PARTHENOGENESIS AND GENETIC VARIABILITY. II. ONE-LOCUS MODELS FOR VARIOUS DIPLOID POPULATIONS[1,2]

JAMES H. ASHER, JR.

The Department of Zoology, The University of Michigan, Ann Arbor, Michigan

Received April 7, 1970

PARTHENOGENESIS in the animal kingdom has been termed an "evolutionary dead end". This view stems from the writings of DARLINGTON (1937), WHITE (1948), SUOMALAINEN (1950), and others who suggested that only two genetic consequences result from such a system of reproduction: (1) complete homozygosity; or (2) complete heterozygosity. These authors described the mechanisms presumed to yield these results for several parthenogenetic species; unfortunately, none of these descriptions utilized rigorous mathematics to analyze the genetic properties of parthenogenetic populations.

The validity of the above hypotheses was challenged by CARSON (1967a) who suggested that automictic parthenogenetic reproduction can *maintain* heterozygosity. He stated that in those species of insects (*Drosophila mangabeirai, Solenobia lichenella, Devorgilla canescens* etc.) which can restore zygoidy either by inhibition of meiosis I or by central fusion, loci which are absolutely linked to the kinetochore could be maintained in a state of permanent heterozygosity. Furthermore, with the addition of chromosomal rearrangements, the amount of heterozygosity preserved in parthenogenetic species could be increased. Thus, he suggested heterozygosity could be maintained in these organisms by at least two mechanisms: (1) absolute linkage to the kinetochore; and (2) chromosomal rearrangement. WHITE (1970), reversing his previous views on heterogeneity in parthenogenetic animals, appears to take a position similar to that of CARSON (1967a); however, his arguments also lack mathematical rigor.

The mathematics needed as a basis for students of natural parthenogenetic populations was developed in part in a previous study (NACE, RICHARDS and ASHER 1970) where a model based upon a mapping function was used to estimate gene–kinetochore distances and "inbreeding" in parthenogenetically produced frogs.* It was noted that although the linkage data were derived from artificial parthenogenetic reproductions, the analytical model should apply to all systems of parthenogenesis, natural or artificial, which restore zygoidy either by inhibition of meiosis II or by terminal fusion. Although the paper presented a mathe-

[1] Part of a thesis submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy in The University of Michigan Horace H. Rackham School of Graduate Studies.

[2] These investigations were supported by a National Institutes of Health Genetics Training Grant 5 T01 GM00071-12, and in part by the National Science Foundation grant GB 8187, and by The University of Michigan Computing Center.

* The term inbreeding does not truly apply to the parasexual process described here. No term exists which describes a system of reproduction leading to increased homozygosity independent of the mechanism of reproduction. Rather than formulate a new term, we will use the term "inbreeding" in quotes when it relates specifically to parthenogenetic animals.

matical account of "inbreeding" associated with parthenogenetic reproduction and confirmed previous predictions made by HALDANE (WHITE 1948, footnote p. 243), DARLINGTON (1937), and SUOMALAINEN (1950), it did not consider certain modifying factors which are known to alter the course of "inbreeding" in other systems (HAYMAN and MATHER 1953; HAYMAN 1953; WORKMAN and JAIN 1966; ALLARD, JAIN and WORKMAN 1968). To extend the arguments presented by NACE, RICHARDS and ASHER (1970), this paper proposes to accomplish the following: (1) to develop deterministic models which describe rates of "inbreeding" for three general mechanisms of parthenogenetic reproduction; (2) to extend these models to include selection; and (3) to use these models to describe the theoretical genetic structure of parthenogenetic populations. These arguments, however, are restricted in this paper to one-locus models of diploid species which have a closed breeding system.

THEORETICAL CONSIDERATIONS

Mapping function: As previously demonstrated (NACE, RICHARDS and ASHER 1970), the mapping function developed by BARRATT *et al.* (1954) and normally used to compute linkage relationships in *Neurospora crassa* can also be used: (1) to construct linkage maps in vertebrates and other organisms in which second-division segregants can be detected; and (2) to obtain "inbreeding" estimates for parthenogenetic populations in which the homozygosity at a given generation is proportional to the frequency of recombination between a given locus and its kinetochore.

Restoration of zygoidy: In the automictic parthenogenetic species described by WHITE (1948), SUOMALAINEN (1950), and by WHITE, CHENEY and KEY (1963), zygoidy tends to be restored by one of six mechanisms: (1) premeiotic replication of the chromosomes followed by a normal meiosis; (2) normal meiosis followed by the fusion of the first or second cleavage nuclei; (3) abnormal meiosis I followed by a normal meiosis II where kinetochore replication occurs; (4) normal meiosis I with meiosis II aberrant, or equivalently the second polar body fuses with the egg nucleus; (5) abnormal meiosis I and II in which kinetochores replicate and two of the four chromatids are randomly distributed between a single polar body and the egg nucleus; and (6) inhibition of meiosis I with restoration of zygoidy by utilization of meiosis II products as the first cleavage nuclei.

Mechanism 1: Because chromosomal pairing in mechanism 1, as observed in the grasshopper *Moraba virgo* (WHITE, CHENEY and KEY 1963), is usually restricted to daughter chromosomes, meiosis restores the egg nucleus to a genetic condition exactly equivalent to that of the oogonial cell, provided mutation has not occurred. In this case, existing heterozygosity is maintained and is increased by mutation.

Mechanism 2: As the cleavage nuclei of the moth *Solenobia triquetrella* (SUOMALAINEN 1950), which reproduces by this mechanism, are haploid and genetically identical, restoration of the zygoid state by fusion of these nuclei leads

to total homozygosity in a single generation. The equivalent of this mode of reproduction, inhibition of first cleavage mitosis, can be artificially induced in amphibians (NACE and RICHARDS, personal communication).

Mechanism 3: A diagrammatic representation of the restoration of zygoidy by central fusion is presented in Figure 1. It is apparent that this mechanism, which occurs in *Drosophila parthenogenetica* and *D. mangabeirai* (STALKER 1956; MURDY and CARSON 1959), is genetically equivalent to an inhibition of meiosis I followed by a normal meiosis II, which is seen in the parasitic wasp *Devorgilla canescens* (SPEICHER 1937; SPEICHER, SPEICHER and ROBERTS 1965).

Mechanism 4: The restoration of zygoidy by inhibition of meiosis II was used by NACE, RICHARDS and ASHER (1970) to obtain second-division segregants of frogs heterozygous for various mutant genes. Figure 2 demonstrates that this mechanism is equivalent to terminal fusion regardless of the cytological mechanisms involved. This type of mechanism has been recognized in *D. parthenogenetica*, *D. mangabeirai*, the homopteran, *Lecanium hesperidium* (STALKER 1954, 1956; MURDY and CARSON 1959; SUOMALAINEN 1950), and other insect species.

Mechanism 5: The restoration of zygoidy by a totally abnormal meiosis is represented in Figure 3. This mechanism has been observed in the moth *Solenobia lichenella*, the nematode *Rhabditis monohystera*, and has been suggested for races of the brine shrimp *Artemia salina* (SUOMALAINEN 1950).

Mechanism 6: A sixth mechanism, described by SUOMALAINEN (1950), restores zygoidy by inhibition of meiosis I followed by meiosis II which produces two nuclei that become the first cleavage nuclei. As in the gall wasp *Neuroterus baccarum*, cytokinesis then occurs giving rise to mosaic zygoids made up of homozygous *AA* and *aa* cells, or to heterozygotes (*Aa*), depending upon whether recombination occurred.

Consideration of these parthenogenetic mechanisms reveals that the genetic structures of populations reproducing by mechanisms 1 and 2 can be understood without recourse to rigorous mathematical treatment and that they produce either complete homozygosity or heterozygosity as predicted by earlier descriptions. On the other hand, a description of the consequences of mechanism 6 requires knowledge of the breeding properties of the mosaics. This is lacking at present. Thus, parthenogenetic mechanisms 1, 2, and 6 will not be further considered here. Examination of parthenogenetic mechanisms 3, 4, and 5, however, suggests the possibility of constructing models to describe the genetic structure of populations reproducing by these mechanisms.

