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Original article

# Numerical Modeling of the Functioning of Oyster Farm in Donuzlav Bay and its Impact on Water Area

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*Abstract*
*Purpose*. This study aims to develop and apply a mathematical model for comprehensively assessing the ecological impact of an oyster farm on the coastal waters of the Black Sea through model experiments designed to investigate the interactions between marine farms and the environment.
*Methods and Results*. The oyster farm in Donuzlav Bay was simulated using a two-dimensional chemical-biological object-oriented marine ecosystem model. Numerical experiments simulated the operation of an oyster farm (capacity: ~ 100 tons of wet weight, area: 80 hectares) located in the central part of Donuzlav Bay. Calculations related to oysters in their first, second and third year of cultivation were performed for the period from May to October. Results indicate that during the first year of cultivation, when oyster wet weight of soft tissues ranges from 1.2 to 4.5 g, the farm's impact on the marine ecosystem is insignificant. In the second and third years of cultivation, an increase in the bottom sediments volume was observed, primarily attributed to the oyster plantation.
*Conclusions*. The simulation results highlight the need to optimize farm configuration and the number of cultivated mollusks to minimize negative impacts on the water area. The qualitative and quantitative characteristics of flat oyster life obtained from the model are consistent with the data from a previously developed one-dimensional mollusk growth model and field data from monitoring the European oyster cultivation in Donuzlav Bay.

**Keywords:** European oyster, Donuzlav Bay, chemical-biological model, coastal ecosystem, object-oriented modeling

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## Introduction

Active mariculture cultivation raises numerous questions regarding the functioning of marine ecosystems in the coastal zone, which are characterized by a complex interplay of physical, chemical, and biological processes. Consequently, components of coastal ecosystems interact with each other and with the marine environment through multiple direct and feedback mechanisms. The success of a marine farm depends on how effectively mariculture species integrate into the established ecosystem of the selected marine area. The exchange of matter and energy between mariculture and the environment must support sustainable growth of the cultivated species while avoiding degradation of the ecosystem and, where possible, enhancing its condition. These interaction processes can be evaluated using comprehensive ecological models that integrate physical, chemical, and biological components. This study considers several existing models that simulate the functioning of mariculture in relation to its environmental interactions.

The study [1] presents results on the impact of mussel (*Mytilus galloprovincialis*) mariculture on the marine environment, derived through mathematical modeling. The authors employed a population model based on dynamic energy budget theory, integrated with field data on seston content and the chemical composition of mussel tissues. These data were collected in 2006–2007 from three mussel farms located in Italy and Slovenia in the Adriatic Sea. The dynamics of carbon, nitrogen, and phosphorus fluxes were evaluated over a 10-month cultivation period. Calculations revealed that the nitrogen and phosphorus released by mussels as feces and pseudofeces during their life cycle are, respectively, two and five times greater than those incorporated into the mollusks' tissues. The obtained results underscore the need for a comprehensive approach to mariculture site selection, accounting for the environmental impact of marine farming.

The study [2] evaluates the influence of the Apalachicola River (Florida, USA) discharge on the population of the giant oyster *Magallana gigas*. The authors integrated a three-dimensional hydrodynamic circulation model with field data on the oyster life cycle to develop stochastic models. The results identify several environmental factors affecting oyster growth dynamics, with the hydrological regime of the Apalachicola River established as the primary factor. Although the influence of the marine environment on oyster population has been thoroughly studied, the impact of oyster farms on the water area ecosystem remains underexplored. A clearer understanding of the interactions between mariculture and the environment can be achieved by integrating a hydrodynamic model with a biological model.

The study [3] investigates the impact of an oyster farm on the ecosystem of the tidal zone in Marennes-Oléron Bay, France, with a primary focus on the structure of the bay's food chain. A carbon-based food chain model was employed to assess the influence of the oyster farm on the bay ecosystem. The analysis revealed that the presence of oysters alters the interactions between benthic and pelagic organisms, with benthic animals becoming the primary consumers of organic carbon. Doubling the area of the oyster farm increased secondary production, providing additional food for juvenile nekton. Through mathematical modeling, the authors demonstrated how bivalve mollusk mariculture affects the species composition of the tidal zone fauna. During growth, oysters release significant amounts of ammonium and phosphates; however, the direct impact of these compounds on the ecosystem was not investigated in the referenced study.

The efficiency of mariculture cultivation is often evaluated using the ecological carrying capacity of the water area as an indicator. Studies [4–6] describe several models developed to assess the ecological carrying capacity of water areas hosting mariculture operations. In [4], a two-dimensional physical-biogeochemical model applied to Sungo Bay, China, is presented. The findings from [4, 7], along with other studies, informed the strategic placement of a marine farm cultivating polyculture in Sungo Bay. Despite 60 years of active exploitation, the bay's ecosystems remain healthy due to the implementation of scientific recommendations for marine farm management [8].

Literature analysis reveals the widespread use of comprehensive ecological models for studying ecosystems that include mariculture. Studies [1, 3, 6, 8] demonstrate the potential of these models for assessing nutrient and carbon fluxes in ecosystems. Additionally, comprehensive ecological models enable evaluation of the influence of the hydrochemical regime on the productivity of cultivated species [2, 7, 9] and forecasting economic profitability [6, 8]. Analysis of the reviewed models indicates that they are geographically specific, with simulation results heavily dependent on local conditions. A promising approach involves using an individual-based model of the cultivated species as the core of the biological component in these models.

This study aims to develop a two-dimensional model of a marine coastal ecosystem incorporating European oyster mariculture. Using this model, numerical experiments are conducted to investigate and quantitatively assess the impact of an oyster farm on the ecosystem of Donuzlav Bay.

## Materials and methods

Subject and object of research. The European oyster (*Ostrea edulis*), a commercially significant species in the last century, experienced a substantial decline in population, leading to the loss of its commercial importance [1]. The cultivation of *O. edulis* is of interest due to its relevance for restoring wild oyster population and supporting mariculture [2, 3] [10]. Donuzlav Bay was selected as the object of simulation modeling because it hosts several operational marine farms cultivating mussels and oysters [11]. The availability of field data on the dynamics of morphometric characteristics of the flat oyster in this region [3] further supported the choice of Donuzlav Bay as the location for the model plantation.

Model concept. The two-dimensional model of a marine coastal ecosystem is developed using object-oriented modeling (OOM) principles. The modeled ecosystem comprises the marine environment and marine plant and animal

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[1] Krakatitsa, T.F., 1976. [*Biology of the Black Sea Oyster Ostrea edulis L. in Relation to Issues of Its Reproduction*]. Kiev: Naukova Dumka, 80 p. (in Russian).

