES DERIVED FROM
117       C PARENT GENOTYPES BY INDEPENDENT SEGREGATION AND CROSSOVER
118       C WITH PROBABILITIES PCROS AND PCROL OF CHIASMA BETWEEN
119       C ADJACENT SEGMENTS AND ADJACENT LOCI RESPECTIVELY
120       76      CALL INVER(CP,NSEG,PINV)
121               CALL TRANS(CP,NSEG,PTRA)
122               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
123               CALL MUTAT(S,NSEG,PMUT)
124       C PRINT CHROMOSOME STRUCTURE DURING LAST GENERATION IF IPCS = 1
125               IF(IGEN.EQ.LGEN.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
126       C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
```

```
127     C ZYGOTE IS INVIABLE
128             IF(VIAB(S,NSEG))GO TO 77
129             NIZ=NIZ+1
130             GO TO 70
131     C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
132     C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
133     C GENERATION IF IPAF = 1
134     77      IF(IPAF.EQ.0)GO TO 80
135             CALL CA(IGEN,LGEN,IND,NPOP,NSEG)
136     C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
137     C BY NDVLP
138     80      GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
139     81      CALL SGA1(NSEG,S,NPAR,X)
140             GO TO 90
141     82      CALL SGA2(NSEG,S,NPAR,X)
142             GO TO 90
143     83      CALL SGA3(NSEG,S,NPAR,X)
144             GO TO 90
145     84      CALL SGA4(NSEG,S,NPAR,X)
146             GO TO 90
147     85      CALL SGA5(NSEG,S,NPAR,X)
148             GO TO 90
149     86      CALL SGA6(NSEG,S,NPAR,X)
150             GO TO 90
151     87      CALL SGA7(NSEG,S,NPAR,X)
152             GO TO 90
153     88      CALL SGA8(NSEG,S,NPAR,X)
154             GO TO 90
155     89      CALL SGA9(NSEG,S,NPAR,X)
156             GO TO 90
157     810     CALL SGA10(NSEG,S,NPAR,X)
158             GO TO 90
159     811     CALL SGA11(NSEG,S,NPAR,X)
160             GO TO 90
161     812     CALL SGA12(NSEG,S,NPAR,X)
162     C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
163     C FUNCTION SPECIFIED BY NVALU
164     90      GO TO(91,92,93,94,95,96),NVALU
165     91      CALL V1(NPAR,X,V(IND))
166             GO TO 97
167     92      CALL V2(NPAR,X,V(IND))
168             GO TO 97
169     93      CALL V3(NPAR,X,V(IND))
170             GO TO 97
171     94      CALL V4(NPAR,X,V(IND))
172             GO TO 97
173     95      CALL V5(NPAR,X,V(IND))
174             GO TO 97
175     96      CALL V6(NPAR,X,V(IND))
176     C INCREMENT INDIVIDUAL COUNTER
177     97      INDIV=INDIV+1
178     C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
179     C ARE WITHIN THE ADMISSIBLE DOMAIN
```

```
180             IF(V(IND).LT.CV)GO TO 100
181             NTR=NTR+1
182             NTRT=NTRT+1
183             VSUM=VSUM+V(IND)
184             IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
185       C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
186       C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
187       C OF ALL PRECEDING INDIVIDUALS
188       100   IF(IPBP.EQ.1)GO TO 101
189             IF(IPAP.EQ.1)GO TO 102
190             GO TO 110
191       101   IF(V(IND).LE.HIV)GO TO 110
192             HIV=V(IND)
193       102   IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
194       105   FORMAT(1X,I5,F10.3,8I7)
195             IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
196       106   FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
197       110   IK=0
198       C BRANCH ON GENERATION AND FAMILY MEMBER
199             IF(IGEN.EQ.2)GO TO 121
200             K=IFAM+ISTOR
201             IF(IFM.GT.1)GO TO 120
202       C STORE FIRST INDIVIDUAL OF EACH FAMILY
203             VS(IFAM)=V(IND)
204             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
205             IF(ITOG(1).EQ.1)GO TO 125
206             GO TO 130
207       C REPLACE FAMILY REPRESENTATIVE WITH THIS INDIVIDUAL
208       C IF THIS INDIVIDUAL HAS HIGHER PHENOTYPIC VALUE
209       120   IF(V(IND).LT.VS(IFAM))GO TO 130
210             VS(IFAM)=V(IND)
211             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
212             IF(ITOG(1).EQ.1)GO TO 125
213             GO TO 130
214       C STORE FIRST NSEL GENOTYPES DURING F2 GENERATION
215       121   IF(IND.GT.NSEL)GO TO 122
216             K=IND+ISTOR
217             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
218             VS(IND)=V(IND)
219             IF(ITOG(1).EQ.1)GO TO 125
220             GO TO 130
221       C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
222       C F2 GENERATION IF VALUE OF THIS INDIVIDUAL EXCEEDS
223       C THE LOWEST VALUE
224       122   LOW=1
225             DO 123 I=1,NSEL
226             IF(VS(I).LT.VS(LOW))LOW=I
227       123   CONTINUE
228             IF(V(IND).LT.VS(LOW))GO TO 130
229             K=LOW+ISTOR
230             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
231             VS(LOW)=V(IND)
232       C PRINT GENERATION, INDIVIDUAL, VALUE, AND LOCATION IF
233       C GENOTYPE IS STORED IN F1 AND PEDIGREE IS REQUESTED
```

```
234      125      IF(ITOG(1).EQ.1)WRITE(6,126)IGEN,IND,V(IND),K
235      126      FORMAT(2I6,F11.3,I6)
236               IK=1
237      C PRINT GENERATION, INDIVIDUAL, AND VALUE IF PEDIGREE
238      C IS REQUESTED
239      130      IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)IGEN,IND,V(IND)
240               IF(IND.EQ.NPOP)GO TO 140
241               IND=IND+1
242               GO TO 70
243      C END GENERATION IGEN
244      C LIST FAMILIES ACCORDING TO SUPERIOR FAMILY MEMBER
245      140      CALL LIST(VS,NSEL,R)
246      C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
247               CALL ASD(VS,NSEL,AVGS,STDS)
248      C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
249               CALL ASD(V,NPOP,AVG,STD)
250      C STORE IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
251               K=(IRUN-1)*LGEN+IGEN
252               WRITE(2'K,150)IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR
253      150      FORMAT(1X,I3,5F10.3,2I10)
254      C TEST FOR END OF RUN
255               IF(IGEN.EQ.LGEN)GO TO 160
256      C BEGIN NEW GENERATION
257               IGEN=IGEN+1
258               IDRAW=IDRAW+50
259               IF(IDRAW.GT.50)IDRAW=0
260               ISTOR=ISTOR+50
261               IF(ISTOR.GT.50)ISTOR=0
262               GO TO 60
263      C TEST FOR END OF REPLICATE RUNS
264      160      IF(IRUN.EQ.NREP)GO TO 170
265               IRUN=IRUN+1
266               GO TO 50
267      C MEAN AND EXTREMES OF REPLICATE RUNS
268      170      CALL MERR(LGEN,NREP)
269      C CLOSE FILES
270               CALL CLOSE(1)
271               CALL CLOSE(2)
272               CALL CLOSE(3)
273               CALL CLOSE(7)
274      C TEST FOR STOP
275               IF(CDATA(1).EQ.STOP)STOP
276      C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
277      C IF ITOG(2) = 2
278               IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
279      180      FORMAT(1X,'RESTART AT ',A5)
280               IF(ITOG(2).EQ.2)PAUSE
281      C CONTINUE USING INPUT DATA IN FILE CDATA
282               CALL SEEK(1,CDATA)
283               GO TO 10
284               END
```

Pedigree Method 2 (PM2)

PDP-9 CHAIN/EXECUTE System

```
DOS-15 V1A
$B PR

DOS-15 V1A
$$JOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>PM2
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MPM2,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:PDFSV
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
        16646-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          60001
PM2 7/9/73
NDVLP           6
NVALU           1
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.0500
PMUT       0.0000
CV         0.0000
NPOP           32   32   16    8    4    2    2    2    2    2
NSEL           16   16    8    4    2    1    1    1    1    1
LGEN           10
NPAR            2
NSEG            2
NVAR            6
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
          STOP
```

Main Program (MPM2)

```
001       C MPM2 V1
002       C PEDIGREE METHOD 2
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM PM2
004             INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005             LOGICAL EVENT,VIAB
006             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
007             1,V(100),VS(100),NP(10),NS(10),VV(2)
008             COMMON /CPS/CP,S
009             DATA F1(1),F2(1),F3(1)/5HF1   ,5HF2   ,5HF3   /
010             1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
011             1,STOP/5HSTOP /,PFILE(1)/5HPM2  /
012       C READ PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,
013       C CV,NP,NS,LGEN,NPAR,NSEG,NVAR,IX,IPAP,IPBP,IPAF,IPCS,
014       C CDATA FROM DISK FILE
015             IF(ITOG(2).EQ.0)GO TO 6
016             WRITE(6,1)
017       1     FORMAT(1X,'DATA FILE')
018             READ(5,5)PFILE(1)
019       5     FORMAT(A5)
020       6     CALL SEEK(1,PFILE)
```

```
021      10       READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
022               1,PCROS,PCROL,PMUT,CV
023      15       FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
024               READ(1,20)(NP(I),I=1,10),(NS(J),J=1,10)
025      20       FORMAT(10X,10I5/10X,10I5)
026               READ(1,25)LGEN,NPAR,NSEG,NVAR,IX
027      25       FORMAT(9X,I6,4(/9X,I6))
028               READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
029      30       FORMAT(9X,I6,3(/9X,I6)/9X,A5)
030               CALL CLOSE(1)
031      C DELETE AND RECREATE PRINT FILE
032               CALL DLETE(7,PFILE,I)
033               CALL ENTER(7,PFILE)
034      C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,
035      C CV,NP,NS,LGEN,NPAR,NSEG,NVAR,IX,IPAP,IPBP,IPAF,IPCS,
036      C CDATA INTO PRINT FILE PFILE
037               WRITE(7,35)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
038               1,PCROS,PCROL,PMUT,CV
039      35       FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
040               1/' PINV',F11.4/' PTRA',F11.4
041               1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
042               1/' CV',F13.4)
043               WRITE(7,40)(NP(I),I=1,10),(NS(J),J=1,10)
044      40       FORMAT(' NPOP',I11,9I5/' NSEL',I11,9I5)
045               WRITE(7,45)LGEN,NPAR,NSEG,NVAR,IX,IPAP,IPBP
046               1,IPAF,IPCS,CDATA(1)
047      45       FORMAT(' LGEN',I11/' NPAR',I11/' NSEG',I11/' NVAR',I11
048               1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
049               1/' IPCS',I11/10X,A5)
050      C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
051      C UP TO 102 CHROMOSOME ARRAYS
052               CALL DLETE(1,F1,I)
053               CALL DEFINE(1,4*NSEG,102,F1,IV1,0,0,0)
054      C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
055      C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH GENERATION
056               CALL DLETE(2,F2,I)
057               CALL DEFINE(2,80,NVAR*LGEN,F2,IV2,1,0,0)
058      C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
059      C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
060      C AND GENERATION
061               CALL DLETE(3,F3,I)
062               CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
063      C START RANDOM NUMBER GENERATOR AT IX
064               IX=-IX
065               CALL URN(IX,U)
066      C INITIALIZE VARIETY COUNTER AND BEGIN VARIETY IVAR
067               IVAR=1
068      50       INDIV=0
069               NTRT=0
070               VSUM=0.
071               E=0.
072               IGEN=1
073               HIV=0.
```

```
074               ISTOR=0
075               IDRAW=50
076       C BEGIN GENERATION IGEN
077       60      IND=1
078               NIZ=0
079               NTR=0
080               NPOP=NP(IGEN)
081               NSEL=NS(IGEN)
082               NFSZ=NPOP/NSEL
083       C SELECT PARENTAL GENOTYPES AND LOAD ARRAYS CP AND S
084       61      IF(IGEN.GT.1)GO TO 72
085               IF(IVAR.GT.2)GO TO 63
086       C FORM RANDOM HOMOZYGOUS PARENT GENOTYPE FOR INITIAL CROSS
087               DO 62 K=1,2
088               DO 62 I=1,NSEG
089               CALL URN(IX,U)
090               IS=IX
091               IF(EVENT(.5))IS=-IX-1
092               DO 62 J=1,2
093               N=(I-1)/8+1
094               M=I-(N-1)*8
095               CP(I,J,K)=IPAC(N,M)
096               S(I,J,K)=IS
097       62      CONTINUE
098               GO TO 76
099       C FETCH PARENTS OF VARIETAL CROSS
100       63      READ(1'101)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
101               READ(1'102)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
102               GO TO 76
103       C FETCH PARENT
104       72      IFAM=(IND-1)/NFSZ+1
105               IF(IND.EQ.1)GO TO 75
106       73      IFM=IFM+1
107               IF(IFAM.NE.IFAMO)GO TO 75
108               IF(ITOG(1).EQ.1)WRITE(6,74)IFAM,IFM,I1
109       74      FORMAT(29X,3I6)
110               GO TO 76
111       75      I1=R(IFAM)+IDRAW
112               I2=I1
113               READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
114               READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
115               IFAMO=IFAM
116               IFM=0
117               GO TO 73
118       C FORM ZYGOTE GENOTYPE BY UNION OF GAMETES DERIVED FROM
119       C PARENT GENOTYPES BY INDEPENDENT SEGREGATION AND CROSSOVER
120       C WITH PROBABILITIES PCROS AND PCROL OF CHIASMA BETWEEN
121       C ADJACENT SEGMENTS AND ADJACENT LOCI RESPECTIVELY
122       76      CALL INVER(CP,NSEG,PINV)
123               CALL TRANS(CP,NSEG,PTRA)
124               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
125               CALL MUTAT(S,NSEG,PMUT)
126       C PRINT CHROMOSOME STRUCTURE DURING LAST GENERATION IF IPCS = 1
127               IF(IGEN.EQ.LGEN.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
```

```
      C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
      C ZYGOTE IS INVIABLE
            IF(VIAB(S,NSEG))GO TO 77
            NIZ=NIZ+1
            GO TO 61
      C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
      C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
      C GENERATION IF IPAF = 1
      77    IF(IPAF.EQ.0)GO TO 80
            CALL CA(IGEN,LGEN,IND,NPOP,NSEG)
      C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
      C BY NDVLP
      80    GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
      81    CALL SGA1(NSEG,S,NPAR,X)
            GO TO 90
      82    CALL SGA2(NSEG,S,NPAR,X)
            GO TO 90
      83    CALL SGA3(NSEG,S,NPAR,X)
            GO TO 90
      84    CALL SGA4(NSEG,S,NPAR,X)
            GO TO 90
      85    CALL SGA5(NSEG,S,NPAR,X)
            GO TO 90
      86    CALL SGA6(NSEG,S,NPAR,X)
            GO TO 90
      87    CALL SGA7(NSEG,S,NPAR,X)
            GO TO 90
      88    CALL SGA8(NSEG,S,NPAR,X)
            GO TO 90
      89    CALL SGA9(NSEG,S,NPAR,X)
            GO TO 90
      810   CALL SGA10(NSEG,S,NPAR,X)
            GO TO 90
      811   CALL SGA11(NSEG,S,NPAR,X)
            GO TO 90
      812   CALL SGA12(NSEG,S,NPAR,X)
      C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
      C FUNCTION SPECIFIED BY NVALU
      90    GO TO(91,92,93,94,95,96),NVALU
      91    CALL V1(NPAR,X,V(IND))
            GO TO 97
      92    CALL V2(NPAR,X,V(IND))
            GO TO 97
      93    CALL V3(NPAR,X,V(IND))
            GO TO 97
      94    CALL V4(NPAR,X,V(IND))
            GO TO 97
      95    CALL V5(NPAR,X,V(IND))
            GO TO 97
      96    CALL V6(NPAR,X,V(IND))
      C INCREMENT INDIVIDUAL COUNTER
      97    INDIV=INDIV+1
      C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
      C ARE WITHIN THE ADMISSIBLE DOMAIN
```

