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Bayesian Morphometric Analysis for Archaeological Seed Identification: *Phoenix* (Arecaceae) Palms from the Canary Islands (Spain)

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Abstract: The taxonomic complexity of *Phoenix* palms in the Canary Islands, where multiple morphotypes representing at least four taxa currently exist, presents significant challenges for archaeobotanical identification. We developed a Bayesian probabilistic framework to identify archaeological *Phoenix* seeds within the context of genus-wide morphological diversity. Our analysis incorporated thousands of specimens including modern reference collections, archaeological materials from pre-Hispanic sites in Gran Canaria and La Gomera (3–16th centuries CE), and fossil remains. We recorded quantitative measurements and qualitative characteristics for each specimen. To understand taphonomic effects, we conducted experimental carbonization of modern *P. canariensis* seeds and documented the resulting morphological alterations. We performed a hierarchical cluster analysis using Ward's minimum variance method and calculated taxonomic assignment probabilities for archaeological specimens using Bayesian inference, where likelihood was derived from taxon proportions within assigned clusters. The results indicated a high probability (0.69–1.00) that the archaeological specimens belong to *P. canariensis* var. *canariensis*, with no evidence for *P. dactylifera* presence. These findings provide critical insights into pre-Hispanic exploitation of Phoenix palms, particularly the endemic *P. canariensis*, which served as a vital resource, providing food, fiber, and construction materials. Our methodological approach offers a robust framework for addressing taxonomic uncertainty in archaeobotanical research while enhancing understanding of historical palm biogeography and resource use patterns in the Canary Islands.

Keywords: date palms; *Phoenix canariensis*; Archaeobotany; Bayesian inference; Canary Islands; taxonomic identification; carbonization; morphometrics

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1. Introduction

1.1. Taxonomic Overview of Phoenix Palms

The genus *Phoenix* (Arecaceae) encompasses 13–20 date-bearing palm species, characterized by significant taxonomic complexity arising from genetic, biogeographic, and morphological variations [1–6]. Among these, *Phoenix canariensis* H.Wildpret (Figure 1) and *Phoenix dactylifera* L. are particularly noteworthy for their economic and cultural significance [7–11].

Figure 1. Morphological diversity of *Phoenix canariensis* varieties: habit and seed characteristics. (**A**–**C**): Mature palm fruits: (**A**) *P. canariensis* var. *canariensis*; (**B**) var. *macrocarpa*; (**C**) var. *porphyrococca*; (**D**,**E**): Mature palm specimens: (**D**) var. *macrocarpa*; (**E**) var. *porphyrococca*. (**F**,**J**): Representative seed morphotypes: (**F**) var. *canariensis* from Maria Serena gardens, Menton, France; (**G**) var. *macrocarpa* from Moraira, Alicante, Spain; (**H**) var. *canariensis* from Moraira, Alicante, Spain; (**I**) var. *porphyrococca* from Torrijos, Toledo, Spain; (**J**) var. *macrocarpa* from Ibiza, Spain. Scale bars = 10 mm. All photographs by D. Rivera and C. Obón.

1.2. Morphological and Genetic Characteristics of P. canariensis

Endemic to the Canary Islands, *Phoenix canariensis* exhibits significant morphological diversity, particularly in its fruit characteristics and leaf structure. However, in stark contrast to this variability, its spheroid echinate phytoliths—microscopic silica structures formed within specific plant cell types, including epidermal and parenchyma cells, as well as fruit tissues—display remarkable uniformity. These microfossil structures, commonly found in both archaeological and natural sedimentary contexts, exhibit minimal polymorphic variation, maintaining a highly consistent morphological profile [12]. Furthermore, *P. canariensis* demonstrates a distinct pattern of genetic differentiation across the archipelago, following a stepping-stone model that aligns with the chronological sequence of island emergence.

1.3. Ethnobotanical Significance and Cultural Integration

Phoenix canariensis has historically held significant ethnobotanical importance in the Canary Islands [7,13,14]. Archaeological evidence, including carbonized and desiccated stem fragments found in Aboriginal domestic and granary contexts, confirms its cultural significance [15]. This cultural embeddedness is particularly evident on La Gomera Island, where a rich Guanche-Spanish lexicon demonstrates a sophisticated ethnolinguistic classification of the palm's various morphological structures and agricultural products. This specialized nomenclature encompasses reproductive and vegetative components, including female inflorescences (escoba), unripe fruits (gamame), stem-extracted sap (guarapo), leaf-base fibrous sheaths (jarropón), infructescence peduncles (palanqueta), individual leaves (penca), leaf rachises (pirguán/pírgano), sub-basal acanthophyll-bearing leaf regions (talajague), and mature fruits (támbara/támara) [16–18]. This intricate vernacular taxonomy underscores the palm's deep integration into indigenous agricultural systems and its profound socioeconomic and cultural significance [17,19].

1.4. Taxonomic Complexity and Hybridization

The taxonomic complexity within the *Phoenix* genus is further substantiated by documented instances of interspecific hybridization and genetic introgression, particularly exemplified by infraspecific variants such as *P. canariensis* var. *porphyrococca*. The occurrence of spontaneous hybridization events between *P. canariensis* and *P. dactylifera* has resulted in complex patterns of genetic admixture, manifesting in intermediate morphological characteristics and altered physiological traits. This genetic permeability between closely related *Phoenix* species presents significant challenges for taxonomic delimitation and phylogenetic reconstruction. The documented introgression patterns suggest historical and contemporary gene flow events, potentially influenced by both natural processes and anthropogenic factors, including cultivation practices. These hybridization dynamics not only contribute to the species' phenotypic plasticity but also raise important questions regarding species boundaries and evolutionary trajectories within the genus [14,20,21]. Such genetic complexity necessitates a nuanced approach to taxonomic classification that acknowledges the fluid nature of species boundaries in actively evolving plant lineages.

1.5. Theoretical Framework: Domestication as Coevolution

The intricate relationships between local human populations and palms, particularly in the context of domestication, demand nuanced scholarly attention. The concept of domestication is frequently misconstrued, with prevailing definitions often exhibiting an anthropocentric bias that overemphasizes human intentionality. Such perspectives critically undermine the significance of unconscious selection processes and artificially constrain our understanding by excluding non-human domesticators.

A more biologically sophisticated conceptualization of domestication recognizes it as a complex coevolutionary phenomenon arising from specialized mutualisms, wherein one species systematically influences another's fitness to secure essential resources or services [22]. Contemporary scientific discourse increasingly acknowledges that some of the most transformative evolutionary events have originated directly from coevolutionary interactions [23].

Empirical evidence supports the notion that numerous species characteristics are intrinsically linked to interactions with other organisms. These interactions encompass a diverse array of ecological dynamics, including generalized competition, character displacement, predator-prey relationships, host-parasite interactions, mutualism, foraging strategies, and plant toxicity mechanisms. Consequently, the coevolution of species groups, rather than the isolated evolution of individual species, emerges as a critically important analytical framework [24–26]

1.6. Geographical Context

Archaeological evidence substantiates the early exploitation of *P. canariensis* by Berber-like populations who colonized the Canary Islands between 70 CE and 500 CE, remaining isolated until European exploration circa 1300 CE [27–29]. Historical documentation from 1350–1600 CE reveals extensive palm utilization, particularly in Gran Canaria and La Gomera, encompassing nutritional and material applications including food production and fiber-based artifact manufacturing [30–33].

Palaeobotanical investigations confirm the presence of *Phoenix* through Holocene pollen records, leaf fragments, and archaeological seed remains [34–36]. Gran Canaria and La Gomera exhibit archaeological palm-derived artifacts, with their extraordinary preservation attributed to climatic aridity and stable cave environmental conditions. Documented uses include textile production, basketry, architectural elements, and various utilitarian implements [36–38].

Archaeological seed recovery has been challenging due to their diminutive size and inconsistent archaeological processing methodologies. Systematic sampling has yielded carbonized date remains from multiple sites in Gran Canaria (La Cerera, Guayedra, El Tejar, Lomo los Melones, Cueva Pintada, Lomo de los Gatos) and La Gomera (El Alto del Garajonay, La Cañada de la Gurona, Sobrado de los Gomeros), with limited representation in Tenerife (Cueva de la Higuera Cota Tegueste) [33,39–44].

1.7. Research Objectives and Methodological Approach

This research aims to develop a Bayesian probabilistic method for identifying archaeological palm seeds, with implications extending beyond archaeology to contemporary biodiversity conservation and agricultural management. By integrating comprehensive morphological analyses of both modern and archaeological specimens alongside experimental carbonization protocols, this study seeks to reconstruct historical vegetation dynamics, identify potential indicators of domestication, and assess the taxonomic diversity of *Phoenix* species in the Canary Islands.

The proposed methodological framework has significant practical applications for modern palm conservation strategies. These include the identification and preservation of historically adapted populations for climate resilience programs, the development of evidence-based habitat restoration protocols, the authentication of indigenous varieties for sustainable agriculture, and the establishment of baseline taxonomic data for biodiversity monitoring. Furthermore, by providing historical ecological data, this research offers valuable insights into species responses to environmental change, informing contemporary resource management practices. Additionally, the methodology supports germplasm conservation initiatives by enabling more precise taxonomic identification in modern breeding programs and ensuring the genetic authenticity of threatened palm populations.

A key challenge in archaeological seed identification lies in its reliance on empirical comparisons with non-carbonized reference collections. This study addresses these limitations by refining identification protocols through Bayesian probabilistic modeling, enhancing their applicability not only in archaeology but also in contemporary palm taxonomy. The improved identification framework facilitates more accurate species delineation in conservation contexts, supports agricultural development by preserving indigenous varieties and fostering climate-resilient cultivars, and strengthens ecosystem restoration efforts by informing evidence-based habitat rehabilitation strategies through more precise historical ecological reconstructions.

2. Materials and Methods

2.1. Archaeological Context

The analyzed archaeological *Phoenix canariensis* seeds, radiocarbon-dated between the 7th and 16th centuries CE, were recovered from sedimentary contexts alongside food remains, suggesting their consumption by indigenous Canarian populations of African origin [33,42].

Archaeological investigations of *P. canariensis* seeds were conducted at three significant pre-Hispanic sites in Gran Canaria: Cueva Pintada, Guayedra, and Lomo de Los Gatos.

Cueva Pintada, located in northwestern Gran Canaria (28°08′35′′ N, 15°39′17′′ W), represents a complex settlement with residential and potentially ritualistic spaces, dated between the 7th and 16th centuries CE [45]. Three carbonized *P. canariensis* seeds were identified within ′stone structure 25′, a domestic context from the 13–15th centuries CE. This domestic context, characterized by evidence of cooking and storage activities, yielded *Phoenix* cf. *canariensis* seeds alongside charred barley (*Hordeum vulgare*) and fig (*Ficus carica*) remains [33,46].

The Guayedra site, a stone dwelling structure located in western Gran Canaria (28°04′58′′ N, 15°42′17′′ W), is part of the ′Majada de Altabaca′ settlement. Radiocarbon dating of a wood sample indicates occupation between 720–820 cal. CE, with archaeological evidence suggesting continued use until the 14–15th centuries CE [47]. A single charred *P. canariensis* seed was recovered from an ash layer within the structure and deposited at El Museo Canario in Las Palmas [46].

Lomo de Los Gatos, situated in southern Gran Canaria (27°49′05′′ N, 15°45′37′′ W), encompasses a substantial settlement with residential and funerary structures. Twenty-one carbonized *Phoenix* cf. *canariensis* seeds were extracted from a midden associated with a dwelling structure, radiocarbon-dated between 1400–1630 cal. CE. This contextual assemblage, characterized by a complex depositary matrix including ash, wood charcoal, crop seeds, marine shells, and faunal remains, suggests occupation during both pre-Hispanic and early colonial periods [46].

Archaeological investigations of *P. canariensis* seeds on La Gomera Island were conducted at two distinct sites: Alto del Garajonay and Sobrado de los Gomeros.

Alto del Garajonay, situated at the island's summit (28°06′35′′ N, 17°14′54′ W) at an elevation of 1487 m above sea level, comprises an extensive stone structure interpreted as a ritualistic sacrificial altar. The site, characterized by multiple hearths and substantial faunal remains from ovicaprids (*Ovis aries/Capra hircus*) and pig (*Sus scrofa*), provides evidence of ceremonial food offerings [48]. Fifteen charred *Phoenix* seeds were recovered alongside carbonized barley and wild plant seeds, with radiocarbon dating indicating occupation between 790 and 1030 cal. CE [41]. Four of these seeds are illustrated in Figure 2.

