

The Tutu Archaeological Village Site: A Multidisciplinary Case Study In Human Adaptation

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Quantitative paleodietary reconstruction with complex foodwebs: An isotopic case study from the Caribbean

William J. Pestle^{a,*}, Jason Laffoon^{b,c}

^a Department of Anthropology, Merrick Hall 1022, University of Miami, Coral Gables, FL 33124-2005, United States
^b Faculty of Archaeology, Leiden University, Eersteeweg 2, 2333CC Leiden, The Netherlands
^c Faculty of Earth and Life Sciences, Vrije Universiteit, De Boelelaan 1085, 1081HV Amsterdam, The Netherlands

ABSTRACT

Stable isotope analysis has a long history in Caribbean archaeology. The Caribbean region, however, possesses a highly complex isotopic ecology, including both a large number of isotopically variable food sources, and a high degree of isotopic overlap between different food groups. As such, to date, most regional paleodietary studies have been limited to descriptive and qualitative conclusions concerning the relative contributions of different food sources. In this study we apply an iterative Bayesian multi-source mixing model (FRUITS) to skeletal stable isotope data from the prehistoric population of Tutu, St. Thomas, USVI, to test the feasibility of such models to generate quantitative and probabilistic individual paleodietary reconstructions. The isotope data set includes both bone collagen ($\delta^{13}\text{C}_{\text{coll}}$ and $\delta^{15}\text{N}_{\text{coll}}$) and apatite ($\delta^{13}\text{C}_{\text{apat}}$) data. The results of two different dietary models using four and five distinct food groupings, respectively, are compared and assessed relative to other relevant archaeological evidence pertaining to past diet at the site. We highlight the potentials and limitations of multi-source mixing models for regional paleodietary studies, and their relevance to ongoing debates within Caribbean archaeology concerning the relative importance of different food sources such as manioc, maize, and seafood.

1. Introduction

Recent years have seen a notable increase in the use of mixture models, many of which employ Bayesian principles, in isotopic studies of paleodiet (Fernandes et al., 2014, 2015; Lubetkin and Simenstad, 2004; Moore and Semmens, 2008; Newsome et al., 2004; Parnell et al., 2010, 2012; Phillips, 2001; Phillips and Gregg, 2001; Stock and Semmens, 2013). Many of these applications have been made in continental settings (e.g. Fernandes et al., 2015; Pestle et al., 2016a, 2016b), however, which tend to possess comparatively simple foodwebs featuring little overlap in the isotopic signatures of source groups. In comparison, few examples of the use of such models are to be found in Caribbean paleodietary literature (the only exceptions being Pestle, 2016a and Clinique et al., 2015). In large part, the paucity of Caribbean applications can be attributed to the incredible complexity of the region's foodweb (Pestle, 2010b, 2013). Not only do the floral and faunal foodwebs of the region comprise hundreds and hundreds of edible taxa but the isotopic signatures of different food groups (established based on taxon, ecological niche, supposed trophic position) are non-overlapping. This stands in stark opposition to many of the continental regions in which stable isotope analysis was first developed and

applied. The huge number of potential sources and the lack of discrete, non-overlapping clusters of ecologically similar organisms tend to produce overly broad and non-definitive solutions in multi-source mixture models.

The lack of such studies is unfortunate, as these Bayesian tools can provide quantitative and probabilistic solutions to individual diet and, "offer a powerful means to interpret data because they can incorporate prior information, integrate across sources of uncertainty and explicitly compare the strength of support for competing models or parameter values" (Moore and Semmens, 2008: 471). The capability to compare models/competing hypotheses could be of particular utility in the Caribbean, where some long-held assumptions about diet (e.g. the primacy of manioc/cassava) are/have been challenged (e.g. McKeiburn and Pagan-Jiménez, 2012; Pagan-Jiménez, 2013). Moreover, these approaches are inherently stronger in that they are model-bound, and allow testing of possible alternatives fitting the observed data following Bayesian principles, instead of traditional approaches that fit possible explanations of diet only after patterns in the data are defined (See Pestle et al., 2016b). Finally, these models have significant interpretive value in that they move discussions beyond isotopes or macronutrients to actual assessment of food intake, a metric that would

* Corresponding author.

E-mail address: w.pestle@miami.edu (W.J. Pestle).

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