```
182             IF(V(IND).LT.CV)GO TO 100
183             NTR=NTR+1
184             NTRT=NTRT+1
185             VSUM=VSUM+V(IND)
186             IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
187       C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
188       C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
189       C OF ALL PRECEDING INDIVIDUALS
190       100   IF(IPBP.EQ.1)GO TO 101
191             IF(IPAP.EQ.1)GO TO 102
192             GO TO 110
193       101   IF(V(IND).LE.HIV)GO TO 110
194             HIV=V(IND)
195       102   IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
196       105   FORMAT(1X,I5,F10.3,8I7)
197             IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
198       106   FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
199       110   IK=0
200       C BRANCH ON GENERATION AND FAMILY MEMBER
201             IF(IGEN.EQ.1)GO TO 121
202             K=IFAM+ISTOR
203             IF(IFM.GT.1)GO TO 120
204       C STORE FIRST INDIVIDUAL OF EACH FAMILY
205             VS(IFAM)=V(IND)
206             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
207             IF(ITOG(1).EQ.1)GO TO 125
208             GO TO 130
209       C REPLACE FAMILY REPRESENTATIVE WITH THIS INDIVIDUAL
210       C IF THIS INDIVIDUAL HAS HIGHER PHENOTYPIC VALUE
211       120   IF(V(IND).LT.VS(IFAM))GO TO 130
212             VS(IFAM)=V(IND)
213             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
214             IF(ITOG(1).EQ.1)GO TO 125
215             GO TO 130
216       C STORE FIRST NSEL GENOTYPES DURING F1 GENERATION
217       121   IF(IND.GT.NSEL)GO TO 122
218             K=IND+ISTOR
219             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
220             VS(IND)=V(IND)
221             IF(ITOG(1).EQ.1)GO TO 125
222             GO TO 130
223       C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
224       C F2 GENERATION IF VALUE OF THIS INDIVIDUAL EXCEEDS
225       C THE LOWEST VALUE
226       122   LOW=1
227             DO 123 I=1,NSEL
228             IF(VS(I).LT.VS(LOW))LOW=I
229       123   CONTINUE
230             IF(V(IND).LT.VS(LOW))GO TO 130
231             K=LOW+ISTOR
232             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
233             VS(LOW)=V(IND)
234       C PRINT GENERATION, INDIVIDUAL, VALUE, AND LOCATION IF
235       C GENOTYPE IS STORED IN F1 AND PEDIGREE IS REQUESTED
```

```
      125      IF(ITOG(1).EQ.1)WRITE(6,126)IGEN,IND,V(IND),K
      126      FORMAT(2I6,F11.3,I6)
               IK=1
      C PRINT GENERATION, INDIVIDUAL, AND VALUE IF PEDIGREE
      C IS REQUESTED
      130      IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)IGEN,IND,V(IND)
               IF(IND.EQ.NPOP)GO TO 140
               IND=IND+1
               GO TO 61
      C END GENERATION IGEN
      C LIST FAMILIES ACCORDING TO SUPERIOR FAMILY MEMBER
      140      CALL LIST(VS,NSEL,R)
      C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
               CALL ASD(VS,NSEL,AVGS,STDS)
      C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
               CALL ASD(V,NPOP,AVG,STD)
      C STORE IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
               K=(IVAR-1)*LGEN+IGEN
               WRITE(2'K,150)IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR
      150      FORMAT(1X,I3,5F10.3,2I10)
      C TEST FOR END OF VARIETY
               IF(IGEN.EQ.LGEN)GO TO 160
      C BEGIN NEW GENERATION
               IGEN=IGEN+1
               IDRAW=IDRAW+50
               IF(IDRAW.GT.50)IDRAW=0
               ISTOR=ISTOR+50
               IF(ISTOR.GT.50)ISTOR=0
               GO TO 60
      C TEST FOR END OF RUN
      160      K=R(1)
               WRITE(6,161)VS(K),VV
      161      FORMAT(1X,'VS='F10.3/' VV='2F10.3)
               LOW=IVAR
               IF(IVAR.LE.2)GO TO 163
               LOW=1
               DO 162 I=1,2
               IF(VV(I).LT.VV(LOW))LOW=I
      162      CONTINUE
      163      IF(VS(K).LT.VV(LOW))GO TO 164
               VV(LOW)=VS(K)
               K=K+ISTOR
               READ(1'K)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
               K=100+LOW
               WRITE(1'K)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
      164      IF(IVAR.EQ.NVAR)GO TO 170
               IVAR=IVAR+1
               GO TO 50
      C PRINT DATA FROM SUCCESSIVE VARIETIES
      170      CALL PDFSV(LGEN,NVAR)
      C CLOSE FILES
               CALL CLOSE(1)
               CALL CLOSE(2)
               CALL CLOSE(3)
```

```
290               CALL CLOSE(7)
291         C TEST FOR STOP
292               IF(CDATA(1),EQ,STOP)STOP
293         C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
294         C IF ITOG(2) = 2
295               IF(ITOG(2),EQ,2)WRITE(6,180)CDATA(1)
296         180   FORMAT(1X,'RESTART AT ',A5)
297               IF(ITOG(2),EQ,2)PAUSE
298         C CONTINUE USING INPUT DATA IN FILE CDATA
299               CALL SEEK(1,CDATA)
300               GO TO 10
301               END
```

Bulk Population Breeding 1 (BPB1)

PDP-9 CHAIN/EXECUTE System

```
 B PR

DOS-15 V1A
$$JOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>BPB1
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MBPB1,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:MERR
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
       15532-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          20001
BPB1 6/7/73
NDVLP           1
NVALU           6
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
POUCR      0.0000
CV         0.0000
NPOP            32
NSEL            32
LGEN            10
NPAR             2
NSEG             8
NREP             5
IX               1
IPAP             0
IPBP             1
IPAF             0
IPCS             0
         STOP
```

Main Program (MBPB1)

```
001      C MBPB1 V1
002      C BULK POPULATION BREEDING 1
003      C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM BPB1
004            INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005            LOGICAL EVENT,VIAB
006            DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
007            1,V(100),VS(100),F(100)
008            COMMON /CPS/CP,S
009            DATA F1(1),F2(1),F3(1)/5HF1    ,5HF2    ,5HF3    /
010            1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
011            1,STOP/5HSTOP /,PFILE(1)/5HBPB1 /
012      C READ PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,
013      C POUCR,CV,NPOP,NSEL,LGEN,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,
014      C IPCS,CDATA FROM DISK FILE
015            IF(ITOG(2).EQ.0)GO TO 6
016            WRITE(6,1)
017      1     FORMAT(1X,'DATA FILE')
018            READ(5,5)PFILE(1)
019      5     FORMAT(A5)
020      6     CALL SEEK(1,PFILE)
021      10    READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
```

```
022               1,PCROS,PCROL,PMUT,POUCR,CV
023      15       FORMAT(9X,A5/12A5,2(/9X,I6),6(/9X,F6.4)/8X,F7.4)
024               READ(1,20)NPOP,NSEL,LGEN
025      20       FORMAT(9X,I6,2(/9X,I6))
026               READ(1,25)NPAR,NSEG,NREP,IX
027      25       FORMAT(9X,I6,3(/9X,I6))
028               READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
029      30       FORMAT(9X,I6,3(/9X,I6)/9X,A5)
030               CALL CLOSE(1)
031      C DELETE AND RECREATE PRINT FILE
032               CALL DLETE(7,PFILE,I)
033               CALL ENTER(7,PFILE)
034      C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT
035      C POUCR,CV,NPOP,NSEL,LGEN,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,
036      C IPCS,CDATA INTO PRINT FILE PFILE
037               WRITE(7,40)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
038               1,PCROS,PCROL,PMUT,POUCR,CV,NPOP,NSEL,LGEN,NPAR
039               1,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
040      40       FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
041               1/' PINV',F11.4/' PTRA',F11.4
042               1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
043               1/' POUCR',F10.4/' CV',F13.4/' NPOP',I11/' NSEL',I11
044               1/' LGEN',I11/' NPAR',I11/' NSEG',I11/' NREP',I11
045               1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
046               1/'IPCS',I11/10X,A5)
047      C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
048      C UP TO 2*NSEL CHROMOSOME ARRAYS
049               CALL DLETE(1,F1,I)
050               CALL DEFINE(1,4*NSEG,2*NSEL,F1,IV1,0,0,0)
051      C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
052      C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH GENERATION
053               CALL DLETE(2,F2,I)
054               CALL DEFINE(2,80,(NREP+3)*LGEN,F2,IV2,1,0,0)
055      C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
056      C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
057      C AND GENERATION
058               CALL DLETE(3,F3,I)
059               CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
060      C START RANDOM NUMBER GENERATOR AT IX
061               IX=-IX
062               CALL URN(IX,U)
063      C INITIALIZE RUN COUNTER AND BEGIN RUN IRUN
064               IRUN=1
065      50       INDIV=0
066               NTRT=0
067               VSUM=0.
068               E=0.
069               IGEN=1
070               HIV=0.
071               ISTOR=0
072               IDRAW=NSEL
073      C BEGIN GENERATION IGEN
074      60       IND=1
075               NIZ=0
```

```
076             NTR=0
077       C SELECT PARENTAL GENOTYPES AND LOAD INTO CORE
078       C ARRAYS CP AND S
079       70    IF(IGEN.GT.1)GO TO 72
080       C FORM RANDOM HETEROZYGOUS PARENTS
081             DO 71 K=1,2
082             DO 71 I=1,NSEG
083             CALL URN(IX,U)
084             DO 71 J=1,2
085             N=(I-1)/8+1
086             M=I-(N-1)*8
087             CP(I,J,K)=IPAC(N,M)
088             IF(J.EQ.1)S(I,J,K)=IX
089             IF(J.EQ.2)S(I,J,K)=-IX-1
090       71    CONTINUE
091             GO TO 79
092       C FETCH PARENT
093       72    IF(IND.GT.1)GO TO 75
094             N=R(1)
095             F(1)=V(N)
096             DO 73 I=2,NSEL
097             N=R(I)
098       73    F(I)=F(I-1)+V(N)
099             DO 74 I=1,NSEL
100       74    F(I)=F(I)/F(NSEL)
101       75    CALL URN(L,U)
102             DO 76 I=1,NSEL
103             IF(U.LE.F(I))GO TO 77
104       76    CONTINUE
105       77    I1=R(I)+IDRAW
106             I2=I1
107       C OUTCROSS SELECTED INDIVIDUAL WITH PROBABILITY POUCR
108             IF(EVENT(POUCR))I2=IRAND(1,NSEL)+IDRAW
109             READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
110             READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
111             IF(ITOG(1).EQ.1)WRITE(6,78)I1,I2
112       78    FORMAT(29X,2I6)
113       C FORM ZYGOTE GENOTYPE BY UNION OF GAMETES DERIVED FROM
114       C PARENT GENOTYPES BY INDEPENDENT SEGREGATION AND CROSSOVER
115       C WITH PROBABILITIES PCROS AND PCROL OF CHIASMA BETWEEN
116       C ADJACENT SEGMENTS AND ADJACENT LOCI RESPECTIVELY
117       79    CALL INVER(CP,NSEG,PINV)
118             CALL TRANS(CP,NSEG,PTRA)
119             CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
120             CALL MUTAT(S,NSEG,PMUT)
121       C PRINT CHROMOSOME STRUCTURE DURING LAST GENERATION IF IPCS = 1
122             IF(IGEN.EQ.LGEN.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
123       C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
124       C ZYGOTE IS INVIABLE
125             IF(VIAB(S,NSEG))GO TO 790
126             NIZ=NIZ+1
127             GO TO 70
128       C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
129       C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
```

```
C GENERATION IF IPAF = 1
790      IF(IPAF.EQ.0)GO TO 80
         CALL CA(IGEN,LGEN,IND,NPOP,NSEG)
C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
C BY NDVLP
80       GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
81       CALL SGA1(NSEG,S,NPAR,X)
         GO TO 90
82       CALL SGA2(NSEG,S,NPAR,X)
         GO TO 90
83       CALL SGA3(NSEG,S,NPAR,X)
         GO TO 90
84       CALL SGA4(NSEG,S,NPAR,X)
         GO TO 90
85       CALL SGA5(NSEG,S,NPAR,X)
         GO TO 90
86       CALL SGA6(NSEG,S,NPAR,X)
         GO TO 90
87       CALL SGA7(NSEG,S,NPAR,X)
         GO TO 90
88       CALL SGA8(NSEG,S,NPAR,X)
         GO TO 90
89       CALL SGA9(NSEG,S,NPAR,X)
         GO TO 90
810      CALL SGA10(NSEG,S,NPAR,X)
         GO TO 90
811      CALL SGA11(NSEG,S,NPAR,X)
         GO TO 90
812      CALL SGA12(NSEG,S,NPAR,X)
C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
C FUNCTION SPECIFIED BY NVALU
90       GO TO(91,92,93,94,95,96),NVALU
91       CALL V1(NPAR,X,V(IND))
         GO TO 97
92       CALL V2(NPAR,X,V(IND))
         GO TO 97
93       CALL V3(NPAR,X,V(IND))
         GO TO 97
94       CALL V4(NPAR,X,V(IND))
         GO TO 97
95       CALL V5(NPAR,X,V(IND))
         GO TO 97
96       CALL V6(NPAR,X,V(IND))
C INCREMENT INDIVIDUAL COUNTER
97       INDIV=INDIV+1
C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
C ARE WITHIN THE ADMISSIBLE DOMAIN
         IF(V(IND).LT.CV)GO TO 100
         NTR=NTR+1
         NTRT=NTRT+1
         VSUM=VSUM+V(IND)
         IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
```

```
184      C OF ALL PRECEDING INDIVIDUALS
185      100     IF(IPBP.EQ.1)GO TO 101
186              IF(IPAP.EQ.1)GO TO 102
187              GO TO 110
188      101     IF(V(IND).LE.HIV)GO TO 110
189              HIV=V(IND)
190      102     IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
191      105     FORMAT(1X,I5,F10.3,8I7)
192              IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
193      106     FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
194      110     IK=0
195      C STORE FIRST NSEL GENOTYPES
196              IF(IND.GT.NSEL)GO TO 115
197              K=IND+ISTOR
198              WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
199              VS(IND)=V(IND)
200              IF(ITOG(1).EQ.1)GO TO 125
201              GO TO 130
202      C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
203      C F2 GENERATION IF VALUE OF THIS INDIVIDUAL EXCEEDS
204      C THE LOWEST VALUE
205      115     LOW=1
206              DO 120 I=1,NSEL
207              IF(VS(I).LT.VS(LOW))LOW=I
208      120     CONTINUE
209              IF(V(IND).LT.VS(LOW))GO TO 130
210              K=LOW+ISTOR
211              WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
212              VS(LOW)=V(IND)
213      C PRINT GENERATION, INDIVIDUAL, VALUE, AND LOCATION IF
214      C GENOTYPE IS STORED IN F1
215      125     IF(ITOG(1).EQ.1)WRITE(6,126)IGEN,IND,V(IND),K
216      126     FORMAT(2I6,F11.3,I6)
217              IK=1
218      C PRINT GENERATION, INDIVIDUAL, AND VALUE
219      130     IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)IGEN,IND,V(INL,
220              IF(IND.EQ.NPOP)GO TO 140
221              IND=IND+1
222              GO TO 70
223      C END GENERATION IGEN
224      C LIST INDIVIDUALS ACCORDING TO PHENOTYPIC VALUE
225      140     CALL LIST(VS,NSEL,R)
226      C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
227              CALL ASD(VS,NSEL,AVGS,STDS)
228      C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
229              CALL ASD(V,NPOP,AVG,STD)
230      C STORE IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
231              K=(IRUN-1)*LGEN+IGEN
232              WRITE(2'K,150)IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR
233      150     FORMAT(1X,I3,5F10.3,2I10)
234      C TEST FOR END OF RUN
235              IF(IGEN.EQ.LGEN)GO TO 160
236      C BEGIN NEW GENERATION
237              IGEN=IGEN+1
```

```
238               IDRAW=IDRAW+NSEL
239               IF(IDRAW.GT.NSEL)IDRAW=0
240               ISTOR=ISTOR+NSEL
241               IF(ISTOR.GT.NSEL)ISTOR=0
242               GO TO 60
243         C TEST FOR END OF REPLICATE RUNS
244         160   IF(IRUN.EQ.NREP)GO TO 170
245               IRUN=IRUN+1
246               GO TO 50
247         C MEAN AND EXTREMES OF REPLICATE RUNS
248         170   CALL MERR(LGEN,NREP)
249         C CLOSE FILES
250               CALL CLOSE(1)
251               CALL CLOSE(2)
252               CALL CLOSE(3)
253               CALL CLOSE(7)
254         C TEST FOR STOP
255               IF(CDATA(1).EQ.STOP)STOP
256         C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
257         C IF ITOG(2) = 2
258               IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
259         180   FORMAT(1X,'RESTART AT ',A5)
260               IF(ITOG(2).EQ.2)PAUSE
261         C CONTINUE USING INPUT DATA IN FILE CDATA
262               CALL SEEK(1,CDATA)
263               GO TO 10
264               END
```

Mass Selection 1 (MS1)

PDP-9 CHAIN/EXECUTE System

```
 B PR

DOS-15 V1A
$SJOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>MS1
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MMS1,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:MERR
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
       17214-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          30001
MS1 6/7/73
NDVLP          1
NVALU          6
PINV      0.0010
PTRA      0.0010
PCROS     0.5000
PCROL     0.5000
PMUT      0.0010
CV        0.0000
NPOP           32
NSEL           16
LGEN           10
NPAR            2
NSEG            8
NREP            5
IX              1
IPAP            0
IPBP            1
IPAF            1
IPCS            1
          STOP
```

Main Program (MMS1)

