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Research Article

Features of the Supramolecular Cell-Genetic Organization of E. Coli in Engineering Aspects of Biotechnology

Evilina Alekseevna Ivanova

Ufa Institute of Biology UFIC RAS, Ufa, Russia

ORCID

Evilina Alekseevna Ivanova; 0000-0002-8511-4044

Abstract. Recently, there has been a keen interest in the physicochemical features of self-organizing spatio-temporal, heteropolymer-supramolecular assemblies, in which the system of components of the fluctuation dynamics of surface protein groups is evolutionarily selected for the implementation of morphogenetic processes of ontogenesis.That is, evolution created chemical compounds, the exceptional organization of which ensured the fulfillment of the most complex and precise tasks.In this research, the bacterial cell of*E. coli* was considered in the concept of supramolecular science, where, in accordance with the informational development program based on the principles of molecular recognition, phase ensembles appear, which are characterized by a certain organization, depending on the phase growth of the population culture. In this respect, proteomic *super*-molecular physicochemistry can be considered as physicochemical or molecular informatics.Arginine is of interest because almost all of its molecule is active and undergoes obligatory interactions both with DNA and with other histones and non-histones. The results of this study demonstrated the super-protein surface of supramolecular assemblies, the flexible system PPCC-*E.coli,* active zones, dynamics of continuity, positioning topological-spatio-temporal *Arg*-protease-processing, local areas of the nucleoid system, and interrelations at the level of: Bp-liquid crystal-bacterioplasma; NsCo-fragile, PsCo-tightly bound to the cell remainder; and in the Co-cell remainder itself. These data may be of practical interest in various engineering aspects of biotechnology.

Keywords: arginine protease processing, supramolecules, *E.coli,* phase protein, *super*-molecules.

Corresponding Author: Evilina Alekseevna Ivanova; email: fiona_belobor@mail.ru

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1. Introduction

Based on theoretical developments alone, it is impossible to predict the prediction of the conformational states of biomacromolecules, and even more so of supramolecular assemblies. Theoretical predictions must necessarily be combined with experimental data from molecular biology.Biological evolution repeatedly strengthens, consolidates and presents to researchers the consequences of those physical principles on which molecular interactions are based separately in a protein, and then in its *super*-molecules included in supramolecular assemblies. All experimental protein physics is now mainly

the physics of small proteins, and the physics of large protein *super*-molecules and their complexes is just beginning to develop. Understanding of biological processes is much easier achieved with the help of model organisms, in which the cellular level of organization of vital activity can be viewed from the position of self-organization of supramolecular structures constantly interacting with each other and the environment. In this respect, supramolecular chemistry can be considered as chemical or molecular informatics.

A well-characterized universal unicellular prokaryotic organism *E.coli* - intestinal gram-negative eubacteria was chosen as a model object of the study.It is believed that *E, coli* is the most powerful and diverse in nature karyogenomic object. It is known that the cytoplasm of a cell is highly structured, divided by membranes and is all permeated with cytoskeleton filaments, from this point of view, intracellular reactions can be more adequately described only by the supramolecular chemistry of immobilized enzymes, where interactions of many macromolecules are already integrated.

The purpose of this work is to present a cell (based on patents developed in the laboratory [1-7]) in the form of: Bp-bacterioplasma, NsCo-fragile, PsCo-tightly bound to the Co-cell remainder of supramolecular assemblies, in the molecules of which the genetic memory of self-organization and its realization in cycles, and morphogenetic phases of growth and development, with the participation of *Arg*-protease-processing.

2. Methods

The biochemical approach to this goal was based on the previously developed methodological principles for the study of the eukaryotic system [8]. Fractionation of supramolecular assemblies was carried out on the basis developed for protein chemistry, the rupture of weak and strong supramolecular interactions using first linear. and then a stepped salt gradient.Accordingly, the isolated supramolecular ensembles of *E.coli* cells were presented as a heteropolymer base: bacterioplasma – Bp (0.14M NaCl); loosely bound-NsCo (0.35 M NaCl) and tightly bound -PsCo (2M NaCl) with the cell debris and the cell debris itself - Co (13% GuHCl).Along with protein components, supramolecular assemblies include DNA, RNA, and hexoses[3]. The amount of protein in the supramolecular assemblies was determined by the Bradford method as modified [4]. *Arg* protease processing was evaluated by cleavage of *Arg*-X bonds in an arginine-rich protein, protamine (Merk) [5-7].The protamine molecule - Salmine-A-I, consists of 33 amino acids: *Arg*-22 molecules; Ser - 4 molecules; Pro - 3 molecules; Gly-, Val- 2

molecules each. The activity was expressed in nmol arginine / (s -1 • μg protein) in 1.5 ml of population periodic culture medium containing supramolecular assemblies of *E. coli* - (PPCC-*E.coli*).

