NUMERICAL TESTING OF EVOLUTION THEORIES

PART I

THEORETICAL INTRODUCTION AND BASIC TESTS [1]

by

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NOTE BY THE AUTHOR

A few introductory remarks may be helpful to avoid possible misinterpretations when a relatively new subject is presented.

It is not the intention of the author to face the reader with a new type of life or new living forms. The numerical symbioorganisms presented in this paper are not living, not in the sense commonly attributed to this term. It is, however, the purpose of this paper to present a part of the rapidly growing evidence to the effect that, what we are used to consider living beings (terrestrial life forms) are a particular type of symbioorganisms and are subject to the same evolutionary improvements and to many other "biophenomena" which are common to a large class of symbioorganisms.

There is nothing more peculiar about this statement, except for its more recent discovery, than about statements like the following:

1) living organisms are physical bodies and are subject to the same mechanical and physical laws followed by all physical bodies.

2) living organisms are formed by chemical compounds and are subject to the same kind of chemical reactions, which are the object of biochemistry.

The investigation of physical, chemical and symbiogenetical phenomena are all important for the understanding of different aspects of the process which is designated by the common term "LIFE".

If the reader at any stage should fall for the temptation to attribute to the numerical symbioorganisms a little too many of the properties of living beings, please do not make the mistake of believing that this was the intention of the author. The properties of symbioorganisms are clearly and specifically described and they should be understood s t a t e m e n t b y s t a t e m e n t the way they are presented.

As to the terminology used the following principles have been followed: concepts presenting some form of similarity or analogy with a biological concept have been designated by the same or a similar term. For example: "symbioorganism" corresponding to the biologic term "organism"; or "symbiosis" (also termed "utility association") corresponding to the biologic term "symbiosis"; and "mutation" to disignate hereditary

1) The investigation presented in this paper was supported in part by research grants RG-6980 and C-2306 from the National Institutes of Health, United States Public Health Service. The first part of the investigation was performed while the author was a temporary member of the Institute for Advanced Study in Princeton, New Jersey, and the evolution experiments and competition tests were performed by the electronic computer of the Institute.

changes which are not normal crossing results, the same term used for such hereditary changes in biology. This terminology has the advantage of being easy to remember and of making the analogies with biological concepts immediately clear to the reader without requiring tedious explanations. However, the reader should be careful not to confuse a term used in connection with symbioorganisms with the same, or a similar term used in biology. The reader who is aware of this will have no difficulty in keeping the record straight. The terms and concepts used in connection with symbioorganisms are in no case identical to biological concepts; they are mathematical concepts (see appendix) usually applicable to a large variety of symbioorganisms. The biological terms are often selected by the common use of the language and they usually refer to empirical objects and observed biologic phenomena.

Empirical models of symbioorganisms, such as the numerical symbioorganisms developed in a particular experiment are to be considered as empirical representations of a mathematical entity in the same sense as a circular object can be used to represent a circle as a mean of investigation or description. The same terminology used in the mathematical entity investigated will of course also be used in its empirical models.

1. INTRODUCTION

This is the first of two papers the purpose of which is to give an orientation on the present stage and recent developments in the investigation of numeric evolution phenomena. The second paper (BARRICELLI, 1962) will appear in this journal later.

The Darwinian idea that evolution takes place by random hereditary changes and selection has from the beginning been handicapped by the fact that no proper test had been found to decide whether such evolution was possible and how it would develop under controlled conditions. A test using living organisms in rapid evolution (viruses or bacteria) would have the serious drawback that the causes of adaptation or evolution would be difficult to state unequivocally, and Lamarckian or other kinds of interpretation would be difficult to exclude. However if, instead of using living organisms, one could experiment with entities which, without any doubt could evolve exclusively by "mutations" and selection, then and only then would a successful evolution experiment give conclusive evidence; the better if the environmental factors also are under control as for example if they are limited to some sort of competition between the entities used.

The author has shown in several publications (BARRICELLI, 1954 and 1957) that evolution processes in many respects similar to biological evolution can now be obtained using self-reproducing entities of numerical nature whose properties are completely under control. Mutation and selection alone, however, proved insufficient to explain evolutionary phenomena. Another fundamental idea (to be explained in sections 2 and 3) had to be added to the theory before it was possible to obtain evolutionary processes and other phenomena characteristic of living organisms, which are listed in section 6.

It may appear that the properties one would have to assign to a population

of self-reproducing elements in order to obtain Darwinian evolution are of a spectacular simplicity. The elements would only have to:

1. Be selfreproducing and
2. Undergo hereditary changes (mutations) in order to permit evolution by a process based on the survival of the fittest.

Such evolution would actually have the characteristics of a purely statistical phenomenon which may well occur in other than biological contexts.

In fact, examples of self-reproducing entities are well known and it is no problem to define and construct more such entities artificially. It is for instance well known that some chemical compounds, called "autocatalysts," have the ability to catalyze a chemical reaction between other compounds, a reaction whose result is, among other things, an increase of the catalyst itself. Such an autocatalyst will therefore become more and more abundant as the reaction proceeds, or in other words, it reproduces itself. At the same time, some compounds (called substrates) originally present will be consumed, while other compounds (called by-products) may, by the same reaction, be produced together with the autocatalyst.

Also in atomic physics, autocatalytic phenomena similar to the one above described are well known. For instance a neutron may start a chain reaction by hitting a uranium U_{235} atom producing among other things two or more neutrons, and thus reproduces itself by a process having the characteristics of what may be considered atomic autocatalysis. The Uranium U_{235} atoms act as the substrate of the nuclear reaction, which, in addition to neutrons also produces some by-products (some elements of atomic weight roughly half the weight of Uranium).

It is easy to construct artificial objects or define entities, for instance of arithmetic nature, which are able to reproduce themselves. In this case one may also choose the definition in such a way that the factors which are not indispensable, conceptually, such as substrates and by-products, will not be included among the elements to be operated upon. For instance, one may use as self-reproducing entities a group of numbers written in the first line of a crossection paper — see fig. 1, where negative numbers are underlined — and one may choose arbitrarily a reproduction rule for these numbers. The reproduction rule used in fig. 1 is the following: in one time unit (generation) a positive number m is reproduced m squares to the right and a negative number n is reproduced $-n$ squares to the left. The result obtained from the first line by following this reproduction rule is recorded in the second line. Applying the same reproduction rule to the second line, one obtains the third line, *etc.* Of course, in order to prosecute the operation, one would have

to state some rule to decide what to do in the cases in which two different numbers happen to fall (collide) in the same square. This will be done below.

The other property essential for Darwinian evolution, *viz.*, undergoing hereditary changes, is probably not as common outside the living organisms as is the faculty to reproduce. There is little point in trying to enumerate phenomena which might be interpreted as examples of hereditary change. For the purposes of this paper, it is sufficient to recall that the genes of a cell and the viruses are examples of self-reproducing elements with the ability to undergo hereditary changes. In both cases the ability to reproduce and to undergo hereditary changes seems to be a property of the nucleic acid which is an important constituent of these structures.

There is no difficulty in defining mathematical entities which besides the faculty to reproduce have the property of undergoing hereditary changes. In the numerical entities defined above, one may for instance choose some mutation rules to apply when two numbers collide in the same square. The number to be put in the collision square may be different from the two colliding numbers and may therefore represent a mutation.

The following mutation rule has been applied in fig. 1 : two numbers which

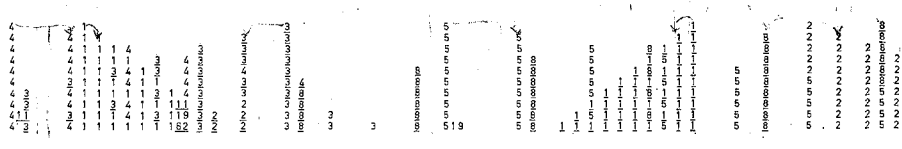

Fig. 1. Selfreproducing numbers (see text). Adaptive selection but no extensive evolution phenomena are possible.

collide in a square are added together, and from the result one subtracts the content of the square above the collision square (except when the square above the collision square is empty, in which case nothing will be subtracted). If three numbers collide in the same square, they are added together, and from the result one subtracts twice the content of the square above the collision place, and so on.

In this manner we have created a class of numbers which are able to reproduce and to undergo hereditary changes. The conditions for an evolution process according to the principle of Darwin's theory would appear to be present. The numbers which have the greatest survival in the environment created in fig. 1 by the rules stated above, will survive. The other numbers will be eliminated little by little. A process of adaptation to the environmental conditions, that is, a process of Darwinian evolution, will take place.