```
001       C MMS1 V1
002       C MASS SELECTION 1
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM MS1
004             INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005             LOGICAL EVENT,VIAB
006             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
007             1,V(100),VS(100)
008             COMMON /CPS/CP,S
009             DATA F1(1),F2(1),F3(1)/5HF1   ,5HF2   ,5HF3   /
010             1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
011             1,STOP/5HSTOP /,PFILE(1)/5HMS1  /
012       C READ PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
013       C NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA
014       C FROM DISK FILE
015             IF(ITOG(2).EQ.0)GO TO 6
016             WRITE(6,1)
017       1     FORMAT(1X,'DATA FILE')
018             READ(5,5)PFILE(1)
019       5     FORMAT(A5)
020       6     CALL SEEK(1,PFILE)
021       10    READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
```

```
022               1,PCROS,PCROL,PMUT,CV
023      15       FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
024               READ(1,20)NPOP,NSEL,LGEN
025      20       FORMAT(9X,I6,2(/9X,I6))
026               READ(1,25)NPAR,NSEG,NREP,IX
027      25       FORMAT(9X,I6,3(/9X,I6))
028               READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
029      30       FORMAT(9X,I6,3(/9X,I6)/9X,A5)
030               CALL CLOSE(1)
031      C DELETE AND RECREATE PRINT FILE
032               CALL DLETE(7,PFILE,I)
033               CALL ENTER(7,PFILE)
034      C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV
035      C NPOP,NSEL,LGEN,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,
036      C CDATA INTO PRINT FILE PFILE
037               WRITE(7,40)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
038               1,PCROS,PCROL,PMUT,CV,NPOP,NSEL,LGEN,NPAR
039               1,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
040      40       FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
041               1/' PINV',F11.4/' PTRA',F11.4
042               1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
043               1/' CV',F13.4/' NPOP',I11/' NSEL',I11
044               1/' LGEN',I11/' NPAR',I11/' NSEG',I11/' NREP',I11
045               1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
046               1/' IPCS',I11/10X,A5)
047      C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
048      C UP TO 2*NSEL CHROMOSOME ARRAYS
049               CALL DLETE(1,F1,I)
050               CALL DEFINE(1,4*NSEG,2*NSEL,F1,IV1,0,0,0)
051      C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
052      C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH GENERATION
053               CALL DLETE(2,F2,I)
054               CALL DEFINE(2,80,(NREP+3)*LGEN,F2,IV2,1,0,0)
055      C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
056      C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
057      C AND GENERATION
058               CALL DLETE(3,F3,I)
059               CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
060      C START RANDOM NUMBER GENERATOR AT IX
061               IX=-IX
062               CALL URN(IX,U)
063      C INITIALIZE RUN COUNTER AND BEGIN RUN IRUN
064               IRUN=1
065      50       INDIV=0
066               NTRT=0
067               VSUM=0.
068               E=0.
069               IGEN=1
070               HIV=0.
071               ISTOR=0
072               IDRAW=NSEL
073      C BEGIN GENERATION IGEN
074      60       IND=1
075               NIZ=0
```

```
076               NTR=0
077         C SELECT PARENTAL GENOTYPES AND LOAD INTO CORE
078         C ARRAYS CP AND S
079         70    IF(IGEN.GT.1)GO TO 72
080         C FORM RANDOM HETEROZYGOUS PARENT GENOTYPES
081               DO 71 K=1,2
082               DO 71 I=1,NSEG
083               CALL URN(IX,U)
084               DO 71 J=1,2
085               N=(I-1)/8+1
086               M=I-(N-1)*8
087               CP(I,J,K)=IPAC(N,M)
088               IF(J.EQ.1)S(I,J,K)=IX
089               IF(J.EQ.2)S(I,J,K)=-IX-1
090         71    CONTINUE
091               GO TO 74
092         72    I1=IRAND(1,NSEL)+IDRAW
093               I2=IRAND(1,NSEL)+IDRAW
094               READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
095               READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
096               IF(ITUG(1).EQ.1)WRITE(6,73)I1,I2
097         73    FORMAT(29X,2I6)
098         C FORM ZYGOTE GENOTYPE BY UNION OF GAMETES DERIVED FROM
099         C PARENT GENOTYPES BY INDEPENDENT SEGREGATION AND CROSSOVER
100         C WITH PROBABILITIES PCROS AND PCROL OF CHIASMA BETWEEN
101         C ADJACENT SEGMENTS AND ADJACENT LOCI RESPECTIVELY
102         74    CALL INVER(CP,NSEG,PINV)
103               CALL TRANS(CP,NSEG,PTRA)
104               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
105               CALL MUTAT(S,NSEG,PMUT)
106         C PRINT CHROMOSOME STRUCTURE DURING LAST GENERATION IF IPCS = 1
107               IF(IGEN.EQ.LGEN.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
108         C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
109         C ZYGOTE IS INVIABLE
110               IF(VIAB(S,NSEG))GO TO 75
111               NIZ=NIZ+1
112               GO TO 70
113         C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
114         C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
115         C GENERATION IF IPAF = 1
116         75    IF(IPAF.EQ.0)GO TO 80
117               CALL CA(IGEN,LGEN,IND,NPOP,NSEG)
118         C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
119         C BY NDVLP
120         80    GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
121         81    CALL SGA1(NSEG,S,NPAR,X)
122               GO TO 90
123         82    CALL SGA2(NSEG,S,NPAR,X)
124               GO TO 90
125         83    CALL SGA3(NSEG,S,NPAR,X)
126               GO TO 90
127         84    CALL SGA4(NSEG,S,NPAR,X)
128               GO TO 90
```

```
      85       CALL SGA5(NSEG,S,NPAR,X)
               GO TO 90
      86       CALL SGA6(NSEG,S,NPAR,X)
               GO TO 90
      87       CALL SGA7(NSEG,S,NPAR,X)
               GO TO 90
      88       CALL SGA8(NSEG,S,NPAR,X)
               GO TO 90
      89       CALL SGA9(NSEG,S,NPAR,X)
               GO TO 90
      810      CALL SGA10(NSEG,S,NPAR,X)
               GO TO 90
      811      CALL SGA11(NSEG,S,NPAR,X)
               GO TO 90
      812      CALL SGA12(NSEG,S,NPAR,X)
      C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
      C FUNCTION SPECIFIED BY NVALU
      90       GO TO(91,92,93,94,95,96),NVALU
      91       CALL V1(NPAR,X,V(IND))
               GO TO 97
      92       CALL V2(NPAR,X,V(IND))
               GO TO 97
      93       CALL V3(NPAR,X,V(IND))
               GO TO 97
      94       CALL V4(NPAR,X,V(IND))
               GO TO 97
      95       CALL V5(NPAR,X,V(IND))
               GO TO 97
      96       CALL V6(NPAR,X,V(IND))
      C INCREMENT INDIVIDUAL COUNTER
      97       INDIV=INDIV+1
      C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
      C ARE WITHIN THE ADMISSIBLE DOMAIN
               IF(V(IND).LT.CV)GO TO 100
               NTR=NTR+1
               NTRT=NTRT+1
               VSUM=VSUM+V(IND)
               IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
      C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
      C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
      C OF ALL PRECEDING INDIVIDUALS
      100      IF(IPBP.EQ.1)GO TO 101
               IF(IPAP.EQ.1)GO TO 102
               GO TO 110
      101      IF(V(IND).LE.HIV)GO TO 110
               HIV=V(IND)
      102      IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
      105      FORMAT(1X,I5,F10.3,8I7)
               IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
      106      FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
      110      IK=0
      C STORE FIRST NSEL GENOTYPES
               IF(IND.GT.NSEL)GO TO 115
               K=IND+ISTOR
```

```
183             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
184             VS(IND)=V(IND)
185             IF(ITOG(1).EQ.1)GO TO 125
186             GO TO 130
187       C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
188       C F2 GENERATION IF VALUE OF THIS INDIVIDUAL EXCEEDS
189       C THE LOWEST VALUE
190       115   LOW=1
191             DO 120 I=1,NSEL
192             IF(VS(I).LT.VS(LOW))LOW=I
193       120   CONTINUE
194             IF(V(IND).LT.VS(LOW))GO TO 130
195             K=LOW+ISTOR
196             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
197             VS(LOW)=V(IND)
198       C PRINT GENERATION, INDIVIDUAL, VALUE, AND LOCATION IF
199       C GENOTYPE IS STORED IN F1
200       125   IF(ITOG(1).EQ.1)WRITE(6,126)IGEN,IND,V(IND),K
201       126   FORMAT(2I6,F11.3,I6)
202             IK=1
203       C PRINT GENERATION, INDIVIDUAL, AND VALUE
204       130   IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)IGEN,IND,V(IND)
205             IF(IND.EQ.NPOP)GO TO 140
206             IND=IND+1
207             GO TO 70
208       C END GENERATION IGEN
209       C LIST INDIVIDUALS ACCORDING TO PHENOTYPIC VALUE
210       140   CALL LIST(VS,NSEL,R)
211       C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
212             CALL ASD(VS,NSEL,AVGS,STDS)
213       C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
214             CALL ASD(V,NPOP,AVG,STD)
215       C STORE IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
216             K=(IRUN-1)*LGEN+IGEN
217             WRITE(2'K,150)IGEN,E,AVG,STD,AVGS,STDS,NIZ,NTR
218       150   FORMAT(1X,I3,5F10.3,2I10)
219       C TEST FOR END OF RUN
220             IF(IGEN.EQ.LGEN)GO TO 160
221       C BEGIN NEW GENERATION
222             IGEN=IGEN+1
223             IDRAW=IDRAW+NSEL
224             IF(IDRAW.GT.NSEL)IDRAW=0
225             ISTOR=ISTOR+NSEL
226             IF(ISTOR.GT.NSEL)ISTOR=0
227             GO TO 60
228       C TEST FOR END OF REPLICATE RUNS
229       160   IF(IRUN.EQ.NREP)GO TO 170
230             IRUN=IRUN+1
231             GO TO 50
232       C MEAN AND EXTREMES OF REPLICATE RUNS
233       170   CALL MERR(LGEN,NREP)
234       C CLOSE FILES
235             CALL CLOSE(1)
```

```
236               CALL CLOSE(2)
237               CALL CLOSE(3)
238               CALL CLOSE(7)
239      C TEST FOR STOP
240               IF(CDATA(1).EQ.STOP)STOP
241      C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
242      C IF ITOG(2) = 2
243               IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
244      180      FORMAT(1X,'RESTART AT ',A5)
245               IF(ITOG(2).EQ.2)PAUSE
246      C CONTINUE USING INPUT DATA IN FILE CDATA
247               CALL SEEK(1,CDATA)
248               GO TO 10
249               END
```

Simple Recurrent Selection 1 (SRS1)

PDP-9 CHAIN/EXECUTE System

```
 B PR

DOS-15 V1A
$$JOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>SRS1
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MSRS1,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:MERR
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
        14607-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          40001
SRS1 6/7/73
NOVLP           1
NVALU           1
PINV       0.0000
PTRA       0.0000
PCROS      0.5000
PCROL      0.5000
PMUT       0.0000
CV         0.0000
NPOP           28
NSEL            8
LCYC           10
NPAR            8
NSEG           32
NREP            1
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
          40002
```

Main Program (MSRS1)

```
001       C MSRS1 V1
002       C SIMPLE RECURRENT SELECTION 1
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM SRS1
004             INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005            1,TCP(256,2),TS(256,2)
006             LOGICAL EVENT,VIAB
007             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
008            1,V(100),VS(100)
009             COMMON /CPS/CP,S
010             DATA F1(1),F2(1),F3(1)/5HF1   ,5HF2   ,5HF3   /
011            1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
012            1,STOP/5HSTOP /,PFILE(1)/5HSRS1 /
013       C READ PFILE,NOVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
014       C NPOP,NSEL,LCYC,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS
015       C CDATA(1) FROM DISK FILE
016             IF(ITOG(2).EQ.0)GO TO 6
017             WRITE(6,1)
018       1     FORMAT(1X,'DATA FILE')
019             READ(5,5)PFILE(1)
020       5     FORMAT(A5)
021       6     CALL SEEK(1,PFILE)
```

```
022     10      READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
023             1,PCROS,PCROL,PMUT,CV
024     15      FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
025             READ(1,20)NPOP,NSEL,LCYC
026     20      FORMAT(9X,I6,2(/9X,I6))
027             READ(1,25)NPAR,NSEG,NREP,IX
028     25      FORMAT(9X,I6,3(/9X,I6))
029             READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
030     30      FORMAT(9X,I6,3(/9X,I6)/9X,A5)
031             CALL CLOSE(1)
032     C DELETE AND RECREATE PRINT FILE
033             CALL DLETE(7,PFILE,I)
034             CALL ENTER(7,PFILE)
035     C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
036     C NPOP,NSEL,LCYC,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS
037     C CDATA(1) INTO PRINT FILE PFILE
038             WRITE(7,40)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
039             1,PCROS,PCROL,PMUT,CV,NPOP,NSEL,LCYC,NPAR
040             1,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
041     40      FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
042             1/' PINV',F11.4/' PTRA',F11.4
043             1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
044             1/' CV',F13.4/' NPOP',I11/' NSEL',I11
045             1/' LCYC',I11/' NPAR',I11/' NSEG',I11/' NREP',I11
046             1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
047             1/' IPCS',I11/10X,A5)
048     C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
049     C UP TO 2*NSEL CHROMOSOME ARRAYS
050             CALL DLETE(1,F1,I)
051             CALL DEFINE(1,4*NSEG,2*NSEL,F1,IV1,0,0,0)
052     C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
053     C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH CYCLE
054             CALL DLETE(2,F2,I)
055             CALL DEFINE(2,80,(NREP+3)*LCYC,F2,IV2,1,0,0)
056     C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
057     C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
058     C AND CYCLE
059             CALL DLETE(3,F3,I)
060             CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
061     C START RANDOM NUMBER GENERATOR AT IX
062             IX=-IX
063             CALL URN(IX,U)
064     C INITIALIZE RUN COUNTER AND BEGIN RUN IRUN
065             IRUN=1
066     50      INDIV=0
067             NTRT=0
068             VSUM=0.
069             E=0.
070             ICYC=1
071             HIV=0.
072             ISTOR=0
073             IDRAW=NSEL
074     C BEGIN CYCLE ICYC
075     60      IND=1
```

```
076               NIZ=0
077               NTR=0
078               N1=1
079               N2=1
080         65    IF(ICYC.GT.1)GO TO 67
081         C FORM RANDOM HETEROZYGOTES OF SOURCE POPULATION
082               DO 66 I=1,NSEG
083               CALL URN(IX,U)
084               DO 66 J=1,2
085               N=(I-1)/8+1
086               M=I-(N-1)*8
087               CP(I,J,3)=IPAC(N,M)
088               IF(J.EQ.1)S(I,J,3)=IX
089               IF(J.EQ.2)S(I,J,3)=-IX-1
090         66    CONTINUE
091               GO TO 74
092         C DETERMINE PARENTS OF DIALLEL CROSS
093         67    N2=N2+1
094               IF(N2.LE.NSEL)GO TO 68
095               N1=N1+1
096               IF(N1.EQ.NSEL)N1=1
097               N2=N1+1
098         C PRODUCE FIRST PARENT OF DIALLEL CROSS BY SELFING AN
099         C INDIVIDUAL SELECTED FROM THE SOURCE POPULATION OR
100         C PREVIOUS CYCLE
101         68    I1=N1+IDRAW
102               READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
103               READ(1'I1)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
104               CALL INVER(CP,NSEG,PINV)
105               CALL TRANS(CP,NSEG,PTRA)
106               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
107               CALL MUTAT(S,NSEG,PMUT)
108         C STORE FIRST PARENT IN TCP,TS
109         69    DO 70 J=1,2
110               DO 70 I=1,NSEG
111               TCP(I,J)=CP(I,J,3)
112         70    TS(I,J)=S(I,J,3)
113         C PRODUCE SECOND PARENT OF DIALLEL CROSS BY SELFING AN
114         C INDIVIDUAL SELECTED FROM THE SOURCE POPULATION OR
115         C PREVIOUS CYCLE
116               I2=N2+IDRAW
117               READ(1'I2)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
118               READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
119               CALL INVER(CP,NSEG,PINV)
120               CALL TRANS(CP,NSEG,PTRA)
121               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
122               CALL MUTAT(S,NSEG,PMUT)
123         C PRINT PEDIGREE IF REQUESTED
124               IF(ITOG(1).EQ.1)WRITE(6,71)N1,N2,I1,I2
125         71    FORMAT(29X,4I6)
126         C DIALLEL CROSS OF SECOND-YEAR PROGENY OF PREVIOUS CYCLE
127               DO 72 J=1,2
128               DO 72 I=1,NSEG
```