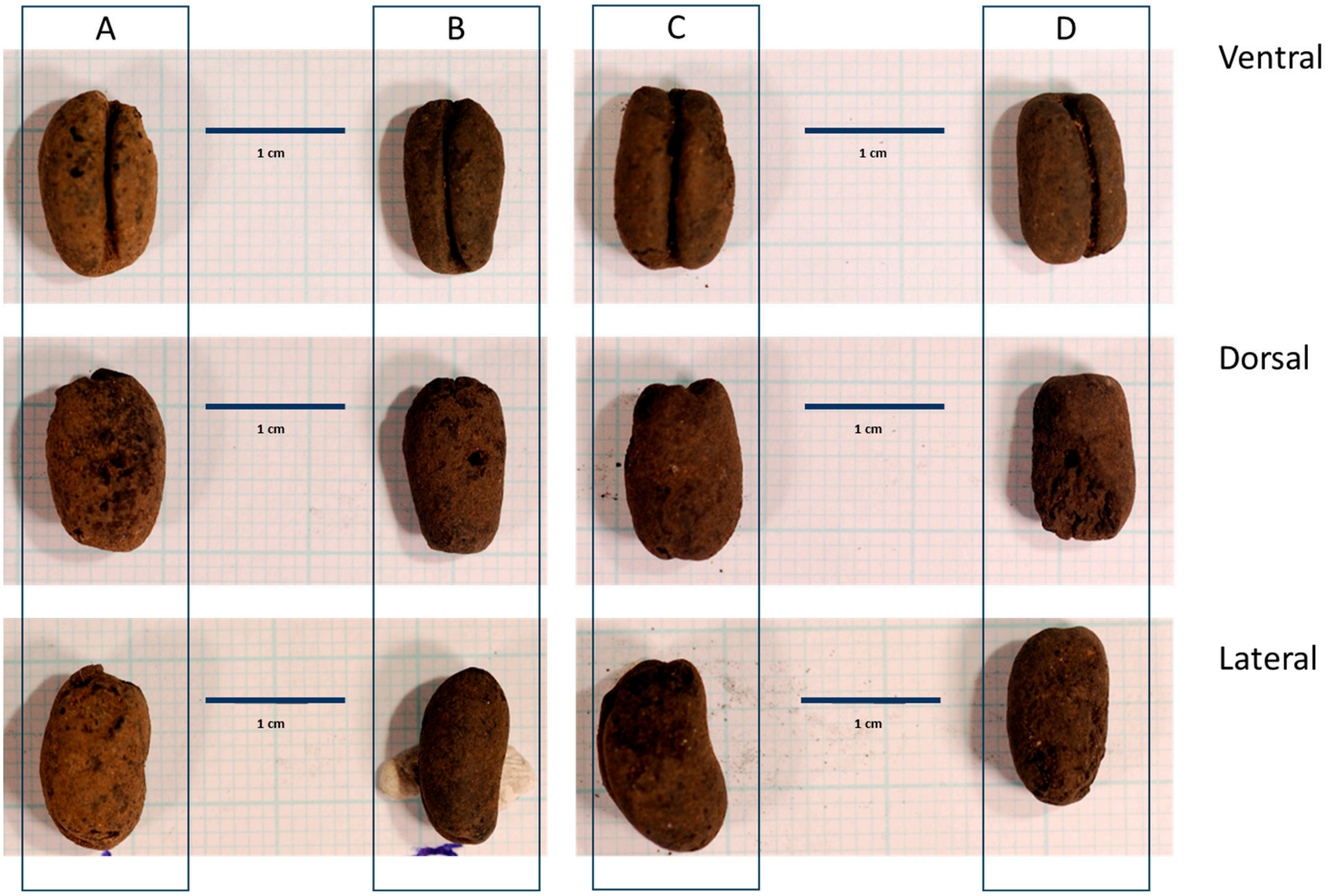


Figure 2. *Phoenix* seeds recovered from pre-Hispanic archaeological contexts at Alto del Garajonay site, with radiocarbon dating indicating occupation between 790 and 1030 cal. CE (La Gomera, Canary Islands, Spain). Photographs by J. Morales and D. Rivera. Scale bar = 10 mm.

Sobrado de los Gomeros, an open-air archaeological site in western La Gomera (28°05′07″ N, 17°19′10″ W) at an elevation of 527 m, provides evidence of pre-Hispanic domestic activities through the presence of lithic artifacts and ceramic assemblages. Three charred *Phoenix* cf. *canariensis* seeds (Figure 3) were recovered from archaeological deposits, alongside carbonized barley and wild plant seeds [40,49]. However, the site lacks precise radiocarbon chronological data, limiting definitive temporal interpretation.

2.2. *Phoenix* Seed Morphology

Seeds were analyzed for taxonomic identification using established diagnostic criteria [1,2,5]. Primary characteristics assessed included shape (ellipsoidal, ovate, cylindrical, oblong, or fusiform), ventral furrow configuration, dorsal micropyle position, and base/apex morphology. Quantitative measurements were recorded for length, width, and thickness, with *P. dactylifera* specimens ranging from 21–27 × 8 − 9.5 × 7–8 mm and *P. canariensis* from 14–16 × 8.5 − 9.6 × 8–8.8 mm. Surface texture features, including transverse striations in *P. dactylifera* and longitudinal striations in *P. canariensis*, were documented. Taphonomic alterations, particularly carbonization effects common in Canary Islands archaeological deposits, were assessed and incorporated into identification confidence estimates. A probabilistic analytical framework was employed to account for intra- and inter-specific morphological variation and preservation-related feature modifications.

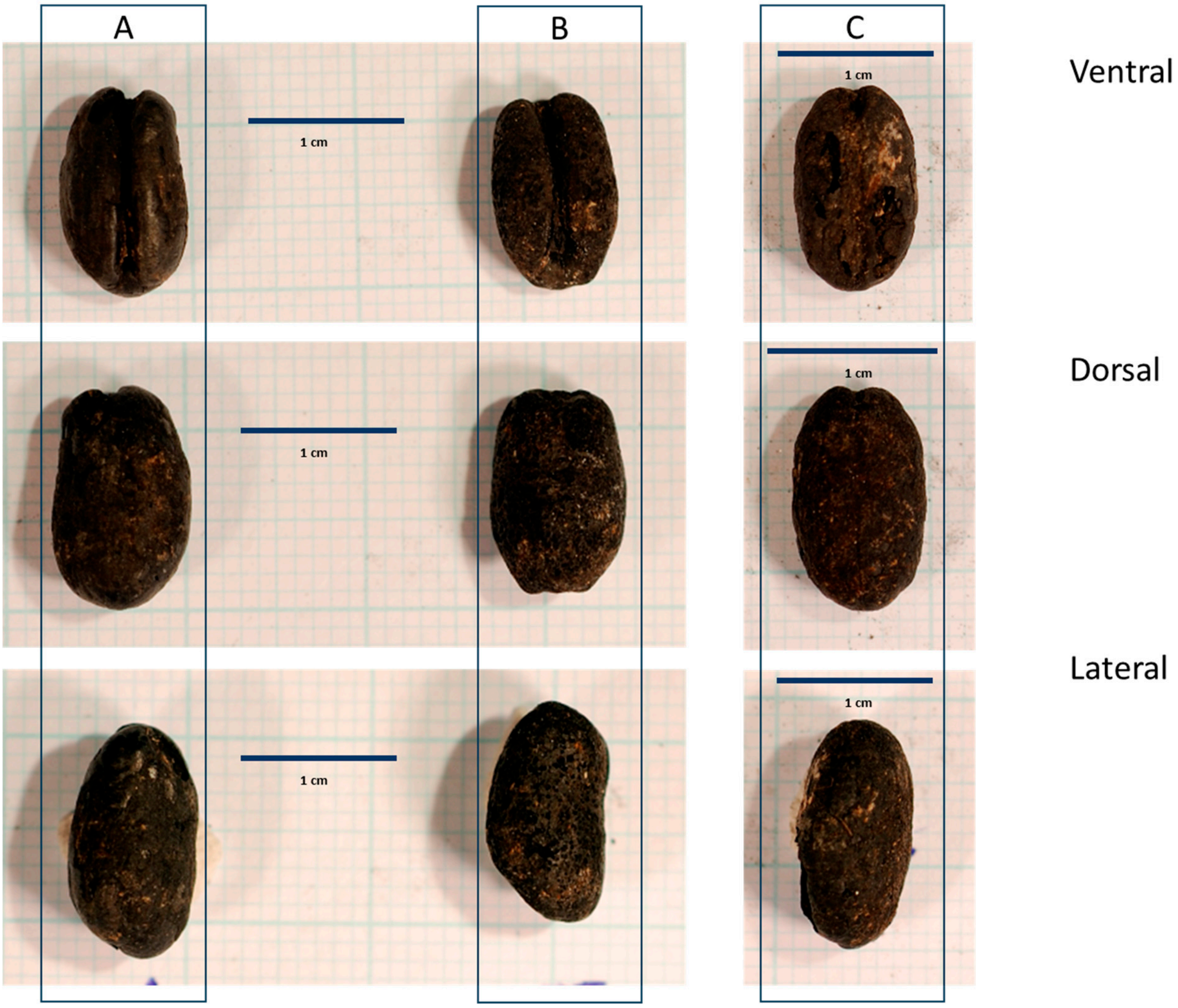


Figure 3. *Phoenix* seeds recovered from pre-Hispanic archaeological contexts at Sobrado de los Gomeros site (La Gomera, Canary Islands, Spain). Photographs by J. Morales and D. Rivera. Scale bar = 10 mm.

2.3. Morphometric Seed Analysis

Our comprehensive study analyzed 1096 seed samples comprising 982 modern, 103 archaeological, and 11 fossilized samples. Each sample comprised 15 individual seeds in the case of modern specimens, whereas archaeobotanical and fossil samples contained a smaller and more variable number of seeds. This variability resulted in an approximate average of 10 seeds per sample, with a total of 10,066 seeds analyzed—9336 of which originated from the 982 modern samples. This sample size exceeds previous research by Rivera et al. [5], primarily due to an exhaustive collection of *P. canariensis* samples from the Canary Islands and international locations (the list of samples analyzed, and their taxonomic identity, is available as Table S1). With the exception of type specimens, fossils, and archaeological samples, all modern samples are preserved in the Herbarium UMH and the Spanish Palm Germplasm Bank at the Escuela Politécnica Superior of Orihuela, Universidad Miguel Hernández de Elche (Spain), initially funded by the National Institute for Agricultural Research (INIA). The bank was established to facilitate the collection, propagation, preservation, and characterization of *Phoenix* species and other related palms. Currently, the Palm Germplasm Bank houses over 600 living accessions, representing 19 species and subspecies, as well as 4 interspecific hybrids [17]. As of 2024, the National

Phoenix Collection has documented 1675 accessions, highlighting the extensive range of palm genetic resources stored in this repository.

Modern seed samples underwent standardized processing: desiccation to 20% moisture content using a Sicco Auto-Star Desiccator (Bohlender GmbH, Grünsfeld, Germany), preservation with Scharlau silica gel with a humidity indicator at 5 °C in two Liebherr K 42 refrigerators (Liebherr-International Austria GmbH, Bischofshofen, Austria), and taxonomic verification through morphological characterization of mother plants and germinated specimens. Samples represented *Phoenix* species, cultivars, and four outgroup taxa, with approximately 15 seeds per sample. Voucher specimens are deposited in the UMH herbarium and carpological collection [50].

Seed morphological characterization employed a comprehensive 20-descriptor protocol: three quantitative metrics (length, breadth, depth), two allometric relationships (breadth/length ratio and depth/breadth ratio), one volumetric dimension (length × breadth × depth), and 14 qualitative attributes with 41 distinct states. The morphological characteristics of seeds include various shapes such as ovoid-conical-triangular, ellipsoidal, elliptic-oblong, cylindrical-linear, globose, hemispherical, and fusiform. The apex of the seed exhibits different forms, including obtuse, acute, retuse, oblique, and truncate. Similarly, the seed base can be obtuse, acute, oblique, or truncate. The surface texture of seeds is classified as either smooth or rugose.

Regarding other surface features, seeds may present longitudinal striations. Wrinkling patterns can be irregular or transversely grooved. The position of the micropyle is either central or basal. The ventral groove varies in prominence and shape, appearing as either not pronounced, V-shaped, or U-shaped. Seed curvature is described as dorsoventrally bent or straight. Additionally, some seeds exhibit protuberances in the form of ridges and/or wings.

