Original Article

Gene-mating dynamic evolution theory II: global stability of N-gender-mating polyploid systems

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Abstract
Extending the previous 2-gender dioecious diploid gene-mating evolution model, we attempt to answer “whether the Hardy–Weinberg global stability and the exact analytic dynamical solutions can be found in the generalized N-gender N-polyploid gene-mating system with arbitrary number of alleles?” For a 2-gender gene-mating evolution model, a pair of male and female determines the trait of their offspring. Each of the pair contributes one inherited character, the allele, to combine into the genotype of their offspring. Hence, for an N-gender N-polypoid gene-mating model, each of N different genders contributes one allele to combine into the genotype of their offspring. We exactly solve the analytic solution of N-gender-mating $(n+1)$-alleles governing highly nonlinear coupled differential equations in the genotype frequency parameter space for any positive integer N and $n$. For an analogy, the 2-gender to N-gender gene-mating equation generalization is analogs to the 2-body collision to the N-body collision Boltzmann equations with continuous distribution functions of discretized variables instead of continuous variables. We find their globally stable solution as a continuous manifold and find no chaos. Our solution implies that the Laws of Nature, under our assumptions, provide no obstruction and no chaos to support an N-gender gene-mating stable system.

Keywords Population genetics and evolutionary biology · Chaotic dynamics · Blood types and biological physics · Exactly solvable models · Time-dependent nonlinear differential equations · Hardy-Weinberg manifold

Introduction
Dynamical (time-dependent) evolution of population percentages labeled by biological traits or genetic characteristics in a population system is a primary focus of studies for population genetics and evolutionary biology (Wright 1921; Fisher 1930; Crow and Kimura 1970; Waltman 1983; Edwards 2000; Ewens 2004 and references therein). Their governing laws involve genetics, which can be traced back to Mendel’s foundational work (Mendel 1865). In a previous work Wang and Chen (2020), we had surveyed the time evolution of genotype frequency in a 2-gender dioecious diploid population system. We derive our governing equations based on our four fundamental assumptions,

(a) The mating of gene-holders is (approximately) closed in a population system.
(b) The mating probability for certain gene-type to another gene-type, due to average-and-random mating mechanism, is proportional to the product of their population (e.g., quadratic forms for 2-gender, cubic forms for 3-gender, and their generalizations: degree-N polynomial forms for N-gender mating.).
(c) The probability of a gene-type for newborn generation obeys the Mendelian inheritance.
(d) The accumulation of human population obeys the exponential growth law, for both the birth and the death evolution.

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We had derived the governing equations in the parameter space of the genotype frequencies, and we had solved the analytical solution of the governing equations within a single locus and arbitrary number of alleles mating process. However, our previous work only focus on 2-gender mating, normally one male and one female. We can analytically prove the global stability and Hardy–Weinberg equilibrium (Hardy 1908; Weinberg 1908). For biological and mathematical interests, we ponder whether the N-gender case, where N is an arbitrary integer number, will bring interesting and surprising new results. In other words, we like to consider a mating system of N different genders. The mating process of the system will be successful if and only if there is a group of N different genders participate in the mating process. For a certain genotype (or a biological trait), each of these different N genders contributes an allele, together combine into the inherited genotype of their offspring.

The questions we ask and aim to address are: Whether 2-gender mating is special for \( N = 2 \), so that it assures the global stability for the system under time evolution? Whether 2-gender mating is special so that there exist exact analytic solutions? Whether there is chaos for N-gender mating system at some integer N? Is it possible to solve the analytic solution for arbitrary N? Is there a specific integer number M, such that for gender number smaller than M, the system has the global stability; if the gender number is larger than M, then the chaos appears (from global stability to chaos)? If so, what is the integer M?

Since the 1-gender mating is just a trivial asexual reproduction, and the 2-gender mating is a case with a global stable solution, one might expect that the 2-gender mating is a transitional case for the dynamical properties of N-gender mating system. In other words, for \( N > 2 \), there might exist chaos or more complicated time-evolution phase diagrams. However, as we will show later, for the general N-gender gene-mating system, there is always a global stable manifold as long as the system satisfies the previous four assumptions. Throughout the article, we focus on the standard equations without considering the mutation and natural selection. From the mathematic viewpoint, the highly symmetric governing equations result in a continuous global stable manifold. This higher dimensional curved manifold is a global stable attractor, under time evolution attracting all points in the Euclidean fiber attached at every manifold point. The stable manifold and the fibers together form a fiber bundle completely filling in the whole genotype-frequency parameter space. We solve the analytical solutions exactly for the general N-gender \( (n + 1) \)-alleles gene-mating system (see Wang and Chen 2020 and the footnote 1).

