

Using whole-genome sequences to guide whale conservation efforts.

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Resumo da palestra: Whale conservation is a complicated and complex task due to the highly migratory nature of baleen whales and the resulting unprecise census size estimations. It is still unknown how much certain species were affected by industrial whaling efforts or present-day human influences. Especially the fin whale (*Balaenoptera physalus*) was one of the most sought-after species and industrial scaled hunting depleted populations worldwide until local overexploitations led to a collapse of the whaling industry followed by whaling restrictions established in the 1960s and 1970s. To that day, it is still difficult to assess how much these events affected their population sizes and if or how much they recovered from it. However, with the rise of modern genome sequencing technologies, it is now possible to make comprehensive statements about their genetic past and actual “wellbeing”. Using 51 whole genome sequences, we were able to construct demographic models showing that around 80% of the former population were depleted by whaling. We also analyzed three different dimensions of genetic consequences that we would expect after such a depletion. Doing so, we were not able to find a markedly reduction of the genetic diversity compared to other baleen whales or mammals. We also found no signs of frequent inbreeding or increased numbers of mutations with a supposedly negative impact for the individual fitness. Eventually, we compared found results to single genomes of other whale species and showed that other whales might suffer more from recent inbreeding and negative mutations. Thus, historical whaling may have affected genomes of different baleen whale species in different ways, suggesting that genome-wide assessments of other species and populations are essential for future, more specific, conservation efforts.

Biografia: I am interested in the evolution of genomes and genomic diversity in general, including phylogenetic as well as population genetic questions. In my current work, I try to uncover the impact of bottleneck events on the genetic diversity of baleen whales, and I would like to understand how depleting population sizes affect these genomes. Therefore, I analyze gene flow and hybridization patterns between whales, but I also aim for new genome publications and phylogenetic insides. With this, I hope to support the conservation and management of whales. Additionally, I worked a lot with genomes of parasitic fungi that possess fast evolving and diverse contents of genes responsible for their pathogenetic behavior, called effectors. In so doing, I tried new machine learning tools that predict these effectors and evaluate their reliability. Eventually, this will speed up our process of finding and analyzing those genes.

