Let $A$ and $a$ be the alleles. Then the genotypes of zygotes are

$$AA,\ aa,\ Aa \equiv aA.$$

Let the corresponding fitness coefficients be $\lambda_{11}$, $\lambda_{22}$, $\lambda_{12}=\lambda_{21}$. They are nonnegative and at least one of them is not zero.

THERE ARE 4 PHENOTYPICAL SITUATIONS:

I) The genotypes are phenotypically distinguished. Then $\lambda_{ik}$ ($i \leq k$) are *independent* variables.

II) The genotypes $AA$ and $Aa$ have the same phenotype but the phenotype of $aa$ is different. This is just the case of *Mendel dominance*. In this case there is a *dependence* between variables $\lambda_{ik}$, namely,

$$\lambda_{11} = \lambda_{12} \qquad (1)$$

but $\lambda_{22}$ is independent of $\lambda_{11}$.

III) The genotypes $AA$ and $aa$ have the same phenotype but the phenotype of $Aa$ is different. Then

$$\lambda_{11} = \lambda_{22} \qquad (2)$$

but $\lambda_{12}$ is independent of $\lambda_{11}$.

IV) All genotypes have the same phenotype. This is just the *selectively neutral* case,

$$\lambda_{11} = \lambda_{22} = \lambda_{12} \qquad (3)$$

Let us stress that $\lambda_{ik}$ must be considered up to a common multiple factor. This means that the number of independent variables must be reduced by 1. Thus, the space of our systems is of dimension 2 in the case (I), of dimension 1 in the case (II) and of (III) and dimension 0 in the case (IV).

In any case with fixed $\lambda_{ik}$ we have a dynamical system whose states are the probabilistic pair

$$(p, q)\ (p \geq 0,\ q \geq 0,\ p+q=1).$$

That the space of states is the closed interval so that, the space is 1-dimensional. The evolutionary equation for this system was done by Ronald Fisher in 1922. This is the following:

$$p' = p(\lambda_{11}p + \lambda_{12}q) \,/\, W \qquad (4)$$

$$q' = q(\lambda_{21}p + \lambda_{22}q) \,/\, W \qquad (5)$$

where

$$W = \lambda_{11}p^2 + 2\lambda_{12}\, pq + \lambda_{22}\, q^2, \qquad (6)$$

the so-called *mean fitness* of the population. If $(p,q)$ is a state in a generation then $(p', q')$ is the state in the next generation.

The dynamical system (4)-(5) by itself is a point in the space of triples

$$\Lambda = (\lambda_{11} : \lambda_{22} : \lambda_{12})$$

considered up to proportionality. The space of all such systems is the positive part of the 2-dimensional real projective space $\mathbf{RP}^2$. Equivalently, this space is the 2-dimensional basis simplex in $\mathbf{R}^3$:

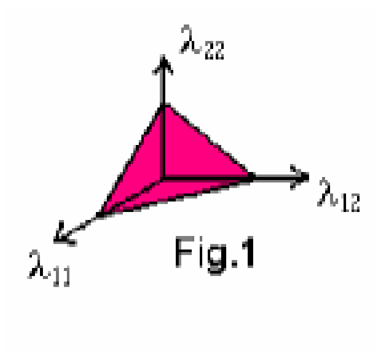


Fig.1

In the case (I) we consider all such systems. In the case (II) the space of systems under consideration is the red interval on the Figure 2.

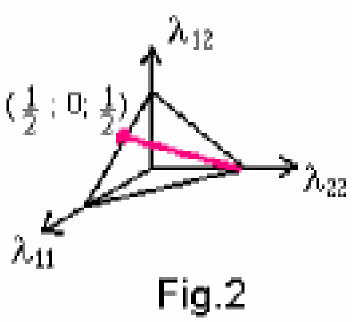


Fig.2

Similarly, in the case (III) we have

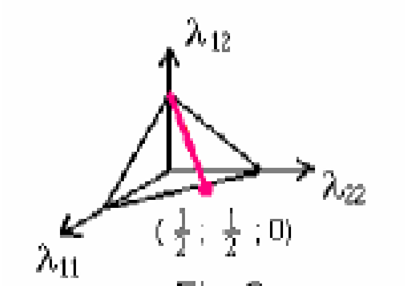

Fig.3

Finally, in the case (IV) the only center point of the simplex corresponds to a considered system.

