Supplementary Information for
Earliest Evidence of Primate Captivity and Translocation Supports Gift Diplomacy Between Teotihuacan and the Maya

Nawa Sugiyama¹, Saburo Sugiyama², Clarissa Cagnato³, Christine A.M. France⁴, Atsushi Iriki⁵, Karissa S. Hughes⁶, Robin R. Singleton⁶, Erin Thornton⁷, Courtney A. Hofman⁶

Nawa Sugiyama
Email: nawa.sugiyama@ucr.edu

This PDF file includes:

- Supplementary text
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Other supplementary materials for this manuscript include the following:

- 3D Model S1 to S2
- Supplementary Dataset
Supplementary Text: Materials and Methods

Radiocarbon and Ceramic Dating. A bone (eagle) and carbon sample from Offering D4 were sent to the University of Arizona AMS Laboratory for radiocarbon analysis. The uncalibrated dates were modelled as a single phase in OxCal 4.4 program modeled with the INTCAL 13 calibration curve (1) (Figure S1). Values can be consulted in the manuscript, Table 1.

Ceramics from the fill of Offering D4 (n=177) and from the general fill of the 1.8(L)x1.7(W)x1.1m(H) area where Offering D4 was found (Tunnel 5) (n=842) was analyzed by Guillermo García Roma, project member of Project Plaza of the Columns Complex using general ceramic categories following Rattray (2). Absolute date ranges followed Sugiyama and Sugiyama (3). Results of the ceramic analysis are presented in Table S1.

Zooarchaeological Analysis. We applied standard zooarchaeological methods for species, age, sex, and other surface modification detection (4). Photogrammetry model of the dentition was also taken to study wear patterns (3D Model S1 and S2). Published literature and direct consultation with the primatology collection housed at the Smithsonian Institution’s National Museum of Natural History informed age, sex, and species identification. Morphometric traits of the Mexican spider monkey (Ateles geoffroyi vellerosus) and Yucatan spider monkey (Ateles geoffroyi yucatanensis) were recorded by N. Sugiyama and Y.T. Hsu in 2019. Additional subspecies including A. geoffroyi geoffroyi (Nicaragua and Costa Rica) and A. geoffroyi ornatus (Costa Rica and Panama) were consulted, though their morphometric traits and species distribution range eliminated them as possible contenders for the Mound 25C specimen. Notable cranial features of A. g. vellerosus include the following: a more prognathic shape, less elongated cranial vault, rounded and outward facing external auditory meatus (which faces inferiorly for A. geoffroyi yucatanensis), larger infraorbital foramen, more gracile and sharper orbital ridge (thick and rounded for yucatanensis), thinner zygomatic, thicker nasal bridge, acute and well defined posterior orbital constriction that is v-shaped (more rounded in yucatanensis) (Figure S2). Mandibular characteristics of A. g. verollerosus include the following: a slightly thinner canine, and a straight body (yucatanensis tends to have a ventrally curved body as it narrows towards the symphysis) (Figure S3). Based on these features, we argue the Mound 25C specimen has a closer affinity to A.g. vellerosus, though we were unable to conduct systematic recording to capture within species variability. Thus, we tentatively assign the species as A.g. cf. verollerosus. As spider monkeys are sexually dimorphic, with females characteristically being more gracile and with smaller canines, the Mound 25C specimen is likely to be that of a female though its young age makes this a tentative designation.

A. geoffroyi canines erupt relatively late in the dental sequence. They are among the last four teeth to erupt, beginning with the lower canine, upper canine, and finally the lower and upper M3 (5, 6). Unfortunately, published eruption sequence could not be correlated with known age. Carpenter (7) mentions that the permanent lower first incisor erupts at about one year of age, and all four incisors erupt by 15 months in captive spider monkeys. Henderson (5) reports Ateles sp. have one of the slowest dental eruption sequences among New World primates. Based on this published data, B. Holly Smith (8) estimates canine eruption to be roughly twice as slow as the squirrel monkey (Saimiri sciureus), whose canines erupt roughly between 18 (lower canine) and 20 (upper canine) months (9). Based on her estimate, we suspect Ateles
canines likely erupt between 3 and 3 ½ years of age. It is important to note that the isotope value of tooth enamel reflects the diet/environment of the organism at the time of tooth formation and not tooth eruption, yet the temporal span of canine tooth formation remains undetermined. Nonetheless, we can infer the lower and upper canine isotope values that reflect a transition into captive state were incorporated sometime prior to circa three years of age when the canines were still forming.