Limiting assumptions: In treating these three mechanisms, only a single locus with two alleles (*A* and *a*) will be considered. The relative survival or fitness values of *AA*, *Aa*, and *aa* are assumed to be $W_{AA}:1:W_{aa}$. Figure 4 illustrates a population of parthenogenetically reproducing organisms carrying these alleles, and describes the way each organism contributes to the next generation. This contribution can be modified by selection acting upon: (1) fecundity; (2) meiosis; and (3) zygoid survival (Figure 4). While the fitness of a given genotype may

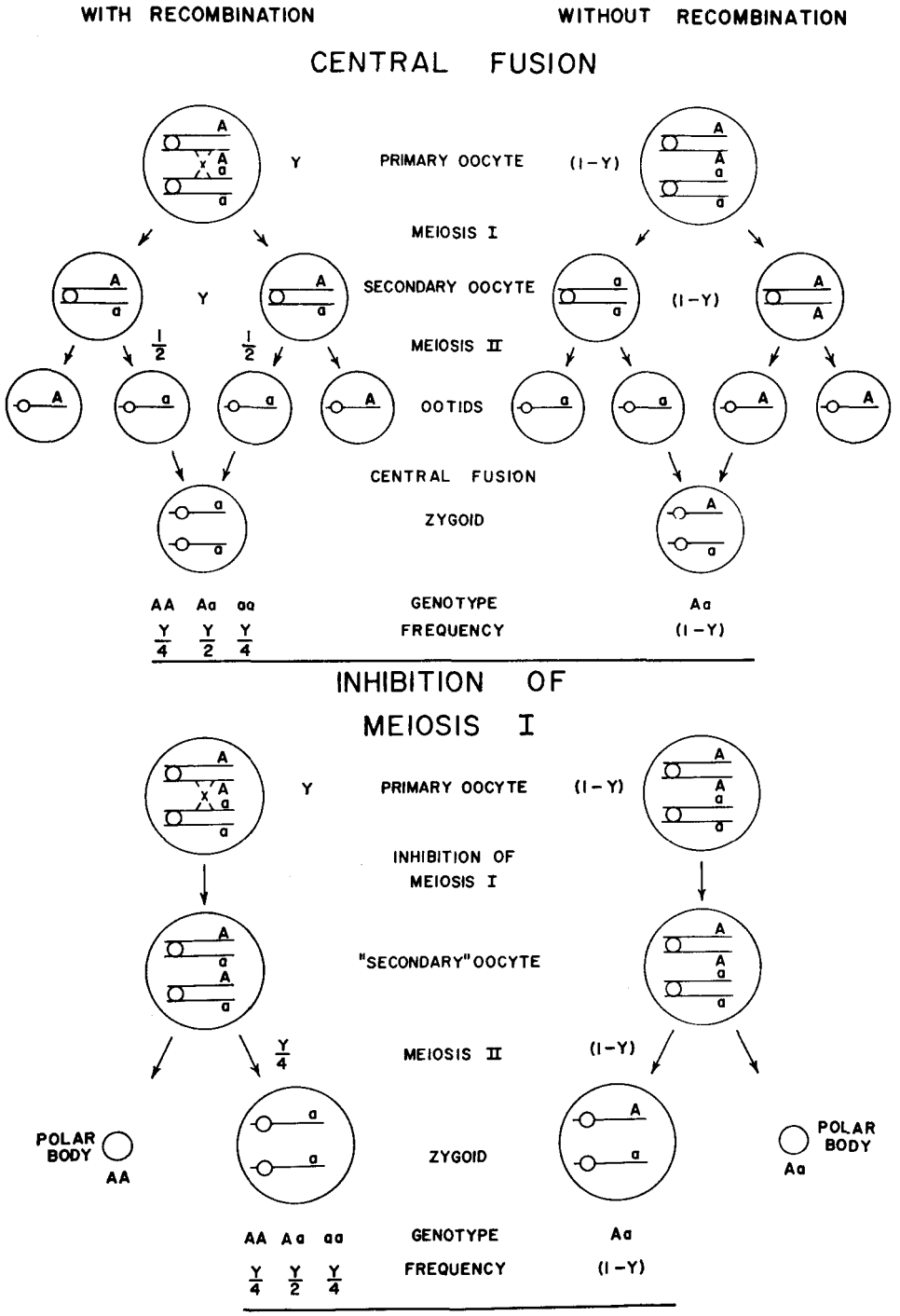

FIGURE 1.—Diagrammatic representation of the meiotic events of mechanism 3 (represented by E_2 in the equations) for the parthenogenetic species, *Drosophila mangabeirai*, restoring zygoidy in part by central fusion; and in the parastic wasp, *Devorgilla canescens*, restoring zygoidy by inhibition of meiosis I. Note that in central fusion the products of different secondary oocytes fuse and that geometric restrictions within the species involved prevent fusion of the two products of a single secondary oocyte. A single locus with two alleles (A and a) is considered where Y is the probability of a recombination between the locus and kinetochore.

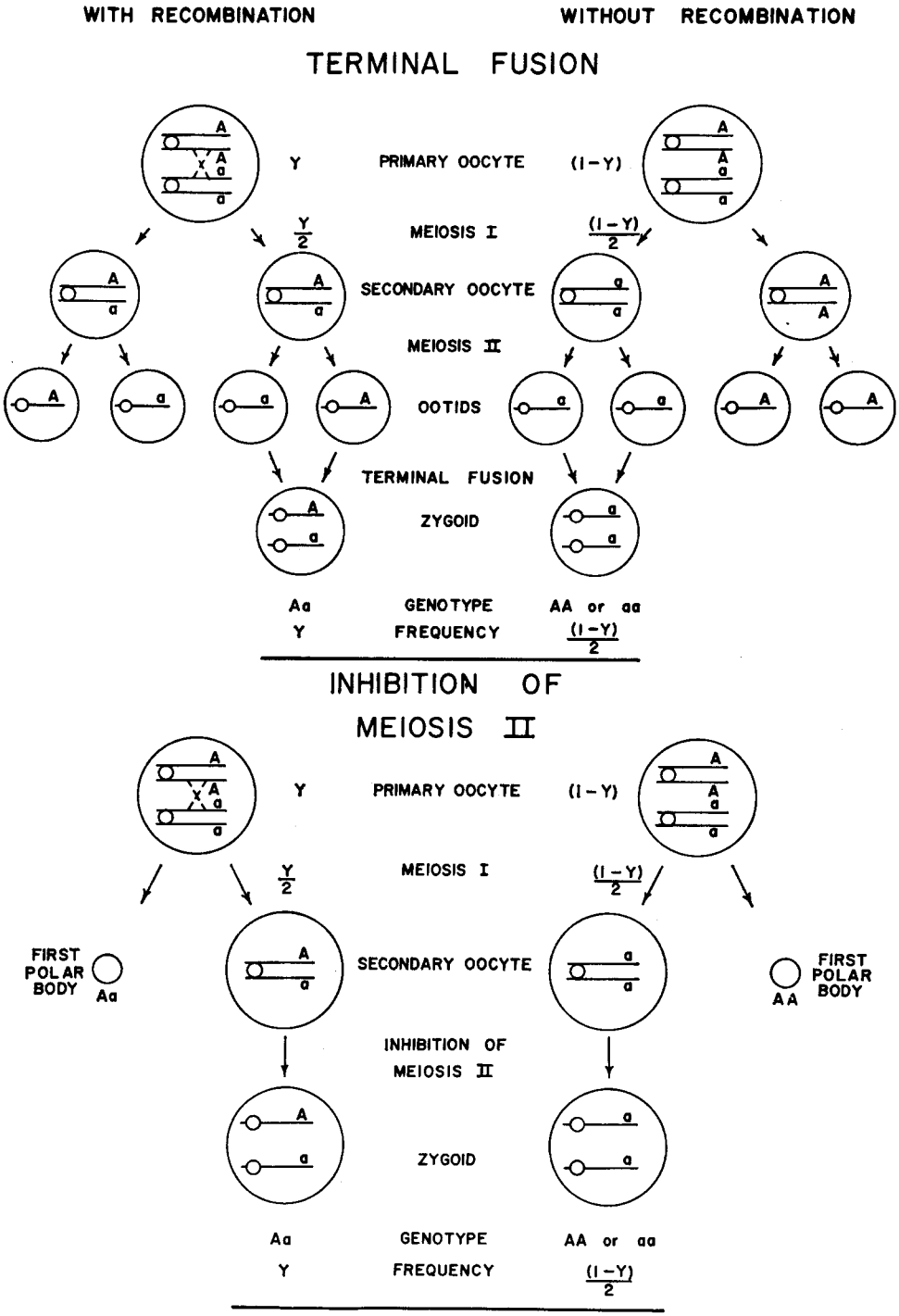

FIGURE 2.—Diagrammatic representation of the meiotic events of mechanism 4 (represented by E_1 in the equations) for the parthenogenetic species *Drosophila mangabeirai* restoring zygoidy in part by terminal fusion; and for the homopteran, *Lecanium hesperidum*, restoring zygoidy by inhibition of meiosis II. Note that in terminal fusion, the products of a single secondary oocyte fuse while geometric restrictions within the species involved prevents fusion of the products from two different secondary oocytes. A single locus with two alleles is treated as in Figure 1.