Although the parchment layer and seed color, and the base or apex being mucronate or not, are relevant descriptors in botanical studies, they are not considered as identity-defining characteristics in archaeological seed samples due to degradation over time [5].

Quantitative measurements utilized a Mitutoyo Absolute Digimatic 500-202-21 digital caliper (0.01 mm precision, accuracy ±0.02 mm) (Mitutoyo Europe GmbH, Neuss, Germany), while qualitative characteristics were analyzed using an Olympus SZ11 trinocular stereomicroscope equipped with wide-field 10×/22 eyepieces and a continuous zoom magnification system (zoom ratio 6.1:1) providing a magnification range of 1.8× to 11×. The microscope was mounted on an integrated Olympus SZ-STU1 universal stand with an SZ-STB1 boom stand system, offering enhanced stability and precise three-dimensional positioning capability (Olympus Corporation, Tokyo, Japan). Image acquisition was performed using a Leica EC3 digital camera (resolution 3.1 megapixels) featuring a 1/2-inch CMOS sensor, mounted on the dedicated trinocular port for documentation and analysis. (Leica Camera AG, Wetzlar, Germany) and macro photographic documentation (Lumix FZ60 camera with a Leica DC lens, Panasonic Holdings Corporation, Osaka, Japan).

The analytical methodology entailed converting individual seed measurements into discrete classes and corresponding frequencies, thereby enabling comparative analyses beyond mere average values. Continuous parameters were categorized into four to six classes, facilitating an integrated quantitative–qualitative matrix analysis. Consequently, a comprehensive database was developed that systematized 1096 seed samples across 67 descriptors, capturing both the frequencies of qualitative states and the classes of quantitative parameters. Additionally, archaeological seed samples were preliminarily evaluated for preservation state, with morphological characteristics being documented from scaled imagery.

2.4. Experimental Carbonization

Because the archaeological seeds recovered presented evidence of carbonization, to comprehensively assess the impact of carbonization on *P. canariensis* seed morphology, an experimental protocol was developed utilizing microwave-assisted carbonization (Bluesky-Carrefour, Massy, France). Microwave irradiation, increasingly employed in organic sample processing, offers advantages including rapid processing and minimal physical sample degradation [51,52].

The experimental design involved systematically carbonizing modern, desiccated, *P. canariensis* seeds. Two *P. canariensis* seed samples—one from *P. canariensis* var. *canariensis* population cultivated in the Campus de Espinardo of the Murcia University and another commercial (Vilmorin, Paris, France)—were subjected to controlled carbonization. Twelve seeds were randomly selected, comprehensively characterized prior to carbonization, and then heated at full power (1000 W) for 10 min until carbonization.

Post-carbonization, each seed was re-examined to quantify morphological transformations. Preliminary analyses revealed primary alterations in dimensional metrics and chromatic properties. A simple linear regression model (Figure 4A–C) was developed to mathematically characterize seed metamorphosis, represented by the generalized formula $y = \beta 1 + \beta 2x + \epsilon$, enabling quantitative documentation of carbonization-induced morphological variations. Where each term represents:

- y: the dependent variable (outcome or response variable).
- $\beta 1$: the intercept (the value of y when $x = 0$).
- $\beta 2$: the slope coefficient (the change in y for a one-unit increase in x).
- x: the independent variable (predictor or explanatory variable).
- ε: the error term, which represents the unexplained variation in y that is not accounted for by the linear relationship with x. It accounts for randomness, measurement errors, or influences from other variables not included in the model. It ensures that the equation acknowledges real-world data variability rather than assuming a perfect deterministic relationship between x and y.

For L, length Equation (1)

$$\beta_1 = -0.54 \pm 0.43 \text{ mm};\ \beta 2 = 0.986 \pm 0.031;\ \sigma = 0.25 \text{ mm} \tag{1}$$

For B, breadth Equation (2)

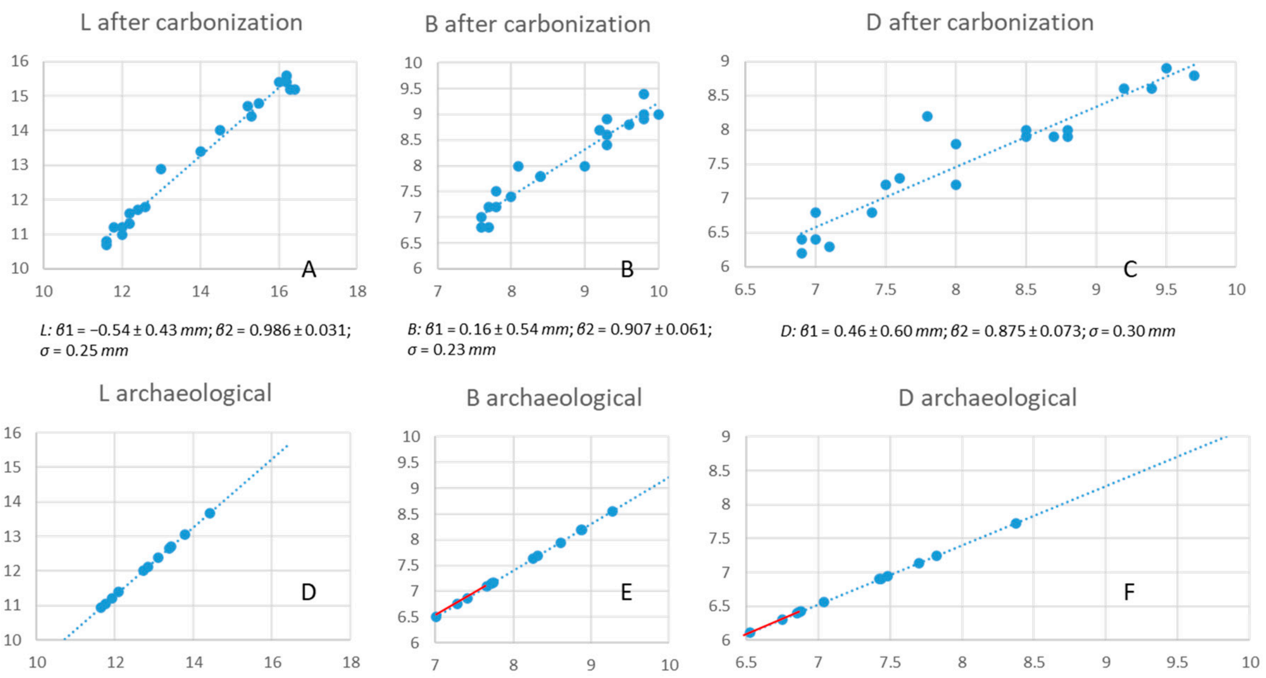
$$\beta_1 = 0.16 \pm 0.54 \text{ mm};\ \beta 2 = 0.907 \pm 0.061;\ \sigma = 0.23 \text{ mm} \tag{2}$$

For D, depth Equation (3)

$$\beta_1 = 0.46 \pm 0.60 \text{ mm};\ \beta 2 = 0.875 \pm 0.073;\ \sigma = 0.30 \text{ mm} \tag{3}$$

where y is the value of the parameter after carbonization, x is the value before carbonization and σ is the standard error.

The regression models developed in this study enable the reconstruction of carbonized seed dimensions by statistically inferring their original morphological characteristics. This methodological approach facilitates direct comparative analyses between archaeological and modern seed specimens.



L after carbonization

B after carbonization

D after carbonization

$L: \beta 1 = -0.54 \pm 0.43\ mm; \beta 2 = 0.986 \pm 0.031; \sigma = 0.25\ mm$

$B: \beta 1 = 0.16 \pm 0.54\ mm; \beta 2 = 0.907 \pm 0.061; \sigma = 0.23\ mm$

$D: \beta 1 = 0.46 \pm 0.60\ mm; \beta 2 = 0.875 \pm 0.073; \sigma = 0.30\ mm$

L archaeological

B archaeological

D archaeological

Figure 4. Dimensional changes in *Phoenix canariensis* seeds due to carbonization and reconstruction of original archaeological seed dimensions. (**A**–**C**) Linear regression models showing the relationship between pre- and post-carbonization measurements for experimentally charred seeds, where L = length, B = breadth, D = depth. Regression equation: $y = \beta_1 + \beta_2 x + \epsilon$, and σ = standard error. (**D**–**F**) Application of regression models to estimate original dimensions of archaeological seeds. In all plots, x and y axes show dimensions in millimeters. (**A**–**C**): x = dimensions of desiccated seeds before carbonization, y = dimensions after carbonization. (**D**–**F**): x = reconstructed original dimensions, y = measured dimensions of archaeological seeds. Red lines indicate values falling below the experimental model predictions.

To rigorously assess the archaeological *Phoenix* seed samples, a comprehensive analytical strategy was implemented encompassing four distinct methodological scenarios:

- Site-level analysis using original, uncorrected data (five aggregated samples).
- Individual seed-level analysis using original, uncorrected data (twelve discrete samples).
- Site-level analysis incorporating carbonization-induced morphological corrections (five aggregated samples).
- Individual seed-level analysis incorporating carbonization-induced morphological corrections (twelve discrete samples).

This multi-scenario approach enhances methodological robustness by mitigating potential systematic biases and facilitating a nuanced interpretation of archaeological seed morphological variability.

2.5. Data Analysis

2.5.1. Classification of Samples

The morphometric parameters were systematically transformed into a comprehensive dissimilarity matrix utilizing DARwin V.6.0.17 (25 April 2018) software [53–55].

To compare numerous samples, each consisting of 15 seeds, we constructed an ordered sequence of character states encompassing qualitative traits, discrete quantitative traits, and discretized quantitative traits. Each individual cell within this sequence represents the relative frequency of seeds in the sample that fall into the corresponding category. Consequently, each sample was characterized by an artificial spectrum of these frequencies. Two samples were considered identical if they exhibited identical values across all corresponding cells in the sequence. This implies that, in a series of samples, each column of cells was treated as a distinct variable, regardless of whether it corresponded to a categorical trait, a discrete set, or a discretized continuous set. Consequently, the data matrix maintains a consistent number of variables across all samples.

An effective discretization method should partition the domain of a continuous variable into intervals such that their cut points are close to decision boundaries and their widths are sufficiently large. This requirement is not difficult to achieve for many data sets; as a result, a wide variety of discretization methods can exhibit similar performance regardless of their complexities [56]. Discretization of continuous variables is a crucial topic in data preprocessing and machine learning, often improving classification performance in algorithms such as Support Vector Machines, Random Forests, and Naive Bayes [57]. Beyond transforming continuous values into discrete ones, discretization serves as a variable selection method, particularly in high-dimensional genomic and proteomic data. While it simplifies data and accelerates learning, it may also cause information loss [58,59]. The main challenge is determining optimal thresholds for discretization. Fayyad and Irani [60] introduced an entropy-based method that selects partition points to minimize joint entropy between continuous and classification variables, enhancing feature selection. Dougherty, Kohavi, and Sahami [61] compared discretization methods and found that a Minimum Description Length (MDL) metric led to improved classifications in decision trees and Naive Bayes classifiers. Hong [62] proposed a K-nearest neighbor clustering-based metric to determine the optimal number of partitions. Decision trees also facilitate discretization by selecting cut-points that maximize class separation using entropy or Gini impurity [58]. Ultimately, the classification performance gains from discretization stem primarily from variable selection rather than merely transforming continuous data into discrete values.

Here, we selected partition points based on the assumption that our continuous variables follow a Gaussian distribution. To preserve this distributional pattern, the continuous variable was divided into equal intervals, ensuring that the resulting discrete categories align as closely as possible with the expected Gaussian structure.

We implemented a nuanced data reduction strategy by consolidating quantitative and qualitative morphological characteristics into a single analytical matrix. Quantitative variables were discretized into predefined classes to standardize comparative analysis. For example, the breadth-to-length ratio (B/L) was systematically categorized into eight hierarchical ordinal strata, defined by progressively refined quantitative thresholds ranging from 0.1 to $\leq$0.9 in increments of 0.1. This approach ensures a granular and methodical segmentation of the continuous variable, facilitating nuanced analytical distinctions.

Similarly, other quantitative variables were categorized into graduated intervals:

- Length (L): 15 intervals, ranging from 4 to $\leq$60 mm.
- Breadth (B): 9 intervals, ranging from 3 to $\leq$19 mm.
- Depth (D): 6 intervals, ranging from 0.1 to $\leq$18 mm.
- Depth-to-breadth ratio (D/B): 6 intervals, ranging from 0.3 to $\leq$1.5.
- Volumetric dimension (L × B × D): 13 intervals, ranging from 36 to $\leq$1200 mm^3.