It is also unclear when *Ateles* sp. permanent dentition is completed. Other New World monkeys obtain full permanent dentition by 4 ¼ years, as reported among *Lagothrix lagothricha* (4.25), *Cebus apella* (3.25 years), *Alouatta palliata* (3 years), *Saimiri sciureus* (1.71 years), *Aotus trivirgatus* (1.25 years), *Callithrix jacchus* (0.88 years), and *Saguinus fuscicollis* (0.81 years) (8). From this, we can infer the Mound 25C spider monkey was likely at least 4 ½ years of age when it was sacrificed.

All postcranial elements were unfused, indicating the spider monkey was still of subadult or juvenile age. The Mound 25C spider monkey had a closed metopic suture, and the mandibular symphysis was partially fused, which are both early fusing elements. Other cranial sutures remained unfused or only partially fused. Schultz’s (10) suture closure table illustrates *Ateles* sp. coronal, sagittal, and lambdoid sutures tend to remain open or only partly fused until much later age than other New World primate species, though no absolute age was assigned. Spider monkey age categories are infant <2 years, juvenile 2-5 years, subadult 5-8 years (when they become independent from mothers and sexually active), and adult >8 years (11). Based on the complete permanent dentition, and mostly unfused cranial and post-cranial elements, we interpret the Mound 25C specimen was a subadult between 5-8 years old.

It is notable that Schultz (6) reports some adults (3.2%) and older individuals (14.3%) with caries (n=156). No adults and only 7.9% of old individuals had closed alveolus. Greater frequency of caries in captive, rather than wild primate populations, particularly on their first incisor and first molars was recorded (6).

Dental wear patterns were assessed via visual inspection with a microscope and a 3D photogrammetry model created with Agisoft. Figure S4 (red arrow) indicates the upper maxillary 1st premolar is absent and the corresponding alveolus is closed. Microscope photographs document extreme wear of its incisors exposing the underlying dentine (Figure S5). The general poor oral health of the individual can also be verified in the 3D Model S1 and S2. Given the relatively young age of the Teotihuacan spider monkey, its closed alveolus and extensive wear pattern is likely caused by abnormal diet and stress due to its captive status.

**Light Isotopes.** Carbonate and collagen isotopes for the majority of the samples were run at the Smithsonian Museum Conservation Institute Stable Isotope Mass Spectrometry Laboratory by Sugiyama and France. One sample, NS353e, was processed for structural carbonate extraction by Thornton in the Washington State University Department of Anthropology Stable Isotope Prep Lab. Collagen extraction of bone and/or dentine followed protocol published by Longin (12) and modified per France et al (13). Samples were not consolidated prior to isotope testing. Solid fragments were demineralized with 0.6 M hydrochloric acid in 4°C, rotating the solution every 24 h until reactions ceased, and samples were neutralized in ultrapure water. Samples were then submerged in a 0.125 M sodium hydroxide solution over night at room temperature to remove hemic and fulvic acids. Remaining organic materials (once neutralized) were solubilized by soaking in 0.03 M HCl (95°C, 24 h). Purified collagen was extracted through
isolating the soluble phases via freeze-drying, and weighed into tin cups. A Costech 4010 Elemental Analyzer coupled to a Thermo Delta V Advantage mass spectrometer was used for combustion and stable isotope ratio measurements following standard delta notation: \( \delta X = \left( \frac{R_{\text{sample}} - R_{\text{standard}}}{R_{\text{standard}}} \right) \times 1000 \); where \( X \) is the heavy isotope of interest (\( ^{15}N, ^{13}C, ^{18}O \)), \( R \) is the isotope ratio (\( ^{15}N/^{14}N, ^{13}C/^{12}C, ^{18}O/^{16}O \)). \( \delta^{15}N_{\text{collagen}} \) and \( \delta^{15}N_{\text{collagen}} \) values were calibrated against internal acetanilide and urea_UIN3 reference materials, both of which are calibrated to USGS40 and USGS 41 (14). Collagen diagenesis was evaluated by calculating the percent collagen yield (>1%) and C:N ratio (2.8-3.6).

Structural carbonate extraction protocol followed modified methods of Bryant et al. (15). Bone, dentine, and enamel were ground into a fine powder by an agate mortar and pestle and soaked in 2.5% sodium hypochlorite solution (24 h) to remove organics. Neutralized samples were then soaked for four hours in 1 M acetic acid solution buffered with 1 M calcium acetate (pH ~4.5) to remove secondary labile carbonates (16, 17). Samples were neutralized and dried at 60°C and weighed into Exetainer vials, and reacted with concentrated phosphoric acid (SG > 1.92) at 25°C. Samples were run on a Thermo Gas Bench II connected to a Thermo Delta V Advantage mass spectrometer. The \( \delta^{13}C_{\text{carbonate}} \) and \( \delta^{18}O_{\text{carbonate}} \) values were calibrated against NBS-19 and LSVEC carbonate reference materials and have an error of ± 0.2‰ (1σ) based on replicates of reference materials and selected samples. Carbonate diagenesis was tested with FTIR-ATR spectroscopy utilizing values reported in France et al. (18) for C/P (bone 0.05-0.32, dentin 0.05-0.3, enamel 0.08-0.2) and IRSF (bone 2.5-4.3, dentine 3.1-4.3, and enamel 3.1-4.0). Values that failed diagenesis test for collagen and carbonate samples are underlined in Table 2a.