[2] Kryuchkov, V.G., 2014. [*Oyster Farm. Explanatory Note and Economic Calculations*]. Kerch, 92 p. (in Russian).

[3] Sytnik, N.A., 2014. *Functional Ecology of the Flat Oyster (Ostrea edulis L., 1758, Ostereidae, Bivalvia) of the Black Sea*. Thesis Cand. Biol. Sci., Kerch, 174 p. (in Russian).

organisms. These components are represented as a set of objects or fields on a regular grid.

An object in the OOM framework is defined as a group of identical organisms and their immediate living space (ILS), such as a phytoplankton aggregation, a small area of the seafloor occupied by macroalgae of a certain species, a mussel collector, or an oyster cage. The ILS represents the area where exchange processes between organisms and the environment occur. Geometrically, model objects are represented as cylinders, the dimensions corresponding to the physical dimensions of the designated ILS for a given set of marine organisms. The model assumes a homogeneous distribution of biomass within each object. For cylindrical objects, the height and base radius are defined. The initial positions of objects in the model space can be specified or randomly distributed. When modeling marine farms, objects representing cultivated mariculture are positioned according to the farm's layout. Phytoplankton and phytobenthos objects are distributed randomly.

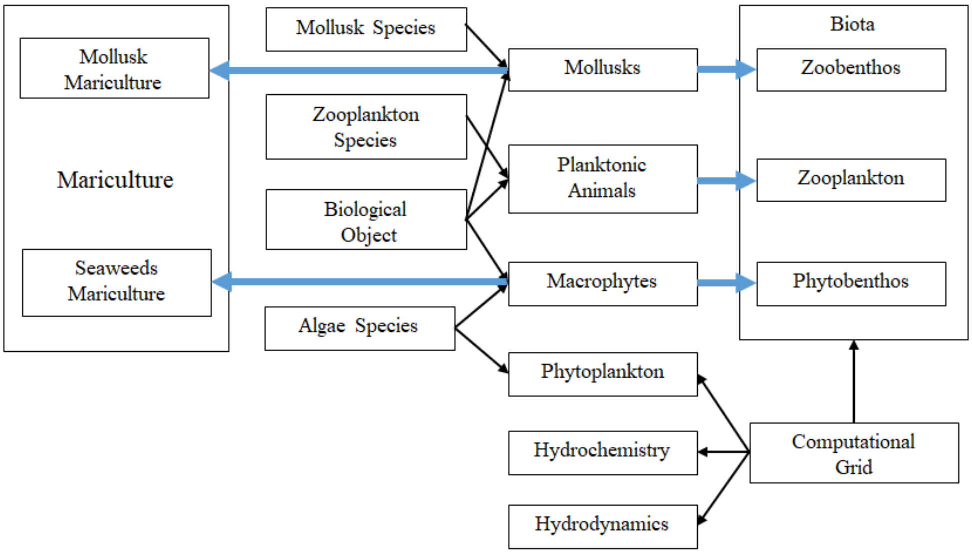
The sizes of objects may change over time. The maximum radius of an object's horizontal projection is set equal to the grid step. When this threshold is exceeded, the object splits into two new objects, with their combined volumes equaling that of the initial object. The mass is distributed equally between the new objects.

The biomass of an object can increase during growth and decrease due to a lack of resources. To save computational power, the program includes a procedure for removing objects with biomass below a threshold level from the calculation area. In this case, the object's biomass is transferred to the pool of particulate organic matter (POM).

The marine environment is represented by a set of hydrophysical and hydrochemical fields defined on a regular grid. The control variables in the model are air temperature, wind velocity, and illumination at the sea surface. The model calculates concentrations of inorganic compounds of nitrogen, phosphorus, and sulfur, POM, dissolved organic matter (DOM), and the concentration of dissolved oxygen in the water. The resource available to an object is calculated as a weighted average of the values in the grid cells partially or fully overlapped by the object's horizontal projection. Weight coefficients are proportional to the area of cell overlap by the object.

The developed simulation model of coastal ecosystem dynamics provides quantitative estimates of environmental characteristics and biological objects at any time. This representation enables the study of the dynamics of all parameters defining the state of the coastal ecosystem and the identification of relationships between its components. Quantitative assessment of material fluxes between ecosystem components allows for accurate determination of the degree and nature of the marine farm's impact on the coastal ecosystem.

OOM of a marine farm. Based on the principles outlined above, a two-dimensional chemical-biological OOM of a marine farm was previously developed [12]. To simulate the operation of an oyster farm and its interactions with the marine environment, a new method was incorporated into the "Mollusks" class, built upon a one-dimensional dynamic energy budget (DEB) model for the European oyster [13]. This method mathematically describes the processes of filtration, feeding, respiration, excretion, growth, and reproduction of the oyster. Model verification results demonstrated strong agreement between the calculated values of linear and weight growth of oysters and those measured during a field experiment in Donuzlav Bay from 2001 to 2003. The structure of the OOM classes is examined in greater detail below (Fig. 1).



**F i g. 1.** Class diagram of the chemical-biological object-oriented model of marine ecosystem. Black arrows indicate heredity, blue ones – inclusion of multiple objects of one class into the properties of another higher class

The “Computational Grid” class defines the coordinates of the calculation domain and a regular grid, at the nodes of which hydrophysical and hydrochemical variables are specified. Class properties include water body depth ($H$), grid steps in the zonal ($dx$) and meridional ($dy$) directions, domain dimensions ($Ndx \times Mdy$), spatial boundaries of the water body, and the time step ($dt$).