2. CRITICISM OF THE DARWINIAN EVOLUTION PRINCIPLE

The last example of Darwinian evolution clearly shows that something more is needed to understand the formation of organs and properties with a complexity comparable to those of living organisms. No matter how many mutations occur, the numbers of fig. 1 will never become anything more complex than plain numbers.

One may object that the situation is different for genes and viruses because of the greater complexity of the nucleic acid molecules which might be expected to present far greater evolutionary possibilities.

If the situation is different for the simplest self-reproducing elements of hereditary material, that must be for some other reason, but certainly not for the evolutionary possibilities of each individual element. If one considers the recombinational genes — which are the smallest fragments of hereditary material which can be separated from adjacent hereditary material by crossing over — as the self-reproducing elements from which the hereditary material is formed, one finds the following situation. In most recombinational genes only two allelic states are found; more rarely one finds 3 or more allelic states. A recombinational gene with n allelic states is a gene which can exist only in n different varities which can be reached by one or several consecutive mutations. The evolutionary possibilities of such a recombinational gene are therefore very limited. Evolution can do nothing better than select the fittest of the n possible states. It is hard to visualize how such a selfreproducing element could, simply by mutations and selection, develop into a "homo sapiens" or anything able to construct a homo sapiens even if allowance is made for the fact that the number of allelic states may be generally or very often underestimated.

As far as evolutionary possibilities are concerned, the situation does not seem to be any better for the recombinational genes, in spite of their apparent complexity, than it is for the numbers recorded in fig. 1.

If the Darwinian evolutionary principle is to explain the complexity and efficiency reached by living organisms, it must be applicable to the simplest elements which are able to reproduce and mutate. One cannot start with entities of considerable complexity and efficiency, as for example cells, even if relatively simple unicellular organisms, such as amoebae, are chosen. It is obvious that amoebae have a complexity, efficiency and evolutionary possibility far greater than the numbers in fig. 1. But these faculties of the amoeba are part of the properties which evolution theory is supposed to explain rather than to postulate as a prerequisite for evolution.

In conclusion, the selection principle of Darwin's theory is not sufficient to explain the evolution of living organisms if one starts with entities having

only the property to reproduce and mutate. At least one more theoretical principle is needed, a principle which would explain how self-reproducting entities could give rise to organisms with the variability and evolutionary possibilities which characterize living organisms.

3. THE SYMBIOGENESIS THEORY

A solution of this difficulty is provided by a theory which can be introduced as a possible interpretation of the startling analogies existing between intracellular viruses and genes. Intracellular viruses and genes are probably both segments of nucleic acid with autocatalytic properties and with the ability to acquire hereditary changes. Examples of intermediate stages between viruses and genes have been found (*cf.* plasmagenes in *Paramecium,* SONNEBORN, 1949). Often the only way to distinguish a symbiotic virus from a gene is provided by the virus' ability to be transmitted by infection, because both are inherited in a similar way (*cf.* LEDERBERG & LEDERBERG, 1952). In recent years the study of bacterial genetics and the relation between bacteria and temperate phages has shown that an appreciable section of genetic material of the *E. Coli* bacterium K_{12} consists of symbiotic viruses. An interesting theory, "the symbiogenesis theory," provides a possible interpretation of the mentioned analogies between viruses and genes. Originally the term "symbiogenesis" was used to qualify any theory implying that the first cell were formed by a symbiotic association of several entities (MERESCHKOWSKY, 1910). A more recent version of symbiogenesis theory, which has proved most fruitful assumes that the genes and possibly other selfreproducing entities in the cell spring from originally independent viruses or virus-like organisms which by symbiosis have been united with the rest of the cell (KOZO-POLIANSKY, 1924; BARRICELLI, 1947, 1952, 1955). According to the symbiogenesis theory the evolution process which led to the formation of the cell was initiated by a symbiotic association between several virus-like organisms. Little by little an increasing number of symbionts of the same nature may have joined the group, and the evolution process thus initiated may have led to the formation of the various organs and properties of the cell.

This theory solves the dilemma in which we were placed by pushing Darwin's evolutionary principle to its ultimate consequences. Even if every recombinational gene were assumed to have only two allelic stages, the association of n genes (or primitive viruses) would yield an organism with 2^n possible varieties. Among these many varieties natural selection undoubtedly has a good choice. If the number n of genes is in the usual range of several thousand, it may not appear so incredibly fantastic to imagine that among the

2^n possible combinations there may be some which correspond to organisms as complex as *Drosophila* or possibly as complex as Man.

In short, the situation is completely reversed, and the limited number of allelic states in each self-reproducing element does not represent an important limitation if the symbiogenesis theory is correct. [2]

Until recently the possibilities of testing the theory were very limited. With the development of bacterial and virus genetics testing possibilities previously unsuspected became available. On a theoretical basis the use of high speed computers makes it possible today to decide what an evolution process would look like when developing in accordance to the symbiogenesis theory.

4. THE SYMBIOGENETIC INTERPRETATION OF CROSSING

An important success of the symbiogenesis theory is that it can explain in a simple way how sexual reproduction originated, a phenomenon whose interpretation was a complete mystery before this theory appeared. In fact, if the genes associated into larger organisms by symbiotic phenomena, they had from the beginning the capacity to change hosts and associate with new organisms as parasites and symbionts usually do. This capacity, already at the outset, conferred to the gene-association the adaptivity of organisms with sexual reproduction which is based on the fact that a large number of useful mutations — one in each gene — can expand in the population contempora-

2) This fact remains a fundamental difficulty in all non symbiogenetic attempts to explain the origin of life; namely, the enormous variability, and consequently, the enormous complexity of the first selfreproducing entity required by such explanations. This difficulty is partly recognized by the authors of non symbiogenetic explanations, since they all imply that life on this planet may have arisen only once in a period of several billion years. The possibility that life in a primitive form (microorganisms) might have been transmitted from other planets, by different types of space diffusion phenomena, has also been considered.

When the variability of the selfreproducing entities is limited to very few allelic states, the origin of such entities is no longer a problem. As a matter of fact, no variability is strictly required in each individual self-reproducing entity. The presence or the absence of a self-reproducing entity with the respective phenotypic effects these two alternatives may have on the organism, are in themselves two allelic hereditary characters.

Nobody knows at what rate new autocatalysts are being created by chance on this planet. But, to put it mildly, every chemist would probably suggest that the rate per second, or even better per microsecond, should be used as a unit rather than the rate per billion years.

The origin of the selfreproducing entities is, therefore, no problem. The problems are: (1) Whether a symbiotic association of a large group of autocatalysts is likely to be formed. (2) Whether the symbiotic association of a large group of selfreproducing entities is possible on statistical and mathematical grounds.

The second question is the one which is being directly answered in this paper. However, the nature of the answer and the results which will be presented are strongly suggestive that also the answer to the first question would be affirmative, and that terestrinal life is one result of such symbiotic associations.

neously. This will sooner or later provide for the necessary reassociation of all the positively selected genes into the final organism. A great number of phenotypic problems can in this way be solved contemporaneously without delaying one another, a fact which permits an increase in the rate of evolutionary adaptation by a factor of several thousand (R. A. Fisher, p. 122-123, 1930).

According to the symbiogenesis theory sexual reproduction is the result of an adaptive improvement of the original ability of the genes to change host organisms and recombine. Examples will be shown in this paper of crossing mechanisms and crossing phenomena observed during a series of artificial evolution phenomena developed as a test of the symbiogenesis theory (see also BARRICELLI, 1957). On this theory crossing mechanisms can be expected to exist in all organisms, even the most primitive ones.

Among the experimental facts in support of this interpretation of the origin of crossing and sexual reproduction one may cite:

1. Crossing in viruses. Crossing mechanisms are found in many viruses, particularly in bacterial viruses (phages). ADAMS, 1959, page 377).
2. Composite viruses. Examples are known of a virus which can carry the genetic material of one or even two different viruses in the same protein coat (JACOB, 1955; ADAMS, 1959). This is a startling example of symbiosis which might easily lead to the formation of a single virus with the genetic material of two or several different viruses.
3. Transduction in the *E. Coli* bacterium K_{12}. This form of transduction is due to the fact that a genetic segment containing several hereditary characters of the bacterium is still able, under certain conditions, to act as a virulent phage (parasite). Under other conditions it will act as a symbiont which is able to change the host organism and bring with it the hereditary characters which are localized in the genetic segment it represents. (ADAMS, 1959; BARRICELLI, 1956; various papers relevant to this point by LEDERBERG, JACOB, CAMPBELL, FUERST and others, are quoted by ADAMS, 1959).
4. Provirus region in K_{12}. An appreciable segment of genetic material in K_{12} bacteria, the provirus region, is formed by symbiotic viruses of the kind just described.
5. Defective phages. By mutation a virus may become unable to act as a parasite and hence in order to be transmitted to another host organism it may often be dependent on some mechanism different from the kind of transduction described above. Two such mechanisms (*Sal-*

monella transduction and regular cross) are described below. Usually a phage-genetic segment adapted to perform a function in the bacterium is no longer apt to perform its original function in the phage (too many mutations and substitutions). Transducing phages are therefore defective.

