

Runs of homozygosity in killer whale genomes provide a global record of demographic histories

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Abstract

Runs of homozygosity (ROH) occur when offspring inherit haplotypes that are identical by descent from each parent. Length distributions of ROH are informative about population history; specifically the probability of inbreeding mediated by mating system and/or population demography. Here, we investigate whether variation in killer whale (*Orcinus orca*) demographic history is reflected in genome-wide heterozygosity and ROH length distributions, using a global dataset of 26 genomes representative of geographic and ecotypic variation in this species, and two F1 admixed individuals with Pacific-Atlantic parentage. We first reconstruct demographic history for each population as changes in effective population size through time using the

pairwise sequential Markovian coalescent (PSMC) method. We find a subset of populations declined in effective population size during the Late Pleistocene, while others had more stable demography. Genomes inferred to have undergone ancestral declines in effective population size, were autozygous at hundreds of short ROH ($<1\text{Mb}$), reflecting high background relatedness due to coalescence of haplotypes deep within the pedigree. In contrast, longer and therefore younger ROH ($>1.5\text{ Mb}$) were found in low latitude populations and populations of known conservation concern, including a Scottish population, for which 37.8% of the autosomes comprised of ROH $>1.5\text{ Mb}$ in length.

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ROH_Draft_Revision.pdf available at <https://authorea.com/users/422578/articles/528298-runs-of-homozygosity-in-killer-whale-genomes-provide-a-global-record-of-demographic-histories>