

New genomic study provides a glimpse of how whales could adapt to ocean

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In a paper published in *Nature Genetics*, researchers from Korea Institute of Ocean Science and Technology, Korea Genome Research Foundation, BGI, and other institutes presented the first high-depth minke whale genome and their new findings on how whales successfully adapted to ocean environment. The data yielded in this study will contribute to future studies of marine mammal diseases, conservation and evolution.

Whales roam throughout all of the world's oceans, living in the water but breathing air like humans. At the top of the food chain, [whales](#) are vital to the health of the marine environment, whereas 7 out of the 13 great whale species are endangered or vulnerable. The minke whale is the most abundant baleen whale. Its wide distribution makes it an ideal candidate for whole reference genome sequencing.

In this study, researchers conducted de novo sequencing on a minke whale with 128x average depth of coverage, and re-sequenced three [minke whales](#), a fin whale (*Balaenoptera physalus*), a bottlenose dolphin, and a finless porpoise (*Neophocaena phocaenoides*). The yielded data may help to improve scientists' understanding of the evolutionary changes adapted to ocean environment from whole genome level.

The adaptation of whale to ocean life was notably marked by resistance to physiological stresses caused by a lack of oxygen, increased reactive oxygen species, and high salt level. In this study, researchers investigated a number of whale-specific genes that were strongly associated with stress resistance, such as the peroxiredoxin (PRDX) family, O-linked N-

acetylglucosaminylation (O-GlcNAcylation). The results revealed that the gene families associated with stress-responsive proteins and anaerobic metabolism were expanded.

Perhaps the most dramatic environmental adaptation for a whale is deep diving, which can induce hypoxia. Under the hypoxic conditions, the body might produce more [reactive oxygen species](#) (ROS), harmful compounds that can damage DNA. Glutathione is a well-known antioxidant that prevents damage to important cellular components by ROS. In this study, researchers provided evidence to support that there is an increased ratio of reduced glutathione/glutathione disulfide when suffering hypoxic or oxidative stress.

Minke whales and other Mysticeti whale species grow baleen instead of teeth. It's previously reported that the genes ENAM, MMP, and AMEL might play a role in tooth enamel formation and biomineralization. This study showed that these genes may be pseudogenes with early stop codons in the [baleen whales](#). In addition, researchers found that the gene families related to whale's body hair and sensory receptors were contracted, such as Keratin-related [gene families](#) associated with hair formation, several Hox genes that play an important role in the body plan and embryonic development.

Xuanmin Guang, project manager from BGI, said, "Minke whale is the first marine mammal that has been sequenced with such high-depth genome coverage. The genome data not only can help us know much more about the adaptation mechanisms underlying minke whale, but also provides invaluable resource for marine mammal's future studies such as diseases control and prevention, species conservation, and protection."

More information: Minke whale genome and aquatic adaptation in cetaceans, [DOI: 10.1038/ng.2835](https://doi.org/10.1038/ng.2835)

Provided by BGI Shenzhen

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