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**A model for biodegradation of polymer fibers made
 of poly-3-hydroxybutyrate poly(3HB)
 and poly-3-hydroxybutyrate-co-3-hydroxyvalerate poly(3HB-co-3HV)
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Abstract

Biodegradation of medical devices is a complex process that depends on many factors, ranging from the methods of polymer synthesis to the concentration of active enzymes in the medium. Mathematical modeling of the biodegradation of polyhydroxyalkanoates (PHAs) is of great practical importance as it allows the degradation of the material to be analyzed with different parameters and different product forms to be considered without the need for many lengthy experiments. Considering the kinetics and mechanisms of enzymatic degradation of PHA, two main processes can be distinguished: adsorption and hydrolysis. The first step is the adsorption of the enzyme onto the polymer surface, and the second step is the hydrolysis of the polymer chain. In finite element modeling, adsorption can be described by surface homogeneous diffusion and hydrolysis by a reaction equation, similar to models for polylactides. To find the unknown model parameters, a nonlinear optimization problem is solved using Sparse Nonlinear OPTimizer (SNOPT) and experimental data on the biodegradation of poly(3HB) and poly(3HB-co-3HV) polymer fibers in three biological environments (human blood, blood serum, and *in vivo*). Based on the simulation results, numerical and experimental results were compared, and the influence of model parameters on the biodegradation profile was analyzed. The model was also applied to assess the biodegradation of other polymeric medical devices such as a vascular stent and a bone implant. The proposed finite element model allows for assessing the biodegradation of polymeric medical devices made from PHA in various biological environments. The biodegradation simulation results are in good agreement with experimental data. This model is the first step towards modeling the biodegradation of PHA and does not include the change in crystallinity, the characteristics of the enzyme during degradation, which may be a further aim of the work.

Keywords

biodegradation model, finite element method, polyhydroxyalkanoates, adsorption, hydrolysis, polymer medical devices

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Модель биodeградации полимерных нитей, изготовленных из поли-3-гидроксibuтирата (P3HB) и поли-3-гидроксibuтирата-co-3-гидроксивалерата (P3HB-co-3HV)

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Аннотация

Введение. Биodeградация медицинских изделий зависит от множества факторов, начиная от методов синтеза полимеров и заканчивая концентрацией активных ферментов в среде. Математическое моделирование биodeградации полигидроксialканоатов (ПГА) имеет большое практическое значение, поскольку позволяет анализировать деградацию материала с различными параметрами и рассматривать разные формы изделий без необходимости проведения множества длительных экспериментов. **Метод.** Рассматривая кинетику и механизмы ферментативной деградации ПГА, можно выделить два основных процесса: адсорбцию и гидролиз. В предлагаемой конечно-элементной модели адсорбция описывается уравнением гомогенной диффузии на поверхности, гидролиз — уравнением реакции, аналогично моделям для полилактидов. Для поиска неизвестных параметров модели решается задача нелинейной оптимизации с помощью Sparse Nonlinear OPTimizer и экспериментальных данных биodeградации полимерных нитей из poly(3HB) и poly(3HB-co-3HV) в трех биологических средах (человеческая кровь, сыворотка крови и *in vivo*). **Основные результаты.** По результатам моделирования проведено сравнение численных и экспериментальных результатов, проанализировано влияние параметров модели на профиль биodeградации. Разработанная модель применена для оценки биodeградации полимерных медицинских изделий, таких как сосудистый стент и костный имплантат. **Обсуждение.** Предложенная конечно-элементная модель позволяет оценить биodeградацию полимерных медицинских изделий из ПГА в различных биологических средах. Результаты моделирования биodeградации хорошо согласуются с экспериментальными данными. Модель является первым шагом к моделированию биodeградации ПГА и не включает изменение кристалличности, характеристики фермента в процессе деградации, что может стать целью дальнейшей работы.

Ключевые слова

модель биodeградации, метод конечных элементов, полигидроксialканоаты, адсорбция, гидролиз, полимерные медицинские изделия

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Introduction

Biodegradation of medical devices is a complex process that depends on many factors, ranging from the methods of polymer synthesis to the concentration of active enzymes in the medium. Mathematical modeling of the biodegradation of polyhydroxyalkanoates (PHAs) is of great practical importance, as it allows the degradation of the material to be analyzed with different parameters and different product forms to be considered without the need for many lengthy experiments — one experiment may run for 180 days of degradation, for example [1].

