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Exploring the Development of a Complex Agricultural System in the Maya Lowlands
through the Analysis of eDNA

The main objective of the proposed study is to investigate the emergence and growth of the agricultural economy in Maya lowlands from the earliest settlements in the early Middle Preclassic (1000-600 BCE) to the establishment of the state level society in the Late Preclassic (300 BCE-150 CE). Despite intensive investigations throughout the Maya lowlands, we still understand little of the early processes that led to the domestication and commodification of many cultigens, nor do we have a clear picture of the range of plants cultivated by the early Maya. Therefore, we will employ advanced analysis of ancient plant DNA extracted from two sources, macrobotanical remains and sediments, recovered from early agricultural fields and nearby water storage features, to provide a detailed picture of the selection processes that shaped complex agriculture in the tropics. The study will be conducted at Yaxnohcah, an extensive settlement situated in the middle of the Central Karstic Uplands, a region including most of southern Campeche, Mexico and northern Petén, Guatemala. After five years of investigations, we have established an occupational history for the site beginning at ca. 900 BCE through to 850 CE, with no breaks in the sequence. Additionally, we have identified numerous agricultural field and terraces, as well as nearby reservoirs.

To obtain the most reliable results, we will couple eDNA metagenomics with classical paleobotanical studies for sedimentary deposits from two distinct types of features at Yaxnohcah, namely the ancient fields in which the crops were grown and the sediments accumulated in the reservoirs, to identify ancient cultigens and reconstruct past agricultural systems. We have selected five fields in different vegetation zones for testing: three fields in an upland forest, one field in a transitional forest, and one field in a wetland. Two test units of 1 x 1 m will be placed in each field and a total of thirty eDNA samples will be extracted from the profiles of each unit. In addition, we will extract two sediment cores each from five reservoirs located near the identified fields. A total of fifty eDNA samples will be extracted from two sediment cores taken from five different reservoirs.

The team will use shotgun metagenomics methods to sequence ancient eDNA (environmental DNA) sequencing. This cutting-edge technology has not been applied to eDNA strands recovered from sediments formed in a tropical environment. Moreover, we will be using a targeted enrichment process, which preferentially sequences strands of interest, regardless of strand length. This study will be the first to apply this method to bulk eDNA samples. Specifically, the team will enrich important genes in relevant crops, such as maize and cotton, to identify the varieties in use at different times and to characterize genomic selective processes over the period in which the sites were inhabited. We will conduct classical paleobotanical analyses to confirm the results of the eDNA analyses.

Because our study focuses on the application of innovative methods for extracting and identifying ancient DNA in sediments, it will open new avenues of research for processes of domestication, agricultural practices, and environmental reconstruction. Moreover, the cross-disciplinary collaboration among the team members will allow us to make stronger and broader interpretations that will resonate across related disciplines. Finally, the advanced techniques we are implementing will provide an environmental record for the past 3000+ years, which is crucial for understanding the transformations that occurred due to climate change and has profound implications for addressing current environmental challenges in both Canada and Mexico.