This ordinal classification enables precise quantitative stratification while maintaining a structured, incremental progression of defined intervals.

The matrix construction followed a meticulous protocol: each row, totalizing 67 cells, represented individual seed samples, and columns corresponded to both 26 quantitative class intervals and 41 qualitative character states. Cell values represent percentage frequencies of seeds within each defined parameter range or qualitative state, calculated from the primary dataset. Each cell within a row indicates the proportion of seeds of this particular sample displaying specific quantitative or qualitative characteristics.

The comparative metric employed was the chi-square dissimilarity index, which is methodologically optimal for this data typology [53–55]. The chi-square dissimilarity index is particularly well-suited for analyzing data structured as frequency counts, such as the matrix in this study, where each cell represents the percentage frequency of seeds exhibiting specific quantitative classes or qualitative character states. This index measures the divergence between observed and expected frequencies, effectively capturing the dissimilarity between samples based on their distributional characteristics. By accounting for both the magnitude and distribution of frequencies across categories, the chi-square dissimilarity index provides a nuanced assessment of differences between samples, making it a methodologically optimal choice for this type of data [63,64].

This index quantifies each variable's x_{ik} value through its contribution to the aggregate x_i across all variables, facilitating a comprehensive profile comparison Equation (4).

The underlying comparative principle asserts that seed samples are considered morphometrically equivalent when their frequency distributions are statistically identical across all characterized classes and states.

$$d_{ij}^2 = \sum_{k=1}^{K} \left(\frac{x_{ik}}{x_{i.}} - \frac{x_{jk}}{x_{j.}} \right)^2 \left(\frac{x_{..}}{x_{.k}} \right) \tag{4}$$

For $j \neq i$, let d_{ij} represent the dissimilarity metric between sampling units i and j, where:

$i, j \in \{1, 2, \ldots, \mathrm{N}\}$, with N = 1096 representing the total number of samples.

$k \in \{1, 2, \ldots, \mathrm{K}\}$, with K denoting the number of bins or variables (columns)

This mathematical notation precisely defines the pairwise dissimilarity calculation across the comprehensive dataset, enabling systematic comparative analysis of morphometric characteristics Equation (5).

The formulation establishes a rigorous framework for quantitative intercomparison, where each unique pair of samples (i and j) can be systematically evaluated through their multivariate morphological descriptors.

$$K = \sum_{c=1}^{C=67} K_c \tag{5}$$

Let the following notation define the multivariate morphometric analysis parameters:

- K: Total number of variables
- $c \in \{1, 2, \ldots, \mathrm{C}\}$, where C = 67 represents the descriptive morphological parameters
- K_c: Number of states for each descriptor c (approximately 10 states per descriptor)
- x_{ik}, x_{jk}: Specific values of variable k for sampling units i and j, respectively
- $x_{i}.$: Mean value for sampling unit i Equation (6)
- $x_{j}.$: Mean value for sampling unit j
- $x_{.k}$: Mean value for variable k Equation (7)
- $x_{..}$: Comprehensive overall mean Equation (8)

$$x_{i.} = \frac{1}{K} \sum_{k=1}^{K} x_{ik} \tag{6}$$

$$x_{.k} = \frac{1}{\mathrm{N}} \sum_{i=1}^{N} x_{ik} \tag{7}$$

$$x_{..} = \frac{1}{K} \sum_{k=1}^{K} x_{.k} = \frac{1}{\mathrm{N}} \sum_{i=1}^{N} x_{i.} = \frac{1}{NK} \sum_{i=1}^{N} \sum_{k=1}^{K} x_{ik} \tag{8}$$

This notation provides a precise mathematical framework for characterizing the intricate morphological variations across seed samples, enabling systematic multivariate statistical analysis.

The formulation allows for a comprehensive, standardized approach to quantifying morphometric diversity by establishing clear definitional parameters for each analytical component. The dissimilarity metric d_{ij} is operationalized as a normalized index bounded between 0 and 1, where:

- $d_{ij} = 0$ indicates complete morphological congruence, signifying that samples i and j are statistically indistinguishable across all analyzed variables
- $d_{ij} = 1$ represents maximal morphological divergence, indicating that samples i and j exhibit complete heterogeneity across the entire suite of descriptive parameters

This binary boundary condition establishes a rigorous quantitative framework for assessing morphological similarity and differentiation, enabling precise comparative analysis of seed sample characteristics. The metric allows researchers to systematically quantify the degree of morphological variation, facilitating nuanced taxonomic and ecological interpretations based on multivariate morphometric data.

To construct a comprehensive representation of morphological relationships, we employed a hierarchical clustering approach using an agglomerative hierarchical method. This technique systematically aggregates individual sampling units into progressively more inclusive clusters based on their morphometric dissimilarities [54].

The methodological approach aimed to approximate the complex dissimilarity matrix d through a tree-based distance representation δ. Hierarchical clustering methods are distinguished by three critical computational decisions at each iterative step:

- Definition of 'neighborhood' proximity.
- Algorithmic updating of the dissimilarity matrix.
- Estimation of intercluster edge lengths.

We employed the Ward criterion for updating the dissimilarity matrix, an approach that strategically minimizes within-group variance while maximizing between-group inertia. This method facilitates the formation of homogeneous clusters that accurately reflect the expected morphological diversity and align closely with anticipated taxonomic differentiation. Ward's minimum variance criterion, introduced by Joe H. Ward Jr. in 1963 [65], represents a robust hierarchical clustering technique, particularly suited for dissimilarity matrices with values ranging from 0 to 1. By systematically minimizing within-cluster variance, this method provides a rigorous mathematical framework for clustering, ensuring statistically coherent groupings. The methodology distinguishes itself through several critical theoretical contributions:

- Objective Function Methodology: Ward's approach is fundamentally grounded in an optimization principle that minimizes the incremental variance resulting from cluster mergers. This mathematical precision offers a transparent and systematic mechanism for hierarchical clustering, enabling researchers to objectively quantify cluster formation [66].
- Variance Minimization Strategy: By emphasizing the reduction of within-cluster variance, the method preferentially generates compact, spherical clusters. This characteristic is particularly valuable when investigating complex dissimilarity matrices, as it facilitates the identification of inherent data groupings [67].
- Metric Adaptability: Although initially conceived for squared Euclidean distances, Ward's method demonstrates remarkable versatility, allowing adaptation to diverse distance metrics and dissimilarity matrices [68].

The theoretical development of this approach can be traced through several seminal publications. Ward's original paper [65] introduced the fundamental agglomerative hierarchical clustering procedure based on an optimization objective, laying the groundwork for the minimum variance method. Subsequent scholarly contributions significantly refined and expanded its theoretical understanding. Notably, Murtagh and Legendre [69] dispelled previous misconceptions about the method, providing researchers with a comprehensive explication of its implementation across various distance matrix configurations. Székely and Rizzo [70] further extended the method's theoretical boundaries by exploring potential generalizations and metric adaptations. In conclusion, Ward's minimum variance criterion remains a robust and versatile approach to hierarchical clustering [71].

The resulting hierarchical structure was graphically rendered using FigTree version 1.4.3 [72], providing a visually accessible representation of the morphometric relationships among seed samples.

2.5.2. Identification of Samples

Given that the taxonomic classification of most samples within each cluster or morphotype was known a priori, and that these samples originate from previously identified sources based on conventional vegetative and reproductive characters commonly used in *Phoenix* taxonomy, it can be probabilistically inferred that the unclassified specimens (i.e., archaeobotanical materials) within a clearly defined taxonomic cluster belong to the same taxonomic group. This inference is supported by the low proportion of unidentified samples within each cluster.

However, it is crucial to recognize that some morphological clusters may include samples from multiple species or varieties, thereby rendering them taxonomically heterogeneous. As a result, the botanical identification of archaeological samples, particularly within taxonomically diverse groups, requires a nuanced, quantitative approach that is grounded in probabilistic methodologies.

Conditional probabilities provide a logical and intuitive means of integrating prior empirical knowledge to constrain epistemic uncertainty. The Bayesian framework offers a particularly robust analytical approach for systematically evaluating the potential taxonomic affiliation of seeds within a given morphotype and/or taxon.

The hypothetical space (H_i) for *Phoenix* seed identification comprises 24 mutually exclusive and exhaustive operative taxonomic units, which can be systematically categorized into three principal groups (Table 1): *Phoenix canariensis* H.Wilpret complex [*P. canariensis* var. *canariensis, P. canariensis* var. *porphyrococca* (Red Date Group), *P. canariensis* Wildpret's Large Date Group, *and P.* × *arehuquensis (P. canariensis* × *P. reclinata* hybrid)]. *Phoenix dactylifera* L. [*P. dactylifera* Eastern Group, *P. dactylifera* Western Group, and *P. dactylifera* hybrid variants]. And additional *Phoenix* species and cultivars.

It is essential to distinguish between the number of taxonomic units and the number of recognized morphotypes, as seeds from a single species may be distributed across multiple morphological categories, while a single morphotype may also include seeds from different species.

Bayesian probability provides a quantitative framework for assessing propositional plausibility in cases where incomplete empirical data prevent definitive categorical classification. This probabilistic approach operates on a continuous scale from 0 to 1, where 0 denotes absolute certainty of falsehood and 1 represents absolute certainty of truth [58].

Table 1. Frequencies of *Phoenix* taxa in the ensemble of seeds analyzed.

Taxa	Seeds Analyzed	Prior Probability $p(H_i \mid I)$
P. canariensis H.Wildpret var. *canariensis*	2808	0.301
P. canariensis var. *porphyrococca* Vasc. & Franco	135	0.014
P. canariensis Wildpret's Large Date Group	928	0.099
P. × *arehuquensis* (*P. canariensis* × *P. reclinata* hybrid) (*)	57	0.006
P. canariensis Subtotal	3928	0.421
P. dactylifera Eastern group	867	0.093
P. dactylifera hybrids	233	0.025
P. dactylifera Western group (**)	2749	0.295
P. dactylifera Subtotal	3849	0.413
P. 'Palmer'	59	0.006
P. abyssinica Drude.	15	0.002
P. acaulis Roxb.	61	0.007
P. andamanensis auct.	32	0.003
P. arabica Burret	44	0.005
P. caespitosa Chiov.	15	0.002
P. farinifera Roxb.	47	0.005
P. loureiroi Kunth	294	0.032
P. loureiroi var. *hanceana*	78	0.008
P. paludosa Roxb.	62	0.007
P. pusilla Gaertn.	5	0.001
P. reclinata Jacq.	161	0.017
P. roebelenii O'Brien	156	0.017
P. rupicola T.Anderson	80	0.009
P. rupicola 'Medipalm'	8	0.001
P. sylvestris (L.)Roxb.	178	0.019
P. theophrasti Greuter	264	0.028
P. other Subtotal	1559	0.166

(*) P. × arehuquensis [57]; (**) Including P. atlantica and P. iberica.

In Bayesian probability theory, the framework for probabilistic inference involves three key components: the hypothesis (H_i), the observed data (D), and the background information (I) that contextualizes their relationship. The primary objective is to assess the relative veracity of a hypothesis considering empirical evidence. We use the general theorem Bayes—Laplace, which, mathematically expressed, can be represented as Equation (9)

$$p(H_i|D,I) = p(H_i|I).\frac{p(D|H_i,I)}{p(D|I)} \tag{9}$$

Bayes' theorem provides a rigorous mathematical mechanism for dynamically updating probabilistic assessments as new information becomes available. The posterior probability $p(H_i \mid D,I)$ represents the refined probability of a hypothesis after incorporating observational data (D) to the background information (I), fundamentally transforming our understanding through systematic probabilistic reasoning. The posterior probability is mathematically derived through a structured computational process:

- Prior probability $p(H_i \mid I)$: The initial probabilistic assessment of the hypothesis based on pre-existing knowledge (background information).
- Likelihood $p(D \mid H_i,I)$: The probability of observing the specific data given the hypothesis and background information.

- Normalization constant $p(D \mid I)$: A probabilistic scaling factor that ensures the total probability across all hypotheses equals unity, expressed by the marginal probability of data (*D*) given the background information (*I*).

The prior probability $p(H_i \mid I)$ represents the most subjectively determined component of Bayesian inference. However, this subjectivity is not a methodological weakness but a transparent feature of the approach. By explicitly stating initial assumptions, Bayesian methodology ensures that all probabilistic reasoning elements are openly articulated and criticizable.