In the field of biodegradation modeling, one often finds models based on a phenomenological approach, where one does not try to include all possible processes during degradation, but selects some of the most important

components. For example, finite element models of polylactide (PLA) biodegradation have been proposed based on the description of polymer hydrolysis [2–4]. There is also a similar work that solves the heat transfer problem to study the biodegradation of coronary stents [5]. Unfortunately, such models are difficult to apply to PHA polymers because of their hydrophobicity and virtually no autocatalytic component. Biodegradation of PHA occurs only in the presence of specific enzymes — depolymerases. The rate of enzymatic hydrolysis of PHA is a complex process and depends on the availability of ester bonds with water or enzymes, hydrophilicity, morphology, molecular weight, monomers, and other physical properties [6].

In the case of biodegradation of PHA polymers, we can distinguish a model of poly(3HB) synthesis in a bioreactor

[7], a metabolic model [8], a hybrid model to describe PHA production [9], and a neural model to model and predict the behavior of nonlinear abiotic hydrolysis of PLA/PHA tissues [10]. Considering the kinetics and mechanisms of enzymatic degradation of PHA, two main processes can be distinguished: adsorption and hydrolysis. The first step is the adsorption of the enzyme onto the polymer surface, and the second step is the hydrolysis of the polymer chain [11–13]. In finite element modeling, adsorption can be described by surface homogeneous diffusion [14, 15] and hydrolysis by a reaction equation, similar to models for polylactides.

In this paper, a finite element model of the biodegradation of two polymers poly(3HB) and poly(3HB-co-3HV) in three biological media (human blood anticoagulated with sodium citrate), blood serum, *in vivo*) is proposed. The degradation of two polymeric products was also modeled: a vascular stent and a bone implant (Fig. 1).

Materials and Methods

The experimental protocol is described in detail in a previous article [16]. The polymer fibers synthesis process and degradation experiments are briefly described in the following sections.

Fiber synthesis

The monofilament samples were prepared from a homopolymer of polyhydroxybutyrate poly(3HB) (340 kDa, degree of crystallinity 70–78 %) and its copolymer with β -hydroxyvalerate poly(3HB-co-3HV) (295–360 kDa, degree of crystallinity 55 %) containing 15 mol% of hydroxyvalerate [1]. For this study the polymers were extruded at 170 °C and collected on a drum rotating at a

linear speed of about 40 m/min. The extruded fibers were drawn on a hot plate at 100 °C at a draw ratio of 7–8 [16].

Experimental section

The kinetics of fiber biodegradation was studied for *in vitro* and *in vivo* model systems. Phosphate buffer (pH 4.5, 5.9 and 7.0), human blood anti-coagulated with sodium citrate, and blood serum were used as model systems. The samples were exposed at 38 °C for 180 days. To study the dynamics of polymer fiber biodegradation *in vivo*, characterized and weighed samples (2–3 cm long) were placed in diffusion chambers, which were implanted under sterile conditions subcutaneously in the neck fold of Wistar rats under inhalation anesthesia (diethyl ether). During the experiments, fiber samples were periodically removed from the model systems, washed, and examined after drying.

Regardless of the chemical composition and initial physical and chemical properties of the polymer material used for filament production, they did not degrade in phosphate buffer (pH 5.2) at 37 °C. No significant change in fiber weight was observed during the whole observation period (180 days). A similar picture was obtained at other pH values (5.9 and 7.0). Thus, the absence of chemical hydrolysis of PHA fibers in saline solutions was confirmed [16]. Parameters of the polymer are given in Table 1. A similar profile of polymer mass change in the *in vivo* case and others can also be found in other works [17–20].

Degradation of PHA fibers

Enzymatic hydrolysis of PHA is a complex process, and its rate depends on the availability of ester linkages to water or enzymes, hydrophilicity, morphology, molecular weight, monomers, and other physical properties [6]. Enzymatic hydrolysis is more pronounced than non-enzymatic hydrolysis at a later stage of *in vivo* degradation. This