```
129               CP(I,J,1)=TCP(1,J)
130               S(I,J,1)=TS(I,J)
131               CP(I,J,2)=CP(I,J,3)
132     72        S(I,J,2)=S(I,J,3)
133               CALL INVER(CP,NSEG,PINV)
134               CALL TRANS(CP,NSEG,PTRA)
135               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
136               CALL MUTAT(S,NSEG,PMUT)
137     C PRINT CHROMOSOME STRUCTURE DURING LAST CYCLE IF IPCS = 1
138               IF(ICYC.EQ.LCYC.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
139     C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
140     C ZYGOTE IS INVIABLE
141     74        IF(VIAB(S,NSEG))GO TO 75
142               NIZ=NIZ+1
143               GO TO 65
144     C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
145     C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
146     C CYCLE IF IPAF = 1
147     75        IF(IPAF.EQ.0)GO TO 80
148               CALL CA(ICYC,LCYC,IND,NPOP,NSEG)
149     C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
150     C BY NDVLP
151     80        GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
152     81        CALL SGA1(NSEG,S,NPAR,X)
153               GO TO 90
154     82        CALL SGA2(NSEG,S,NPAR,X)
155               GO TO 90
156     83        CALL SGA3(NSEG,S,NPAR,X)
157               GO TO 90
158     84        CALL SGA4(NSEG,S,NPAR,X)
159               GO TO 90
160     85        CALL SGA5(NSEG,S,NPAR,X)
161               GO TO 90
162     86        CALL SGA6(NSEG,S,NPAR,X)
163               GO TO 90
164     87        CALL SGA7(NSEG,S,NPAR,X)
165               GO TO 90
166     88        CALL SGA8(NSEG,S,NPAR,X)
167               GO TO 90
168     89        CALL SGA9(NSEG,S,NPAR,X)
169               GO TO 90
170     810       CALL SGA10(NSEG,S,NPAR,X)
171               GO TO 90
172     811       CALL SGA11(NSEG,S,NPAR,X)
173               GO TO 90
174     812       CALL SGA12(NSEG,S,NPAR,X)
175     C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
176     C FUNCTION SPECIFIED BY NVALU
177     90        GO TO(91,92,93,94,95,96),NVALU
178     91        CALL V1(NPAR,X,V(IND))
179               GO TO 97
180     92        CALL V2(NPAR,X,V(IND))
181               GO TO 97
182     93        CALL V3(NPAR,X,V(IND))
```

```
183               GO TO 97
184       94      CALL V4(NPAR,X,V(IND))
185               GO TO 97
186       95      CALL V5(NPAR,X,V(IND))
187               GO TO 97
188       96      CALL V6(NPAR,X,V(IND))
189       C INCREMENT INDIVIDUAL COUNTER
190       97      INDIV=INDIV+1
191       C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
192       C ARE WITHIN THE ADMISSIBLE DOMAIN
193               IF(V(IND).LT.CV)GO TO 100
194               NTR=NTR+1
195               NTRT=NTRT+1
196               VSUM=VSUM+V(IND)
197               IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
198       C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
199       C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
200       C OF ALL PRECEDING INDIVIDUALS
201       100     IF(IPBP.EQ.1)GO TO 101
202               IF(IPAP.EQ.1)GO TO 102
203               GO TO 110
204       101     IF(V(IND).LE.HIV)GO TO 110
205               HIV=V(IND)
206       102     IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
207       105     FORMAT(1X,I5,F10.3,8I7)
208               IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
209       106     FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
210       110     IK=0
211       C STORE FIRST NSEL GENOTYPES
212               IF(IND.GT.NSEL)GO TO 115
213               K=IND+ISTOR
214               WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
215               VS(IND)=V(IND)
216               IF(ITOG(1).EQ.1)GO TO 125
217               GO TO 130
218       C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
219       C F2 CYCLE IF VALUE OF THIS INDIVIDUAL EXCEEDS
220       C THE LOWEST VALUE
221       115     LOW=1
222               DO 120 I=1,NSEL
223               IF(VS(I).LT.VS(LOW))LOW=I
224       120     CONTINUE
225               IF(V(IND).LT.VS(LOW))GO TO 130
226               K=LOW+ISTOR
227               WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
228               VS(LOW)=V(IND)
229       C PRINT CYCLE, INDIVIDUAL, VALUE, AND LOCATION IF
230       C GENOTYPE IS STORED IN F1
231       125     IF(ITOG(1).EQ.1)WRITE(6,126)ICYC,IND,V(IND),K
232       126     FORMAT(2I6,F11.3,I6)
233               IK=1
234       C PRINT CYCLE, INDIVIDUAL, AND VALUE
235       130     IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)ICYC,IND,V(IND)
```

```
236             IF(IND.EQ.NPOP)GO TO 140
237             IND=IND+1
238             GO TO 65
239       C END CYCLE ICYC
240       C LIST INDIVIDUALS ACCORDING TO PHENOTYPIC VALUE
241       140   CALL LIST(VS,NSEL,R)
242       C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
243             CALL ASD(VS,NSEL,AVGS,STDS)
244       C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
245             CALL ASD(V,NPOP,AVG,STD)
246       C STORE ICYC,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
247             K=(IRUN-1)*LCYC+ICYC
248             WRITE(2'K,150)ICYC,E,AVG,STD,AVGS,STDS,NIZ,NTR
249       150   FORMAT(1X,I3,5F10.3,2I10)
250       C TEST FOR END OF RUN
251             IF(ICYC.EQ.LCYC)GO TO 160
252       C BEGIN NEW CYCLE
253             ICYC=ICYC+1
254             IDRAW=IDRAW+NSEL
255             IF(IDRAW.GT.NSEL)IDRAW=0
256             ISTOR=ISTOR+NSEL
257             IF(ISTOR.GT.NSEL)ISTOR=0
258             GO TO 60
259       C TEST FOR END OF REPLICATE RUNS
260       160   IF(IRUN.EQ.NREP)GO TO 170
261             IRUN=IRUN+1
262             GO TO 50
263       C MEAN AND EXTREMES OF REPLICATE RUNS
264       170   CALL MERR(LCYC,NREP)
265       C CLOSE FILES
266             CALL CLOSE(1)
267             CALL CLOSE(2)
268             CALL CLOSE(3)
269             CALL CLOSE(7)
270       C TEST FOR STOP
271             IF(CDATA(1).EQ.STOP)STOP
272       C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
273       C IF ITOG(2) = 2
274             IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
275       180   FORMAT(1X,'RESTART AT ',A5)
276             IF(ITOG(2).EQ.2)PAUSE
277       C CONTINUE USING INPUT DATA IN FILE CDATA
278             CALL SEEK(1,CDATA)
279             GO TO 10
280             END
```

Simple Recurrent Selection 2 (SRS2)

PDP-9 CHAIN/EXECUTE System

```
DOS-15 V1A
$B PR

DOS-15 V1A
$$JOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>SRS2
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MSRS2,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:PDFSV
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
       15060-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          80001
SRS2 7/12/73
NDVLP          4
NVALU          1
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      0.0000
CV        0.0000
NPOP           32
NSEL            8
LCYC           10
NPAR            8
NSEG           32
NVAR            5
IX              1
IPAP            1
IPBP            0
IPAF            0
IPCS            0
          STOP
```

Main Program (MSRS2)

```
001       C MSRS2 V1
002       C SIMPLE RECURRENT SELECTION 2
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM SRS2
004             INTEGER CP(256,2,3),S(256,2,3),R(100),X(256)
005             1,TCP(256,2),TS(256,2)
006             LOGICAL EVENT,VIA8
007             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
008             1,V(100),VS(100),VV(2)
009             COMMON /CPS/CP,S
010             DATA F1(1),F2(1),F3(1)/5HF1   ,5HF2   ,5HF3   /
011             1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
012             1,STOP/5HSTOP /,PFILE(1)/5HSRS2 /
013       C READ PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
014       C NPOP,NSEL,LCYC,NPAR,NSEG,NVAR,IX,IPAP,IPBP,IPAF,IPCS
015       C CDATA(1) FROM DISK FILE
016             IF(ITOG(2).EQ.0)GO TO 6
017             WRITE(6,1)
018       1     FORMAT(1X,'DATA FILE')
019             READ(5,5)PFILE(1)
020       5     FORMAT(A5)
```

```
021      6        CALL SEEK(1,PFILE)
022      10       READ(1,15)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
023               1,PCROS,PCROL,PMUT,CV
024      15       FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
025               READ(1,20)NPOP,NSEL,LCYC
026      20       FORMAT(9X,I6,2(/9X,I6))
027               READ(1,25)NPAR,NSEG,NVAR,IX
028      25       FORMAT(9X,I6,3(/9X,I6))
029               READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
030      30       FORMAT(9X,I6,3(/9X,I6)/9X,A5)
031               CALL CLOSE(1)
032      C DELETE AND RECREATE PRINT FILE
033               CALL DLETE(7,PFILE,I)
034               CALL ENTER(7,PFILE)
035      C WRITE PFILE,NDVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
036      C NPOP,NSEL,LCYC,NPAR,NSEG,NVAR,IX,IPAP,IPBP,IPAF,IPCS
037      C CDATA(1) INTO PRINT FILE PFILE
038               WRITE(7,40)PFILE(1),A,NDVLP,NVALU,PINV,PTRA
039               1,PCROS,PCROL,PMUT,CV,NPOP,NSEL,LCYC,NPAR
040               1,NSEG,NVAR,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
041      40       FORMAT(10X,A5/1X,12A5/' NDVLP',I10/' NVALU',I10
042               1/' PINV',F11.4/' PTRA',F11.4
043               1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
044               1/' CV',F13.4/' NPOP',I11/' NSEL',I11
045               1/' LCYC',I11/' NPAR',I11/' NSEG',I11/' NVAR',I11
046               1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
047               1/' IPCS',I11/10X,A5)
048      C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
049      C UP TO 2*NSEL+2 CHROMOSOME ARRAYS
050               CALL DLETE(1,F1,I)
051               CALL DEFINE(1,4*NSEG,2*NSEL+2,F1,IV1,0,0,0)
052               KV=2*NSEL
053      C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
054      C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH CYCLE
055               CALL DLETE(2,F2,I)
056               CALL DEFINE(2,80,NVAR*LCYC,F2,IV2,1,0,0)
057      C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
058      C THE NUMBER OF "1" ALLELES IN THE POPULATION AT EACH LOCUS
059      C AND CYCLE
060               CALL DLETE(3,F3,I)
061               CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
062      C START RANDOM NUMBER GENERATOR AT IX
063               IX=-IX
064               CALL URN(IX,U)
065      C INITIALIZE VARIETY COUNTER AND BEGIN VARIETY IVAR
066               IVAR=1
067      50       INDIV=0
068               NTRT=0
069               VSUM=0.
070               E=0.
071               ICYC=1
072               HIV=0.
073               ISTOR=0
074               IDRAW=NSEL
```

```
075     C BEGIN CYCLE ICYC
076     60      IND=1
077             NIZ=0
078             NTR=0
079             N1=1
080             N2=1
081     C SELECT PARENTAL GENOTYPES AND LOAD ARRAYS CP AND S
082     61      IF(ICYC.GT.1)GO TO 67
083             IF(IVAR.GT.2)GO TO 63
084     C FORM RANDOM HETEROZYGOTES OF SOURCE POPULATION
085             DO 62 I=1,NSEG
086             CALL URN(IX,U)
087             DO 62 J=1,2
088             N=(I-1)/8+1
089             M=I-(N-1)*8
090             CP(I,J,3)=IPAC(N,M)
091             IF(J.EQ.1)S(I,J,3)=IX
092             IF(J.EQ.2)S(I,J,3)=-IX-1
093     62      CONTINUE
094             GO TO 74
095     C FETCH PARENTS OF VARIETAL CROSS
096     63      K=KV+1
097             READ(1'K)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
098             K=K+1
099             READ(1'K)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
100             GO TO 73
101     C DETERMINE PARENTS OF DIALLEL CROSS
102     67      N2=N2+1
103             IF(N2.LE.NSEL)GO TO 68
104             N1=N1+1
105             IF(N1.EQ.NSEL)N1=1
106             N2=N1+1
107     C PRODUCE FIRST PARENT OF DIALLEL CROSS BY SELFING AN
108     C INDIVIDUAL SELECTED FROM THE SOURCE POPULATION OR
109     C PREVIOUS CYCLE
110     68      I1=N1+IDRAW
111             READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
112             READ(1'I1)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
113             CALL INVER(CP,NSEG,PINV)
114             CALL TRANS(CP,NSEG,PTRA)
115             CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
116             CALL MUTAT(S,NSEG,PMUT)
117     C STORE FIRST PARENT IN TCP,TS
118     69      DO 70 J=1,2
119             DO 70 I=1,NSEG
120             TCP(I,J)=CP(I,J,3)
121     70      TS(I,J)=S(I,J,3)
122     C PRODUCE SECOND PARENT OF DIALLEL CROSS BY SELFING AN
123     C INDIVIDUAL SELECTED FROM THE SOURCE POPULATION OR
124     C PREVIOUS CYCLE
125             I2=N2+IDRAW
126             READ(1'I2)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
127             READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
128             CALL INVER(CP,NSEG,PINV)
```

```
129             CALL TRANS(CP,NSEG,PTRA)
130             CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
131             CALL MUTAT(S,NSEG,PMUT)
132     C PRINT PEDIGREE IF REQUESTED
133             IF(ITOG(1).EQ.1)WRITE(6,71)N1,N2,I1,I2
134     71      FORMAT(29X,4I6)
135     C DIALLEL CROSS OF SECOND-YEAR PROGENY OF PREVIOUS CYCLE
136             DO 72 J=1,2
137             DO 72 I=1,NSEG
138             CP(I,J,1)=TCP(I,J)
139             S(I,J,1)=TS(I,J)
140             CP(I,J,2)=CP(I,J,3)
141     72      S(I,J,2)=S(I,J,3)
142     73      CALL INVER(CP,NSEG,PINV)
143             CALL TRANS(CP,NSEG,PTRA)
144             CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
145             CALL MUTAT(S,NSEG,PMUT)
146     C PRINT CHROMOSOME STRUCTURE DURING LAST CYCLE IF IPCS = 1
147             IF(ICYC.EQ.LCYC.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
148     C ABORT INDIVIDUAL AND RETURN TO SELECT NEW PARENT IF
149     C ZYGOTE IS INVIABLE
150     74      IF(VIAB(S,NSEG))GO TO 75
151             NIZ=NIZ+1
152             GO TO 61
153     C INCREMENT COUNT OF "1" ALLELES AT EACH INDIVIDUAL AND
154     C PRINT NUMBER OF "1" ALLELES AT EACH LOCUS AT END OF EACH
155     C CYCLE IF IPAF = 1
156     75      IF(IPAF.EQ.0)GO TO 80
157             CALL CA(ICYC,LCYC,IND,NPOP,NSEG)
158     C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
159     C BY NDVLP
160     80      GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
161     81      CALL SGA1(NSEG,S,NPAR,X)
162             GO TO 90
163     82      CALL SGA2(NSEG,S,NPAR,X)
164             GO TO 90
165     83      CALL SGA3(NSEG,S,NPAR,X)
166             GO TO 90
167     84      CALL SGA4(NSEG,S,NPAR,X)
168             GO TO 90
169     85      CALL SGA5(NSEG,S,NPAR,X)
170             GO TO 90
171     86      CALL SGA6(NSEG,S,NPAR,X)
172             GO TO 90
173     87      CALL SGA7(NSEG,S,NPAR,X)
174             GO TO 90
175     88      CALL SGA8(NSEG,S,NPAR,X)
176             GO TO 90
177     89      CALL SGA9(NSEG,S,NPAR,X)
178             GO TO 90
179     810     CALL SGA10(NSEG,S,NPAR,X)
180             GO TO 90
181     811     CALL SGA11(NSEG,S,NPAR,X)
182             GO TO 90
```

```
183      812      CALL SGA12(NSEG,S,NPAR,X)
184      C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
185      C FUNCTION SPECIFIED BY NVALU
186      90       GO TO(91,92,93,94,95,96),NVALU
187      91       CALL V1(NPAR,X,V(IND))
188               GO TO 97
189      92       CALL V2(NPAR,X,V(IND))
190               GO TO 97
191      93       CALL V3(NPAR,X,V(IND))
192               GO TO 97
193      94       CALL V4(NPAR,X,V(IND))
194               GO TO 97
195      95       CALL V5(NPAR,X,V(IND))
196               GO TO 97
197      96       CALL V6(NPAR,X,V(IND))
198      C INCREMENT INDIVIDUAL COUNTER
199      97       INDIV=INDIV+1
200      C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
201      C ARE WITHIN THE ADMISSIBLE DOMAIN
202               IF(V(IND).LT.CV)GO TO 100
203               NTR=NTR+1
204               NTRT=NTRT+1
205               VSUM=VSUM+V(IND)
206               IF(IND.EQ.NPOP)E=VSUM/FLOAT(NTRT)
207      C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
208      C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
209      C OF ALL PRECEDING INDIVIDUALS
210      100      IF(IPBP.EQ.1)GO TO 101
211               IF(IPAP.EQ.1)GO TO 102
212               GO TO 110
213      101      IF(V(IND).LE.HIV)GO TO 110
214               HIV=V(IND)
215      102      IF(NPAR.LE.8)WRITE(7,105)INDIV,V(IND),(X(I),I=1,NPAR)
216      105      FORMAT(1X,I5,F10.3,8I7)
217               IF(NPAR.GT.8)WRITE(7,106)INDIV,V(IND),(X(I),I=1,NPAR)
218      106      FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
219      110      IK=0
220      C STORE FIRST NSEL GENOTYPES
221               IF(IND.GT.NSEL)GO TO 115
222               K=IND+ISTOR
223               WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
224               VS(IND)=V(IND)
225               IF(ITOG(1).EQ.1)GO TO 125
226               GO TO 130
227      C REPLACE LOWEST-VALUED GENOTYPE STORED SO FAR DURING
228      C F2 CYCLE IF VALUE OF THIS INDIVIDUAL EXCEEDS
229      C THE LOWEST VALUE
230      115      LOW=1
231               DO 120 I=1,NSEL
232               IF(VS(I).LT.VS(LOW))LOW=I
233      120      CONTINUE
234               IF(V(IND).LT.VS(LOW))GO TO 130
235               K=LOW+ISTOR
```

