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Abstracts submitted to the 44th FEBS Congress, taking place in Krakow, Poland from 6th to 11th July 2019, and accepted by the Congress Organizing Committee are published in this Supplement of *FEBS Open Bio*. Late-breaking abstracts are not included in this issue.

About these abstracts

Abstracts submitted to the Congress are **not peer-reviewed**. In addition, abstracts are published as submitted and are **not copyedited** prior to publication.

We are unable to make **corrections of any kind** to the abstracts once they are published.

Indexing

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differentiation, cell proliferation, embryonic development. Even slight shift in miRNA level could lead to significant changes of transcriptome, and in a result of cell phenotype. In the last decade, over 2500 human mature miRNA sequences were deposited in miRBase. The function of many of them have been found and anti-miRNA, as potential therapy tools have been designed. Despite of an enormous data of miRNA, there are still many questions concerning miRNA function to be solved. The generally accepted model of the miRNA-guided RNA down-regulation suggests that mature miRNA targets mRNA in a nucleotide sequence-specific manner. Recently, we analyzed the nucleotide content of human mature miRNAs and showed that the most abundant nucleotide in miRNAs is guanosine. We identified guanosine-rich miRNAs and found that the level of G in some miRNAs is even over 90%. We noticed that some miRNAs (179 of 2565 human ones) have quadruplex specific motif GGN(1-7)GGN(1-7)GGN(1-7)GG. Furthermore, we found that at least 50% of miRNAs may adopt tertiary structure. Using specific nucleases, NMR, UV/Vis and CD spectroscopies, small-angle X-ray solution scattering (SAXS) as well as and molecular dynamics, as the first ones, we gave evidences that some miRNAs may adopt quadruplexes, e.g. miR-3620, 4507, hairpin and/or homoduplex structures, e.g. miR-21, miR-93 and miR-296. We also showed that the structure of miRNA has functional consequences and suggested that miRNAs may function also beyond RISC and are even more sophisticated regulators, that it was previously expected. We think that the knowledge of the miRNA structure and its dynamic may give a new insight into miRNA-dependent gene regulation mechanism and be a step forward in the understanding their function and involvement in cancerogenesis.

P-26-003
Bacterial 6S RNAs under stress conditions

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6S RNA is a highly abundant small non-coding RNA found in diverse classes of prokaryotes, including bacteria with an extremely small genome, that indicates an important role of 6S RNA in the cell. 6S RNA has a unique secondary structure which mimics DNA promoter, thus 6S RNA is able to bind RNA polymerase (RNAP) holoenzyme and inhibit transcription in case of an unfavorable environment. Moreover, DNA-dependent RNAP can use 6S RNA as a template for synthesis of short pRNAs, when it needs to release from 6S RNA and proceed transcription of genes. Under normal conditions 6S RNA knockout does not affect *E. coli* growth, while it becomes essential for cell adaptivity to starvation and alkaline stress. Some other bacteria express 6S RNA at highest levels under standard cultivation conditions. These facts raise a number of questions, like (i) what is the mechanism of 6S RNA-dependent transcription inhibition (and its retraction) in these bacteria, (ii) whether 6S RNA is involved in some stress responses, and (3) what type of genes are affected. In the present work we characterized properties and functions of 6S RNAs from *B.* subtilis and *R.* sphaeroides in comparison to *E. coli*. It was shown that in B. subtilis 6S RNA knockouts leads to widespread changes in cellular transcriptome and proteome and results into high cell viability under alkaline conditions. For the first time, *R.* sphaeroides 6S RNA was characterized and osmotic and oxidative phenotypes of cells with deletion of 6S RNA gene were found. Surprisingly, decreased viability of *E. coli* 6S RNA knockout strain was observed in case of response to one of the stress, and some genes affected by the lack of 6S RNA under these conditions were revealed by qRT-PCR. Thus, for the first time we experimentally proved a great variety of 6S RNA functions in different bacteria and its involvement into diverse cellular stress responses. This work was supported by the Russian Foundation for Basic Research (project No. 19-04-00791).

P-26-004
MIR3648 and MIR3867 target heterochromatin

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Non coding RNAs (ncRNAs) participate in various biological processes from regulating enzymatic activities to sustaining spatial organization of the genome. MicroRNAs, whose canonical function is suppressing mRNA translation in the cytoplasm via RNA interference, occur in the nucleus as well where these miRNAs may pair with other ncRNAs localized in certain genome regions and trigger repression or activation of these regions. Here we studied RNA-DNA interactome of the human erythroleukemia cell line K562 by a new method, which is based on adapter-mediated RNA-DNA ligation in cross-linked nuclei followed by sequencing. We identified several hundreds of ncRNAs enriched in active or repressed chromatin. Of particular interest are MIR3648 and MIR3867. We found that these miRNAs establish contacts genome-wide and are ranked among the first in localization to repressed chromatin and the inactive spatial chromatin compartment among all ncRNAs identified in the study. MIR3648 and MIR3867 favor bulk heterochromatin over Polycomb repressed chromatin. They associate with regions of late replication and lamina associated domains, are depleted from the bodies of transcribed genes and enriched in gene deserts. The frequency of contacts of MIR3648 and MIR3867 with gene poor chromosome 18 is about 2 times higher than genome average. Interestingly, MIR3648 and MIR3867 genes are hosted within the 5' external transcribed spacer of the 45S rRNA operon. Importantly, the rRNA itself does not show preferences for active or repressed chromatin. Based on the above observations we speculate that MIR3648 and MIR3867 play a role in heterochromatin formation at the genome scale. Of note, previous studies have revealed multiple examples of miRNA involvement in transcriptional silencing of individual genes. However, MIR3648 and MIR3867 represent the first example of miRNAs associated with inactive chromatin genome-wide. This work was supported by the Russian Science Foundation (grant 18-14-00011).

P-26-005
Inhibition of SIRT1/p53 pathway by miR-211 and induction of cell death in breast cancer cells

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Sirtuin1 (SIRT1), a class III histone deacetylase enzyme, can deacetylate various proteins including p53 and regulate diverse physiological and pathological processes. SIRT1 has been suggested as a promoting factor in tumor development and