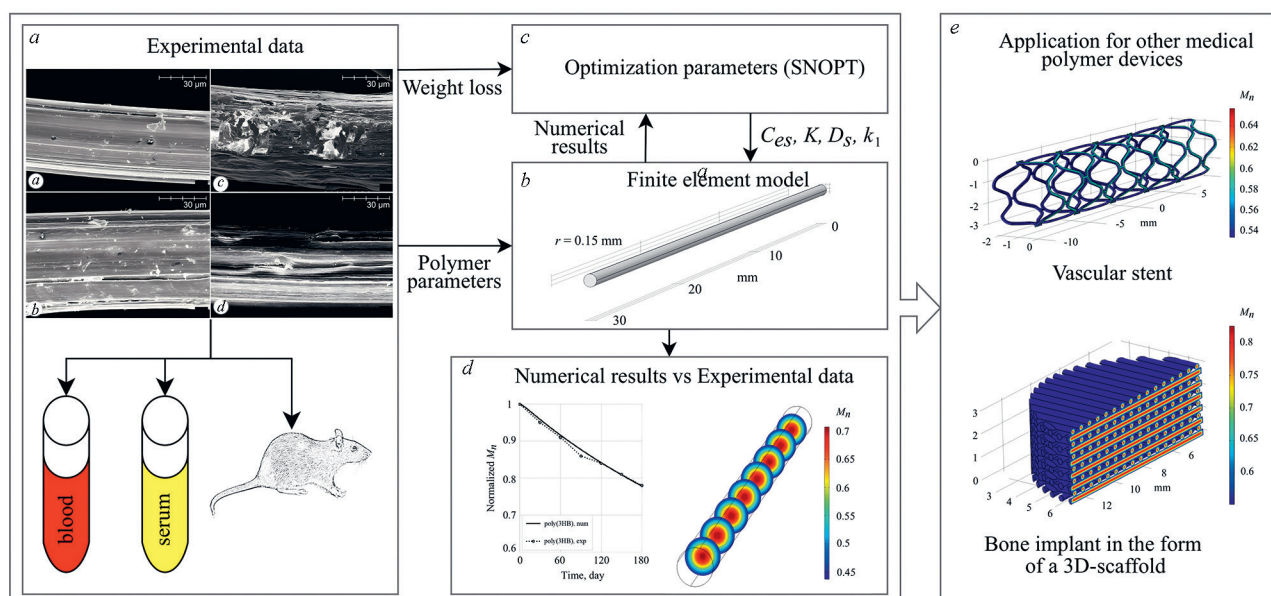


Fig. 1. Scheme of research: experimental data [16] on biodegradation of suture fibers in three biological media (a); construction of finite element model of biodegradation (b); search for unknown parameters by solving the inverse problem (SNOPT algorithm) (c); comparison of numerical and experimental results (d); application of the model for other polymer devices (3D scaffold, vascular stent) (e).

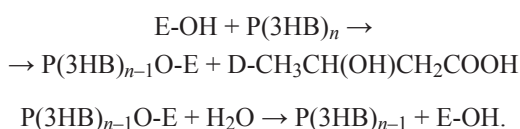
C_{es} is the concentration of enzyme on the surface; K is the mass transfer coefficient; D_s is the diffusion coefficient of enzyme in degrading polymer; r is radius; k_1 is the rate constant of hydrolysis reaction; M_n is the average molecular weight of the polymer

Table 1. Parameters of polymers

Parameters	poly(3HB)	poly(3HB-co-3HV)
Initial concentration of polymer chain esters, C_{p0} , mol/m ³	20,560	20,035
The molar mass of the polymer, M_0 , g/mol	86	88
The initial average molecular mass of the polymer, M_{n0} , kDa	340	350

degradation mechanism was suggested in a study where the *in vitro* biodegradation of poly(3HB-co-3HV) copolymer films was studied in nutrient-depleted activated sludge for a period of 6 weeks [20].

When considering the kinetics of enzymatic degradation, two steps are usually distinguished: adsorption and hydrolysis. The first step is the adsorption of the enzyme onto the polymer surface by the binding domain, and the second step is the hydrolysis of the polymer chain into water-soluble products by the catalytic center [11–13]. One study [12] proposed a reaction scheme for the biodegradation of poly(3HB):



Mathematical model of degradation

In this paper, a model for the biodegradation of PHA polymers is proposed which includes two main processes: adsorption and hydrolysis. Adsorption can be described by the homogeneous surface diffusion model (HSDM) [14, 15], and hydrolysis by the reaction equation.

We assume that a homogeneous polymer is immersed in a medium containing a sufficient amount of enzyme. In addition, the adsorption rate depends on the surface diffusion coefficient and the flux at the polymer surface. The resistance to mass transfer at the surface is considered sufficiently small. The presence of a non-zero concentration of adsorbate is sufficient for hydrolysis. The initial parameters of the polymer, its density, molecular weight, and degree of polymerization are used to calculate the mass.

Determinant ratios of PHA biodegradation are:

$$\begin{aligned} \frac{\partial C_{ep}}{\partial t} &= \nabla(D_s \nabla C_{ep}), \\ \frac{\partial R_s}{\partial t} &= C_{ep} k_1, \end{aligned}$$

where C_{ep} is the mole concentration of adsorbate; D_s is the diffusion coefficient of enzyme in degrading polymer; R_s is the mole concentration of polymer chain scissions; k_1 is the rate constant of hydrolysis reaction.

