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Revisiting Jiahu's 9000-Year-Old Fermented Beverage: New Microfossil Evidence for Early *Qu*-Based and Malt-Based Brewing Technologies in North China

Li Liu [1,2,*], Yahui He [2], Jingpu Li [1,2], Juzhong Zhang [3] and Wuhong Luo [3]

[1] Department of East Asian Languages and Cultures, Stanford University, Stanford, CA 94305, USA; lijingpu@stanford.edu
[2] Stanford Archaeology Center, Stanford University, Stanford, CA 94305, USA; yahuihe@stanford.edu
[3] Department for the History of Science and Scientific Archaeology, University of Science and Technology of China, Hefei 230026, China; juzhzh@ustc.edu.cn (J.Z.); lwh0551@ustc.edu.cn (W.L.)
* Correspondence: liliu@stanford.edu

Abstract

The Jiahu site (ca. 9000–7500 cal. BP) in the Huai River valley has yielded the earliest reported evidence of fermented alcoholic beverages in China. Previous chemical residue analyses interpreted these beverages as a mixture of rice, honey, and fruit, differing markedly from brewing traditions documented at other Neolithic sites in China. To reassess Jiahu brewing practices, we analyzed microfossils preserved in residues from 16 pottery sherds. The residues contained abundant starch granules, phytoliths, and fungal remains, including *Monascus* cleistothecia, hyphae, and yeast cells, together with starch damage patterns resulting from enzymatic hydrolysis, mashing, and cooking-induced gelatinization. Plant remains included rice, Panicoideae and Triticeae cereals, Job's tears, foxnut, underground storage organs (USOs), and other taxa. Rice starches and *Monascus* remains were the most ubiquitous components, indicating that rice and *Monascus* formed the basis of *qu*-based brewing, while evidence consistent with malt saccharification was also identified. Together with previous chemical analyses, these findings suggest that Jiahu brewing relied primarily on *qu*-based saccharification, with contributions from malt-based processing, while honey and fruits may have supplied additional fermentable sugars. Integrating chemical and microfossil evidence provides a robust framework for reconstructing ancient brewing technologies.

Keywords: Jiahu; pottery residues; *Monascus*; *qu*-based brewing; malt saccharification; Neolithic China

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1. Introduction

China has a long history of alcoholic production. Fermented alcoholic beverages have traditionally been dominated by cereal-based brewing processes. Three key terms are used throughout this paper to describe different stages of ancient alcohol production. The first is saccharification, the conversion of starches into fermentable sugars through enzymatic activities. The second is fermentation, the conversion of these sugars into ethanol through yeast activities. The third is brewing, the overarching technological and cultural process of producing alcoholic beverages, encompassing saccharification, fermentation, and related preparation steps.

Traditional Chinese brewing employs two principal approaches to saccharification and fermentation. (1) The *Qu*-based method uses *qu* starters containing filamentous fungi

that secrete hydrolytic enzymes, together with yeasts and bacteria. In this system, saccharification and alcoholic fermentation occur simultaneously, a process known as Simultaneous Saccharification and Fermentation (SSF). (2) The malt-based method relies on the malting of cereals to activate endogenous hydrolytic enzymes present in the grains. Saccharification is completed before alcoholic fermentation, which is subsequently carried out by yeasts naturally present in the environment or intentionally added to the mash [1–3].

The current archaeological record for alcoholic production shows a gradual development and dispersal from south to north, which can be divided into three major spatiotemporal stages.

First, the earliest archaeological evidence for brewing dates back to 10,000–8500 years ago at the early Neolithic Shangshan culture sites in the lower Yangzi River region, such as Shangshan, Xiaohuangshan, and Qiaotou. Alcohol production practices involved rice in combination with filamentous fungi, such as *Monascus*, *Aspergillus*, and *Rhizopus*, to produce *qu* starters, while rice, together with other wild cereals, tubers, and nuts, served as the primary brewing substrates [4–6].

Second, brewing technologies appear farther north in the Huai River valley by around 9000 cal. BP, as represented by the Jiahu site. Previous residue analyses interpreted Jiahu beverages as a mixed fermented beverage composed of rice, honey, and fruit [7].

Third, alcohol production further developed in the Yellow River valley by ca. 8000–7000 cal. BP, as evidenced at early Neolithic Peiligang and Laoguantai-Baijia culture sites, where evidence for both *qu*-based and malt-based saccharification has been identified. At the Peiligang, Shuiquan, and Guantaoyuan sites, filamentous fungi including *Monascus*, *Aspergillus*, and *Rhizopus* have been recorded, together with rice, other cereals, and tubers as the dominant brewing ingredients, indicating close technological links with Shangshan traditions [8,9]. In addition, starch granules exhibiting damage consistent with the mashing of malted cereals have been identified at the Lingkou site, suggesting that the malt-based method was also practiced in the region [9] (Figure 1).

Located in the Huai River valley between the Yangzi and Yellow River regions, Jiahu occupies a pivotal geographic and cultural position in the early development of Chinese brewing traditions (Figure 1). Notably, in contrast to the *qu*-based practices documented at neighboring Early Neolithic sites, previous residue analyses interpreted Jiahu beverages as a mixed fermented beverage composed of rice, honey, and fruit [7].

Qu-based and malt-based production systems continued throughout the Neolithic and early Bronze Age in the Yellow River region (ca. 7000–3100 cal. BP), where fermented beverages were produced primarily from cereals and tubers [10–13].

