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Some Genetic Features of Population Migration

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Abstract

The differential equation for moving genome of panmictic and inbred populations is found. These equations have allowed find the dependence of the population movement speed on various parameters: average time of a generation alternation, the area of the territory developed by the population for certain time, length of a wave of the moving population and inbreeding factor. The nonlinear differential equation of the third order reflecting natural selection in a population is found. Research of the migrating inbred population at present of natural selection has allowed to fined a condition of the allele frequency preservation at women in X-chromosomes.

Key words: A population; Moving genome; Nonlinear genetics; Inbreeding; Natural selection; Hardy-Weinberg law

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INTRODUCTION

The history of a human population development is connected to migration of its parts in various regions of Globe. During movement of primitive people from Africa to Europe, there were various genetic processes which have been caused by the adaptation of a population to new conditions of existence. The most known example of a migratory processes consequences the change of the human skin pigmentation at migration of people from Africa where their occurrence is supposed in higher latitudes that has been caused by the adaptation of a population to new conditions of existence. At the same time, the process of a population motion influenced on its genome.

Moving of the population individuals are not equivalent to moving of the genome. But individuals of the population are carriers of genome therefore moving of the population individuals and moving of genome are closely connected with each other.

The purpose of article is the genetic analysis of features of the population movement, finding of the laws and characteristic genetic parameters of such movement.

1. MIGRATION OF PANMICTIC POPULATIONS

Let’s begin with the elementary case of migration of a panmictic populations.

Let’s assume that at the migration of the population keeps it panmictic character. Though such assumption is the big idealization but for the initial analysis it is allowable especially if the moving part of the population is great enough i.e. contains a plenty of family trees.

For the solving of our problem it is necessary to have, first of all, the basic equation which describes the genome of the moving population. We shall consider requirements which are necessary such equation to satisfy.

First of all, this equation should include Hardy-Weinberg law i.e. to pass in Hardy-Weinberg law at absence of a population movement.

Second, the equation should reflect indifferent character of genome balance for moving panmictic populations.

Thirdly, since movement of a population represents some wave process including elements of individual diffusion in space it is possible to assume that the equation for moving genome should have diffusive-wave character.

For a basis we shall accept the differential equation reflecting balance of genome of the motionless panmictic population or Hardy - Weinberg balance (Volobuev, Romanchuk, & Malishev, 2013):

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}n^2}+\ln 2\frac{\mathrm{d}q_f}{\mathrm{d}n}=0, \tag{1}$$

where q_f there is frequency of the some recessive allele of two-allele systems in the X-chromosome at the woman, $n=\frac{t}{T}$ - dimensionless time, t - current time, T - the normalizing time equal to the average period of generations alternation in the moving population ($T\approx 25$ years).

Taking into account required diffusive-wave character of the equation we shall write down the basic equation for genome of the moving population as:

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}n^2}+\ln 2\frac{\mathrm{d}q_f}{\mathrm{d}n}=D\frac{\mathrm{d}^2 q_f}{\mathrm{d}X^2}, \tag{2}$$

where $D=D^*T$ there is the normalized factor of diffusion, D^* - factor of diffusion of the population individuals, and hence of genome in space. This factor is multiplied on normalizing time T with the purpose of dimensionless time use in the unit of factor D measurements, X - spatial coordinate of the population moving.

Let's note that the Equation (2) simultaneously reflects indifferent character of the genome balance of the moving population since satisfies to the solving q_f=const.

The Equation (2) allows analysis moving of the population and it genome in the certain direction X that most frequently took place in a history of mankind. If moving of a population occurs simultaneously in different directions it is necessary to use the equation:

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}n^2}+\ln 2\frac{\mathrm{d}q_f}{\mathrm{d}n}=D\Delta q_f, \tag{3}$$

where Δq_f there is the Laplacian of the functions q_f.

With the purpose of the solving finding of the Equation (2) we shall make replacement of the variable under the formula:

$$q_f(n,X)=e^{-\left(\frac{1}{2}\ln 2\right)n}u(n,X), \tag{4}$$

where $u(n,X)$ there is new variable dependent on dimensionless time and coordinate of moving.

