

MCF-7 and wild-type cells. The p60+/p70-/p85- MCF-7 cell line was found to express vimentin, a mesenchymal cell marker, as indicated by western blot and immunofluorescence analysis. In addition to up-regulated levels of vimentin, the qPCR analysis also revealed elevated levels of N-cadherin (mesenchymal marker) and down-regulated expression of E-cadherin (epithelial marker) in the cells with selective expression of p60-S6K1 demonstrating features of the mesenchymal-like phenotype of these cells. Meanwhile, p60-/p70-/p85- MCF-7 and wild-type MCF-7 showed the reverse expression levels of the indicated EMT marker genes. The results of qPCR also revealed the EMT transcription program switching in p60+/p70-/p85- MCF-7 since these cells have up-regulated expression of Twist1 and ZEB2 transcription factors which are critical for the initiation of the EMT program. These data imply that the p60+/p70-/p85- MCF-7 cells underwent EMT, whereas p60-/p70-/p85 MCF-7 retained an epithelial-like phenotype. **Conclusions.** Differential expression of S6K1 isoforms under the conditions of p70- and/or p85-S6K1 knockdown and retaining of p60-S6K1 expression initiates EMT in the breast cancer cells MCF-7. This observation indicates a possible role of the p60-S6K1 isoform in the induction of EMT, and this function of p60-S6K1 is likely to be suppressed by the expression of p70- and/or p85-S6K1 isoforms.

## CURRENT STATE AND PROSPECTS OF BIOINFORMATICS DEVELOPMENT

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**Background.** Bioinformatics is usually understood as usage of computer technology for solution of biological problems, such as studying the specific algorithms and methods for analyzing large amounts of data, working mainly with genomic and protein sequences. Main reasons for the development of bioinformatics as a science were factors such as the development of medical biology and the necessity to create arrays of data obtained by experimental methods of medical biology. The **aim** of the work is to analyze the state of bioinformatics as a branch of science and to identify the prospects for its development. The methods are the exploration of the problems and achievements of bioinformatics and the definition of promising directions for the development of science in future. **Results.** The current development of molecular biology requires the active using of effective data analysis methods and usage of modern information technologies. In connection with this, there was a need to solve such practical tasks as the necessarily for work with a large amount of data, complex calculations and special requirements for the performance of computer technology. Bioinformatics uses methods of applied mathematics, statistics, theory and history, computer science and heuristic methods. Basics of the research areas of bioinformatics are alignment of sequences of genomes, gene search, a collection of genomes, alignment of protein structures, anticipating the structure of proteins, prediction of gene expression and protein-protein interaction and reconstruction of the evolution process. A special place has the receipt of high-quality sequences of genomes with fragments of sequences obtained using traditional DNA sequencing methods and designing of accounting for the strong factors for DNA-microchip data. An important role in bioinformatics plays the visualization of research results, such as browser of genomes. The genome is a one-dimensional map that displays any nucleotide awareness. Information is usually structured into blocks which are superimposed on tracks. The most popular are the Integrated Genome and the Browser Integrative Genomic Viewer. Results The development of bioinformatics has allowed us to quickly and reliably decode the human genome. Due to the achievements of bioinformatics that were able to create an artificial bacterium, it was possible to cure some types of cancer. Considering the specifics of data processing operations in bioinformatics and their volume, it seems effective the solution to the wide application of parallel computing technology to significantly improve productivity in solving many

problems, in particular genome alignment, their search and assembly, preservation, and the ability to visualize the results of the researchers.

## DNA FRAGMENTATION OF CRYOPRESERVED HUMAN SPERM IN MEN WITH PATOSPERMIA

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**Introduction.** The level of sperm DNA integrity has an independent diagnostic and prognostic value for patients undergoing the infertility treatment using assisted reproductive technology (ART). According to WHO standards, the amount of sperm with damaged DNA should not exceed 30% in men with normozoospermia (WHO, 2010). An integral part of ART is spermatozoa cryopreservation which can lead to appearance of additional damages of DNA structure that cause not only a decrease of their fertilizing abilities, but also the abnormal development of the embryo derived from the in vitro fertilization. **Aim.** The aim was to study the influence of cryopreservation factors on the sperm DNA fragmentation level in the case of patospermia. **Methods.** The study included the data obtained during diagnostics of men, undergoing infertility treatment at the Medical Center "Clinic of Reproductive Medicine of ART" with their written informed consent. The research groups included ejaculatory spermatozoa obtained from men with oligoasthenoteratozoospermia (group 2) and testicular spermatozoa of men with obstructive azoospermia obtained by epididymis aspiration or extraction (group 3). The comparison group was spermatozoa of men with normozoospermia (group 1). Sperm cryopreservation was carried out by two-step method using 7% glycerol. The level of DNA fragmentation in sperm was determined using fluorescence microscopy and acridine orange staining. **Results.** It has been established that the number of spermatozoa with damaged DNA in ejaculatory spermatozoa was higher than in testicular ones. Thus, the level of DNA fragmentation in group 1 was  $(17.5 \pm 3.02)\%$ , in group 2  $(32.7 \pm 7.7)\%$  and in group 3 was  $(6.2 \pm 1.3)\%$ . After cryopreservation this indicator increased in all studied groups and amounted to  $(27.2 \pm 1.9)\%$ ,  $(41.6 \pm 5.7)\%$  and  $(10.8 \pm 2.3)\%$  for groups 1–3, respectively. **Conclusions.** The level of DNA fragmentation is higher in freshly isolated spermatozoa from oligoasthenoteratozoospermic men than in case of normozoospermia and obstructive azoospermia. Testicular sperm cells are characterized by a low level of DNA fragmentation. Cryopreservation causes an increase in the level of sperm DNA fragmentation regardless of the spermatogenesis state. The results of research should be confirmed during the infertility treatment by ART methods.

## CULTIVATION OF NEWBORN RABBIT VIBRISSA DERMAL PAPILLA CELLS IN VITRO

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**Background.** The dermal papilla (DP) formation is associated with a complex process of neural crest cells migration. DP contains pluripotent cells that support renewal of a hair follicle over a long period. The possibility of culturing DP cells of several species (mouse, rat, human, and sheep) was shown. **The aim** of our study was to demonstrate the possibility of culturing DP cells of rabbit vibrissae. **Methods.** Cell cultures were isolated from explants by the method of Sieber-Blum, 2004.