6. Transduction in *Salmonella*. Instead of carrying another virus or several other viruses in its protein coat, a phage may carry bacterial genes or genetic segments which no longer are able to act as parasites or individual organisms. This crossing mechanism is very common in the genus *Salmonella*.
7. Regular cross in K_{12}. In some cases two bacteria may attach together in order to permit the transmission of a genetic segment which would be unable to perform the operation without such assistance from the bacterial hosts. The genetic segment is transmitted from a "donor" (male) to a "recipient" (female) bacterium. In K_{12} the transmitted segment is usually different for different strains of donor bacteria used. The transmitted segment will, moreover, be shorter if the mating is interrupted. By interrupting the mating it is therefore possible to find out which part of the genetic segment is transmitted first and may be considered as the beginning or "origin" of the segment and which part represents the end of the segment. In all donor strains studied so far, the origin was represented by genetic material which at present is unable to act as a parasite and according to present knowledge has no autonomous means of transmitting itself to other bacteria. The ends of the transmitted segments, on the contrary, are all in or at the edge of the provirus region. This region consists of genetic segments which have their own mechanisms by which they may be transmitted to other bacteria (by the transduction mechanism of K_{12} bacteria). Therefore, they do not need the assistance of the bacterium in order to perform this operation.

   The function of regular crossing in K_{12} is apparently to assist in the transmission of a genetic segment (probably a conglomerate of many defective viruses) which no longer has its own mechanism of transmission to other bacteria.

Several of the phenomena described above were predicted (BARRICELLI, 1947, 1952, 1955) by the symbiogenesis theory. The same phenomena give a fairly good picture of the way in which the relation between symbiotic viruses and cells may have developed from infection to a crossing mechanism. From regular crossing in K_{12}, with large genetic segments exchanged between copulating cells, a small step farther would apparently lead to a crossing mechanism like that of *Paramecium* with exchange of whole gametic nuclei between the copulating cells.

This is the symbiogenetic interpretation of the origin of sexual reproduction.

One may now ask: What about the origin of biologic evolution? Can the symbiogenesis theory explain a phenomenon like this?

5. THE FORMATION OF SYMBIOORGANISMS BY NUMERICAL ELEMENTS [3]

To test the symbiogenesis theory and find out whether it can explain how an evolution process like the biological one may arise, one may once again make use of numerical entities. All one has to do it to modify the reproduction rules used in fig. 1 in such a way that some kind of cooperation or "symbiosis" between different numerical entities will be promoted. This way one will find out whether it is true that by putting together elements with the fundamental properties of self-reproduction, mutability, and reciprocal (symbiotic) interdependency one can initiate an evolutionary process similar to biological evolution.

In order to promote symbiosis one may change in the following way the reproduction rules of fig. 1:

a) A number n will not be repeated in the square below it, as in fig. 1, but only n squares to the right (if positive) or $-n$ squares to the left (if negative) in the next row (see fig. 2 and 3). This operation will be called "translation to square (n) of next row without reproduction."

b) If the new position (n) happens to be below a square occupied by a different number m then a second n will be placed in position (m), which means m squares to the right (if m is positive) or $-m$ squares to the left (if m is negative) of the original n, but in the next row. This way a number n can reproduce if another number m different from n is present (see fig. 4).

If in this process the number n happens to come several times below different numbers it may reproduce several times (see fig. 5, where the number 4 from the second row appears 3 times in the third row).

The above reproduction rules are made with the purpose of permitting reproduction only when a numerical entity is together with other entities different from itself. A symbiotic cooperation between different numerical entities is thereby rendered necessary for reproduction.

3) All terms borrowed from biology when used in connection with symbiogenetic phenomena represent mathematical, not biological concepts (see appendix and note by the author at the beginning of this paper). They are in no case identical to the biologic concepts designated by the same or a similar term.

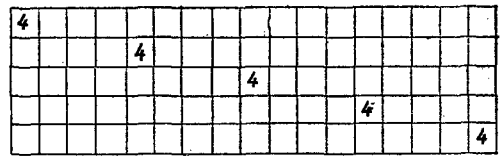

Fig. 2.

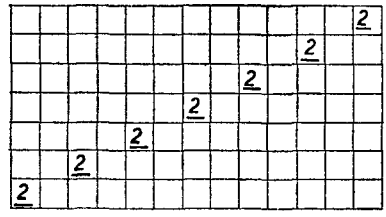

Fig. 3.

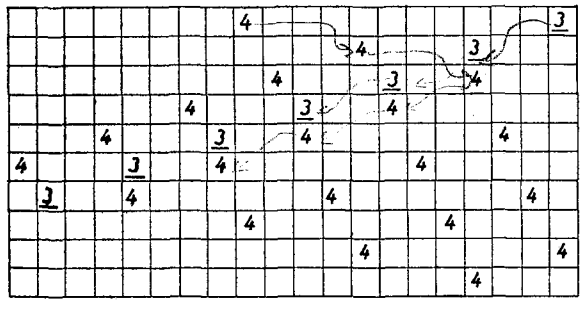

Fig. 4.

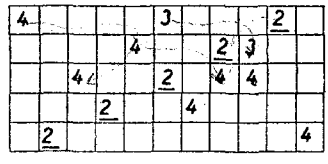

Fig. 5.

Fig. 2, 3, 4, 5. Reproduction rules requiring symbiosis (see text).

To the above reproduction rules one may add arbitrary mutation rules, for instance by taking advantage of the cases in which two different numbers collide in the same square. To begin with, a rule will be used in which no mutation can occur. The square in which two different numbers collide will be left empty, only marked by a cross (X) or "collision sign." If two identical numbers collide, one of them remains in the collision square.

In fig. 6 the absence of mutations is clearly manifested by the fact that the original numbers 5, 1 and -3 are present everywhere and no new number appears. However, in a few generations the numbers organize themselves into a stable configuration (5, -3, 1, -3, 0, -3, 1, 0 where an 0 marks an empty square) which is present everywhere in the figure. This kind of stable configurations will be called "numerical symbioorganisms." In the rest of this paper it will be shown that symbioorganisms have many properties similar to those observed in living structures. Some of the life-like properties of symbioorganisms which will be presented below are termed:

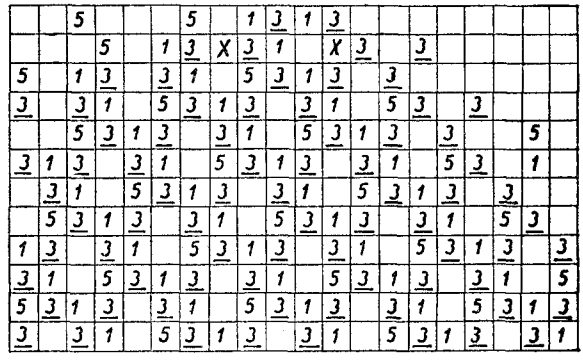

Fig. 6.

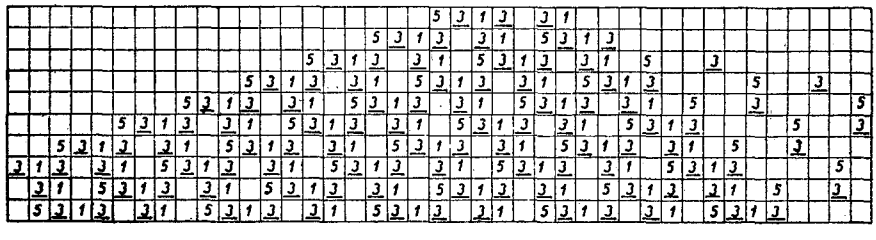

Fig. 7.

Fig. 6 and 7. Formation of a symbioorganism (6) and its reproduction characteristics (7).

