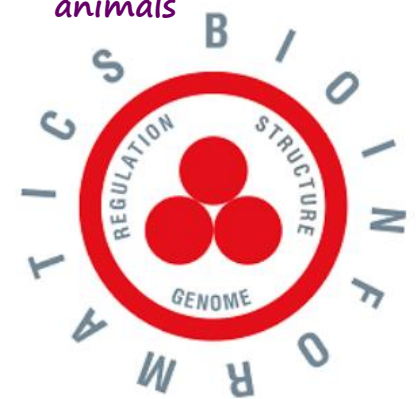


*Domestication explains 2/3 of differential gene expression variance between domestic and wild animals; the remaining 1/3 reflects intraspecific and interspecific variation*



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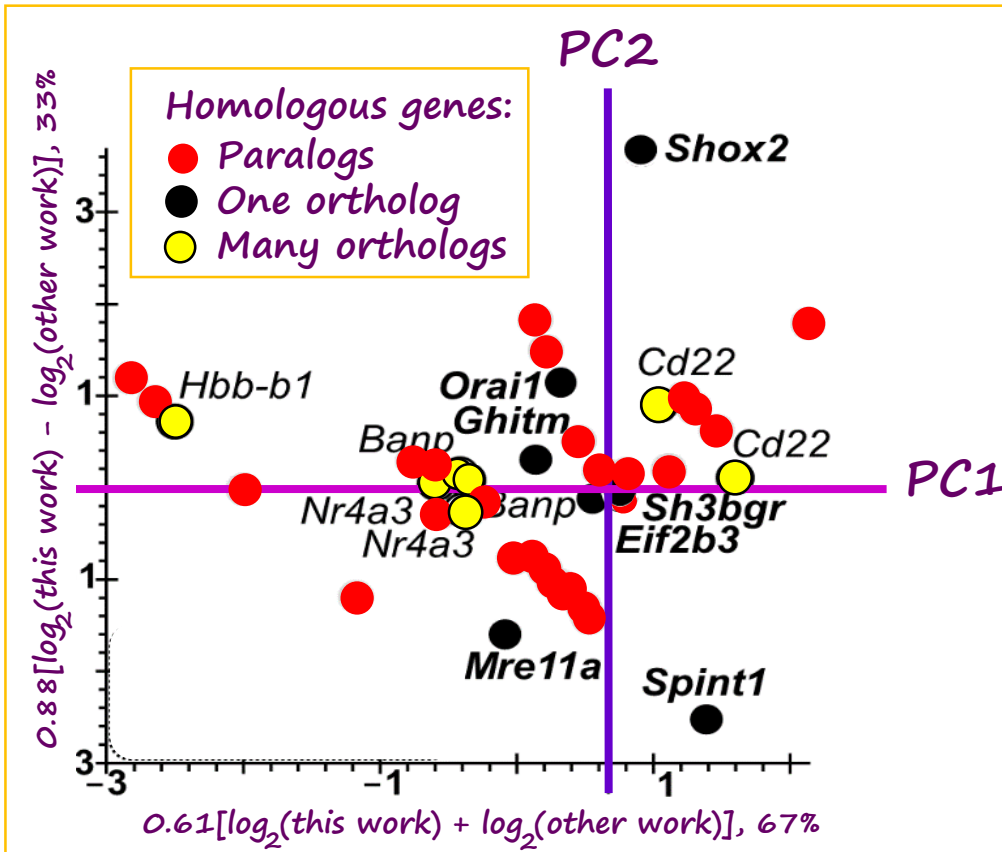
*Section of Animal genetics, bioinformatics and systems computational biology: Population and evolutionary genomics of wild and domestic animals*



<https://doi.org/10.3390/ani11092667>

1. Today, known genomes of domestic and wild animals arouse interest in a common whole-genome pattern of animal domestication that may at least explain differences between the effects of natural and artificial environments on organisms

2. Here we sequenced hypothalamic transcriptomes of tame and aggressive rats, identified their differentially expressed genes (DEGs), and applied principal component analysis to compare them with all the known DEGs of domestic versus wild animals that we could find. Two principal components, PC1 and PC2, respectively explained 67% and 33% of DEGs variance between domestic and wild animals



3. The results of principal component analysis of the hypothalamic DEGs of tame versus aggressive rats found in our work in comparison with known homologous DEGs in domestic animals versus their wild congeners.