3. Results and discussion

To understand the regularities of the integrity of the mechanisms of the molecular genetic foundations of individual development, using the example of a unicellular organism, it is advisable to represent the biological organization in the hierarchy of the systemic approach: population → organism → supramolecular ensembles (Bp → NsCo → PsCo → Co) → their super-protein interfaces, according to by which *Arg-X* signaling-processing moves, announcing the topological-spatio-temporal reorganization of *E.coli* in life (from division to division) and phase (active → deceleration → stationary-transition to growth arrest) development cycles.When the cells of the bacterial population are fragmented, a molecular-mechanical information-sensory system opens up in supramolecular assemblies at the interface, where the guanidine groups of arginine are the anion binding center and can act as zones of localization of conformational changes, the emergence of autowaves and superconductivity in genetic structures.The entire giant bacterial DNA molecule is a replication unit, the remodeling of which is provided with the participation of nucleoid (histone-like - basic) proteins, the composition of which, and interaction with other environmental factors, changes not only from division to division, but also depending on the growth phase of the bacterial cells. A significant role in this process belongs to the proteolytic system, in which *Arg-X* protease processing is involved.

In spatio-temporal movement, the inoculum PPCC-E.coli, inoculated into a fresh medium, immediately exhibits synchronously *Arg-X* protease processing in the supramolecular assemblies of NsCo and PsCo. This, apparently, is associated with morphological and functional processes at the level of the nucleoid system. In different phases of bacterial cell growth, the nucleoid continuously changes its shape due to relaxation and condensation of DNA loops, which, apparently, is associated with the transcriptional activity of certain bacterial genes.

After the introduction of an inoculum exhibiting functional activity in the suprastructural ensembles of NsCo, PCKo; after a lag period of one cell generation, in the active phase of PPCC-*E.coli* growth, a stepwise cyclicity of *Arg-X* protease processing appears, which begins from the surface layer of the Co system, followed by a more powerful and

prolonged repeated transition to the NsCo level. The cell systems of the Co surface layer formed in the active phase are interconnected with the cytoskeleton and are considered in the literature as a source of epigenetic information for morphogenesis. In this case, here, apparently, a significant role belongs to the dynamic foundations of the CSMP system: Co → Bp → NsCo → PsCo morphogenetic processes, which, according to [9], are universal dynamic variables of all morphogenesis, where all supramolecular systems are interconnected with the cytoskeleton and Co. These data can characterize the identification of resistance and instability in biological processes. And also the identification of the fundamental property of all living systems - the ability to survive in extreme environmental conditions, which is the path to the theoretical basis of ontogenesis.

During the transition to the deceleration phase, lag-period intervals are included in one cell generation, then the cyclicity of *Arg-X* protease processing is switched on first in Bp, followed by a transition to Co and again with a transition to Bpcyclicity.

The phase of the transition to growth arrest, which is called stationary, is accompanied by a prolonged increasing cyclic burst of *Arg-X* protease processing in Bp. The proteins released as a result of proteolysis are probably used for the synthesis of new proteins, as well as polyamines, peptides that promote proliferation and, in some cases, inhibit apoptosis. In cells under conditions of starvation and depletion of the energy source, as well as the repression of most bacterial genes, the modulation of the nucleoid plays an essential role in the preservation of DNA. It is likely that in the stationary phase, functioning proteins accumulate to protect the DNA.

The life cycle of bacterial cells lasts from division to division. In their evolution, they did not develop special mechanisms for the strict division of the cell cycle, as it happens in the eukaryotic kingdom, but something similar is observed in slowly growing cells [10]. Each type of bacteria in its own way decides the mechanisms of initiation of replication and the strategy of cell growth. A description of the behavior of the *E. coli* model object, based on the molecular genetic mechanisms of regulation of replication initiation, depending on the exponential and linear laws of cell growth, is presented in [11].

Evolutionary biological systems of prokaryotes have developed alternative mechanisms of protection for the control of proteolysis. This is mainly the “protease and its inhibitor” system. The specificity of the functioning of the “protease and inhibitor” system is interconnected with intracellular localization, and rapid biological control depends on the physiological state and biochemical supraorganization of the biological system of the cell as a whole organism, protection of the regulation of proteinase

activity by inhibitors.Our works show that at all growth phases: active → deceleration → stationary-as a transition to a stop; *Arg-X* protease processing is, respectively, under the synchronous control of trypsin inhibitors, which linearly smoothly accompanies the *Arg-X* protease processing of the surface layer of PsCo*super*-molecules, at an exponential phase, to stepwise cyclicity in phases of slowdown → transition to stop [12].

That is, in the presented experiment, after taking the inoculum with the removed rigid cell membranes, a synchronous rhythm of the dynamics of localization of the "proteases and their inhibitors" system is also established, which acts as an active dynamic direction of the life cycles of bacterial growth. Apparently, this is the information, topological-spatially-geometric synchronized propagation of modes, parametrization of local dynamics of the system "proteases and their inhibitors" in life (from divisions to division) and phase (active → deceleration → stationary-transition to growth arrest) development cycles on the interface of *super*-molecules of supramolecular assemblies PPCC-*E.coli*.

Abbreviations:*E.coli*-Escherichia coli, *Arg*-arginine, Bp-bacterioplasma, NsCo-fragile, PsCo-tightly bound to the cell remainder,Co-cell remainder itself, PPCC-*E.coli*-population-periodic culture*E.coli*, CSMP-cytoskeletal membrane transformations

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