A limited primate isotope baseline was obtained from Schoeninger et al. (19) that examined the canopy effect. Carbon isotope values divided species that inhabit close canopies (capuchin and spider monkeys) versus those that prefer open canopy forests (muriqui or woolly-spider and howler monkeys). Nitrogen showed trophic level effect between frugivorous folivores with >40% legumes (howlers), frugivorous folivores (spider monkey and muriqui or woolly spider), and omnivores (capuchin). Raw modern primate isotope data was modified to account for hair-bone offset for \( \delta^{13}C_{\text{collagen}} \) (+0.86) and \( \delta^{15}N_{\text{collagen}} \) (+1.4) following O’Connell et al. (20). As modern samples are influenced by atmospheric CO2, known as the Suess Effect, a 1.5‰ correction on \( \delta^{13}C_{\text{collagen}} \) was applied to the modern values(21). These offsets are summarized in Table S2.

Modern plant specimens of maize (\( \text{Zea mays} \)) and prickly pear fruit (\( \text{Opuntia} \) sp.) from published reports obtained largely from the marketplace in Oaxaca and Central Mexico provide isotopic baselines of these two potential resources that contributed to the elevated C4/CAM signature of the Mound 25C spider monkey (Table S3). Maize \( \delta^{13}C \) value averaged -11.7±0.7‰ (1σ) while \( \delta^{15}N \) averaged 3.7±2.2‰. Prickly pear fruit \( \delta^{13}C \) mean was -12.7±0.8‰ while \( \delta^{15}N \) mean was 3.6±2.1‰. Prickly pear stem \( \delta^{13}C \) average was -13.2±0.9‰, while \( \delta^{15}N \) average was significantly higher at 7.7±3.2‰. \( \delta^{13}C \) values of maize and tuna fruit are not distinct enough to differentiate. The general greater variance in \( \delta^{15}N \) standard deviation may reflect diverse cultivation practices that influence nitrogen isotope values and many of the plants sampled were purchased in the marketplace.

Strontium isotopes. Strontium isotope ratios (\( ^{87}Sr/^{86}Sr \)) were measured using a ThermoFinnigan Neptune MC-ICPMS housed in the Washington State University Radiogenic Isotope and Geochronology Laboratory (WSU RIGL). Instrument accuracy was monitored and confirmed through replicate measurements of the strontium standard NBS-987. Tooth enamel
was cleaned and prepared in a HEPA—filtered class 1000 clean lab within the WSU RIGL to prevent contamination from exogenous Sr. Enamel was abraded using a dental drill to remove dirt, debris and any adhering dentin, and then pretreated in a 5% acetic acid solution to remove post-depositional contaminants. Following pretreatment, samples were hot-digested in 50% nitric acid (HNO₃ optima) and loaded into cation exchange columns packed with Eichrom strontium-selective resin to isolate strontium from other ions.

**Ancient DNA.**

*DNA extraction.* All pre-amplification work was conducted in the LMAMR ancient DNA lab, which is a positively pressured clean room with unidirectional workflow. The aDNA laboratory adheres to international ancient DNA research standards and is routinely monitored for contamination. The sample was extracted following a protocol as described by Dabney et al. (22), with minor modifications added according to Morales-Arce et al. (23). The extraction used 24.7 mg from one root of the maxillary second left molar and an extraction negative control, to which no DNA was added, to monitor potential contamination. The entire tooth was decontaminated with one minute of UV treatment per side, and then by using 8.25% bleach solution and nuclease free water and gently abrading the sample. Samples were decalcified and digested at room temperature, with a 15-minute pre-digestion, over ~9 days using 2mL of EDTA and 150μL of proteinase K, in two washes. DNA was bound to and purified on a Qiagen MinElute column, using 13mL of Qiagen PB buffer to remove salts/impurities and to concentrate the DNA extract. Extracts were eluted in 60 ul of EB buffer (Qiagen). The DNA concentrations of the extracts were measured using the dsDNA HS kit for Qubit 3 Fluorometer.