Substituting (4) in (2), we shall receive the equation:

$$\frac{\partial^2 u}{\partial n^2}=D\left(\frac{\partial^2 u}{\partial X^2}\right)+\left(\frac{1}{2}\ln 2\right)^2 u. \tag{5}$$

The result of the solution of Cauchy problem for the given equation has rather complex character for the analysis. For example, for initial conditions: at n=0 the function $q_f=q_{f0}=u_0$=const, and $\frac{\partial q_f}{\partial n}=\frac{\partial u_0}{\partial n}=0$ (initial constant on time value of recessive allele frequency), and also in spatial area $-\infty<X<\infty$ the solution of the Equation (5) looks like (Zajtsev & Polanin, 1996):

$$u=\frac{1}{2}\left[f\left(X+\sqrt{D}n\right)+f\left(X-\sqrt{D}n\right)\right]+ + u_0\frac{n\ln 2}{4\sqrt{D}}\int_{X-\sqrt{D}n}^{X+\sqrt{D}n}\frac{I_1\left(\frac{1}{2}\ln 2\sqrt{n^2-\frac{(X-\xi)^2}{D}}\right)}{\sqrt{n^2-\frac{(X-\xi)^2}{D}}}\mathrm{d}\xi, \tag{6}$$

where f there is any function of coordinates $X+\sqrt{D}n$ and $X-\sqrt{D}n$, ξ-variable of integration, $I_1(z)$- modified Bessel function of the first order.

Function $f\left(X-\sqrt{D}n\right)$ means a wave of the population genome, and hence the wave of the population spread to the right, and $f\left(X+\sqrt{D}n\right)$ - to the left.

Let's consider in more detail the form of a migrating population wave. It is obvious that approximation of uniform movement in this case is rather rough. The population goes then after a while stops and develops the certain territory. Then, after an exhaustion of resources the movement renews, etc.. In Figure 1 the front of a genomic wave of moving population is shown.

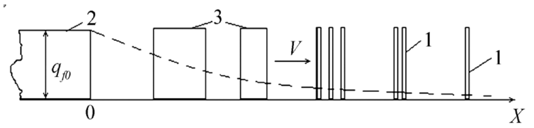

Figure 1
Front of Genomic Wave of Migrating Population

Each man is the carrier of all genome. Therefore examined allele frequency we shall assume an identical at each individual of a population $q_f=q_{f0}$=const. Some individuals, for example, hunters, scouts 1, can leave the basic file of a population 2 on rather big distance. A part of individuals-collectors of a plants fruits 3 leave on smaller distance. In the analysis it is possible to replace such complex character of the forward front of a moving population some dotted line shown on Figure 1.

For our purposes is allowable to use the exponential kind of function f. Also we shall examine only a wave of the population genome propagating to the right. In this case the solving of the Equation (5) can be written down as:

$$u=u_0 e^{-(kX-\omega n)}. \tag{7}$$

In the Equation (7) we shall be interested the parameters of the wave phase k and ω instead of the wave front which according to the solution (6) can be anyone. Substituting (7) in (5) we shall find dependence between parameters of the wave phase and factor of diffusion D:

$$\omega^2 = Dk^2 + \left(\frac{1}{2}\ln 2\right)^2. \tag{8}$$

Substituting (7) in (4) we shall pass to former function q_f:

$$q_f = q_{f0} e^{-\left(kX - \left(\omega - \frac{1}{2}\ln 2\right)n\right)}. \tag{9}$$

Once again we shall note that is real any change of function q_f is not present since each individual carries a full genome. Equation (9) reflects the conditional change shown on Figure 1 by dotted line.

In the Equation (9) $k = \frac{2\pi}{\lambda}$ there is the wave number and $\left(\omega - \frac{1}{2}\ln 2\right)$ - dimensionless cyclic frequency of the wave population genome, λ - length of front of the moving population wave. Equality of initial sizes of functions $q_f = q_{f0} =$const is used also.

First of all we shall find speed of the wave front propagation of population genome. If the population at the movement keeps the panmictic character of the Hardy - Weinberg balance is indifferent and should be observed $q_f = q_{f0} =$const.

Hence, according to (9) the phase of the wave is equal:

$$kX - \left(\omega - \frac{1}{2}\ln 2\right)n = 0. \tag{10}$$

Speed of the wave front movement of population genome according to (10), Figure 1, is equal:

$$V = \frac{X}{t} = \frac{X}{nT} = \frac{\omega - \frac{1}{2}\ln 2}{kT}. \tag{11}$$

Expression (11) has completely general character which has been not connected to the concrete form of a population front wave (9).