The likelihood function $p(D \mid H_i,I)$, alternatively conceptualized as the sampling distribution, quantifies the probative value of the observed data under a specific hypothetical framework. The global likelihood $p(D \mid I)$ serves a normalization function, integrating the probabilities across all potential hypotheses to maintain probabilistic coherence.

Mathematically, this can be expressed as Equation (10):

$$p(D|I) = \sum_{i=1}^{n} p(H_i|I)p\ (D|H_i, I) \tag{10}$$

This formulation facilitates a systematic, transparent approach to probabilistic inference, where each stage of reasoning is explicitly defined and mathematically tractable.

In this context, H_i represents the hypothetical adscription to taxonomic groups, specifically encompassing the 24 operative taxonomic units including species, subspecies, and cultivar groups. The data (*D*) derives from comprehensive seed morphological and taxonomic analyses, focusing on the assigned archaeological seed morphotypes and their corresponding taxonomic representations.

For the background information (*I*), methodologically, two complementary approaches to prior probability assignment are viable:

- Principle of Indifference: Uniform probability distribution across 24 taxonomic units, with $p(Hi) = 1/24$ for each hypothesis. The Principle of Indifference (alternatively termed the Principle of Insufficient Reason)—a fundamental probabilistic heuristic. When confronted with *N* mutually exclusive and exhaustive propositions (*H*) and an absence of discriminating evidence, this principle prescribes an equiprobable distribution, such that each proposition is assigned an equal probability $p(H_i) = 1/N$.
- Empirical Frequency-Based Priors: Alternatively, one can establish prior probabilities based on the observed frequency distribution of taxonomic groups within the comprehensive seed ensemble utilized in the analysis (Table 1).

The frequency-based approach offers a more nuanced prior probability specification, grounded in the empirical composition of the reference seed collection. This method leverages existing taxonomic representation to modulate initial probabilistic assessments, thereby introducing a degree of informative constraint into the Bayesian inference framework.

$$p(H_i) = \frac{n_i}{\sum_{i=1}^{24} n_i} \tag{11}$$

In this formulation, n_i represents the cardinal count of seeds belonging to a specific taxonomic unit t_i. Consequently, the prior probability $p(H_i)$ is directly proportional to the relative frequency of each taxonomic group within the comprehensive seed collection, mathematically expressed as:

$$p(H_i) = n_i/N$$

where:

- n_i denotes the number of seeds associated with taxonomic unit t_i

- N represents the total number of seeds in the analytical ensemble
- $p(H_i)$ quantifies the prior probability as the frequency-weighted representation of each taxonomic group

This approach transforms the raw taxonomic enumeration into a probabilistic framework, wherein the frequency of occurrence serves as the foundational metric for prior probability estimation. By directly mapping the empirical seed distribution onto the probabilistic space, we establish a data-driven foundation for subsequent Bayesian inference.

The frequency-based prior method offers a rigorous, empirically grounded alternative to the Principle of Indifference, utilizing the intrinsic taxonomic composition of the seed collection to calibrate initial probabilistic assessments.

3. Results

3.1. Key Diagnostic Characters

Dimensional morphometrics emerged as a critical taxonomic discriminant, with seed size serving as a primary classificatory parameter (Table S2). The quantitative analysis focused on fundamental seed metrics, including length, breadth, and volumetric dimensions, with this last being latter calculated as the product of length × breadth × depth (expressed in mm^3).

A volumetric analysis revealed distinct clustering patterns that provided significant taxonomic insights. Large-volume morphotypes (1–2 and 6–8) were characteristic of *P. dactylifera* specimens, while morphotype 11 notably encompassed relatively large seeds from *P. canariensis* and Miocene *Phoenix bohemica* fossils. Approximately 50% of these samples were associated with the “Wildpret’s Large Date Group,” with the remainder representing typical *P. canariensis* specimens (Table S2).

In contrast, morphotypes with minimal seed volumes (less than 1000 mm^3) exhibited the highest degree of taxonomic heterogeneity. This pronounced variability complicated the classification of smaller *P. canariensis* seeds, which were distributed across morphotypes 13, 14, and 18. These findings underscore the analytical challenges inherent in the identification of archaeological *Phoenix* seeds, particularly when dealing with morphologically ambiguous or poorly preserved specimens (Table S2).

Beyond dimensional analysis, qualitative morphological descriptors posed additional challenges due to preservation constraints in archaeological samples. However, nine morphological attributes emerged as particularly informative: (1) seed shape (ellipsoidal in *P. canariensis* var. *canariensis* and var. *macrocarpa*, elliptic-oblong in *P. canariensis* var. *porphyrococca*); (2) apex morphology (obtuse in all *P. canariensis* varieties); (3) base configuration (truncate in all *P. canariensis* varieties); (4) surface texture (smooth in *P. canariensis* var. *canariensis* and var. *macrocarpa*, smooth but occasionally rugose in *P. canariensis* var. *porphyrococca*); (5) striation patterns (longitudinal striations in all *P. canariensis* varieties); (6) micropyle positioning (central in all *P. canariensis* varieties); (7) ventral groove characteristics (predominantly U-shaped in all *P. canariensis* varieties, but also occasionally not pronounced or V-shaped); (8) seed curvature (straight in all *P. canariensis* varieties); and (9) wing morphology (absence of ridges and wings in all *P. canariensis* varieties) (Table S2, Figure 1).

By integrating dimensional and morphological data, this study has constructed a robust, multidimensional taxonomic classification framework for archaeobotanical *Phoenix* seed specimens (Table S2). This methodological approach underscores the analytical rigor required in contemporary archaeobotanical research, balancing quantitative precision with nuanced morphological interpretation. By synthesizing comprehensive morphometric analysis with careful consideration of preservation-related limitations, this study provides a refined and systematic approach to the taxonomic classification of archaeological *Phoenix* seeds.

3.2. Morphotypes and Species

The morphological diversity of *Phoenix* seeds closely aligns with the taxonomic patterns delineated by Rivera et al. [5], revealing a complex and nuanced morphological landscape. A comprehensive analysis identified 23 morphological groups, with 20 directly corresponding to *Phoenix* species and species aggregates (Figure 5).

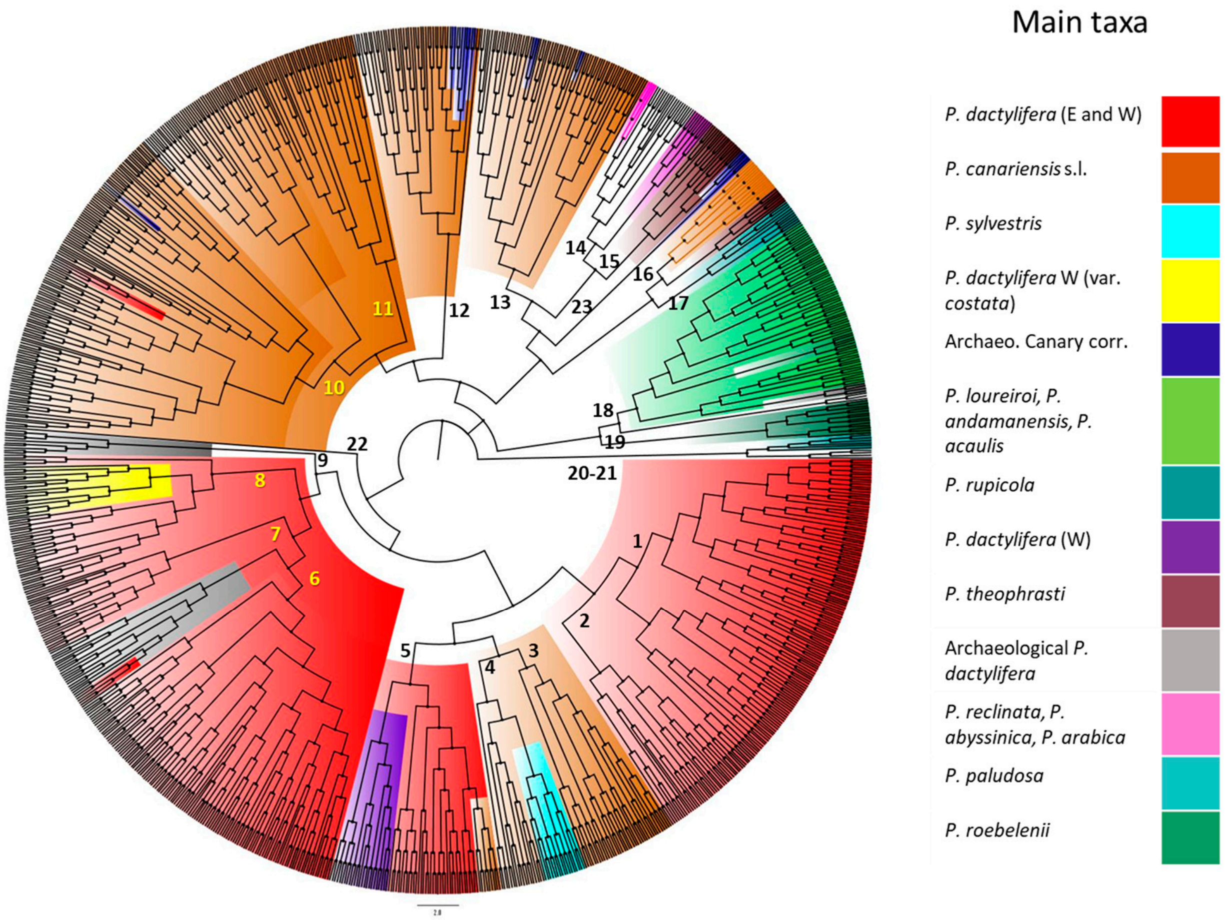


Figure 5. Circular dendrogram of *Phoenix* morphotype relationships generated through agglomerative Ward's minimum variance clustering. Numbers indicate distinct morphotypes, with colors corresponding to different taxa (see Tables S2 and S3 for detailed morphotype descriptions and taxonomic assignments). Tree visualization generated using Darwin 6.0 and FigTree 1.42 based on morphometric data compiled through 22 April 2018 in file Seeds_21_1_2019Canary.xlx [53–55,73].

The taxonomic classification revealed remarkable heterogeneity, with morphotypes ranging from monospecific configurations to those encompassing multiple species (Table S3). Specifically, nine morphotypes represented single species, five incorporated two species, two included four species, and one morphotype encompassed each three, six, eight, or ten species. Three morphotypes contained exclusively archaeological and fossilized seed samples or outgroup taxa (*Washingtonia*, *Euterpe*, and *Chamaerops* seeds), rendering them unsuitable for identification purposes. This intricate classification highlights critical limitations in seed morphometric discrimination. Certain operational taxonomic units proved indistinguishable based solely on seed morphology, while some species, notably *Phoenix dactylifera* and *P. canariensis*, exhibited extraordinary morphological diversity across multiple morphotypes.

The morphological characteristics of *Phoenix reclinata* seeds reveal exceptional complexity with its seeds falling in clusters 14 and 16 to 19 (Figure 6).

Figure 6. Representative examples of *Phoenix* date palm morphotypes. (**A**) Morphotype 13, *P. canariensis*, Pájara, Fuerteventura, Spain; (**B**) Morphotype 12, *P. canariensis*, Colombres, Asturias, Spain; (**C**) Morphotype 11, *P. canariensis*, Jerez, Spain; (**D**) Morphotype 10, *P. canariensis*, Palais Carnolès, Menton, France; (**E**) Morphotype 3, *P. reclinata*, Rwanda, Riverside, USA; (**F**) Morphotype 15, *P. theophrasti*, Vai, Crete, Greece; (**G**) Morphotype 18, *P. loureiroi*, Kalimpong, India; (**H**) Morphotype 19, *P. reclinata*, USDA, Riverside, CA, USA; (**I**) Morphotype 19, *P. roebelenii*, Olocau, Valencia, Spain. Images by D. Rivera.

Seed samples from morphotypes 13–19 exhibit intriguing diversity, sparingly distributed with *P. reclinata*, *P. theophrasti* or a few samples of *P. dactylifera* clustered intermixed with *P. canariensis and P. roebelenii* seeds (Figure 6). These specimens consistently present diminutive dimensions, measuring less than 1000 mm^3, which introduces notable taxonomic disambiguation challenges, particularly when contrasted with the smaller seed types of *P. canariensis.*

The morphological profile of *Phoenix dactylifera* reveals extensive seed morphology variation, without significant overlap with *P. canariensis.* Although samples of both species occur, but with inequal proportions across morphotypes 3 to 5, 7, 9, 13–14, 16 and 18. Distinctive surface characteristics for *P. dactylifera* include rough surfaces, transversal striation, prominent wrinkles, and minimal longitudinal striation.