To date, residue analyses have been conducted on several hundred pottery vessels from at least 38 Neolithic and Early Bronze Age sites in China. The results indicate that *qu*-based and malt-based traditions constituted the dominant brewing technologies throughout this approximately 7000-year period. In particular, the co-occurrence of rice and *Monascus* is widespread, having been identified at 20 of the 38 sites (52.6%) (Supplementary Materials Table S1 for details and references).

The malt-based and *qu*-based techniques identified in the archaeological record correspond closely with the conventional understanding of early Chinese alcohol production methods, first recorded in oracle-bone inscriptions of the late Shang dynasty (ca. 1250–1046 BC) and later described in the *Zhou Li* (*Rites of Zhou*) during the Eastern Zhou period by the fifth century BC. These textual sources document two distinct methods: one employing malted grains as saccharification agents and the other involving the preparation of *qu* starters, corresponding broadly to *li* and *jiu* alcoholic beverages, respectively [2,3].

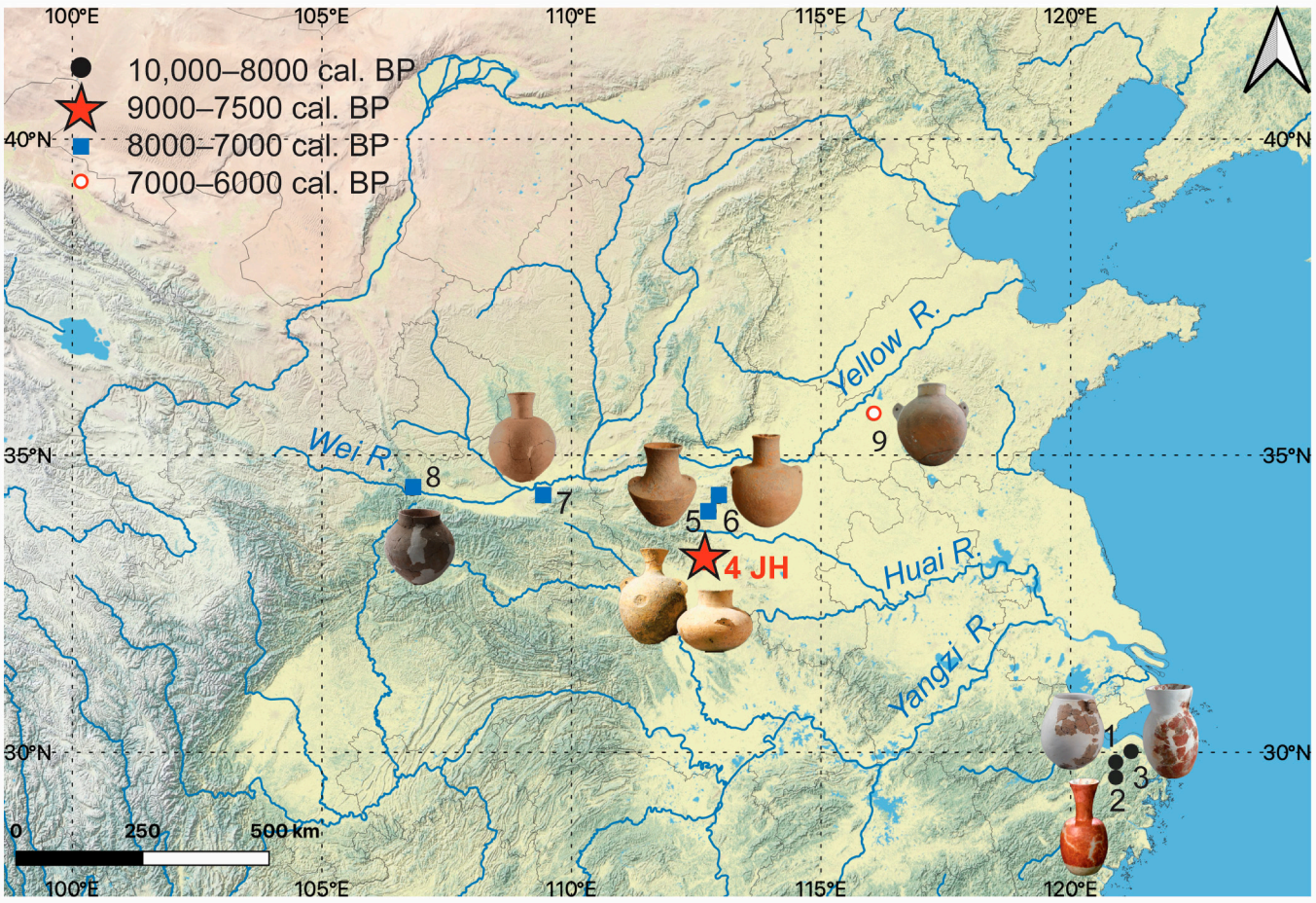


Figure 1. Locations of Neolithic sites associated with fermented alcoholic beverages discussed in this study. (1) Shangshan; (2) Qiaotou; (3) Xiaohuangshan; (4) Jiahu (JH); (5) Shuiquan; (6) Peiligang; (7) Lingkou; (8) Guantaoyuan; (9) Dongjiabai.

In combination, these lines of evidence suggest that the brewing method proposed for Jiahu—namely, a mixed fermentation involving rice, honey, and fruit—differs from most other known Neolithic and early Bronze Age alcohol production traditions in China. This discrepancy therefore warrants further investigation. We suggest that it may stem, at least in part, from differences in analytical approaches rather than reflecting an actual historical divergence.

