

Bioinformatics study of genes expression in rat brain areas by RT-PCR and their role in behavior

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Motivation and Aim: We studied mechanisms of hereditary-mediated aggressive behavior on laboratory animal models based on transcriptome profiling. Set of experiments in different model animals were used to compile the data set of genes related to behavior and estimate their conservation across species in a database prototype.

Methods and Algorithms: We used unique experimental model of grey rats (*Rattus norvegicus*) selected by aggressive behavior toward human. We estimated the gene expression in rat brain areas [1]. RNA-seq sequencing of rat brain areas samples was done using Illumina HiSeq. Next we used RT-PCR.

Results: We tested several genes presumably associated with the manifestation of aggressive behavior. We have studied the following genes expression in rat hypothalamus: *Egr1*, *Gabrd*, *Zic2*, *Shank3*. All the genes were differentially expressed in a hypothalamus of tame and aggressive rats. *Egr1* had lower expression in tame rat hypothalamus than in aggressive rats. 3 other genes – *Gabrd*, *Zic2* and *Shank3* had significantly higher expression in tame rat hypothalamus than in aggressive rats (P-value less than 5E-5). *GABRD* codes the gamma-aminobutyric acid type A (GABA-A) receptor delta subunit. GABA-A receptors are ligand-gated chloride channels. Alternatively spliced transcript variants have been described for this gene, but their biological validity has not been determined. The protein encoded by *EGR1* gene belongs to the EGR (early growth response) family of C2H2-type zinc-finger proteins. Studies suggest this is a cancer suppressor gene. *Zic2*. The protein encoded by this gene is a *Zic* family member 2 and acts as a transcriptional repressor and may regulate tissue – specific expression of dopamine receptor D1. Dopaminergic transmission is associated with motivation, learning and cognition. The set of computer tools and data processing pipelines helped to find genes and gene regulation patterns applied to behavior models [1].

Conclusion: Many synapse-related genes have statistically significant deviation in splicing depending on brain region and aggressive/tame status in rat. It is a novel phenomenon of the transcriptome data related to aggressive behavior

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References

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