Phoenix canariensis exhibits canonical seed morphological characteristics: an ellipsoidal configuration with a truncated base, an obtuse (rarely truncated) apex, and a smooth surface. Additional defining features include longitudinal striations, a central micropyle, a U- or V-shaped ventral furrow, a straight and unbent orientation, and the absence of wings or crests.

Morphotype-specific nuances further elucidate taxonomic complexity. For example, Morphotype 3 presents an elliptic-oblong variant with slightly elongated dimensions and marginally divergent base-to-length index values. Morphotypes 3–4 and, notably, 10–13 comprehensively encompass the variability observed in modern *P. canariensis* seeds (Table S3, Figures 5 and 6), while Morphotype 15, characterized by *P. theophrasti*, remains distinguishable by its distinctive ovoid seed configuration and obtuse base morphology (Figure 6).

Geographical and archaeological distributions provide additional insights. Modern Canary Islands seed samples cluster in Morphotypes 10, 11, 12, and 13. Archaeological *P. canariensis* samples demonstrate consistent distribution, with Morphotype 12 exhibiting the highest prevalence (Table 2). Morphotype 15, associated with *P. theophrasti* (Figure 6), includes a single archaeological seed from Alto Garajonay (Table 2).

Table 2. Probabilistic Classification of Archaeological *Phoenix* Seed Specimens across Morphological Typologies under Integrated Analytical Conditions.

Sites	Island	Seed Numbers	10	12	13	15	23
Alto del Garajonay	La Gomera	4	-	0.875	-	0.125	-
Sobrado de los Gomeros	La Gomera	3	0.167	0.167	0.5	-	0.167
Cueva Pintada	Gran Canaria	2	-	1	-	-	-
Lomo de los Gatos	Gran Canaria	2	-	-	1	-	-
Guayedra	Gran Canaria	1	-	-	1	-	-

Methodological Note: The integrated analytical scenario represents the mean probability derived from corrected archaeological seed assemblages, encompassing both composite samples and individual seed specimens. Dimensional correction factors were empirically determined through experimental carbonization of contemporary *Phoenix canariensis* seeds to enable robust comparative analyses of uncharred and carbonized botanical remains. Probabilistic calculations assume an equiprobable scenario (p = 0.5) of seed provenance: either originating from a single botanical source or representing multiple discrete sources. Probability values are constrained within the standard statistical range of 0 to 1.

A marginal yet intriguing observation involves Morphotype 23, represented by a unique archaeological specimen from Sobrado de Los Gomeros. This seed exhibits morphological proximity to Morphotypes 15 and 13, further underscoring the complex interrelationships within *Phoenix* seed taxonomy.

The findings underscore the significant limitations of morphometric classification and emphasize the necessity for multifaceted taxonomic approaches. These approaches should include molecular data, when available, and the use of machine learning tools, which extend beyond traditional morphological analyses.

3.3. Identification of Phoenix Archaeological Seed Samples from the Canary Islands

Phoenix seed samples from archaeological sites on Gran Canaria and La Gomera exhibited morphological diversity across morphotypes 10, 12, 13, 15, 18, and 23, with variations depending on the analytical scenario (Table S4). To reconstruct the original seed dimensions, the present researchers applied algorithms that quantify the impact of carbonization.

The analysis explored four analytical scenarios, systematically combining single versus whole sample methods and original "carbonized" versus corrected "uncarbonized" datasets. Based on preliminary results, the "whole sample and corrected 'uncarbonized'" approach was identified as the most effective method (Table S4).

Only seed classifications derived from the corrected data were retained, enabling the reconstruction of dimensions prior to carbonization. To validate the standard linear regression model, a Bayesian framework based on Zellner's methodology [74–77] was employed.

The Bayesian regression model produced comparable results while also estimating the probability distribution for each inferred parameter Equation (12).

Please note that, in this context, the symbol $\propto$ means 'is proportional to'.

$$p(x|y_0DI) \propto p(x|DI)p(y_0|xDI) \propto p(y_0|xDI) \tag{12}$$

This probabilistic approach demonstrated particular robustness when the prior was relatively uninformative (high standard deviation) and the regression exhibited high accuracy, as illustrated in the representative probability distributions presented in Figure 7A,B, in contrast to Figure 7C,D. This methodological approach enables nuanced interpretation of archaeological seed morphometrics, surpassing traditional linear analytical techniques.

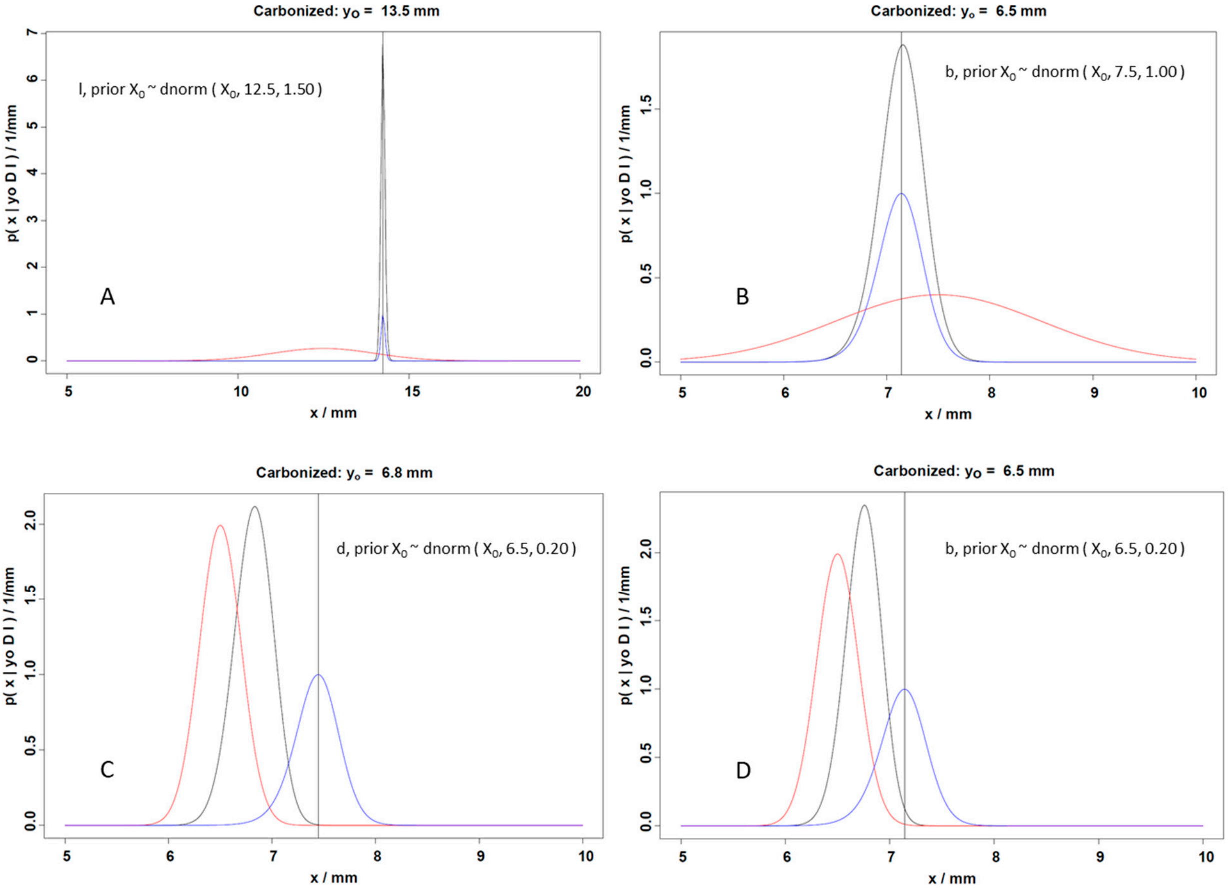


Figure 7. Examples of Bayesian predictive distributions for desiccated seed parameters, given the same parameters observed in carbonized seeds. (**A**) Displays a predictive distribution for length (l); (**B**) Represents the posterior distribution of breadth (b); (**C**) Depicts the posterior distribution of depth (d); (**D**) Represents the posterior distribution of breadth (b) with a much narrower prior standard deviation, Abbreviations: *l* (length), *b* (breadth), *d* (depth). Graph Elements and Color Coding: The red curve represents the prior probability distribution, $p\ (x/DI)$, which encodes prior knowledge about the parameter of interest (x) based on the experimental design or external data sources. The blue curve denotes the likelihood function, $p(y_0/xDI)$, which represents how the observed data (y_0) informs the relationship between the measured parameter and the prior distribution. The black curve illustrates the posterior predictive distribution, $p(x/y_0\ DI)$, which is proportional to $p(x/DI)p(y_0/xDI)$, integrating prior knowledge with observed data to update beliefs about the parameter.

Figure 7 presents four panels (A–D), each corresponding to a specific parameter (length, breadth, or depth), demonstrating the application of Bayesian analysis to predict original seed dimensional characteristics from carbonized archaeological material.

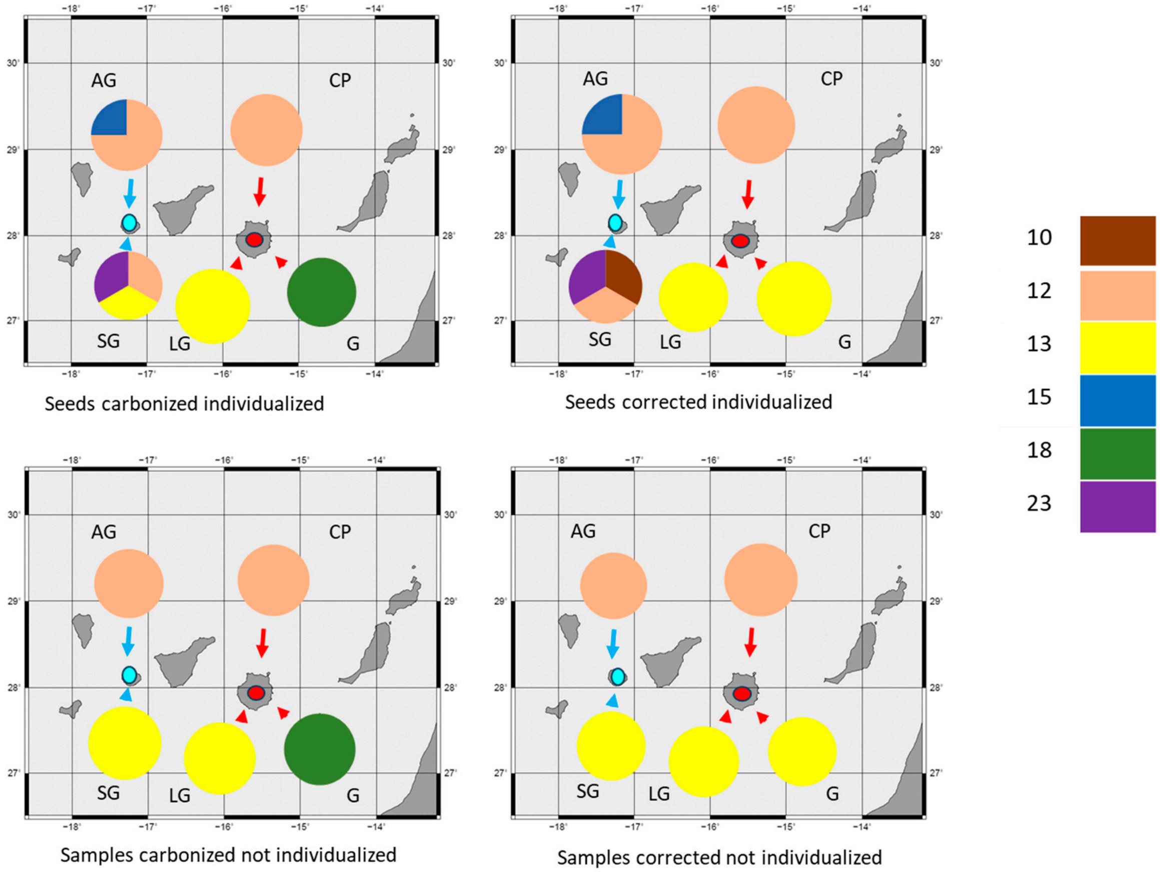
- Panel A: Displays a predictive distribution for length (l), given a dnorm(X_0, 12.5, 1.50) prior. With a prior centered around X_0 = 12.5 mm and a relatively high standard deviation (1.50), the y-axis represents probability density, and the x-axis represents length (x) in millimeters. The posterior (black curve) aligns closely with the observed data, indicating that the likelihood strongly influences the posterior due to the narrow spread of the likelihood function (blue).
- Panel B: Represents the posterior distribution of breadth (b), given a dnorm(X_0, 7.5, 1.00) prior. With a prior centered around X_0 = 7.5 mm and moderate standard deviation (1.00), the posterior distribution, where the carbonized seed dimension (Y_0) is 6.5 mm, shifts significantly compared to the prior, reflecting an interplay between prior assumptions and observed data.
- Panel C: Depicts the posterior distribution of depth (d), given a dnorm(X_0, 6.5, 0.20) prior. With a prior centered around X_0 = 6.5 mm and a low standard deviation (0.20), the narrow prior strongly influences the posterior, where the carbonized seed dimension (Y_0) is 6.8 mm, which aligns closely with the prior distribution.
- Panel D: Also pertains to breadth (b) and thus shows the posterior distribution of breadth, given a dnorm(X_0, 6.5, 0.20) prior. With a prior centered around X_0 = 6.5 mm and a much narrower prior standard deviation (0.20), the prior significantly restricts the posterior's range, where the carbonized seed dimension (Y_0) is 6.5 mm.