Although all previous studies focused on residues preserved on pottery sherds, the Jiahu materials were examined primarily through chemical analysis, whereas other Neolithic pottery vessels have been investigated mostly using microfossil analysis. Consequently, they address different components of ancient brewing rather than competing explanations for the same evidence. Chemical analysis identifies molecular compounds and biomarkers that may indicate fermentation products, whereas microfossil analysis directly documents the botanical and microbial remains associated with brewing practices. Consequently, the two approaches may yield different reconstructions of ancient brewing practices. To test this proposition, we reexamined pottery samples from Jiahu using microfossil analysis to document starch granules, phytoliths, and fungal remains.

The objectives of this study are threefold: (1) to identify the brewing methods and ingredients at Jiahu; (2) to examine vessel functions in relation to alcoholic production and consumption at the site; and (3) to evaluate the role of Jiahu in the development and spread of brewing technologies during the Early Neolithic in North China.

2. The Jiahu Site and Re-Evaluation of the Original Pottery Residue Analyses

2.1. Jiahu Site

The Jiahu site, located in Wuyang County of Henan Province, is an early Neolithic settlement (ca. 9000–7500 cal. BP) situated in the Huai River valley (Figure 1: 4). More than four decades of archaeological investigations have yielded an exceptionally rich assemblage of material remains [14,15]. The site is best known for several remarkable discoveries, including early evidence of rice cultivation [16], the crafting of the world's oldest playable flutes [17], inscribed symbols on turtle shells [18], and residue evidence for fermented beverages [7].

The identification of fermented beverage residues in pottery jars from Jiahu [7] represented a groundbreaking discovery in Chinese archaeology two decades ago, opening a new window for understanding food practices and ritual behavior at the onset of the Neolithic transition. The original study analyzed residues from 16 pottery sherds using GC-MS, HPLC-MS, FT-IR, stable isotope analysis, and Feigl spot tests. The results revealed broadly consistent chemical profiles across the samples and identified biomarkers interpreted as evidence for rice, honey, and fruit (grape or Chinese hawthorn), including tartaric acid/tartrate and long-chain *n*-alkanes derived from beeswax. Stable isotope values further suggested that C_3 plants, such as rice and grape, constituted the primary ingredients.

Because the original interpretation has had a profound influence on subsequent discussions of early Chinese alcohol production, it is important to reassess both the analytical methods and the resulting interpretations of the original study in light of methodological advances in residue analysis over the past two decades.

2.2. Methodological Evaluation of Previous Research

The principal conclusion of the original study was that the Jiahu inhabitants consumed a fermented beverage made from a mixture of honey, rice, and fruits (hawthorn and/or grape) [7]. The primary evidence for honey is the detection of a series of *n*-alkanes (C23, C25, C27, and C29). These odd-carbon long-chain alkanes are commonly regarded as biomarkers for plant waxes. However, more robust identification of beeswax requires consideration of the distribution and relative abundances of additional compounds, including even-carbon long-chain alcohols and long-chain fatty acids [19].

The evidence for rice is based on stable isotope analysis of two samples, whose δ13C values were interpreted as consistent with rice or grapes. The inclusion of rice among the ingredients is highly plausible, but definitive confirmation of this hypothesis requires direct evidence, such as rice starch granules or rice-specific biomarkers. The primary evidence for fruits is the detection of tartaric acid. However, two critical methodological issues limit the confidence in this interpretation (fermented grapes or hawthorns): first, the reliability of tartaric acid as a criterion for grape wine; and second, the reliability of the analytical methods employed for its detection in previous research.

The chief concern pertains to the indicative significance of tartaric acid. Tartaric acid is commonly regarded as a biomarker for fruit-based alcoholic beverages derived from grape, wild grape, hawthorn, and related taxa [20,21]. However, it lacks both strong biological specificity for these taxa and a direct biochemical relationship to alcoholic fermentation. In addition to grape and hawthorn, many other plants, including kiwifruit, tamarind, pomegranate, gourd, calabash, wheat, and rice, also contain tartaric acid [22–29]. Owing to its widespread occurrence in fruits, vegetables, and grains, tartaric acid has been identified not only in grape wine but also in other alcoholic beverages, including beer and Chinese *qu*-based fermented drinks [30–35]. Tartaric acid may persist through association with soil, ceramic matrices and other organic compounds (such as benzoic acid) [22,36–39], thereby

increasing its archaeological visibility. Consequently, tartaric acid derived from a variety of sources may be preserved in archaeological samples. Recent studies have also highlighted potential contamination sources, including soil environments [40] and plastic products [27]. Furthermore, tartaric acid alone does not provide evidence for fermentation. Therefore, the detection of trace amounts of tartaric acid alone, without supporting evidence, has limited interpretive value.

Considering the relatively weak specificity of tartaric acid, at least two criteria should ideally be satisfied to chemically distinguish grape-derived products from other plant-based products in archaeological context: (1) a high concentration of tartaric acid, significantly exceeding that of control and environmental samples; and (2) a higher tartaric acid content compared to other organic acids commonly found in alcoholic beverages. An effective quantitative method has been established that satisfies the second criterion: the relative proportion of tartaric acid (TA) to malic acid (MA), expressed as %TA and calculated as TA divided by the sum of TA and MA. In grapes and grape-derived products, %TA typically exceeds 30% [41]. To further demonstrate that ancient grape products were fermented (i.e., wine), independent evidence for the fermentation process is required.

