THE MODELS OF POPULATION DYNAMICS AS TOOL FOR STUDYING OF GENETIC POLYMORPHISM OF BAIKALIAN POLYCHAETS

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SUMMARY

In some cases it is difficult to interpret accurately the results obtained with molecular genetic analysis. One of such examples is the case of fresh-water polychaets from Lake Baikal. The observable picture of genetic differentiation in this group of organisms does not correspond to the standard Wright’s (Wright, 1943) model “Isolation by Distance”. To obtain the more correct explanation, the methods of population dynamics simulating the processes of neutral molecular evolution are used. With this model we estimated possible results of different scenarios of migration and interaction of organisms and determined stationary state of neutral DNA polymorphism. If DNA polymorphism in the model fits the pattern observed, it allows us to make assumption that causes of genetic polymorphism in the model and in the real population are similar.

INTRODUCTION

In this work we try to explain the mechanisms generating the pattern of genetic polymorphism in populations of organisms by means the population dynamics. This necessity has arisen since for some groups of organisms where it is difficult to propose adequate explanation for the pattern observed. One of such groups of organisms is Baikal polychaete genus Manayunkia.

Baikal polychaets of genus Manayunkia Leidy, 1859 (Sedentaria, Sabellidae) is not well-studied group. These organisms are representatives of one of few polychaets genera, living in fresh or brackish waters. The species, described by M.M. Kozhov (Kozhov, 1962) as Manayunkia baicalensis, was recently subdivided into three separate species on the basis of morphological and ecological features (Sitnikova et al., 1997). It’s also confirmed with 18S rRNA data (Sitnikova et al., 1995). Baicalian polychaets also have relatively low mobility, and one to suppose, that vicariance can play the important role in diversification of these animals. It means, that intraspecies genetic distances in the given group of organisms should be described by model of “Isolation by Distance” (Wright, 1943).

EXPERIMENTAL DATA

In order to study intra-populationary polymorphism, we took the species M. godlewskii. This species inhabits generally on the silting bottom and has body size slightly more then two other ones. The animals were collected during the expeditions and fixed with 70 %
EtOH, or delivered alive. The DNA extraction was carried out with standard phenol chloroform method (Sambrook et al., 1967). As a marker for molecular phylogenetic researches we choose Folmer’s fragment of 1 subunit of cytochrom-c-oxidase gene (mtCO1) (Folmer et al., 1994). The sequences obtained were aligned with using the program Bio Edit, version 5.0.9. All data obtained were classified according to location into four groups: 1) cape Berezovyi on south-western coast of Baikal, 2) Varnachka, 3) bay Peschanaya, and 4) Sahurta (strait Olkhonskie Vorota). These groups, in turn, are clustered into two groups: #1 (Berezovyi-Varnachka), and #2 (Peschanaya-Sahurta).

The analysis of genetic polymorphism was carried out by using of criterion $F_{st}$ for DNA sequence data (Hudson et al., 1992). Values of the criterion vary in range from 0 up to 1. Small values of $F_{st}$ correspond to higher gene flow between populations. The dependence of the criterion value on the physical distance between samples was obtained. For almost immobile organisms one may expect rapid growth of the values with the increase of distance between localities. But in our case it was found that the distance between localities and criterion value are not correlated (Table 1).

Table 1. $F_{st}$ criterion in real population and different theoretical model

<table>
<thead>
<tr>
<th>Distance (relative unit)</th>
<th>$F_{st}$ in real population (M. godlewskii)</th>
<th>$F_{st}$ in model population (one species)</th>
<th>$F_{st}$ in model population (two species)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$F_{st}$ Distance (relative unit)</td>
<td>$F_{st}$ Distance (relative unit)</td>
<td>$F_{st}$ Distance (relative unit)</td>
</tr>
<tr>
<td>0.08</td>
<td>0.25</td>
<td>0.08</td>
<td>0.1</td>
</tr>
<tr>
<td>0.33</td>
<td>0.2</td>
<td>0.33</td>
<td>0.15</td>
</tr>
<tr>
<td>0.41</td>
<td>0.13</td>
<td>0.41</td>
<td>0.3</td>
</tr>
<tr>
<td>0.63</td>
<td>0.52</td>
<td>0.63</td>
<td>0.6</td>
</tr>
<tr>
<td>0.94</td>
<td>0.22</td>
<td>0.94</td>
<td>0.7</td>
</tr>
<tr>
<td>1</td>
<td>0.3</td>
<td>1</td>
<td>0.75</td>
</tr>
</tbody>
</table>