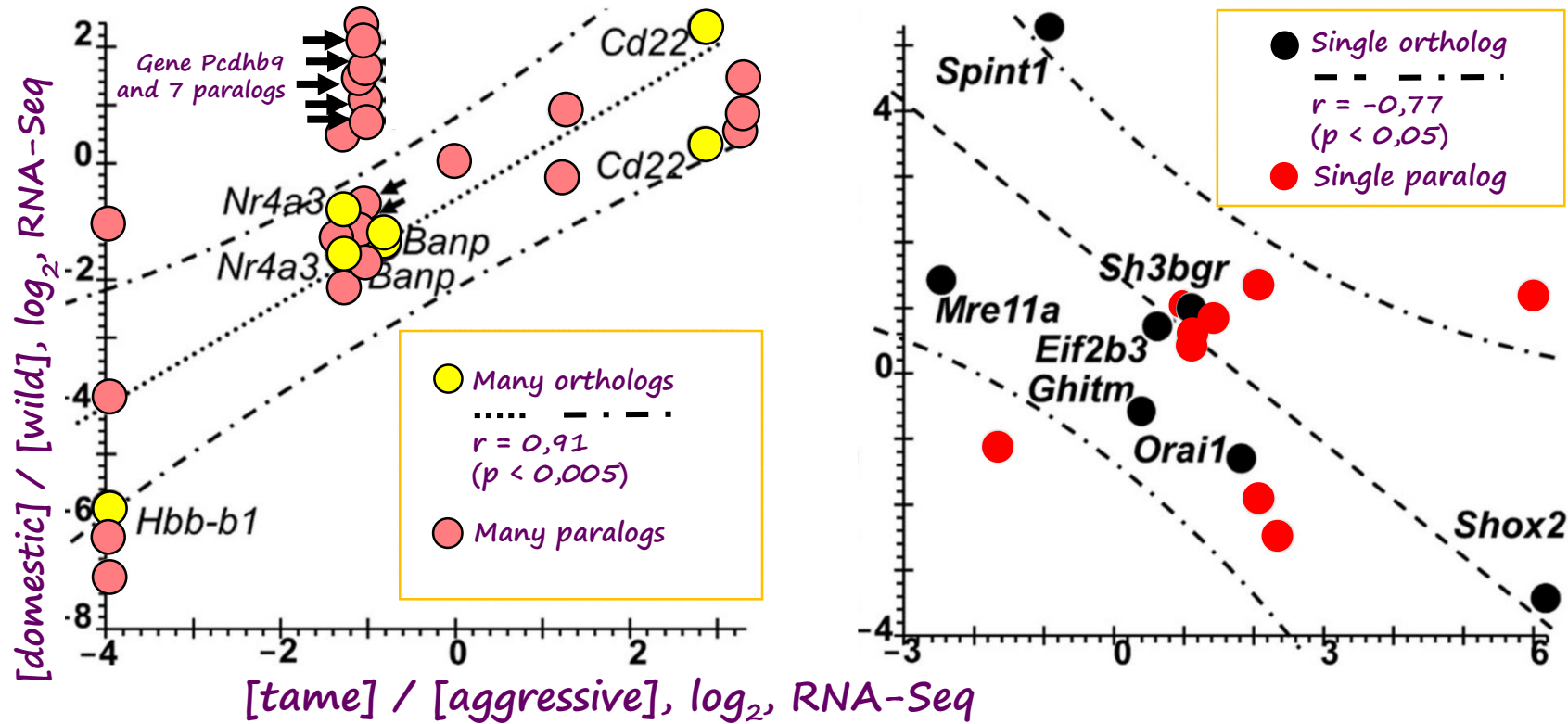
Legend:

black circles are seven single orthologs Eif2b3, Ghitm, Mre11a, Orai1, Sh3bgr, Shox2, and Spint1 grouped along the purple line;  
 yellow circles are pairs of seven orthologs supported by other homologs Banp, Cd22, Nr4a3, and Hbb-b1 grouped along the pink line;  
 red circles are all the remaining paralogs.

log<sub>2</sub> (this work) and log<sub>2</sub> (other works);  
 PC1 and PC2: first (major) and second (minor) principal components calculated by means of software package Statistica; they are parallel to the purple and pink lines, respectively



#### 4. Correlation of Expression Levels of Homologous Genes in Domestic/Wild Animals and Tame/Aggressive Rats



#### 5. Materials and method:

##### Animals

The study was performed on adult male gray rats (*Rattus norvegicus*) selectively bred for over 90 generations for either aggressive or domesticated behavior (as two outbred lines)

RNA-Seq and qPCR of hypothalamus samples of tame and aggressive rats (bioinformatics and molecular biology methods)

Comparison of available RNA-Seq datasets from transcriptomes of domestic and wild animals with our data

Statistical Analysis: principal component analysis

#### 6. Conclusion:

- ✓ On a laboratory model of the animal domestication, tame and aggressive rats, the relationship of differential gene expression with two factors was shown - with artificial selection (domestication) and intraspecific variability
- ✓ Two processes were quantified, domestication and microevolution at the same scale (genome-wide analysis)
- ✓ They respectively explain 2/3 and 1/3 of the differences in differential gene expression in domestic and wild animals as a response of genomes to the impact of artificial and natural habitat factors

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This study was supported by the Russian Science Foundation (grant No. 19-74-10041)