

Highlights

- We generated the first mitochondrial genomes of the extinct flat-headed peccary.
- Molecular phylogeny reveals flat-headed peccary is sister-taxon to living peccaries.
- Divergence date estimates help to clarify peccary biogeographic evolution.
- No genetic signature of population decline prior to flat-headed peccary extinction.

Introduction

- Peccaries are even-toed ungulates belonging to the family Tayassuidae.
- There are three extant species: collared peccary, white-lipped peccary and Chacoan peccary [1][2].
- Currently these species are distributed through Central and South America, with the collared peccary extending into southern United States (Figure 1).
- However, peccaries were once widespread across all of North America [3].
- Phylogenetic relationships and biogeographic histories of extant peccary species still unclear.
- The extinct North American flat-headed peccary (*Platygonus compressus*) is a good candidate for inclusion in a molecular phylogenetic study due to its recent extinction in the late Pleistocene (~11 thousand years ago).
- Subfossils should be amenable to extract ancient DNA (aDNA) [4]
- Flat-headed peccary is hypothesised to be closely related or synonymous to the Chacoan peccary due to morphological similarities [5][6].
- Abundant flat-headed peccary subfossil remains have been recovered from Sheriden Cave [7], an exceptional archaeological and palaeontological site with dated stratigraphy in North-Western Wyandot County, Ohio (Figure 1).



Figure 1: Geographic distribution of the extinct flat-headed peccary and the three extant peccary species in the Americas. Grey dots indicate Pleistocene fossil localities yielding remains of the extinct flat-headed peccary; Sheriden Cave, Ohio is marked with a grey cross. Flat-headed peccary depiction shown in the same grey. Current distributions of collared peccary (blue), white-lipped peccary (orange) and Chacoan peccary (yellow) are reproduced from the IUCN red list database [8].

Aims

- Confidently resolve the phylogeny of peccaries, including the extinct flat-headed peccary, by sequencing complete mitochondrial genomes for each species.
- Use molecular dating analyses to explore whether diversification of modern peccaries occurred in North or South America.
- Perform a preliminary survey of flat-headed peccary genetic diversity at Sheriden Cave to assess whether diversity and aDNA preservation are adequate for the flat-headed peccary to serve as a future model species for studying late Pleistocene megafaunal extinctions.