The "Hydrodynamics" class is the inheritor of the " Computational Grid" class. Its primary method is a simplified integral model of the Black Sea’s upper layer [14, 15], which describes the spatiotemporal dynamics of the upper mixed layer’s temperature ($T^0$, °C) and depth ($h$, m), as well as the temperature of the lower layer ($T^h$, °C). These layers are assumed to be homogeneous in density. Given that the spatial variability of wind and air temperature fields over the sea, particularly in summer, exceeds the size of the computational domain, a one-dimensional version of the model is employed:

$$h\frac{\partial T^0}{\partial t} = \Gamma^0 - \Gamma^{h-0},$$

$$
\begin{gathered}
\Gamma^0 = a(T^0 - T_{\mathrm{a}}), \\
\frac{\partial h}{\partial t} = \frac{1}{T^0 - T^h}(\Gamma^{h-0} - \Gamma^{h+0}), \\
G - D = 0.5\alpha g h \rho_w (\Gamma^0 + \Gamma^{h-0}), \qquad (1) \\
G = C_g V_*^3,\ D = \rho V_*^3 \left(f\left(\frac{h}{L_1}\right) + \frac{a_2 h}{L|N|}\right), \\
f\left(\frac{h}{L_1}\right) = \left\{\begin{matrix} \frac{a_1 h}{L_1} \text{ at } h \le \frac{C_g}{a_1} L_1 \\ C_g \text{ at } h > \frac{C_g}{a_1} L_1 \end{matrix}\right\},
\end{gathered}
$$

where $\Gamma^0$ is the heat flux through the sea surface; $\Gamma^{h\text{-}0}$ and $\Gamma^{h+0}$ are the heat fluxes at the lower boundary of the mixed layer and the upper boundary of the lower layer, respectively; $T_{\mathrm{a}}$ is the air temperature (°C); $\alpha$ is the coefficient of thermal expansion of water; $\rho_w$ is the water density (kg/m$^3$); $G, D$ represent the integral generation and dissipation of turbulent energy, respectively; $V_* = \sqrt{\frac{\tau_0}{\rho_w}}$ is the dynamic friction velocity in water; $\tau_0$ is the wind stress at the surface; $L$ is the Monin–Obukhov length scale (m); $L_1$ is the boundary layer thickness scale; $N = L/L_1$ is the dimensionless Kazansky–Monin stratification parameter; and $C_g$, $a$, $a_1$, $a_2$ are empirical coefficients.

Equation (1) defines the condition for switching between two regimes of upper layer dynamics: entrainment and detrainment of water mass into or from the upper layer. Entrainment occurs when $G - D - 0.5\rho_w \alpha g h \Gamma^0 > 0$, resulting in changes to the characteristics of the upper mixed layer while the lower layer remains unchanged. Otherwise, detrainment occurs, altering the characteristics of the lower layer while the upper layer remains unchanged. However, gas and heat exchange through the surface may modify the temperature and oxygen content in the upper layer. Thus, the two-layer model with a time-variable upper layer incorporates an additional term to the equations for hydrochemical variables of the upper layer [16]:

$$
\frac{\partial Y_i^0}{\partial t} + U\frac{\partial Y_i^0}{\partial x} + V\frac{\partial Y_i^0}{\partial y} = K_x\left(\frac{\partial^2 Y_i^0}{\partial x^2} + \frac{\partial^2 Y_i^0}{\partial y^2}\right) + G_i^0 + A_i^0 + \frac{\Gamma^{h-0} - \Gamma^{h+0}}{(T^0 - T^h)h}(Y_i^h - Y_i^0) \quad (2)
$$

and the lower layer:

$$
\frac{\partial Y_i^h}{\partial t} + U\frac{\partial Y_i^h}{\partial x} + V\frac{\partial Y_i^h}{\partial y} = K_x\left(\frac{\partial^2 Y_i^h}{\partial x^2} + \frac{\partial^2 Y_i^h}{\partial y^2}\right) + G_i^h + A_i^h + \frac{\Gamma^{h-0} - \Gamma^{h+0}}{(T^0 - T^h)(H-h)}(Y_i^h - Y_i^0), \quad (3)
$$

where $Y_i^0$ and $Y_i^h$ represent variables of the “Hydrochemistry” block in the upper and lower layers (μM); $U$, $V$ are the layer-averaged current velocities (m/s); $G_i$, $A_i$ are source (sink) functions determined by chemical and biological processes, respectively; the superscripts “0” and “$h$” indicate association with the upper or lower layer, respectively; $H$ is the basin depth (m); and $K_x$ is the horizontal diffusion coefficient.

The “Hydrochemistry” class inherits from the “Computational Grid” class and is characterized by the following properties: concentrations of nitrates, nitrites, phosphates, dissolved oxygen, hydrogen sulfide, sulfates, sulfites, sulfur, and dissolved and particulate organic nitrogen at the nodes of the regular grid; coefficients in the parameterizing chemical reactions; and diffusion coefficients for suspended and dissolved substances. The class includes the following methods:

– a one-dimensional chemical-biological model that describes the coupled nitrogen and sulfur cycles under aerobic and anaerobic conditions, developed for modeling processes in the redox zone of the Black Sea (provides the setting of $G_i$ functions in equations (2) and (3)). The chemical reaction equations and parameter values used in the calculations are detailed in [17];

– a procedure for calculating advection, diffusion, and vertical mixing at the boundary of two layers, with adjustments to hydrochemical variables;

– a procedure for incorporating the discharge and input of dissolved and suspended substances from the biological components of the model.

The “Phytoplankton” class is the inheritor of the “Computational Grid” and “Algae Species” classes. In the current model version, phytoplankton is represented as a passive tracer, simplifying the model and reducing computational time while maintaining acceptable error margins [18]. The primary method of this class is a model of phytoplankton field evolution, influenced by external conditions and interactions with mollusk mariculture objects. It is a two-dimensional adaptation of a previously developed and validated one-dimensional model [19]:

$$\frac{\partial B}{\partial t}+U\frac{\partial B}{\partial x}+V\frac{\partial B}{\partial y}=K_x\left(\frac{\partial^2 B}{\partial x^2}+\frac{\partial^2 B}{\partial y^2}\right)+(P_{\mathrm{r}}(1-k_{\mathrm{r}})-k_{\mathrm{e}}-m)B-\sum A_i, \qquad (4)$$

$$\frac{\partial Q_{\mathrm{N}}}{\partial t}+U\frac{\partial Q_{\mathrm{N}}}{\partial x}+V\frac{\partial Q_{\mathrm{N}}}{\partial y}=K_x\left(\frac{\partial^2 Q_{\mathrm{N}}}{\partial x^2}+\frac{\partial^2 Q_{\mathrm{N}}}{\partial y^2}\right)+V_{\mathrm{NO_3}}^{\max}\big(1-f(Q_{\mathrm{N}})\big)\frac{[\mathrm{NO_3}]}{K_{\mathrm{NO_3}}+[\mathrm{NO_3}]}+$$
$$+V_{\mathrm{NH_4}}^{\max}\big(1-f(Q_{\mathrm{N}})\big)\frac{[\mathrm{NH_4}]}{K_{\mathrm{NH_4}}+[\mathrm{NH_4}]}-P_{\mathrm{r}}Q_{\mathrm{N}}, \qquad (5)$$