(A) Selfreproduction; (B) Crossing; (C) Great variability; (D) Mutation (if the rules stated above are changed in order to permit mutation); (E) Spontaneous formation; (F) Parasitism; (G) Repairing mechanisms; (H) Evolution.

6. GENERAL PROPERTIES OF SYMBIOORGANISMS

Symbioorganisms do not have to be of numerical nature. Any elements with the property of self-reproduction and symbiotic cooperation may associate into symbioorganisms of some sort, no matter wheter they are of

numerical, chemical, or any other nature. According to the symbiogenesis theory, living organisms are the particular kind of symbioorganisms which arise when organic molecules are used as self-reproducing elements.

Some general properties which one may expect to find very often in symbioorganisms and all of which are to be found in numerical symbioorganisms are the following:

A) Selfreproduction. In fig. 7 it is shown that the symbioorganism (5, -3, 1, -3, 0, -3, 1, 0) — which arose in fig. 6 — is able to reproduce itself.

B) Crossing. In fig. 8 and 9 the two symbioorganisms (9, -11, 1, -7) and (5, -11, 1, -3) are crossed. The second parent organism differs from the first one by two hereditay characters, 5 instead of 9 and -3 instead of -7. In fig. 8, where the first organism was placed to the left, the second to the right, the crossing product obtained was the recombinant (5, -11, 1, -7). In fig. 9 on the contrary, where the order of the two parent organisms was reversed, the complementary recombinant (9, -11, 1, -3) was obtained. If these two crossing products are crossed with one another, one can obtain again the parental structures of the previous crosses as shown in fig. 10 and 11. Not all symbioorganisms do cross as neatly as these. Often one or two of the crossing products are not competetive in the presence of the parent organisms and can simply not arise, nor could they survive if they did. Nevertheless, the very existence of so simple a solution of the crossing problem is of great theoretical significance.

C) Great variability. Each symbioorganism may consist of any number of elements (genes or numbers) and each element may have several allelic states. The number of varieties which can arise is practically unlimited. This does not mean that every symbioorganism, no matter how primitive will show a great variability. But under proper conditions many symbioorganisms will (see fig. 24, generations 600, 1000, 1200, 1300, 1400, 1500, 1600, 1700 and 1800).

D) Mutation. To obtain mutations it is sufficient to change the rules for collision of different numerical elements. The change will have to be rather gentle if one wishes to keep the properties listed above.

All mutation rules which will be used in this paper consist in replacing some of the collision signs X (marking squares in which two different numbers have collided) by a new number or mutation.

One example of such mutation rules is the following (Rule A):

1) An X (collision sign) which happens to be under an occupied square remains.

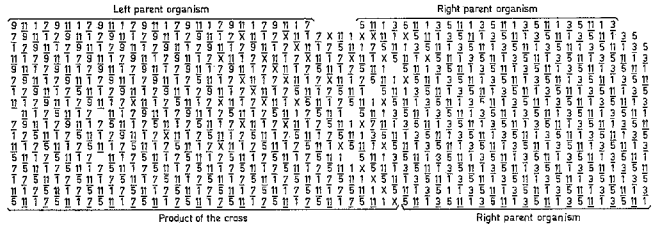

Fig. 8.

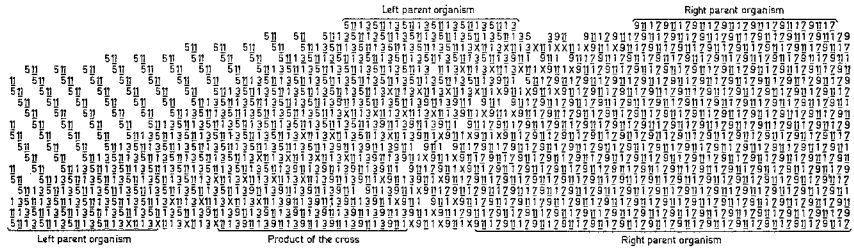

Fig. 9.

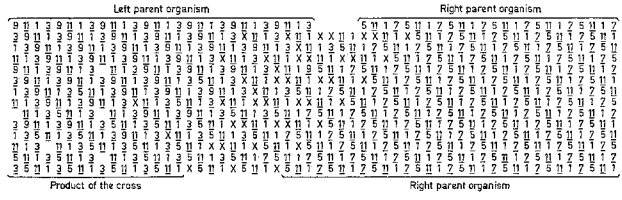

Fig. 10.

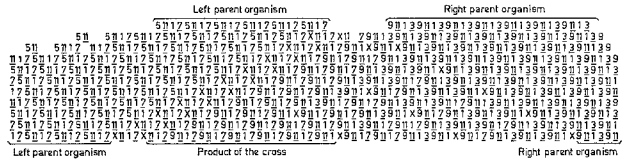

Fig. 11.

Fig. 8. 9. 10, 11. Crossbreeding in numeric symbioorganisms (see text). Crossing rules similar to those of haploid organisms.

2) An X which happens to be under an empty square or under another X is replaced by a number M (mutation) whose absolute value is equal to the distance between the closest number to the left and the closest number to the right of the empty square in question (the distance is measured in number of squares). If the two numbers have

the same sign, the mutation M will be the positive distance (sign +); if the two numbers have different signs, the mutation M will be taken equal to the negative distance (sign —).

3) If there is no number to the right or to the left of the empty square above the X (collision close to a border of figure) the X remains.

For instance, in fig. 12 at the second line where the two numbers 3 and —4 collide, one finds + 5 instead of an X because the distance between the closest number to the right and the closest number to the left in the line above is 5 squares and because they have the same sign (both are positive). On the other hand in fig. 13 the place where the

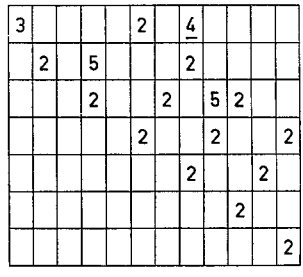

Fig. 12.

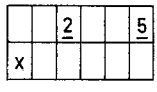

Fig. 13.

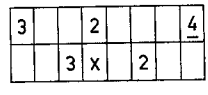

Fig. 14.

Fig. 12, 13, 14. The A-mutation rule.

two numbers —2 and —5 collide is marked with an X because there is no number to the left of X in the line above. Likewise in fig. 14 the X remains where the two numbers 3 and —4 collide since the square above the collision place is not empty.

Several other mutation rules which have been used in evolution experiments will be defined in this paper. Although the mutation rule may influence the kind of symbioorganisms which arise, the general character of the phenomena remains the same. [4]

4. In earlier experiments mutations based on random numbers have also been tried with comparable results. Some of the methods used in this paper will also yield fairly random mutations when a symbioorganism — as very often is the case — collides with invading numbers generated in an adjourned disorganized region. The frontier between two different symbioorganisms is usually disorganized.

E) Spontaneous formation. In fig. 15 the first row contains only the numbers 1, —1, or empty squares selected by a random procedure (heads and tails was played with two coins; two heads indicate 1, two tails —1, one head and one tail indicates an empty square). In the following generations other numbers than 1 and — 1 arose by mutation and various organisms recorded in the figures 16, 17, 18, 19, 20, 21, and 22 were formed.

This experiment shows that under favourable conditions symbioorganisms can be formed quite frequently and the formation of a symbioorganism is not a rare event. But of course if the environment is modified by the presence of other symbioorganisms such spontaneous formation can be prevented.

F) Parasitism. One may note that one of the symbioorganisms (1, —2, 1, 1, —2, 0) a so called tregener which arose near the upper right border of fig. 15 in the above experiment (the one which is recorded in fig. 17) does not reproduce completely. In fig. 17 the symbioorganism loses its elements one by one and at the end nothing remains. However, If the same symbioorganism is sowed together with the symbioorganism (1, —1) which acts as its host it will reproduce normally as shown in fig. 18. At the same time, the host is destroyed little by little. This relationship between two symbioorganisms is very similar to the phenomenon which in biology is called parasitism. The same terminology may be used here. The symbioorganism (1, —2, 1, 1, —2, 0) shall be called a parasite of (1, —1).

Parasitism is a very common phenomenon among symbioorganisms and it constitutes one of the major difficulties in the performance of numerical evolution experiments. Often an evolution process will end with the destruction of the species by a parasite which also will die out once the host is destroyed.

G) Repairing mechanism. Damages are usually repaired by cooperation among several neighboring symbioorganisms. The repairing process may often be partially or completely successful even if all the symbioorganisms present are damaged by removing (cancelling) some of their genes. In this case the repairing is more likely to succeed the greater the number of symbioorganisms cooperating.

