

Ancient bears provide insights into Pleistocene ice age refugia in Southeast Alaska

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Abstract

During the Late Pleistocene, major parts of North America were periodically covered by ice sheets. However, there are still open questions about whether ice-free refugia were present in the Alexander Archipelago along the Southeast (SE) Alaska coast during the Last Glacial Maximum (LGM). Numerous subfossils have been recovered from caves in SE Alaska, including American black (*Ursus americanus*) and brown (*U. arctos*) bears, which today are found in the Alexander Archipelago but are genetically distinct from mainland bear populations. Hence, these bear species offer an ideal system to investigate long-term occupation, potential refugial survival, and lineage turnover. Here we present genetic analyses based on 99 new complete mitochondrial genomes from ancient and modern brown and black bears spanning the last ~45,000 years. Black bears form two SE Alaskan subclades that diverged >100,000 years ago, one preglacial and one postglacial. All postglacial ancient brown bears are closely related to modern bears in the archipelago, while a single preglacial brown bear is found in a distantly related clade. A hiatus in the bear subfossil record around the LGM and the deep split of their pre- and post-glacial subclades fail to support a hypothesis of continuous occupancy in SE Alaska throughout the LGM for either species. Our results are consistent with an absence of refugia along the SE Alaska coast, but indicate that vegetation quickly expanded after deglaciation, allowing bears to recolonize the area after a short-lived LGM peak.

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