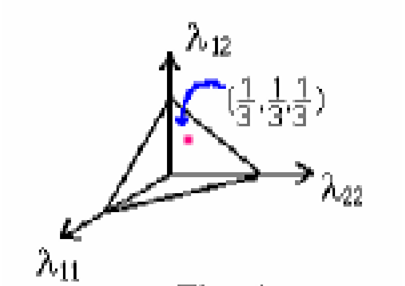

Fig.4

The equilibria set of any system (4)-(5) can be easily found. This set turns out to be finite beyond the selectively neutral situation. (It the latter situation all states are equilibria). This selectively neutral situation is in fact, exceptional. *In cases (I), (II), (III) the equilibria set is finite generically.* In order to pass from this observation to a general theorem about multilocus multiallele populations we need in a general mathematical concept of phenotype. This concept was introduced by Lyubich (1983) as follows.

Consider the set $Z$ of all zygote genotypes in a population. Any partition of $Z$ onto pairwise intersected nonempty classes is called a *phenotypical structure* of $Z$. The class $\Phi(z)$ of a zygote $z \in Z$ is called its *phenotype*. If $F$ is the set of all phenotypes then the mapping $\varphi: Z \to F$ is called the *gene control.* Formally, a phenotypical structure can be described as a triple $(Z, F, \varphi)$.

Conversely, given a set $F$ and a mapping $\varphi: Z \to F$, then there exists a unique phenotypical structure on $Z$ with the set $F$ of phenotypes and the gene control $\varphi$.

The Mendel dominance (our case II) is the phenotypical structure with the classes $F_1=\{AA, Aa\}$ and $F_2=\{aa\}$. The gene control $\varphi$ in this case is

$\varphi$:

| $AA$ | $aa$ | $Aa$ |
|---|---|---|
| $F_1$ | $F_2$ | $F_1$ |

The phenotypes of the homozygotes *AA*, *aa* are different here.

In the case (III) the classes are $F_1=\{AA, aa\}$, $F_2=\{Aa\}$, the gene control is

$\varphi$:

| *AA* | *aa* | *Aa* |
|---|---|---|
| $F_1$ | $F_1$ | $F_2$ |

Here the phenotypes of the homozygotes are the same.

In order to formulate our general result, we, first of all, consider the set Γ of all gametes. Every zygote can be considered as an unordered pair of gametes. The *homozygotes* $(\gamma,\gamma)$ bijectively correspond to the gametes $\gamma\in\Gamma$.

Definition. Consider a gamete γ and the phenotype $\varphi(\gamma,\gamma)=\{z_1,\ldots,z_s\}$. For a gamete $g\in\Gamma$, we write $g\leq\gamma$ if $g$ is contained in the gamete pool of the zygotes $z_1,\ldots,z_s$. A phenotypical structure $(Z,F,\varphi)$ is called *regular* if the binary relation $g\leq\gamma$ is partial order on the set Γ. This means that

$$a)\quad \left.\begin{matrix} g\leq\gamma \\ \gamma\leq h \end{matrix}\right\} \longrightarrow g\leq h \qquad \textit{transitivity}$$

$$b)\quad \left.\begin{matrix} g\leq\gamma \\ \gamma\leq g \end{matrix}\right\} \longrightarrow g=\gamma \qquad \textit{antisimmetry}.$$

If is convenient to extend this partial order to a linear one.

Theorem. *Given a regular phenotypical structure with fitness coefficient* $\lambda(g,\gamma)$ *which depend only on the phenotypes. Then the equilibria set is finite except for a surface in the simplex*

$$\sum_{g\leq\gamma}\lambda(g,h)=1,\ \lambda(g,h)\geq 0.$$

This result can be applied to many natural situations. For instance, if the phenotype of any homozygote is different from the phenotypes of all other zygotes then the phenotypical structure is regular. We can also consider a very general scheme of dominance even for multilocus systems and this situation, turns out to be regular as well.