One essential remark is that the coefficients of the governing equations for N-gender mating can be derived explicitly from the coefficient of \( \sum_{k_0+k_1+\cdots+k_n=N}^{N} \binom{N}{k_0,k_1,\ldots,k_n} \) in the well-known multinomial theorem:

\[
(G_0 + G_1 + \cdots + G_n)^N = \sum_{k_0+k_1+\cdots+k_n=N}^{N} \binom{N}{k_0,k_1,\ldots,k_n} G_0^{k_0} G_1^{k_1} \cdots G_n^{k_n}.
\]

Here we denote the inherited character (commonly known as the allele) as \( G_j \) where \( j = 0, 1, \ldots, n \) for \( (n + 1) \) types of alleles. We can count the number of population carrying a certain genotype \( G_0^{k_0} G_1^{k_1} \cdots G_n^{k_n} \) (from the set of alleles \( G_j \) inherited from each of the N-gender parents) as \( G_0 \cdots G_1 \cdots G_n \) where \( k_i \) is an labeling inherited with this specific allele \( G_j \). So we have a map from the set of alleles to a certain genotype, then to a total number of population with this genotype:

\[
G_0^{k_0} G_1^{k_1} \cdots G_n^{k_n} \rightarrow G_0 a_0 a_1 \cdots a_m \cdots a_m
\]

So far we only define our notations, later in main sections, we will write down the governing dynamical equations for the population evolution as in Wang and Chen (2020). We will also renormalize the \( G_j \) via dividing it by the total population \( P \),

\[
\sum_{k_0+k_1+\cdots+k_n=N}^{N} G_0 \cdots G_1 \cdots G_n \equiv P,
\]

and redefine the \( G' \) as in the discussion below, we will explicitly write down the coefficients for the simple case of \( N = 1, 2 \), as in second and third sections and in Wang and Chen (2020). We can also explicitly write down

1. For example, in Wang and Chen (2020), the \( (n + 1) \)-alleles can be regarded as \( n \) dominant alleles and 1 recessive allele in a single locus. We can denote the 1 recessive allele as \( G_0 \), and the \( n \) dominant alleles as \( G_1, \ldots, G_n \).

2. For the sake of keeping the minimal amount of notations, later in all sections, we will map the genotype population \( G_j \) to genotype frequency \( G_j' \) \( \equiv \frac{G_j}{P} \), then rename the genotype frequency as \( G_j' \).
the coefficients of the governing equations for N-gender mating (for $N = 3$ in fourth section and for a general $N$ in fifth section) from the coefficient of $\left(k_0, k_1, \ldots, k_N\right)$ of multinomial theorem, but we leave this coefficient implicit to simplify the notations. Another remark is that our governing equation shall also be viewed as generalizing the diploid system to the N-polyploid system. For the N-gender-mating N-polyploid system, if the previous four assumptions are obeyed, we prove that the global stability of genotype frequencies can be shown to be robust even for N-gender-mating.

1-Gender gene-mating model (asexual)

Here we start from the asexual mating system. There exists only one gender in a system, such that each gender could self-produce its offspring exactly the same as itself. Then, we denote the population number of certain genotype as $G_a$, where $a$ is arbitrary integer number. Thus, parallel to the work Wang and Chen (2020), based on the assumptions done in first section, we can derive the governing equations for population

$$\frac{d}{dt} G_a = k_b G_a - k_d G_a,$$

where $k_b$ is birth rate and $k_d$ is death rate. Apparently we can normalize the $G_a$ by the total population $P$, and we will relabel

$$\frac{G_a}{P} \rightarrow G_a$$

as the genotype frequency. Hereafter, we will re-parameterize the equation in terms of the genotype frequency $G_a$, and we obtain the governing equations for genotype frequencies

$$\frac{d}{dt} G_a = 0.$$

Hence, any point in the genotype frequency parameter space is stable for 1-gender asexual system. The genotype frequency is within the range of $[0, 1]$.

