

# Statistical flaws undermine pre-Columbian chicken debate

Thomson et al. (1) recently used analyses of modern and ancient chicken DNA in an attempt to overturn evidence of Polynesian dispersal of chickens to pre-Columbian South America. There are, however, significant methodological and statistical problems in the analyses carried out by Thomson et al., problems that seriously undermine their conclusions.

Thomson et al. (1) conduct an approximate Bayesian computation comparison of different models for the ancestral migration patterns of chickens. Their analysis is based on an approximate migration matrix (tables S4 and S5 in ref. 1) that is specified without justification. In these tables, the “backward” rates for South America are 0 for all regions except Europe. That means that any migration to South America will be from Europe with a probability of 1.

It could be that the migration matrices used in the analysis have just been misreported, or that rows and columns were switched by mistake. Whichever the case, the outcome of any model comparison will be significantly determined by the choice of migration matrix. Thomson et al. (1) give no evidence that the data (rather than the

a priori migration matrix) provides support for or against the pre-Columbian chicken hypothesis.

A second set of issues relate to the conflict reported by Thomson et al. (1) between proportions of D and E haplotypes reported in early work and their failure to observe an E haplotype [Thomson et al. observed 0 E haplotypes from 22 ancient samples, whereas Storey et al. (2) observed 15 E haplotypes from 31 samples]. Thomson et al. (1) make two mistakes when arguing that these observed proportions are significantly different. The first mistake is to compute *P* values by fixing one proportion and testing the other sample. This approach underestimates variability because both proportions will have sampling error. The authors should instead conduct a two-sample test, which reduces the level of significance by many orders-of-magnitude.

The second mistake is to treat each individual as an independent sample, making an implicit assumption that individuals from the same island have independent haplotypes. Note that the 31 samples tested by Thomson et al. (1) come from two sites in Niue, one site in Hawai’i, and 12 from a single

site in Rapa Nui. One would expect very strong correlation between samples at the same site, and this necessarily increases estimates of variability in the observed proportions, to the point that the observed proportions are highly unlikely to be statistically significant.

In summary, the statistical evidence used by Thomson et al. (1) to argue their case is lacking and should be either revised or rejected.

**David Bryant<sup>1</sup>**

Allan Wilson Centre, Department of Mathematics and Statistics, University of Otago, Dunedin, Otago 9054, New Zealand

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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. (2012) Investigating the global dispersal of chickens in prehistory using ancient mitochondrial DNA signatures. *PLoS ONE* 7(7):e39171.

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<sup>1</sup>Email: david.bryant@otago.ac.nz.