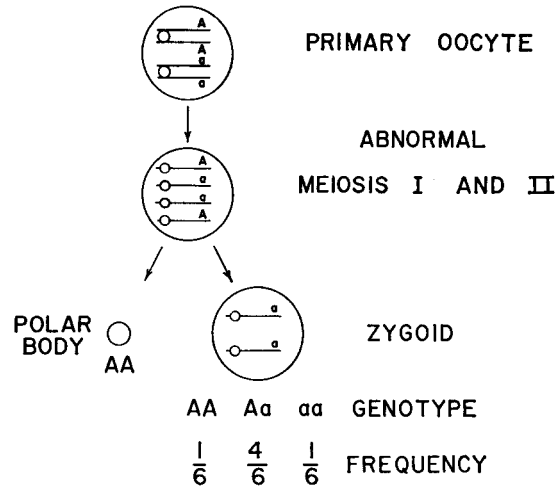

FIGURE 3.—Diagrammatic representation of the meiotic events of mechanism 5 in a parthenogenetic species, e.g., the moth, *Solenobia lichenella*, which restores the zygoid condition by an abnormal meiosis I and II. A single locus with two alleles is treated as in Figures 1 and 2. The ratios are derived by assuming independent assortment of the locus and its kinetochore and are thus not influenced by linkage.

be related to all three processes, it is examined here on the limiting assumption that selection occurs upon only one process in the life cycle of the organism, namely zygoid survival (process 3 of Figure 4).

The following additional limiting assumptions have also been made. First, given a gene–kinetochore distance (x), a mapping function [expressions (1) and (2) in NACE, RICHARDS and ASHER (1970)] is assumed to predict the frequency of heterozygotes (Aa) produced in each generation. This frequency is proportional to the frequency of recombination (y) and assumes no selection upon either process 1 or 2 (Figure 4). Second, it is assumed neither mutation, migration, nor

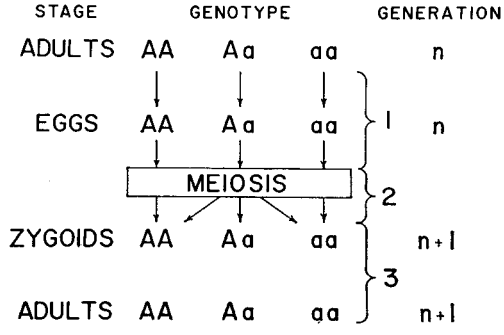

FIGURE 4.—A schematic representation of a parthenogenetically reproducing population at the n and $n+1$ generations showing that selection may affect: (1) fecundity; (2) meiosis; and (3) zygoid survival.

cross-fertilization influences gene frequencies, i.e., that these are closed breeding systems.

Model I: As mechanisms 3 and 4 occur simultaneously in several species (*D. parthenogenetica* and *D. mangabeirai*), independently in other species (*Devorgilla canescens* and *L. hesperidum*), and have or can be induced in still other species (*Rana pipiens* etc.), model I has been constructed to describe populations which reproduce by either or both mechanisms 3 and 4. Considering such parthenogenetic populations, the initial genotypic frequencies are given by:

$$P_n = \text{frequency of } AA \text{ at generation } n$$
$$Q_n = \text{frequency of } aa \text{ at generation } n$$
$$R_n = 1 - P_n - Q_n = \text{frequency of } Aa \text{ at } n$$

The frequencies of homozygotes and heterozygotes in successive generations, then, are described by the following equations derived from a consideration of Figures 1, 2, and 4:

$$P_{n+1} \propto \{P_n + R_n[E_1(1-\gamma)/2 + E_2\gamma/4]\}\, W_{AA} \tag{1}$$

$$Q_{n+1} \propto \{Q_n + R_n[E_1(1-\gamma)/2 + E_2\gamma/4]\}\, W_{aa} \tag{2}$$

$$R_{n+1} \propto R_n[E_1\gamma + E_2(1-\gamma/2)]\, W_{Aa} \tag{3}$$

where

γ = the probability of recombination at locus A, a corrected map distance (x) from its kinetochore
E_1 = proportion of eggs developing by mechanism 4 (Figure 2)
E_2 = proportion of eggs developing by mechanism 3 (Figure 1)
$E_2 = 1 - E_1$
W_{AA} = proportion of AA surviving
W_{aa} = proportion of aa surviving
W_{Aa} = proportion of Aa surviving = 1

The equilibrium equations describing a population reproducing by either or both mechanisms 3 and 4 with zygoid selection can be developed using techniques presented by HAYMAN (1953), WORKMAN and JAIN (1966), and ALLARD, JAIN and WORKMAN (1968) to describe mixed selfing and random mating systems. At equilibrium, when the values of P, Q, and R are the same for each successive generation (n, $n+1$, . . . , i), the condition $P_{n+1}/P_n = Q_{n+1}/Q_n = R_{n+1}/R_n$ must hold. This yields the following equations derived from equations (1), (2), and (3):

$$P_i = \frac{R_i[E_1(1-\gamma)/2 + E_2\gamma/4]W_{AA}}{E_1\gamma + E_2(1-\gamma/2) - W_{AA}} \tag{4}$$

$$Q_i = \frac{R_i[E_1(1-\gamma)/2 + E_2\gamma/4]W_{aa}}{E_1\gamma + E_2(1-\gamma/2) - W_{aa}} \tag{5}$$

Letting

$$K_1 = E_1(1-\gamma)/2 + E_2\gamma/4 \tag{6}$$

$$K_2 = E_1\gamma + E_2(1-\gamma/2) \tag{7}$$

and substituting these values and equations (4) and (5) into $P_i + Q_i + R_i = 1$, the equation for heterozygosity at equilibrium (R_{eq}) is given by:

$$R_{eq} = R_i = \frac{1}{\frac{K_1 W_{AA}}{K_2 - W_{AA}} + \frac{K_1 W_{aa}}{K_2 - W_{aa}} + 1} \tag{8}$$

Thus, the frequency of heterozygotes at equilibrium is proportional to: (1) the fitness of both homozygotes (assuming $W_{Aa} = 1$); (2) the proportion of eggs reproducing by central or terminal fusion (mechanisms 3 and 4); and (3) the probability of recombination, which is itself related to the distance of the locus from its kinetochore. As the value for the fitness of both homozygotes approaches the value for K_2 from zero ($W_{AA} \rightarrow K_2$ and $W_{aa} \rightarrow K_2$) which is determined by specific values of E_1, E_2, and γ, R_{eq} approaches zero, and the population approaches complete homozygosity.

Using these expressions, equilibrium phase diagrams (Figure 5) similar to those developed by HAYMAN and MATHER (1953) and used by HAYMAN (1953) and by WORKMAN and JAIN (1966) to describe mixed selfing and random mating systems can be developed for a strictly parthenogenetic species. These phase diagrams describe the genetic structure of all populations having varying values of W_{AA} and W_{aa} for a *constant* value of K_2. For a given value of W_{AA} and W_{aa}, the phase diagram indicates whether the population at equilibrium will be completely homozygous (A and B of Figure 5) or will sustain heterozygosity (C and D of Figure 5). The positions of the boundaries separating the four areas of a given phase diagram are dependent upon the value of K_2 chosen for analysis. As noted above, this latter value is in turn dependent upon the values of E_1, E_2, and γ.

The three straight lines of this figure represent the first set of boundary conditions separating populations which are completely homozygous (A and B, Figure 5) from each other and from those maintaining heterozygosity (C and D). These boundary conditions result from allowing $R_{eq} \rightarrow 0$ in equations (4) and (5) and are given by:

$$W_{AA} = K_2 \tag{9}$$

$$W_{aa} = K_2 \tag{10}$$

$$W_{AA} = W_{aa} \text{ (where } W_{AA} \text{ and } W_{aa} > K_2) \tag{11}$$

Within the boundaries defined by (9) and (10), the values of either W_{AA} or W_{aa} go from K_2 to 0 while R_{eq} takes on values of 0 to 1 (Figure 5, right column). As W_{AA} or W_{aa} take on these values, a second boundary (the hyperbolic curve between C and D, Figure 5) is passed which satisfies the Hardy-Weinberg equilibrium and is derived by substituting equations (4) and (5) into $4PQ - R^2 = 0$, a restatement of the Hardy-Weinberg equation. This boundary, given by:

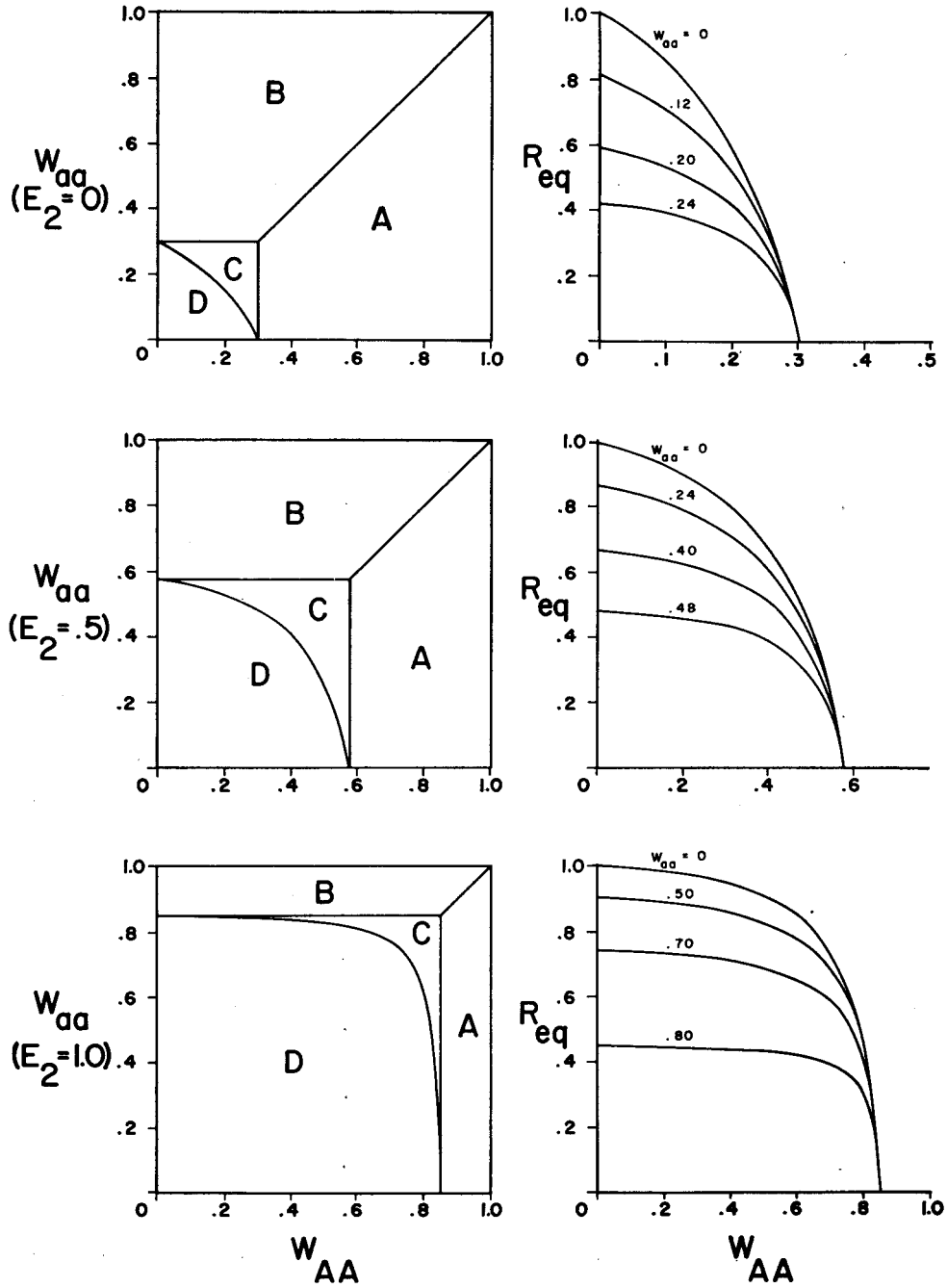

FIGURE 5.—Equilibrium phase diagrams for Model I, with corresponding values of R_{eq} (equilibrium heterozygosity) for one linkage distance ($x = 20$ map units), one value of the coefficient of coincidence ($k = 1.0$), and three values of central fusion ($E_2 = 1.0, .5, 0$). Area A indicates populations that are totally homozygous for A; B—homozygous for a; C—with less heterozygosity than a Hardy-Weinberg population; D—with more heterozygosity than a Hardy-Weinberg population.

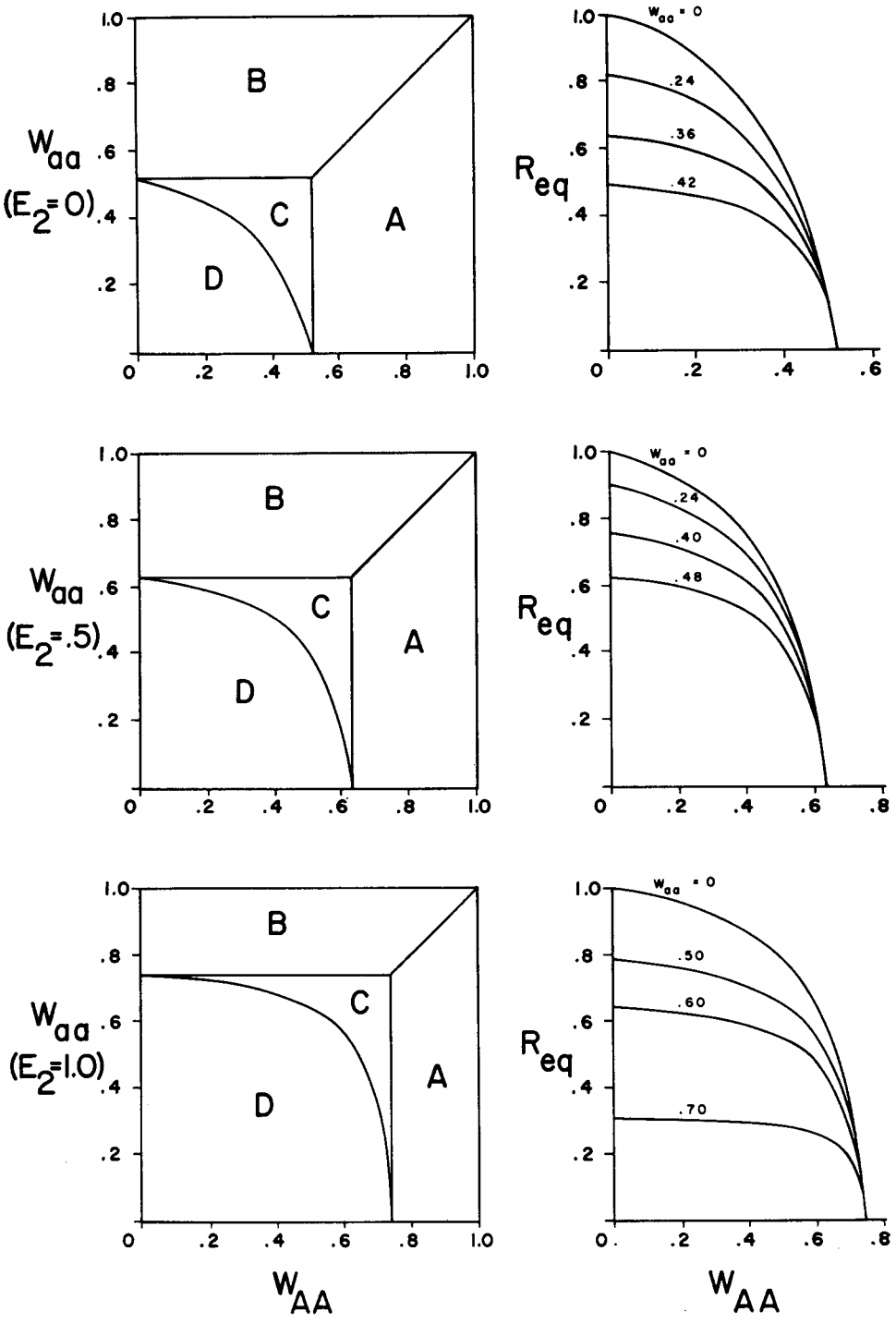

FIGURE 6.—Equilibrium phase diagrams for model I, with corresponding values of R_{eq} (equilibrium heterozygosity) for one linkage distance ($x = 50$ map units). The values of E_2 and k are defined in Figure 5 as are the meanings of A, B, C, and D.

