Signatures of selection and adaptation to subterranean lifestyle across the transcriptomes of Arvicolinae (Rodentia, Cricetidae)

P-01.3-17

O. Bondareva[I], S. Bodrov[I], E. Genelt-Yanovskiy[I], T. Petrova[I], N. Abramson[I]

[I]Zoological Institute RAS, Saint-Petersburg, Russia

Subterranean rodents from the Arvicolinae subfamily constitute an ideal model to test hypotheses about adaptive evolution due to ecological shifts. We obtained raw RNA-seq reads for ten representatives of the subfamily to detect adaptive signatures of subterranean species. For seven species raw reads were available in the NCBI SRA. In addition, we used previously assembled *M. ochrogaster* and *C. griseus* transcriptomes. Data covered such specialized subterranean species as *P. schaposchnikowi*, *E. lutescens*, *L. mandarinus* and *T. subterraneus* as well as closely related terrestrial species. We revealed 112 single-copy orthologs, which were subsequently analyzed for signatures of natural selection. The median dN/dS value (free model) was higher for subterranean voles compared to terrestrial ones. However, when evaluating the selection independently for each line of subterranean rodents (branch model) genes with significant differences were not found. We found at least ten genes with parallel amino acid substitutions that were specific for subterranean rodents: Erp29, Rad23b, Hikeshi, Zadh2, Mrps14, Pycr2, Ccdc86, GTPBP2, Snapc2 and Ttll12. These genes can potentially be involved in the process of rodent adaptation to the subterranean lifestyle: Mrps14 regulates the mitochondrial translation process. The Rad23b and Pycr2 genes are associated with DNA repair processes and the response to oxidative stress, respectively. Genes Zadh2 (production of prostaglandins), CCdc86 (viral response), and Ttll12 (regulation of interferon) are involved in changing the immune response and adaptation of rodents to a new infectious background. It could occur, in particular, due to high humidity in burrows. The remaining genes we found are involved in general regulatory processes: protein folding - Erp29, stress response with HSP70 - Hikeshi, transcription (Snapc2), and translation (GTPBP2). This study was conducted with financial support from the Russian Science Foundation grant N19-74-20110.