Boundary and initial conditions are also set:

$$\begin{aligned} C_{ep} &= 0, \quad t = 0, \\ \frac{\partial C_{ep}}{\partial t} &= 0, \quad t = 0, \\ -\mathbf{n}(D_s \nabla C_{ep})|_{\Gamma_s} &= K(C_{es} - C_{ep}), \\ R_s &= 0, \quad t = 0, \end{aligned}$$

$$\frac{\partial R_s}{\partial t} = 0, \quad t = 0,$$

where Γ_s is the outer surface; K is the mass transfer coefficient; C_{es} is the concentration of enzyme on the surface; $\mathbf{n}$ is the outward unit normal vector on a normal to surface Γ_s ; t is time.

Averaged molecular weight excluding the short chains [21] is then calculated as

$$M_n = \frac{1 - (R_s/C_{p0})}{1 + (M_{n0}/M_0)((R_s/C_{p0}) - (1/m)(R_s/C_{p0}))},$$

where M_{n0} is the initial average molecular mass of the polymer; $m = 4$ is the average degree of polymerisation of the short chains, usually from 4 to 6 [21].

Implementation of the Mathematical Model in COMSOL Multiphysics

In the General Form Partial Differential Equation (PDE) module in COMSOL, a transient general type PDE with a flow on the boundary is:

$$\begin{cases} e_u \frac{\partial^2 u}{\partial t^2} + d_a \frac{\partial u}{\partial t} + \nabla \Gamma = f \text{ in } \Omega, \\ -\mathbf{n} \Gamma = g - qu \text{ on } \partial \Omega \end{cases},$$

where Ω is the calculated volume domain and $\partial \Omega$ is the domain boundary; u is the dependent variable; f, g, q, Γ are user-defined coefficients; e_u is the mass coefficient; d_a is a damping coefficient or mass coefficient; $g = C_{es}K, q = K$.

There are two equations in our system, so we need to add two General Form PDEs. The initial values for C_{ep} and R_s are zero.

The diffusion equations describing the adsorption of an enzyme:

$$\begin{cases} d_{C_{ep}} \frac{\partial C_{ep}}{\partial t} + \nabla(D_s \nabla C_{ep}) = 0, \\ -\mathbf{n}(D_s \nabla C_{ep}) = K(C_{es} - C_{ep}) \end{cases},$$

where the coefficients are $e_{C_{ep}} = 0; d_{C_{ep}} = 1; f = 0;$

$\Gamma_{C_{ep}} = \left\{ -D_s \frac{\partial C_{ep}}{\partial x}, -\frac{\partial C_{ep}}{\partial y}, -D_s \frac{\partial C_{ep}}{\partial z} \right\}; \Gamma_{C_{ep}}$ is the flux vector for a dependent variable C_{ep} ; x, y и z are the Cartesian coordinates.

The hydrolysis equation has the following form:

$$d_{R_s} \frac{\partial R_s}{\partial t} = C_{ep} k_1,$$

where the coefficients are $e_{R_s} = 0, d_{R_s} = 1, f = C_{ep} k_1, \Gamma_{R_s} = 0; d_{R_s}$ is the damping coefficient or mass coefficient for a dependent variable R_s ; e_{R_s} is the mass coefficient for a

dependent variable R_s ; Γ_{R_s} is the flux vector for a dependent variable R_s .

The data that supports the findings of this study are openly available in Mendeley Data¹.

Calculating model parameters

A mathematical finite element model using the software COMSOL Multiphysics was constructed from the biodegradation data of polymer fibers made of poly(3HB-co-3HV) [16]. The fiber was represented as a cylinder with a length of 30 mm and a radius of 0.15 mm (Fig. 2), and a flux describing the adsorption of the enzyme was set on the outer surface of the filament.

To search for unknown reaction rate coefficients, we solved the inverse problem using the Sparse Nonlinear OPTimizer (SNOPT) algorithm [22] and the experimental data discussed above [16]. The biodegradation parameters of the modeled polymer fibers of poly(3HB) and poly(3HB-

co-3HV) are given in Tables 1 and 2. For all cases, the parameter $K = 2.5 \cdot 10^{-4}$ m/day.

Results and discussion

Comparison of numerical and experimental results

The biodegradation of polymer yarns with these parameters was modeled using the finite element method. Comparison of the results of numerical and in-situ experiments is presented in Fig. 3, which makes it possible to assert a good agreement between the results of modeling and experiments. The standard deviation between the results is presented in Table 3.

The presented model of PHA biodegradation allows us to describe the loss of polymer mass by surface diffusion of enzymes and hydrolysis but does not consider the change in crystallinity and erosion. It should also be noted that this model does not consider changes in the concentration of active enzymes involved in the polymer degradation process.