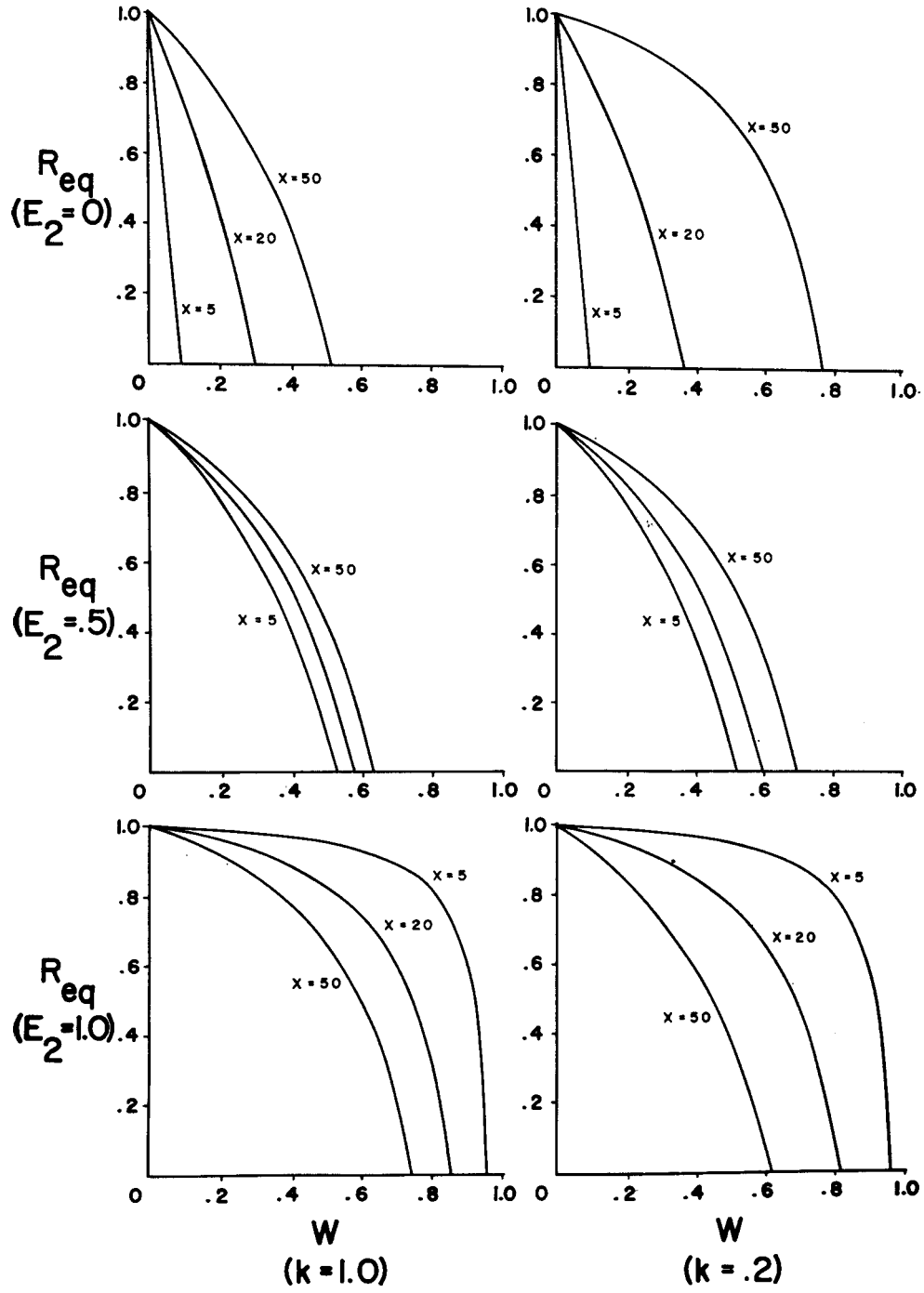

FIGURE 7.—The values of R_{eq} (equilibrium heterozygosity) where W_{AA} and W_{aa} are equal and are given the symbol W. Three values of linkage ($x = 5$, 20, and 50 map units), three values of central fusion ($E_2 = 1.0$, .5, and 0), and two values of the coefficient of coincidence ($k = 1.0$ and .2) are considered.

$$W_{AA} = \frac{K_2(K_2 - W_{aa})}{W_{aa}(4K_1^2 - 1) + K_2} \tag{12}$$

separates area C which represents populations with less heterozygosity than would be found in a Hardy-Weinberg population, from D representing populations of greater heterozygosity.

Thus equations (4) through (12) represent the genetic structure of all possible parthenogenetic populations which reproduce by either or both mechanisms 3 and 4. The phase diagrams, Figures 5 and 6, are visual representations of some of these populations where specific values have been chosen for E_1, E_2, and γ. Some sample values of equilibrium heterozygosity (R_{eq}) for these phase diagrams are given in the right column of Figures 5 and 6 and in Figure 7.

Although representing a wide range of conditions, these diagrams do not consider two extreme conditions described by the equations: (1) absolute linkage ($\gamma \to 0$); and (2) independent assortment of the locus and kinetochore ($\gamma \to 2/3$). As absolute linkage has been stated to maintain heterozygosity in species reproducing by central fusion (CARSON 1967a), these extremes will be treated separately for central and terminal fusion.

The equilibrium conditions for a population reproducing solely by central fusion, derived by setting $E_2 = 1$ and $E_1 = 0$ in equation (6) and (7) and substituting these values into equation (8), is given by:

$$R_{eq} = \frac{1}{\dfrac{W_{AA}\gamma}{4(1 - \gamma/2 - W_{AA})} + \dfrac{W_{aa}\gamma}{4(1 - \gamma/2 - W_{aa})} + 1} \tag{13}$$

The influence of absolute linkage upon equilibrium in such populations can be observed by allowing $\gamma \to 0$ in equation (13). If W_{AA} and $W_{aa} < 1$, then $R_{eq} \to 1$. On the other hand, if W_{AA} and $W_{aa} = 1$, the amount of heterozygosity at equilibrium will be exactly the same as at the initiation of "inbreeding," since heterozygotes no longer contribute to the proportion of homozygotes produced each generation.

The equilibrium condition for genes that segregate independently from their kinetochores is derived by substituting $\gamma = 2/3$ into equation (13) and is given by:

$$R_{eq} = \frac{1}{\dfrac{W_{AA}}{6(2/3 - W_{AA})} + \dfrac{W_{aa}}{6(2/3 - W_{aa})} + 1} \tag{14}$$

From this equation, we see that R_{eq} may have values from $1 \to 0$ as W_{AA} and W_{aa} take on values from $0 \to 2/3$.

The equilibrium condition for a population reproducing solely by terminal fusion, derived by setting $E_2 = 0$ and $E_1 = 1$ in equation (8), is given by:

$$R_{eq} = \frac{1}{\dfrac{W_{AA}(1 - \gamma)}{2(\gamma - W_{AA})} + \dfrac{W_{aa}(1 - \gamma)}{2(\gamma - W_{aa})} + 1} \tag{15}$$

The influence of absolute linkage upon such populations can be observed by allowing $\gamma \to 0$ in equation (15). Regardless of the value of W_{AA} and W_{aa} which, however, must be less than γ to maintain heterozygosity, $R_{eq} \to 0$ as $\gamma \to 0$. Thus, for populations which reproduce by terminal fusion, absolute linkage leads to complete homozygosity. For genes that segregate independently from their kinetochores, the equilibrium condition which is derived by substituting $\gamma = 2/3$ into equation (15), is identical to equation (14), demonstrating that central and terminal fusion produce the same result for independently segregating genes.

From the previous considerations of equations (13) and (15), we see that close linkage has an opposite effect upon equilibrium depending upon whether the populations reproduce by central or terminal fusion. These equilibrium values are also influenced by the effect of chromosome interference $(1 - k)$ on γ. Increased interference lowers the probability of double recombinations occurring between a given gene and its kinetochore and thus increases γ. It is evident, therefore, from a consideration of Figures 1 and 2, that increased interference will increase the frequency of homozygotes in species which reproduce entirely by central fusion, and decrease the frequency of homozygotes in species reproducing entirely by terminal fusion. Clearly the genetic composition at each parthenogenetic generation, and thus the rate of gain of homozygosity as well, is dependent upon γ, and γ is dependent upon both interference and linkage. It is therefore necessary to determine what proportion of central and terminal fusion minimizes the influences of interference and linkage on the population structure, as stated either in terms of the frequency of homozygotes or heterozygotes. This value of central fusion (E_2) can be obtained by letting k (the coefficient of coincidence) take the values k_1 and k_2 which give the values γ_1 and γ_2 for a given value of x (linkage). These values of γ yield two different values for K_2 (equation (7)) and are expressed by:

$$\begin{aligned} K_2' &= E_1\gamma_1 + E_2(1 - \gamma_1/2) \\ K_2'' &= E_1\gamma_2 + E_2(1 - \gamma_2/2) \end{aligned} \tag{16}$$

Setting $K_2' = K_2''$, eliminating the γ values and solving for E_2, where $E_1 = 1 - E_2$, we find that $E_2 = 2/3$. This means that interference has no effect upon the levels of homozygosity when central fusion (E_2) occurs in 2/3 and terminal fusion (E_1) occurs in 1/3 of the eggs. Similar arguments can be stated concerning the relationship of linkage (x) with respect to γ; consequently, this proportion eliminates the influence of both linkage and interference upon the levels of homozygosity.

From these considerations, we may describe parthenogenetic populations which reproduce by either or both mechanisms 3 and 4 by the following (model I): (1) equation (8) represents the general equilibrium conditions for R_{eq} under all conditions; (2) if all progeny have equal fitness, the population will be completely homozygous at equilibrium; (3) if the gene is absolutely linked to the kinetochore and the population reproduces by central fusion (mechanism 3), $R_{eq} \to 1$ where W_{AA} and $W_{aa} < 1$, or, $R_{eq} = R_0$ where W_{AA} and $W_{aa} = W_{Aa} = 1$;

(4) if the gene is absolutely linked to the kinetochore and the population reproduces by terminal fusion (mechanism 4), the population will be totally homozygous at equilibrium; (5) as $\gamma \to 2/3$, which represents independent segregation of a gene and its kinetochore, the equilibrium value of heterozygotes is given by equation (14) and applies to all populations reproducing by either or both mechanisms 3 and 4; (6) all equilibrium states can be represented by equilibrium phase diagrams derived from equations (8) through (12); (7) where $E_2 = 2/3$, linkage and interference have no effect upon equilibrium states; (8) these equilibrium states are independent of the initial values of P (frequency of AA), Q (frequency of aa), and R (frequency of Aa).

