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Names and affiliations of applicants (* indicates experimentalists):

LOIKO Nataliya*, KOVALENKO Vladislav*, KRUPYANSKIY Yury*, TERESHKIN Eduard*

Semenov Institute of Chemical Physics Laboratory of biopolymer dynamics Structure of Matter Department RU - MOSCOW

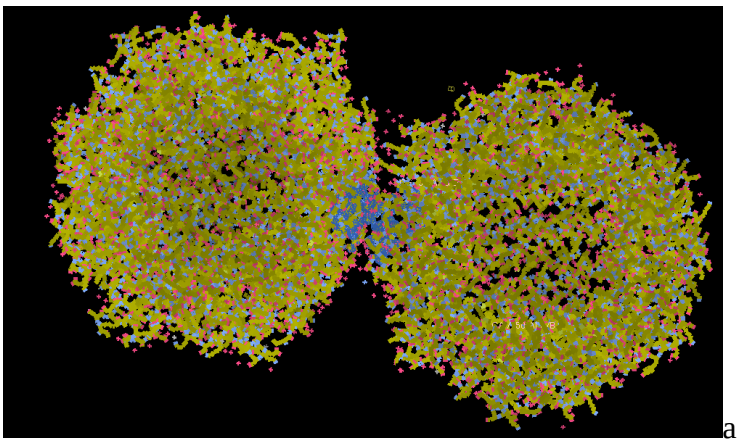
Report:

In the present work, the adaptation process is considered for the simplest example of the bacterial E. coli nucleoid. Experimental studies performed recently on prokaryotic bacterial cells, the simplest living organisms, have demonstrated that, under unfavorable environmental conditions (for example, starvation), bacterial cells can use biocrystallization, a special mechanism of protection of the genetic apparatus (nucleoid), generally untypical of living organisms. This mechanism helps to protect the nucleoid from damage and resume the activity of the bacterial cells later, upon improvement of the external conditions. We study the DNA-binding protein from starved cells (DPS) with DNA of bacteria.

During this two sessions of experiments, the dynamical changes in the structure of *in vivo* and *in vitro* crystals were studied. *In vivo* researches had shown an enlargement of scattered intensity at the zone corresponding to resolution from 140 Å to 90 Å. Also, during these sessions we had grown 12 crystals of DNA-Dps complexes, 3 of them were obtained with short linear DNA with 24 b/p, other 9 crystals were grown with the addition of pBluescript sequence (length is about 2500 b/p). With these crystals we were managed to collect a data, which help us to find a solvation of the crystal structure of a Dps-DNA complex at the resolution with 2.4 - 3.4 Å.

Concentrated solutions of DPS protein (up to 3.1 mg / ml) mixed with DNA solutions (in weight ratios from 12.6: 1 to 5: 1) were incubated for 30 minutes at a temperature of 18 ° C. Then, the resulting solution was diluted with a precipitator in a ratio of 1:1 and applied by drops of 5 μl to the inner surface of the glass. Concentrated (30%) solutions of ammonium sulfate or polyethylene glycol with different molecular weights were used as a precipitant. The glass was placed over the wells of a crystallographic plate filled with a concentrated solution of the precipitant. The plates were incubated at 18° C for two weeks. Due to the diffusion of the vapor, a slow increase in the concentration of the precipitating substance occurred in the drop of the protein-DNA solution, which contributed to the appearance in 3-5 days of small crystals. By day 14 some of them reached a size of 50-100 μm in length and had the shape of a flat parallelepiped. It should be noted that the magnitude, shape and quantity of obtained crystals were varied depending on the conditions for their production. Even crystals from the same plate had a different unit cell parameters, but all of them were releated to the same symmetry group named P 1 2 1. Differences in linear parameters of a unit cell of all crystals weren't higher than 0.5 Å. We hope that these differences means that position of DNA in our crystals

were chaotic, this point also explains why we miss the DNA on the obtained electron density map. Although DNA molecules are missed in obtained crystal structure, it wasn't published in Protein Data Bank yet, despite of the fact that researches aimed on a solvation of crystal structure of a pure Dps were succsesfully carried out (its structure is releated to a different symmetry group named P 2 2 2). It was also shown that in the control experiments using only solutions of the DPS protein (without DNA), the crystallization process passed much more slowly, and the resulting crystals had smaller size. As it was mentioned above, two types of DNA were used in our experements, namely, extracted bacterial nucleoid and short DNA molecules with a length of 24 base pairs. The best crystal was obtained from DPS with short DNA mixture. On Fig. 1 you can see the fitting of electron density map and coordinates of atoms of obtained crystal. On Fig. 2 you can see the diffraction picture of this crystal. On Fig. 3 it is shown the elementary cell of the crystal of the DPS protein, which consists of four molecules.