2-Gender gene-mating model

This section briefly summarizes the analytic solution studied in our previous work Wang and Chen (2020). We had studied the governing equations for genotype frequencies:

$$\frac{d}{dt} G_{aa} = k_b \left( G_{aa} + \sum_{j=0}^{n} G_{aj} + \frac{1}{2} \sum_{i \neq a, j \neq a} G_{ai} G_{aj} - G_{aa} \right),$$

$$\frac{d}{dt} G_{a\beta} = k_b \left( 2G_{a\beta} G_{\beta\beta} + \sum_{i=0}^{n} G_{ai} G_{\beta\beta} + \sum_{j=0}^{n} G_{aa} G_{\beta\jmath} + \frac{1}{2} \sum_{i=0}^{n} \sum_{j=0}^{n} G_{ai} G_{\beta\jmath} - G_{a\beta} \right).$$

Recall that the death rate $k_d$ has no net effect on the genotype frequencies, because it is a universal linear effect on each genotype population which does not change genotype frequency. Note that $G_{aa}$ means the genotype frequency contributed from the same alleles $a$ from both parents. $G_{a\beta}$ means the genotype frequency contributed from the alleles $a$ and $\beta$ from each of the parents, respectively. Hereafter, we will identify $G_{a\beta}$ and its $G_{a\alpha}$ as the same genotype frequency, therefore the governing equations have taken account of the combined effects of $G_{a\beta}$ and its $G_{a\alpha}$. We had found an exact analytic parameterization of the global stable manifold:

$$G_{aa, eq}(\theta) = \sum_{i=1}^{n} \left( \frac{\sin^2(\theta)}{(\cos(\theta) + \sin(\theta))^2} \right),$$

$$G_{a\beta, eq}(\theta) = \sum_{j=1}^{n} \left( \frac{\sin^2(\theta)}{(\cos(\theta) + \sin(\theta))^2} \right).$$

Her $\theta_i$ is within the range $[0, \pi/2]$. More conveniently, we find that a new parametrization of coordinates

$$G_{aa} = G_{aa, eq}(\theta) + \sum_{i=1, j \neq a}^{n} s_{ai},$$

$$G_{a\beta} = G_{a\beta, eq}(\theta) - 2s_{a\beta},$$

providing an inverse transformation mapping between the two kinds of parametrizations.
\[
\theta_k = \tan^{-1}\left( \left\{ \sum_{i=k}^{n} \left( 2G_{ki} + \sum_{j=0}^{n} G_{kj} \right) \right\} / \left( 2G_{k-1,k-1} + \sum_{j=0}^{n} G_{k-1,j} \right) \right), \quad 1 \leq k \leq n, \text{ with } n \text{ formulas}
\]

\[
s_{ij} \text{ can be solved from the following equations:
}\]

\[
\tan^2(\theta_k) = \frac{\sum_{i=k}^{n} G_{ij} - \sum_{j=0}^{n} s_{k-1,j}}{G_{k-1,k-1} - \sum_{j=0}^{n} s_{k-1,j}}, \quad 1 \leq k \leq n, \text{ with } n \text{ equations}
\]

\[
\tan(\theta_k) = \left( \sum_{i=k}^{n} (G_{mi} + 2s_{mi}) \right) / (G_{m,k-1} + 2s_{m,k-1}), \quad 2 \leq k \leq n, \quad 0 \leq m \leq k - 2, \quad \text{with } \binom{n}{2} \text{ equations}
\]

Given any given initial values of \( G_{ij} \) parameters as the input data and the starting point of time-evolution, we are able to find the final equilibrium point solution \( G_{ij,eq} \):

\[
\begin{align*}
G_{aa,eq} & = \frac{1}{4} \left( 2G_{aa} + \sum_{i \neq a} G_{ai} \right), \\
G_{a\beta,eq} & = \frac{1}{2} \left( 2G_{aa} + \sum_{i \neq a} G_{ai} \right) \left( 2G_{\beta\beta} + \sum_{i \neq \beta} G_{\beta i} \right),
\end{align*}
\]

By the above relation, we can simplify the inverse transformation, the function \( s_{\alpha\beta}(G_{ij}) \)

\[
\begin{align*}
\theta_{\mu+1} & = \tan^{-1}\left( \left\{ \sum_{\alpha=\mu+1}^{n} \left( 2G_{aa} + \sum_{i=0}^{n} G_{ai} \right) \right\} / \left( 2G_{\mu\mu} + \sum_{i=0}^{n} G_{\mu i} \right) \right), \quad 0 \leq \mu \leq n - 1, \text{ with } n \text{ formulas.}
\end{align*}
\]

\[
s_{\alpha\beta} = \frac{1}{2} (G_{\alpha\beta,eq}(G_{ij}) - G_{\alpha\beta}), \quad 0 \leq \alpha, \beta \leq n,
\]