Substituting in (11) parameter ω from (8) and taking into account $D = D^*T$ we shall find:

$$V = \frac{\sqrt{Dk^2 + \left(\frac{1}{2}\ln 2\right)^2} - \frac{1}{2}\ln 2}{kT} = \sqrt{\frac{D^*}{T} + \left(\frac{1}{2kT}\ln 2\right)^2} - \frac{1}{2kT}\ln 2. \tag{12}$$

Let's note that in (12) the condition is observed: At $D^*=0$ the population is motionless $V=0$.

Using length of the population wave front under the formula $\lambda = \frac{2\pi}{k}$ we shall find:

$$V = \sqrt{\frac{D^*}{T} + \left(\frac{\lambda}{4\pi T}\ln 2\right)^2} - \frac{\lambda}{4\pi T}\ln 2. \tag{13}$$

It is interesting to analyse on extremum the function of speed $V(T,\lambda)$. Simple transformations of derivatives $\frac{\partial V}{\partial T}$ and $\frac{\partial V}{\partial \lambda}$, and equating of these derivatives with zero result in a trivial conclusion that the minimal size of speed $V(T,\lambda)=0$ is determined by the condition $D^*=0$ i.e. a motionless population.

In Figure 2 dependence of the speed of the population genome moving on the average period T of the generation alternation in population plotted under Equation (13) is shown.

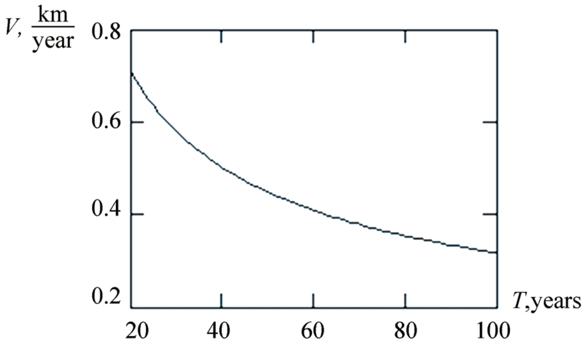

Figure 2
Dependence of Speed of Moving Genome of Panmictic Populations on the Average Period *T* of Generations Alternation.

At calculation the length of the population front wave was accepted $\lambda=0.4$km, factor of diffusion $D^* = 10\frac{\text{km}^2}{\text{year}}$.

Calculation shows that with increase in the period of a generation alternation the speed of the population and it genome movement to become less. It is correct since younger individuals are more dynamical i.e. if the generations are more often are alternated the population faster move. At the period of the generation alternation $T \approx 25$years the calculated speed of genome movement, and hence the population is equal $V \approx 0.63\frac{\text{km}}{\text{year}}$. It is obvious that this speed basically is caused by a gradual exhaustion of resources on a way of the population movement.

Believing, that during migration from Africa primitive people have passed about 5,000 km it is possible to find the time of movement ~ 8,000 years. At this time 320 generations were alternated.

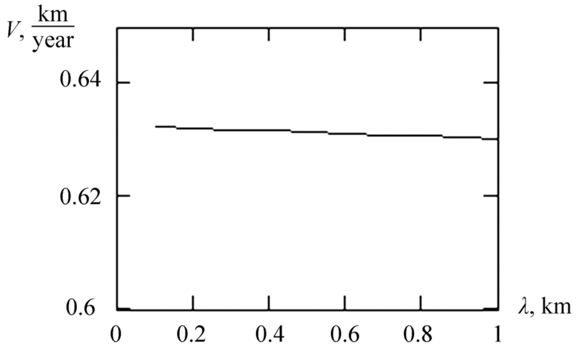

Figure 3
Dependence of Speed of Panmictic Populations Movement on Length of a Wave Front *λ*

In Figure 3 the dependence of speed of the population movement on length λ of the wave front is shown at period of the generation alternation equal $T \approx 25$years, plotted under Equation (13). From the graph it is visible that with increase in length of the wave the speed of the population movement falls. It is correct since more compact populations should move with the greater speed than less compact. But this dependence is not so strong.

At the analysis of the Equation (13) there is a question on sense of diffusion factor D^*. This parameter reflects the area developed by the population within year at each stage of movement. Actually this parameter reflects the resources necessary for vital activity and movement of the population. We shall notice that the parameter $D=D^*T$ is meaning of the area developed by the population during a life of one generation.

