

Re: First Americans Arrived Recently, Settled Pacific Coast, DNA Study Says

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In sci.archaeology message [news:equil0\\$edv\\$1@xxxxxxxxxx](mailto:news:equil0edv1@xxxxxxxxxx) by "Uwe Müller" <uwemueller@xxxxxxxxxx> . . . :

"Jack Linthicum" <jacklinthicum@xxxxxxxxxxxx> schrieb im Newsbeitrag news:1171209545.500210.272980@xx

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By measuring the rate of mutation, Kemp found that so-called molecular evolution—the process by which genetic material changes over time—had taken place two to four times faster than researchers believed mtDNA could evolve.

That, Kemp said, suggests people entered the Americas within the last 15,000 years, because the DNA has evolved too fast for the arrival to have occurred any earlier.

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The first paragraph boils down to something like: all dates arrived at via genetic dating could be divided by 2 or even 4. That would have enormous consequences for the population/repopulation—after—the—ice—age—scenarios in Europe.

The second paragraph seems to imply some doubts about the dating. If the dating is correct, an age of 10300 for the sample, no method of dating given, than the mutation rate should have to be roughly trebled. If the mutation rate is trebled, the amount of genetic change apparent in modern descendants would argue against an earlier arrival than ca.

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15000.

If the dating of the tooth was not correct, the mutation rate may remain unchanged, or could be changed according to personal preferences. There would be no argument against earlier arrivals.

So everything rests on one tooth, and how it was dated. Does anyone know how it was done? A carbon 14 dating could be easily off because of the influence of marine carbon, as they were said to exploit coastal resources. Was it dated by the date of the layer of extraction?

Their conclusions are not warranted, the 96% confidence interval for the persistence of a founding haplotype is $0.04 = 1/2^N$ where $N =$ number of half-lives. $2^N = 25 N \sim 4.5$ half-lives. If the estimated rate of evolution is 1 event per locus of 9 to 28 ky then the rejectable timings would be

40 ky + 10,000 years. Therefore the conclusion of the abstract is not

scientifically secure and a bad use of statistics. Even if they were using genomic DNA which has 5 times the number of relevant mutations their rejection criteria would be in excess of 15,000 years or more.