$$\frac{\partial Q_{\mathrm{P}}}{\partial t}+U\frac{\partial Q_{\mathrm{P}}}{\partial x}+V\frac{\partial Q_{\mathrm{P}}}{\partial y}=K_x\left(\frac{\partial^2 Q_{\mathrm{P}}}{\partial x^2}+\frac{\partial^2 Q_{\mathrm{P}}}{\partial y^2}\right)+V_{\mathrm{P}}^{\max}\big(1-f(Q_{\mathrm{P}})\big)\frac{[\mathrm{P}]}{K_{\mathrm{P}}+[\mathrm{P}]}-P_{\mathrm{r}}Q_{\mathrm{P}}, \qquad (6)$$

$$P_{\mathrm{r}}=\mu\cdot\min(f(Q_{\mathrm{N}}),f(Q_{\mathrm{P}})),$$

where $B$ represents phytoplankton biomass (mg/m$^3$); $t$ is time (days); $U$, $V$ are vertically averaged advection velocities (m/s); $\mu$ is the maximum specific rate of gross phytoplankton production (1/day); $P_{\mathrm{r}}$ is the realized specific rate of gross production (1/day); $k_{\mathrm{r}}$ is the coefficient determining energy expenditure on respiration; $k_{\mathrm{e}}$ is the coefficient of organic matter release (exudation); $m$ is the phytoplankton cell mortality rate (1/day); $Q_{\mathrm{N}}$ and $Q_{\mathrm{P}}$ are the internal nitrogen and phosphorus content in phytoplankton cells, respectively (pmol/cell); $Q_{\mathrm{N}}^{\max}$, $Q_{\mathrm{N}}^{\min}$, $Q_{\mathrm{P}}^{\max}$, $Q_{\mathrm{P}}^{\min}$ are the maximum and minimum nitrogen and phosphorus content in phytoplankton cells (pmol/cell); [$\mathrm{NO_3}$], [$\mathrm{NH_4}$], [P] are the concentration of nitrates, ammonium, and phosphorus in water (μM); $V_{\mathrm{NO_3}}$, $V_{\mathrm{NH_4}}$, $V_{\mathrm{P}}$ are the uptake rates of nitrates, ammonium, and phosphorus in water (pmol/(cell day)); $V_{NO_3}^{max}$, $V_{NH_4}^{max}$, $V_P^{max}$ are the maximum nutrient uptake rates (pmol/(cell day); $K_P$, $K_{NO_3}$, $K_{NH_4}$ are half-saturation constants (μM); and $\sum A_i$ represents the cumulative impact of oyster farm objects on the phytoplankton field. The number of phytoplankton cells per unit volume is calculated based on the carbon content in a cell $Q_C$, which is assumed to be constant, unlike $Q_N$ and $Q_P$. For diatoms, $Q_C$ = 12 pmol/cell. Given a phytoplankton biomass $B$ = 0.083 mmol C/m$^3$, the number of cells $K = \frac{0.083}{12} \frac{B}{Q_C} 10^9 = 6.9 \cdot 10^6 B(\text{cell/m}^3)$.

The numerical parameters of the phytoplankton species *Thalassiosira pseudo* used in this study are presented in Table 1.

Table 1

**Numerical values of phytoplankton parameters**

| Parameter | *Thalassiosira pseudo* |
|---|---|
| $Q_N^{max}$, pmol/cell | 0.286 |
| $Q_N^{min}$, pmol/cell | 0.050 |
| $Q_P^{max}$, pmol/cell | 0.020 |
| $Q_P^{min}$, pmol/cell | 0.001 |
| $V_{NO_3}^{max}$, pmol/(cell day) | 0.257 |
| $V_{NH_4}^{max}$, pmol/(cell day) | 0.744 |
| $V_P^{max}$, pmol/(cell day) | 0.210 |
| $K_P$, μM | 0.580 |
| $K_{NO_3}$, μM | 0.860 |
| $K_{NH_4}$, μM | 0.200 |
| $k_r$, 1/day | 0.150 |
| $k_e$, 1/day | 0.250 |
| $m$, 1/day | 0.250 |
| $P_{max}$, mg $O_2$/g DW/h | 1.250 |
| $R_d$, mg $O_2$/g DW/h | 0.310 |
| α | 0.110 |

The “Biological Object” class defines properties including the object’s coordinates within the modeling domain, its vertical and horizontal dimensions, mass, and the range of possible variations in biomass and size.

The “Mollusk Species” class encompasses all parameters necessary for describing the energy balance of various mollusk species. The “Mollusks” class inherits from both the “Mollusk Species” and “Biological Object” classes, providing a comprehensive description of the carrier (collector or raft) and the group of cultivated mollusks. This includes parameters of the DEB model, which describes their growth on the carrier and interactions with the environment. The primary method of the "Mollusks" class is the DEB model adapted to the specific mollusk species [13]:

$$K_{\mathrm{d}} \frac{dW_{\mathrm{d}}}{dt} = \left(P_{\mathrm{som}} + P_{\mathrm{gen}}\right),$$
$$P = P_{\mathrm{som}} + P_{\mathrm{gen}} + P_{\mathrm{sh}} = A_{\mathrm{e}} F K_{\mathrm{c}} C - R - E_{\mathrm{x}},$$

where $K_{\mathrm{d}}$ represents the caloric content of mollusk tissues (cal/(g dry weight)); $W_{\mathrm{d}}$ is the dry weight of soft tissues (g); $P_{\mathrm{som}}$ is the energy costs for somatic tissue growth (cal/h); $P_{\mathrm{gen}}$ is the energy costs for generative tissue growth (cal/h); $P_{\mathrm{sh}}$ is the energy expenditure for shell growth (cal/h); $R$ is the energy expended on mollusk respiration (cal/h); $E_{\mathrm{x}}$ is the excreted energy (cal/h); $F$ is the filtration rate (L/h); $K_{\mathrm{c}}$ is the caloric content of food suspension (cal/mg); $C$ is the concentration of the food suspension (mg/L); and $A_{\mathrm{e}}$ is the food assimilation coefficient.

The current version of the ecological model incorporates two variants of the DEB model: one for the Black Sea mussel (*Mytilus galloprovincialis*) and one for the flat oyster (*Ostrea edulis*). This enables the model to simulate the operation of different mollusk species within a single area. Detailed DEB models describing the growth of oysters and mussels, along with approximations of their life processes, are provided in [13, 20].

The "Mariculture" class includes a set of objects from the "Mollusks" class. This class defines general and integral characteristics of the marine plantation, including its spatial configuration, length, volume, arrangement of collectors relative to the surface, total mass of cultivated mollusks, their production characteristics, and the quantities of consumed and released substances.

Similarly, an object of the "Mollusks" class can represent a group of identical bivalve mollusk individuals occupying a fixed area of the seabed with known dimensions and coordinates. In this case, a collection of such objects forms the "Zoobenthos" array.

