

 GENOME EVOLUTION

Evolutionary insights from comparative bear genomics

The divergence time between the polar bear (*Ursus maritimus*) and its closest relative the brown bear (*Ursus arctos*) is much shorter than previously anticipated (<500,000 years), according to the results of a new study in *Cell*. This finding implies that polar bears have adapted to life in the High Arctic and to a diet rich in fatty acids in a fairly short evolutionary period.

The researchers were interested in understanding the genetic changes that species undergo when adapting to new ecological niches, particularly evolutionary changes related to the adaptation to a diet high in fat content. “By understanding the genetic components involved in this change, we might gain a better understanding of the genetic components related to fitness consequences of

a high-fat diet in general,” explains Rasmus Nielsen, one of three corresponding authors of the study. “For example, polar bears have very high cholesterol levels, and it is unclear how they are able to cope with these when humans generally cannot.”

The population genomics approach involved deep sequencing and *de novo* assembly of a polar bear reference genome, as well as resequencing of 79 Greenlandic polar bear genomes and 10 brown bear genomes. Notably, the authors found that, in polar bears, the genes under strong positive selection — the genetic signature of adaptation — were highly enriched for genes with a function in the cardiovascular system in humans. For example, *APOB*, which encodes apolipoprotein B — the major protein component of

low-density lipoprotein cholesterol — had the strongest selection signal in polar bears, the study showed.

The fact that the polar bear has evolved several unique characteristics in only a few hundred thousand years makes this non-model organism particularly fascinating from an evolutionary standpoint. Moreover, the team believe that direct tests of functional hypotheses are the way forward. “It could be very interesting to investigate the effects of the particular mutations observed in the polar bear *APOB* gene in a mouse model,” concludes Nielsen.

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ORIGINAL RESEARCH PAPER Liu, S. et al.
Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. *Cell* 157, 785–794 (2014)



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