On Figure 4 the dependence of speed of the population movement on diffusion factor D^* is shown.

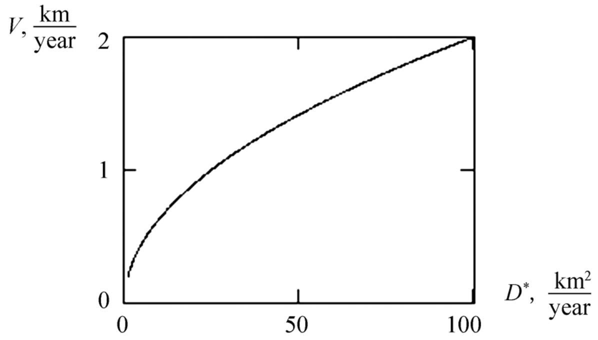

Figure 4
Dependence of Speed of Panmictic Populations Movement on the Area of Territory Developed by the Population for a Year D^*

The found dependence is rather strong. It shows that the big resource area the population can develop for the year at the movement the faster it moves.

The basic lack of the carried out analysis of the moving population is the assumption about it panmictic character. Actually the migration of the human population part in various directions occurred rather small groups, tribes or separate communities of tribes. Of these tribes there was to be relatively small number of family trees therefore consanguineous mating, i.e. inbreeding has been widespread.

2. MIGRATION OF INBRED POPULATIONS

As it was already specified above in primitive populations, for example, leaving of Africa and moving aside northern European influence of inbreeding was important. Therefore, we shall consider influence of inbreeding on a migrating population.

The way of the inbreeding account for a motionless population has been analysed in (Volobuev, Romanchuk, & Malishev, 2014). Adding in the equation for allele frequency q_f motionless inbred populations the item reflecting movement of a population we shall find the general equation for a condition of genome in a moving inbred population:

$$\frac{d^2 q_f}{dn^2} + \frac{3}{2\Delta n}\frac{dq_f}{dn} = D\frac{d^2 q_f}{dX^2} + \frac{F}{\Delta n^2(1-F)}q_f^2, \qquad (14)$$

where F there is inbreeding factor.

The found equation is the nonlinear differential equation of the second order with square-law nonlinearity.

We shall search the solution of the Equation (14) as a traveling wave $q_f=f(\zeta)$ where $\zeta=kX-\omega n$. In this case the Equation (14) will be transformed to the kind:

$$\frac{d^2 q_f}{d\varsigma^2}\left(\omega^2 - Dk^2\right) - \frac{3}{2\Delta n}\frac{dq_f}{d\varsigma}\omega = \frac{F}{\Delta n^2(1-F)}q_f^2. \qquad (15)$$

Let's lower the order of the Equation (15) having designated $\frac{dq_f}{d\varsigma} = Z\frac{\frac{3}{2\Delta n}\omega}{\omega^2 - Dk^2}$. We shall receive Abel's differential equation:

$$Z\left[\frac{dZ}{dq_f} - 1\right] = \frac{\left(\omega^2 - Dk^2\right)}{\left(\frac{3}{2\Delta n}\right)^2\omega^2}\frac{F}{\Delta n^2(1-F)}q_f^2 = \frac{4}{9}\left(1 - \frac{D}{V^2}\right)\frac{F}{(1-F)}q_f^2, \qquad (16)$$

where $\frac{\omega}{k} = V$ there is speed of the population movement. Let's note that the received differential equation does not depend on size Δn.

The analytical solution of the Equation (16) does not exist. However the greatest interest has dependence of the population movement speed V on inbreeding factor F. This dependence can be found without the solving of the Equation (16).

Let's consider the right part of the Equation (16) which defines the inbreeding in a population. The inbreeding factor F is present both at numerator, and in the denominator. Factor F serves in numerator for establishment of all right part existence in the equation (16). At F=0 the right part of the Equation (16) disappears and the population to become panmictic i.e. in this case $q_f = q_{f0}$=const. If $F \neq 0$ the recessive allele frequency q_f grows (Volobuev, Romanchuk, & Malishev, 2014) i.e. inbreeding factor in numerator is responsible for dynamics of the function q_f growth. Therefore the inbreeding factor in numerator of the Equation (16) right part should be kept at any transformations.