MODELS OF POPULATION DYNAMICS

Methods of population dynamics were applied in order to model the accumulation of genetic difference in highly viscous population(s). The model is based on the following assumptions: 1) all organisms do not move except for offspring at early stages, 2) the probability of fertilization of a female by male depends on distance between them and drops with the increase of distance, 3) the probability of death of each organism depends on a competition with other organisms, intensity of a competition depends on the density of organisms. All these assumptions follow the characteristics of the organisms studied. The general of the equations population dynamics thus will look as follows:

$$\frac{\partial N(x,t)}{\partial t} = rN(x,t) \left\{ \int_{y_{\min}}^{y_{\max}} \frac{C(x-y)N(y)dy}{K} - D \frac{\partial^2 N(x,t)}{\partial x^2} \right\} (1)$$

In this equation $N(x,t)$ there is a number of organisms in a point of space with coordinate $x$, $r$ there is a speed of reproduction, $K$ there is a capacity of an environment, $D$ the factor of diffusion determining speed of distribution of organisms. Function $C(x-y)$ defines dependence of intensity of a competition on remoteness of organisms in space, in our model $C(x-y) = \frac{1}{2\pi \sigma} \exp \left( -\frac{(x-y)^2}{2\sigma^2} \right)$.
Being based the equation (1), individually based model describing population
dynamics of investigated organisms has been developed. The probability of death on each
time step is defined by the following ratio:

\[
P_x = r \frac{\sum_{i=1}^{N} C(x - y_i)}{K} \, dt
\]  

In this equation \( P_x \) is the probability of death of an organism with coordinate \( x \), \( dt \) is
the interval of integration. The probability of fertilization of the female by a given male
depends on the distance between them according to Gaussian function
\( C_r(x_m - x_f, \sigma_r) \) where \( x_f \) and \( x_m \) there are coordinates of the female and the male. Thus \( \sigma_r \)
equals \( \sigma_c \). It means that sufficiently distant organisms don’t interact. Distribution of the
offspring is believed to follow the Gauss function \( C(x, \sigma_D) \) where \( \sigma_D \) is proportional
diffusion factor. Each organism in our model has neutral nucleotide sequence with length
500 base pairs long. Sequence is transferred from female to all offspring thus following
neutral molecular evolution in mitochondrial DNA.

The numerical experiments, following initial and boundary conditions were used: the one-
dimensional distribution range was represented by stretch \( l \) unit long with coordinates ranging
from 0 to 1. At a simulation start the organisms had coordinates close to 0 and all neutral
sequences were supposed to be identical. Periodically during calculation genetic sequences of
the organisms living at edges of the range were used for calculation of \( F_{st} \). Calculation was
carried out until then while \( F_{st} \) did not achieve the stationary value (Table 1).

For each set of the nucleotide sequences resulting a simulation \( F_{st} \) criterion was
calculated. Dependence between \( F_{st} \) on the distance between groups of organisms was
found to be nonlinear, for closely located groups of organisms. \( F_{st} \) monotonously
increases with the distance until it reaches saturation. This result correlates with the model
“Isolation by Distance” but contradicts the real data from Baikalian polychaets.

Then the model is changed so that one-dimensional area is inhabited by 2 species of
competing organisms which do not cross-breed. The competition between the organisms
belonging to different species was set to be slightly less then between the conspecific
ones. It was next scenarios of the mechanism of formation of polymorphism in neutral
DNA sequences. The equations of population dynamics in this case will be:

\[
\frac{\partial N_1(x,t)}{\partial t} = r_1N_1(x,t) \left( 1 - \frac{\int_{y_{min}}^{y_{max}} C(x-y)N_1(y)dy}{K} - \alpha \int_{y_{min}}^{y_{max}} C'(x-y)N_1(y)dy \right) - D \frac{\partial^2 N_1(x,t)}{\partial x^2}
\]

\[
\frac{\partial N_2(x,t)}{\partial t} = r_2N_2(x,t) \left( 1 - \frac{\int_{y_{min}}^{y_{max}} C(x-y)N_2(y)dy}{K} - \beta \int_{y_{min}}^{y_{max}} C'(x-y)N_2(y)dy \right) - D \frac{\partial^2 N_2(x,t)}{\partial x^2}
\]

In this equation \( N_1(x,t) \) and \( N_2(x,t) \) is number of organisms of competing species.

Value of \( F_{st} \) criterion was calculated as previous case, we suppose that information
about intraspecies differences is unknown. In this model the value of \( F_{st} \) criterion does not
depend on the distance between groups of organisms. The cause of it is next. Two species
accumulate intraspecific differences connected with remoteness in space and interspecific
differences connected with interspecific isolation. If it is not possible to distinguish the
given organisms and they will be determined as one species in this case among
intraspecies genetic distances there are interspecies genetic distances. It will bring in
distortions at calculation \( F_{st} \).
RESULTS AND DISCUSSION

Summarizing the results obtained it is possible to conclude, that the \textit{Manayunkia} behaves according to the second model which assumes two species. Therefore the pattern of genetic diversity observed may be explained by assumption that \textit{M.godlewskii} in fact consists of at least two sibling species which do not cross-breed.

REFERENCES