Biodegradation map

The results of the analysis of the influence of model parameters on the product degradation profile are illustrated in Fig. 4. According to research, the diffusion

¹ Fotin A. A model for biodegradation of polymer fibers made of poly-3-hydroxybutyrate (P3HB) and poly-3-hydroxybutyrate-co-3-hydroxyvalerate (P3HB-co-3HV). Biodegradation model file (Comsol) for P3HB, in vivo // Mendeley Data. 2025. V. 2. doi: 10.17632/x358g47nnz.2

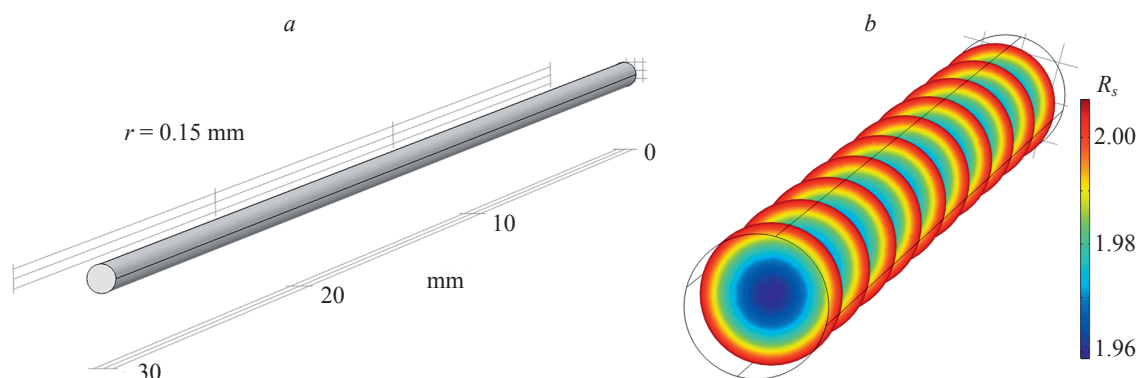


Fig. 2. The polymer fiber model: simplified fiber geometry, cylinder with a length of 30 mm and a radius of 0.15 mm (a); the result of numerical simulation, the value of R_s (the mole concentration of polymer chain scissions) for 180 days, poly(3HB), blood (b)

Table 2. Model parameters for poly(3HB) and poly(3HB-co-3HV) in three media

Parameters	Human blood (anti-coagulated with sodium citrate)	Blood serum	<i>in vivo</i>
poly(3HB)			
C_{es} , mol/m ³	$9.3 \cdot 10^{-3}$	$9.4 \cdot 10^{-3}$	$10.6 \cdot 10^{-3}$
D_s , m ² /day	$1.3 \cdot 10^{-9}$	$5.57 \cdot 10^{-8}$	$2.8 \cdot 10^{-11}$
k_1 , day ⁻¹	1.19	1.19	1.98
poly(3HB-co-3HV)			
C_{es} , mol/m ³	$1.68 \cdot 10^{-2}$	$1.5 \cdot 10^{-2}$	$1.92 \cdot 10^{-2}$
D_s , m ² /day	$1.1 \cdot 10^{-8}$	$2.1 \cdot 10^{-8}$	$3.63 \cdot 10^{-11}$
k_1 , day ⁻¹	1.24	1.3	1.69

Table 3. Standard deviation for numerical and experimental results

Copolymers	Human blood (anti-coagulated with sodium citrate)	Blood serum	<i>in vivo</i>
poly(3HB)	0.0038	0.0092	0.0076
poly(3HB-co-3HV)	0.0068	0.0083	0.0112

