Researchers reveal molecular mechanism of freeze tolerance adaptation in Amur sleeper

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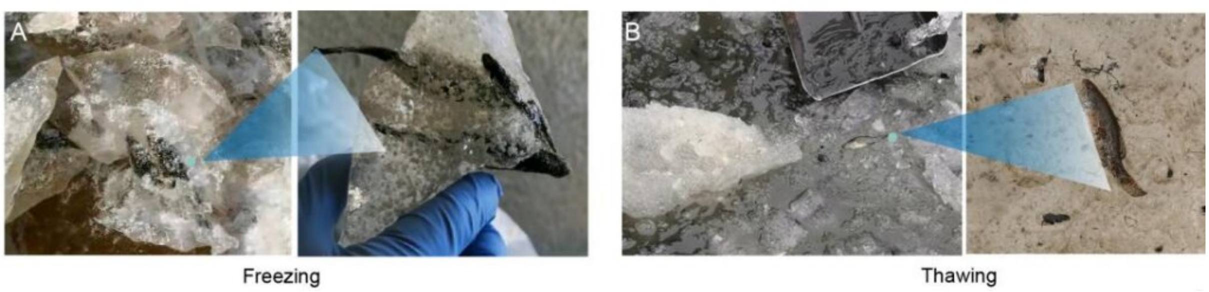

Genes and metabolites related to hypometabolism and the cell stress response. Photographs of the Amur sleeper during freezing (A) and thawing (B). Credit: *Molecular Biology and Evolution* (2023). DOI: 10.1093/molbev/msad040

Some thermostatic vertebrates hibernate in extremely cold environments, while ectothermic animals migrate to relatively warmer areas or produce antifreeze proteins to prevent their body fluids from freezing, as in the case of Antarctic ice fish (Chaenocephalus aceratus). Few ectothermic animals, such as the wood frog, adopt freeze tolerance, an uncommon survival strategy of an organism to withstand the freezing of body water as extracellular ice.

Although there are many studies on the mechanism of freeze tolerance, the genetic basis in ectothermic vertebrates remains largely unknown.

Recently, a research group led by Prof. He Shunping from the Institute of Hydrobiology (IHB) of the Chinese Academy of Sciences revealed the key genetic innovation and regulatory mechanisms associated with freeze tolerance of Amur sleeper (Perccottus glenii), the only known freeze-tolerant fish species. The study was published in *Molecular Biology and Evolution*.

The researchers generated the de novo genome for P. glenii and the closely related but non-cold-hardy Neodontobutis hainanensis. Comparative genomic, transcriptomic and metabolomic analyses showed that P. glenii and N. hainanensis diverged from a common ancestor about 15.07 million years ago and P. glenii experienced a high rate of protein evolution.

A set of genes associated with hypometabolism (nadufaf6 and atp5f1d), cellular stress response (shc1, oxr1, hspa12b, ercc8 and ercc6l2), cytoskeleton stability (kntc2, spc24, haus3, CTT complex, tppp), cryoprotectant accumulation (g6pc and g3pp) and transmembrane transport (aqp3, aqp4, glut2), as well as neural activity (adora, gabrg2, mglur5 and fbxo2) were found to be under positive selection, rapid evolution or specific expansion in P. glenii genome.

The researchers revealed the expression regulation of related genes during activity, freezing and thawing periods. These changes may play an important role in the freeze tolerance of P. glenii.

Metabonomic analyses further revealed the content changes of metabolites related to the antioxidant stress response. The researchers found that a variety of carbohydrates, alcohols and amino acids may be used as the cryoprotectant of P. glenii.

This study elucidated the key genetic innovation and regulatory mechanisms of freeze tolerance in the P. glenii. It not only provides a genetic resource for exploring the adaptative evolutionary mechanism of freeze tolerance in ectothermic vertebrates, but also has potential implications for the development of better cryopreservation technologies and the exploration of the causes of mental diseases in biomedicine, since many genes reported here are associated with multiple neurological and neuropsychiatric disorders in humans.

More information: Haifeng Jiang et al, Multi-omics investigation of freeze tolerance in the Amur sleeper, an aquatic ectothermic vertebrate, *Molecular Biology and Evolution* (2023). DOI: 10.1093/molbev/msad040

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