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Simulating Pleistocene climate effect on archaic human interbreeding

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Genomic data document multiple episodes of interbreeding among Neanderthals, Denisovans and *Homo sapiens*. When, where and how often the interbreeding between these hominin populations took place remains unclear. Here, we study the Neanderthal-Denisovan admixture during the past 400 thousand years using a novel habitat model that integrates extensive fossil, archeological, and genetic data with unprecedented transient Coupled General Circulation Model simulations of global climate and vegetation. Our Pleistocene hindcast of habitat suitability reveals pronounced climate-driven zonal shifts in the main overlap region of Denisovans and Neanderthals in central Eurasia. These shifts, which influenced timing and intensity of potential interbreeding events, can be attributed to the response of climate and vegetation to past variations in atmospheric CO₂ and northern hemisphere ice-sheet volume. Therefore glacial/interglacial climate swings likely played an important role in archaic human gene flow and genetic diversification.