a

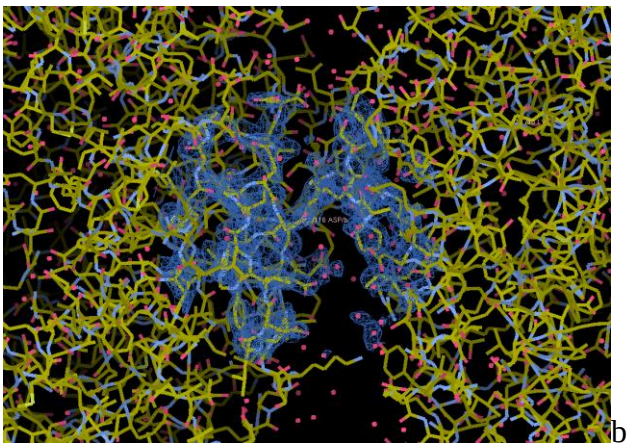

b

Fig. 1 (a) Fitting of electron density map and coordinates of atoms of obtained crystal; (b) Zone of possible DNA location, contact zone of two DPS molecules with increased electron density.

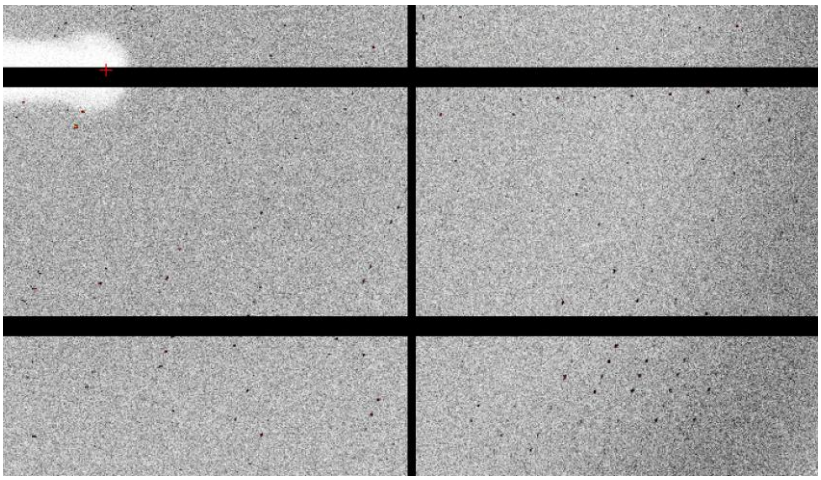


Fig. 2 The picture of the crystal diffraction

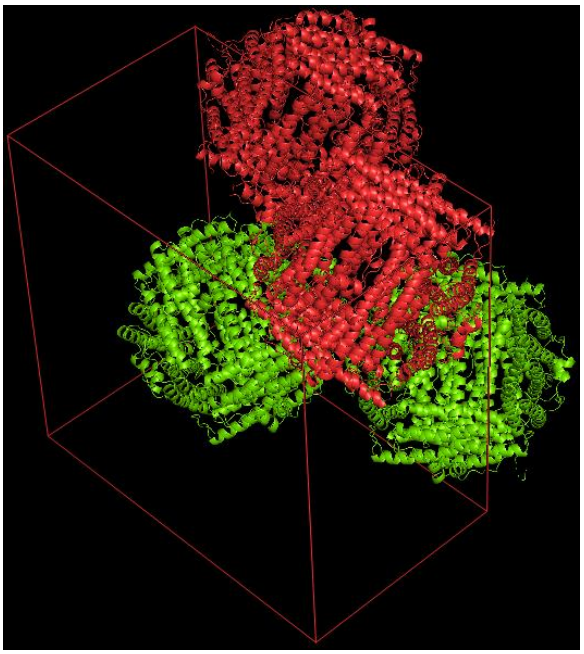


Fig. 3 The view of the unit cell of the obtained crystal.

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