

Summary of: The application of baleen whale genomes in conservation and evolutionary research.

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Baleen whales (Mysticeti) are a clade of highly adapted carnivorous marine mammals that can reach extremely large body sizes and feature characteristic keratinaceous baleen plates used for obligate filter feeding. From a conservation perspective, nearly all baleen whale species were hunted extensively over a roughly 100 years lasting time period that depleted many of the respective whale stocks with so far unknown consequences for e.g. their molecular viability. From an evolutionary perspective, the lack of fossil records together with conflicting molecular patterns resulted in a still unclear and debated phylogeny of modern baleen whales, particularly in rorquals (Balaenopteridae). In this dissertation, I will demonstrate the application of baleen whale genomes to tackle these open questions by using modern approaches of conservation and evolutionary genomics.

Conservation genomic aspects of baleen whales were addressed in two projects, both using whole genome data of either an Icelandic fin whale (*Balaenoptera physalus*) population or multiple blue whale (*Balaenoptera musculus*) populations to evaluate the impact of the industrial whaling era on their molecular viability. The results suggest a substantial drop in effective population size of both species but also a lack of manifestation in genotypes of the fin whale population when compared to the blue whale populations. Especially the rare and short runs of homozygosity (ROH), usually indicative for inbreeding, suggest frequent outcrossing in fin whales while all analyzed blue whale populations featured long and frequent ROH. In addition to these analyses, genome data of blue whale populations was further used to evaluate if northern hemisphere blue whales diverged into different subspecies. Population genetic and gene flow analyses showed clearly separated and well isolated populations in accordance with their assumed geographical distance. In contrast, the genome-wide divergence between all blue whale populations was low compared to other cetacean populations and to the next closely related sei whale species. Because this includes the morphologically different and well recognized pygmy blue whale subspecies, a proposal was made to equally categorize the two northern-hemisphere blue whale populations as subspecies.

Evolutionary aspects were addressed in a third project, by constructing the genome of the pygmy right whale (*Caperea marginata*) and testing its potential in phylogenetics and cancer research. Phylogenomic analyses using fragments of a whole-genome alignment featuring nearly all extant baleen whales, allowed the revision of the complex evolutionary relationships of rorquals by quantifying and characterizing the amounts of conflicts in early diverging branches. These relationships were further used to identify phylogenetically independent pairs of baleen whales with a maximum of diverging body size differences to compare rates of positive selection between their genomes. The results suggest nearly evenly distributed frequencies of alternative topologies which supports the representation of the early divergence of rorquals as a hard polytomy with high amounts of introgression and incomplete lineage sorting. Within the set of available genomic data, three independent pairs of baleen whales with diverging body sizes were found and comparisons of positive selection rates resulted in many potentially body size and cancer related genes. The lack of conserved selection patterns, however, suggest a more convergent evolution of size and cancer resistance like previously discussed in paleontology.

In conclusion, the application of whole genome data using methods of conservation genetics allowed for a comprehensive estimation about the molecular viability of blue and fin whales as well as an assessment of the taxonomic status of northern-hemisphere blue whale populations. The rather different results between blue and fin whales underlines the importance of genomic monitoring of baleen whales because different species show rather different molecular consequences of their potentially varying depletions. Furthermore, as showcased for the northern-hemisphere blue whale, many important isolated populations of baleen whales may still be unknown to conservation management and genome-wide comparisons will most likely contribute to overcome this under-classification problem. The application of whole genome data in evolutionary research allowed the characterization of the complex patterns of molecular conflicts within baleen whales and especially rorquals that will contribute to the still rather unclear understanding of their evolution. The here found molecular support for the idea of convergent evolution of gigantism in whales will further guide the search for molecular patterns responsible for Peto's paradox.