This phenomenon presents a startling analogy with the repairing mechanism known in bacterial viruses as "reactivation by multiple infection with inactivated (for ex. irradiated) phages."

In all the 5 odd symbioorganisms of line 9 in fig. 23, a large fraction of the numerical elements, selected by a random procedure, are can-

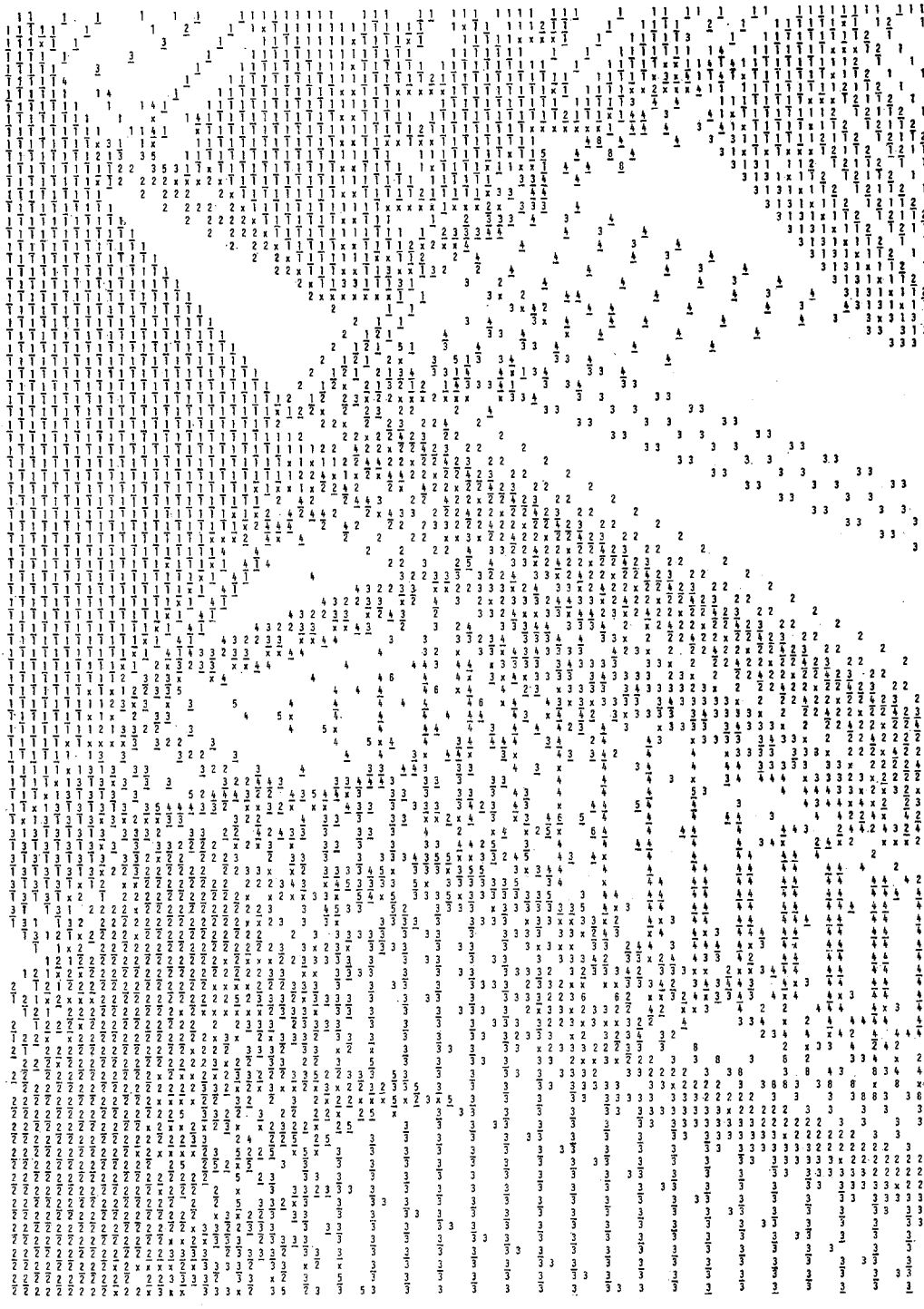

Fig. 15. Spontaneous formation of symbioorganisms in an experiment started with random numbers

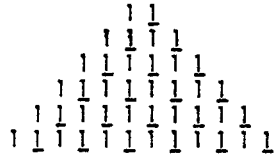

Fig. 16

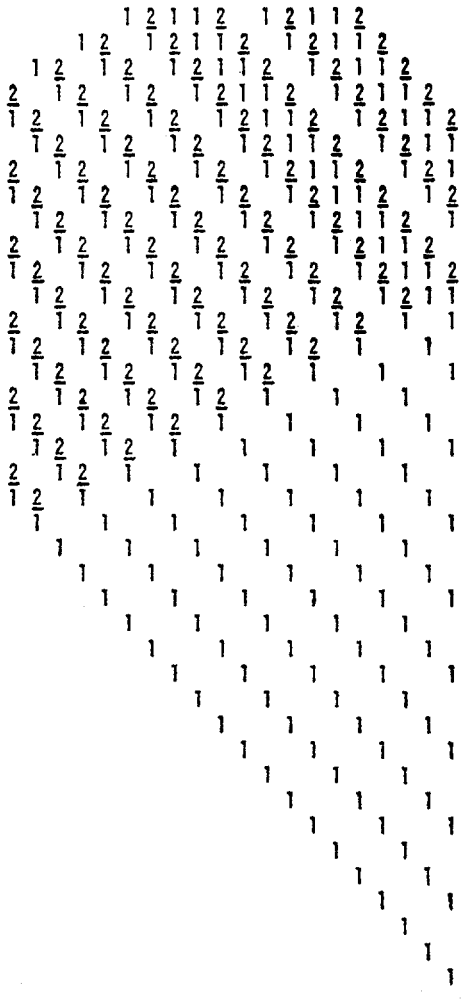

Fig. 17

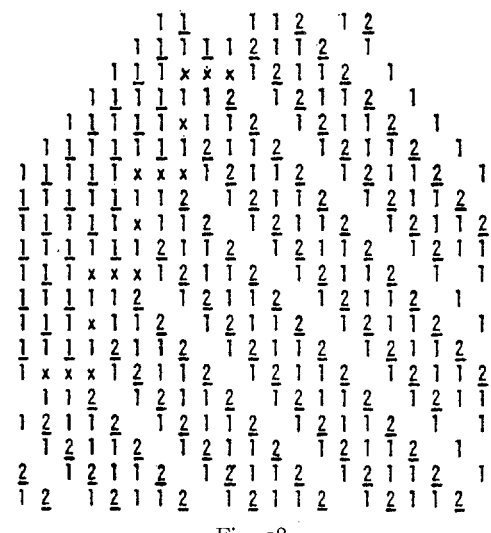

Fig. 18

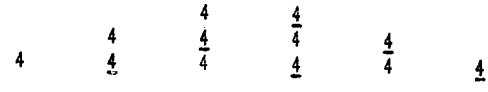

Fig. 19

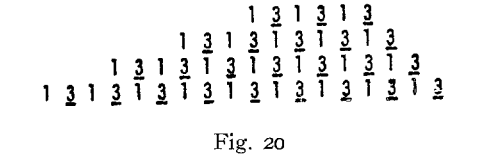

Fig. 20

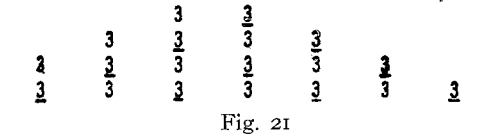

Fig. 21

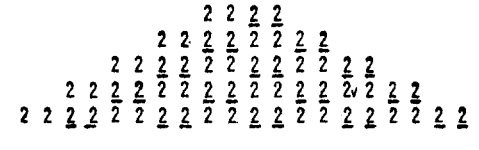

Fig. 22

Fig. 16, 17, 18, 19, 20, 21, 22. Reproduction of symbioorganisms which arose in the experiment of fig. 15. One organism (parasite Fig. 17) does not reproduce succesfully when alone. However in association with its host organism (Fig. 18) it reproduces normally.