Taking into account the given position we shall transform the right part (16) as follows:

$$Z\left[\frac{dZ}{dq_f} - 1\right] = \frac{4}{9}\left(\frac{1}{1-F} - \frac{D}{\left(V\sqrt{1-F}\right)^2}\right)Fq_f^2. \qquad (17)$$

All parameters connected to the wave phase are present only at the second addend in brackets of the right part (17). Therefore it is possible to conclude that for the account of the inbreeding factor influence on the moving population speed it is necessary to multiply the speed of the population wave in $\sqrt{1-F}$.

Hence Equations (12) and (13) for the genome speed of moving population and itself population can be transformed to the kind:

$$V = \left(\frac{\sqrt{Dk^2 + \left(\frac{1}{2}\ln 2\right)^2} - \frac{1}{2}\ln 2}{kT} \right) \sqrt{1-F} = \\ = \left(\sqrt{\frac{D^*}{T} + \left(\frac{\lambda}{4\pi T}\ln 2\right)^2} - \frac{\lambda}{4\pi T}\ln 2 \right) \sqrt{1-F} \quad . \qquad (18)$$

In Figure 5 the dependence of the moving population speed of inbreeding factor is shown for the following parameters: λ=0.4 km, $D^* = 10\,\frac{\text{km}^2}{\text{year}}$, $T \approx 25$ years.

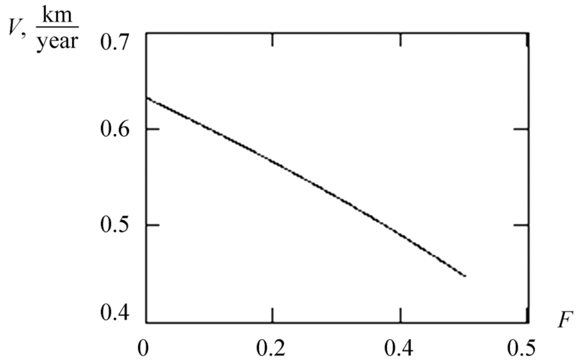

Figure 5
Dependence of Speed of Inbred Population Movement on the Inbreeding Factor *F*

The received result, Figure 5, can be interpreted as follows. At increase of inbreeding in the moving population its speed of movement decreases. Biologically it can be connected by that in the population with consanguineous mating the individuals become more weakened and during moving by less dynamical.

At F=1 according to (18) the population stops. The cause of this step there is fast and full degeneration of the population. If to address to the equation (Volobuev, Romanchuk, & Malishev, 2014) for the motionless population (or (14) at D=0) at $F \to 1$ the right part of the equation which determines the inbreeding quickly grows aspiring to infinity. This increase can be compensated only to increase in velocity of frequency q_f growth in the left part of the equation. But this speed is limited by the biologo-reproductive opportunities of the population. Therefore in a reality achievement F=1 does not occur because the population quickly degenerates.

Thus, migration of human populations in various regions of Globe is caused by moving as individuals of a population so of a population genome which is transferred to the given individuals. The found differential equation for moving genome of panmictic populations (2) allows to find dependence of speed of a moving population on various parameters in particular average time of a generation alternation, the area developed by a population for certain time, length of a wave of a moving population.

During migration of populations owing to small number of individuals the role of consanguineous mating was great. The found differential Equation (14) of the moving inbred populations allows to analyse reduction in speed of a population movement depending on inbreeding factor.

3. NATURAL SELECTION IN A POPULATION AS A PROBLEM OF NONLINEAR GENETICS. POWER OF SELECTION

The problem of natural selection has been mentioned for a family tree in and for a population in (Volobuev, Romanchuk, & Malishev, 2013). The basic characteristics of selection have been introduced: parameter of selection s and fitness of a genotype 1-s. However in (Volobuev, Romanchuk, & Malishev, 2013) the simplified technique of algebraic interrelation reception between the blood recessive allele O frequency q_f at women in case of a hemophilia and dimensionless time n at present of selection has been used.

In the given article we shall solve a problem of selection in a population using a standard way of transition from finite-differential equation characteristic for a family tree to the differential equation correct for a population. This way is submitted in (Volobuev, Romanchuk, & Malishev, 2013).

As well as earlier the analysis of natural selection we shall we shall carry out by the example of selection against of a recessive homozygotes.