```
236             WRITE(1'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
237             VS(LOW)=V(IND)
238         C PRINT CYCLE, INDIVIDUAL, VALUE, AND LOCATION IF
239         C GENOTYPE IS STORED IN F1
240         125     IF(ITOG(1).EQ.1)WRITE(6,126)ICYC,IND,V(IND),K
241         126     FORMAT(2I6,F11.3,I6)
242             IK=1
243         C PRINT CYCLE, INDIVIDUAL, AND VALUE
244         130     IF(ITOG(1).EQ.1.AND.IK.EQ.0)WRITE(6,126)ICYC,IND,V(IND)
245             IF(IND.EQ.NPOP)GO TO 140
246             IND=IND+1
247             GO TO 61
248         C END CYCLE ICYC
249         C LIST INDIVIDUALS ACCORDING TO PHENOTYPIC VALUE
250         140     CALL LIST(VS,NSEL,R)
251         C AVERAGE VALUE AND STANDARD DEVIATION OF SELECTED INDIVIDUALS
252             CALL ASD(VS,NSEL,AVGS,STDS)
253         C AVERAGE VALUE AND STANDARD DEVIATION OF POPULATION
254             CALL ASD(V,NPOP,AVG,STD)
255         C STORE ICYC,E,AVG,STD,AVGS,STDS,NIZ,NTR IN F2
256             K=(IVAR-1)*LCYC+ICYC
257             WRITE(2'K,150)ICYC,E,AVG,STD,AVGS,STDS,NIZ,NTR
258         150     FORMAT(1X,I3,5F10.3,2I10)
259         C TEST FOR END OF VARIETY
260             IF(ICYC.EQ.LCYC)GO TO 160
261         C BEGIN NEW CYCLE
262             ICYC=ICYC+1
263             IDRAW=IDRAW+NSEL
264             IF(IDRAW.GT.NSEL)IDRAW=0
265             ISTOR=ISTOR+NSEL
266             IF(ISTOR.GT.NSEL)ISTOR=0
267             GO TO 60
268         C TEST FOR END OF RUN
269         160     K=R(1)
270             IF(ITOG(1).EQ.1)WRITE(6,161)VS(K),VV
271         161     FORMAT(1X,'VS='F10.3/' VV='2F10.3)
272             LOW=IVAR
273             IF(IVAR.LE.2)GO TO 163
274             LOW=1
275             DO 162 I=1,2
276             IF(VV(I).LT.VV(LOW))LOW=I
277         162     CONTINUE
278         163     IF(VS(K).LT.VV(LOW))GO TO 164
279             VV(LOW)=VS(K)
280             K=K+ISTOR
281             READ(1'K)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
282             K=KV+LOW
283             WRITE(1'K)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
284         164     IF(IVAR.EQ.NVAR)GO TO 170
285             IVAR=IVAR+1
286             GO TO 50
287         C PRINT DATA FROM SUCCESSIVE VARIETIES
288         170     CALL PDFSV(LCYC,NVAR)
289         C CLOSE FILES
```

```
290               CALL CLOSE(1)
291               CALL CLOSE(2)
292               CALL CLOSE(3)
293               CALL CLOSE(7)
294       C TEST FOR STOP
295               IF(CDATA(1).EQ.STOP)STOP
296       C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
297       C IF ITOG(2) = 2
298               IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
299       180     FORMAT(1X,'RESTART AT ',A5)
300               IF(ITOG(2).EQ.2)PAUSE
301       C CONTINUE USING INPUT DATA IN FILE CDATA
302               CALL SEEK(1,CDATA)
303               GO TO 10
304               END
```

Reciprocal Recurrent Selection 1 (RRS1)

PDP-9 CHAIN/EXECUTE System

```
DOS-15 V1A
$B PR

DOS-15 V1A
$$JOB
A DKA -1,-4

$CHAIN
CHAIN V7A

NAME XCT FILE
>RRS1
LIST OPTIONS & PARAMETERS
>NM
DEFINE RESIDENT CODE
>MRRS1,INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST,
-ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA
DESCRIBE LINKS & STRUCTURE
>G1=SGA1,PGA1
>G2=SGA2,PGA2
>G3=SGA3,PGA3
>G4=SGA4,PGA4
>G5=SGA5,PGA5
>G6=SGA6,PGA6
>G7=SGA7,PGA7
>G8=SGA8,PGA8
>G9=SGA9,PGA9
>G10=SGA10,PGA10
>G11=SGA11,PGA11
>G12=SGA12,PGA12
>G1:G2:G3:G4:G5:G6:G7:G8:G9:G10:G11:G12:MERR
>V1:V2:V3:V4:V5:V6
>

CORE REQ'D
        15532-57636

DOS-15 V1A
$$EXIT
```

Input Data

```
          50001
RRS1 6/25/73
NOVLP          1
NVALU          1
PINV      0.0000
PTRA      0.0000
PCROS     0.5000
PCROL     0.5000
PMUT      1.0000
CV        0.0000
NPOP           8
NSEL           4
NSAMP          2
LCYC          10
NPAR           8
NSEG          32
NREP           1
IX             1
IPAP           1
IPBP           0
IPAF           0
IPCS           0
          STOP
```

Main Program (MRRS1)

```
001       C MRRS1 V1
002       C RECIPROCAL RECURRENT SELECTION 1
003       C MAIN PROGRAM OF GENETIC PROGRAMMING SYSTEM RRS1
004             INTEGER CP(256,2,3),S(256,2,3),RA(100),RB(100),X(256)
005             LOGICAL EVENT,VIAB
006             DIMENSION A(12),CDATA(2),F1(2),F2(2),F3(2),PFILE(2)
007             1,VA(100),VB(100)
008             COMMON /CPS/CP,S
009             DATA F1(1),F2(1),F3(1)/5HF1   ,5HF2   ,5HF3   /
010             1,F1(2),F2(2),F3(2),PFILE(2),CDATA(2)/5*4H SRC/
011             1,STOP/5HSTOP /,PFILE(1)/5HRRS1 /
012       C READ PFILE,NOVLP,NVALU,PINV,PTRA,PCROSPCROL,PMUT,CV,
013       C NPOP,NSEL,NSAMP,LCYC,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS
014       C CDATA(1) FROM DISK FILE
015             IF(TTOG(2).EQ.0)GO TO 6
016             WRITE(6,1)
017       1     FORMAT(1X,'DATA FILE')
018             READ(5,5)PFILE(1)
019       5     FORMAT(A5)
020       6     CALL SEEK(1,PFILE)
021       10    READ(1,15)PFILE(1),A,NOVLP,NVALU,PINV,PTRA
```

```
022               1,PCROS,PCROL,PMUT,CV
023     15        FORMAT(9X,A5/12A5,2(/9X,I6),5(/9X,F6.4)/8X,F7.4)
024               READ(1,20)NPOP,NSEL,NSAMP,LCYC
025     20        FORMAT(9X,I6,3(/9X,I6))
026               READ(1,25)NPAR,NSEG,NREP,IX
027     25        FORMAT(9X,I6,3(/9X,I6))
028               READ(1,30)IPAP,IPBP,IPAF,IPCS,CDATA(1)
029     30        FORMAT(9X,I6,3(/9X,I6)/9X,A5)
030               CALL CLOSE(1)
031     C DELETE AND RECREATE PRINT FILE
032               CALL DLETE(7,PFILE,I)
033               CALL ENTER(7,PFILE)
034     C WRITE PFILE,NOVLP,NVALU,PINV,PTRA,PCROS,PCROL,PMUT,CV,
035     C NPOP,NSEL,NSAMP,LCYC,NPAR,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS
036     C CDATA INTO PRINT FILE PFILE
037               WRITE(7,40)PFILE(1),A,NOVLP,NVALU,PINV,PTRA
038               1,PCROS,PCROL,PMUT,CV,NPOP,NSEL,NSAMP,LCYC,NPAR
039               1,NSEG,NREP,IX,IPAP,IPBP,IPAF,IPCS,CDATA(1)
040     40        FORMAT(10X,A5/1X,12A5/' NOVLP',I10/' NVALU',I10
041               1/' PINV',F11.4/' PTRA',F11.4
042               1/' PCROS',F10.4/' PCROL',F10.4/' PMUT',F11.4
043               1/' CV',F13.4/' NPOP',I11/' NSEL',I11/' NSAMP',I10
044               1/' LCYC',I11/' NPAR',I11/' NSEG',I11/' NREP',I11
045               1/' IX',I13/' IPAP',I11/' IPBP',I11/' IPAF',I11
046               1/' IPCS',I11/10X,A5)
047     C DELETE AND REDEFINE DIRECT ACCESS FILE F1 USED TO STORE
048     C UP TO 4*NPOP CHROMOSOME ARRAYS
049               CALL DLETE(1,F1,I)
050               CALL DEFINE(1,4*NSEG,4*NPOP,F1,IV1,0,0,0)
051     C DELETE AND REDEFINE DIRECT ACCESS FILE F2 USED TO STORE
052     C EFF, AVG, STD, AVGS, STDS, NIZ, NTR FOR EACH CYCLE
053               CALL DLETE(2,F2,I)
054               CALL DEFINE(2,80,(NREP+3)*LCYC,F2,IV2,1,0,0)
055     C DELETE AND REDEFINE DIRECT ACCESS FILE F3 USED TO COUNT
056     C THE NUMBER OF "1" ALLELES IN THE A AND B POPULATIONS
057     C AT EACH LOCUS AND CYCLE
058               CALL DLETE(3,F3,I)
059               CALL DEFINE(3,16,NSEG,F3,IV3,0,0,0)
060     C START RANDOM NUMBER GENERATOR AT IX
061               IX=-IX
062               CALL URN(IX,U)
063     C INITIALIZE COUNTERS AND BEGIN RUN IRUN
064               NBPOP=NPOP+NPOP
065               NHYB=NBPOP*NSAMP
066               IRUN=1
067     50        INCIV=0
068               NTRT=0
069               VSUM=0.
070               E=0.
071               ICYC=1
072               HIV=0.
073               IDRAW=0
074               ISTOR=NBPOP
075     C FORM RANDOM HETEROZYGOUS SOURCE POPULATIONS
```

```
076               DO 55 K=1,NBPOP
077               DO 54 I=1,NSEG
078               CALL URN(IX,U)
079               DO 54 J=1,2
080               N=(I-1)/8+1
081               M=I-(N-1)*8
082               CP(I,J,3)=IPAC(N,M)
083               IF(J.EQ.1)S(I,J,3)=IX
084               IF(J.EQ.2)S(I,J,3)=-IX-1
085        54     CONTINUE
086               WRITE(11'K)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
087        C INCREMENT COUNT OF "1" ALLELES AT EACH LOCUS OF INDIVIDUALS
088        C IN THE SOURCE POPULATIONS IF IPAF = 1
089               IF(IPAF.EQ.0)GO TO 55
090               IF(K.LE.NPOP)KK=K
091               IF(K.GT.NPOP)KK=K-NPOP
092               CALL CA(ICYC,LCYC,KK,NPOP,NSEG)
093        55     CONTINUE
094        C BEGIN CYCLE ICYC
095        60     IND=1
096               NIZ=0
097               NTR=0
098        C DETERMINE PARENTS IN RECIPROCAL CROSS
099               IFM=0
100               N1=1
101               VA(1)=-1000.
102        65     IFM=IFM+1
103               IF(IFM.LE.NSAMP)GO TO 70
104               N1=N1+1
105               IF(N1.GT.NPOP)NB=N1-NPOP
106               IF(N1.LE.NPOP)VA(N1)=-1000.
107               IF(N1.GT.NPOP)VB(NB)=-1000.
108               IFM=1
109        70     IF(N1.LE.NPOP)N2=IRAND(NPOP+1,NBPOP)
110               IF(N1.GT.NPOP)N2=IRAND(1,NPOP)
111        C FORM HYBRID GENOTYPE OF CROSSBRED ZYGOTE
112               I1=N1+IDRAW
113               I2=N2+IDRAW
114               READ(11'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
115               READ(11'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
116               CALL INVER(CP,NSEG,PINV)
117               CALL TRANS(CP,NSEG,PTRA)
118               CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
119               CALL MUTAT(S,NSEG,PMUT)
120        C PRINT CHROMOSOME STRUCTURE DURING LAST CYCLE IF IPCS = 1
121               IF(ICYC.EQ.LCYC.AND.IPCS.EQ.1)CALL DCS(IND,CP,NSEG)
122        C PRINT PEDIGREE IF REQUESTED
123               IF(ITOG(1).EQ.1)WRITE(6,71)N1,N2,I1,I2
124        71     FORMAT(29X,4I6)
125        C ABORT INDIVIDUAL AND RETURN TO SELECT NEW RANDOM PARENT IF
126        C ZYGOTE IS INVIABLE
127               IF(VIAB(S,NSEG))GO TO 80
128               NIZ=NIZ+1
129               GO TO 70
```

```
C DEVELOP PARAMETER VALUES USING GENE ACTION SPECIFIED
C BY NDVLP
80      GO TO(81,82,83,84,85,86,87,88,89,810,811,812),NDVLP
81      CALL SGA1(NSEG,S,NPAR,X)
        GO TO 90
82      CALL SGA2(NSEG,S,NPAR,X)
        GO TO 90
83      CALL SGA3(NSEG,S,NPAR,X)
        GO TO 90
84      CALL SGA4(NSEG,S,NPAR,X)
        GO TO 90
85      CALL SGA5(NSEG,S,NPAR,X)
        GO TO 90
86      CALL SGA6(NSEG,S,NPAR,X)
        GO TO 90
87      CALL SGA7(NSEG,S,NPAR,X)
        GO TO 90
88      CALL SGA8(NSEG,S,NPAR,X)
        GO TO 90
89      CALL SGA9(NSEG,S,NPAR,X)
        GO TO 90
810     CALL SGA10(NSEG,S,NPAR,X)
        GO TO 90
811     CALL SGA11(NSEG,S,NPAR,X)
        GO TO 90
812     CALL SGA12(NSEG,S,NPAR,X)
C EVALUATE INDIVIDUAL PHENOTYPIC VALUE USING TEST
C FUNCTION SPECIFIED BY NVALU
90      GO TO(91,92,93,94,95,96),NVALU
91      CALL V1(NPAR,X,VIND)
        GO TO 97
92      CALL V2(NPAR,X,VIND)
        GO TO 97
93      CALL V3(NPAR,X,VIND)
        GO TO 97
94      CALL V4(NPAR,X,VIND)
        GO TO 97
95      CALL V5(NPAR,X,VIND)
        GO TO 97
96      CALL V6(NPAR,X,VIND)
C INCREMENT INDIVIDUAL COUNTER
97      INDIV=INDIV+1
C RECORD HIGHEST PROGENY VALUE OF RECURRENT PARENT
        IF(N1.GT.NPOP)GO TO 98
        IF(VIND.GE.VA(N1))VA(N1)=VIND
        GO TO 99
98      NB=N1-NPOP
        IF(VIND.GE.VB(NB))VB(NB)=VIND
C UPDATE TRIAL COUNTERS AND EFFICIENCY IF PARAMETERS
C ARE WITHIN THE ADMISSIBLE DOMAIN
99      IF(VIND.LT.CV)GO TO 100
        NTR=NTR+1
        NTRT=NTRT+1
        VSUM=VSUM+VIND
```