Since the decoupled governing equations are the simple exponential-decay type differential equations, we obtain the exact solution of governing equations:

\[
\begin{align*}
\frac{dx_{a\beta}}{dt} & = -k_{a\beta} s_{a\beta}, \quad 0 \leq \alpha < \beta \leq n, \\
\frac{dx_{a\beta}}{dt} & = 0, \quad 1 \leq \mu \leq n.
\end{align*}
\]

The importance of the new parametrization is that the original governing equations are simplified to a set of decoupled governing equations in the new coordinates:

\[
\begin{align*}
\frac{dx_{a\beta}}{dt} & = -k_{a\beta} s_{a\beta}, \quad 0 \leq \alpha < \beta \leq n, \\
\frac{dx_{a\beta}}{dt} & = 0, \quad 1 \leq \mu \leq n.
\end{align*}
\]

Since the decoupled governing equations are the simple exponential-decay type differential equations, we obtain the exact solution of governing equations:

In the following sections, we will generalize the 2-gender gene-mating model to N-gender gene-mating model.

### 3-Gender gene-mating model

Hereafter we do not bother to write down the coefficients of the governing equations, which could be easily determined by the multinomial theorem Eq. (1), the basic mating rules

\[
\begin{align*}
\frac{d}{dt} G_{aaa}(t) & = \sum_{0 \leq i \leq n} \tilde{a}_{aa} e^{-k_{aa}} G_{aa} G_{ii} - G_{aaa}, \\
\frac{d}{dt} G_{a\alpha\beta}(t) & = \sum_{0 \leq i \leq n} \tilde{a}_{a\alpha\beta} e^{-k_{a\alpha\beta}} G_{aa} G_{i\alpha} G_{\beta\beta} - G_{a\alpha\beta}, \\
\frac{d}{dt} G_{a\alpha\beta\gamma}(t) & = \sum_{0 \leq i \leq n} \tilde{a}_{a\alpha\beta\gamma} e^{-k_{a\alpha\beta\gamma}} G_{aa} G_{i\alpha} G_{i\beta} G_{\beta\gamma} - G_{a\alpha\beta\gamma},
\end{align*}
\]

where \( i_1 \leq i_2 \leq i_3; \ i_4 \leq i_5 \leq i_6; \ i_7 \leq i_8 \leq i_9 \). We should remember that there will be a permutation factor for \( G_{i_1 i_2 i_3} G_{i_4 i_5 i_6} G_{i_7 i_8 i_9} \), if genotypes of three genders are not the same. Again, we note that \( G_{a\alpha\beta\gamma} \) means the genotype frequency contributed from the alleles \( \alpha, \beta \) and \( \gamma \) from each of the three genders, respectively. Hereafter, we will identify

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\[ G_{\alpha\beta\gamma} \text{ and its index permutation } G_{\beta\alpha\gamma}, G_{\gamma\alpha\beta}, \text{ etc., as the same genotype frequency. In our notation, we will define the genotype frequency } G_{\alpha\beta} \text{ such that } \alpha \leq \beta \leq \gamma. \]

Interestingly, regardless of the nonlinear governing equations are generalized to the more complicated 3-gender cubic form (instead of the 2-gender quadratic form in third section), we can still solve the governing equations and its global stability. We find an analytic parametrization of a continuous global stable manifold as follows:

\[
G_{aaa,eq}(\theta_\mu) = \left[ \prod_{i=1}^{\alpha} \frac{\sin^3(\theta_i)}{(\cos(\theta_i) + \sin(\theta_i))^3} \right] \frac{\cos^3(\theta_{a+1})}{(\cos(\theta_{a+1}) + \sin(\theta_{a+1}))^3},
\]

\[
\begin{align*}
G_{aab,eq}(\theta_\mu) & = \left[ \prod_{i=1}^{\alpha} \frac{\sin^3(\theta_i)}{(\cos(\theta_i) + \sin(\theta_i))^3} \right] \frac{3 \cos^3(\theta_{a+1}) \sin(\theta_{a+1})}{(\cos(\theta_{a+1}) + \sin(\theta_{a+1}))^3} \\
& \cdot \left[ \prod_{j=a+2}^{\beta} \frac{\sin(\theta_j)}{\cos(\theta_j) + \sin(\theta_j)} \right] \frac{\cos^3(\theta_{\beta+1})}{(\cos(\theta_{\beta+1}) + \sin(\theta_{\beta+1}))^3}.
\end{align*}
\]

