Molecular adaptations of subterranean rodents to underground lifestyle

Olga Bondareva
Zoological Institute RAS, Saint-Petersburg, Russia olga.v.bondareva@gmail.com

Raisa Chetverikova
The Carl von Ossietzky University of Oldenburg, Oldenburg, Germany
raisa.chetverikova@gmail.com

Mike Rayko
University of California, San Diego, USA mike.rayko@gmail.com

Natalja I. Abramson
Zoological Institute RAS, Saint-Petersburg, Russia natalia_abr@mail.ru

Subterranean rodents comprise approximately 250 species that spend their entire lives in underground, unventilated tunnels, distributed along all continents except Australia and Antarctica. Subterranean rodents escape from predators and extreme climatic fluctuations in their underground habitats, but subject to various stressors such as darkness, oxygen deficiency, hypercapnia, food shortage and high infectivity. Since environmental stress is considered as an important evolutionary driving force, most of subterranean rodents share convergent evolutions in adaptation to a shared ecotope, e.g. all of them have more or less regressive vision ability and progressive hypoxia and hypercapnia tolerance. In the meanwhile, they show divergent adaptations to their separated feeding niches and different phylogenies. With the fast-developing of NGS technology, recent progress in rodent comparative genomics offers an inimitable opportunity for the investigation on convergent and divergent evolution, and the discovery of molecular mechanisms that underlie underground adaptations.

5 transcripts of 5 phylogenetically distant underground species (*Fucomys damarensis, Ctenomys sociabilis, Eospalax baileyi, Tachyoryctes splendens, Nannospalax galili)* from differents tissues were obtained from NCBI SRA database. All transcripts were aligned to *Mus musculus* cDNA with bwa program, SNP calling was performed with GATK package. Then we selected all SNPs presented in all alignments using bedtools.

We found 30 075 SNP in 3 464 genes. Density of this genes was maximum on 11 and 19 Mus chromosomes. It was more that median of the density + SD (fig.1). The least density was on X-chromosome (less than median - SD) that we can explain with long non-coding regions on it. There was no genes of our interest on Y chromosome and in MT genome.

To analyse SNP we used standard nucleotide tests: ratio of substitutions in different codon positions (first, second, third), amount of transitions and transversions, amount of synomymous and not-synonymous substitutions. The number of third-place replacement were almost like in first and in second positions - to our surprise - 9 495, 9 985 and 10 595 for first, second and third positions, respectively. The transition number was almost twice higher than transversions amount - 9 262 and 10 910. The amount of non-synonymous substitutions were surprisingly in 1.6 times higher than amount of synonymous substitutions - 18 909 и 11 166, respectively.

We made GO-terms analysis of all genes of interest. It showed statistical enrichment of 4 term. GO:0036303 and GO:0060854, they were closely connected with lymph vessel morphogenesis (fig.2), GO:0031021 and GO:0002133 were involved in microtubule organisation and were part of polycystin protein complex. We have determined 3 genes, that were functionally stand out: Mzt1, Wdr60 and Pkd1. Mzt1 is component of fission spindle and connects with gamma-tubulin. Wdr60 connects dynein and take a part in embryonal skeletal muscle morphogenesis. Pkd1 replies for ion channels activity and connection of protein-kinases. Maybe this genes play roles in underground adaptation.

