the non-coding DNA is repeats either scattered through genome (dispersed repeats) or tandemly organized (tandem repeats, TR or satellite DNA). These repeats are transcribed and the transcripts are involved in different processes including early preimplantation embryogenesis. However it is still unknown are the tandem repeats transcripts accumulated during oogenesis or the repeats are transcribed de novo in early embryo prior after the genome activation. The aim of the study was to check the presence of pericentromeric TR transcripts in preovulatory oocytes and to reveal its intracellular distribution. Methods. The TR of pericentromeric satellite 3 (HS3) as well as its transcripts distribution in GV, MI and MII oocytes was studied with DNA-DNA and RNA-DNA FISH, respectively. The colocalisation of HS3 DNA and RNA with RNA-helicase p68 (DDX5) involved in the HS3 transcription regulation was estimated by immunoFISH. The GV and MI preovulatory oocytes were obtained from donors after the informed consent had been signed. GV and MI donor oocytes are not used for gametes banking and are usually discarded. They were donated for scientific purposes after the ethic committee permission was granted. The presence of HS3 transcripts in transcriptome was verified with bioinformatics' methods of analysis of published preovulatory oocytes transcriptome (Zhang *et al.*, 2018). Results. The probe used was hybridized to pericentromeric regions of all chromosomes excluding 2,6,8,11,12,18,19 on lymphocytes chromosome spreads in DNA-DNA FISH experiments. In GV oocytes, the probe was revealed as the part of condensed heterochromatic ring included in the inverted karyosphere . In M1 and M2, the probe was localized to pericentromeric chromosome regions. In DNA-RNA FISH, the probe revealed 1 mkm granules in ooplasm in M1, M2 but not in GV oocytes. Pretreatment with RNAse eliminated the hybridization signal. The HS3 RNA granules were associated with the granules of RNA helicase p68 (DDX5). The analysis of transcriptome revealed a polyadenilated HS3 transcript, that contained a sequence homological to the probe used in the experiment. The transcript contained also the sequence we describe previously as actively transcribed in senescent and malignant cells (Enukashvily *et al.*, 2007). Conclusion. HS3 transcripts are accumulated in human oocyte after the transition from GV to M1. The transcripts are not associated with chromosomes but are adjacent to granules of RNA helicase p68.

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F-1. AEDL peptide and NaCl affect on the ultrastructure and expression of DNA and lysine methyltransferase *genes in Nicotian*a tabacum L. regenerants

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Due to its fixed nature, plants have a developed system of adaptation to environmental changes. The most studied epigenetic modifications of

the genome are DNA methylation and histone proteins. Unlike animals, in which the epigenetic status is updated in each generation, in plants, epimutations can be steadily inherited, and therefore are important for evolution. Salinity is the most important abiotic stress for plants. Along with morphological changes as a result of the action of a high concentration (150 mM) of NaCl on tobacco regenerants (*Nicotiana tabacum* L.), changes in the ultrastructure of cell compartments in plant tissues, in particular nuclei and mitochondria, were observed. The mutual transformation of heterochromatin and euchromatin is primarily due to modifications of the histone proteins and the main modifications are the methylation of lysine residues. The presence of NaCl leads to an increase in the expression of the lysine methyltransferase gene - SUVR3, methylated H3K9, and decreased in the expression of the ASHR3 gene encoding the lysine methyltransferase, methylated H3K4. Sodium chloride causes an increase in the expression of the gene SNF2, an actin-dependent chromatin remodulator, 2 times. Proteins of the SNF2 complex untie the bonds between DNA and histones, increasing access to DNA. De novo methylation in plants is carried out by the unique enzyme DRM2, which is absent in animals. A high salt concentration causes an increase in the expression gene of DNA methyltransferase - DRM2 by 30 %. Moreover, the expressions of DNA-supporting methyltransferases genes remains almost unchanged. The short tetrapeptide AlaGluAspLeu (AEDL) at a concentration of 10-8M significantly stimulates the growth and development of tobacco calluses Nicotiana tabacum. Significant differences in the packing of chromatin in the presence of AEDL were detected both in normal conditions and under the action of NaCl. Significant differences in the packing of chromatin in the presence of AEDL were detected both in normal conditions and under the action of NaCl. In the presence of tetrapeptide, a significant decrease in the expression of genes of the SNF2 family is observed, the level of gene expression genes of methyltransferase DNA remains practically unchanged, the expression of histone methyltransferase genes also remains unchanged or decreases even. In the presence of the tetrapeptide AlaGluAspLeu and sodium chloride together, the expression of the lysine methyltransferase gene, SUVR3, increases, as in the case of the presence of sodium chloride only. An almost 3-fold increase in expression of the SNF2 chromatin modulator, which encodes an ATP-dependent helicase, which is necessary for DNA methylation, was also noted. Such an increase in the expression of chromatin remodulator is accompanied by an increase in the expression of DRM2 almost 3 times.

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F-2. Probing the chromatin structure of ribosomal DNA using extended chromatin fibers

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