Orca’s Survival during the Ice Age

In the ocean, the killer whale rules as a top predator, feeding on everything from seals to sharks. Being at the apex of the food chain, killer whales’ geographic distribution and population size can also serve as a sentinel species regarding past and future ocean ecosystems and environmental change.

In a recent study in Molecular Biology and Evolution, Moura et al. (2014) assembled 2.23 Gb of northern hemisphere killer whale genomic data and mitochondrial DNA from 616 samples worldwide. Would the data analysis reveal patterns of past climate change that may have impacted food availability? Also, what happened to the diversity of killer whales over time during the last great ice age?

From this data set, the authors used an evolutionary coalescent model to conclude that killer whales were stable in population size during most of the Pleistocene (2.5 million–11,000 years ago) followed by a rapid decline and bottleneck during the last great period of ice age (110,000–12,000 years ago). Although most populations declined, a population off of southern Africa remained stable. Consistent with the population bottleneck, they also showed low genetic diversity, with the exception of a refuge population off the coast of South Africa.

“Our data supports the idea of a population bottleneck affecting killer whales over a wide geographic range and leading to the loss of diversity,” said Moura et al. (2014), “The South African population stands out as an exception, which may be due to local conditions that were productive and stable over the last million years or so.”

Thus, the recent ice age may have been detrimental to the ocean’s top predator and significantly affected diversity among living populations.

Reference

Largest Evolutionary Study of Sponges Sheds New Light on Animal Evolution

Sponges are an important animal for marine and freshwater ecology and represent a rich animal diversity found throughout the world, from tropical climates to the arctic poles. For evolutionary biologists, they also present an interesting animal for comparative study, because they are simple filter feeders that lack nervous, digestive, or circulatory systems, suggesting that they diverged early from other animals.

To provide a wider framework for understanding the molecular complexity behind the evolution of sponges, authors Riesgo et al. (2014) performed the largest sequencing study to date on the genes of representatives from eight sponge genera covering all four currently recognized sponge classes. They performed comparative analysis of animal genes important for signaling, neuronal and ionic conduction, epithelia, immunity, and reproduction.

One of the remarkable results of this work, published in Molecular Biology and Evolution, is the understanding that most higher animal genes, or the greater complement of genes involved in more complex gene pathways, are also present in all sponge groups. They found a number of genes that previously had been associated with complex structures of higher animals and were thought to be absent in sponges. This provides an important new resource to the question which molecules might have been present in early animal groups, and more importantly, provides the framework for posing new hypotheses on determining gene function in sponges and the evolution of animal complexity.

Reference