These panels demonstrate how Bayesian updating adapts prior distributions based on new evidence (likelihood), emphasizing the relative influence of prior assumptions and data quality on posterior distributions. A tighter prior standard deviation results in less influence from the observed data (Figure 7C,D), whereas a broader prior allows for greater adjustment based on the likelihood function (Figure 7A,B).

This methodology, illustrated in Figure 7, is crucial for accurately modeling seed traits when direct measurements are limited or noisy. By leveraging prior knowledge and observational data, this approach ensures robust and precise estimations of seed length, breadth, and depth, facilitating downstream applications in taxonomy, agriculture, and evolutionary studies. This Bayesian framework underscores the power of combining prior knowledge with observed evidence to refine predictions about biological parameters, as clearly illustrated in Figure 7.

To address inherent sampling uncertainties in archaeological *Phoenix* seeds, and specifically, whether specimens originated from single or multiple individuals, we implemented a probabilistic framework with equal prior probabilities (0.5) for both scenarios (Table 2). This approach examined whether source uncertainty significantly influenced size-based classification probabilities, testing the hypothesis that single-source specimens would exhibit greater morphometric homogeneity under normal distribution assumptions. Analysis revealed site-specific patterns: morphotype assignments remained stable despite source uncertainty at Cueva Pintada, Lomo de los Gatos, and Guayedra. However, Alto de Garajonay and Sobrado de los Gomeros demonstrated complex morphological variability requiring additional analytical considerations.

Morphotype classification demonstrated site-specific patterns. Cueva Pintada specimens were consistently allocated to morphotype 12 across all analytical scenarios (corrected/uncorrected carbonization, single/aggregate samples; Figure 8). Lomo de los Gatos specimens similarly showed consistent allocation to morphotype 13, while the single Guayedra specimen was classified as morphotype 13 after carbonization correction.


Seeds carbonized individualized

Seeds corrected individualized

Samples carbonized not individualized

Samples corrected not individualized

Figure 8. Allocation of pre-Hispanic archaeobotanical seeds to *Phoenix* seed morphotypes under different classification scenarios. Note: The classification considers individual seeds versus sample-based (not individualized) analyses and accounts for potential changes in seed dimensions due to carbonization. Abbreviations: Locations on Gomera Island (blue dots and arrows) include AG (*Alto del Garajonay*) and SG (*El Sobrado de Los Gomeros*). Locations on Gran Canaria Island (red dots and arrows) include CP (*Cueva Pintada*), LG (*Lomo los Gatos*), and G (*Guayedra*). Image generated by F. Alcaraz and D. Rivera using GMT 6, Excel, and PowerPoint [73,78,79].

An initial analysis of Sobrado de los Gomeros revealed apparent morphological heterogeneity among individual seeds (Table S4, Figure 8). However, aggregate analysis under single-source assumptions resulted in consistent classification within morphotype 13. Alto de Garajonay exhibited comparable complexity: one seed displayed reduced dimensions and conical morphology suggesting morphotype 15, while two aligned with morphotype 12 (Figure 8). Collective analysis supported morphotype 12 classification.

Notably absent from archaeological assemblages were morphotypes 3, 4, 11, and 16, which constitute significant proportions of modern *P. canariensis* populations (Table S3). This absence is particularly significant for the elliptic-oblong morphotype 3 and large-seeded morphotype 11 (>1150 mm^3; Table S2). These findings highlight the necessity of integrating multiple analytical approaches to address uncertainties in archaeological seed provenance and morphological variation.

4. Discussion

Our analysis demonstrates the extensive morphological diversity within *Phoenix* seeds, emphasizing the necessity of comprehensive sampling for accurate morphotype characterization. While *P. dactylifera* and *P. canariensis* are well-represented in our dataset, *P. reclinata* and other species require additional sampling for complete morphological assessment.

This research contributes to morphometry-based archaeobotanical identification methodologies. Archaeological plant remains, being non-fossilized materials, require comparisons with modern reference collections of hypothesized related taxa [80]. Such identifications must be contextualized within broader biogeographical and phylogenetic frameworks before asserting taxonomic assignments [81].

Carbonization represents a primary taphonomic process affecting archaeological seed morphology. Experimental carbonization—typically conducted at 220–240 °C under oxygen-limited conditions—provides insights into preservation mechanisms and optimal charring conditions [82]. This approach enables direct comparison between experimentally charred modern specimens and archaeological materials, informing interpretations of ancient plant use, food processing techniques, and agricultural practices. Originally developed for cereals, this methodology now encompasses diverse taxa including *Vitis*, *Quercus*, *Gossypium*, *Oryza*, *Helianthus*, and various pulses [83–89].

Key findings from experimental carbonization studies have revealed several significant patterns:

The preservation potential varies systematically among plant structures, with cereal grains demonstrating superior preservation compared to glume bases, which in turn preserve better than culm nodes [82]. This hierarchical pattern of preservation aids archaeobotanists in interpreting the relative frequencies of plant components in archaeological assemblages.

Carbonization induces substantial morphological alterations in seed dimensions and form. Research on wheat and pea grains has demonstrated that anoxic heating conditions significantly influence their morphometric characteristics [84,85]. The extent of these modifications correlates directly with both temperature exposure and duration, with different plant species and structures exhibiting distinct optimal preservation parameters [86].

Species-specific carbonization responses play a crucial role in archaeobotanical identification. Our research demonstrates that while carbonization had minimal impact on the primary identification characteristics of Phoenix seeds, it significantly compromised their structural integrity. This surface fragility subsequently enhanced their susceptibility to other taphonomic processes, resulting in the gradual erosion and deterioration of diagnostic features, particularly the longitudinal striation patterns. This observation provides important insights into the complex interplay between carbonization and long-term preservation processes in archaeobotanical assemblages.

Morphometric studies on archaeological *Phoenix* seeds have provided crucial insights into date palm domestication and historical biogeography. Notable research includes Sallon et al.'s [90] examination of 2000-year-old Judean seeds, which were significantly larger than modern varieties; archaeobotanical analysis at Ra's al-Jinz in Oman documenting Bronze Age *Phoenix dactylifera* consumption [91]; and comprehensive morphometric analyses identifying domestication syndrome traits [92].

A significant methodological advancement came from Terral et al. [93], who analyzed 64 equally spaced points along seed outlines from both dorsal and lateral views. Their sample included 45 cultivars, 9 wild specimens, 5 *Phoenix* species, and archaeological seeds from seven Egyptian sites. Using elliptic Fourier transform (EFT) for geometric morphometrics combined with Linear Discriminant Analysis (LDA), they successfully differentiated between species and identified most archaeological samples as *P. dactylifera*, with one 5th century BCE specimen from Áyn-Ziyâda classified as *P. reclinata*.

Rivera et al. [5] analyzed 3920 seeds across 364 samples, including modern *Phoenix* species (304 samples with type specimens), archaeological (51) and fossil (9) seeds. The study examined 67 descriptors: 41 qualitative states and 26 quantitative parameters. Eight species (*P. acaulis*, *P. canariensis*, *P. paludosa*, *P. reclinata*, *P. roebelenii*, *P. rupicola*, *P. sylvestris* and *P. theophrasti*) showed distinctive characteristics based on size, surface features, apex and base shape, and ventral furrow morphology. By analyzing modern, fossil, and archaeological materials together, they successfully matched archaeobotanical samples to modern *Phoenix* morphotypes, primarily *P. dactylifera*, with some specimens corresponding to *P. reclinata, P. caespitosa, P. atlantica, P. theophrasti, P. pusilla* and *P. canariensis*.

Key findings across these studies revealed that cultivated date palm seeds are distinctively longer and more elongated compared to other *Phoenix* species, notably *P. canariensis*, though the domestication syndrome definition awaits definitive identification of wild relatives.

Historical analyses, particularly of Judean desert specimens, indicate that ancient seeds were there larger than modern varieties, suggesting changes in cultivation practices over time [90]. However, the decline and eventual near-extinction of date palms in Palestine, the Jordan Valley, and neighboring regions represents a complex historical process spanning multiple centuries, which can be behind this decrease in seed and fruit dimension. This deterioration can be traced to several interconnected historical factors. The Roman-Jewish wars of 66–73 CE and 132–136 CE precipitated significant demographic disruption through population deportation and displacement, severely impacting the sophisticated cultivation practices required for date palm agriculture. The subsequent collapse of Judea proved particularly devastating to the preservation of elite cultivars, as the expertise required for vegetative propagation and seedling selection was largely lost. Over time, these carefully cultivated specimens were gradually superseded by unsupervised seedling populations and feral trees that produced markedly inferior fruit [90]. The temporal progression of this decline is well-documented across multiple centuries. By the eleventh century, date palms had already become notably scarce in the region, though some areas maintained their cultivation traditions longer than others. The Jericho and Zoara regions, for instance, sustained extensive date palm cultivation until the fourteenth century, when the agricultural economy collapsed during the Mamluk period. The fifteenth century marked a crucial turning point, as date palms vanished entirely from the Jericho-Ein Gedi region—a development potentially attributable to anthropogenic factors or climatic changes affecting water resources. By the nineteenth century, the transformation was complete: the original cultivated varieties had been entirely displaced by spontaneous seedling populations and feral specimens [94].

This long-term decline culminated in the early twentieth century, when the once-flourishing date palm industry of Palestine and the Jordan Valley had been reduced to negligible levels. Perhaps most notably, the Judean date palm, a variety of particular historical and agricultural significance, was considered extinct in its traditional habitat [94]. This case illustrates how complex historical, political, biological [95] and environmental factors can combine to transform not only an agricultural landscape over time but also the prevailing seed morphology in cultivated plants such as date palm.

This body of research has enhanced our understanding of *Phoenix* species differentiation, wild versus cultivated variants, and the evolution of cultivation practices, while demonstrating the effectiveness of morphometric analysis in archaeological contexts.

Methodological precision emerges as a critical determinant in taxonomic analysis, where nuanced morphological observations can precipitate substantial taxonomic reclassifications. The Lomo de Los Gatos archaeological assemblage exemplifies this methodological complexity: subtle morphological variations—particularly base obliquity and longitudinal striation patterns—can fundamentally alter taxonomic clustering outcomes. This observation illuminates a dual limitation in current archaeobotanical identification methodologies. First, the approaches demand exceptionally well-preserved archaeological materials that retain both structural integrity and surface detail despite taphonomic processes and carbonization. Second, and perhaps more significantly, the inherent constraints of archaeological sampling often yield numerically limited assemblages, potentially obscuring the full spectrum of morphological variation within ancient populations. This sampling limitation may result in under-representation of certain morphotypes and could potentially skew taxonomic interpretations. Such constraints underscore the necessity for developing robust statistical frameworks that can account for both preservation bias and small sample sizes in archaeological contexts.

Contemporary *Phoenix* populations in the Canary Islands predominantly comprise typical *P. canariensis*, including the Wildpret's Large Date Group and the *P. canariensis* var. *porphyrococca* (Red Date Group) [19] (Figure 9). Historical documentation supports the early introduction of the date palm (*Phoenix dactylifera*) following Spanish arrival, with Fuerteventura Island exhibiting a notably high proportion of *P. dactylifera* and related variants (Figure 9) [96].

