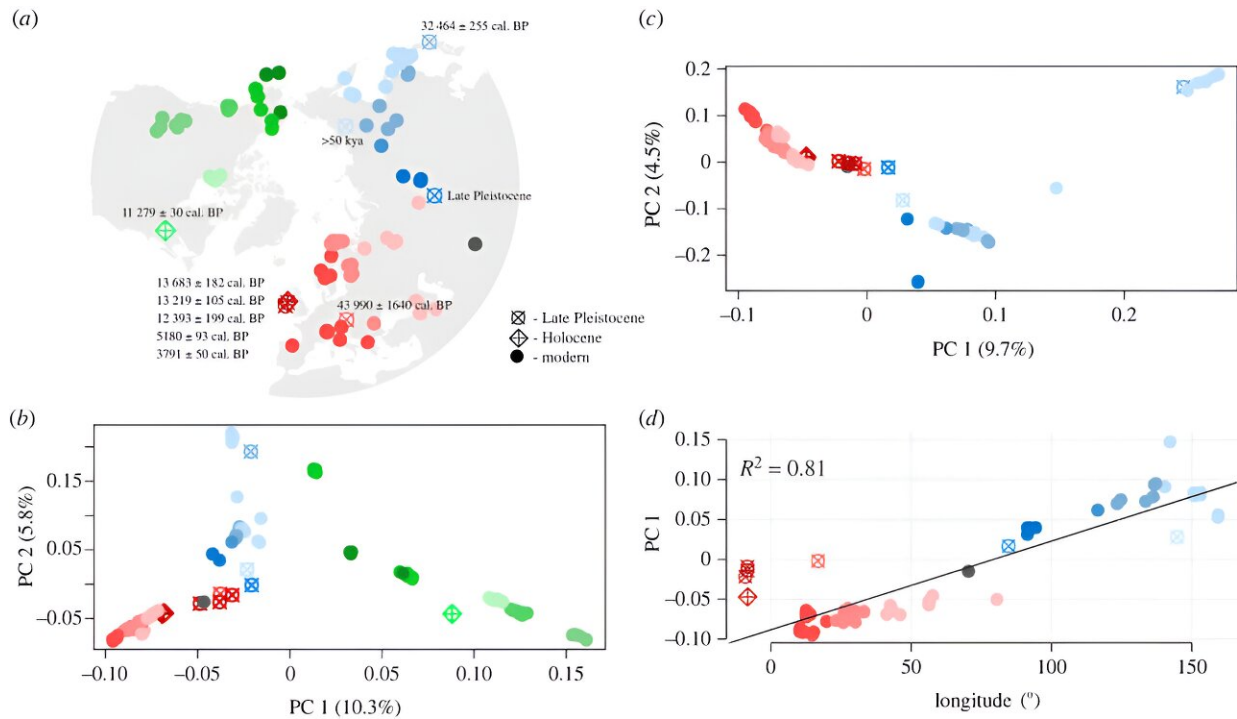


Ancient brown bear genomes shed light on Ice Age losses and survival

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Brown bear sample localities and population structure. (a) Map showing the localities of the ancient and contemporary brown bear genomes analyzed. Calibrated radiocarbon ages of the ancient samples are listed next to their locality. "Late Pleistocene" next to Denisova_LP indicates a direct age is unknown, but it is listed as Late Pleistocene in the original publication [26]. CGG_1_020006 was dated to beyond the limit of radiocarbon dating (greater than 50 kya) but molecularly dated to 61 826 years BP [HPD 95%: 27 866–96 783 years BP] [22]. (b) PCA generated from genotype likelihoods of all samples. (c) PCA generated from genotype likelihoods of the Eurasian samples only. Percentage values in parentheses on the X and Y axes show the percentage of

variation explained by the principal component. (d) PC1 versus degrees longitude for the Eurasian individuals, excluding the Japanese individuals. Colors and symbols represent geography and age, respectively. Dark gray circle shows the single Himalayan individual. The color of CentralRussia1 was changed to light red due to its geographical position in the Ural mountains and European-like clustering in the PCA. Credit: *Proceedings of the Royal Society B: Biological Sciences* (2024). DOI: 10.1098/rspb.2023.2411

The brown bear is one of the largest living terrestrial carnivores, and is widely distributed across the Northern Hemisphere. Unlike many other large carnivores that went extinct at the end of the last Ice Age (cave bear, sabretoothed cats, cave hyena), the brown bear is one of the lucky survivors that made it through to the present. The question has puzzled biologists for close to a century: How was this so?

Brown bears are ecologically flexible and have a broad dietary range. While they are carnivores, their diets can also consist primarily of [plant matter](#) making them adaptable to environmental changes. However, brown bears also experienced extensive range reductions and regional extinctions during the last Ice Age. Brown bears used to occupy a much wider range including Ireland; Honshu, the largest island of Japan; and Quebec (Canada).

Did the decline or disappearance of bear populations in certain areas happen because bears left those places for better ones that they still currently live, or did unique groups of bears with distinct genes inhabit those areas and go extinct, leading to a loss in the overall diversity of the species?

By studying the genomes of ancient brown bears dated to between 3,800 and 60,000 years old, including several individuals from outside their [current range](#), researchers from the University of Copenhagen, Denmark

and the University of Yamanashi, Japan sought to address this question by investigating the [evolutionary relationships](#) between brown bears across space and time.

Their research is [published](#) in the journal *Proceedings of the Royal Society B: Biological Sciences*.

Their study showed that brown bears did not simply move with the shifting environment, but populations went extinct. "Our analyses showed that ancient brown bears represent genetic diversity absent in today's populations" says Takahiro Segawa, lead author of the study. "While brown bears survived global extinction, they suffered considerable losses of their historical range and [genetic diversity](#)."

This new perspective highlights a crucial period in the [brown bears'](#) history, and that they also faced challenges during and after the last Ice Age.

"As we continue to grapple with the challenges of coexistence between humans and wildlife, insights from the deep past are invaluable in shaping a sustainable future." adds Michael Westbury, the senior author of the study. "Although studying recent specimens can provide some insights, by including samples from the past and from areas a species no longer exists, we can better quantify how patterns of current diversity arose, and inform predictions about how they may respond to future environmental change."

More information: Takahiro Segawa et al, The origins and diversification of Holarctic brown bear populations inferred from genomes of past and present populations, *Proceedings of the Royal Society B: Biological Sciences* (2024). [DOI: 10.1098/rspb.2023.2411](https://doi.org/10.1098/rspb.2023.2411)

Provided by University of Copenhagen

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