```
184             IF(IND.EQ.NHYB)E=VSUM/FLOAT(NTRT)
185       C WRITE INDIV,VALUE,AND PARAMETERS INTO PFILE IF IPAP = 1
186       C OR IPBP = 1 AND VALUE OF INDIVIDUAL EXCEEDS VALUE
187       C OF ALL PRECEDING INDIVIDUALS
188       100   IF(IPBP.EQ.1)GO TO 101
189             IF(IPAP.EQ.1)GO TO 102
190             GO TO 130
191       101   IF(VIND.LE.HIV)GO TO 130
192             HIV=VIND
193       102   IF(NPAR.LE.8)WRITE(7,105)INDIV,VIND,(X(I),I=1,NPAR)
194       105   FORMAT(1X,I5,F10.3,8I7)
195             IF(NPAR.GT.8)WRITE(7,106)INDIV,VIND,(X(I),I=1,NPAR)
196       106   FORMAT(1X,I5,F10.3,8I7/(16X,8I7))
197       C PRINT CYCLE, INDIVIDUAL, AND VALUE
198       130   IF(ITOG(1).EQ.1)WRITE(6,131)ICYC,IND,VIND
199       131   FORMAT(2I6,F11.3)
200             IF(IND.EQ.NHYB)GO TO 140
201             IND=IND+1
202             GO TO 85
203       C END CYCLE ICYC
204       C LIST INDIVIDUALS ACCORDING TO PHENOTYPIC VALUE
205       140   CALL LIST(VA,NPOP,RA)
206             CALL LIST(VB,NPOP,RB)
207       C AVERAGE VALUE AND STANDARD DEVIATION OF A PROGENY
208             CALL ASD(VA,NPOP,AVGA,STDA)
209       C AVERAGE VALUE AND STANDARD DEVIATION OF B PROGENY
210             CALL ASD(VB,NPOP,AVGB,STDB)
211       C STORE ICYC,E,AVGA,STDA,AVGB,STDB,NIZ,NTR IN F2
212             K=(TRUN-1)*LCYC+ICYC
213             WRITE(2'K,150)ICYC,E,AVGA,STDA,AVGB,STDB,NIZ,NTR
214       150   FORMAT(1X,I3,5F10.3,2I10)
215       C TEST FOR END OF RUN
216             IF(ICYC.EQ.LCYC)GO TO 160
217       C BEGIN NEW CYCLE
218             ICYC=ICYC+1
219       C SELF NSEL INDIVIDUALS WITH HIGHEST PROGENY VALUE
220       C TO PROPAGATE POPULATIONS A AND B
221             N1=0
222             DO 155 K=1,NBPOP
223             N1=N1+1
224             IF(N1.GT.NSEL)N1=1
225             IF(K.LE.NPOP)I1=RA(N1)+IDRAW
226             IF(K.GT.NPOP)I1=RB(N1)+NPOP+IDRAW
227             I2=I1
228             READ(1'I1)((CP(I,J,1),S(I,J,1),I=1,NSEG),J=1,2)
229             READ(1'I2)((CP(I,J,2),S(I,J,2),I=1,NSEG),J=1,2)
230             CALL INVER(CP,NSEG,PINV)
231             CALL TRANS(CP,NSEG,PTRA)
232             CALL FZYGO(CP,S,NSEG,PCROS,PCROL)
233             CALL MUTAT(S,NSEG,PMUT)
234             I3=K+ISTOR
235             WRITE(1'I3)((CP(I,J,3),S(I,J,3),I=1,NSEG),J=1,2)
```

```
C INCREMENT COUNT OF "1" ALLELES AT EACH LOCUS OF INDIVIDUALS
C IN THE NEW A AND B POPULATIONS IF IPAF = 1
        IF(IPAF.EQ.0)GO TO 155
        IF(K.LE.NPOP)KK=K
        IF(K.GT.NPOP)KK=K-NPOP
        CALL CA(ICYC,LCYC,KK,NPOP,NSEG)
155     CONTINUE
C RESET BASE LOCATIONS OF F1
        IDRAW=IDRAW+N3POP
        IF(IDRAW.GT.N3POP)IDRAW=0
        ISTOR=ISTOR+N3POP
        IF(ISTOR.GT.N3POP)ISTOR=0
        GO TO 50
C TEST FOR END OF REPLICATE RUNS
160     IF(IRUN.EQ.NREP)GO TO 170
        IRUN=IRUN+1
        GO TO 50
C MEAN AND EXTREMES OF REPLICATE RUNS
170     CALL MERR(LCYC,NREP)
C CLOSE FILES
        CALL CLOSE(1)
        CALL CLOSE(2)
        CALL CLOSE(3)
        CALL CLOSE(7)
C TEST FOR STOP
        IF(CDATA(1).EQ.STOP)STOP
C PRINT NAME OF NEXT DATA FILE IN SEQUENCE AND PAUSE
C IF ITOG(2) = 2
        IF(ITOG(2).EQ.2)WRITE(6,180)CDATA(1)
180     FORMAT(1X,'RESTART AT ',A5)
        IF(ITOG(2).EQ.2)PAUSE
C CONTINUE USING INPUT DATA IN FILE CDATA
        CALL SEEK(1,CDATA)
        GO TO 10
        END
```

Resident Subroutines: INVER,TRANS,FZYGO,CWS,MUTAT,MUT,VIAB,LIST, ASD,URN,IRAND,EVENT,IPAC,NPAC,DCS,CA,SA

```
C INVER V1
      SUBROUTINE INVER(CP,NSEG,PINV)
      INTEGER CP(256,2,3)
      LOGICAL EVENT
      IF(PINV.EQ.0.)RETURN
      DO 20 K=1,2
      DO 20 J=1,2
      DO 20 I=1,NSEG
      IF(.NOT.EVENT(PINV))GO TO 20
      CALL NPAC(CP(I,J,K),IC,M)
      IF(M.EQ.1)GO TO 20
      N=IRAND(1,M-1)
      IF(ITOG(1).EQ.1)WRITE(6,5)IC,N,M,K,J
5     FORMAT(1X,'INVERSION',5I6)
      DO 10 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,IP)
      IF(LC.NE.IC)GO TO 10
      IF(IP.LT.N.OR.IP.GT.M)GO TO 10
      CP(L,J,K)=IPAC(IC,M+N-IP)
10    CONTINUE
20    CONTINUE
      RETURN
      END
```

```
C TRANS V1
      SUBROUTINE TRANS(CP,NSEG,PTRA)
      INTEGER CP(256,2,3)
      LOGICAL EVENT
      IF(PTRA.EQ.0.)RETURN
      DO 120 K=1,2
      DO 120 J=1,2
      DO 120 I=1,NSEG
      IF(.NOT.EVENT(PTRA))GO TO 120
      CALL NPAC(CP(I,J,K),NC,NP)
      L=IRAND(1,NSEG)
      CALL NPAC(CP(L,J,K),MC,MP)
      IF(MC.EQ.NC)GO TO 120
      N=IRAND(1,4)
      IF(ITOG(1).EQ.1)WRITE(6,15)N,NC,NP,MC,MP,K,J
15    FORMAT(1X,'TRANLOCATION',7I6)
      GO TO (20,40,60,90),N
C EXCHANGE UPPER ARMS
20    DO 30 L=1,NSEG
```

```
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(LC.EQ.NC.AND.LP.LE.NP)IC=MC
      IF(LC.EQ.MC.AND.LP.LE.MP)IC=NC
      IF(LC.EQ.NC.AND.LP.GT.NP)IP=LP-NP+MP
      IF(LC.EQ.MC.AND.LP.GT.MP)IP=LP-MP+NP
      CP(L,J,K)=IPAC(IC,IP)
30    CONTINUE
      GO TO 120
C EXCHANGE LOWER ARMS
40    DO 50 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(.NOT.LC.EQ.NC.AND.LP.GE.NP)GO TO 45
      CP(L,J,K)=IPAC(MC,LP-NP+MP)
45    IF(.NOT.LC.EQ.MC.AND.LP.GE.MP)GO TO 50
      CP(L,J,K)=IPAC(NC,LP-MP+NP)
50    CONTINUE
      GO TO 120
C EXCHANGE UPPER ARM OF NC CHROMOSOME WITH LOWER ARM OF MC CHROMOSOM
60    MX=0
      DO 70 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(LC.EQ.MC.AND.LP.GT.MX)MX=LP
70    CONTINUE
      DO 80 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(.NOT.LC.EQ.NC.AND.LP.LE.NP)GO TO 75
      CP(L,J,K)=IPAC(MC,NP+MP-LP)
75    IF(LC.EQ.NC.AND.LP.GT.NP)CP(L,J,K)=IPAC(LC,LP-NP+MX-MP+1)
      IF(.NOT.LC.EQ.MC.AND.LP.GE.MP)GO TO 80
      CP(L,J,K)=IPAC(NC,MX-LP+1)
80    CONTINUE
      GO TO 120
C EXCHANGE LOWER ARM OF NC CHROMOSOME WITH UPPER ARM OF MC CHROMOSOM
90    NX=0
      DO 100 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(LC.EQ.NC.AND.LP.GT.NX)NX=LP
100   CONTINUE
      DO 110 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,LP)
      IF(.NOT.LC.EQ.NC.AND.LP.GE.NP)GO TO 105
      CP(L,J,K)=IPAC(MC,NX-LP+1)
105   IF(.NOT.LC.EQ.MC.AND.LP.LE.MP)GO TO 106
      CP(L,J,K)=IPAC(NC,MP+NP-LP)
106   IF(LC.EQ.MC.AND.LP.GT.MP)CP(L,J,K)=IPAC(LC,LP-MP+NX-NP+1)
110   CONTINUE
120   CONTINUE
      RETURN
      END
```

```
C FZYGO V1
      SUBROUTINE FZYGO(CP,S,NSEG,PCROS,PCROL)
      INTEGER CP(256,2,3),S(256,2,3),H(32,4)
     1,F(2),LP(256),RP(256)
      LOGICAL EVENT
      DATA F(1),F(2)/2,1/
C ZERO ZYGOTE ARRAY
      DO 10 J=1,2
      DO 10 L=1,NSEG
      CP(L,J,3)=0
10    S(L,J,3)=0
C GENERATE GAMETE FROM EACH PARENT
      DO 120 K=1,2
C ZERO DATA ARRAY
      DO 20 J=1,4
      DO 20 I=1,32
20    H(I,J)=0
C UNPACK DATA AT LOCI IN BOTH GENOMES AND FILL ARRAY H
      NSC=0
      DO 40 I=1,NSEG
      CALL NPAC(CP(I,1,K),IC1,IP1)
      CALL NPAC(CP(I,2,K),IC2,IP2)
      IF(H(IC1,1).EQ.0.OR.H(IC1,1).EQ.2)H(IC1,1)=H(IC1,1)+1
      IF(H(IC2,1).EQ.0.OR.H(IC2,1).EQ.1)H(IC2,1)=H(IC2,1)+2
      IF(IP1.GT.H(IC1,2))H(IC1,2)=IP1
      IF(IP2.GT.H(IC2,3))H(IC2,3)=IP2
      IF(IC1.EQ.IC2)GO TO 40
      IF(H(IC1,4).EQ.0.AND.H(IC2,4).EQ.0)GO TO 30
      IF(H(IC1,4).EQ.0.AND.H(IC2,4).NE.0)H(IC1,4)=H(IC2,4)
      IF(H(IC1,4).NE.0.AND.H(IC2,4).EQ.0)H(IC2,4)=H(IC1,4)
      IF(H(IC1,4).EQ.H(IC2,4))GO TO 40
      DO 25 J=1,32
      IF(J.NE.IC2.AND.H(J,4).EQ.H(IC2,4))H(J,4)=H(IC1,4)
25    CONTINUE
      H(IC2,4)=H(IC1,4)
      GO TO 40
30    NSC=NSC+1
      H(IC1,4)=NSC
      H(IC2,4)=NSC
40    CONTINUE
C ASSIGN SOURCE GENOMES TO EACH CHROMOSOME I IN H(I,1)
      DO 50 I=1,32
      IF(H(I,1).EQ.0)GO TO 50
      IF(H(I,1).EQ.3)H(I,1)=IRAND(1,2)
      DO 45 J=I,32
      IF(H(J,1).EQ.0.OR.H(J,4).EQ.0)GO TO 45
      IF(H(J,4).EQ.H(I,4))H(J,1)=H(I,1)
45    CONTINUE
50    CONTINUE
C SEGREGATION WITH CROSSOVER INHIBITED BY INVERSION AND
C TRANSLOCATION
      DO 120 I=1,32
      IF(H(I,1).EQ.0)GO TO 120
      J=H(I,1)
```

```
      JH=F(J)
C ARRANGE LOCI ON SOURCE CHROMOSOME BY POSITION
      DO 60 L=1,NSEG
      CALL NPAC(CP(L,J,K),LC,M)
      IF(LC.NE.I)GO TO 60
      LP(M)=L
60    CONTINUE
C IDENTIFY SECTION OF SOURCE CHROMOSOME SYNAPSED WITH ANOTHER
C CHROMOSOME
      N1=1
      N2=H(I,J+1)
70    L1=LP(N1)
      DO 80 N=N1,N2
      LN=LP(N)
      CALL NPAC(CP(LN,JH,K),LNC,LNP)
      CALL NPAC(CP(L1,JH,K),L1C,L1P)
      IF(LNC.NE.L1C)GO TO 90
      RP(N)=IABS(LNP-L1P+N1)
80    CONTINUE
90    NF=N-1
C SELECT GAMETE SEGMENTS FROM PARENTAL CHROMOSOMES WITH PCROS
C PROBABILITY OF FUNCTIONAL CROSSOVER BETWEEN SEGMENTS
      JC=J
      DO 110 N=N1,NF
      IF(EVENT(PCROS))JC=F(JC)
      IF(RP(N).NE.N)JC=J
      IF(N.GT.N1.AND.RP(N-1).NE.N-1)JC=J
100   L=LP(N)
      CP(L,K,3)=CP(L,J,K)
      JCH=F(JC)
      M=0
      JCC=1
      DO 105 KK=1,16
      IF(EVENT(PCROL))JCC=F(JCC+1)-1
105   M=M*2+JCC
      CALL CWS(S(L,JC,K),S(L,JCH,K),M,S(L,K,3))
110   CONTINUE
      IF(NF.EQ.N2)GO TO 120
      N1=NF+1
      GO TO 70
120   CONTINUE
      RETURN
      END
```

```
/CWS V1
/SUBROUTINE CWS(SJC,SJCH,M,SK3)
      .TITLE CWS
      .GLOBL  .DA,CWS
CWS   0
      JMS*    .DA
```

```
        JMP     .+5
SJC     .DSA    0
SJCH    .DSA    0
M       .DSA    0
SK3     .DSA    0
        LAC*    M
        CMA
        DAC     MBAR
        LAC*    SJC
        AND*    M
        DAC     TEMP
        LAC*    SJCH
        AND     MBAR
        TAD     TEMP
        DAC*    SK3
        JMP*    CWS
MBAR    0
TEMP    0
        .END
```

```
C MUTAT V1
        SUBROUTINE MUTAT(S,NSEG,PMUT)
        INTEGER S(256,2,3)
        LOGICAL EVENT
        IF(PMUT.EQ.0.)RETURN
        DO 20 J=1,2
        DO 20 L=1,NSEG
        M=0
        DO 10 K=1,17
        IF(.NOT.EVENT(PMUT))GO TO 10
        M=M+2**(K-1)
10      CONTINUE
        IF(M.GT.0)CALL MUT(S(L,J,3),M)
20      CONTINUE
        RETURN
        END
```

```
/MUT V1
/SUBROUTINE MUT(I,M)
        .TITLE MUT
        .GLOBL  .DA,MUT
MUT     0
        JMS*    .DA
        JMP     .+3
I       .DSA    0
M       .DSA    0
        LAC*    I
```

```
         XOR*     M
         AND      (177777
         DAC*     I
         JMP*     MUT
         .END



C VIAB V1
         LOGICAL FUNCTION VIAB(S,NSEG)
         INTEGER S(256,2,3)
         VIAB=.TRUE.
         RETURN
         END



C LIST V1
         SUBROUTINE LIST(V,N,S)
         INTEGER S(100)
         DIMENSION V(100)
         DO 10 I=1,N
10       S(I)=I
         NM1=N-1
         DO 20 I=1,NM1
         IP1=I+1
         DO 20 K=IP1,N
         IS=S(I)
         KS=S(K)
         IF(V(KS).LT.V(IS))GO TO 20
         M=S(I)
         S(I)=S(K)
         S(K)=M
20       CONTINUE
         RETURN
         END



C ASD V1
         SUBROUTINE ASD(V,N,AVG,STD)
         DIMENSION V(100)
         S=0.
         DO 10 I=1,N
10       S=S+V(I)
         AVG=S/FLOAT(N)
         STD=0.
         DO 20 I=1,N
20       STD=STD+(V(I)-AVG)**2
```

```
      IF(N.GT.1)STD=SQRT(STD/FLOAT(N-1))
      IF(N.EQ.1)STD=0.
      RETURN
      END
```

```
/URN V1
/SUBROUTINE URN(IX,U)
      .TITLE URN
      .GLOBL .DA,URN
URN   0
      JMS*    .DA
      JMP     .+3
IX    .DSA    0
U     .DSA    0
      LAC*    IX
      SMA
      JMP     START
      CMA
      TAD     (1
      DAC     I
START LAC     U
      TAD     (1
      DAC     UP1
      LAC     I
      CLL
      MUL               /MULTIPLY BY 259
      403               /DECIMAL 259 = OCTAL 403
      LACQ
      AND     (77777    /MODULO 32768
      DAC*    IX
      DAC     I
      RTL               /POSITION FOR 18-BIT WORD
      CLQ
      NORM
      DAC*    UP1       /DEPOSIT MANTISSA
      LACS              /GET STEP COUNTER
      TAD     (-34
      CMA
      TAD     (1
      AND     (777
      DAC*    U         /DEPOSIT EXPONENT
      JMP*    URN
I     0
UP1   0
```