In addition to the indicative significance of tartaric acid, significant concern pertains to the analytical methods employed for its detection. Given the analytical limitations of the techniques available at the time, the methods used to identify tartaric acid in earlier works [20,21,42] are now considered less reliable than modern analytical techniques. This limitation was also acknowledged by McGovern [43]. For instance, McGovern utilized the Feigl spot test and Fourier-transform infrared spectroscopy (FT-IR) to identify tartaric acid in Jiahu's pottery sherds. The Feigl test has limited specificity, as it cannot reliably distinguish tartaric acid from compounds such as gluconic acid, glucuronic acid, dihydroxytartaric acid, and malic acid, and it requires relatively high concentrations (ca. 5–10 mg/mL) for detection [22,44]. FT-IR is likewise problematic for archaeological materials, which are typically complex mixtures, making it difficult to differentiate tartaric acid or tartrates from other organic substances such as resins [22].

In recent years, mass spectrometry has been widely recognized for its superior capacity to identify and quantify organic acids in archaeological samples [22,27,45,46]. McGovern likewise acknowledged that more reliable analytical approaches include liquid chromatography–tandem mass spectrometry (LC-MS/MS) and liquid chromatography–high-resolution mass spectrometry (LC-HRMS) [47]. Accordingly, some early studies, including the Jiahu case, would benefit from reexamination using new methods.

Another important limitation of the original interpretation is the lack of an explanation for how saccharification was achieved in Jiahu fermented alcoholic beverages [7]. If rice was one of the primary starchy ingredients, the brewing process would necessarily have involved two stages: saccharification and fermentation. Although the incorporation of honey and fruits may have contributed fermentable sugars, their presence in rice-rich fermentation ingredients does not account for the saccharification process. To address this issue, microfossil analysis offers a particularly effective approach because it can directly document both the plant ingredients and the biological agents involved in saccharification and fermentation.

It should be emphasized that this study is not intended to overturn the conclusions of McGovern et al.'s pioneering investigation. Rather, our microfossil-based reassessment provides an independent and complementary line of evidence, particularly through the analysis of starch granules and fungal remains, that addresses aspects of the brewing process—such as saccharification—that could not be directly evaluated using the organic residue analytical methods available at the time.

We acknowledge that, without parallel reanalysis of the original pottery samples using modern chemical techniques (e.g., LC-MS/MS or LC-HRMS), it is not possible to fully evaluate the original chemical interpretation. Accordingly, the methodological considerations discussed here are intended to highlight the strengths and limitations of different analytical approaches rather than to reject the earlier interpretation. Future studies integrating both advanced chemical residue analysis and microfossil analysis would provide the most comprehensive framework for reconstructing ancient brewing practices.

3. Materials and Methods

3.1. Research Material

The archaeological sequence from Jiahu has been divided into three chronological phases, dating to ca. 9000–7500 cal. BP. In the present study, 16 pottery sherds (POT1-16) represent all three occupational phases. The samples represent a range of vessel types recovered from diverse archaeological contexts, including burials, houses, ash pits, and middens, during the seventh excavation season in 2001 [15]. These sherds comprise fragments of globular jars and bottles of various forms, which have been interpreted as being associated with the production or storage of fermented beverages. The principal distinction between these two vessel types lies in their size, with jars generally being nearly twice as large as bottles. In addition, two basins and one cauldron were included for comparative analysis (Figure 2; Supplementary Materials Table S2).

