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# Cluster Mechanism of Formation of Biological Nanoobjects and Mesoobjects

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***Author's contribution***

*The sole author designed, analyzed and interpreted and prepared the manuscript.*

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***Short Note***

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## ABSTRACT

In this work, we consider a scheme of a direct synthesis of volumetric protein nanoparticles in a system previously consisted of amino acid molecules by using an asymptotic method of kinetics for forming objects having quantum features. A proposed model gives formally calculated sizes, which correspond to characteristic dimensions of protein nanoparticles (hemoglobin, elastin and lipoprotein). In addition, the model provides a mesoscopic range of sizes, which is in keeping with characteristic dimensions of non-dividing cells (erythrocytes and small lymphocytes) as well as of simplest organisms.

*Keywords: Objects; quantum features; protein nanoparticles; cells; characteristic dimensions.*

## 1. INTRODUCTION

One of topical trends of nanoscience and nanotechnology consists in the creation and the study of biological materials, in particular, the study of physical mechanisms of protein biosynthesis [1-4]. In accordance with the results of the investigations the commonly accepted scheme of proteins construction is presented in such a manner that a volumetric-packed nanoparticle that represents an aperiodic crystal, is formed from nanochains with the C–N peptide

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bonds (primary structures) as a result of the twisting and the mutual arrangement of various polypeptides in the presence of nucleic acid molecules.

Besides, in [3] the possibility exists «that the given scheme does not exhaust all ways of a biosynthesis of proteins». In the light of this the quantum nature of biophysical processes should be noted, because thanks to the quantum nature «the main peculiarities of physical behavior of macromolecules are determined by rotational isomerism», because a substance is considered as a dynamic mixture of amino acid molecules located in crossed conformation and in conformations directed to the right and to the left [2]. Hundreds and thousands of vibrations with the frequencies of the order of $10^{12}$–$10^{13}$ $c^{-1}$ [2] occur in a turning time of the order $10^{-10}$ s in a molecule. In the course of these vibrations the bonds can be formed between contiguous molecules – tunnel transition takes place in a quantum-mechanical system as a result of a great number of «attempts». Hence, rotational-vibrational interactions of amino acid molecules can bring about their volumetric polycondensation. Inoculating centers of polycondensation can be nucleic acid molecules, close to which amino acid molecules are clustered in a certain order, prescribed by a preferable formation of C–N bonds in the system volume, as the shortest and strongest bonds in comparison with C–C bonds and C–O bonds (see [5]).

In the current work, on the basis of the asymptotic method [6] for studying kinetics of formation of objects having quantum features, a scheme of a direct synthesis of volumetric protein nanoparticles is considered in a system previously consisted of amino acid molecules with additives of nucleic acid molecules (cytoplasm [1]). A protein synthesis without a formation stage of polypeptide nanochains is seemingly possible owing to phonon excitations of molecules in the whole volume. It is demonstrated in work [6] that the mentioned method is also used in a mesoscopic range of sizes. This makes it possible to use this method to assess a maximum size of biological objects under consideration – cells. It is necessary to note that, in accordance with the classification given in [1], typical sizes of different biological nanoobjects lie in the range of 0.42-140 nanometers (nm), and typical sizes of biological mesoobjects lie in the range of 0.5-15 micrometers (μm).

## 2. METHODOLOGY

We consider the formation of nanoobjects and mesoobjects in conservative stochastic systems determined as total mass-limited assemblies of quantum objects interacting with each other in a random way. A process of irreversible aggregation of objects will be described in terms of distribution density wave $\varphi(a,t)$ in the space of cluster sizes $a$, propagating in time $t$ in direction of cluster size increase. Such a one-dimensional approach enables us not to take into account particle form deviation from the simplest form (a cubic form). On the basis of the universal relation $\Delta a \cdot \Delta k \geq 1/4\pi$ derived from the Fourier theorem for a half-width $\Delta a$ of a wave packet and a half-width $\Delta k$ of a spectral line ($k$ is the wave number), which is true for a wave of any physical nature, we can write «an uncertainty relation » for a coordinate and a momentum in the space $a$ [6]:

$$\Delta a \cdot \Delta p \approx \frac{\hbar}{2}. \quad (1)$$

Here, $\Delta p \sim p = m\Delta a/\Delta t$ is the momentum uncertainty, $m = m_0(a/a_0)^3$ is the particle mass, $m_0$ and $a_0$ are a molecule mass and a molecule size (a size of a seed), $\hbar$ is the reduced Planck constant. Momentum uncertainty in order of magnitude is equal to a momentum, that is, interaction between objects either takes place or not. Physical meaning of relation (1) implies that in the course of the time interval $\Delta t$ of an elementary (single) interaction act of objects an exact particle size can not be defined until this interaction is completed either through a capture of one object by another, or by means of their partial or complete disruption, or via elastic scattering. It is associated with the fact that up to the completion of the elementary act under review it is impossible to determine, which of the objects each of their interacting molecules relates to. This means that uncertainty principle allows a possibility of mutations of biological objects at a molecular level.

