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Life Sciences Reporting Summary

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Experimental design

1. Sample size

   Describe how sample size was determined.

   Data combined from 1 lake record (60 pollen samples and 417 charcoal samples), 3 soil profiles, and six modern vegetation plots (3 pairs from ADE and non-ADE soils.).

   Lake samples were processed, identified, and counted at the University of Exeter Archaeobotany Laboratory following standard procedures (see Methods and SI). We used the standard pollen count size of 300 grains per sample to capture pollen diversity and characterise major vegetation communities in the Neotropics (Gosling et al., 2009). An additional sieving step was added to concentrate crop pollen. Crop pollen was identified using taxonomic key and the reference collection housed at the University of Exeter (see SI methods). Total charcoal counts from 1cm2 at every 0.5cm depth were counted.

   Archaeological soil samples were processed for phytoliths, identified, and counted at the University of Exeter Archaeobotany Laboratory following standard procedures (Piperno, 2006). The standard count size of a minimum of 200 phytoliths were identified in each sample. In order to maximize the recovery of important phytoliths of different size classes, such as those that derive from the rinds of Cucurbita fruits (Bozarth,1987; Piperno et al., 2000) and from leaves and cobs of maize (Iriarte, 2003; Pearsall et al., 2003; Piperno and Pearsall, 1993), soil sediments were separated by wet-sieving into silt (2-50 um) and sand (50 to 2000 um) fractions.

   We set up three pairs of 0.25 ha plots (50 x 50 m) vegetation plots, three in Amazonian Dark Earths (ADE) and three in adjacent non-ADE locations. In each plot, we sampled all live trees with diameter at breast height ≥10 cm (DBH) and at least 1.30 m tall. Botanical inventory data are available in SI.

2. Data exclusions

   Describe any data exclusions.

   No data were excluded from this analysis.

3. Replication

   Describe the measures taken to verify the reproducibility of the experimental findings.

   Lake sediment cores were taken using a Livingston piston corer. Sediment samples showed no signs of bioturbation. This interpretation is supported by the 210Pb and 14C AMS age-depth model (see SI methods for details).
   Standard methods, protocols, and taxon identification were used in pollen and phytolith analysis and detailed in the SI methods section. Three replicate soil profiles were analysed and three pairs of vegetation plots were used as replicates. All botanical inventory data are available in SI along with the updated plant list of edible plants (compiled from publicly available materials). Plants collected for identification were accessioned into the Herbarium in Manaus are publicly available. All statistics were calculated in R open source software using publicly available packages (e.g. vegan community ecology package) and detailed in the SI methods.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   Archaeobotany. Samples were carefully collected by experience archaeologists using column sampling and targeted archaeological features from undisturbed archaeological contexts and soil profiles.

   Palaeoecology. Four different lakes were cored in the region. Lake Carana was selected based on proximity to archaeological site and distance to river (decreased riverine transport).

Botany. The six vegetation plots were selected at random in ADA and non-ADE forests. Due to the high concentration of ADE soils, non-ADE plots were sampled a minimum of 150 m away from the edge of ADE soils.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Blinding was not relevant to our study.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ Test values indicating whether an effect is present *Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.*
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation)

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

Tilia 2.0.37 was used for pollen analysis, C2 was used for phytolith analysis and R-Studio was used for statistical analysis, the Bacon R package was used in R to develop the age-depth model for lake sediement core.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

No unique materials were used.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cells lines were used.

b. Describe the method of cell line authentication used.

No eukaryotic cells lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cells lines were used.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The study did not involve humans.