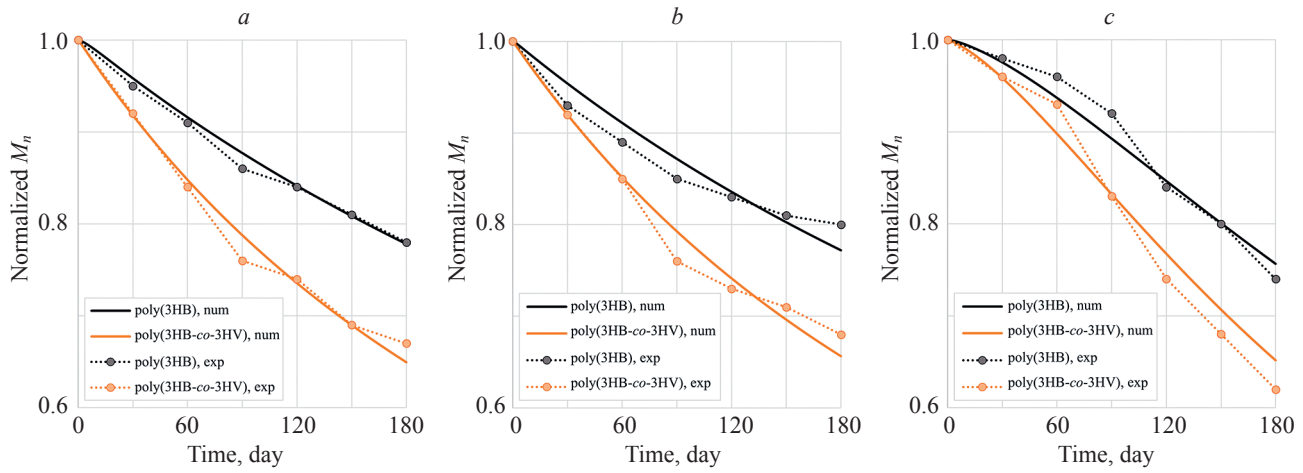


Fig. 3. Plots of loss of average normal molecular weight. Comparison of numerical modeling results with experimental data on the biodegradation of polymer filaments: in human blood (anti-coagulated with sodium citrate) (a); in blood serum (b); *in vivo* (c)