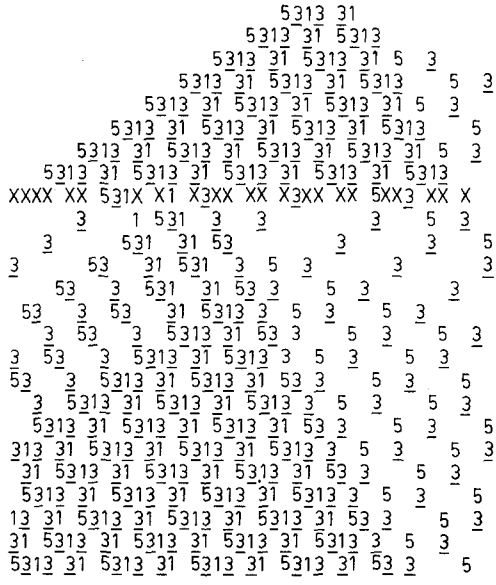

Fig. 23. Repairing mechanism by cooperation of several seriously damaged symbioorganisms. Removed numbers (damages) in the ninth line are marked by X's.

celled (replaced by an X in the fig.). The damaged symbioorganisms left reconstitute the original pattern in a few generations. None of the 5 odd damaged symbioorganisms of line 9 would in itself have been able either to reconstitute the original pattern or else to generate another pattern able to survive and reproduce.

Recovery by the above repairing mechanism is not always complete, and the reconstituted symbioorganism may often show deficiencies (missing genes). A deficiency is not always lethal, and the symbioorganism may therefore survive as a mutant.

H) Evolution. In fig. 15 the only example of hereditary change in a symbioorganism is the change which transformed (1, —1) into (1, —3) at the left side of the figure around generation 60. This change was induced by an external element (—3) entering the symbioorganism. Using high speed computers, evolution experiments have been performed which involved a large number of hereditary changes. Some of these evolution experiments will be described in this paper. The result of such experiments can be summarized as follows:

Symbioorganisms can be completely modified. Their complexity may drastically increase, and they can branch into different species which are unable to interbreed.

The evolution leads to a better adaptation to the artificial environmental conditions and a greater ability to compete with other symbioorganisms (see competition tests, Section 9).

Both mutation and crossing phenomena played a central part in evolution. To begin with, most of the crossing was performed by single elements (genes) which left one symbioorganism and entered another symbioorganism. Later the "regular" crossing mechanism described in fig. 8, 9, 10, and 11 became predominant. Such regular crossing is very similar to the crossing in haploid species of living organisms.

7. EVOLUTION EXPERIMENTS

In order to observe evolutionary phenomena, the experiment of fig. 15 would have to be repeated on a much larger scale and for a much larger number of generations. Such experiments were done in 1953, 1954, and 1956 in Princeton, New Jersey, using the electronic computer of the Institute for Advanced Study. Instead of 100 lines (generations) with 80 numbers each as in fig. 15, the Princeton experiments were continued for more than 5,000 generations using universes of 512 numbers. Moreover, the actual size of the universe was usually increased far beyond 512 numbers by running several parallel experiments with regular interchanging of several (50 to 100) consecutive numbers between two universes every 200 or every 500 generations (see BARRICELLI, 1957). A technical difficulty which showed up at once was the development of a phenomenon which will be called "homogeneity." Within a few hundred generations a single primitive variety of symbioorganism invaded the whole universe. After that stage was reached no collisions leading to new mutations occurred and no evolution was possible. The universe had reached a stage of "organized homogeneity" which would remain unchanged for any number of following generations, and the "final" symbioorganism occupying such universe would remain unchanged.

Attempts to modify the mutation rule did not remove this difficulty, but they often led to a different type of final symbioorganism better adapted to the new mutation rule. In many instances a new mutation rule would lead to a complete disorganization of the whole universe, apparently due to the death by starvation of a parasite, which in this case was the last surviving organism. After this stage of "disorganized homogeneity" was reached, some new organisms could arise again by chance once in a while. But they were always promptly destroyed and the stage of disorganized homogeneity was maintained. The reasons for development of disorganized homogeneity are not entirely understood. But a mutation rule which encourages parasitism

followed by starvation of the parasites once the host organisms are used up, could be expected to give a result like this.

Both homogeneity problems were eventually overcome by using different mutation rules in different sections of each universe. Also slight modifications of the reproduction rule were used in different universes to create different types of environment (BARRICELLI, 1957). Furthermore, by running several parallel experiments and by exchanging segments between two universes every 200 or 500 generations it was possible to break homogeneity whenever it developed in one of the universes.

Successful evolution experiments lasting for several thousand generations have been performed by these methods. However the reasons for the difficulties and for the success of the procedure used are not yet sufficiently understood. Later attempts to apply the same idea (see next paper of this series, BARRICELLI, 1962) have shown that this method is more likely than not to lead to a failure unless the same combination of mutation and reproduction rules is applied again. The rules used are indicated in the legend of fig. 24.

8. RESULTS

Part of an evolution process developed in Princeton in 1956 is described in fig. 24. The figure is obtained by a photographic method from IBM cards punched by the computer and represents a part of the memory of the computer at various stages during the evoution process. In a universe of 512 number locations (the number locations, 0, 100, 200, 300, 400, and 500 are marked in the upper and lower border of fig. 24), 5 generations every 100 are recorded in the figure, starting at generation 300 and ending at generation 2000 with an interruption between generation 600 and 1000. For example, the number 300 at the right border of the figure marks the beginning of the 5 generations 300-304, the location 400 marks the beginning of the 5 generations 400-404 and so forth. The number location and the generation can be used to identify any spot in the figure. The data of the figure are given in binary numbers. In a few cases the binary numbers will be translated into decimal numbers to identify some of the organisms for the reader.

The universe described in fig. 24 represents one of 5 parallel experiments performed by the computer. At regular intervals segments of the universe in fig. 24 were exchanged with two other universes of the same size but with slightly different mutation and reproduction rules. Also inside fig. 24, four different mutation rules were used in four different regions (see legend of fig. 24).

A set of numbers introduced at generation 200 from another universe of a parallel experiment, developed into several symbioorganisms in successive

generations as recorded in the figure. At generation 600 a single species represented by a few different varieties able to interbreed, occupied the whole universe. At generation 1000 the same species and its parasites are still evolving by mutation, crossing, and selection. Its varieties which can be seen in the figure at generation 1000 are:

Symbioorganism	Type	Period	Number Locations
3 3 3 3 3 3	Independ.	2	0-80 and 490-511
3 3 3 3 6 3 3 6 3 3 3 3 3 6 3 3 6 3	Parasite	18	80-250
3 3 3 3 0 3 3 6 3 3 3 3 3 0 3 3 6 3	Parasite	18	250-400
3 3 3 3 9 3	Independ.	6	420-490

Symbioorganisms like these which are formed by multiples of 3 will be called *R*-organisms.

At generation 1100 the universe was almost entirely disorganized, but the *R*-organisms either survived around number location 200 or were reintroduced by an exchange with one of the other two universes. At generation 1200, three *R*-organisms occupied the region between the number locations 180 and 400. After generation 1200 the evolution of *R*-organisms, as can be seen in the figure, leads to a greater and greater complexity. Every number (gene) in the original symbioorganism is replaced several times by new mutations. After generation 1600 all genes are multiples of 6. This is a characteristic property of a type of the symbioorganisms which are called *Q*-organisms (BARRICELLI, 1957). After generation 1800 the *Q*-organisms acquire a periodicity of 72 genes, which will remain their characteristic period to the end of the experiment. After this characteristic periodicity was reached the evolution proceeded at a slower rate until generation 5000 when the experiment was discontinued. The last 3000 generations are not recorded in fig. 24, but the end result, or the *Q*-organism which occupied the same universe at generation 5000 will be shown in fig. 25.

A large number of other symbioorganisms arose after generation 2000. One of these, which will be called *QS*-organism, survived for a long time in competition with the *Q*-organisms. After generation 4000 the *Q*-organisms invaded all 5 universes and the *QS*-organisms were eradicated. The *QS*-organisms arose as a result of a symbiotic association of a *Q*-organism with another species (*S*-organism) whose genes are even numbers but mostly not multiples of 6. Every other gene in a *QS*-organism belongs to a *Q*-organism, and the remaining genes belong to an *S*-organism. Two examples of *QS*-organisms are recorded in fig. 25 in the second competition test. The *QS*-*organism* to the right has a period 16 and 4 alternate generations. Its numeric elements translated into decimals are in the 4 generations.