In (Volobuev, Romanchuk, & Malishev, 2013) has been received the recurrent ratio for the finding of a recessive allele frequency at women if those frequencies in the two previous generations of women are known:

$$q_{fn} = \frac{\frac{1}{2}\left(q_{f(n-1)} + q_{f(n-2)}\right) - q_{f(n-2)}q_{f(n-1)}s}{1 - q_{f(n-2)}q_{f(n-1)}s}. \qquad (19)$$

In the Equation (19) s there is standard parameter of selection against of a recessive homozygotes.

By simple algebraic transformations of the Equation (19) we shall find:

$$q_{f(n-1)} + q_{f(n-2)} - 2q_{fn} = 2s\left(q_{f(n-2)}q_{f(n-1)} - q_{fn}q_{f(n-2)}q_{f(n-1)}\right). \qquad (20)$$

Let's consider the differential equation:

$$\frac{d^2 q_{f(n-1)}}{dn^2} + \eta \frac{dq_{f(n-1)}}{dn} = \alpha s\left(q_{f(n-2)}q_{f(n-1)} - q_{fn}q_{f(n-2)}q_{f(n-1)}\right), \qquad (21)$$

where η and α are some constants. Differentiation in (21) as before goes on dimensionless time n (normalized on average time of generation alternation in a population).

Let’s pass in (21) to finite-differential form of derivatives:

$$\frac{q_{fn} - 2q_{f(n-1)} + q_{f(n-2)}}{\Delta n^2} + \eta\frac{q_{f(n-1)} - q_{f(n-2)}}{\Delta n} = \\ = \alpha s\left(q_{f(n-2)}q_{f(n-1)} - q_{fn}q_{f(n-2)}q_{f(n-1)}\right) \quad (22)$$

Transforming (22) by analogy to (Volobuev, Romanchuk, & Malishev, 2013, & 2014) we shall find:

$$-2q_{fn} + 2(2-\eta\Delta n)q_{f(n-1)} - 2(1-\eta\Delta n)q_{f(n-2)} = \\ = -\alpha 2s\Delta n^2\left(q_{f(n-2)}q_{f(n-1)} - q_{fn}q_{f(n-2)}q_{f(n-1)}\right) \quad (23)$$

Let’s identify the Equation (23) with the Equation (20). In (Volobuev, Romanchuk, & Malishev, 2014) as a result of a similar identification the size $\eta = \frac{3}{2\Delta n}$ has been found. Besides it is possible to see that $\alpha = -\frac{1}{2\Delta n^2}$.

Hence, the differential Equation (21) can be written down as:

$$\frac{\mathrm{d}^2 q_{f(n-1)}}{\mathrm{d}n^2} + \frac{3}{2\Delta n}\frac{\mathrm{d}q_{f(n-1)}}{\mathrm{d}n} = -\frac{1}{2\Delta n^2}s\left(q_{f(n-2)}q_{f(n-1)} - q_{fn}q_{f(n-2)}q_{f(n-1)}\right). \quad (24)$$

At transition to a population the number of generation of a role does not play therefore, we shall receive:

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}n^2} + \frac{3}{2\Delta n}\frac{\mathrm{d}q_f}{\mathrm{d}n} = -\frac{s}{2\Delta n^2}\left(q_f^2 - q_f^3\right). \quad (25)$$

The nonlinear differential Equation (25) allows to calculate frequency q_f of intact recessive allele at women in the *X*-chromosomes of a population at present of selection on mutant alleles.

For convenience of calculation it is used in (25) new independent variable $t = \frac{n}{\Delta n}\sqrt{\frac{s}{2}}$. If to accept $\Delta n = \frac{3}{2\ln 2}$, see (Volobuev, Romanchuk, & Malishev, 2013), we shall find $t = \frac{2\ln 2n}{3}\sqrt{\frac{s}{2}} \approx 0.462n\sqrt{\frac{s}{2}}$.

In view of the new independent variable the Equation (25) will be transformed to the kind:

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}t^2} + \varepsilon\frac{\mathrm{d}q_f}{\mathrm{d}t} = -\left(q_f^2 - q_f^3\right), \quad (26)$$

where it is designated $\varepsilon = \frac{3}{\sqrt{2s}}$. At variation of a selection standard parameter $0 \leqslant s \leqslant 1$ the size $\infty \geq \varepsilon \geq \frac{3}{\sqrt{2}} \approx 2.12$.