References

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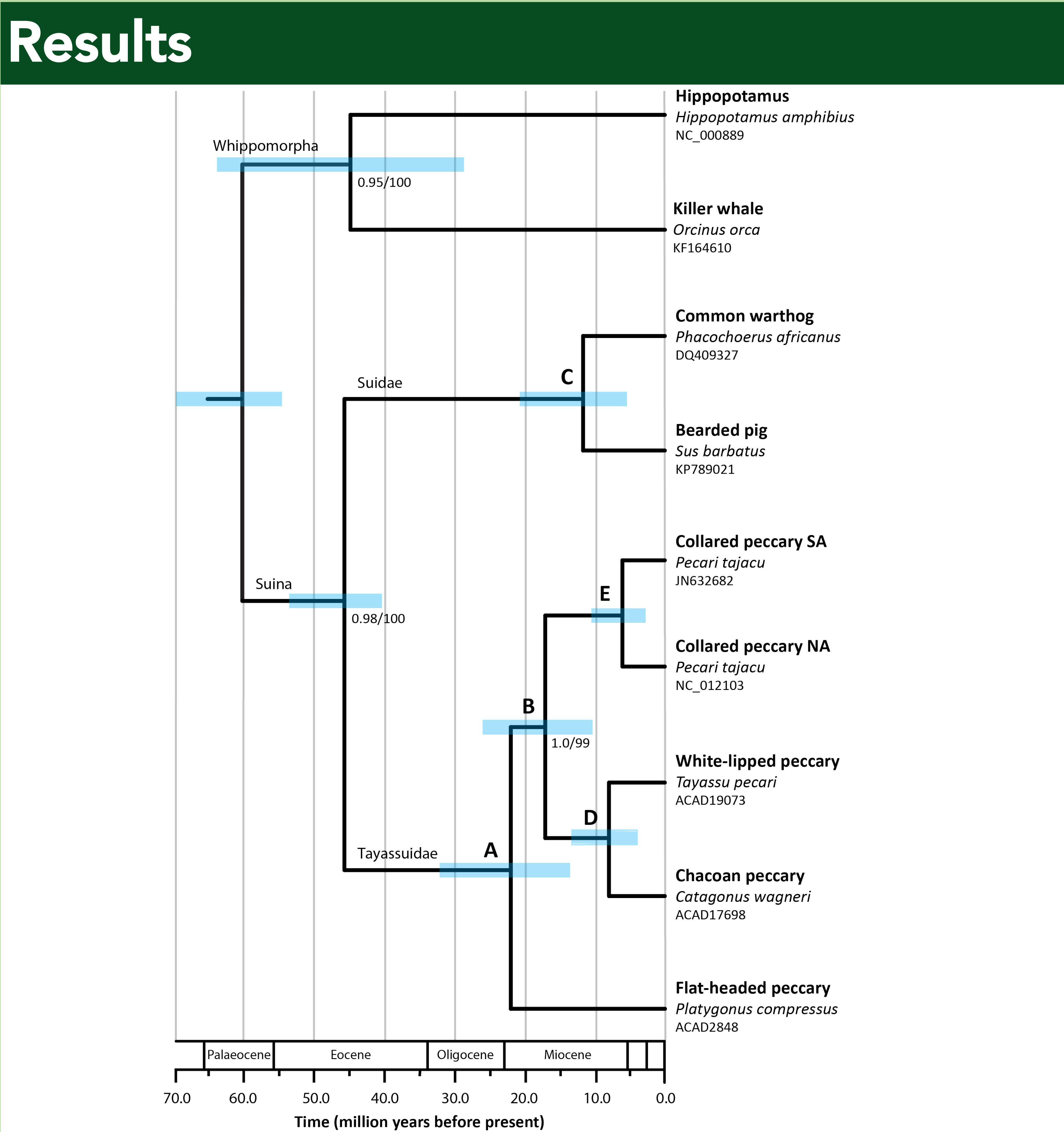


Figure 2: BEAST maximum clade credibility tree. Mean node ages are given and node bars represent the 95% Highest Posterior Density (HPD). Support values (Bayesian Posterior Probability/Maximum Likelihood Bootstrap) are provided for nodes that did not receive maximum support (1.0/100). NA = North America; SA = South America.