The "Planktonic Animals" class inherits from the "Biological Object" and "Zooplankton Species" classes. A collection of such objects ("Zooplankton" in Fig. 1), together with the "Phytobenthos" and "Zoobenthos" arrays, is included in the "Biota" class, which is the inheritor of the "Computational Grid" class. The properties of the "Biota" class encompass fields of all biological components of the ecosystem on a two-dimensional grid, as well as averaged or integrated characteristics essential for analyzing system behavior. The methods of this class enable calculation of all listed characteristics and the conversion of object-based representations into two-dimensional fields suitable for analysis and visualization.

The "Macrophytes" class inherits from the "Algae Species" and "Biological Object" classes, and its object's properties include all necessary information for calculating the production and metabolic processes of macroalgae for a specific species. The primary method of the "Macrophytes" class is the DEB model developed in [21, 22]. For macroalgae and microalgae nearly identical models are used, with minor differences reflecting the specific characteristics of available natural data. Based on these data, the following equations were formulated:

$$\frac{dB_\mathrm{m}}{dt} = (P_\mathrm{r} - k_\mathrm{e} - m)B_\mathrm{m},$$

$$\frac{dQ_\mathrm{N}}{dt} = V_{\mathrm{NO}_3}\frac{[\mathrm{NO}_3]}{K_{\mathrm{NO}_3} + [\mathrm{NO}_3]} + V_{\mathrm{NH}_4}\frac{[\mathrm{NH}_4]}{K_{\mathrm{NH}_4} + [\mathrm{NH}_4]} - P_\mathrm{r}Q_\mathrm{N},$$

$$\frac{dQ_\mathrm{P}}{dt} = V_\mathrm{P}\frac{[\mathrm{P}]}{K_\mathrm{P} + [\mathrm{P}]} - P_\mathrm{r}Q_\mathrm{P},$$

$$P(E) = \left(P_{\max}\tanh\left(\alpha\frac{E}{P_{\max}}\right) - R_\mathrm{d}\right)f(T),$$

$$E = E_0\exp(-\beta z),$$

$$P_\mathrm{r} = P(E)\,k_\mathrm{DW}\min\big(f(Q_\mathrm{N}), f(Q_\mathrm{P})\big)\,C_\mathrm{w},$$

$$f(Q_\mathrm{N}) = \frac{Q_\mathrm{N} - Q_\mathrm{N}^{\min}}{Q_\mathrm{N}^{\max} - Q_\mathrm{N}^{\min}},$$

$$f(Q_\mathrm{P}) = \frac{Q_\mathrm{P} - Q_\mathrm{P}^{\min}}{Q_\mathrm{P}^{\max} - Q_\mathrm{P}^{\min}},$$

$$V_{\mathrm{NO}_3} = V_{\mathrm{NO}_3}^{\max}\big(1 - f(Q_\mathrm{N})\big),$$

$$V_{\mathrm{NH}_4} = V_{\mathrm{NH}_4}^{\max}\big(1 - f(Q_\mathrm{N})\big),$$

$$V_\mathrm{P} = V_\mathrm{P}^{\max}(1 - f(Q_\mathrm{P})),$$

where $E_0$ (μmol photon/m$^2$/s) represents photosynthetically active radiation (PAR) at the water surface, $E$ is the PAR at depth $z$ (m); $B_\mathrm{m}$ is the biomass of the macrophyte object (g dry weight/m$^3$); $P_\mathrm{r}$ is the specific growth rate (1/day); $P(E)$ is the photosynthesis rate (mg $O_2$/g dry weight/h); $P_{\max}$ is the maximum photosynthesis rate; α is the slope of *PE*-curve at low light flux values; $R_\mathrm{d}$ (mg $O_2$/g dry weight/h) is the dark respiration rate, representing the oxygen consumed for respiration in the absence of PAR; $Q_\mathrm{N}$ and $Q_\mathrm{P}$ (μmol/g dry weight) are the concentrations of phosphorus and nitrogen in algal tissues; $Q_\mathrm{N}^{\max}$, $Q_\mathrm{N}^{\min}$, $Q_\mathrm{P}^{\max}$, $Q_\mathrm{P}^{\min}$ (μmol/g dry weight) are the minimum and maximum concentrations of phosphorus and nitrogen in algal tissues; $V_{\mathrm{NO}_3}$, $V_{\mathrm{NH}_4}$, $V_\mathrm{P}$ are the uptake rates of nitrates, ammonium, and phosphorus from water (μmol/g dry weight/h); $V_{\mathrm{NO}_3}^{\max}$, $V_{\mathrm{NH}_4}^{\max}$, $V_\mathrm{P}^{\max}$ are the maximum nutrient uptake rates; $K_\mathrm{P}$, $K_{\mathrm{NO}_3}$, $K_{\mathrm{NH}_4}$ are half-saturation constants (μM); $m$ is the mortality coefficient; $k_\mathrm{e}$ is the exudation rate; and $k_\mathrm{DW}$ is the conversion coefficient from $O_2$ mg to C mg.

The numerical parameters of phytobenthos, comprising two seagrass species (*Zostera noltii* and *Ruppia maritima*), used in this study are presented in Table 2.

A collection of objects of the “Macrophytes” class forms the “Phytobenthos” array, which is a property of the “Biota” class. Analogous to the “Mollusks” class, a collection of objects from the “Macrophytes” class can be included in an object of the “Mariculture” class, which describes a plantation of cultivated macroalgae. The top-level class “Ecosystem” includes instances of the classes “Hydrodynamics”, “Hydrochemistry”, “Phytoplankton”, “Mariculture”, “Biota”.

Table 2

**Numerical values of phytobenthos parameters**

| Parameter | *Zostera noltii* | *Ruppia maritima* |
|---|---|---|
| $Q_N^{max}$, μmol/g DW | 4507 | 4507 |
| $Q_N^{min}$, μmol/g DW | 755 | 755 |
| $Q_P^{max}$, μmol/g DW | 118 | 118 |
| $Q_P^{min}$, μmol/g DW | 30 | 30 |
| $V_{NO_3}^{max}$, μmol/g DW/h | 3.0 | 14.1 |
| $V_{NH_4}^{max}$ , μmol/g DW/h | 19.4 | 75.0 |
| $V_P^{max}$, μmol/g DW/h | 2.42 | 9.30 |
| $K_P$, μM | 1.5 | 1.5 |
| $K_{NO_3}$, μM | 7.0 | 9.2 |
| $K_{NH_4}$, μM | 12.3 | 12.3 |
| $k_e$, 1/h | 0.1 | 0.1 |
| $m$, 1/day | 0.005 | 0.005 |
| $P_{max}$, mg $O_2$/g DW/h | 6.85 | 15.94 |
| $R_d$, mg $O_2$/g DW/h | 1.70 | 1.43 |
| α | 0.046 | 0.060 |

## Results and discussion

The configuration of the model oyster farm was designed based on recommendations for managing oyster farms in Donuzlav Bay [2]. The total area occupied by the oyster plantation is ~ 80 hectares. Oyster cages are suspended from rafts, with each raft designed to hold 500 kg of raw oyster mass (including shells) of marketable size. The rafts are organized into blocks of 8 units each, connected sequentially. The model oyster farm comprises 24 blocks, yielding ~100 tons of marketable products.

