**Supplemental Text 1**

Methods and Instrumentation

*Elemental analysis-isotope ratio mass spectrometry (EA-IRMS)*

Elemental analysis-isotope ratio mass spectrometry was carried out at the CUNY Advanced Science Research Center (directed by Brian Giebel). No pre-treatment of the samples was undertaken prior to analysis (for a discussion, see Craig et al. 2007; Morton and Schwartz 2004). Each sample was weighed in duplicate (c.700μg) into tin capsules, which were analyzed using a Flash 2000 Organic Elemental Analyzer linked to a Delta V Plus isotope ratio mass spectrometer (both from Thermo Scientific). Vienna Pee Dee Belemnite (VPDB) and atmospheric nitrogen (AIR) were used as international standards for δ13C and δ15N measurements, respectively. Carbon and nitrogen isotopes were analyzed in the same analytical run. Samples yielding less than 1% nitrogen were discarded and instrument precision on repeated measurements was always better than 1‰ (and most of the time better than 0.5‰) for both elements, as determined by duplicate measurements.

*Gas Chromatography - Mass Spectrometry (GC-MS)*

Gas Chromatography - Mass Spectrometry analysis was carried out at CUNY Queens College by the senior author. For lipid analysis by gas chromatography-mass spectrometry, charred deposits (50-200 mg scraped from the potsherd interior surface) and ceramic samples (ca. 1–2 g drilled from the interior wall) were weighed and lipids were extracted and methylated according to established protocol by direct acid-catalyzed transesterification to maximize recovery (Craig et al. 2013). Methanol (1 mL) was added and homogenized with the charred deposit, the mixture was ultrasonicated for 15 min and then acidified with concentrated sulphuric acid (200μL). The acidified suspension was heated in sealed tubes for 4 h at 70 °C and then cooled, and lipids were extracted with n-hexane (3×2mL) and dried down under a gentle N2 flow. The extracts were transferred to autosampler vials and 10μg of internal standard (hexatriacontane) was added. To identify dihydroxy fatty acids, acid extracts were treated with BSTFA to obtain their TMS ethers following a protocol described in Lucquin et al. (2016a). Lipids extracted from ceramic matrices and charred deposits were analyzed by GCMS, a technique that allows the separation of complex mixtures and the identification of plant- and animal-derived lipids (e.g., sterols, n-alkanoic acids). GCMS analysis was performed using an Agilent 7890A Series gas chromatograph connected to an Agilent 5975 C Inert XL mass-selective detector with a quadrupole mass analyzer (Agilent Technologies, Cheadle, Cheshire, UK). The splitless injector and interface were maintained at 300 °C and 280 °C respectively. Helium was the carrier gas at constant inlet pressure, and the GC column was inserted directly into the ion source of the mass spectrometer. The ionization energy was70 eV and spectra were obtained by scanning between m/z 50 and 800. All samples were analyzed using a DB5-ms (5%-phenyl)-methyl polysiloxane column (30 m × 0.32 mm × 0.25μm; J&W Scientific, Folsom, CA, USA). The temperature program was 2 min at 50 °C, 10 °C min−1 to 325 °C and 15 min at 325 °C. In addition to the above general scanning, a SIM method was performed to identify specific biomarkers. The column used was DB23 (50%-Cyanopropyl)-methylpolysiloxane column (60m, 250μm & 0.25μm; J & Scientific, Folsom, CA, USA). The temperature program was 2 minutes at 50°C, 10°C/min to 100°C, 4 °C/min to 140 °C, 0.5°C/min to 160°C and 20°C /min to 250°C for 10 minutes. Helium was also used as the carrier gas at a rate flow of 1.5mL/min. Four groups of ions were selected: m/z 74, 87, 213, 270 to identify 4,8,12- trimethyltridecanoic acid ; m/z 74, 88, 101, 312 for pristanic; m/z 74, 101, 171, 326 for phytanic and m/z 74, 105, 262, 290, 318, 346 for ω-(o-alkylphenyl) alkanoic acids corresponding to the carbon length C16 to C22, respectively. This method was also conducted to confirm the source of lipids by calculating the relative contribution of AAPA-C18 isomers (Bondetti et al. 2021) and phytanic’s SRR diastereomer (Lucquin et al. 2016b).