\[
\begin{align*}
G_{ab\beta,eq}(\theta_\mu) & = \left[ \prod_{i=1}^{\alpha} \frac{\sin^3(\theta_i)}{(\cos(\theta_i) + \sin(\theta_i))^3} \right] \frac{3 \cos^3(\theta_{a+1}) \sin^2(\theta_{a+1})}{(\cos(\theta_{a+1}) + \sin(\theta_{a+1}))^3} \\
& \cdot \left[ \prod_{j=a+2}^{\beta} \frac{\sin(\theta_j)}{\cos(\theta_j) + \sin(\theta_j)} \right] \frac{\cos^3(\theta_{\beta+1})}{(\cos(\theta_{\beta+1}) + \sin(\theta_{\beta+1}))^3}.
\end{align*}
\]

\[
\begin{align*}
G_{ab\gamma,eq}(\theta_\mu) & = \left[ \prod_{i=1}^{\alpha} \frac{\sin^3(\theta_i)}{(\cos(\theta_i) + \sin(\theta_i))^3} \right] \frac{2 \cos(\theta_{\beta+1}) \sin(\theta_{\beta+1})}{(\cos(\theta_{\beta+1}) + \sin(\theta_{\beta+1}))^2} \\
& \cdot \left[ \prod_{j=a+2}^{\gamma} \frac{\sin(\theta_j)}{\cos(\theta_j) + \sin(\theta_j)} \right] \frac{\cos(\theta_{\gamma+1})}{(\cos(\theta_{\gamma+1}) + \sin(\theta_{\gamma+1}))^2}.
\end{align*}
\]

\[
G_{aaa,eq} = \left( \frac{1}{3} \right)^3 \left[ 3G_{aaa} + 2 \sum_{i=0}^{n} G_{aai} + \sum_{0 \leq j \leq n} G_{aj} \right]^3,
\]

\[
G_{aab,eq} = \frac{3!}{2!1!1!} \left( \frac{1}{3} \right)^3 \left[ 3G_{aaa} + 2 \sum_{i=0}^{n} G_{aai} + \sum_{0 \leq j \leq n} G_{aj} \right]^2.
\]

\[
G_{ab\beta,eq} = \left( \frac{1}{3} \right)^3 \left[ 3G_{aaa} + 2 \sum_{i=0}^{n} G_{aai} + \sum_{0 \leq j \leq n} G_{aj} \right]
\]

\[
\begin{align*}
\theta_{\mu+1} & = \tan^{-1} \left\{ \sum_{a\mu+1}^{n} \left( \frac{3G_{aaa} + 2 \sum_{i=0}^{n} G_{aai} + \sum_{0 \leq j \leq n} G_{aj}}{3G_{a\mu} + 2 \sum_{i=0}^{n} G_{a\mu i} + \sum_{0 \leq j \leq n} G_{a\mu j}} \right) \right\},
\end{align*}
\]

\[
0 \leq \mu \leq n - 1, \ n \text{ formulas.}
\]

\[
s_{1\alpha\beta} = \frac{1}{2} (G_{aaa,eq}(G_{i\gamma}) + G_{aab,eq}(G_{i\gamma}) - G_{aa\beta} - G_{a\beta\gamma}),
\]

\[
\text{with } \binom{n + 1}{2} \text{ formulas.}
\]

\[
u_{1\alpha\beta} = \frac{1}{6} (G_{ab\beta,eq}(G_{i\gamma}) - G_{aa\beta} - G_{a\beta\gamma}, \text{ with } \binom{n + 1}{3} \text{ formulas.}
\]

Our next key step is deriving the decoupled governing equations in the new coordinates:
Finally, we obtain the exact analytic solution of governing equations for a 3-gender mating system:

\[
\frac{d\theta}{dt} = \frac{\partial}{\partial \theta} f(\theta, \phi, \psi, \theta, \phi, \psi),
\]

where we define \( \alpha_0 \equiv -1 \). All \( \theta \) are within the range \([0, \pi/2]\).

We extend the stable manifold through the following parametrized Euclidean fiber at each fixed point on the stable manifold. This procedure leads to our new parametrization of coordinates. For \( N \)-gender mating of \((n + 1)\) alleles, we separate the parametrization of fiber space to two cases, for \( N \) is an even integer and for \( N \) is an odd integer.

