

New snailfish genome reveals how they adapted to the pressures of deep-sea life

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Yap hadal snailfish (YHS) in situ at 6,903 m (above) and after capture (below).
Credit: Mu Y et al., 2021, PLOS Genetics

A new whole genome sequence for the Yap hadal snailfish provides insights into how the unusual fish survives in some of the deepest parts of the ocean. Xinhua Chen of the Fujian Agriculture and Forestry University and Qiong Shi of the BGI Academy of Marine Sciences published their analysis of the new genome May 13th in the journal *PLOS Genetics*.

Animals living in deep-sea environments face many challenges, including high pressures, low temperatures, little food and almost no light. Fish are the only animals with a backbone that live in the hadal zone—defined as depths below 6,000 meters—and hadal snailfishes live in at least five separate marine trenches. Chen, Shi and their colleagues constructed a high-quality whole [genome](#) sequence from the Yap hadal snailfish to understand how it has adapted to life in the deep sea. The fish was captured from the Yap Trench in the western Pacific Ocean at a depth of about 7,000 meters.

Analysis of the new genome revealed multiple adaptations for living in a cold, dark, [high-pressure](#) environment. The snailfish carries extra genes for DNA repair, which may help keep its genome intact under high pressures. It also has five copies of a gene for an enzyme that takes a compound produced by bacteria in its gut and transforms it into one that stabilizes the structure of proteins under high hydrostatic pressure. The snailfish has also lost certain genes involved in vision, taste and smell, which are likely unnecessary in its dark, food-limited environment.

These new findings offer clues into the mechanisms that snailfish have evolved to survive in oceanic trenches. However, the researchers point out that further studies will be needed to confirm the functions of these genetic changes. Additionally, the high-quality genome sequence can serve as a resource for future in-depth investigations of snailfish and other animals living in the hadal zone.

Chen adds, "Many [genes](#) associated with DNA repair show evidence of positive selection and have expanded copy numbers in the genome of Yap hadal snailfish, which potentially reflect the difficulty of maintaining DNA integrity under high hydrostatic pressure. The five copies of the trimethylamine N-oxide (TMAO)-generating enzyme flavin-containing monooxygenase-3 gene (fmo3) and the abundance of trimethylamine (TMA)-generating bacteria in the gut of Yap hadal [snailfish](#) could provide enough TMAO to improve protein stability under hadal conditions."

More information: Mu Y, Bian C, Liu R, Wang Y, Shao G, Li J, et al. (2021) Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. *PLoS Genet* 17(5): e1009530.
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