*Library Preparation and Indexing.* The library preparation steps were conducted using previously published protocols (24), but with minor modifications. A partial UDG treatment (25) was implemented at the beginning of the protocol on 10.53 ul of DNA extract (5.54 ng of DNA). Following library preparation, the concentration of DNA within the libraries was measured through qPCR. And at this step, the library was deemed unusable. The library preparation was repeated using 30 ul of DNA extract (15.78ng) and a scaled-up protocol. This second library DNA concentration was measured through qPCR and used for further steps. For indexing, a unique pair of DNA barcodes were added to each sample as outlined in Kircher et al. (26), while the samples were amplified in triplicate via PCR. Libraries were amplified in 50uL volumes using 2X Kapa HiFi Hotstart with Uracil mix and 55ug BSA. Another negative was included in the library preparation step to monitor contamination.

*Qualification and Sequencing.* After indexing, concentration for all samples was again determined using the dsDNA HS kit for Qubit 3 Fluorometer and 1ng/μL dilutions were made. These dilutions were quantified on the Agilent Technologies Fragment Analyzer. As there were dimers in the samples, all samples on the sequencing run (including others not in this project) were pooled from 10nM dilutions and processed with the Pippin Prep 2 % gel to select for fragments between 150 and 500 base pairs in size. The pool was sequenced on a 2 x 150-NextSeq run at the Oklahoma Medical Research Foundation (OMRF)’s Clinical Genomics Core.

*Analyses.* Raw reads were quality filtered by removing adapter sequences, trimming low quality bases, and merging R1 and R2 reads with AdapterRemoval2 (version 2.1.7) (27). Low quality reads and reads shorter than 30 base pairs were also filtered out at this point. Trimmed and merged reads were mapped to the reference genome using bwa (version 0.7.17-r1188) (28) with parameters for ancient DNA (-n set to 0.01, seed disabled). SAMtools (version 1.5) (29) was then used to filter out unmapped or poor quality (-q set to 37) reads and duplicate reads, and then sort the alignments by coordinates (Table S4).
Quality filtered reads were first mapped to the *Ateles geoffroyi* (black-handed spider monkey, species id: 75176) genome, as that was the only publicly available spider monkey genome in GenBank. To determine if the mapped DNA molecules have the characteristic patterns expected for degraded DNA, we used the program PMD Tools v0.50 (Figure S6) (30). The sample was also competitively mapped using the dataset from Morales-Jimenez et al. (31)(PopSet id: 631909078), which includes limited mitochondrial data from various spider monkey species and sub-species (Table S5).

Given the limitations of the publicly available genome data, a 600bp segment of CytB and the surrounding region was isolated from the ancient sample for phylogenetic analysis (Supplementary Dataset). This CyB section was aligned with the BLAST algorithm in Geneious (v11.1.5) to identify candidate sequences to create a gene tree. Additional geo-tagged samples were downloaded for comparison from Genbank. These were then aligned to the ancient sample consensus sequence with Mafft v1.4.0 (32) as implemented in Geneious. Phylogenetic analysis was conducted in a maximum likelihood framework with RAxML v8.2.12 (33) and a GTR+CAT substitution model with 100 bootstrap replications (Figure S7A). Given the potential for missing data to impact the phylogenetic reconstruction, the sample phylogeny was re-created using a maximum likelihood method with partial deletion (590 sites) and a Tamura-Nei substitution model in MEGA v10.1.8 (34) with 100 bootstrap replicates (Figure S7B). In both phylogenetic trees, the sample fell within a clade containing both the *A. g. vellerosus* and *A. g. yucatanensis* subspecies. The 600 bp alignment was filtered for variable sites and complete data, yielding 68 sites over 43 sequences. This new alignment was used for the median-joining network analysis in PopART (v: 1.7) (35).

For sex determination, samples were mapped to the *Callithrix jacchus* (white-tufted-ear marmoset, species id: 1965096), as this was the closest relative with a published chromosomal genome (Table S4B). A modified version of the sex-determination script published in Mittnik et al (36) was then used, which calculated the ratio of autosomal chromosome reads to X chromosome reads in order to determine sex. This analysis supported zooarchaeological sex assignment of female (Rx 1.147305, 95%CI 1.106341-1.188268).

**Paleobotany.**

*Collecting the samples.* Samples were taken by Ariel Texis in Teotihuacan 2021 and analyzed by Cagnato. Prior to taking the archaeological samples, a control sample (distilled water in a container) was placed on the table in the same room where the samples were taken. The table was bleached prior to sampling, and the dental picks and containers to hold the samples were sterilized prior to their use. Non-powdered gloves were used while sampling. The teeth were all photographed before and after sampling.

The monkey teeth presented very faint marks of dental calculus, and in some cases the teeth could not be removed from the bones: we therefore had to adapt the sampling. We used two methods, wet and dry. The first is inspired by a “dental wash” protocol, carried out by Boyadjian et al. (37) on teeth from Brazilian shellmound (Sambaqui) burials. The procedure was slightly modified by using a lower concentration of hydrochloric acid (HCL) and by omitting soaking the teeth in the acid for long periods of time to avoid tooth damage.