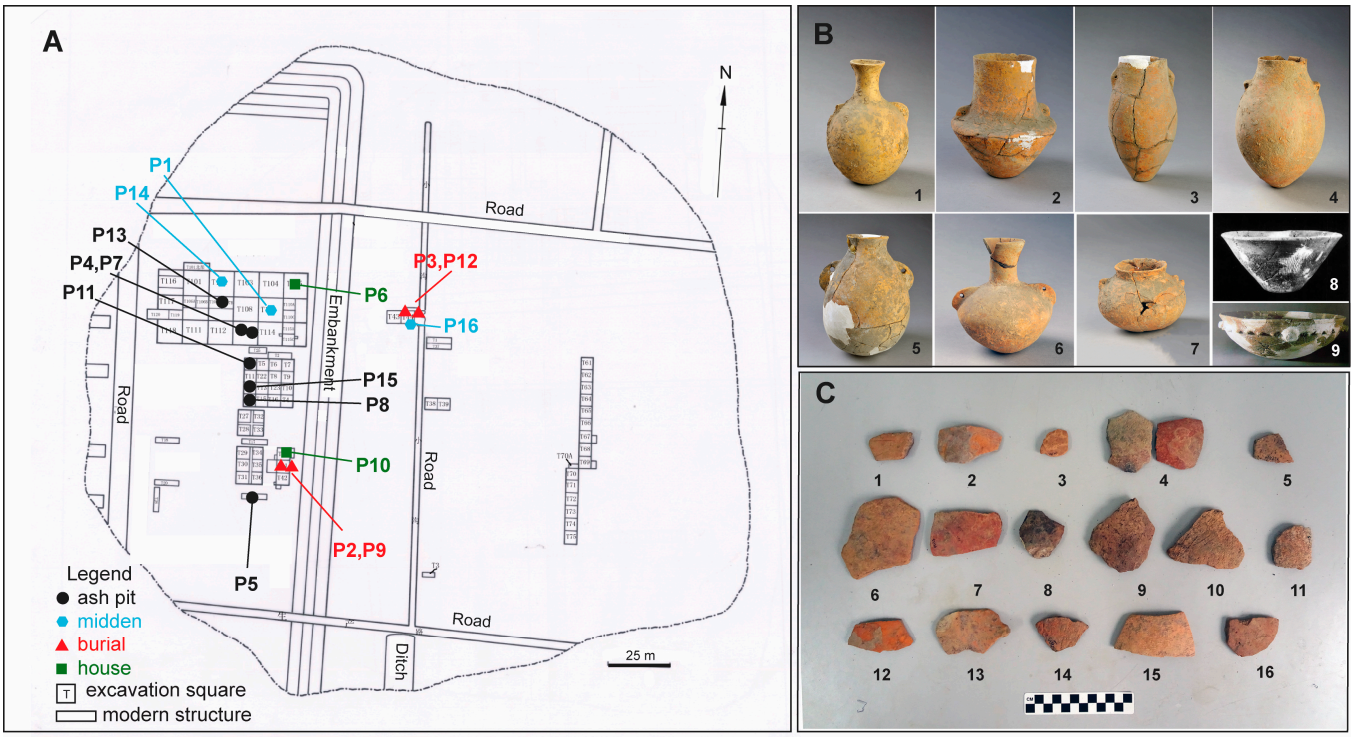


Figure 2. Jiahu site excavation map and pottery samples analyzed. (**A**) Jiahu excavation map and location of pottery sherds analyzed. (**B**) Representative pottery vessels comparable to the analyzed sherds: (1–3) *Hu* bottles; (4–7) various forms of two-handled globular jars; (8) *pen* basin; (9) *fu* cauldron. (**C**) Pottery sherds analyzed: (1) *pen* basin; (2–4) *hu* bottle; (5) *fu* cauldron; (6) *pen* basin; (7–9) *guan* globular jar; (10–16) *shuang'erguan* two-handled globular jar.

Although these sherds were briefly washed during post-excavation processing, previous archaeological studies have shown that microfossils preserved within absorbed residues and surface crevices generally survive such cleaning procedures.

The sherds had been stored at the University of Science and Technology of China in Hefei after excavation. To assess the possibility of contamination, we analyzed six control samples: five collected from the exterior surfaces of selected analyzed sherds (POT2, POT11, POT14, POT15, and POT16), and one consisting of soil adhering to sherd POT7.

3.2. Methods

Microfossil analysis was conducted to recover starch granules, phytoliths, and fungal remains (including filamentous fungi and yeast cells) preserved in residues adhering to the interior surfaces of the pottery sherds. Prior to sampling, all sherds were gently cleaned with unused disposable toothbrushes to remove loose surface sediments. Residues were extracted from the interior surfaces using a sterilized ultrasonic toothbrush, and the resulting wet suspensions were transferred to sterile tubes for storage. In addition, dry adhering residues were carefully scraped from the vessel surfaces using clean stainless-steel blades and sealed in sterile plastic bags as dry samples. Wet samples were analyzed immediately following extraction, whereas dry samples were retained for subsequent analyses.

The wet residue samples were processed following standard microfossil extraction protocols established at the Stanford Archaeology Center. The procedure involved two primary steps: (1) dispersion using 0.5 M ethylenediaminetetraacetic acid (EDTA; pH 8.0) to disaggregate microaggregates and release embedded microparticles; and (2) heavy-liquid separation using sodium polytungstate (SPT; density = 2.35 g/cm^3) to isolate microbotanical remains.

To minimize modern contamination, strict laboratory cleaning procedures were followed throughout the study. All equipment and work surfaces were thoroughly cleaned after each use, and the laboratory was cleaned weekly. Modern reference materials and archaeological samples were processed in separate laboratory facilities using dedicated equipment and toolkits to prevent cross-contamination. Test tubes and microscope slides were inspected before use to ensure that they were free of microfossil remains.

The recovered extracts were mounted on glass slides in a 1:1 (v/v) mixture of glycerol and distilled water and examined under a Zeiss Axio Scope A1 microscope equipped with polarizing filters and differential interference contrast (DIC) optics at 200× and 400× magnification. Photomicrographs were captured using a Zeiss Axiocam HRc digital camera and processed with ZEN 2.3 Light software.

Microfossil analysis also offers practical advantages for archaeological residue studies. Because it requires only minimal sampling of adhering residues, it can be applied to complete pottery vessels without destructive removal of pottery fragments. In addition, the method can be carried out using relatively modest laboratory facilities and does not require specialized chemical analytical instrumentation.

3.3. Microfossil Criteria for Identifying Ancient Brewing Methods

Microfossil remains were identified based on morphological characteristics through comparison with modern reference collections curated at the Stanford Archaeology Center, supplemented by published identification manuals/references for starch granules [48–51], phytoliths [52–54], and fungi, including molds and yeasts [3] (pp. 166–169), [55–58], ref. [59] (pp. 154–156).

The identification of brewing-related morphological alterations in starch granules is essential for distinguishing different brewing methods. As a representative example of malt-based brewing, we investigated a traditional millet beer that is still widely produced in northern Shaanxi. In this process, ground malted wheat is mixed with steamed millet flour,

hot water is added to produce a mash, and the mixture is fermented for approximately 24 h. The resulting beverage is an unfiltered, low-alcohol millet beer [9] (Figure 3).

