

## **Workshop proposal: Genetics insights into killer whale evolution**

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At the time of the last orca symposium, the decade-long first human genome project was not yet complete. Killer whales were then typically studied using mitochondrial D-loop sequences and genotypes at microsatellites. The majority of studies were population- or region-specific.

Genetic studies of killer whales, like most other fields of research on this species, initially focused on the North Pacific ecotypes. Our understanding of this species may be somewhat biased by this – specifically the finding that ecological variation correlates with, and even drives genetic differentiation, is often assumed to be a species-wide trait.

The advent of high-throughput sequencing in the late 2000s marked the start of a dramatic change, making it possible to rapidly sequence complete genomes of tens and even hundreds of whole genome sequences at a reasonable cost. Genomic studies of killer whales have been at the forefront of harnessing this new technology within the field of marine mammal research. The compatibility of genomic datasets and established public archiving of data provide the opportunity for each study to be cumulative, and able to directly compare to, and build upon previously published data. As such, we can progress from regional studies, to an increasingly detailed view of genetic variation within this species at a global scale.

The goals of this workshop are:

- To present a simple global model of genetic variation among and within killer whale populations.
- To review the literature and discuss how past findings fit this model; understanding why some studies have drawn conflicting conclusions and identifying methodological short-comings in some early genomic studies.
- Provide a platform for early career researchers to present their work on local populations, with discussion by all on how these emerging and on-going studies fit the model.
- Work together to draft a synthesis, highlighting where there is consensus or continued outstanding disagreements, best practices identified by the attendees, and presenting an updated version of the model. It is hoped this synthesis can be presented as a talk to the broader symposium.