



No evidence against Polynesian dispersal of chickens to pre-Columbian South America

Thomson et al. (1) claim that previous results using ancient DNA to track prehistoric chicken dispersals across the Pacific (2) “have been impacted by contamination with modern chicken DNA and, that as a result, there is no evidence for Polynesian dispersal of chickens to pre-Columbian South America.” We challenge this statement and argue that their research design and interpretations are flawed.

In the original and subsequent papers, we have shown that mitochondrial DNA haplotype E, identified in ancient chicken remains from the Pacific and Chile, was the first haplotype introduced into the Pacific, around 2000 B.C. (2, 3). Later introductions resulted in the distribution of haplotype D, found at high frequency throughout Central/East Polynesia. Of the 15 E haplotypes identified in ancient Pacific chickens, 12 come from sites predating A.D. 1000, where no D haplotypes have been found. All analyses and simulations reported to produce contrary results (1) relate to modern chickens or bones obtained from Central/East Polynesia, which was not settled until after A.D. 1000. Unlike those processed by Storey et al. (2, 3), none of Thomson et al.’s (1) samples were directly dated. We would expect that their samples would result in a high frequency of D haplotypes, given their age and archaeological context. This expectation in no way refutes the sequencing or dating results of the pre-Columbian Chilean chickens.

Thomson et al. (1) argue that the ancient E sequences obtained are the result of a “well-

known problem” of contamination of laboratory reagents. The cited paper (4) actually states: “Of the 779 no-template PCR control reactions done ..., 763 did not yield any product. All contaminant PCR products were sequenced and identified. ... The most common contaminant identified was cow (14/16...), followed by pig and chicken (each 1/16...)” Thus, 1 in 779 reactions was contaminated by chicken DNA. It is unlikely that such contamination could be the source of all E haplotypes observed in ancient chickens. “E”s were never found in our extraction blanks and several critical E sequences from Chile and Vanuatu (2, 3) were reproduced in an independent laboratory using different methods and reagents. There is no compelling evidence to discard a priori these or other ancient E sequences.

Thomson et al. (1) identify multiple haplotypes (D, E, and A) in their results for individual bones, yet none of their reported contamination was identified through sequencing negative controls. Instead, the authors claim that once samples were processed with Shrimp DNase, which supposedly removes contamination in reagents, only D sequences were obtained. Interestingly, in a subsequent paper in PNAS by several of the coauthors (5), these authors accept the ubiquitous presence of E sequences in ancient European chickens (including sequences we published) and did not use Shrimp DNase in their protocols. Apparently,

protocols and interpretations they rejected in the Pacific are acceptable for Europe? The authors also point out “that lineage replacement (often rapid and geographically widespread) was common” (5). Thus, it may be expected that D sequences would rapidly replace E, particularly in East Polynesia. Thomson et al. (1) provide no data to justifiably reject the evidence for Polynesian dispersal of chickens to pre-Columbian South America.

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1 Thomson VA, et al. (2014) Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across the Pacific. *Proc Natl Acad Sci USA* 111(13):4826–4831.

2 Storey AA, et al. (2007) Radiocarbon and DNA evidence for a pre-Columbian introduction of Polynesian chickens to Chile. *Proc Natl Acad Sci USA* 104(25):10335–10339.

3 Storey AA, et al. (2010) Mitochondrial DNA from 3000-year old chickens at the Teouma site, Vanuatu. *J Archaeol Sci* 37(10):2459–2468.

4 Leonard JA, et al. (2007) Animal DNA in PCR reagents plagues ancient DNA research. *J Archaeol Sci* 34(9):1361–1366.

5 Girdland Flink L, et al. (2014) Establishing the validity of domestication genes using DNA from ancient chickens. *Proc Natl Acad Sci USA* 111(17):6184–6189.

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