



International Young Scientists Conference dedicated to the 50-th Anniversary of the Institute of Molecular Biology NAS RA

“NEW TRENDS IN LIFE SCIENCE”

26-28, SEPTEMBER 2016

ABSTRACTS



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Yerevan, Armenia

THE ROLE OF NON-CODING DNA IN ONTOGENY AND EVOLUTION

T. Shkurat

Southern Federal University, Russia

Non-coding DNA sequences represent a new frontier in molecular genetics, genomics, proteomics, and transcriptomics. They have great potential to advance our full understanding of biological processes in ontogeny and evolution. Many mechanisms of functioning and localization of the protein non-coding DNA regulatory sequences in eukaryotic genomes have not been found yet. We used molecular and bioinformatics approaches to study the genome functional elements that regulate genes responsible for the formation of a genetically determined and evolutionary fixed characteristics, such as species, life expectancy, height, weight, number of dominant follicles in 37 species of mammals. One of the important regulatory elements of gene expression is microRNA. High copies number per cell of *hsa-mir-5096* and *hsa-mir-1268* genes in mammals' genomes was discovered. Regularities of microRNA molecules localization in the vicinity of the somatotropic axis genes and animals growth, hypothalamic-pituitary-gonadal genes and the dominant follicles number were found. For example, the number of microRNA molecules localized around the chorionic gonadotropin alpha chain gene (CGA) positively correlated with duration of pregnancy ($r=0.89$); birth weight ($r -0.86$); lifetime of the form ($r -0.7$). A negative correlation with the number of pups in a litter ($r -0.82$) was detected. The interaction model of non-coding genome elements with coding one is considered. It is shown that the annotation of the non-coding DNA nucleotide sequences, their classification and identification of structural-functional organization allows, on the one hand, to understand the scenario of the evolution of non-coding DNA elements, while on the other it assists to formulate an idea about their role in various biological processes. This study was supported by Russian Ministry of Science and Education, grant №6.703.2014/K.