- **(1) For** \( N \in \text{even}, N = 2k \):

  There are 3 types of vectors spanning the extended Euclidean bundle space.

  \[
  \hat{s}_{i \alpha \beta} = \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right) - 2\hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right)
  \]

- **(2) For** \( N \in \text{odd}, N = 2k + 1 \):

  There are 3 types of vectors spanning the extended Euclidean bundle space.

  \[
  \hat{u}_{i \alpha \beta} = \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right) - \left( k + 1 - i \right) \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right)
  \]

**N-gender gene-mating model**

Now we will generalize the above analysis to the \( N \)-gender gene-mating model. Each genotype frequency parameter can be written as, \( G_{\alpha_1 \alpha_2 \cdots \alpha_m \alpha_{m+1} \cdots \alpha_n} \), each is within the range \([0, 1]\), and we find the existence of the global stable fixed points as a continuous manifold and the parametrization of the global stable manifold as:

\[
G_{\alpha_1 \cdots \alpha_m \alpha_{m+1} \cdots \alpha_n}(\theta_\gamma) = \left( \prod_{i=1}^{n} \prod_{j=1}^{n} \frac{\sin^2(\theta_{\gamma_1}) \sin(\theta_{\gamma_2}) \sin(\theta_{\gamma_3}) \cdots \sin(\theta_{\gamma_{n-1}}) \sin(\theta_{\gamma_n})}{\cos(\theta_{\gamma_1}) + \sin(\theta_{\gamma_1})^n} \right)^{N-1}...
\]

where \( n = n_1 + n_2 + \cdots + n_m = \sum_{i=1}^{n} \).

- **(2)** \( N \in \text{odd}, N = 2k + 1 \): There are 3 types of vectors spanning the extended Euclidean bundle space.

  - **(a) The symmetry type for** \( \alpha \leftrightarrow \beta \):

    \[
    \hat{m}_{\alpha \beta} = \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right) - \left( k + 1 - i \right) \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right)
    \]

  - **(b) The anti-symmetry type for** \( \alpha \leftrightarrow \beta \):

    \[
    \hat{u}_{i \alpha \beta} = \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right) - \left( k + 1 - i \right) \hat{G}_{\alpha \beta} \cdot \alpha \left( \alpha \beta \right) \left( \beta \right)
    \]

  - **(c) The mixed of multiple-genes (mixed type number \( \geq 3 \)) vector:**

    \[
    \hat{m}_{\alpha_1 \alpha_2 \cdots \alpha_m \alpha_{m+1} \cdots \alpha_n} = \left( \prod_{i=1}^{n} \prod_{j=1}^{n} \frac{\sin^2(\theta_{\gamma_1}) \sin(\theta_{\gamma_2}) \sin(\theta_{\gamma_3}) \cdots \sin(\theta_{\gamma_{n-1}}) \sin(\theta_{\gamma_n})}{\cos(\theta_{\gamma_1}) + \sin(\theta_{\gamma_1})^n} \right)^{N-1}...
    \]
\[
\hat{a}_{i; \alpha; \beta; \ldots; \beta; \ldots; \beta; \beta} = \hat{G}_{\alpha; \ldots; \alpha; \beta; \ldots; \beta} \quad \text{where } 1 \leq i \leq k.
\]

(26)

(b) The anti-symmetry for \( a \leftrightarrow \beta \):

\[
\hat{u}_{i; \alpha; \beta; \ldots; \beta} = -2i \hat{G}_{\alpha; \ldots; \alpha; \beta; \ldots; \beta} + (2k + 3 - 2i) \hat{G}_{\alpha; \ldots; \alpha; \beta; \ldots; \beta} - \hat{G}_{\alpha; \ldots; \alpha; \beta; \ldots; \beta},
\]

(27)

(c) The vector of mixed multiple-genes (mixed type number \( \geq 3 \)):

\[
\hat{m}_{\alpha_1; \ldots; \alpha_t; \alpha_s; \ldots; \alpha_m; \ldots; \alpha_m} = n_1 \hat{G}_{\alpha_1; \ldots; \alpha_t; \alpha_s; \ldots; \alpha_m} + n_2 \hat{G}_{\alpha_1; \ldots; \alpha_t; \alpha_s; \ldots; \alpha_m},
\]

(28)

The parametrization of the genotype frequency space for the \( N \)-gender gene-mating of \((n + 1)\) alleles system is like the parametrization of the fiber bundle space including both the global stable base manifold and the fibers attached on the manifold. We obtain:

\[
\sum_{\substack{0 \leq j_1 \leq \ldots \leq j_k \leq n}} G_{j_1; \ldots; j_k; \ldots; j_k} \hat{G}_{j_1; \ldots; j_k; \ldots; j_k} \hat{G}_{j_1; \ldots; j_k; \ldots; j_k}
\]

\[
= \sum_{\substack{0 \leq j_1 \leq \ldots \leq j_k \leq n}} G_{j_1; \ldots; j_k; \ldots; j_k} \hat{G}_{j_1; \ldots; j_k; \ldots; j_k} \hat{G}_{j_1; \ldots; j_k; \ldots; j_k}
\]