Model II: If a population reproduces by mechanism 5 in which zygoidy is restored following completely abnormal meiotic divisions (Figure 3) and zygoid selection occurs (Figure 4, process 3), the recurrent equations are given by:

$$\begin{aligned} P_{n+1} &\propto (P_n + R_n/6)W_{AA} \\ Q_{n+1} &\propto (Q_n + R_n/6)W_{aa} \\ R_{n+1} &\propto (4R_n/6)W_{Aa} \end{aligned} \tag{17}$$

The equilibrium equations from such a population with $W_{Aa} = 1$ derived as were equations (4), (5), and (8) are:

$$P_i = \frac{R_i W_{AA}}{6(2/3 - W_{AA})} \tag{18}$$

$$Q_i = \frac{R_i W_{aa}}{6(2/3 - W_{aa})} \tag{19}$$

$$R_{eq} = R_i = \frac{1}{\dfrac{W_{AA}}{6(2/3 - W_{AA})} + \dfrac{W_{aa}}{6(2/3 - W_{aa})} + 1} \tag{20}$$

A comparison of equations (14) and (20) shows that for individual loci the equilibrium values for mechanism 5 are equivalent to the values for mechanisms 3 and 4 where $\gamma \to 2/3$. The boundary conditions of the phase diagrams for this kind of parthenogenetic reproduction at $R_{eq} = 0$ are given by:

$$\begin{aligned} &W_{AA} = 2/3 \\ &W_{aa} = 2/3 \\ &W_{AA} = W_{aa} \text{ (where } W_{AA} \text{ and } W_{aa} > 2/3) \end{aligned} \tag{21}$$

and the boundary which satisfies the condition of Hardy-Weinberg equilibrium is given by:

$$W_{AA} = \frac{2 - 3W_{aa}}{3 - 4W_{aa}} \tag{22}$$

The single phase diagram described by these equations is given in Figure 8.

From these considerations, the following conclusions can be made concerning populations reproducing by mechanism 5 (model II): (1) equation (20) repre-

sents the general equilibrium conditions for R_{eq} under all conditions; (2) if $W_{AA} = W_{aa} = W_{Aa} = 1$, the population at equilibrium is completely homozygous; (3) linkage and interference play no role with respect to the equilibrium; (4) the equilibrium of any population can be represented by a phase diagram where boundary conditions are given by equations (21) and (22).

Population structures: The deterministic models I and II describe the genetic structure of populations of parthenogenetic species which restore zygoidy: (1) by mechanism 3 (Figure 1); (2) by mechanism 4 (Figure 2); (3) by either or both mechanisms 3 and 4; and (4) by mechanism 5 (Figure 3). These models plus the mapping function and the recurrent equation (equations (1), (2), and (4), NACE, RICHARDS and ASHER 1970) for the calculation of successive fixation indices (F) were used to determine the genetic structures of several parthenogenetic populations at equilibria conditions defined for each of these populations by equations (8) (model I) and (20) (model II).

RESULTS AND DISCUSSION

Model I: The results of calculations for parthenogenetic populations of model I are as follows. In the absence of selection, the gain in homozygosity occurs at a very rapid rate in forms reproducing with central fusion (E_2), terminal fusion (E_1), or a combination of these mechanisms (Table 1 and Figure 9). These results confirm previous predictions made by many investigators and reported in part by

TABLE 1

The influence of interference (1 — k) *upon the rates of increase in homozygosity in parthenogenetic species reproducing by either or both central and terminal fusion as indicated by the fixation indices* (F) *at each generation for a locus 20 map units from the kinetochore*

$W_{AA} = W_{Aa} = W_{aa} = 1$

E_1*=	1.0		.7		.5		.3		0	
E_2=	0		.3		.5		.7		1.0	
Generations k =	1.0	.2	1.0	.2	1.0	.2	1.0	.2	1.0	.2
0	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
1	.699	.628	.535	.495	.425	.407	.315	.319	.105	.186
2	.910	.861	.783	.745	.669	.648	.531	.536	.278	.318
3	.973	.946	.899	.871	.810	.791	.679	.684	.387	.461
4	.992	.981	.953	.935	.891	.876	.780	.784	.479	.561
5	.997	.993	.978	.967	.937	.927	.849	.853	.557	.643
6	.999	.997	.990	.983	.964	.956	.897	.900	.623	.710
7		.999	.995	.992	.979	.974	.929	.932	.680	.764
8			.998	.996	.988	.985	.951	.954	.729	.808
9				.998	.993	.991	.967	.968	.769	.843
10					.996	.995	.977	.978	.804	.873
20						.999	.999	.999	.962	.981
30									.992	.998

* E_1 = the proportion of eggs reproducing by terminal fusion; E_2 = the proportion of central fusion; k = the coefficient of coincidence.

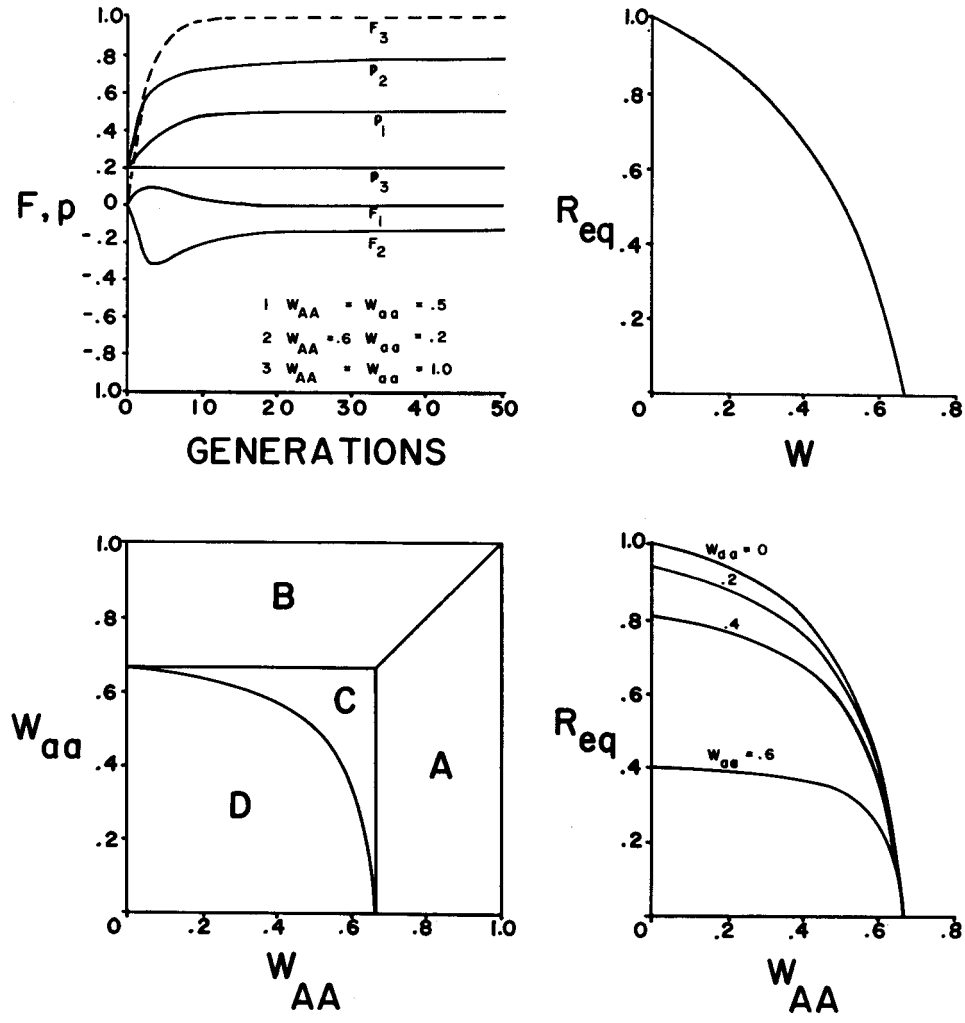

FIGURE 8.—Equilibrium phase diagram with corresponding values of R_{eq} (equilibrium heterozygosity), fixation indices (F), and the frequencies of the gene A (p) for various parthenogenetic populations reproducing according to mechanism 5 (model II, Figure 3).

