

Domestication explains two-thirds of differential gene expression variance between domestic and wild animals; the remaining one-third reflects intraspecific and interspecific variation

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Before genomes were sequenced, zoologists had discovered destabilizing selection as a general pattern of animal domestication that in foxes and minks had yielded fur colors never seen in the wild. Today, known genomes of humans and 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. Here we sequenced hypothalamic transcriptomes of tame and aggressive rats, identified their differentially expressed genes (DEGs), and, for the first time, 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 differential-gene-expression variance (hereinafter: log2 value) between domestic and wild animals. PC1 corresponded to multiple orthologous DEGs supported by homologs; these DEGs kept the log2 value sign from species to species and from tissue to tissue (i.e., a common domestication pattern). PC2 represented stand-alone homologous DEG pairs reversing the log2 value sign from one species to another and from tissue to tissue (i.e., representing intraspecific and interspecific variation). Accordingly, here we found that the artificial environment of domestic animals alters activities of genes in the same direction as that seen in corresponding human genes during human diseases, whereas the natural environment maintains a normal gene expression pattern in wild animals (matching human health). *Acknowledgements:* This work was supported by Russian government project FWNR-2022-0020.