

## Computer analysis of genes expression, involved in the serotonergic and dopaminergic systems work, in the ventral tegmental brain area of aggressive and non-aggressive rats

A.O. Bragin\*, A.L. Markel, R.V. Kozhemyakina, Y.L. Orlov

*Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

\* e-mail: [ibragim@bionet.nsc.ru](mailto:ibragim@bionet.nsc.ru)

**Key words:** serotonergic system, dopaminergic systems, aggressive rats, computer analysis, gene expression

*Motivation and Aim:* Aggression remains one of the important problems even in developed countries. It is known, that aggressive behavior can be caused not only by social factors, but also by genetic factors. For this reason, the analysis of gene expression patterns – associated with aggressive behavior – is an urgent task. For the analysis of the genetic basis of aggressive behavior in the Institute of Cytology and Genetics SB RAS two rat lines were developed: aggressive and tolerant (non-aggressive).

*Methods and Algorithms:* In the work, the ventral tegmental area of the rat brain was analyzed, containing dopaminergic neurons and responsible for motivation. RNA-sequencing of the samples of the ventral tegmental region of the brain of aggressive and non-aggressive rats was performed [1].

*Results:* As a result of the computer analysis of RNA-seq data, the expression of protein genes – associated with dopamine and serotonin in the brain tissue of aggressive and non-aggressive rats was assessed. Significant differences in the expression of the serotonin and dopamine receptors, the dopamine transporter and the enzymes – responsible for the synthesis and catabolism of serotonin and dopamine – were found.

*Conclusion:* The obtained results may be of interest both for the problem of aggressiveness in fundamental science and for industry, for example, for breeders of animals.

*Acknowledgements:* The research has been supported by RFBR (grant No. 18-34-00496).

### *References*

1. Babenko V.N. et al. (2016) Analysis of differential gene expression by RNA-seq data in brain areas of laboratory animals. *Journal Integrative Bioinformatics*. 13(4):292.