NACE, RICHARDS and ASHER (1970). They are true for all loci in species which reproduce by terminal fusion regardless of linkage. For those populations reproducing by central fusion, all loci will also become completely homozygous, except those absolutely linked to the kinetochore. In practice, however, even these loci may become homozygous as altered adjacent nucleotides (in bacteria) show approximately .001 percent recombination (GUEST and YANOFSKY 1966).

The rate at which this homozygosity is attained is shown in Figure 9, which indicates that populations reproducing by central fusion approach complete homozygosity more slowly than do those using terminal fusion or those repro-

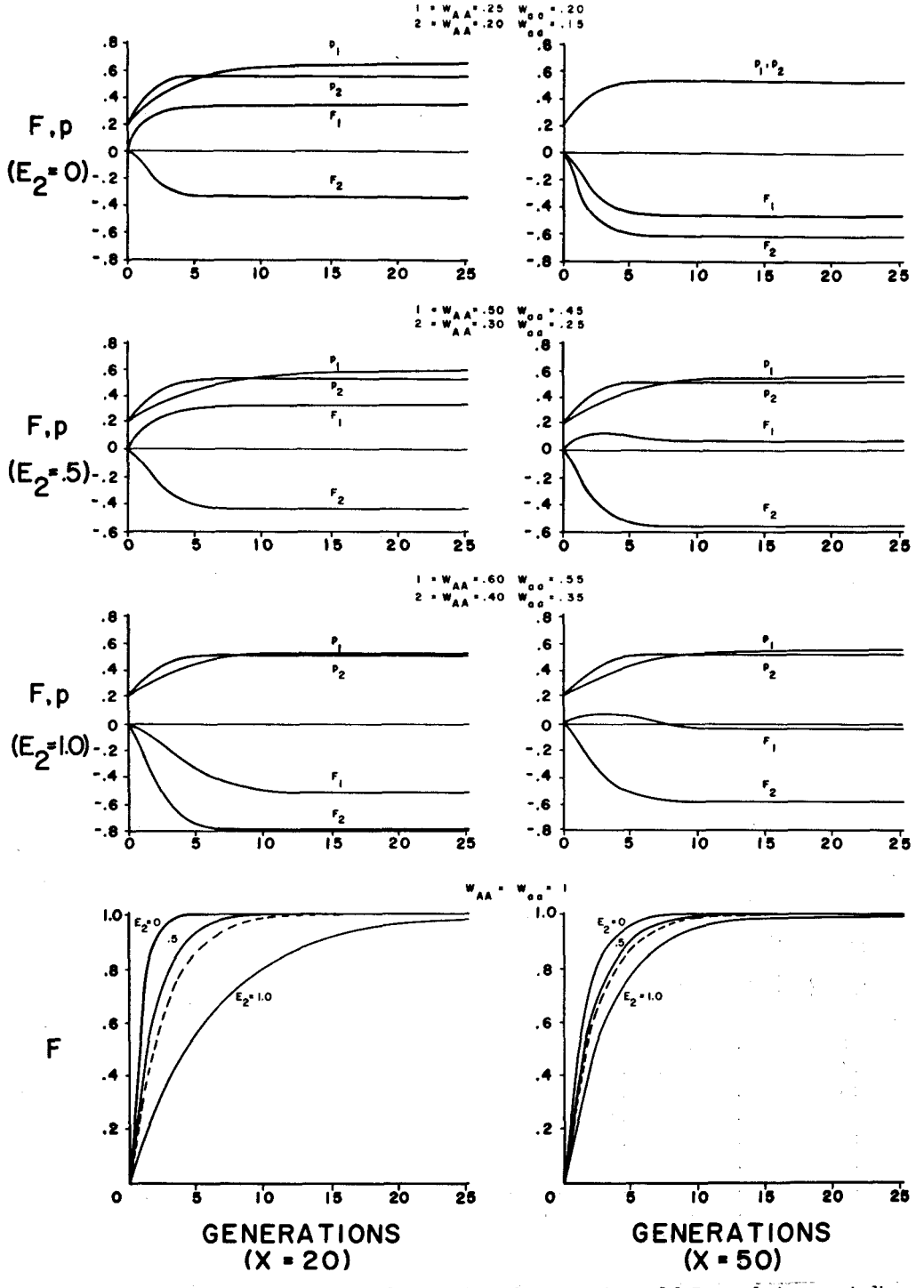

FIGURE 9.—The approach to equilibrium of parthenogenetic model I populations as indicated by the fixation indices (F) and the frequency of the gene A (p) for two values of linkage ($x = 20$ and 50 map units), three values of central fusion ($E_2 = 1.0$, .5, and 0), one value of the coefficient of coincidence ($k = 1.0$), and various values of W_{AA} and W_{aa}. The dashed line ($W_{AA} = W_{aa} = 1$) represents the gain in homozygosity where the gene A segregates independently of its kinetochore or where $E_1 = 1/3$ and $E_2 = 2/3$.

ducing by selfing (Table 10; NACE *et al.* 1970). Table 1 also demonstrates that interference has a different effect upon the rates of "inbreeding" depending upon the mode of reproduction. In the case of populations using central fusion ($E_2 = 1$), interference enhances the rate of gain of homozygosity; in terminal fusion ($E_1 = 1$), this rate is retarded (Table 1). However, as derived from equation (16) and seen in Table 2, neither interference nor in fact linkage affects the gain in homozygosity when the proportion of central fusion in model I is ⅔ ($E_2 = ⅔$). The rate of gain of homozygosity in such a population is equivalent to the rate either in model I where γ approaches ⅔ (independent segregation of the gene and kinetochore), or in model II (compare the dashed curves in Figures 8 and 9). Considering model I, the homozygosity gained each generation ($1 - \gamma$ for terminal fusion and $\gamma/2$ for central fusion), with few exceptions, greatly exceeds the mutation rate, thus mutation is not a force which could maintain heterozygosity in these parthenogenetic species.

If, on the other hand, parthenogenetic reproduction is accompanied by a significant heterozygote advantage or by experimental selection for heterozygosity (as with the establishment of "congenic" strains of amphibians, NACE 1968; NACE, RICHARDS and ASHER 1970), heterozygosity can be maintained in parthenogenetic populations as it is in selfing and mixed selfing and random mating populations (HAYMAN and MATHER 1953; HAYMAN 1953; WORKMAN and JAIN 1966; ALLARD, JAIN and WORKMAN 1968). The amount of heterozygosity maintained

TABLE 2

The influence of interference and linkage upon population equilibria as indicated by values of W_{AA} *and* W_{aa} *at the boundary where* $R_{eq} = 0$ *as in the equilibrium phase diagrams* (Figure 5) *for ten linkage values* (x), *six values of central* (E_2) *and terminal fusion* (E_1) *and two values of coincidence* (k)

	E_1 =	1.0		.8		.6		.333*		.2		0	
linkage distance in map units	E_2 =	0		.2		.4		.666		.8		1.0	
	k =	1.0	.2	1.0	.2	1.0	.2	1.0	.2	1.0	.2	1.0	.2
5		.093	.098	.265	.269	.437	.439	.667	.667	.781	.780	.954	.951
10		.173	.194	.321	.335	.469	.472	.667	.667	.765	.761	.914	.903
15		.242	.285	.369	.400	.497	.514	.667	.667	.752	.743	.879	.875
20		.301	.375	.411	.461	.520	.549	.667	.667	.740	.726	.850	.814
25		.352	.455	.446	.519	.541	.582	.667	.667	.720	.709	.824	.772
30		.396	.533	.477	.573	.558	.613	.667	.667	.721	.693	.802	.734
35		.433	.604	.503	.623	.573	.642	.667	.667	.713	.679	.783	.698
40		.466	.669	.526	.668	.586	.667	.667	.667	.707	.666	.767	.666
45		.494	.724	.546	.707	.598	.690	.667	.667	.701	.655	.753	.638
50		.518	.707	.563	.739	.607	.708	.667	.667	.696	.646	.741	.615

* A value of $E_1 = 1/3$ has the effect of eliminating the influence of linkage and interference ($1 - k$) upon the strength of selection needed to maintain heterozygosity ($R_{eq} > 0$) in parthenogenetic species reproducing by model I.

is dependent upon: (1) linkage and interference; (2) proportion of central and terminal fusion; and (3) degree of selection. Sample equilibrium phase diagrams have been presented in Figures 5 and 6 which describe numerous conditions leading to the maintenance of heterozygosity in parthenogenetic populations reproducing according to model I. The fitness values of the homozygotes needed to maintain heterozygosity at any level are given by W_{AA} and $W_{aa} < K_2$. Table 2 gives these values of fitness where $R_{eq} = 0$. Smaller values than these will allow heterozygosity to be maintained. In terms of the coefficient of selection ($S = 1 - W$), these values indicate that selection against homozygotes with intensities of S_{AA} and $S_{aa} > .05$ to .91 could maintain heterozygosity under the conditions described in Table 2. Thus a comparison of these values and those indicated in Figures 5, 6, and 9, shows that central fusion requires a smaller selection coefficient (S_{AA} and $S_{aa} = 0$ to .33) to maintain a given level of equilibrium heterozygosity than is required by terminal fusion (S_{AA} and $S_{aa} = 1$ to .33). The approach to this equilibrium is represented by the curves of Figure 9, which describe the progress of inbreeding at successive generations for sample model I populations. It is noted that equilibrium is attained rapidly (within 10 to 15 generations for the examples given).

