

Tissue-specific transcriptional profile in the edible dormice is strongly affected by hibernation

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Some living organisms can survive adverse environmental conditions (extreme temperatures, lack of water, food, oxygen, etc.) by drastic changes in metabolism. In such state, the metabolism is reduced up to 50-100% (complete ametabolism) depending on the type of organism and the external environment. One of the most intriguing hypometabolism examples is hibernation of edible dormice (*Glis glis*). Hibernating dormice can slow the metabolism for a long period (up to 11 months), when their body temperature drops up to 4°C during torpid bouts (Hoelzl et al., 2015). However, torpor state alternates with interbout arousals, when the animals wake up and their body temperature rises for a short time (Carey et al., 2003; Ruf and Geiser, 2015). At the same time, edible dormouse has long, compared to other rodents, lifespan: up to 12 years.

During hibernation, all of systems of organs undergo alterations in their metabolic activity and physiology similar to different physiological conditions associated with human diseases and injuries, which represent a proper model for studying new approaches in clinical treatment. A thorough understanding of differential gene expression between active and torpid states is required to translate of lessons from hibernating animals to biomedicine. Furthermore, this information can provide a variety of hypometabolic strategies that improve human health.

In current study, in the frame of Edible Dormice Genome Project initiative, we aimed to identify transcriptional profile alteration associated with hibernation in edible dormice. For this purpose, we examined three groups of animals: active, torpid and aroused between torpor bouts and conducted whole-genome analysis of mRNA expression using Illumina HiSeq

2500 platform in muscle (m. soleus and m. EDL) and lumbar spinal cord samples.

Analysis of differential gene expression reveals a drastic alteration in transcriptional program in response to hibernation in all investigated tissues. Noticeably, interbout arousal – important step in physiology of hibernation – is transcriptionally most similar to torpor state than to active state. The main categories of differential expressed genes and molecular pathways associated with hibernation and interbout arousal in edible dormice were determined.

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