**Wet sampling.** Wet samples were collected only from teeth that could be removed (i.e., not stuck to the bone), therefore 3 teeth from the mandible were selected: 2nd and 3rd molar, and the left incisor. A clean, new toothbrush was used for each tooth. The tooth was gently brushed prior to
sampling to remove any dust, and the occlusal and outer surfaces washed using a 7.5 % solution of HCL. We also gently picked the occlusal surface with a pick and placed the material in the same vial. The brushes were rinsed with distilled water and the residues placed in the containers. Once completed, the tooth was rinsed with distilled water and left to dry, before being carefully stored.

**Dry sampling.** Dry samples were taken from teeth that could not be removed from the maxillary bone. Dry sampling avoids tooth damage and conflating which tooth samples were taken from. Three teeth were chosen: 1st and 3rd molar, and an incisor. Using sterilized dental picks, any visible residue on the occlusal surface and outer surfaces was gently scrapped and placed in aluminum foil before placing it in clean containers. The resulting samples were extremely light and can be described as powder (i.e., no bulky particles).

**Laboratory processing.** The dental wash samples were placed in 50 ml centrifuge tubes, filled with distilled water, and centrifuged for 2 minutes at 2000 RPM. The supernatant was discarded, and this was repeated twice more to rinse out all the acid from the sample.

The dry samples were decalcified by adding 5 ml of 7.5% HCL and centrifuging for 5 minutes at 5000 RPM. The supernatant was discarded, and the tube refilled with distilled water. This was done twice more to rinse the sample completely. The control sample was reduced by centrifuging, and the supernatant discarded. The remaining liquid was placed on a slide (see below).

Slides were prepared by placing a drop of the clean sample, and a drop of a 1:1 glycerin: water solution, which was added to allow rotation of the starch grains and other elements. A cover slide was added, and viewed with a transmitted light microscope (Nikon E600 POL). Starch grains were photographed under transmitted and cross-polarized light at 10-60 x magnification using a Zeiss Axiocam 208 color. Starch grain identification was based on consulting an available reference collection of plants native to Central Mexico and the Maya Lowlands.

**Results: Microbotanical remains and other elements.**

**Phytoliths:** These were generally found as single-cell particles. Only one grass silica skeleton was recovered, composed of articulated short (bilobate) and long cells. Elongate entire (Figure S8m) and elongate dentate cells (Figure S8n) were also found, and these are common in the plant kingdom, although they represent the majority of the long cells in monocots (38). Bulliform flabellate phytoliths reported in Poaceae and Cyperaceae (sedge family) leaves were also identified (38). Acute bulbosus phytoliths present in numerous grasses, other monocots (sedges), and in a few dicots and palms (38) were also extant. Short cell phytoliths of bilobate (Figure S8o), saddle (Figure S8p), and rondel forms found in the grass family were also present in the samples.

**Trichomes:** Trichomes are fine unicellular or multicellular appendages found on a variety of surfaces of plant organs and tissues. Different types of trichomes were found in the samples, likely indicating different species.

**Crystals:** Two types of calcium oxalate crystals were present: hexagonal prismatic crystals measuring on average between 10-12 microns in length (Figure S8r) and larger ones, which can be described more as styloids (Figure 5k). No further identification could be reached, but it should be noted that crystals appear in both dicots and monocots (39) and have been reported from almost all parts of a plant (40).
Vascular tissue: Different types of plant vessel elements (Figure S8s-t), as well as vasicentric tracheids, indicative of hardwoods (angiosperms), were recovered. On the other hand, the presence of softwoods (gymnosperms) is evidenced by fragments with taxodioid or cupressoid cross-field pitting (Figure 5I) and fiber tracheid fragments with uniseriate tracheid pitting (Figure S8u).

Other non-vegetal remains: Non-vegetal remains include a mammal hair fragment, which measures 8.5 mm (minimum) lengthwise, and 17 μm at its widest. Sandra Koch identified this element as mammalian underfur that cannot be morphologically identified to species (Figure S8v-w). Finally, fungal spores (likely *Alternaria* sp., Figure S8x) were present.

The control sample contained unidentified fibers and other particles, but nothing that resembles the remains found in the archaeological samples described above.
Figure S1. Bayesian statistical model of eagle bone (EL-D449) and radiocarbon sample (M-D3050) as one phase run by OxCal v4.4.
Figure S2. Spider monkey cranium of *A. g. vellerosus* (left) and *A. g. yucatanensis* (right) from the National Museum of Natural History. Top: superior view, middle: lateral view, bottom: inferior view.
Figure S3. Spider monkey mandible of *A. g. vellerosus* (left) and *A. g. yucatanensis* (right) from the National Museum of Natural History. Top: superior view, middle: lateral view, bottom: ventral view.
Figure S4. Mound 25C spider monkey maxilla A) frontal view, B) inferior view. Red arrow indicates location where right Pm1 is absent and alveolar cavity is filled in.
Figure S5. Mound 25C spider monkey maxillary incisors with extensive wear; A) labial view, B) lingual view. Microscope images, bar indicates 2 mm.