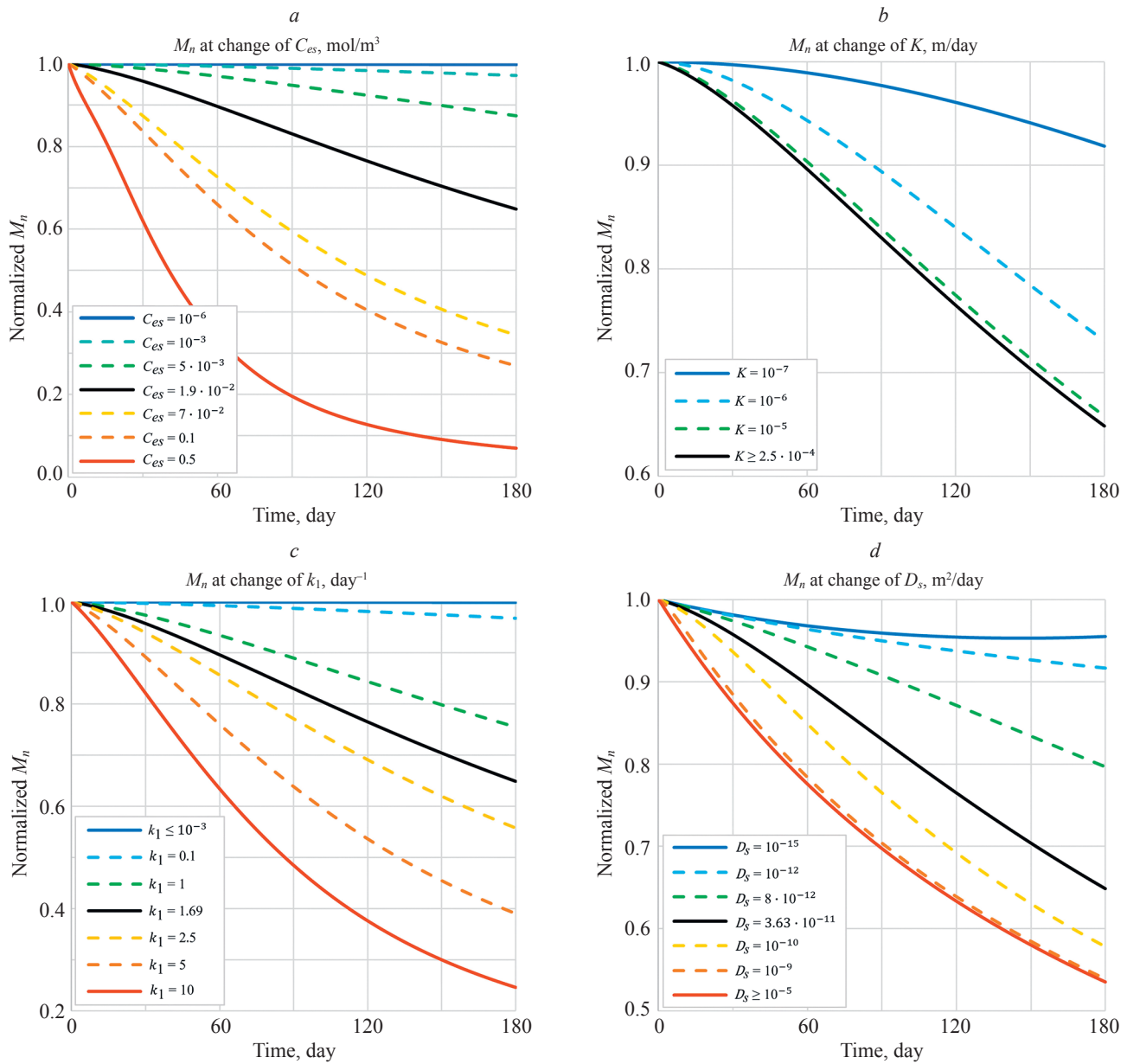


Fig. 4. Effect of model parameters on the degradation profile of suture fiber. Biodegradation parameters poly(3HB-co-3HV) *in vivo* were taken as initial parameters. The black line indicates results with initial parameters. The red and blue solid lines show the results for the boundary values of the parameters. Dotted lines show results for intermediate values: for $0.5 \leq C_{es} \leq 10^{-4}$ mol/m³ (a); for $0.1 \leq K \leq 10^{-7}$ m/day (b); for $10 \leq k_1 \leq 10^{-3}$ day⁻¹ (c); for $10^{-5} \leq D_s \leq 10^{-15}$ m²/day (d)

coefficient $D_s < 10^{-5}$ m²/day [23–26], the mass transfer coefficient $10^{-7} < K < 0.1$ m/day [27]. The remaining parameters C_{es} , k_1 varied in an arbitrary range from their initial values. Initial parameter: $C_{p0} = 20,560$ mol/m³; $M_0 = 86$ g/mol, $M_{n0} = 340 \cdot 10^3$ g/mol; $K = 2.5 \cdot 10^{-4}$ m/day; $C_{es} = 1.92 \cdot 10^{-2}$ mol/m³; $D_s = 3.63 \cdot 10^{-11}$ m²/day; $k_1 = 1.69$ day⁻¹.

From the data obtained, it can be stated that the degradation profile does not change any more with the variation of parameters in the boundaries: $K > 10^{-4}$, $D_s > 10^{-4}$. It can also be assumed that the degradation is most influenced by the enzyme activity, which is embedded in the parameter C_{es} .

Application for other polymer devices

This model can be used to analyze the degradation of different polymer products. Parameters for poly(3HB-co-3HV) in *in vivo* media were used for further calculations.

For example, in one article, a similar polymer, P(3HB-co-3HV), was used to make a bone replacement implant in the form of a cylindrical lattice. This implant was implanted

in the bones of animals. According to the results of the *in vivo* experiment, the polymer material of the remaining 3D scaffold fragments was 25 % smaller than the cross-sectional diameter of the original filament when 3D printed and was surrounded by lamellar bone tissue [28]. If we assume that the density of the material is uniform, then the mass loss is about 43 %. It should be noted that no experiments on the degradation of the 3D scaffold were carried out, and conclusions on mass loss are based only on the change in filament diameter on some slices. Based on this data, a numerical experiment was conducted the results of which are shown in Fig. 5. As can be seen from the graph, the implant lost about 25 % of its weight by day 150. This discrepancy can be explained by the different methods of manufacturing the polymer product and by the different media (in the first case blood in the subcutaneous fold of the rat, in the second case femur of the pig).

A numerical biodegradation experiment was also performed for the arbitrary cardiovascular stent geometry, and the results are shown in Fig. 6. Flow was set on