```
C IRAND V1
      FUNCTION IRAND(IL,IU)
      DATA IX/1/
      CALL URN(IX,U)
      IRAND=IL+IFIX(FLOAT(IU-IL+1)*U)
      IF(IRAND.EQ.IU+1)IRAND=IU
      RETURN
      END



C EVENT V1
      LOGICAL FUNCTION EVENT(PROB)
      DATA IX/1/
      EVENT=.FALSE.
      CALL URN(IX,U)
      IF(U.LT.PROB)EVENT=.TRUE.
      RETURN
      END



/IPAC V1
/FUNCTION IPAC(N,M)
      .TITLE IPAC
      .GLOBL .DA,IPAC
IPAC  0
      JMS*   .DA
      JMP    .+3
N     0
M     0
      LAC*   N
      TAD    (-1
      LLS    10
      AND    (177400
      DAC    TEMP
      LAC*   M
      TAD    (-1
      AND    (377
      XOR    TEMP
      JMP*   IPAC
TEMP  0
```

```
/NPAC V1
/SUBROUTINE NPAC(CP,C,P)
          .TITLE NPAC
          .GLOBL .DA,NPAC
NPAC      0
          JMS*      .DA
          JMP       .+4
CP        .DSA      0
C         .DSA      0
P         .DSA      0
          LAC*      CP
          AND       (377
          TAD       (1
          DAC*      P
          LAC*      CP
          LRS       10
          AND       (377
          TAD       (1
          DAC*      C
          JMP*      NPAC
```

```
C DCS V1
          SUBROUTINE DCS(IND,CP,NSEG)
          INTEGER CP(256,2,3)
          WRITE(7,10)IND
10        FORMAT(1X,'INDIVIDUAL',I3)
          DO 60 J=1,2
          WRITE(7,20)J
20        FORMAT(1X,'GENOME',I2)
          N=1
25        IPMAX=0
          DO 30 L=1,NSEG
          CALL NPAC(CP(L,J,3),IC,IP)
          IF(IC.NE.N)GO TO 30
          CP(IP,1,1)=L
          IF(IP.GT.IPMAX)IPMAX=IP
30        CONTINUE
          IF(IPMAX.EQ.0)GO TO 60
          WRITE(7,40)N
40        FORMAT(1X,'CHROMOSOME',I3)
          WRITE(7,50)(CP(I,1,1),I=1,IPMAX)
50        FORMAT(1X,10I4)
          N=N+1
          GO TO 25
60        CONTINUE
          RETURN
          END
```

```
C CA V2
      SUBROUTINE CA(IGEN,LGEN,IND,NPOP,NSEG)
      INTEGER CP(256,2,3),S(256,2,3),A(16),B(16)
      COMMON /CPS/CP,S
      IF(IND.GT.1)GO TO 30
      NFIX=2*NPOP
      NFL=0
      DO 10 K=1,16
10    A(K)=0
      DO 20 K=1,NSEG
20    WRITE(3'K)(A(I),I=1,16)
30    DO 50 K=1,NSEG
      CALL SA(S(K,1,3),S(K,2,3),B(1))
      READ(3'K)A
      DO 40 I=1,16
40    A(I)=A(I)+B(I)
      WRITE(3'K)A
50    CONTINUE
      IF(IND.LT.NPOP)RETURN
      WRITE(7,60)IGEN
60    FORMAT(/1X,'GENERATION',I4/1X,'SEG',24X,'NUMBER OF 1 ALLELES')
      DO 80 K=1,NSEG
      READ(3'K)A
      WRITE(7,70)K,(A(-I+17),I=1,16)
70    FORMAT(1X,I3,3X,16I4)
      DO 80 J=1,16
      IF(A(J).EQ.0.OR.A(J).EQ.NFIX)NFL=NFL+1
80    CONTINUE
      WRITE(7,90)NFL
90    FORMAT(1X,'NFL=',I4)
      NFL=0
      RETURN
      END
```

```
/SA V1
/SUBROUTINE SA(S1,S2,B)
      .TITLE SA
      .GLOBL .DA,SA
SA    0
      JMS*   .DA
      JMP    .+4
S1    .DSA   0
S2    .DSA   0
B     .DSA   0
      LAC    B
      TAD    (-1
      DAC    POINT
      LAC*   S1
      XOR*   S2
      DAC    ONE
```

```
          LAC*    S1
          AND*    S2
          DAC     TWO
          LAC     (-20
          DAC     CNT
DO        ISZ     POINT
          LAC     TWO
          AND     (1
          CLL
          RAL
          DAC     TEMP
          LAC     ONE
          AND     (1
          XOR     TEMP
          DAC*    POINT
          LAC     ONE
          RAR
          DAC     ONE
          LAC     TWO
          RAR
          DAC     TWO
          ISZ     CNT
          JMP     DO
          JMP*    SA
POINT     0
CNT       0
TEMP      0
ONE       0
TWO       0
          .END
```

Linked Subroutines: SGA1,PGA1;SGA2,PGA2;SGA3,PGA3;SGA4,PGA4;SGA5,PGA5;SGA6,PGA6;
SGA7,PGA7;SGA8,PGA8;SGA9,PGA9;SGA10,PGA10;SGA11,PGA11;
SGA12,PGA12;SGA2A,PGA2A;SGA5A,PGA5A;SGA8A,PGA8A;SGA11A,PGA11A;
MERR:PDFSV:V1,V2,V3,V4,V5,V6

```
C SGA1 V1
       SUBROUTINE SGA1(NSEG,S,NPAR,X)
       INTEGER S(256,2,3),X(256),W(4)
       DATA W/1,1,120,1920/
       L=0
       DO 20 I=1,NPAR
       N=0
       DO 10 J=1,4
       L=L+1
       CALL PGA1(S(L,1,3),S(L,2,3),M)
       IF(J.EQ.1)M=M*15/32
       IF(J.EQ.2)M=M*15/2
10     N=N+M*W(J)
20     X(I)=N
       RETURN
       END
```

```
/PGA1 V1
/SUBROUTINE PGA1(S1,S2,M)
       .GLOBL .DA,PGA1
PGA1   0
       JMS*    .DA
       JMP     .+4
S1     .DSA    0
S2     .DSA    0
M      .DSA    0
       LAC     (-20
       DAC     CNT
       DZM     N
       LAC*    S1
       XOR*    S2
       DAC     A
W1     AND     (1
       TAD     N
       DAC     N
       LAC     A
       RAR
       DAC     A
       ISZ     CNT
       JMP     W1
       LAC     (-20
       DAC     CNT
```

```
          LAC*     S1
          AND*     S2
          CLL
          RAL
          DAC      A
W2        AND      (2
          TAD      N
          DAC      N
          LAC      A
          RAR
          DAC      A
          ISZ      CNT
          JMP      W2
          LAC      N
          DAC*     M
          JMP*     PGA1
CNT       0
N         0
A         0
          .END
```

```
C SGA2 V1
          SUBROUTINE SGA2(NSEG,S,NPAR,X)
          INTEGER S(256,2,3),X(256)
          DO 10 L=1,NPAR
          CALL PGA2(S(L,1,3),S(L,2,3),X(L))
10        CONTINUE
          RETURN
          END
```

```
/PGA2 V1
/SUBROUTINE PGA2(S1,S2,M)
          .GLOBL   .DA,PGA2
    2     0
          JMS*     .DA
          JMP      .+4
S1        .DSA     0
S2        .DSA     0
M         .DSA     0
          LAC*     S1
          XOR*     S2
          CLL
          RAR
          DAC      TEMP
          LAC*     S1
          AND*     S2
```

```
          TAD       TEMP
          AND       (177777
          DAC*      M
          JMP*      PGA2
TEMP      0
          .END
```

```
C SGA3 V1
          SUBROUTINE SGA3(NSEG,S,NPAR,X)
          INTEGER S(256,2,3),X(256)
          DO 10 L=1,NPAR
          CALL PGA3(S(L,1,3),S(L,2,3),X(L))
10        CONTINUE
          RETURN
          END
```

```
/PGA3 V1
/SUBROUTINE PGA3(S1,S2,M)
          .GLOBL .DA,PGA3
PGA3      0
          JMS*      .DA
          JMP       .+4
S1        .DSA      0
S2        .DSA      0
M         .DSA      0
          LAC*      S1
          XOR*      S2
          DAC       HET
          LAC*      S1
          AND*      S2
          XOR       HET
          AND       (177777
          JMS       CONV
          DAC       TEMP
          LAC*      S1
          AND*      S2
          JMS       CONV
          TAD       TEMP
          RAR
          AND       (177777
          DAC*      M
          JMP*      PGA3
HET       0
TEMP      0
          /SUBROUTINE TO CONVERT ACC FROM GRAY TO BINARY CODE
CONV      0
```

```
        DAC     N       /SAVE ACC
        LAC     (-20    /SET COUNTER
        DAC     CNT
        DZM     A
        LAC     N       /RESTORE ACC
        RTL
        RAL
ROTA    RAL             /ROTATE BITS LEFT INTO POSITION
        DAC     N       /SAVE ACC
        AND     (1
        XOR     A
        DAC     A
        LAC     N       /RESTORE ACC
        AND     (777776 /CLEAR LSB
        XOR     A
        ISZ     CNT
        JMP     ROTA
        CLL
        AND     (177777
        JMP*    CONV
N       0
CNT     0
A       0
        .END
```

```
C SGA4 V1
        SUBROUTINE SGA4(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256),W(4)
        DATA W/1,1,120,1920/
        L=0
        DO 20 I=1,NPAR
        N=0
        DO 10 J=1,4
        L=L+1
        CALL PGA4(S(L,1,3),S(L,2,3),M)
        IF(J.EQ.1)M=M*15/32
        IF(J.EQ.2)M=M*15/2
10      N=N+M*W(J)
        N=N-16384
        IF(N.LT.0)N=-N
        IF(N.GT.32767)N=65535-N
20      X(I)=N*2
        RETURN
        END
```

```
/PGA4 V1
/SUBROUTINE PGA4(S1,S2,M)
          .GLOBL .DA,PGA4
PGA4      0
          JMS*      .DA
          JMP       .+4
S1        .DSA      0
S2        .DSA      0
M         .DSA      0
          LAC       (-20
          DAC       CNT
          DZM       N
          LAC*      S1
          XOR*      S2
          DAC       A
W1        AND       (1
          TAD       N
          DAC       N
          LAC       A
          RAR
          DAC       A
          ISZ       CNT
          JMP       W1
          LAC       (-20
          DAC       CNT
          LAC*      S1
          AND*      S2
          CLL
          RAL
          DAC       A
W2        AND       (2
          TAD       N
          DAC       N
          LAC       A
          RAR
          DAC       A
          ISZ       CNT
          JMP       W2
          LAC       N
          DAC*      M
          JMP*      PGA4
CNT       0
N         0
A         0
          .END
```

```
C SGA5 V1
      SUBROUTINE SGA5(NSEG,S,NPAR,X)
      INTEGER S(256,2,3),X(256)
      DO 10 L=1,NPAR
      CALL PGA5(S(L,1,3),S(L,2,3),N)
      N=N-16384
      IF(N.LT.0)N=-N
      IF(N.GT.32767)N=65535-N
10    X(L)=N*2
      RETURN
      END
```

```
/PGA5 V1
/SUBROUTINE PGA5(S1,S2,M)
      .GLOBL  .DA,PGA5
PGA5  0
      JMS*    .DA
      JMP     .+4
S1    .DSA    0
S2    .DSA    0
M     .DSA    0
      LAC*    S1
      XOR*    S2
      CLL
      RAR
      DAC     TEMP
      LAC*    S1
      AND*    S2
      TAD     TEMP
      AND     (177777
      DAC*    M
      JMP*    PGA5
TEMP  0
      .END
```

```
C SGA6 V1
      SUBROUTINE SGA6(NSEG,S,NPAR,X)
      INTEGER S(256,2,3),X(256)
      DO 10 L=1,NPAR
      CALL PGA6(S(L,1,3),S(L,2,3),N)
      N=N-16384
      IF(N.LT.0)N=-N
      IF(N.GT.32767)N=65535-N
10    X(L)=N*2
      RETURN
      END
```

```
/PGA6 V1
/SUBROUTINE PGA6(S1,S2,M)
        .GLOBL .DA,PGA6
PGA6    0
        JMS*    .DA
        JMP     .+4
S1      .DSA    0
S2      .DSA    0
M       .DSA    0
        LAC*    S1
        XOR*    S2
        DAC     HET
        LAC*    S1
        AND*    S2
        XOR     HET
        AND     (177777
        JMS     CONV
        DAC     TEMP
        LAC*    S1
        AND*    S2
        JMS     CONV
        TAD     TEMP
        RAR
        AND     (177777
        DAC*    M
        JMP*    PGA6
HET     0
TEMP    0
        /SUBROUTINE TO CONVERT ACC FROM GRAY TO BINARY CODE
CONV    0
        DAC     N       /SAVE ACC
        LAC     (-20    /SET COUNTER
        DAC     CNT
        DZM     A
        LAC     N       /RESTORE ACC
        RTL
        RAL
ROTA    RAL             /ROTATE BITS LEFT INTO POSITION
        DAC     N       /SAVE ACC
        AND     (1
        XOR     A
        DAC     A
        LAC     N       /RESTORE ACC
        AND     (777776 /CLEAR LSB
        XOR     A
        ISZ     CNT
        JMP     ROTA
        CLL
        AND     (177777
        JMP*    CONV
N       0
CNT     0
A       0
        .END
```

```
C SGA7 V1
      SUBROUTINE SGA7(NSEG,S,NPAR,X)
      INTEGER S(256,2,3),X(256),W(4)
      DATA W/1,1,120,1920/,IX/1/
      L=-1
      DO 20 I=1,NPAR
      N=0
      DO 10 J=1,4
      L=L+2
      LD=L+1
      CALL URN(IX,U)
      CALL PGA7(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
      IF(J.EQ.1)M=M*15/32
      IF(J.EQ.2)M=M*15/2
10    N=N+M*W(J)
20    X(I)=N
      RETURN
      END
```

```
/PGA7 V1
/SUBROUTINE PGA7(S1,S2,S1D,S2D,IX,M)
      .GLOBL .DA,PGA7
PGA7  0
      JMS*    .DA
      JMP     .+7
S1    .DSA    0
S2    .DSA    0
S1D   .DSA    0
S2D   .DSA    0
IX    .DSA    0
M     .DSA    0
      LAC     (-20
      DAC     CNT
      DZM     N
      LAC*    S1
      AND*    S2
      DAC     A
      LAC*    S1
      XOR*    S2
      DAC     B
      LAC*    S1D
      AND*    S2D
      DAC     C
      LAC*    S1D
      XOR*    S2D
      AND*    IX
      XOR     C
      AND     B
      XOR     A
      CLL
```

```
        RAL
        DAC     A
W2      AND     (2
        TAD     N
        DAC     N
        LAC     A
        RAR
        DAC     A
        ISZ     CNT
        JMP     W2
        LAC     N
        AND     (177777
        DAC*    M
        JMP*    PGA7
CNT     0
N       0
A       0
B       0
C       0
        .END
```

```
C SGA8 V1
        SUBROUTINE SGA8(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256)
        DATA IX/1/
        L=-1
        DO 10 I=1,NPAR
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA8(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
10      X(I)=M
        RETURN
        END
```

```
/PGA8 V1
/SUBROUTINE PGA8(S1,S2,S1D,S2D,IX,M)
        .GLOBL  .DA,PGA8
PGA8    0
        JMS*    .DA
        JMP     .+7
S1      .DSA    0
S2      .DSA    0
S1D     .DSA    0
S2D     .DSA    0
IX      .DSA    0
```

```
M       .DSA    0
        LAC*    S1
        AND*    S2
        DAC     A
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
        XOR     A
        AND     (177777
        DAC*    M
        JMP*    PGA8
A       0
B       0
C       0
        .END
```

```
C SGA9 V1
        SUBROUTINE SGA9(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256)
        DATA IX/1/
        L=-1
        DO 10 I=1,NPAR
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA9(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
10      X(I)=M
        RETURN
        END
```

```
/PGA9 V1
/SUBROUTINE PGA9(S1,S2,S1D,S2D,IX,M)
        .GLOBL .DA,PGA9
PGA9    0
        JMS*    .DA
        JMP     .+7
S1      .DSA    0
S2      .DSA    0
S1D     .DSA    0
```