The initial conditions for model integration include the average dry weight of soft tissues of a single oyster, the total dry weight of all cultivated mollusks on a single raft (carrier), the vertical profile of water temperature, and fields of hydrochemical elements (nitrates, nitrites, ammonium, phosphates, POM and DOM), as well as phytoplankton biomass. The fields of chemical compounds were generated as random variables with specified mean and variance. Average concentrations were adopted from [11]: [$NH_4$] = 3.6 μM; [$NO_3$] = 3.0 μM; [$PO_4$] = 0.25 μM; [POM] = 5 μmol N/l; [DOM] = 5 μmol N/l; $B = 200$ mg/m$^3$. At the grid nodes, with a temporal resolution of three hours, vectors of vertically averaged current velocities were prescribed, calculated previously using a hydrodynamic nonlinear sigma-coordinate circulation model in the hydrostatic approximation [23]. In this model version, the zooplankton and zoobenthos components were disabled.

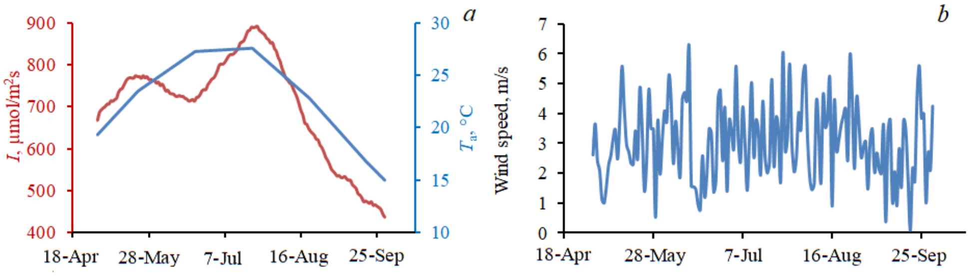
At each integration step, the exchange processes between objects and the environment were calculated. Phytoplankton and macroalgae assimilate carbon, nitrogen, and phosphorus compounds from the environment, releasing oxygen and DOM. Oysters consume phytoplankton and POM from the environment and release phosphates, ammonium, DOM, and POM, with a portion of the POM returning to the suspended matter pool in the water column and another portion contributing to biodeposits (SDM). At each integration step, objects calculate available resources based on the ecosystem's state, modified by prior calculations. This approach simulates competition for resources. When objects intersect or overlap, resource consumption by earlier-processed objects within the same time step can be significant, potentially causing nutrient deficiencies for subsequent objects. To avoid consistently disadvantaging certain objects, the order of calculations at each integration step was randomized.

<u>Initial and boundary conditions.</u> The integration step varied across the biological, chemical, and hydrodynamic components of the model. The dynamics of biological objects and chemical reaction equations were calculated with a time step of three hours, while advection and diffusion of fields were computed with a time step of 36 minutes. At the open boundaries of the computational domain, zero gradient conditions normal to the boundary were applied.

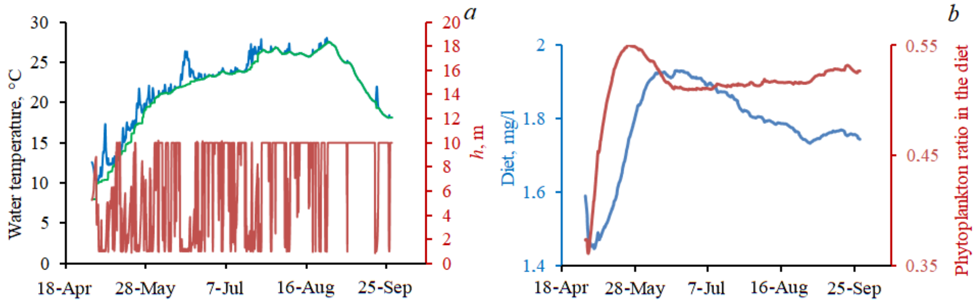
The phytoplankton field was represented as a collection of diatom microalgae objects with a high growth rate. The control variables of the model included surface illumination, air temperature, and wind velocity (Fig. 2). The time series of surface illumination was based on average insolation estimates for the Black Sea [24], with diurnal variability modeled using a sinusoidal function. Air temperature and wind velocity were derived from ERA-Interim data (2007) with a temporal resolution of three hours. The integration period spanned 5 months, from May to October, corresponding to the period of active oyster growth.

The time required for an oyster to reach marketable size from the moment it is placed in a cultivation cage is 27–33 months [2]. Consequently, calculations were performed for two size groups of oysters, corresponding to the second and third years of cultivation, with initial raw weights of soft tissues of 2.3 g and 18.4 g (shell heights of 22 mm and 48 mm, respectively). The impact of the oyster plantation on the ecosystem was evaluated through the dynamics of exchange processes between oysters and the marine environment. The following parameters were calculated: farm-averaged oyster shell height, oyster soft tissue mass, filtration rates, consumption, metabolic costs, excretion, mass of excreted ammonium and phosphates, and average concentrations of hydrochemical components across the entire computational domain and within the oyster farm area.

The conditions of the model marine environment for oyster cultivation are illustrated in Figs. 2 and 3. Fig. 3, a shows the evolution of the vertical temperature profile under the influence of heating and wind stress. The profile, determined by the upper mixed layer (UML) model variables $T^0$, $T^h$ and $h$, evolves as follows: as heating intensifies, mixing extends to the seafloor, effectively eliminating the two-layer structure and establishing homogeneous conditions throughout the depth of the modeled water body. A new UML briefly forms during a sharp increase in wind stress but rapidly dissipates. Fig. 3, *b* depicts the dynamics of the average food suspension concentration across the computational domain and the ratio between its components – phytoplankton and POM. Phytoplankton accounts for approximately half of the mollusk' diet.