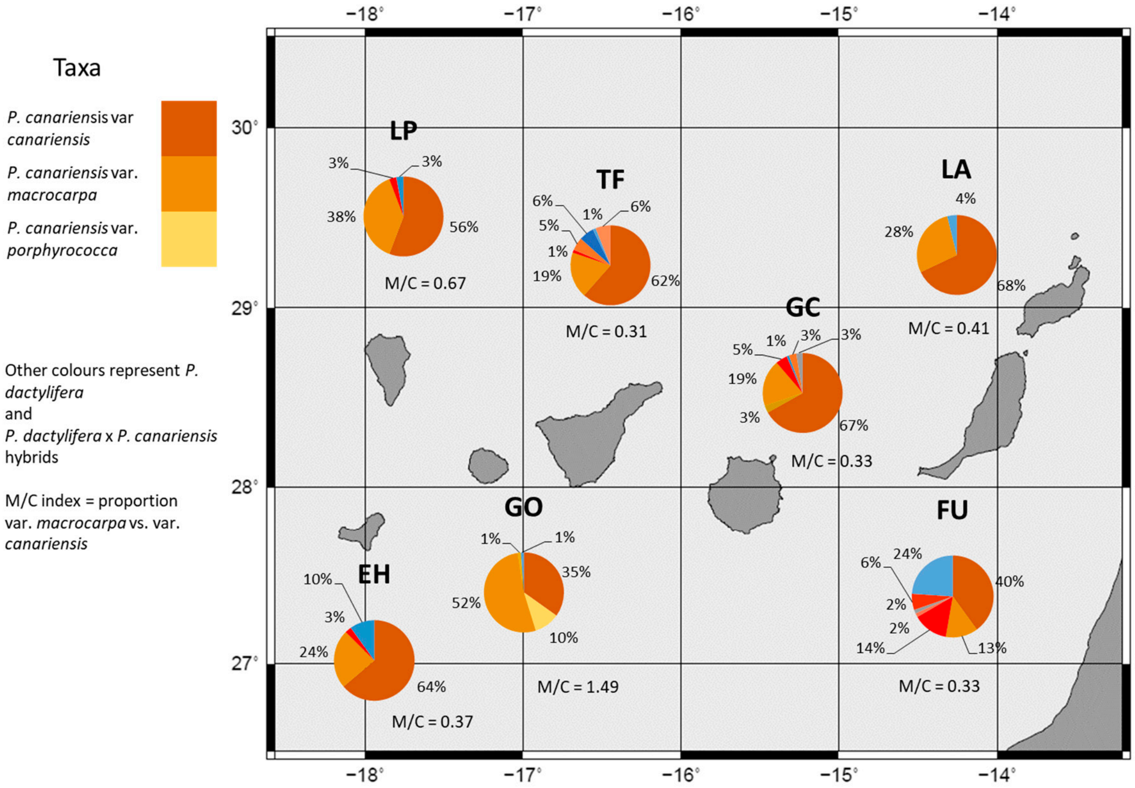


Figure 9. Frequency of *Phoenix* palm populations in the Canary Islands, including *P. canariensis* varieties, *P. dactylifera*, and interspecific hybrids. Data sourced from Phoenix_Spain.org. http://www.phoenix-spain.org/ (accessed on 2 April 2025) [50].

The archaeobotanical record aligns closely with the prevalence of modern *P. canariensis*. The conspicuous absence of elliptical-oblong seed morphotypes and larger seed configurations suggests potential recent evolutionary developments, possibly arising from introgression with *P. dactylifera*. Bayesian probabilistic analyses consistently demonstrate the dominance of *P. canariensis* across the seven morphological types recognized in the Canary Islands (Figure 9).

Typical *P. canariensis var. canariensis* exhibits the smallest seeds within the species (Figure 1A,F,H) and deep green, large leaves with numerous leaflets and robust, yellowish basal spines [97]. The *P. canariensis* Wildpret's Large Date Group encompasses samples characterized by their large seeds (Figure 1B,G,J) with volumetric dimensions (length × breadth × depth) typically exceeding 1000 mm^3, associated with larger fruits. This Canary Islands date palm variety is distinguished not only by this feature but also by its glaucous leaves [19,97–99] (Figure 1D). Hermann Wildpret named this variety *Phoenix canariensis* var. *macrocarpa* [100]. Finally, the *P. canariensis* Red Date Group comprises palms with red fruits of varying dimensions and shapes (Figure 1C,I), characterized by notably glaucous leaves (Figure 1E). This variety is botanically recognized as *P. canariensis* var. *porphyrococca* [8,99]. While its presence in the archaeobotanical record is possible (Table 3), particularly at Sobrado de los Gomeros, it is unlikely given the low proportion of this variety in contemporary *P. canariensis* populations (Figure 9).

Probabilistic reconstructions, incorporating both morphotype and taxonomic considerations, provide nuanced insights. While typical *P. canariensis* demonstrated the highest probability across archaeological sites, subtle variations emerged. Sites like Cueva Pintada and Alto Garajonay exhibited potential associations with the Wildpret's Large Date Group. Notably, samples from Lomo de Los Gatos, Guayedra, and Sobrado de los Gomeros displayed distinctive characteristics, suggesting potential relationships with Tropical African and Asian *Phoenix* populations.

Quantitative identification methodologies, including probability odds of species attribution, substantiate the predominant *P. canariensis* classification (Table 3). Particularly compelling evidence emerged from Cueva Pintada, with unequivocal *P. canariensis* identification. Interestingly, one seed from Sobrado de los Gomeros defied classification within established morphotypes, potentially indicating an extinct *P. canariensis* variety or a methodological anomaly—a rare but not unprecedented archaeobotanical phenomenon. This recalls the extinct wheat species, *Triticum parvicoccum*, described by Kislev [101].

Table 3. Bayesian Probabilistic Taxonomic Characterization of Archaeological *Phoenix* Seed Assemblages from Insular Palaeobotanical Contexts in the Canary Archipelago. Taxa with probabilities lower than 0.05 in all samples were excluded except in *P. canariensis*.

Taxa	Alto Garajonay	Sobrado de los Gomeros	Cueva Pintada	Lomo de los Gatos	Guayedra
P. canariensis var. *canariensis*	0.709	0.590	0.81	0.66	0.66
P. canariensis var. *porphyrococca*	0	0.017	0	0.03	0.03
P. canariensis Wildpret's Large Date Group	0.166	0.080	0.19	0.03	0.03
P. canariensis Subtotal	0.875	0.688	1.00	0.72	0.72
P. dactylifera s.l. Subtotal	0	0.045	0	0.08	0.08
P. farinifera	0	0	0	0.05	0.05
P. roebelenii	0.021	0	0	0.07	0.07
P. theophrasti	0.104	0.015	0	0.03	0.03
Others Subtotal	0.125	0.102	0	0.19	0.19
Probability ratio *P. canariensis* vs. others	7	6.74	∞	3.78	3.78
Probability ratio *P. canariensis* vs. *P. dactylifera* s.l.	∞	15.28	∞	8.25	8.25

Methodological Note: Values of probabilities vary from 0 to 1. Kolmogorov's theorem [1956] implies that probabilities of 0 and 1 correspond to absolute impossibility and certainty within the framework of the model. However: In practical terms [102,103], (p. 5, Remark 2), a probability of 1 does not guarantee that the event will occur (or has occurred) in every real-world scenario; it reflects certainty only within the confines of the model. Similarly, $P(A) = 0$ does not preclude the possibility of the event entirely—it only means the event is negligible in the model's context.

This research provides critical insights into the evolutionary history of *P. canariensis*, revealing a pre-Hispanic prevalence of typical morphotypes characterized by small to medium-sized seeds. Our data indicates that the emergence of larger fruits could be associated with initial cultivation and domestication processes occurring within the Canary Islands.

Intriguingly, inter-island variations in morphotype proportions suggest differential selective pressures. While typical morphological distributions remain consistent, islands like La Gomera exhibit markedly distinct selective patterns, with a pronounced tendency toward large-fruited palm varieties. This suggests nuanced, geographically variable diversification, potentially driven by localized unintentional human selection mechanisms during natural or linked to domestication processes.

Molecular evidence suggests that *Phoenix canariensis* was present in the Canary Islands long before the arrival of the first Canarians, making it unlikely that these early inhabitants introduced any distinct morphotypes [13,14]. Consequently, it is more plausible that the initial stages of *P. canariensis* domestication occurred in situ within the archipelago. However, it appears evident that the domestication process did not progress sufficiently to differentiate cultivated populations from their wild counterparts.

Moreover, the intricate interplay of natural, semi-natural, and anthropogenic habitats where *P. canariensis* is found [19] did not correlate with specific morphotypes. In contrast, a comparison across islands (Figure 9) revealed that the proportion of modern var. *macrocarpa* samples relative to typical *P. canariensis* samples ranges between 0.3 and 0.4, reaching 0.67 on La Palma Island and 1.49 on La Gomera. This pattern suggests stronger selective pressures favoring large-fruited palm trees on La Gomera. Molecular marker investigation is imperative for comprehensively elucidating *Phoenix macrocarpa* population dynamics across La Gomera and Gran Canaria. Our analyses from La Gomera reveal minimal intra-island genetic differentiation, substantiating extensive historical palm cultivation practices that have substantially homogenized local genetic structures. Notably, these genetic profiles demonstrate remarkable similarity to Tenerife populations, though our current dataset's limitations necessitate acknowledging the potential incompleteness of our genetic characterization.

Therefore, it is likely that the incipient domestication of *P. canariensis* was aimed at producing larger fruits but did not occur with uniform intensity across the Canary Islands.

The proposed methodological framework represents a realistic approach to archaeological seed identification, particularly potent when supported by comprehensive germplasm repositories. The methodology's potential extends beyond *Phoenix*, presenting promising applications for taxonomically diverse cultivated plant genera such as grapevine (*Vitis*), olive (*Olea*), oak (*Quercus*), wheat (*Triticum*), barley (*Hordeum*), and numerous pulses such as broad beans (*Vicia*), peas (*Pisum*), lentils (*Lens*), and chickpeas (*Cicer*) among others.

5. Conclusions

The integration of advanced seed morphometric analysis with Bayesian probabilistic frameworks has proven to be a powerful taxonomic identification tool, particularly when supported by comprehensive comparative collections and well-preserved archaeological specimens. This methodological approach has yielded significant insights into the taxonomic composition of archaeological *Phoenix* palm seeds from Indigenous Canarian sites.

Our analysis of specimens from five archaeological locations revealed distinct identification patterns. Seeds from Cueva Pintada (Gran Canaria) showed unambiguous *Phoenix canariensis* classification, while specimens from Alto del Garajonay (La Gomera), Lomo de los Gatos, and Guayedra (Gran Canaria) demonstrated a sufficiently high probabilistic attribution (0.7–0.9) to this species. The Sobrado de los Gomeros (La Gomera) assemblage presented a more nuanced case, with *P. canariensis* identification marginally supported at 0.68, influenced by an anomalously large specimen. Additionally, individually, some seeds from Cueva Pintada and Alto del Garajonay showed elevated probability of belonging to the Wildpret's Large Date Group.

While the complete narrative of *P. dactylifera* introduction to the Canary Islands awaits further archaeological investigation, our findings have immediate implications for contemporary conservation and agricultural management of *P. canariensis*. The methodological framework developed here transcends its archaeological origins, offering valuable applications in modern contexts. The demonstrated capacity to distinguish between closely related taxa makes this approach particularly valuable for contemporary palm taxonomy, biodiversity assessment, and germplasm conservation.

These findings provide crucial baseline data for identifying historically adapted palm populations, potentially informing climate resilience strategies and sustainable resource management. The methodology's broad applicability extends to modern conservation initiatives, agricultural development programs, and breeding efforts aimed at maintaining genetic authenticity. This research thus bridges archaeological investigation with contemporary environmental challenges, offering practical tools for biodiversity conservation and agricultural management in island ecosystems.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/seeds4020019/s1, Table S1: List of *Phoenix* seed samples analyzed. Table S2: Descriptive characters for the 20 morphotypes taxonomically meaningful. Table S3: Probabilities of *Phoenix* taxa given each one of the twenty morphotypes taxonomically meaningful. Table S4: Morphological Classification of Archaeological *Phoenix* Seed Assemblages from the Canary Islands: Taxonomic Attribution across Comparative Scenarios.

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