Figure S6. PMD tools estimated damage patterns for A) *Ateles geoffroyi* mapping and B) comparative mappings.
Figure S7. Phylogenetic analysis of partial cytochrome b gene generated using a maximum likelihood method with 100 bootstrap replicates in A) RAxML v8.2.12 and B) MEGA v10.1.8 with partial deletion. In both trees, the sample fell within a clade that contains the A. g. vellerosus and A. g. yucatanensis subspecies.
Figure S8. Microbotanical remains and other elements recovered from the spider monkey teeth. Starch grains, viewed under transmitted and cross-polarized light (a-d) probable tubers; (e-l) damaged starch grains as evidenced by the loss of the extinction cross. Phytoliths (m-p). trichome (q); prismatic crystals (r); vessel elements (s-t, white arrow indicates intervessel pits); softwood fiber tracheids (u, white arrow indicates uniseriate tracheid pitting); mammalian underfur hair (v-w); fungal spore, cf. *Alternaria* sp. (x). (All photos C. Cagnato)
Table S1. Ceramic counts and percentages of sherds by phase pertaining to the fill of offering D4, and the general fill of Tunnel 5.

| Ceramic Phase    | Dates*  | Offering D4 Only | Tunnel 5 |
|------------------|---------|------------------|----------|
|                  | n      | %    | n      | %    |
| Early Tlamimilolpa | 200-350 CE | 106  | 60   | 502  | 60   |
| Miccaotli        | 150-200 CE | 52   | 29   | 242  | 29   |
| Tzacuali         | 100-150 CE | 11   | 6    | 78   | 9    |
| Non-ID           | 8      | 5    | 20   | 2    |
| Total            | 177    |       | 842  |       |
Table S2. $\delta^{13}C_{\text{collagen}}$ and $\delta^{15}N_{\text{collagen}}$ corrections applied to modern New World monkey values taken from Schoeninger et al. 1997:Table 3.

|                | n  | Original | $\delta^{13}C_{\text{collagen}}$ | $\delta^{15}N_{\text{collagen}}$ |
|----------------|----|----------|-------------------------------|----------------------------------|
|                |    |          | Suess effect (+1.5) | Hair-bone offset (+1.4) | Original | Hair-bone offset (+.86) |
| Spider monkey  | 5  | -24.9    | -23.4                        | -22                             | 5        | 5.86                    | 0.5   |
| Howler monkey  | 12 | -23.4    | -21.9                        | -20.5                           | 3.5      | 4.36                    | 0.7   |
| Capuchin monkey| 4  | -24.6    | -23.1                        | -21.7                           | 7        | 7.86                    | 0.1   |
| Muriqui or woolly-spider monkey | 7 | -23.5 | -22                        | -20.6                           | 5.6      | 6.46                    | 0.4   |
Table S3. Summary of plant isotope data of agricultural maize (*Zea mays*) and nopal cactus/fruit (*Opuntia sp.*) from published literature.

