

Pleistocene Brown Bears in the Mid-Continent of North America

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Current biogeographic models hypothesize that brown bears (*Ursus arctos*) migrated from Asia to North America via east Beringia (unglaciated Alaska and Yukon) ~100 to 50 thousand radiocarbon years ago (ka) but did not reach areas south of Beringia until the opening of a mid-continental ice-free corridor (IFC) ~13 to 12 ka (1, 2). This model has been problematic because migration to the mid-continent was blocked by glacial ice only during the relatively short period ~23 to 12 ka, meaning the mid-continent was largely ice-free before the Last Glacial Maximum (LGM), ~24 to 18 ka (3–5).

Thirty-one brown bear fossils have been radiocarbon-dated in east Beringia (2). Three have infinite ages (>53 ka), the rest are <48 ka, and there is a hiatus in their record from ~35 to 21 ka, suggesting brown bears were absent during that interval (2). Ancient mitochondrial DNA studies have shown that three clades of brown bears inhabited east Beringia before 35 ka: clades 2c, 3c, and 4 (2) (Fig. 1). Populations that recolonized east Beringia after 21 ka all belonged to subclades that were not present before 35 ka (2). Clade 4 never reappeared in east Beringia. After 10 ka, the modern phylogeographic structure of North American brown bears became established: clade 3a in western and central Alaska, clade 3b in extreme eastern Alaska and northwestern Canada, and clade 4 in southern Canada and the contiguous United States (6). It has been difficult to explain the descendency of bears in the mid-continent if clade 4 has been absent from North America since 35 ka.

Here, we report a well-preserved cranial fragment from a brown bear (Provincial

Museum of Alberta no. P98.5.374) collected in fluvial gravels near Edmonton, Alberta (Fig. 1, fig. S1, and table S1). Two accelerator radiocarbon dates on collagen returned ages of $25,210 \pm 560$ years (AA48743) and $27,410 \pm 200$ years (OxA-12902). This find indicates that brown bears reached areas south of Beringia well before the postglacial period and before the coalescence of the Laurentide and Cordilleran glaciers.

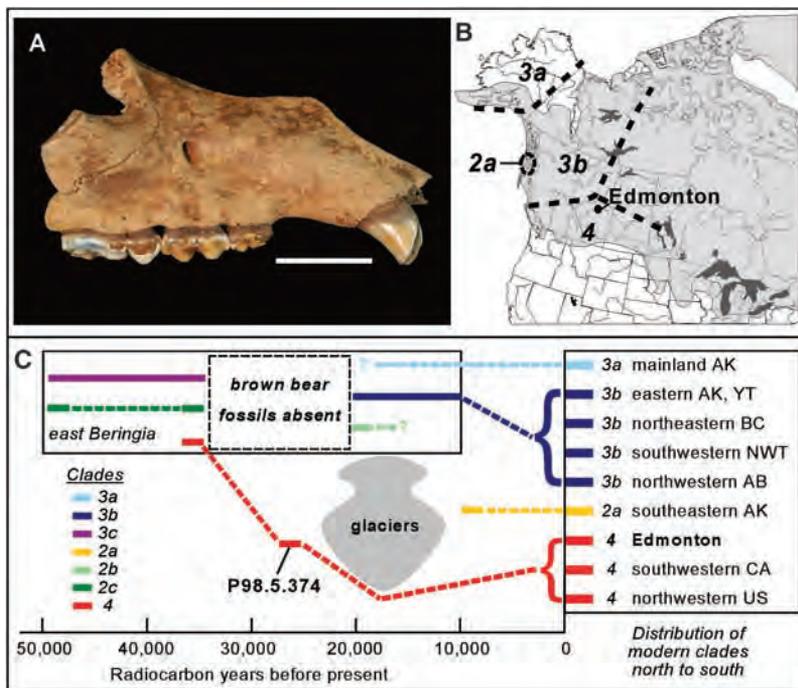


Fig. 1. (A) Brown bear cranial fragment P98.5.374 recovered near Edmonton, Alberta. Scale bar, 3 cm. (B) The maximum extent of glacialiation (gray shading) in northwestern North America during the LGM (4) and the present distribution of brown bear clades (6). (C) Brown bear clades in North America over the past 50,000 years (2, 6). Dashed lines indicate that presence is presumed even though fossils are lacking. The box in the upper left represents populations in Pleistocene east Beringia. AK, Alaska; YT, Yukon Territory; BC, British Columbia; NWT, Northwest Territories; AB, Alberta; CA, Canada; US, United States.

We extracted mitochondrial DNA from ~0.5 g of the root of the specimen's second molar, using established ancient-DNA techniques (2, 7). Two nonoverlapping but highly variable fragments (60 and 135 base pairs) of the control region were amplified, and the sequences obtained show that P98.5.374 belongs to clade 4 (GenBank accession nos. AY796010 and AY796011).

These results challenge the hypothesis that southern brown bears are descended from Beringian populations dispersing through the IFC ~13 to 12 ka, because those dispersers would have belonged to clade 2 or 3. With clade 4 bears inhabiting central Alberta ~26 ka, a more parsimonious model is that clade 4 bears penetrated into southern regions well before the LGM, that they became isolated south of the ice during the LGM, and that modern bears there are descended from in situ populations.

By implication, northern and southern female brown bears in North America have been genetically isolated from each other for at least 35,000 years. Furthermore, the first appearance of brown bears south of the LGM ice margin should not be used to date the earliest availability of a late glacial IFC for human expansion in the New World.

References and Notes

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7. Materials and methods are available on Science Online.
8. Primary DNA sequencing was performed at the Henry Wellcome Ancient Biomolecules Centre, and replication at the Max Planck Institute for Evolutionary Anthropology. Partly supported by the Bureau of Land Management, U.S. Department of the Interior.

Supporting Online Material
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 Materials and Methods
 Fig. S1
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