```
S2D     .DSA    0
IX      .DSA    0
M       .DSA    0
        LAC*    S1
        AND*    S2
        DAC     AA
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
        XOR     AA
        JMS     CONV
        AND     (177777
        DAC*    M
        JMP*    PGA9
AA      0
B       0
C       0
        /SUBROUTINE TO CONVERT ACC FROM GRAY TO BINARY CODE
CONV    0
        DAC     N       /SAVE ACC
        LAC     (-20    /SET COUNTER
        DAC     CNT
        DZM     A
        LAC     N       /RESTORE ACC
        RTL
        RAL
ROTA    RAL             /ROTATE BITS LEFT INTO POSITION
        DAC     N       /SAVE ACC
        AND     (1
        XOR     A
        DAC     A
        LAC     N       /RESTORE ACC
        AND     (777776 /CLEAR LSB
        XOR     A
        ISZ     CNT
        JMP     ROTA
        CLL
        AND     (177777
        JMP*    CONV
N       0
CNT     0
A       0
        .END
```

```
C SGA10 V1
        SUBROUTINE SGA10(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256),W(4)
        DATA W/1,1,120,1920/,IX/1/
        L=-1
        DO 20 I=1,NPAR
        N=0
        DO 10 J=1,4
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA10(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
        IF(J.EQ.1)M=M*15/32
        IF(J.EQ.2)M=M*15/2
10      N=N+M*W(J)
        N=N-16384
        IF(N.LT.0)N=-N
        IF(N.GT.32767)N=65535-N
20      X(I)=N*2
        RETURN
        END



/PGA10 V1
/SUBROUTINE PGA10(S1,S2,S1D,S2D,IX,M)
        .GLOBL .DA,PGA10
PGA10   0
        JMS*    .DA
        JMP     .+7
S1      .DSA    0
S2      .DSA    0
S1D     .DSA    0
S2D     .DSA    0
IX      .DSA    0
M       .DSA    0
        LAC     (-20
        DAC     CNT
        DZM     N
        LAC*    S1
        AND*    S2
        DAC     A
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
```

```
        XOR     A
        CLL
        RAL
        DAC     A
W2      AND     (2
        TAD     N
        DAC     N
        LAC     A
        RAR
        DAC     A
        ISZ     CNT
        JMP     W2
        LAC     N
        AND     (177777
        DAC*    M
        JMP*    PGA10
CNT     0
N       0
A       0
B       0
C       0
        .END
```

```
C SGA11 V1
        SUBROUTINE SGA11(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256)
        DATA IX/1/
        L=-1
        DO 10 I=1,NPAR
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA11(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
        M=M-16384
        IF(M.LT.0)M=-M
        IF(M.GT.32767)M=65535-M
10      X(I)=M*2
        RETURN
        END
```

```
/PGA11 V1
/SUBROUTINE PGA11(S1,S2,S1D,S2D,IX,M)
        .GLOBL  .DA,PGA11
PGA11   0
        JMS*    .DA
        JMP     .+7
```

```
S1      .DSA    0
S2      .DSA    0
S1D     .DSA    0
S2D     .DSA    0
IX      .DSA    0
M       .DSA    0
        LAC*    S1
        AND*    S2
        DAC     A
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
        XOR     A
        AND     (177777
        DAC*    M
        JMP*    PGA11
A       0
B       0
C       0
        .END
```

```
C SGA12 V1
        SUBROUTINE SGA12(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256)
        DATA IX/1/
        L=-1
        DO 10 I=1,NPAR
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA12(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
        M=M-16384
        IF(M.LT.0)M=-M
        IF(M.GT.32767)M=65535-M
10      X(I)=M*2
        RETURN
        END
```

```
/PGA12 V1
/SUBROUTINE PGA12(S1,S2,S1D,S2D,IX,M)
        .GLOBL .DA,PGA12
PGA12   0
        JMS*    .DA
        JMP     .+7
S1      .DSA    0
S2      .DSA    0
S1D     .DSA    0
S2D     .DSA    0
IX      .DSA    0
M       .DSA    0
        LAC*    S1
        AND*    S2
        DAC     AA
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
        XOR     AA
        JMS     CONV
        AND     (177777
        DAC*    M
        JMP*    PGA12
AA      0
B       0
C       0
        /SUBROUTINE TO CONVERT ACC FROM GRAY TO BINARY CODE
CONV    0
        DAC     N       /SAVE ACC
        LAC     (-20    /SET COUNTER
        DAC     CNT
        DZM     A
        LAC     N       /RESTORE ACC
        RTL
        RAL
ROTA    RAL             /ROTATE BITS LEFT INTO POSITION
        DAC     N       /SAVE ACC
        AND     (1
        XOR     A
        DAC     A
        LAC     N       /RESTORE ACC
        AND     (777776 /CLEAR LSB
        XOR     A
        ISZ     CNT
        JMP     ROTA
        CLL
```

```
          AND       (177777
          JMP*      CONV
N         0
CNT       0
A         0
          .END



C SGA2 V2
          SUBROUTINE SGA2(NSEG,S,NPAR,X)
          INTEGER S(256,2,3),X(256)
          DO 10 L=1,NPAR
          CALL PGA2(S(L,1,3),S(L,2,3),M)
10        X(L)=M
          RETURN
          END



/PGA2 V2
/SUBROUTINE PGA2(S1,S2,M)
          .GLOBL    .DA,PGA2
PGA2      0
          JMS*      .DA
          JMP       .+4
S1        .DSA      0
S2        .DSA      0
M         .DSA      0
          LAC*      S1
          AND       (177777
          DAC       A
          AND       (100000
          SNA
          JMP       .+5
          LAC       A
          CMA
          AND       (177777
          DAC       A
          LAC*      S2
          AND       (177777
          DAC       B
          AND       (100000
          SNA
          JMP       .+5
          LAC       B
          CMA
          AND       (177777
          DAC       B
          LAC       A
          TAD       B
```

```
          DAC*     M
          JMP*     PGA2
A         0
B         0
          .END



C SGA5 V2
          SUBROUTINE SGA5(NSEG,S,NPAR,X)
          INTEGER S(256,2,3),X(256)
          DO 10 L=1,NPAR
          CALL PGA5(S(L,1,3),S(L,2,3),M)
          M=M+M
          IF(M.GE.65536)M=M-65536
10        X(L)=M
          RETURN
          END



/PGA5 V2
/SUBROUTINE PGA5(S1,S2,M)
          .GLOBL   .DA,PGA5
PGA5      0
          JMS*     .DA
          JMP      .+4
S1        .DSA     0
S2        .DSA     0
M         .DSA     0
          LAC*     S1
          AND      (177777
          DAC      A
          AND      (100000
          SNA
          JMP      .+5
          LAC      A
          CMA
          AND      (177777
          DAC      A
          LAC*     S2
          AND      (177777
          DAC      B
          AND      (100000
          SNA
          JMP      .+5
          LAC      B
          CMA
          AND      (177777
          DAC      B
```

```
          LAC       A
          TAD       B
          DAC*      M
          JMP*      PGA5
A         0
B         0
          .END



C SGA8 V2
          SUBROUTINE SGA8(NSEG,S,NPAR,X)
          INTEGER S(256,2,3),X(256)
          DATA IX/1/
          L=-1
          DO 10 I=1,NPAR
          L=L+2
          LD=L+1
          CALL URN(IX,U)
          CALL PGA8(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
10        X(I)=M
          RETURN
          END



/PGA8 V2
/SUBROUTINE PGA8(S1,S2,S1D,S2D,IX,M)
          .GLOBL    .DA,PGA8
PGA8      0
          JMS*      .DA
          JMP       .+7
S1        .DSA      0
S2        .DSA      0
S1D       .DSA      0
S2D       .DSA      0
IX        .DSA      0
M         .DSA      0
          LAC*      S1
          AND*      S2
          DAC       A
          LAC*      S1
          XOR*      S2
          DAC       B
          LAC*      S1D
          AND*      S2D
          DAC       C
          LAC*      S1D
          XOR*      S2D
          AND*      IX
```

```
        XOR     C
        AND     B
        XOR     A
        AND     (177777
        DAC     A
        AND     (100000
        SNA
        JMP     .+5
        LAC     A
        CMA
        AND     (177777
        DAC     A
        LAC     A
        CLL
        RAL
        AND     (177777
        DAC*    M
        JMP*    PGA8
A       0
B       0
C       0
        .END
```

```
C SGA11 V2
        SUBROUTINE SGA11(NSEG,S,NPAR,X)
        INTEGER S(256,2,3),X(256)
        DATA IX/1/
        L=-1
        DO 10 I=1,NPAR
        L=L+2
        LD=L+1
        CALL URN(IX,U)
        CALL PGA11(S(L,1,3),S(L,2,3),S(LD,1,3),S(LD,2,3),IX,M)
        M=M+M
        IF(M.GE.65536)M=M-65536
10      X(I)=M
        RETURN
        END
```

```
/PGA11 V2
/SUBROUTINE PGA11(S1,S2,S1D,S2D,IX,M)
        .GLOBL  .DA,PGA11
PGA11   0
        JMS*    .DA
        JMP     .+7
S1      .DSA    0
```

```
S2      .DSA    0
S1D     .DSA    0
S2D     .DSA    0
IX      .DSA    0
M       .DSA    0
        LAC*    S1
        AND*    S2
        DAC     A
        LAC*    S1
        XOR*    S2
        DAC     B
        LAC*    S1D
        AND*    S2D
        DAC     C
        LAC*    S1D
        XOR*    S2D
        AND*    IX
        XOR     C
        AND     B
        XOR     A
        AND     (177777
        DAC     A
        AND     (100000
        SNA
        JMP     .+5
        LAC     A
        CMA
        AND     (177777
        DAC     A
        LAC     A
        CLL
        RAL
        AND     (177777
        DAC*    M
        JMP*    PGA11
A       0
B       0
C       0
        .END
```

```
C MERR V1
        SUBROUTINE MERR(LGEN,NREP)
        DIMENSION A(7),AMAX(7),AMIN(7),R(7),IR(2)
        DO 60 J=1,LGEN
        DO 10 I=1,7
        A(I)=0.
        AMAX(I)=-1000.
10      AMIN(I)=1000.
        DO 30 I=1,NREP
        K=(I-1)*LGEN+J
        READ(2'K,20)IGEN,(R(L),L=1,5),IR(1),IR(2)
```

```
20      FORMAT(I3,5F10.3,2I10)
        R(6)=FLOAT(IR(1))
        R(7)=FLOAT(IR(2))
        DO 30 K=1,7
        A(K)=A(K)+R(K)
        IF(R(K).GT.AMAX(K))AMAX(K)=R(K)
        IF(R(K).LT.AMIN(K))AMIN(K)=R(K)
30      CONTINUE
        B=FLOAT(NREP)
        DO 40 I=1,7
40      A(I)=A(I)/B
        K=NREP*LGEN+J
        WRITE(2'K,50)J,A
50      FORMAT(1X,I3,7F10.3)
        K=K+LGEN
        WRITE(2'K,50)J,AMAX
        K=K+LGEN
60      WRITE(2'K,50)J,AMIN
        WRITE(7,70)
70      FORMAT(/1X,'AVERAGE VALUES'
        1/1X,'GEN',7X,'EFF',7X,'AVG',7X,'STD',6X,'AVGS',6X,
        1'STDS',7X,'NIZ',7X,'NTR')
        DO 90 J=1,LGEN
        K=NREP*LGEN+J
        READ(2'K,80)IGEN,R
80      FORMAT(I3,7F10.3)
90      WRITE(7,50)IGEN,R
        IF(NREP.EQ.1)RETURN
        WRITE(7,100)
100     FORMAT(/1X,'MAXIMUM VALUES'
        1/1X,'GEN',7X,'EFF',7X,'AVG',7X,'STD',6X,'AVGS',6X,
        1'STDS',7X,'NIZ',7X,'NTR')
        DO 110 J=1,LGEN
        K=(NREP+1)*LGEN+J
        READ(2'K,80)IGEN,R
        IR(1)=IFIX(R(6))
        IR(2)=IFIX(R(7))
110     WRITE(7,120)IGEN,(R(K),K=1,5),IR(1),IR(2)
120     FORMAT(1X,I3,5F10.3,2I10)
        WRITE(7,130)
130     FORMAT(/1X,'MINIMUM VALUES'
        1/1X,'GEN',7X,'EFF',7X,'AVG',7X,'STD',6X,'AVGS',6X,
        1'STDS',7X,'NIZ',7X,'NTR')
        DO 140 J=1,LGEN
        K=(NREP+2)*LGEN+J
        READ(2'K,80)IGEN,R
        IR(1)=IFIX(R(6))
        IR(2)=IFIX(R(7))
140     WRITE(7,120)IGEN,(R(K),K=1,5),IR(1),IR(2)
        RETURN
        END
```

```
001       C PDFSV V1
002                 SUBROUTINE PDFSV(LGEN,NVAR)
003                 DIMENSION A(7),R(7),IR(2)
004                 DO 40 I=1,NVAR
005                 WRITE(7,10)I
006       10        FORMAT(1X'VARIETY',I3/1X'GEN'7X'EFF'7X'AVG'7X'STD
007                 1X'AVGS'6X'STDS'7X'NIZ'7X'NTR')
008                 DO 40 J=1,LGEN
009                 K=(I-1)*LGEN+J
010                 READ(2'K,20)IGEN,(R(L),L=1,5),IR(1),IR(2)
011       20        FORMAT(I3,5F10.3,2I10)
012                 WRITE(7,30)IGEN,(R(L),L=1,5),IR(1),IR(2)
013       30        FORMAT(1X,I3,5F10.3,2I10)
014       40        CONTINUE
015                 RETURN
016                 END
```

```
C V1 V2
          SUBROUTINE V1(N,X,V)
          INTEGER X(256)
          V=0.
          DO 20 I=2,N,2
          X1=FLOAT(X(I-1))/65535.
          X2=FLOAT(X(I))/65535.
20        V=V+50.*((1.-X1)+X2)
          V=V/FLOAT(N/2)
          RETURN
          END
```

```
C V2 V1
          SUBROUTINE V2(N,X,V)
          INTEGER X(256)
          V=0.
          DO 20 I=2,N,2
          X1=FLOAT(X(I-1))/65535.
          X2=FLOAT(X(I))/65535.
          V=V+100.-100.*ABS(X2-X1**2)
          1-35.2*SQRT((1.-X1)**2+(1.-X2)**2)
20        CONTINUE
          V=V/FLOAT(N/2)
          RETURN
          END
```

```
C V3 V1
      SUBROUTINE V3(N,X,V)
      REAL M1,M2
      INTEGER X(256)
      G(P1,P2,M1,M2,S1,S2,RHO)=EXP(-(S2**2*(P1-M1)**2-2.*
     1S1*S2*RHO*(P1-M1)*(P2-M2)+
     1S1**2*(P2-M2)**2)/(2.*S1**2*S2**2*(1.-RHO**2)))
      V=0.
      DO 20 I=2,N,2
      X1=FLOAT(X(I-1))/655.35
      X2=FLOAT(X(I))/655.35
      V=V+60.*G(X1,X2,0.,50.,10.,10.,.0)
     1+100.*G(X1,X2,75.,75.,10.,10.,.95)
     1+40.*G(X1,X2,40.,10.,10.,10.,.0)
20    CONTINUE
      V=V/FLOAT(N/2)
      RETURN
      END

C V4 V1
      SUBROUTINE V4(N,X,V)
      REAL M1,M2
      INTEGER X(256)
      G(P1,P2,M1,M2,S1,S2,RHO)=EXP(-(S2**2*(P1-M1)**2-2.*
     1S1*S2*RHO*(P1-M1)*(P2-M2)+
     1S1**2*(P2-M2)**2)/(2.*S1**2*S2**2*(1.-RHO**2)))
      V=0.
      DO 20 I=2,N,2
      X1=FLOAT(X(I-1))/655.35
      X2=FLOAT(X(I))/655.35
      V=V+100.*G(X1,X2,0.,50.,10.,10.,.0)
     1+60.*G(X1,X2,75.,75.,10.,10.,.95)
     1+40.*G(X1,X2,40.,10.,10.,10.,.0)
20    CONTINUE
      V=V/FLOAT(N/2)
      RETURN
      END

C V5 V1
      SUBROUTINE V5(N,X,V)
      REAL M1,M2
      INTEGER X(256)
      G(P1,P2,M1,M2,S1,S2,RHO)=EXP(-(S2**2*(P1-M1)**2-2.*
     1S1*S2*RHO*(P1-M1)*(P2-M2)+
     1S1**2*(P2-M2)**2)/(2.*S1**2*S2**2*(1.-RHO**2)))
      V=0.
      DO 20 I=2,N,2
```

```
      X1=FLOAT(X(I-1))/655.35
      X2=FLOAT(X(I))/655.35
      V=V+60.*G(X1,X2,0.,50.,10.,10.,.0)
     1+40.*G(X1,X2,75.,75.,10.,10.,.95)
     1+100.*G(X1,X2,40.,10.,10.,10.,.0)
20    CONTINUE
      V=V/FLOAT(N/2)
      RETURN
      END



C V6 V2
      SUBROUTINE V6(N,X,V)
      INTEGER X(256)
      V=0.
      DO 20 I=1,N
      S=FLOAT(X(I)-32767)/32767.
20    V=V+S*S
      V=100.-100.*V/FLOAT(N)
      RETURN
      END
```