The parameter $\Delta t$ is defined by using the Heisenberg rule as a life time of an excited state of an isolated quantum-mechanical system connected with a width of the energy level $\Delta E$ of this state:

$$\Delta t \approx \frac{\hbar}{\Delta E}. \quad (2)$$

Let us consider formally systems consisting of a seeds in the shape of molecules of the «greatest» amino acid [1] – tryptophan $C_{11}H_{12}N_2O_2$, whose structure includes elements of structures of smaller amino acids, or in the form of nucleotides – of the smallest amino acids/the greatest amino acids of DNA (cytosine / guanine phosphate [1]). Assessments show that according to data [7] for characteristic temperatures $\theta_\nu$ of extension of crystal-forming chemical bonds C–C, C=C, C–N, C–O, which are approximately equal to each other and amount to about 1500 K, effective characteristic vibration frequency of a tryptophan molecule is circa $\nu = k_B\theta_\nu / b2\pi\hbar \approx 2\cdot10^{12}$ s$^{-1}$ ($k_B$ is the Boltzmann constant, $b$ = 16 is the general number of the mentioned chemical bonds [1]). The parameter $2\pi\hbar\nu/k_BT \approx 0.3$ at a representative temperature of protein synthesis $T \approx 310$ K (for example, a normal temperature of human blood is equal to 309.6 K). Then on the basis of notions [7] concerning molecular crystals at low energy levels in the approximation of harmonic vibrations [8] it can be assumed that $\Delta E = 3N2\pi\hbar\nu\left(\exp\frac{2\pi\hbar\nu}{k_BT}-1\right)^{-1} \approx 3Nk_BT$, where $N$ is the number of molecules covered by phonon excitations. Analogous considerations are true for amino acids of DNA. After rewriting relation (1) for the average size $\langle a\rangle$, from (1) and (2) we get the following approximate differential relation for describing a growth of an average size of particles having a cubic form:

$$\frac{\langle a\rangle^{3/2}}{N^{1/2}}\,d\langle a\rangle \cong \left(\frac{3k_BTa_0^3}{2m_0}\right)^{1/2} dt\ ,\ \langle a\rangle(t=0)=0\ . \quad (3)$$

Having determined the dependence $N(\langle a\rangle)$ for a given mode of a process and by solving the equation (3) in quadratures, we can obtain approximate growth laws of average-size particles with time. Such a simplified formal approach not taking into account sophisticated biochemistry of formation processes of the objects under consideration makes it possible to calculate characteristic dimensions of proteins and protein structures – enzymes [1,2].

In a proposed simple model the building elements of proteins are nanoparticles with the critical size $a_* = 2a_0$ (translation symmetry), with which a quasi-long-range crystalline order arises in them. With a small flow (sf) of these elements, when each of them has time to occupy its place at a surface of a growing particle till the onset of its interaction with a subsequent element, a size of a region of phonon excitation is approximately equal to $a_*$ and a number of excited molecules is equal to 8. From equation (3) we get that a growth law takes the following form:

$$\langle a\rangle_{sf} \approx \left(\frac{75k_BTa_0^3}{m_0}\right)^{1/5} t^{2/5}\ . \quad (4)$$

Under the homogeneous «simultaneous» influence (hs) on a system, it turned out that all molecules of two interacting particles are excited: $N = 2(\langle a\rangle/a_0)^3$. Then from equation (3) we obtain the following expression:

$$\langle a\rangle_{hs} \approx \left(\frac{3k_BT}{m_0}\right)^{1/2} t\ . \quad (5)$$

In work [6] from uncertainty relation (1) and a condition of mass conservation in an elementary interaction act of a big cluster and a seed, when $\Delta a \approx a_0^3/3a^2$, the following expression has been gained for a maximum object size:

$$a_{\max} \approx \frac{2}{9}\frac{m_0}{\hbar}\frac{a_0^3}{\Delta t_{\min}}\ . \quad (6)$$

Here $\Delta t_{\min}$ is the minimal time interval of elementary objects interaction act, determined by a physical nature of a process. In the case under consideration, the given parameter can be defined as $\Delta t_{\min} = 2\pi\hbar/k_B\theta_\nu \approx 3\cdot10^{-14}$ s. Formula derivation (6) does not depend on a relationship between phonon energy and thermal energy. Therefore, this formula, which a temperature does not enter into, is true for any seed and gives mesoscopic limits for objects being considered.