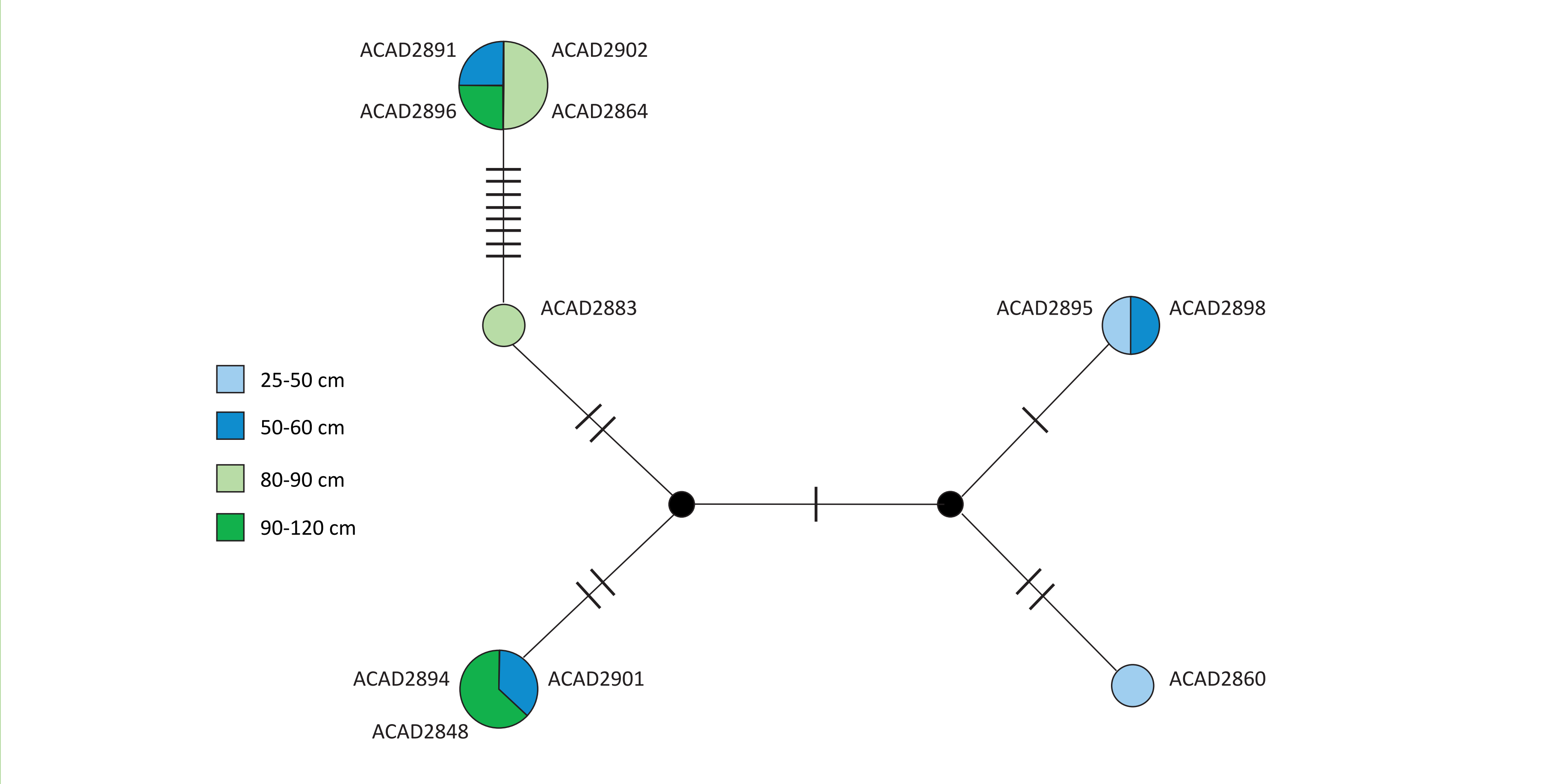


Figure 3: Haplotype network of flat-headed peccary samples. Haplotypes are labelled with their corresponding identification number. Sizes of spheres represent number of individuals per haplotype. Colour represents stratigraphic depth of sample; age of fossil increases with depth. Perpendicular lines represent the number of nucleotide changes along each branch.

Conclusions – Phylogeny & Biogeography

- Divergence between the extinct flat-headed peccary and the extant South American species occurred in the early Miocene, around 22 million years ago (mya; Figure 2).
- Our phylogeny refutes previous suggestions that the flat-headed and Chacoan peccaries are closely related or synonymous [5][6].
- Our age estimates suggest that for a South American diversification of living peccaries, their most recent common ancestor (MRCA) must have reached South America more than 10 mya – well before the complete joining of the American continents [9].
- If the MRCA of living peccaries did not itself migrate to South America, then our divergence date estimates likely reflect an initial North American diversification followed by independent migrations to South America.

Conclusions – Population Analysis

- For the Sheriden Cave flat-headed peccary population we anticipated seeing a population with low diversity, possibly reflecting a small population size as they neared extinction.
- Instead, the haplotype network (Figure 3) showed no apparent decline through time; the negative value for Fu’s FS (-5.92; p-value = 0.002) suggests population expansion.
- Lack of a signal of population decline in the flat-headed peccaries may reflect favourable local environmental conditions prior to their extinction.
- The flat-headed peccary shows promise as a model species for future investigation into Pleistocene megafaunal extinctions due to sufficient aDNA preservation, abundant fossils, widespread distribution (Figure 1) and apparent genetic diversity.