ABSTRACT: The evolutionary genetic relationship between polar bears (Ursus maritimus) and brown bears (U. arctos) is a subject of continuing controversy. To address this we generated genome-wide sequence data for seven polar bears, two brown bears, including one from the enigmatic ABC Islands population, and a black bear (U. americanus).

These data reveal remarkable genetic homogeneity within polar bears and clear evidence of past hybridization with brown bears. Hybridization, however, appears to be limited to habitat islands, where isolated polar bears are gradually converted into brown bears via male-mediated dispersal and sex-biased gene flow. Our simplified and comprehensive model for the origin and evolution of polar bears resolves conflicting interpretations of mitochondrial and nuclear genetic data, and highlights the potential effect of natural climate change on long-term evolutionary processes.

BIOGRAPHY: Ed Green was born and raised in Atlanta, Georgia, USA. He graduated from the University of Georgia (BS 1997 – Genetics) and then was a Peace Corps volunteer in Eritrea. In graduate school, he worked with Steven Brenner at UC Berkeley on alternative splicing and sequence alignment algorithms. As an NSF post-doc with Svante Paabo in Leipzig, Germany he led the analysis consortium that described the genome of the Neandertal, human's closest extinct relative. He is now an Assistant Professor in the Department of Biomolecular Engineering at the UC Santa Cruz. He is a Searle Scholar, A Sloan Fellow, and the recipient of the Newcomb Cleveland Prize.