## 3. RESULTS AND DISCUSSION

From formula (4) we get that in a system previously composed of tryptophan molecules (the greatest amino acid with $m_0 = 204m_u$, $m_u$ is the atomic mass unit, $a_0$ = 0.67 nm [1]), at $T \approx$ 310 K in the course of turning time $t \approx 10^{-10}$ s in the regime of adding of building elements the particles having a characteristic dimension of 4.9 nm are generated. In a system composed of

nucleotides (cytosine phosphate with $m_0$ = 309$m_u$, $a_0$ = 0.81 nm or guanine phosphate with $m_0$ = 361$m_u$, $a_0$ = 0.86 nm [1]), a characteristic dimension of the particles generated under the same conditions is equal to 5 nm. The obtained calculated sizes correspond approximately to proteins of elastin (5 nm [1]) and hemoglobin (4.5×7 nm [1]) as well as to enzymes with a molecular weight $M$ = 72000 ($a$ = 0.12$M^{1/3}$ [1]). In the case of simultaneous excitation of a system (formula (5)) preliminary consisted of tryptophan molecules, in the course of turning time $t \approx 10^{-10}$ s the particles having a characteristic dimension of 19.8 nm are formed. This dimension is approximately in keeping with lipoprotein (20 nm [1]). A size of 20.8 nm is gained by using formula (4) at «slow» biological processes [4] with a typical time scale of $10^{-7}$ s.

From formula (6) we have that a maximum size of biological mesoobjects, which are formed as a result of tryptophan molecule aggregation, accounts for 7.5 μm. This magnitude corresponds formally to non-dividing cells: 1) it correlates with a diameter of human erythrocyte (7.2–7.5 μm [9]); 2) it limits the sizes of small lymphocytes (4.5–6.5 μm [10]) from above. If molecules of the «smallest» amino acid – glycine ($m_0$ = 75$m_u$, $a_0$ = 0.42 nm [1]) are regarded as seeds (germs), from formula (6) we gain that the greatest size of objects is equal to 0.65 μm. This value corresponds to a characteristic dimension of an organelle lysosome consisted of enzymes (0.7 μm [1]).

It should be noted that a calculated range of sizes of mesoobjects 0.65–7.5 μm fits into a range of sizes 0.1–15 μm of simplest organisms – archaeas [11]. Thus, a proposed model is true for determining sizes of non-proliferating cells. It can be hoped that the proposed method and the presented estimates are found to be useful in choosing conditions of the laboratory simulation of a synthesis of simplest organisms.

In particular, under extremal natural conditions (for instance, at the impact of meteorites, in craters, in hydrothermal springs etc.), under which amino acid molecules are fractured, fragments of molecules can be seeds of biological structures. For example, if a tryptophan molecule [1] divides into a group containing saccharide structures (carbon rings) and into a group containing three carbon atoms, a nitrogen atom and an oxygen atom, we can consider as a seed a «volumetric» atomic cluster $C_3H_6NO_2$ with a molecular weight $M$ = 88 and with a size of 0.34 nm. In this case, from formula (6) we get that the greatest size of objects is equal to 0.4 μm ($\Delta t_{min} = 2\pi\hbar/k_B\theta_v = 3\cdot10^{-14}$ s). This magnitude is in agreement with a size of nanosized symbiont [12].

If we consider as seeds some fragments of glycine molecules [1] with a disrupt C–C bond: the clusters $CH_4N$ ($M$ = 30) and $CHO_2$ ($M$ = 45) with the sizes of about 0,20 nm, from formula (6) we obtain that the maximum sizes of objects are equal to $a_{max} \approx$ 30 nm and 45 nm, respectively. These values correspond formally to ribosomes [13], in which a protein biosynthesis takes place. The protein biosynthesis has been uncovered in cells of all living organisms (bacteria, plants and animals) without exception. In this case, the first calculated magnitude $a_{max} \approx$ 30 nm restricts a diameter $d$ = 20-30 nm of ribosomes of the class 70SP in the cells not having a formed nucleus (procaryotes: bacteria, green algae); and the second magnitude $a_{max} \approx$ 45 nm restrains the sizes up to 40 nm of ribosomes of the class 80SP in cytoplasm of all eukaryotes – organisms with formed cell nuclei (karyons).

The obtained correspondence between calculated values and observed data allows us to put for consideration the issue about an existence of other forms of organisms being unknown at present. It can be expected that the proposed phenomenological approach in combination with fundamental ideas given in [14] and methods for discovering new species elaborated in [15] will help us to clear the above mentioned issue.

## 4. CONCLUSION

The uncertainty principle admits a synthesis of volumetric protein nanoparticles without the formation of polypeptide nanochains. It determines a possibility of mutations of biological objects at a molecular level. A supposed simple model gives formally rated sizes of biological nano-objects and meso-objects corresponding to characteristic dimensions of some proteins and enzymes (ferments), of non-dividing cells as well as simplest organisms. At the same time, the issue remains open, whether the uncertainty principle allows the existence of other forms of organisms being unknown at present?

## COMPETING INTERESTS

Author has declared that no competing interests exist.

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