The nonlinear differential Equation (26) can be solved only numerically.

Initial conditions, first of all, are necessary for the solution of the differential Equation (26): Initial frequency of the recessive allele *a* q_{f0} and initial speed of falling of this frequency $\left(\frac{\mathrm{d}q_f}{\mathrm{d}t}\right)_0$ or $\left(\frac{\mathrm{d}q_f}{\mathrm{d}n}\right)_0$.

Initial frequency q_{f0} at t=0 or n=0 as well as in (Volobuev, Romanchuk, & Malishev, 2013 and Vogel & Motulsky, 1990) was accepted q_{f0}=0.605. Initial speed of falling of the allele frequency we shall accept such that the solution of the Equation (26) approximately corresponded to (Volobuev, Romanchuk, & Malishev, 2013). In this case $\left(\frac{\mathrm{d}q_f}{\mathrm{d}t}\right)_0 = -0.6$ and $\left(\frac{\mathrm{d}q_f}{\mathrm{d}n}\right)_0 = -0.165$ for characteristic for a hemophilia the parameter of selection s=0.71.

The step of calculation on a variable t equal Δt=0.001 and numbre of steps 20,000 was used.

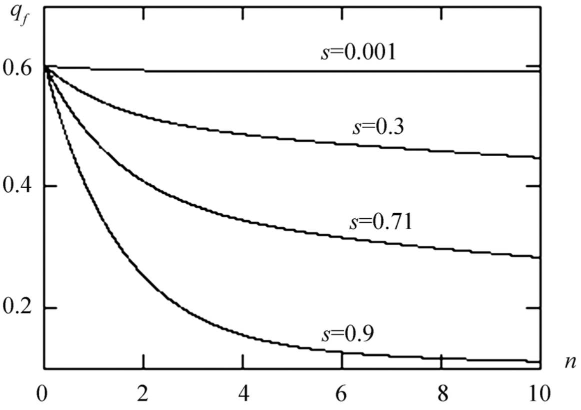

Figure 6
Dependence of Intact Recessive Allele Frequency q_f in *X*-Chromosomes in Women in a Population on Dimensionless Time *n* at Various Parameters of Selection *s*

In Figure 6 the graphs of dependence of intact recessive allele frequency q_f in *X*-chromosomes at women in a population on dimensionless time *n* are shown at various parameters of selection *s*.

In conclusion of the given section we shall consider the some general-biological questions connected to functioning of natural selection.

There is pays to attention very high degree of nonlinearity-the third-of the differential Equation (26) describing natural selection in populations. It has important general-biological importance. The degree of nonlinearity of natural selection defines its opportunities, i.e. power of selection. We did not was success to find out mutational processes with higher degree of nonlinearity. The inbred mutational processes have the second degree of nonlinearity.

Other processes, for example, hemophilia or induced mutagenesis under action of radiation (Volobuev, 2005) have the first degree of nonlinearity or in other words these processes are linear. It means that any mutational processes in populations of the Earth can be leveled by natural selection. From this point of view of H. Muller (Muller, 1950) fear about danger of the future biological degeneration of mankind owing to accumulation of a genetic load for the account of inbreeding (Volobuev, Romanchuk, & Malishev, 2014) unlikely it is possible to assume grounded.

Damage of a genome by mutational processes in earthly populations can cause destruction of a considerable part of individuals, including people. It is the extremely unpleasant and with it is necessary to resist in the various ways: creation of new medical products, protection from ionizing radiations, etc. But as a whole these negative processes practically do not threaten populations, since natural selection gradually restores genetic norm in a population.

4. MIGRATION OF INBRED POPULATIONS AT PRESENCE OF SELECTION

The population is in process of migration usually enough long time. During migration of a population there is an alternation of generations and natural selection operates.

Using Equations (14) and (25), it is possible to write down the differential equation migrating inbred populations in which natural selection operates.

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}n^2} + \frac{3}{2\Delta n}\frac{\mathrm{d}q_f}{\mathrm{d}n} = D\frac{\mathrm{d}^2 q_f}{\mathrm{d}X^2} + \frac{F}{\Delta n^2(1-F)}q_f^2 - \frac{s}{2\Delta n^2}\left(q_f^2 - q_f^3\right). \tag{27}$$

The received nonlinear equation is too difficult for the analysis. However, taking into account cubic nonlinearity of the differential equation of the second order it is possible to assume the presence of solutions as solitary population waves (Dodd, Eilbek, Ghibbon, & Morris, 1998). Apparently, the migrating population represents such solitary wave.