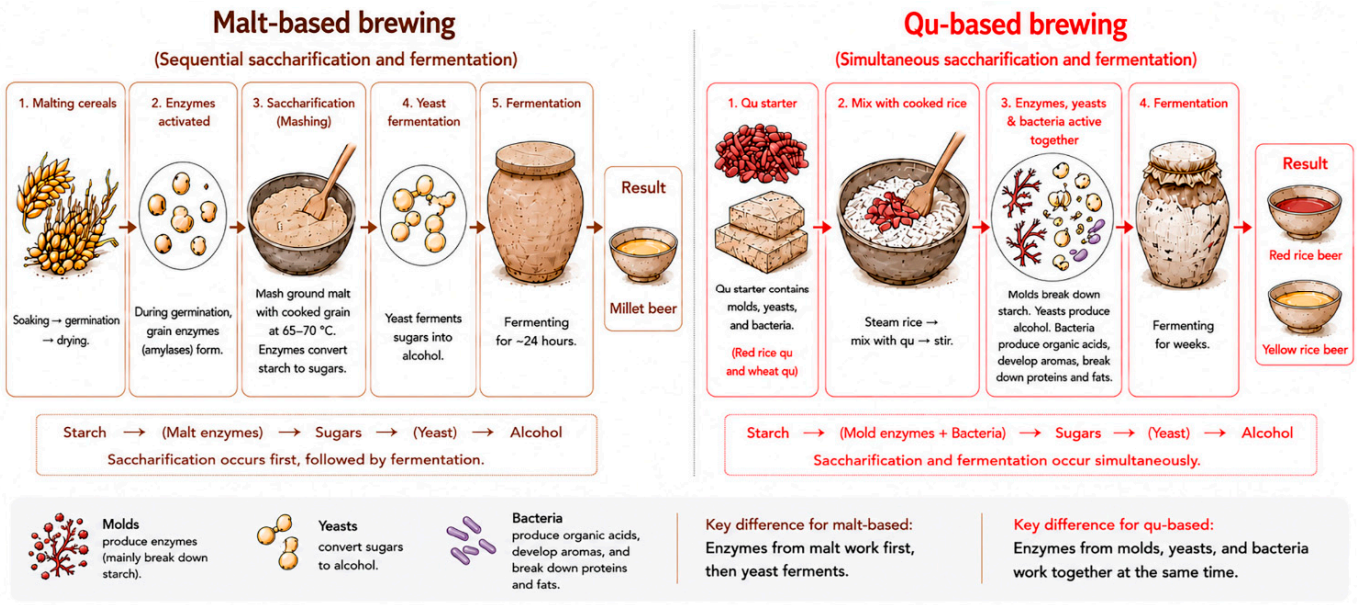


Figure 3. Schematic illustration of the brewing processes of malt-based and *qu*-based technologies in ancient China (Illustration created by the authors with the assistance of OpenAI's ChatGPT Plus).

Experimental studies have shown that starch granules in malt-based brewing undergo enzymatic hydrolysis during grain germination, followed by additional modification during mashing. These processes produce a series of distinctive microscopic alterations, including pitting, deep fissures, exposed lamellae, broken edges, loss of birefringence, central depressions, mild gelatinization, and hollowed centers surrounded by relatively intact peripheries. The latter two morphologies, particularly the "pizza crust-shaped" form, are especially characteristic of Triticeae (wheat and barley) starch granules subjected to mashing at 65–70 °C [48] (Figure 4). In traditional North Shaanxi millet beer, we identified three characteristic types of damaged starch granules: enzymatically digested starches produced during grain germination, "pizza crust-shaped" starches formed during mashing, and heavily gelatinized aggregates resulting from steaming.

In contrast, *qu* was traditionally prepared from uncooked or semi-cooked cereals (such as rice or wheat) inoculated with fungal cultures and subsequently combined with boiled or steamed starchy ingredients to initiate saccharification and fermentation [2,3] (Figure 3). Experimental and ethnographic studies of *qu*-based brewing have shown that the resulting fermented beverages contained diverse microbial communities [50,60,61]. Starch granules from the uncooked ingredients used in the *qu* starter exhibit damage caused by enzymatic hydrolysis, similar to that observed in malted cereals, whereas starch gelatinization caused by high-temperature cooking (steaming or boiling) produces uniformly expanded surfaces, with granules often fusing into larger aggregated masses (Figure 4). Notably, in a wheat *qu*-based brewing experiment, the characteristic "pizza crust-shaped" damaged starch granules were not observed [50].

Furthermore, because malt production does not require the removal of cereal husks, husk phytoliths may be retained in the final alcoholic product. Consequently, a relatively high abundance of cereal husk phytoliths in residue assemblages may provide supporting evidence for malt-based brewing. However, husk phytoliths can also result from incomplete dehusking during routine cereal processing and are therefore not diagnostic on their own.

Their interpretation should be evaluated in conjunction with starch damage associated with malting and mashing to assess whether the residue is consistent with malt-based brewing.