Model II: As in the case of central and terminal fusion, parthenogenetic reproduction using a totally aberrant meiosis (Figure 3, model II) leads to complete homozygosity in the absence of selection (Figure 8). With selection, however, heterozygosity can be maintained. As in the case of model I where $\gamma \rightarrow \frac{2}{3}$ or where $E_2 = \frac{2}{3}$, the coefficient of selection needed to maintain heterozygosity in model II must be S_{AA} and $S_{aa} > .33$. Thus with respect to the ability to maintain heterozygosity, it would appear that reproduction by mechanisms 4 and 5 would be evolutionarily more costly than would reproduction by mechanism 3.

Evidently, heterozygosity can be maintained in at least three ways in an automictic parthenogenetically reproducing species: (1) by absolute linkage to the kinetochore in species which restore zygoidy by central fusion; (2) by chromosomal rearrangements; and (3) by selection.

Evolutionary implications: The abandonment of sexuality has in general been considered an evolutionary detriment. This conclusion stems from the idea that asexual reproduction necessarily eliminates the genetic plasticity that would allow adaptation to new environmental conditions. According to this idea, automictic parthenogenetic reproduction, representing the strongest form of natural "inbreeding," should eliminate this genetic plasticity in a very few generations. Species using this mode of reproduction should therefore represent evolutionary dead ends, as they should lack genetic plasticity.

The data of Table 2 challenge this view and show that for central fusion, loci within 10 map units of the kinetochore *can* be maintained in a heterozygous condition when S_{AA} and $S_{aa} > .09$. This value is not considered excessive when compared to selection coefficients observed in various populations of random mating animals ($S = .3$ and .7) (DOBZHANSKY 1947) and in populations of selfing and random mating plant species ($S = .3$ to .7) (WORKMAN and JAIN 1966; ALLARD, JAIN and WORKMAN 1968). In order to maintain heterozygosity for

these same loci in populations reproducing by terminal fusion, S_{AA} and $S_{aa} > .8$. Such values, though high, are in the range reported for plant inbreeding systems (WORKMAN and JAIN 1966; ALLARD, JAIN and WORKMAN 1968) and may be tolerated by parthenogenetically reproducing animal populations.

Thus, two general conclusions may be drawn regarding parthenogenetic populations: (1) heterozygosity *can be maintained* where overdominance exists; and (2) populations reproducing by central fusion can sustain heterozygosity at a lower cost to the population than can populations reproducing by other parthenogenetic mechanisms.

From these conclusions several predictions can be made. First, if an organism has a higher fitness by having a portion of its genome heterozygous, then within a given population, parthenogenetic reproduction by central fusion should have a selective advantage over reproduction by terminal fusion. Thus we would expect more species to have evolved the parthenogenetic mechanism of central fusion or its equivalent inhibition of meiosis I than to have evolved the other mechanisms of parthenogenesis considered in this paper. Second, provided selection favors heterozygosity, these populations should be polymorphic for some loci, probably those more closely linked to the kinetochore. This prediction: (1) contradicts the statement that these species represent evolutionary dead ends; (2) confirms CARSON's opinion (1967a) concerning the ability of central fusion to maintain heterozygosity; and (3) suggests selection in addition to absolute linkage and chromosomal rearrangement (CARSON 1967a) as a third way of maintaining heterozygosity in parthenogenetic species.

Several experiments can be suggested to test these predictions. First, parthenogenetic species could be surveyed cytologically to determine whether central fusion occurs more frequently than other automictic reproductive mechanisms. Second, populations of parthenogenetic species could be surveyed to determine whether genetic polymorphism exists. If a population lacks chromosomal rearrangements, the level of heterozygosity observed could be used to determine directly the values of W_{AA} and W_{aa}. Given the theoretical and actual genetic structure of these parthenogenetic populations, one can then ask whether or not selection favors parthenogenetic populations which have many polymorphic loci.

The above considerations allow the description of the genetic structure of preexisting parthenogenetic populations. These models could also be used to describe the gene flow associated with the evolution of parthenogenesis in bisexual species. CARSON (1967b) has experimentally studied this evolutionary process by developing various strains of Drosophila which have a very high incidence of spontaneous parthenogenesis. This step in the evolution of a parthenogenetic species can be described in terms of models I and II. By substituting $\bar{\gamma}$ (NACE, RICHARDS and ASHER 1970) for γ in these models, the number of genes involved in the selection for parthenogenetic reproduction can be estimated. Additional steps in this evolutionary process can be described if models I and II are generalized to include mixed modes of reproduction, parthenogenesis accompanied by random or sibling matings, as well as the ploidy values of the species involved. These generalizations

will be developed at a later time and will include both one- and two-locus models.

Thus, the data presented here indicate that automictic parthenogenetic reproduction can sustain varying degrees of genetic plasticity provided selection favors the heterozygote. This plasticity would be maintained at a cost which is higher than that typically required for sexually reproducing species. However, the successful use of parthenogenesis must balance at least three factors: (1) selection favoring asexual reproduction itself; (2) selection favoring general genetic plasticity; and (3) cost of maintaining this plasticity. If these asexually reproducing species are evolutionary dead ends, they are so because they cannot maintain the appropriate balance of these factors.

Artificial parthenogenesis: The previous considerations have been restricted to natural parthenogenetic populations. These findings, however, equally apply to bisexual species which, by laboratory manipulations, can reproduce by parthenogenesis. If the aim of the research is to produce "inbred" strains (NACE 1968; NACE, RICHARDS and ASHER 1970), the most effective means of reproduction is terminal fusion or inhibition of meiosis II. Alternatively, fusion of cleavage nuclei or inhibition of first cleavage could be used, but because severe "inbreeding" depression in the first generation leads to low productivity (NACE and RICHARDS, personal communication), this mechanism cannot be efficiently applied to the organisms studied, at least in the initial generations. The sequential application of inhibition of meiosis II and inhibition of first cleavage, however, should minimize this problem.

As an "inbreeding" system, inhibition of meiosis II, in the absence of selection, leads to complete homozygosity faster than do other conventional breeding systems used to develop inbred strains of mice and other vertebrates. With selection, this mode of reproduction would lead to the development of "congenic" strains. At present, the application of such an artificial breeding system to vertebrates has been successful only in amphibians (KAWAMURA 1939; KAWAMURA and NISHIOKA 1967; NACE and RICHARDS 1969; NACE, RICHARDS and ASHER 1970; MORIWAKI 1963), although PURDOM (1969), whose work was considered in NACE, RICHARDS and ASHER (1970), has attempted an application to fish and gives reference to others who have attempted it.

The author wishes to express his deepest thanks to Dr. GEORGE W. NACE for placing the resources of the Amphibian Facility at the author's disposal, and to Dr. NACE and Dr. CHARLES F. SING for their critical evaluations and guidance during the preparation of this manuscript.

SUMMARY

It has been claimed that parthenogenesis in animals is an evolutionary dead end, as the animals should lack genetic plasticity. To test this claim, this paper presents a rigorous mathematical treatment of the gain in homozygosity in diploid parthenogenetic species which restore zygoidy by: (1) central fusion (inhibition of meiosis I); (2) terminal fusion (inhibition of meiosis II); and (3) by a totally aberrant meiotic division. The models generated consider: (1) linkage and chro-

mosome interference; (2) mechanisms of restoring zygoidy; and (3) selection against homozygotes.——In the absence of selection all populations become completely homozygous. This state is usually attained in less than 10 generations. In the presence of selection with heterozygotes at an advantage, equilibrium heterozygosity is maintained at various levels depending upon: (1) strength of linkage; (2) mode of reproduction; and (3) intensity of selection.——Populations which use central fusion as a mechanism of restoring zygoidy should be able to sustain equilibrium heterozygosity at a lower cost to the population than do parthenogenetic populations using any other mechanism. A mechanism using a mixture of ⅔ central fusion and ⅓ terminal fusion has the effect of eliminating the influence of linkage and interference upon the rates of gain of homozygosity and values of equilibrium heterozygosity. The evolutionary and experimental implications of these findings are briefly considered.——There then appear to be at least three ways in which heterozygosity *can be maintained* in parthenogenetic forms considered at this time: (1) absolute linkage to the kinetochore in species restoring zygoidy by central fusion; (2) chromosomal rearrangements; and (3) selection. These findings appear to contradict the general opinion that parthenogenetic species represent an evolutionary dead end because of their inability to maintain genetic plasticity.

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