| Sample ID | Photosynthetic type | Collection season | Sampled part | Taxa | Common name | $\delta^{13}$C | $\delta^{15}$N | %N | Reference |
|-----------|---------------------|-------------------|--------------|------|-------------|----------------|----------------|-----|-----------|
| WO27      | C4                  | WINTER            | Seed         | *Zea mays* | Maize       | -11.3          | 5.4            | 2.3 | Warriner et al. 2013:Sup Table 1 |
| WO69      | C4                  | WINTER            | Seed         | *Zea mays* | Maize (negro) | -11.8          | 3.0            | 1.0 | Warriner et al. 2013:Sup Table 1 |
| WO68      | C4                  | WINTER            | Seed         | *Zea mays* | Maize (blanco) | -13.4          | 5.0            | 1.9 | Warriner et al. 2013:Sup Table 1 |
| WO70      | C4                  | WINTER            | Seed         | *Zea mays* | Maize (blanco) | -10.7          | 1.3            | 0.9 | Warriner et al. 2013:Sup Table 1 |
| WO71      | C4                  | WINTER            | Seed         | *Zea mays* | Maize       | -11.7          | 0.8            | 1.8 | Warriner et al. 2013:Sup Table 1 |
| WO83      | CAM                 | WINTER            | Alcohol      | *Agave spp.* | Pulque      | -12.2          | 4.2            | 1.4 | Warriner et al. 2013:Sup Table 1 |
| SO38      | CAM                 | SUMMER            | Fruit        | *Opuntia ficus-indica* | Red prickly pear | -12.2          | 5.8            | 1.0 | Warriner et al. 2013:Sup Table 1 |
| SO39      | CAM                 | SUMMER            | Fruit        | *Opuntia ficus-indica* | Green prickly pear | -12.9          | 4.5            | 0.9 | Warriner et al. 2013:Sup Table 1 |
| SO44      | CAM                 | SUMMER            | Fruit        | *Opuntia ficus-indica* | Green prickly pear | -13.8          | 1.4            | 0.7 | Warriner et al. 2013:Sup Table 1 |
| WO13      | CAM                 | WINTER            | Stem         | *Opuntia ficus-indica* | Nopal cactus | -13.7          | 10.2           | 1.7 | Warriner et al. 2013:Sup Table 1 |
| SO36      | CAM                 | SUMMER            | Stem         | *Opuntia ficus-indica* | Nopal cactus | -13.6          | 8.6            | 2.8 | Warriner et al. 2013:Sup Table 1 |
| CAM       | Teotihuacan         | Stem              | Stem         | *Opuntia* | Nopal cactus | -12.7          | 9.3            |     | Morales et al. 2012:Table XI.3 |
| CAM       | Market              | Stem              | Stem         | *Opuntia* | Nopal cactus | -11.9          | 8.6            |     | Morales et al. 2012:Table XI.3 |
| CAM       | Cuicuiaco          | Stem              | Stem         | *Opuntia* | Nopal cactus | -14.2          | 2.1            |     | Morales et al. 2012:Table XI.3 |
| CAM       | Teotihuacan         | Tuna Xoconostle, Cascara | *Opuntia* | Xoconostle | -14.2 | 1.7 | | Morales et al. 2012:Table XI.3 |
| CAM       | Teotihuacan         | Tuna Xxconostle, pulp | *Opuntia* | Xoconostle | -11.8 | 2.1 | | Morales et al. 2012:Table XI.3 |
| CAM       | Teotihuacan         | Tuna Xoconostle, seed | *Opuntia* | Xoconostle | -12.5 | 7.7 | | Morales et al. 2012:Table XI.3 |
| CAM       | Market              | Xoconostle        | *Opuntia* | Xoconostle | -12.4 | 2.1 | | Morales et al. 2012:Table XI.3 |
| CAM       | Teotihuacan         | Fruit, flower     | *Opuntia* | Tuna | -12.2 | 3.2 | | Morales et al. 2012:Table XI.3 |
| CAM       | Teotihuacan         | Fruit, meat       | *Opuntia* | Tuna | -12.6 | 4.1 | | Morales et al. 2012:Table XI.3 |
| C4        | Teotihuacan         | -                 | *Zea mays* | Maiz | -11.8 | -0.5 | | Morales et al. 2012:Table XI.3 |
| C4        | Market              | -                 | *Zea mays* | Maiz (blanco) | -11.5 | 1.4 | | Morales et al. 2012:Table XI.3 |
| C4        | Market              | -                 | *Zea mays* | Maiz (cacao) | -11.7 | 0.1 | | Morales et al. 2012:Table XI.3 |
| C4        | Market              | -                 | *Zea mays averta* | Maiz | -11.7 | 1.7 | | Morales et al. 2012:Table XI.3 |
| C4        | Market              | -                 | *Zea mays averta* | Maiz | -11.5 | -1.1 | | Morales et al. 2012:Table XI.3 |
Table S4. Results of mapping to the A) *Ateles geoffroyi* genome and B) *Callithrix jacchus* genome