(29)

Given any initial values of the genotype frequency \( G \) parameters, we are able to find the final equilibrium \( G \) via the inverse transformation:

\[
G_{\alpha_1; \ldots; \alpha_t; \alpha_s; \ldots; \alpha_m; \ldots; \alpha_m} = \frac{N!}{n_1! \ldots n_m!} \left( \frac{1}{N} \right)^N
\]

(30)

By the above relation, we can simplify the inverse transformation from the old to the new coordinates:
\[ \theta_{\mu+1} = \tan^{-1}\left\{ \sum_{a=\mu+1}^{n} \left[ N G_{a^\mu} + (N-1) \sum_{i=0}^{N \setminus \{ \mu \}} G_{a^i \mu i} + (N-2) \sum_{0 \leq i \leq N-1} G_{a^i \mu i i} + \cdots + \sum_{0 \leq i \leq N-1} G_{a^i \mu i i i} \right] \right\} / \left[ N G_{\mu^\mu} + (N-1) \sum_{i=0}^{N \setminus \{ \mu \}} G_{\mu^i \mu i} + (N-2) \sum_{0 \leq i \leq N-1} G_{\mu^i \mu i i} + \cdots + \sum_{0 \leq i \leq N-1} G_{\mu^i \mu i i i} \right] \]

For \( N = 2k \),

\[
\begin{align*}
\{ s_{1 \alpha \beta} \} &= \frac{1}{2} \left\{ \begin{array}{c}
G_{\alpha \cdots \alpha \beta \cdots \beta} + G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} \\
-2 \sum_{i=2}^{k} s_{1 \alpha \beta}
\end{array} \right\} \quad 2 \leq i \leq k
\end{align*}
\]

For \( N = 2k+1 \),

\[
\begin{align*}
\{ s_{1 \alpha \beta} \} &= \frac{1}{2} \left\{ \begin{array}{c}
G_{\alpha \cdots \alpha \beta \cdots \beta} + G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} \\
-2 \sum_{i=2}^{k} s_{1 \alpha \beta}
\end{array} \right\} \quad 2 \leq i \leq k
\end{align*}
\]

\[
\begin{align*}
\{ u_{1 \alpha \beta} \} &= \frac{1}{2} \left\{ \begin{array}{c}
G_{\alpha \cdots \alpha \beta \cdots \beta} + G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} \\
-2 \sum_{i=2}^{k} u_{1 \alpha \beta}
\end{array} \right\} \quad 2 \leq i \leq k
\end{align*}
\]

\[
\begin{align*}
\{ u_{1 \alpha \beta} \} &= \frac{1}{2} \left\{ \begin{array}{c}
G_{\alpha \cdots \alpha \beta \cdots \beta} + G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} \\
-2 \sum_{i=2}^{k} u_{1 \alpha \beta}
\end{array} \right\} \quad 2 \leq i \leq k
\end{align*}
\]

\[
\begin{align*}
\{ u_{1 \alpha \beta} \} &= \frac{1}{2} \left\{ \begin{array}{c}
G_{\alpha \cdots \alpha \beta \cdots \beta} + G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} - G_{\alpha \cdots \alpha \beta \cdots \beta} \\
-2 \sum_{i=2}^{k} u_{1 \alpha \beta}
\end{array} \right\} \quad 2 \leq i \leq k
\end{align*}
\]

where \( m = \frac{1}{N}(m_{eq} - m) \),

\[
\begin{align*}
m &= \frac{1}{N}(m_{eq} - m)
\end{align*}
\]

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\end{align*}
\]

\[
\begin{align*}
m &= \frac{1}{N}(m_{eq} - m)
\end{align*}
\]
Next we derive the decoupled governing equations in the new coordinates:

\[
\begin{align*}
\frac{d\bar{v}_{i\alpha}}{dt} &= -k_{\beta} s_{i\alpha\beta}, \quad 0 \leq \alpha < \beta \leq n \\
\frac{d\bar{u}_{i\alpha}}{dt} &= -k_{\beta} u_{i\alpha\beta}, \quad 0 \leq \alpha < \beta \leq n \\
\frac{d\bar{r}}{dt} &= -k_{\beta} m, \quad \text{where } m = m_{1} \cdot \alpha_{1} \cdot \alpha_{2} \cdots \alpha_{m} \\
\frac{d\theta}{dt} &= 0, \quad 1 \leq k \leq n.
\end{align*}
\]

