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POSTERS

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main DNA repair systems in eukaryotes. For correct functioning these systems require precise regulation. PARP1 and PARP2 are widely considered as regulators of DNA repair processes, including BER. PARP in response to the DNA damage synthesize polymer of ADP-ribose (PAR) covalently attached to the acceptor proteins including PARP itself. PAR formation can directly influence the acceptor properties and also it is an intracellular signal about DNA damage. PARP1 is well characterized protein but both proteins are under careful attention of researchers. In our work we studied interaction of PARP2 with model DNAs containing several key BER intermediates including AP sites. Moreover AP-site is one of the most frequent types of DNA damages. Using reconstituted systems we made a comparative study of PARP1/PARP2 interaction with several key BER proteins (Pol-beta, FEN1 and APE1) demonstrating inhibitory effect of both PARPs. Wherein in contrast to PARP1 the inhibition caused by PARP2 is hardly regulated by PAR synthesis. We next demonstrated the ability of PARP2 to cross-link with AP site via Schiff base formation like PARP1 does. For both PARPs we determined major role of the N-terminal domains in formation of cross-links with AP DNA. We have also confirmed that DNA binding by PARP2, in contrast to PARP1, is not modulated by autopoly(ADP-ribosyl)ation. Taken together, our results testify to the complicated multilevel regulation of short- and long-patch pathways of BER under coordinated action of PARP1 and PARP2. This work was supported by RSCF project № 17-74-20075.

P.18-007-Mon
Studying of DNA binding proteins using crosslinking reaction with the participation of the cysteine residues

L. Abrosimova[1], M. Monakhova[2], L. Zheleznaya[3], T. Oretskaya[2], D. Rao[4], E. Kubareva[5]
[1]*Department of Chemistry, M.V. Lomonosov Moscow State University, Moscow, Russia,* [2]*Lomonosov Moscow State University, Chemistry Department and Belozersky Institute of Physical and Chemical Biology, Moscow, Russia,* [3]*Institute of Theoretical and Experimental Biophysics, Pushchino, Moscow Region, Russia,* [4]*Department of Biochemistry, Indian Institute of Science, Bangalore, India,* [5]*M.V. Lomonosov Moscow State University, A.N. Belozersky Institute Of Physico-Chemical Biology, Moscow, Russia*

The correction of the errors occurred in the process of DNA replication is performed by DNA mismatch repair (MMR) system. The process of DNA repair is initiated when MutS protein binds to the mismatch. At the next step MutS binds ATP, releases the mismatch and starts moving along DNA as a 'sliding clamp'. This process results in complex formation of MutS with other MMR protein – MutL. The existence of this ternary complex activates DNA repair. This multistage process has been thoroughly studied for *E. coli* MMR system. We suggest investigating the process of DNA repair by MMR system taking place in bacterium *Neisseria gonorrhoeae,* a parasite of mammals. The MutL protein in *N. gonorrhoeae* possesses endonuclease activity contrary to MutL from *E. coli* and initiates MMR by itself. Taking into account the conformation variability and dynamic nature of the MMR proteins themselves and in the complex with DNA, one of the ways to study the interaction of constituents of this complex is their covalent binding. For this purpose, the crosslinking reaction between the MutL cysteine and amino groups of MutS is performed using N-β-maleimidopropyl-oxysuccinimide ester in the presence of DNA. The crosslinked biomolecules are planned to be analyzed by mass spectrometric method. The crosslinking reaction involving cysteine residues was also performed in the case of nicking endonuclease (NE) BspD6I. This enzyme recognizes a specific sequence in DNA and cuts only one strand nearby the recognition site. No crystal data for the complex of NE BspD6I with DNA is available to date. To elucidate the possible contacts of the protein with DNA, the crosslinking reaction was performed. In this case, DNA contained disulfide group in 2′-position of nucleoside that reacted only with cysteine residues. The obtained data allow suggesting which cysteine residues of NE BspD6I can locate in close proximity to DNA during complex formation. The work was funded by RFBR grant № 17-54-45126.

P.18-008-Tue
Low homology FRPs from different cyanobacteria functionally interact with Synechocystis OCP

Y. Slonimskiy[1,2], E. Maksimov[3], N. Sluchanko[2,3]
[1]*M.V. Lomonosov Moscow State University, Department of Biochemistry, Faculty of Biology, Moscow, Russia,* [2]*A.N. Bach Institute of Biochemistry, Federal Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia,* [3]*M.V. Lomonosov Moscow State University, Department of Biophysics, Faculty of Biology, Moscow, Russia*

Photosynthesis requires a balance between efficient light harvesting and protection against photodamage. The cyanobacterial photoprotection system uniquely relies on the functioning of the photoactive orange carotenoid protein (OCP) that under intense illumination provides fluorescence quenching of the light-harvesting antenna complexes, phycobilisomes. The recently identified fluorescence recovery protein (FRP) binds to the photoactivated OCP and accelerates its relaxation into the basal form, completing the regulatory circle. Lately, it was shown that, in addition to the function mentioned above, FRP is able to detach photoactivated OCP from phycobilisomes. At the same time, the molecular mechanism of FRP functioning is largely controversial. Moreover, since the available knowledge has mainly been gained from studying *Synechocystis* proteins, the cross-species conservation of the FRP mechanism remains unexplored. Besides the phylogenetic analysis of FRP sequences, we performed a detailed structural-functional analysis of two selected low-homology FRPs by comparing them with *Synechocystis* FRP (*Syn*FRP). While adopting similar dimeric conformations in solution according to the SAXS data and preserving binding preferences of *Syn*FRP toward various OCP variants, the low-homology FRPs demonstrated distinct binding stoichiometries and differentially accentuated features of this functional interaction. By providing clues to understand the FRP mechanism universally, our results also establish foundations for upcoming structural investigations necessary to elucidate the FRP-dependent regulatory mechanism.

P.18-009-Wed
Analysis of the interaction between 14-3-3 and steroidogenic acute regulatory protein (StAR)

K. Tugaeva[1,2], D. Sotnikov[1], N. Sluchanko[1,3]
[1]*A.N. Bach Institute of Biochemistry, Research Center for Biotechnology of RAS, Moscow, Russia,* [2]*Department of Biochemistry, School of Biology, M.V. Lomonosov Moscow State University, Moscow, Russia,* [3]*Department of Biophysics, School of Biology, M.V. Lomonosov Moscow State University, Moscow, Russia*

14-3-3 proteins participate in different cellular processes through a multitude of interactions with phosphorylated partner proteins. Recently, 14-3-3 proteins were found as components of the multi-

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