Generation																
1	36,	14,	24,	10,	12,	30,	24,	34,	36,	14,	24,	10,	12,	30,	24,	34
2	12,	10,	24,	30,	36,	34,	24,	14,	12,	10,	24,	30,	36,	34,	24,	14
3	36,	30,	24,	34,	12,	14,	24,	10,	36,	30,	24,	34,	12,	14,	24,	10
4	12,	34,	24,	14,	36,	10,	24,	30,	12,	34,	24,	14,	36,	10,	24,	30

Several Q-organisms also show a comparable degree of complexity (for a more detailed description of some evolution processes see BARRICELLI, 1957). Both in the Q- and the QS-organisms every gene was replaced several times during the evolution processes. The number of different varieties which arose either by viable mutations, by crossing, or by invasion of foreign elements must have been at least several thousand in each of the two types of symbioorganisms. Several hundred-thousand mutations (judging from the amount of machine time used and other criteria) arose during the 5 parallel experiments, but less than 1 % of these mutations gave rise to competitive varieties.

9. COMPETITION TESTS

Three experiments made in order to compare the competitivity or fitness reached by several symbioorganisms are recorded in fig. 25. In the first experiment (Test 1) two Q-organisms are compared. To the right (number locations 240-511) is the Q-organism (Q 1800) which occupied the same region at generation 1800 in fig. 24. To the left (number locations 0-240) is a Q-organism (Q 5000) which occupied this region at generation 5000 in the same experiment which is partly recorded in fig. 24. The mutation and reproduction rules used and their distribution according to number location are the same as in fig. 24.

The experiment clearly shows that Q 5000 is much more able to compete under the conditions of fig. 24 and 25 than the Q 1800 organism. In the first 12 generations recorded in the figure Q 1800 is rapidly being destroyed and Q 5000 is rapidly invading its area. At the generations 24-27, which are also recorded in fig. 25, Q 5000 has invaded the whole universe and nothing is left of Q 1800. The reader may have noticed that Q 5000 penetrated into the region of Q 1800 not only from the left but also from the right border. This is because the reproduction rules have been applied considering the universe as circular, or in other words considering number location 0 as identical with 512 and number location 511 as identical with —1. The same has been done in fig. 24, and the reader may notice that the symbioorganism close to the left border is very often the same variety as the symbioorganism close to the right border in the same generation.

In the second experiment (Test 2) two QS-organisms are compared; a QS 2500 to the left (loc. 0-240) with a QS 4000 to the right (loc. 240-511).

Both symbioorganisms appeared in the continuation of the evolution experiment of fig. 24 in generations 2500 and 4000 respectively. In this case the two symbioorganisms are still able to interbreed and may be considered as belonging to the same species, in spite of the 1500 generation interval which separates them. Nevertheless a kind of frontier between the two organisms can easily be seen in the figure, marked by the empty spots due to collisions of different genes. It is evident that the genes of *QS* 4000 are rapidly invading the area of *QS* 2500. After 35 generations the entire universe of fig. 25 (Test 2) was occupied by the genes of *QS* 4000 and every gene of *QS* 2500 had disappeared. Also in this case the variety which had endured a longer period of evolution in the universe of fig. 24 was better fit to compete in this universe.

In the third experiment (Test 3) three symbioorganisms, *Q* 5000, *QS* 4000, and an *R*-organism which appeared in a parellel experiment at generation 1900, are compared. Again the symbioorganism (Q 5000), which had experienced the longest period of evolution, was the one which survived and destroyed the other two.

In any particular universe the survival ability of a symbioorganism is evidently determined by its genetic information, and it is clear that the ability to survive is improved by evolution. The genetic structure of any symbioorganism can rightly be considered as a coded survival strategy program created and developed during its past evolutionary history.

10. ERADICATION OF PRIMITIVE SYMBIOORGANISMS

The tests performed in fig. 25 show one reason why the *Q*-organisms are the only ones which survived at generation 5000: all other symbioorganisms had evidently been eradicated by the more competitive *Q*-varieties.

A glance at the conditions at generation 5000 or even at generation 4000 could easily give the mistaken impression that a symbioorganism had been formed by a lucky accident some time during the experiment, and that this had given rise to all the *Q* and *QS* varieties developed later. The reader who has followed the experiments of fig. 15 and fig. 24 from the beginning is certainly aware that a large number of unrelated symbioorganisms usually arise in such experiments. The only reason why they do not arise also at a later stage is that they have no chance to do so in the presence of far more competitive symbioorganisms developed later. The strong competition is also the reason why all symbioorganisms which survive at the end are related. In any given number of generations there is a finite probability that one or several competitors will be eradicated. At the end only one type of symbio-

organisms (which in the present case happened to be the Q-organisms) will survive.

If this lesson can be applied to living organisms on Earth, the fact, that present life forms seem to be more or less related, is no argument for claiming that symbiogenesis occurred only once on this planet. Nor is the fact that new life forms do not seem to arise any longer an argument for claiming that symbiogenesis could not be frequent under favorable conditions and without competition from preadapted species (see also "oxygen as antibiotic agent," BARRICELLI, 1962, section 12).

11. THE EARLY CROSSING MECHANISMS

Another lesson which can be learned from these investigations is that crossing is a phenomenon which appears very early in a symbiogenetic evolution process and certainly before the symbioorganisms reach the complexity we find in living beings (see next paper of this series BARRICELLI, 1962). All symbioorganisms investigated showed some kind of crossing phenomena. In some cases a crossing process could have the character of an infection or infiltration by a symbiont or a numeric element delivered by another symbioorganism. However in all evolution processes the regular crossing mechanism described in the figures 8, 9, 10, and 11 became rapidly predominant with evolution (for a closer description and classification of the crossing mechanisms observed see BARRICELLI, 1957). The common idea that living beings may have existed for a long time before crossing mechanisms appeared is hardly consistent with a symbiogenetic interpretation. The discovery of crossing in viruses and bacteria support the idea that life may never have developed without crossing phenomena. The accidental loss of crossing ability observed in some cases is usually equivalent to the loss of more than 99.9 % of the potential evolution rapidity (FISHER. 1930). The extinction of the species seems the inevitable result, as soon as possible competitors take advantage of the situation.

12. CONCLUSION

It is clear that many phenomena which were considered peculiar for living beings are common to a large class of symbioorganisms. A question which apparently has troubled many inquirers in these problems is that of the nature of symbioorganisms and their relationship to living organisms. What are the numeric symbioorganisms presented in this paper, and what are all the other types of symbioorganisms, artificial or natural (see next paper of this series BARRICELLI, 1962)? Are they the beginning of, or some sort of,

foreign life forms? Are they only models through which one is able to investigate some properties of living beings and some aspects of biological evolution?

The answers are: (1) They are not models, not any more than living organisms are models. They are a particular class of selfreproducing structures already defined. (2) It does not make sense to ask whether symbioorganisms are living as long as no clearcut definition of "living" has been given (see also: "Note by the author" at the beginning of the present paper). It makes better sense to ask whether the so-called living beings which populate this planet are symbioorganisms, and if so, what kind of symbioorganisms they are. The definition of symbioorganism has already been given and can be summarized as follows: A symbioorganism is a selfreproducing structure constructed by symbiotic association of several selfreproducing entities of any kind.

The numeric symbioorganisms presented in this paper have been developed in order to test a specific prediction of symbiogenesis theory. The prediction is that the phenomena listed in section 6 (general properties of symbioorganisms) and possibly other phenomena until recently considered characteristic of living organisms (biophenomena) are common to a large class of symbioorganisms. The test has given an unequivocal, positive answer. A large group of biophenomena has been detected in the numeric symbioorganisms developed. In the next paper of this series (BARRICELLI, 1962) two more biophenomena (the evolutionary improvement of performance in a specific task and an infection process by a parasite which produces limited injuries but does not destroy the host) will be described.

The answer obtained is also an answer to the question whether symbiogenesis theory can explain the presence of the previously listed biophenomena in living organisms. If living beings are symbioorganisms, they obviously may have the same chance as other symbioorganisms to develop these particular biophenomena.

The properties a class of self-reproducing entities would need in order to build up symbioorganisms and start a symbiogenetic evolution process are extremely simple. There is no reason to believe that billions of years would be needed to develop the biophenomena described. What is needed is not primarily time but a favorable chemical environment in which a large number of interconnected (symbiotic) autocatalytic reactions takes place. The results presented in this paper show that under proper conditions even in the very limited memory of a high speed computer a large number of symbioorganisms can arise by chance in a few seconds. It is only a matter of minutes before all the biophenomena described can be observed. Given

enough time, there is no *a priori* reason why a proper chemical environment could not do the same job.