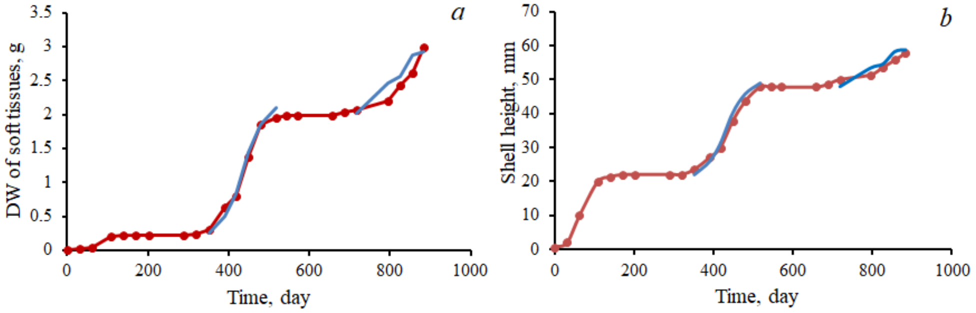


**F i g. 2.** Control variables of the model: insolation at midday (red curve), diurnal maximum air temperature (blue curve) (*a*); wind speed (*b*)



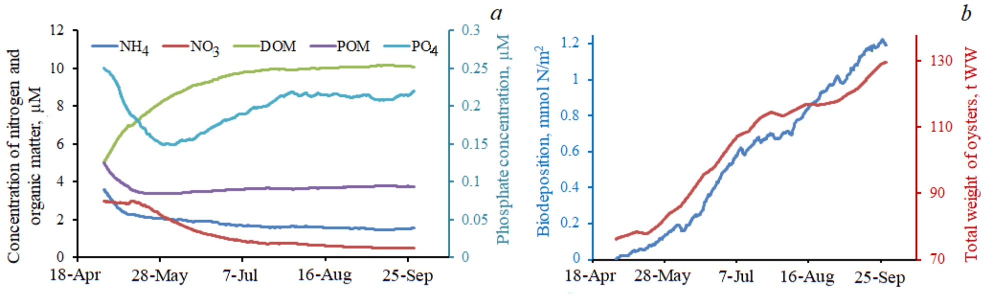
**F i g. 3.** Marine environment conditions: temperature of the upper (blue curve) and lower (green curve) layers, thickness of the upper layer (*a*); concentration of suspended food, and ratio between the mollusk diet components: phytoplankton and suspended organic matter (*b*)

Numerical experiments. The model was validated using the data from work [3], collected at an oyster farm in Donuzlav Bay during 2002–2003. The external conditions of the experiment, including water temperature and food suspension concentration, closely matched observed values. Fig. 4 presents a comparison of field data and model calculations for periods of active mollusk growth in the second and third years of cultivation.



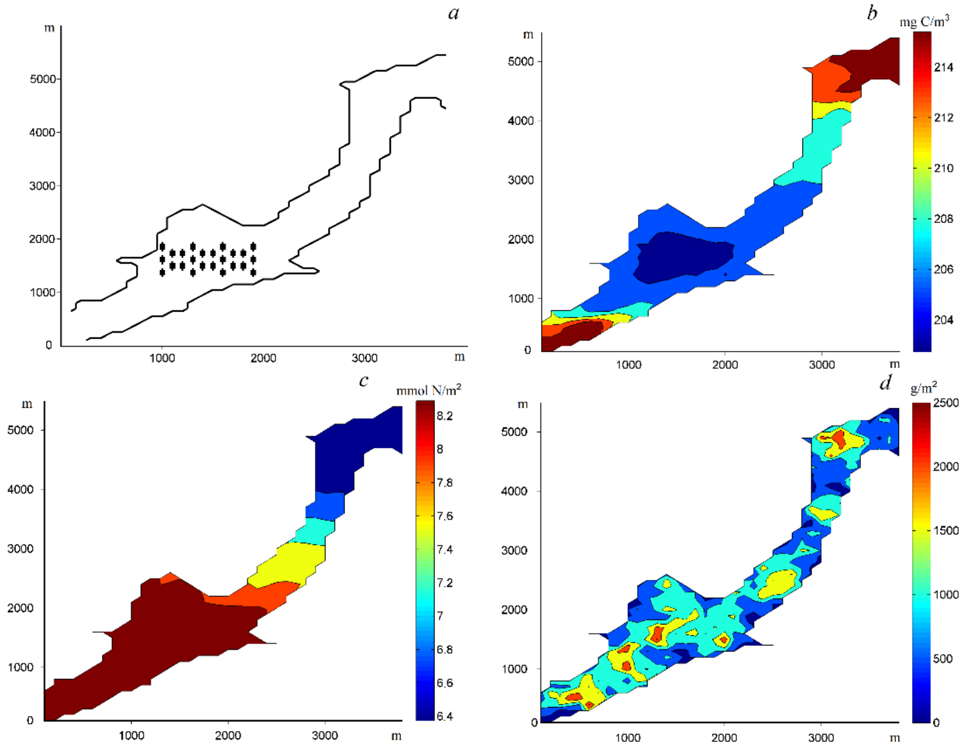
**F i g. 4.** Comparison of model (blue curve) and field (red curve) [3] data by two indicators: dry weight of oyster soft tissues (*a*) and shell height (*b*)

All graphs below refer to calculations for the third year of oyster cultivation, when ecosystem changes are more pronounced. Fig. 5 shows the average values of key hydrochemical characteristics across the computational domain, alongside model data on the growth of the total mass of cultivated oysters and the corresponding biodeposit accumulation over a 5-month period. The concentrations of nitrogen and phosphorus compounds in water, both organic and inorganic, exhibit quasi-stationary values that deviate slightly from those calculated for ecosystem dynamics in the absence of a farm. Within the immediate vicinity of the farm, concentrations differ by 10–20%, but across the entire computational domain, the difference is only 1–2%. The most notable differences in chemical component concentrations occur for organic matter, as inorganic compounds are rapidly assimilated by the plant components of the ecosystem, while POM and DOM persist as traces of autotroph activity.



**F i g. 5.** Dynamic graphs of hydrochemical characteristics for the third year of oyster cultivation (*a*), biodeposits and total mass of cultivated oysters (*b*)

The operation of an oyster plantation with a total mass of ~ 100 tons results in increased biodeposit accumulation and seabed siltation, extending not only directly beneath the farm but also to a considerable distance (Fig. 6).