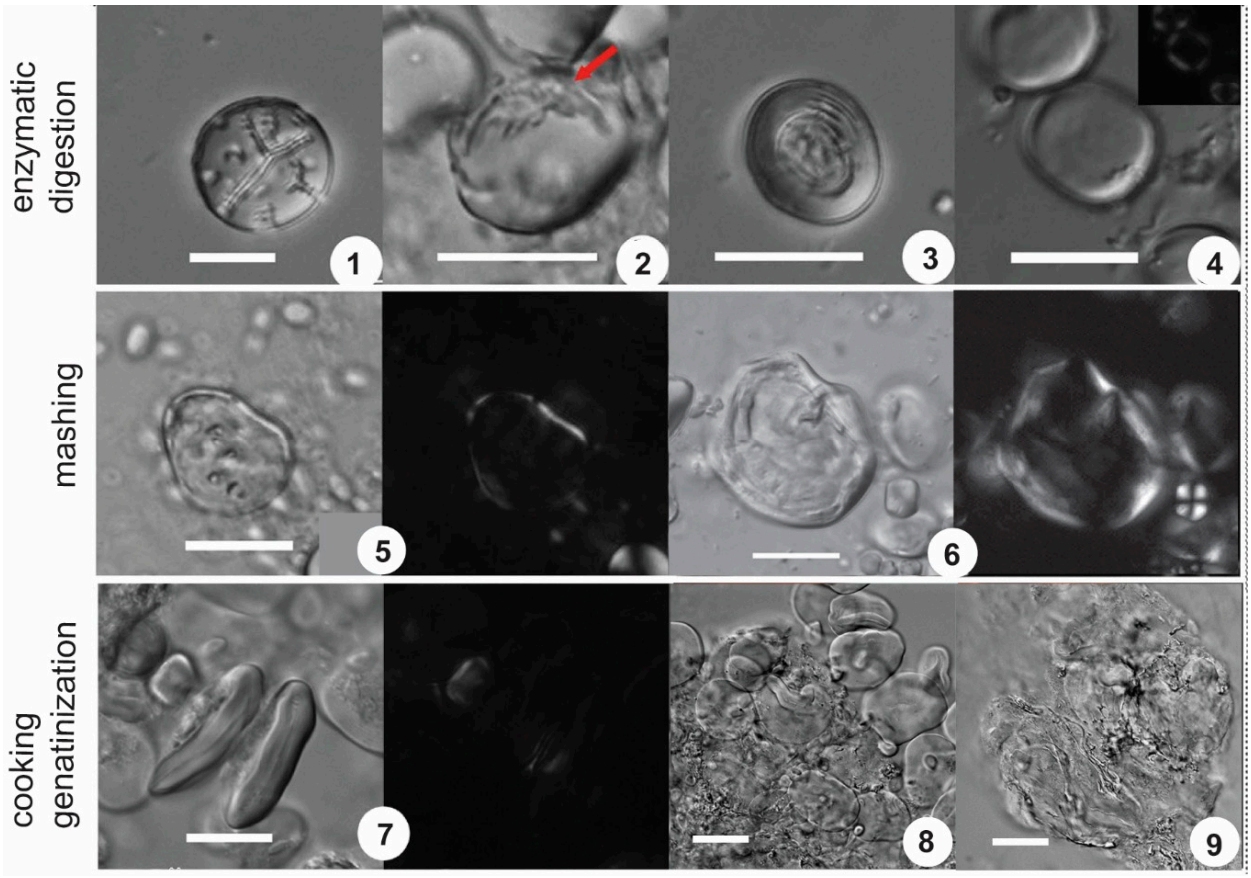


Figure 4. Representative starch damage patterns produced by malt-based and *qu*-based brewing methods. (1–4) Damage caused by enzymatic hydrolysis, including pitting, deep fissures, exposed lamellae, broken edges (pointed by red arrow), loss of birefringence, and central depressions. (5,6) Damage associated with mashing, including mild gelatinization and hollowed centers surrounded by relatively intact peripheries ("pizza crust-shaped"). (7–9) Gelatinization damage caused by cooking, including swollen granules with loss of birefringence and the formation of large aggregates. (Modified from [48] (Figures 5 and 7)).

Although both brewing processes can produce similar types of microfossil assemblages, including phytoliths, yeast cells, and starch granules exhibiting enzymatic hydrolysis, several diagnostic features may help distinguish them. For the malt-based method, the most diagnostic evidence includes cereal starch granules exhibiting central depressions, mild gelatinization, and hollowed centers with relatively intact peripheries, particularly the "pizza crust-shaped" form associated with mashing. In contrast, for the *qu*-based method, the presence of substantial quantities of brewing-related filamentous fungi together with heavily gelatinized starch aggregates constitutes more diagnostic evidence.

The diagnostic features summarized in Table 1 provide a framework for distinguishing malt-based and *qu*-based brewing methods. However, ancient brewers may have reused the same vessels for both techniques. In such cases, residues could preserve diagnostic indicators of both brewing methods, making interpretation more complex. Accordingly, interpretations should be based on the overall microfossil assemblage rather than on any single diagnostic feature.

Table 1. Diagnostic microfossil evidence for distinguishing malt-based and *qu*-based brewing.

Diagnostic Feature	Malt-Based Fermentation	Qu-Based Fermentation
Enzymatically damaged starch	✓	✓
Mashing damage ("pizza crust")	✓	—
Cooking gelatinization	✓	✓
Yeasts	✓	✓
Filamentous fungi	—	*Monascus*, *Aspergillus*, *Rhizopus*
Husk phytoliths	Possible	Possible

4. Results

Abundant microfossil remains (n = 978), ranging from 22 to 262 per sample, were recovered from the residue samples, including starch granules, phytoliths, and fungal elements. Among the three comparative vessels, the P5 cauldron and P6 basin exhibited residue assemblages similar to those of the bottles and jars and were therefore included in the analysis as samples tentatively associated with fermented food processing. In contrast, the P1 incised basin exhibited a distinct pattern, containing abundant phytoliths (n = 112) but virtually no other microfossil remains, and was therefore designated as the control sample. The remaining six control samples each yielded only 0–7 microfossils (Table 2).

Table 2. Jiahu microfossil record.