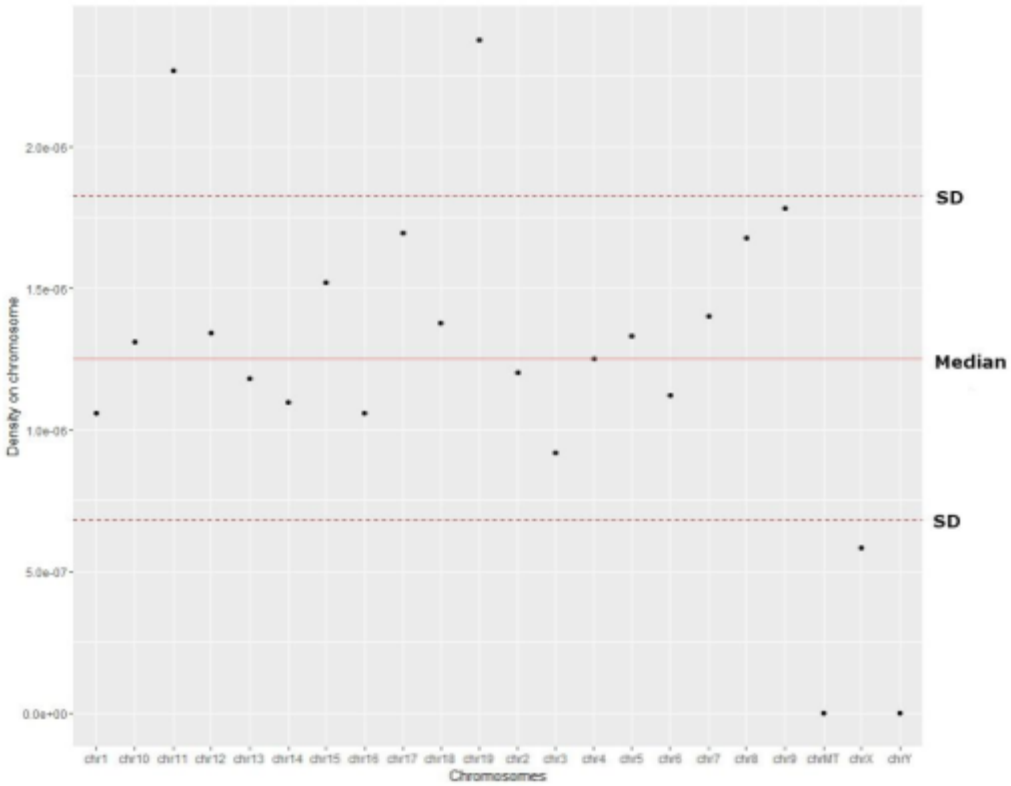

Figure 1. Genes density on Mus chromosomes

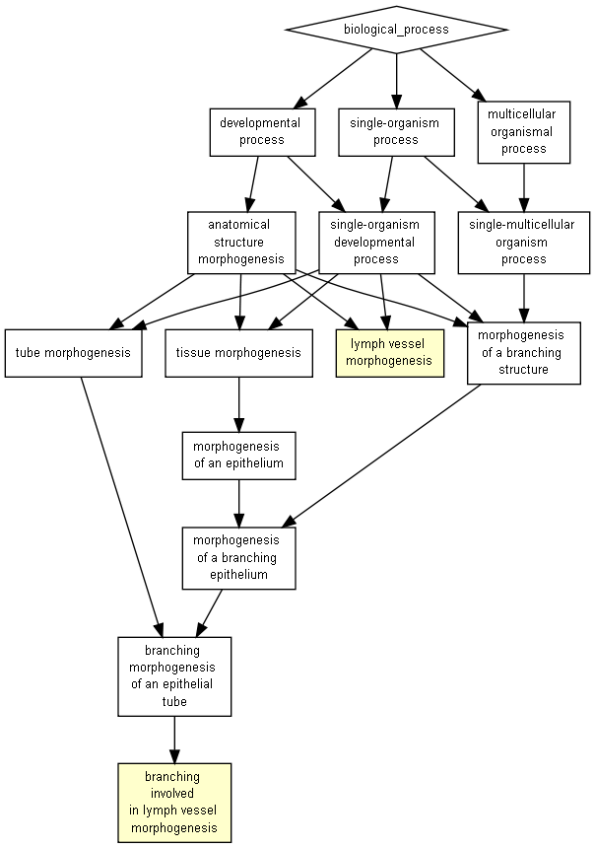

Figure 2. Go-terms enrichment