There are very few important limitations concerning temperature and other environmental conditions required for development of symbioorganisms. Neither the low temperature of the moons of Uranus nor the high temperature of the Sun-side face of Mercury are sufficient arguments to exclude the possibility of symbiogenetic phenomena. The experiment recorded in fig. 24 is a clear demonstration that symbiogenesis can not only take place on a planet or satellite but even in the memory of a high speed computer. To maintain that only conditions similar to those prevailing on Earth could permit symbiogenetic processes would obviously be too great a pretention.

The symbioorganisms evolving in a sufficiently large environment for a sufficiently long period of time may develop properties and organs with any degree of sophistication which could be useful in their particular environment. The number of allelic states and varieties which are possible in a symbioorganism (2^n or more, where n is the number of genes, see section on symbiogenesis theory) is not a serious limitation to the evolutionary possibilities. Unless some other severe limitation is imposed by the conditions of the experiment or the type of universe in which the organism exists (computer, planet, or test tube), there is no *a priori* reason for assuming that other classes of symbioorganisms could not reach the same complexity and efficiency characteristic for living organisms on this planet.

Whether life of the particular form (based on nucleic acid-protein association) which has developed on this planet is frequent or rare or even a unique phenomenon is difficult to say. On the other hand, symbiogenesis in one form or another is likely to have occurred on every planet or satellite where a large number of interconnected autocatalytic reactions are possible or have been possible in the past. The conditions required are too simple for considering symbiogenesis as a unique or even an infrequent phenomenon. However, as shown in the experiments of fig. 24 and 25, once a symbiogenetic process has established itself, it would probably prevent or promptly eradicate any other symbiogenetic activity which could possibly compete or interfere with it. Under these conditions such new symbiogenetic activities may indeed not only be infrequent but for all practical purposes impossible.

APPENDIX

Readers who are familiar with the notion of stochastic time-series will probably remember the definition of a Markovian time-series. An obvious extention of this concept is represented by the notion of a Markovian vector time series, in which each term is a vector V_t with several components (or a set of numbers) instead of a single number.

Definition:

If the probability distribution $P\ (V_{t+1})$ of V_{t+1} exclusively depends on the last preceding term V_t (*i.e.* on the values of the V_t components) the vector-time series is called Markovian. A degenerative case of a Markovian vector time-series is the so called determinístic case in which not just $P\ (V_{t+1})$ *but* V_{t+1} itself is entirely determined when V_t is given. This deterministic case, which would obviously be trival and uninteresting in a normal (numerical) time-series, is neither trival nor uninteresting in a vector time-series, as the reader will have the opportunity to experience. As a matter of fact the so called time t does not necessarily have to be time and could be substituted by any dimension (called pseudo-time) implying the same relationships between consecutive terms of the series. The numeric evolution processes presented in this paper are examples of a Markovian vector time-series, in which every vector (or term) has, as its components, the numbers (inclusive zeros or empty squares) constituting a particular generation of the process. Successive generations are successive terms (vectors) of a Markovian series. In fact every generation V_{t+1} or at least the probability distribution of its terms is completely determined when the preceding generation V_t is given. The Markovian series will be deterministic if the mutation rules applied specify the mutations in every single collision. It will not be deterministic if random numbers are used in the determination of at least part of the mutations.

As a matter of fact it is not necessary to consider only series consisting of vectors or sets of numbers. Instead of numbers one may consider any kind of entities (for example molecules or other gadgets) to be called "Markovian elements". If every term or set of elements V_{t+1} (or at least the probability distribution for the possible alternatives of V_{t+1}) exclusively depends on the preceding term V_t the sample of consecutive sets will be called a timed Markovian universe or shortly a universe. The notions of "deterministic" and "non-deterministic" universes are obvious from previous definitions.

Readers who are familiar with the complexity of time-series problems will be aware that Markovian universes can hardly have been the object of farreaching mathematical investigation. However, the use of high speed data processing computers makes possible the study of particular examples of Markovian phenomena such as the numeric evolution phenomena investigated in this paper.

The notion of Markovian universes and Markovian entities gives the basis for a mathematical definition of the concepts used in symbiogenesis theory. We shall, however, not afflict the reader by presenting a long list of definitions. It will be sufficient to point out that the notions of self-reproducing

Markovian entities, self-reproducing sets of Markovian entities, utility association (symbiosis), symbioorganism, hereditary changes by crossing, mutation *etc.* can be defined in terms of Markovian concepts and are to be considered as mathematical notions.

The numeric evolution processes and probably biologic evolution, if the symbiogenesis theory is correct, are empirical examples of two different symbiogenetic evolution processes. However, this statement does not tell what life is, and can only describe one aspect (the symbiogenetic and evolutionary aspect) of this complex phenomenon.

ZUSAMMENFASSUNG

Das Problem der Erforschung von Evolutionsphänomenen und Theorien unter Verwendung von künstlichen selbst-reproduzierenden Einheiten wird besprochen. Die Notwendigkeit eines theoretischen Prinzips zur Lösung des Variabilitätsproblems wird betont. Es wird gezeigt, dass das Variabilitätsproblem gelöst werden kann unter Annahme, dass selbst-reproduzierende Modelle („Symbio-organismen") von jeder Komplexität gebildet werden können durch eine symbiotische Assoziation von verschiedenen selbst-reproduzierenden Einheiten, jede mit sehr geringer oder gar keiner Variabilität (Symbiogenese-theorie). Weiter wird gezeigt, dass Symbio-organismen entworfen werden können, welche imstande sind, Kreuzungsphänomene verschiedener Art zu erfahren. Schlussfolgerungen, Voraussagungen und empirische Beobachtungen die eine symbiogenetische Interpretation der Entstehung von Kreuzungen in lebendigen Organismen stützen, werden besprochen.

Als einmal das Variabilitätsproblem überwunden war, ergab sich die Möglichkeit, künstliche selbst-reproduzierende Einheiten zu entwerfen, welche imstande sind, eine Anzahl verschiedener Evolutionsphänomene zu entwickeln. Die Symbio-organismen, entwickelt durch die elektronische Rechenmaschine von dem "Institute for Advanced Study, Princeton, N.J.", zeigten auch Kreuzungsphänomene, welche sich schnell zu einem Kreuzungsmechanismus entwickelten, der den Vererbungsgesetzen ähnlich ist, wie sie bei lbendigen Organismen beobachtet werden.

Eine Mannigfaltigkeit von anderen Phänomenen, welche in einer imposanten Weise mit biologischen Phänomenen übereinstimmen, sind in den Abschnitt über allgemeine Eigenschaften von Symbio-organismen aufgenommen. Ein konkurrenz Versuch zwischen mehreren Symbio-organismen, in verschiedenen Stadien eines Evolutionsexperiments gewählt, wurde angestellt. Der Versuch zeigte eine dramatische Verbesserung von Eignung und eine Zunahme von Konkurrenzfähigkeit während des Evolutionsprozesses. Verschiedene Folgerungen von evolutionären Fortgang und Aussterben von untereinander konkurrierenden Symbio-organismen werden besprochen. Die Einfachheit der Bedingungen für Symbiogenese und die grosse Wahrscheinlichkeit, dass symbiogenetische Phänomene verschiedener Art auf anderen Planeten und Satelliten in Entwicklung sein könnten, wird betont.

SUMMARY

The problem of testing evolution phenomena and theories by using artificial self-reproducing entities is discussed. The need of a theoretical principle which can permit the solution of the variability problem is emphasized. It is shown that the variability problem can be solved assuming that self-reproducing patterns (called symbio-organisms) of any complexity can be formed by a symbiotic association of several self-reproducing entities, each with very low variability or no varability at all (symbiogenesis theory).

Furthermore it is shown that symbio-organisms able to undergo crossing phenomena of various types can be designed. Consequences, predictions, and empirical observations supporting a symbiogenetic interpretation of the origin of crossing in living organisms are discussed.

Once the variability problem was overcome, it was possible to design artificial (e.g. numerical) selfreproducing entities able to develop a variety of evolutionary phenomena. The symbio-organisms developed by the electronic computer of the Institute for Advanced Study, Princeton, New Jersey, also showed crossing phenomena which rapidly developed into a crossing mechanism following laws of heredity similar to those observed in living organisms. A variety of other phenomena presenting impressive analogies with biological phenomena are listed in the section on general properties of symbio-organisms.

A competition test between several symbio-organisms selected in different stages of an evolution experiment was performed. The test showed a dramatic improvement of fitness and increase of competitivity during the evolution process. Several consequences of evolutionary improvement and eradication of competitors are discussed.

The simplicity of the conditions for symbiogenesis and the high probability that symbiogenetic phenomena of various kinds may have been developing on other planets and satellites is emphasized.

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