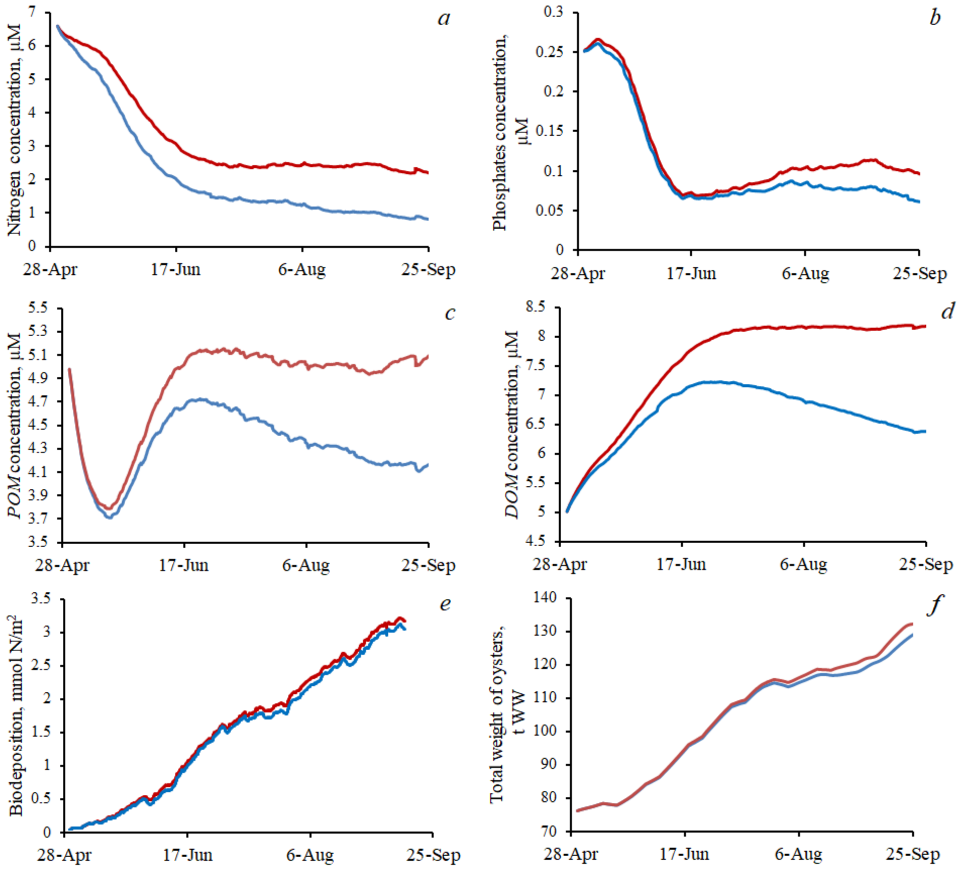


**F i g. 6.** Oyster farm scheme (*a*), phytoplankton biomass (*b*), biodeposits (*c*), phytobenthos biomass (*d*). The submitted fields correspond to the last day of calculation on 30.09.2007

As antisipated, phytoplankton biomass in the farm area is lower than in the surrounding waters, though this difference is minimal. The mass of biodeposits increases toward the southwest, likely due to the specific patterns of water circulation.

The impact of phytobenthos on oyster growth and the ecological state of the water area was investigated. Two scenarios were compared: one with phytobenthos (seagrasses *Ruppia maritima* and *Zostera noltii* with an average total biomass of 770 g raw weight/m$^2$) and one without. The results are presented in Fig. 7. The presence of bottom vegetation significantly reduces the concentrations of inorganic nitrogen and phosphorus compounds, DOM and POM in the water column. Concurrently, the biomass of farm production and the amount of biodeposits decrease slightly.

The beneficial impact of seagrass beds on the ecological state of coastal waters, particularly in areas with limited water exchange with the open sea, is well established. Primarily, phytobenthos ensures an adequate oxygen supply for benthic organisms, supporting their respiration and the oxidation of POM settling to the seafloor. As shown in Fig. 7, seagrass beds also significantly reduce the concentrations of nitrogen and phosphorus compounds in the water column.



**F i g. 7.** Comparison of two numerical experiments – with (blue curve) and without (red curve) inclusion of macrophytobenthos: concentration of the sum of ammonium and nitrates in water (*a*), phosphates (*b*), POM (*c*), DOM (*d*), biodeposits in nitrogen units (*e*), mass of oysters cultivated at the farm (*f*)

Oysters release nitrogen in the form of ammonium at a rate of 0.3 to 0.83 mg N/(g dry weight day) and phosphorus in the form of phosphates at a rate of 0.06 to 0.1 mg/(g dry weight day), with organic nitrogen compounds released at a rate of 0.03 mg N/(g dry weight day). For the entire oyster farm, the total nitrogen release ranges from 0.33 to 1.35 kg N/day, and the total phosphorus release ranges from 0.04 to 0.18 kg P/day. These values double during spawning periods.

## Conclusion

The proposed model yields results consistent with field monitoring data of flat oyster cultivation in Donuzlav Bay and a one-dimensional model (linear and weight growth rates, diet, respiration costs, excretion, and production). The dynamics of these characteristics are driven by external environmental conditions, such as water temperature and food suspension concentration, including POM and phytoplankton. Analysis of simulation results reveal the nature of interactions between the oyster farm and the water body, quantifying exchange processes. The oyster farm is integrated into the carbon, nitrogen, and phosphorus cycles of the ecosystem; mollusks consume food suspension and release detritus, ammonium, and phosphates. Model data indicate that in the first year of cultivation (with an average raw weight of mollusk soft tissues of 1.2–4.5 g), the ecosystem impact is minimal. However, when mollusks exceed 45 mm (17 g raw weight of soft tissues), the farm's impact on the ecosystem becomes noticeable and intensifies as individuals grow.

Concentrations of dissolved compounds in the farm area exceed background levels by ~ 10–20%, but differences across the bay as a whole are negligible. The primary impact of the oyster farm is bottom siltation due to the sedimentation of biodeposits, such as mollusk feces and pseudofeces. The siltation area extends beyond the farm, with its size and configuration determined by the velocity and direction of prevailing currents. Phytobenthos positively affects water quality in the bay reducing ammonium and phosphate concentrations and competing with phytoplankton for nutrients, as confirmed by numerical modeling results.

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**Tatiana A. Filippova** – statement of the problem, development of the biogeochemical model, numerical experiments with the developed model, qualitative and quantitative analysis of the results, preparation of the text and graphic materials for the article

**Vladimir V. Fomin** – numerical modeling of circulation in the Donuzlav Bay during the spring-summer seasons of 2007–2009, preparation of mean current fields for the biogeochemical model

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