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When being obese is healthy: molecular evolution of genes related to metabolism in cetaceans

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Abstract

Energetic homeostasis is the process responsible for balancing the energy rates ingested and expelled from our organism. In most mammals, there is a strict control of the homeostasis and satiety regulation, through anorexigenic and orexigenic peptides. However, some lineages of mammals have different regulation, being able to not feed during months and also going through periods of intense feeding, apparently without getting satisfaction. Notorious examples of this behavior are migrating whales that perform long migrations. This project aims to investigate the genetic evolutionary story of this distinct feeding behavior, that evolved independently in some lineages. Accordingly, we investigated the evolutionary rate in genes involved in the central control of the metabolism (*POMC, MC4R, NPY*) in mammals, focusing on cetacean lineage, to better understand their evolutionary histories.

Key words: *Cetaceans, Migration, Evolutionary Genomics.*

Introduction

Energetic homeostasis is the process responsible for balancing the energy rates ingested and expelled from our organism. In most mammals, there is a strict control of the homeostasis and satiety regulation, through anorexigenic and orexigenic peptides. After eating, POMC, a anorexigenic peptive is active and binds to the MC4R receptor, decreasing the food intake and increasing energy expenditure. In reverse, in caloric insufficiency situations, NPY, a orexigenic peptide is active and blocks the MC4R receptor, increasing the food intake and decreasing energy expenditure. However, some lineages of mammals have different regulation, being able to not feed during months and also going through periods of intense feeding, apparently without getting satisfaction. Notorious examples of this behavior are migrating cetaceans that perform long migrations, such as the humpback whale (*Megaptera novaeangliae),* the blue whale (*Balaenoptera musculus)*, the bowhead whale (*Balaena mysticetus)*, the white whale (*Delphinapterus leucas)* and the common minke whale (*Balaenoptera acutorostrata)*. This project aims to investigate the molecular evolution on metabolic genes that are involved in this distinct feeding behavior. Accordingly, we investigated natural selection analyses in genes involved in the central control of the metabolism (*POMC, MC4R, NPY*) in mammals, focusing on the cetacean species mentioned above, to better understand their evolutionary histories.

Results and Discussion

We performed DNA extraction, PCR and gene sequencing in tissue samples from humpback whale (*Megaptera novaeangliae)* and blue whale (*Balaenoptera musculus)*. All tissue samples were loaned by collaborators from Chile, with the respective permits and licenses. Also, we retrieved sequences from public databases, such a Ensembl and GeneBank, from a comprehensive set of tetrapod species, including representatives from as many mammalian orders as possible and other migrating cetaceans, such as the bowhead whale (*Balaena mysticetus)*, the white whale (*Delphinapterus leucas)* and the common minke whale (*Balaenoptera acutorostrata)*.

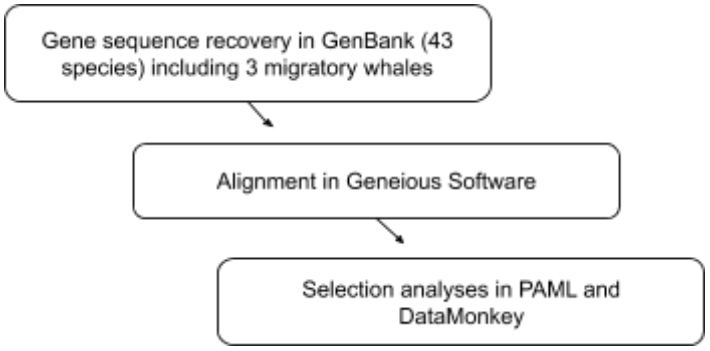

Image 1. Methodoly workflow.

After that, we performed selection analyses using different models implemented in PAML and Datamonkey. Positive or relaxing selection was not observed in NPY. For MC4R and POMC, omega value was significantly greater for the cetacean lineage (0,12 and 0,24, respectively) compared to other mammalian lineages (0,04). A greater value of omega indicates that more nonsynonymous substitutions were fixed along the evolution of migrating lineages, suggesting an acceleration on their evolutionary rate possibly due to a relaxing on purifying selextion acting on both genes .

Conclusions

Our results aid to draw a panorama on selection pressure on these genes along evolution and improve our understanding of molecular evolution of metabolic genes in mammalian history.

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