|       | Total Reads | Merged Reads | Percent of reads merged | Mapped Reads | Q37 Mapped Reads | Unique Reads | Average Read Length |
|-------|-------------|--------------|-------------------------|--------------|------------------|--------------|---------------------|
| **A** |             |              |                         |              |                  |              |                     |
| Sample | 19,057,668  | 16,003,633   | .8397                   | 2,348,746    | 1,962,898        | 1,121,781    | 73.7971             |
| Extract | 2,072,603   | 1,850,982    | .8930                   | 2,414        | 929              | 775          | 58.6929             |
| Library | 86,473      | 37,20        | .4302                   | 4,459        | 1,043            | 145          | 69.131              |
| **B** |             |              |                         |              |                  |              |                     |
| Sample | 19,057,688  | 16,003,633   | .8397                   | 1,291,650    | 800,685          | 461,277      | 66.2132             |
| Species/subspecies                          | GenBank ID      | Geographic Origin                      |
|--------------------------------------------|-----------------|----------------------------------------|
| **Comparative mapping samples**            |                 |                                        |
| *Ateles geoffroyi frontatus*               | KJ186897.1      | Santa Rosa National Park, Costa Rica   |
| *Ateles geoffroyi yucatanensis*            | KJ186879.1      | Cancun, Mexico                         |
| *Ateles geoffroyi ornatus*                 | KJ186887.1      | Panama (Captive)                       |
| *Ateles hybridus*                          | KJ452766.1      | Serrania Las Quinchas, Columbia        |
| *Ateles fusciceps*                         | KJ452770.1      | Ecuador (Captive)                      |
| *Ateles fusciceps*                         | KJ452768.1      | Panama (Captive)                       |
| **Gene tree samples**                      |                 |                                        |
| *Ateles fusciceps rufiventris* (5 samples)*| KJ186857-61     | Darién Province, Panama                |
| *Ateles geoffroyi yucatanensis* (3 samples)| KJ186863-64, 80 | Runaway Creek, Belize                  |
| *Ateles geoffroyi yucatanensis* (10 samples)| KJ186856, 62, 66, 69, 70, 73-77 | Tikal, Guatemala                       |
| *Ateles geoffroyi vellerosus* (8 samples)  | KJ186865, 67, 68, 72, 81-83, 85 | Mexico                                |
| *Ateles geoffroyi yucatanensis* (5 samples) | KJ186871, 78, 79, 84, 86 | Cancun, Mexico                       |
| *Ateles geoffroyi ornatus*                 | KJ186887        | Panama (Captive)                       |
| *Ateles geoffroyi azuerensis* (3 samples)  | KJ186888-90     | Azuero Peninsula, Panama               |
| *Ateles geoffroyi vellerosus* (2 samples)  | KJ186891-92     | El Salvador                            |
| *Ateles geoffroyi frontatus* (3 samples)   | KJ186893-95     | Guadalupe, Nicaragua                   |
| *Ateles geoffroyi frontatus* (2 samples)   | KJ186896-97     | Santa Rosa, Costa Rica                 |
Table S6. Starch grain results from spider monkey teeth extractions. C= Starch Grain Cluster; CR= Crystal; F= Fungus; FB= Fiber; M= Mammal hair; P= Phytolith; S= Softwood fiber; T= Trichome; V= Vessel element. * Numbers in parentheses indicate the starch grains that cannot be identified due to damage.

| TOOTH               | Maize (Zea mays) | Chili Pepper (Capsicum sp.) | Arrowroot (Maranta arundinacea) | Unidentified Tuber A | Unidentified Tuber B | Unidentified Tuber C | Unidentified Starch Grain* | SUB-TOTAL | Other Elements |
|---------------------|------------------|-----------------------------|---------------------------------|----------------------|----------------------|----------------------|---------------------------|-----------|----------------|
| Maxilla             |                  |                             |                                 |                      |                      |                      |                           |           |                |
| 1st molar left      | 3                |                             |                                 |                      |                      |                      |                           | 7         | P              |
| 3rd molar left      | 2                |                             |                                 |                      |                      |                      |                           | 3         |                |
| Incisor left        | 1                |                             |                                 |                      |                      |                      |                           | 2         | F, P, T        |
| Mandible            |                  |                             |                                 |                      |                      |                      |                           |           |                |
| 2nd molar left      | 5                | 5                           | 1                               | 3                    | 1                    |                      | 7(3)                     | 25        | P, S, T        |
| 3rd molar right     | 3                | 3+C                         |                                 |                      |                      |                      | 5(4)                     | 15        | CR, F, FB, S, T, V |
| Incisor left        | 4                | 5+C                         |                                 |                      |                      |                      | 5(2)                     | 17        | CR, FB, M, T   |
| **TOTAL**           | **69**           |                             |                                 |                      |                      |                      |                           |           |                |
Table S7. Phytolith morphotypes recovered from the spider monkey teeth samples.

|                | Acute bulbosus | Blocky | Bulliform flabellate | Elongate entire | Elongate dentate | Grass silica short-cell | Other |
|----------------|----------------|--------|----------------------|-----------------|------------------|-------------------------|-------|
| Maxilla        |                |        |                      |                 |                  |                         |       |
| 1st molar left |                |        |                      | x               |                  |                         |       |
| 3rd molar left |                |        |                      |                 |                  |                         |       |
| Incisor left   |                |        |                      |                 |                  |                         |       |
| Mandible       |                |        |                      |                 |                  |                         |       |
| 2nd molar left | x              | x      | x                    | x               | x                |                         | x     |
| 3rd molar right|                |        |                      |                 |                  |                         |       |
| Incisor left   |                |        |                      |                 |                  |                         |       |
3D Model S1. 3D Photogrammetry model of the Teotihuacan Spider Monkey’s mandible.

3D Model S2. 3D Photogrammetry model of the Teotihuacan Spider Monkey’s maxilla.

Supplementary Dataset. Cytochrome b alignment with Teotihuacan Spider Monkey.

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