Parallel to third and fourth sections analysis, the decoupled governing equations are the exponential-decay type differential equations, we obtain the exact analytic time-evolution solution of governing equations:

\[
\begin{align*}
\frac{dG_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}}}{dt} &= G_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}}(t) \frac{d\bar{G}_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}}}{dt} \\
+ &\sum_{i=1}^{[\frac{N}{2}]} \sum_{0 \leq \alpha \leq \beta \leq N} \tilde{s}_{i\alpha\beta} e^{-k_{\beta} t} \tilde{s}_{i\alpha\beta} G_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}} \\
+ &\sum_{i=1}^{[\frac{N}{2}]} \sum_{0 \leq \alpha \leq \beta \leq N} \tilde{u}_{i\alpha\beta} e^{-k_{\beta} t} \tilde{u}_{i\alpha\beta} G_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}} \\
+ &\sum_{0 \leq \alpha_{1} < \cdots < \alpha_{m} \leq N} \tilde{m}_{\alpha_{1} \alpha_{2} \cdots \alpha_{m}} e^{-k_{\beta} t} \tilde{m}_{\alpha_{1} \alpha_{2} \cdots \alpha_{m}} G_{i_{1}i_{2}i_{3} \cdots i_{N-1}i_{N}}
\end{align*}
\]

Conclusions: global stability of N-gender-mating polyploid systems

The new findings in this work: We have found the exact analytic solutions and proved the global stability of an N-gender gene-mating N-polyploid system. Since there is no chaotic behavior, it seems to suggest that the natural law does not go against N-gender N-polyploid system as far as the global stability is concerned. Presumably, the extraterrestrial aliens or intelligence may have N-gender N-polyploid system with \(N \geq 3\) while the mating system still enjoys the global stability. It is likely that when the mutation and the natural selection process sets in, it will alter the governing equations to be less-symmetric, and thus possibly result in richer or more chaotic behaviors. It will be interesting to study the perturbation away from the symmetric governing equations, with the help of our exact analytic solutions.

The new derivations and analytic solutions in this work: To the best of our knowledge of literature, the analysis closest to ours in the literature is Nagylaki and Crow (1974). In Nagylaki and Crow (1974), some exactly solvable models within a gene pool are analyzed, where the monotonic evolutionary behavior is found. Nagylaki and Crow (1974)’s studies a single locus for an arbitrary number of alleles with or without distinguishing the sex. We study a single locus, arbitrary number alleles in an N-gender multiploid (or polyploid) population. Therefore, we generalize two degrees of freedom, N-gender and N-polyploid, and \((n + 1)\)-alleles, both to arbitrary integers, \(N\) and \(n\).

Related models for the 2-gender diplod find in Edwards (2000) and a systematic derivation in Wang and Chen (2020). It is worthwhile mentioning that some of the previous models mostly focus on solving the “discretized difference equations;” while we focus on solving the idealized “highly-nonlinear coupled continuous differential equations.”

We can also compare the 2-gender to N-gender gene-mating equation to the Boltzmann-like equation. The 2-gender to N-gender gene-mating equations are basically the 2-body collision to the N-body collision Boltzmann equations with continuous distribution functions of discretized variables instead of continuous variables. It may be interesting to find a set of exactly solvable time-dependent Boltzmann equation by generalizing our discretized variables to continuous functional variables. Such a derived Boltzmann-like equation should still provide the global stability and a continuous fixed-point global stable manifold in the infinite-dimensional continuous parameter space (Wang et al. 2020). All these will be left open for future directions.

For more future directions, it may be enlightening to generalize our explicit solutions for the N-gender mating without natural selection rules, to the N-gender mating with selection rules or other modifications: Hofbauer and Sigmund (1988), Akin and Szucs (1994), Nagylaki and Crow (1974), Jost and Pepper (2008).

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\[^{3}\text{Here the genotype label } a_{0} \cdots a_{1} a_{1} \cdots a_{m} \cdots a_{m} \text{ in the continuous genotype frequency distribution function } G_{a_{0} a_{0} \cdots a_{1} a_{1} \cdots a_{m} \cdots a_{m}}(t) \text{ is a discretized labeling, while the time } t \text{ in our model is continuous.}\]

\[^{4}\text{In contrast, the conventional Boltzmann equation has the continuous variables } (\vec{\alpha}, \vec{p}) \text{ in the continuous distribution function } f(\vec{\alpha}, \vec{p}, t), \text{ e.g., } (\vec{\alpha} \in \mathbb{R}, \vec{p} \in \mathbb{R}).\]
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