*GC-combustion-Isotope Ratio MS (GC-c-IRMS)*

To better characterize the lipids extracted from the Dawson site pottery sherds, GC-C-IRMS analysis was conducted in order to ascertain the 13C/12C ratio in the two most abundant fatty acids, i.e., octadecanoic (C18:0) and hexadecanoic (C16:0). These analyses were carried out at the BioArCh labs, University of York (directed by Oliver E. Craig). Samples were analyzed using an Agilent 78,908 GC (Agilent Technologies. Santa Clara. CA. USA) instrument coupled to an Agilent 5975C MSD and an Isoprime 100 IRMS (Isoprime, Cheadle, UK) with an Isoprime GC5 interface (lsoprime, Cheadle, UK). All samples were diluted with hexane and subsequently 1μL of each sample was injected into a DB-5MS (30 m × 0.25 mm × 0.25μm) fused-silica column. The temperature was set for 0.5 min at 50 °C, and raised by 10 °C min−1until 300 °C was reached, and held for 10 min. The carrier gas was ultra-high purity grade helium with a flow rate of 3 mL min−1. The gases eluting from the chromatographic column were split into two streams. One of these was directed into an Agilent 5975C inert mass spectrometer detector (MSD), for sample identification and quantification, while the other was directed through the GC5 furnace held at 850 °C to oxidize all carbon species to CO2. A clear resolution and baseline separation of the analyzed peaks was achieved in both systems. Eluted products were ionized in the mass spectrometer by electron impact. Ion intensities of m/z44, 45, and 46 were monitored in order automatically to compute the13C/12C ratio of each peak in the extracts. Computations were made with Ion Vantage and IonOS Softwares (Isoprime, Cheadle, UK) and were based on comparisons with a standard reference gas (CO2) of known isotopic composition that was repeatedly measured. The results from the analysis are reported in parts per mille (‰) relative to an international standard (V-PDB). The accuracy and precision of the instrument was determined on n-alkanoic acid ester standards of known isotopic composition (Indiana standard F8–3). Archaeological and reference samples were measured in replicate, with archaeological samples having a mean S.D. of 0.06‰ for C16:0 and 0.04‰ for C18:0 and reference samples a mean S.D. of 0.17‰ for C16:0 and 0.15‰ for C18:0. Values were also corrected subsequent to analysis to account for the methylation of the carboxyl group that occurs during extraction. Corrections were based on comparisons with a standard mixture of C16:0 and C18:0 fatty acids of known isotopic composition processed in each batch under identical conditions. In addition, reference samples were corrected (-2.2‰) to account for the Suess effect (Friedli et al. 1986).

*Actualistic experiments*

For the actualistic experiments, modern maize from an organic Amish farm in northern Washington County (New York USA) and Lake Trout from Cayuga Lake (NY USA) were mixed in 10% increments as described in Hart et al. 2018. Briefly, all fish were kept frozen until muscle tissue was sampled. Freeze-dried Lake Trout and dried whole maize kernels were ground into 0.5 mm powders. These were mixed in 10% increments in 1g samples (10% and 90% maize to 90% fish and 10% maize by weight). One gram of sterile clay powder was added to each fish-maize sample and mixed in clean labeled Hach tubes. Lipids were extracted from these samples using the acidified methanol protocol and analysed by gas chromatography-mass spectrometry (GC-MS) and GC-combustion-isotope ratio-MS (GC-C-IRMS) as described above.

*Mixing models*

Simple linear mixing models based on compound specific measurements from published sources were compared with the GC-C-IRMS data from Dawson. In addition to these theoretical mixing lines, single compound isotope values were obtained from measuring authentic mixes of modern maize from an organic Amish farm in northern Washington County (New York USA) and freshwater trout/chain pickerel from Cayuga Lake (NY USA) in 10% increments[[1]](#footnote-1) (Hart et al. 2018). Multiple sources modelling was carried out using the 3.0 Beta version of the Bayesian mixing model FRUITS (Fernandes et al. 2014, available at <http://sourceforge.net/projects/fruits/>). δ13C16:0 and δ13C18:0 values were used as proxies and three food groups as potential sources: freshwater aquatic oils, C4 plant oils, ruminant adipose fats, with δ13C16:0 and δ13C18:0 reference ranges and concentrations as defined in Supplemental Table 5). The δ13C values for each food source was obtained from modern authentic reference fats and oils (Supplemental Table 5) while palmitic and stearic acid concentration values were obtained from the USDA Food Composition Databases (<https://ndb.nal.usda.gov/ndb/>). No additional prior information was added to the model. Uncertainties were derived using a covariance matrix and standard errors of the mean δ13C values for each food source, assuming that the vessels were used repeatedly. Uncertainties were derived from the standard error of the mean values. The concentrations and model outputs are expressed as % of total lipid by dry weight.

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1. Pure freshwater and pure maize samples were not tested in the course of the experiments for which these mixes were originally prepared (Hart et al. 2018) and reference samples were discarded before the senior author could proceed to their analysis in the context of the present study. Due to a manipulation error that occurred during lipid extraction of the authentic mixtures, the 50% maize/50% lake trout sample had to be excluded. [↑](#footnote-ref-1)