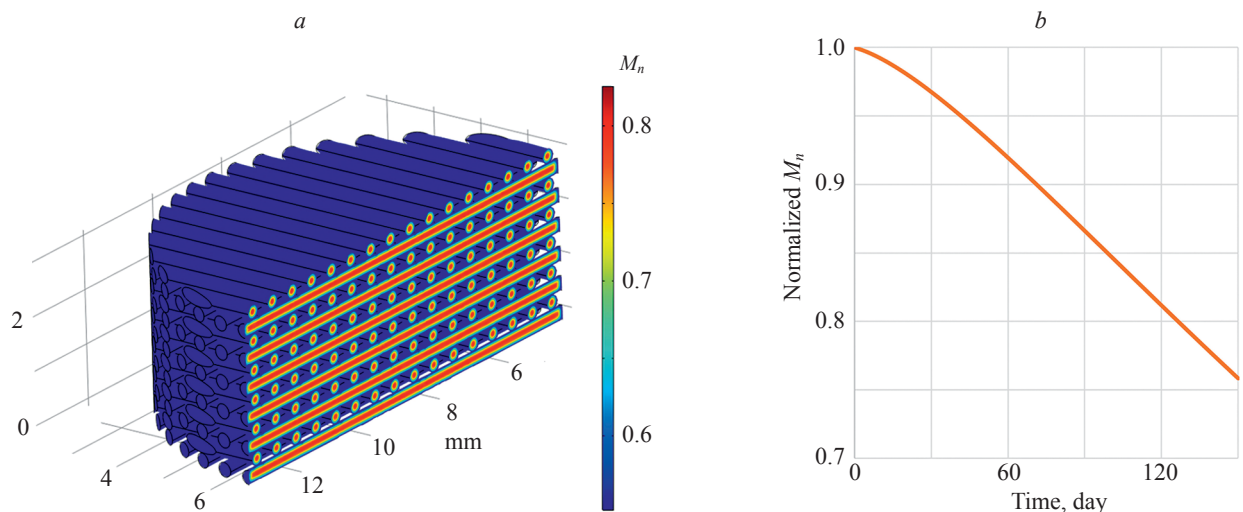


Fig. 5. Modeling the biodegradation of 3D scaffold from poly(3HB-co-3HV), *in vivo*: distribution of normal molecular weight at day 150 (a); plot of the normalized average weight loss (b)

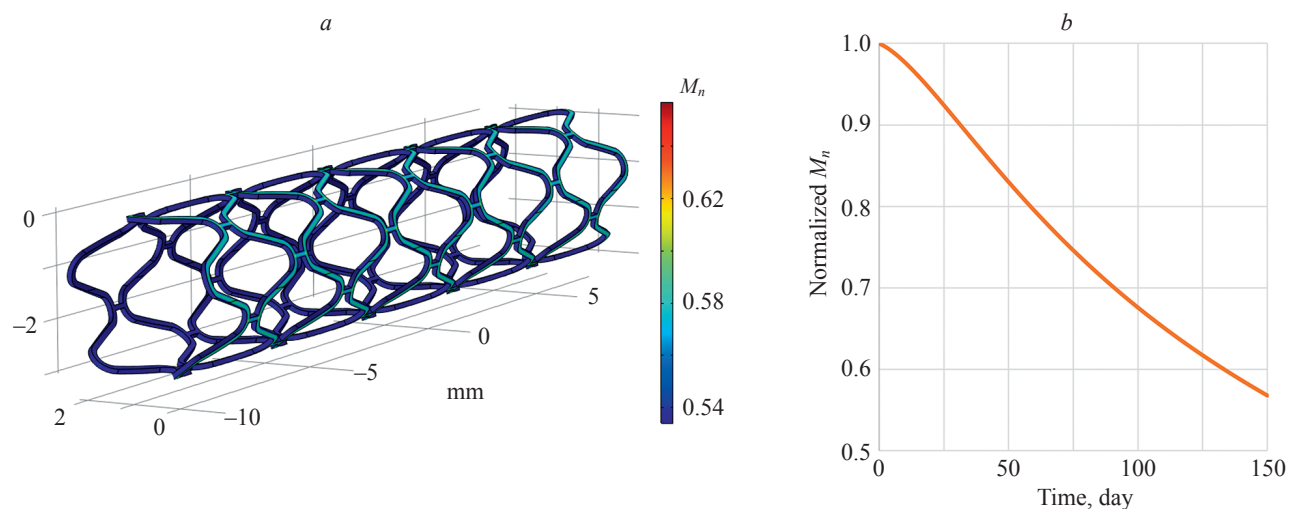


Fig. 6. Modeling the biodegradation of stent from poly(3HB-co-3HV), *in vivo*: distribution of normal molecular weight at day 180 (a); plot of the normalized average weight loss (b)

the outer surfaces of the stent which are not in contact with the vessel wall. Based on the modeling results, the cardiovascular stent is expected to lose approximately 43 % of its initial molecular weight in 180 days. It should be noted that here we ignore the vessel wall healing which can cause the stent struts to be fully covered by the end of this period, changing the boundary conditions [29].

Conclusion

A model for the biodegradation of polyhydroxyalkanoates polymer is proposed based on two processes: adsorption and hydrolysis. The degradation of

polyhydroxyalkanoates sutures in three media (human blood (anticoagulated with sodium citrate), blood serum, *in vivo*) was modeled and unknown parameters of the model were found using the Sparse Nonlinear OPTimizer method. The numerical results were in good agreement with the experimental results. The standard deviation of numerical modeling results from experiments is not more than 0.0012. The model has been applied to study other medical devices such as vascular stents and bone implants. This model is the first step towards modeling the biodegradation of PHA and does not include the change in crystallinity, the characteristics of the enzyme during degradation, which may be a further aim of the work.

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