However, the Equation (27) allows receive very important analytical result. For this purpose it is used wave substitution $\varsigma = \frac{1}{\Delta n^2}(kX - \omega n)$ where k there is wave number, ω - dimensionless cyclic frequency of the population waves. In result we shall find:

$$\frac{\mathrm{d}^2 q_f}{\mathrm{d}\varsigma^2}\left(\omega^2 - Dk^2\right) - \frac{3}{2}\frac{\mathrm{d}q_f}{\mathrm{d}\varsigma}\omega = \left(\frac{F}{1-F} - \frac{s}{2}\right)q_f^2 + \frac{s}{2}q_f^3 \,. \tag{28}$$

Let's find the particular solution of the Equation (28). We shall equate the right part of this equation to zero $\left(\frac{F}{1-F} - \frac{s}{2}\right)q_f^2 + \frac{s}{2}q_f^3 = 0$. In result we have:

$$q_f = \left(1 - \frac{2F}{(1-F)s}\right) = \text{const}\,. \tag{29}$$

Obviously, value of frequency q_f (or $p_f = 1 - q_f = \frac{2F}{(1-F)s}$) in the Equation (29) satisfies to the Equations (27) and (28).

The received expression (29) can be interpreted as follows. If in inbred populations which began to migrate there is some frequency of a recessive allele in *X*-chromosomes at women for preservation of this frequency should be interrelation (29) between inbreeding factor *F*, parameter of selection *s* and this frequency q_f. Equation (29) is correct and for motionless populations.

We assume the frequency of the recessive allele of blood O is equal q_f=0.605 (Vogel & Motulsky, 1990). If to use inbreeding factor F=19×10^{-5}, for example, for Germany (Vogel & Motulsky, 1990) that for a migrating population this frequency did not vary the parameter of selection must be s=9.6×10^{-4}.

The problem of interaction of populations is very important. Obviously, it is connected to a finding of the multiwave solutions of the Equation (27) that is extremely complex mathematical problem. Population waves can cooperate with each other in the various ways. They, for example, can destroy each other as interacting nervous impulses (Volobuev, Neganov & Zajtsev, 1998). Obviously, to this there correspond conflicted interactions of migrating populations.

Population waves can have character of a solitons (Dodd, Eilbek, Ghibbon, & Morris, 1998).

Solitons - it is stable nonlinear solitary waves which in interaction with other local perturbations or with each other show particle like properties. For example, they restore the initial form, i.e. interactions similarly to absolutely elastic particles, for example, to absolutely elastic spheres. As well as spheres the solitons, for example, can be reflected from a barrier. The marked properties of solitons are caused they has the strict balance of the nonlinear processes resulting in increase of a steepness of a wave forward front and dispersive processes lead to destruction a solitary wave, i.e. to reduction of a front steepness. The balance of these processes leads to stability of soliton, i.e. invariability of its form.

We shall note that the third degree of nonlinearity of the differential Equation (27) is sufficient for occurrence of a soliton (Dodd, Eilbek, Ghibbon, & Morris, 1998). In interaction of the solitons the population waves can change directions on opposite on type impacting spheres. I.e. populations try to avoid the destruction. If populations belong to poorly cooperating individuals (elephants and birds) waves of populations in interaction pass through each other practically not influencing one another.

As a whole, the further analysis of interaction of populations has no genetic-mathematical character and passes to area of the social phenomena.

CONCLUSION

Migration of human populations in various regions of Globe is caused by moving as individuals of a population, and population genome which is transferred with the given individuals. The found differential equation for moving genome of panmictic populations has allowed find the dependence of speed of a population movement on various parameters of a migrating population.

During migration of populations the role of a consanguineous mating owing to small number of individuals was great. The found differential equation of a moving inbred population has allowed analyze the decrease in speed of movement of a population depending on inbreeding factor.

The account of natural selection has allowed found interrelation between parameter of selection, inbreeding factor and allele frequency in the *X*-chromosome of the woman in which this frequency is kept by a constant.

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