Sample #	Vessel Type	Excavation Context	Starch	Fungi	Phytoliths	Total
P2	*hu* (bottle)	burial	23	23	12	58
P3	*hu* (bottle)	burial	66	13	7	86
P4	*guanxing hu* (jar-shaped bottle)	ash pit	50	8	204	262
P7	*guan* (jar)	ash pit	17	1	4	22
P8	*guan* (jar)	ash pit	20	1	62	83
P9	*guan* (jar)	burial	16	8	4	28
P10	*shuang'er guan* (two-handled jar)	hourse	10	12	1	23
P11	*shuang'er guan* (two-handled jar)	ash pit	39	20	3	62
P12	*shuang'er guan* (two-handled jar)	burial	19	6	1	26
P13	*shuang'er guan* (two-handled jar)	ash pit	19	9	8	36
P14	*shuang'er guan* (two-handled jar)	midden	57	6	6	69
P15	*shuang'er guan* (two-handled jar)	ash pit	31	7	4	42
P16	*shuang'er guan* (two-handled jar)	burial	26	44	5	75
P6	*pen* (basin)	house	17	11	11	39
P5	*boxing fu* (bowl-shaped cauldron)	ash pit	42	20	5	67
Total N			452	189	337	978
Control samples						
P1	*huawen pen* (incised basin) interior	midden	1	0	111	112
P2 EX	bottle exterior	burial	1	1	1	3
P7 Soil	jar exterior soil	ash pit	0	0	0	0
P11 EX	two-handled jar exterior	ash pit	2	1	0	3
P14 EX	two-handled jar exterior	midden	2	1	3	6
P15 EX	two-handled jar exterior	ash pit	2	2	2	6
P16 EX	two-handled jar exterior	burial	3	2	2	7

4.1. Starch Remains

Among the 16 pottery samples analyzed, starches were recovered from 15, with counts ranging from 10 to 66 granules per sample. By contrast, the control sample yielded only 0–4 starch granules per sample (Table 3).

Table 3. Jiahu starch record.

Starch Type	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**UNID**			**Damaged Starch**			
Starch taxon	Rice compound	Panicoi-deae	Job's tears	Triti ceae	Snake gourd	Foxnut	Yam	Ginger	Tuber	Gelati-nized mass	UNID granule	Starch total	Enzyme	Ferment	Cooked	Damaged total
P2 bottle	5									17	1	23	1	5	17	23
P3 bottle	12	3		6						41	4	66	3	19	41	63
P4 bottle	1	1	1	19	3					22	3	50	10	2	22	34
P7 jar	8			1						8		17	1	8	8	17
P8 jar	6			1	1				1	10	1	20	1	5	10	16
P9 jar	7									9		16		6	9	15
P10 jar	2									8		10		2	8	10
P11 jar	9	11								13	6	39	1	19	13	33
P12 jar	7	1								10	1	19		6	10	16
P13 jar	8								1	9	1	19		8	9	17
P14 jar	5	3		10	29			1	1	4	4	57	5	4	4	13
P15 jar	17	4		1						1	8	31	2	20	1	23
P16 jar	7					4				15		26		11	15	26
P6 basin		4								13		17		4	13	17
P5 cauldron		4		3			1			1	33	42			33	33
Total N	94	31	1	41	33	4	1	1	3	181	62	452	24	119	213	356
Total %	20.8	6.9	0.2	9.1	7.3	0.9	0.2	0.2	0.7	40.0	13.7	100.0	5.3	26.3	47.1	78.8
Ubiquity N.	13	7	1	7	3	1	1	1	3	15	7	15	8	14	15	15
Ubiquity %	86.7	46.7	6.7	46.7	20.0	6.7	6.7	6.7	20.0	100.0	46.7	100.0	53.3	93.3	100.0	100.0
Granule & (compound) measured N.	142	27	1	40	33	19 (4)	1	1	4		18					
Size Min	2.9	7.65	18.41	8.98	3.97	1.5 (16.97)	18.24	16.07	6.17		6.4					
Size Max	7.04	18.88	18.41	38.16	24.04	2.97 (34.14)	18.24	16.07	21.09		22.26					
Size Mean	4.72	12.10	18.41	23.96	10.01	2.25 (22.86)	18.24	16.07	13.29		12.85					
control sample																
P1 basin											1	1				
P2 EX		1										1	1			1
P7 Soil												0				0
P11 EX	1	2									1	4	4			4
P14 EX				2								2		2		2
P15 EX		1		1								2	2			2
P16 EX				1							2	3	1	2		3

A total of 452 starch granules were recovered, of which 209 (46.2% of the total) were assigned to nine taxonomically diagnostic types. Slightly more than half of the assemblage (n = 243; 53.8%) was classified as unidentifiable (UNID) granules or gelatinized masses because the starches were too damaged, gelatinized, or lacked diagnostic morphological features (Table 3).

Most starches (n = 356; 78.8% of the total) exhibit various forms of damage, which can be classified into three categories comparable to experimentally altered starches in our reference database. (1) Enzymatic hydrolysis (n = 24; 5.3% of the total), characterized by random pitting, deep channels, broken edges, central depressions, and the loss of extinction crosses, while retaining weak birefringence (Figure 5: 1, 2, 4, 8; cf. Figure 6: 1, 6, 9). Such alterations may result from several processes, including brewing. (2) Brewing-related processing, including mashing and fermentation (n = 119; 26.3% of the total). Some granules from Panicoideae taxa and Triticeae exhibit hollowed centers with better-preserved peripheries and mild gelatinization, whereas the individual starch granules within rice compound appear blurred or absent, with only a few remaining recognizable (Figure 5: 2, 6, 9; cf. Figure 6: 7, 10). (3) High-temperature gelatinization (steaming or boiling; n = 213; 47.1% of the total), characterized by uniformly expanded surfaces, with starch grains often fused into large masses (Figure 5: 18; cf. Figure 6: 15, 16).

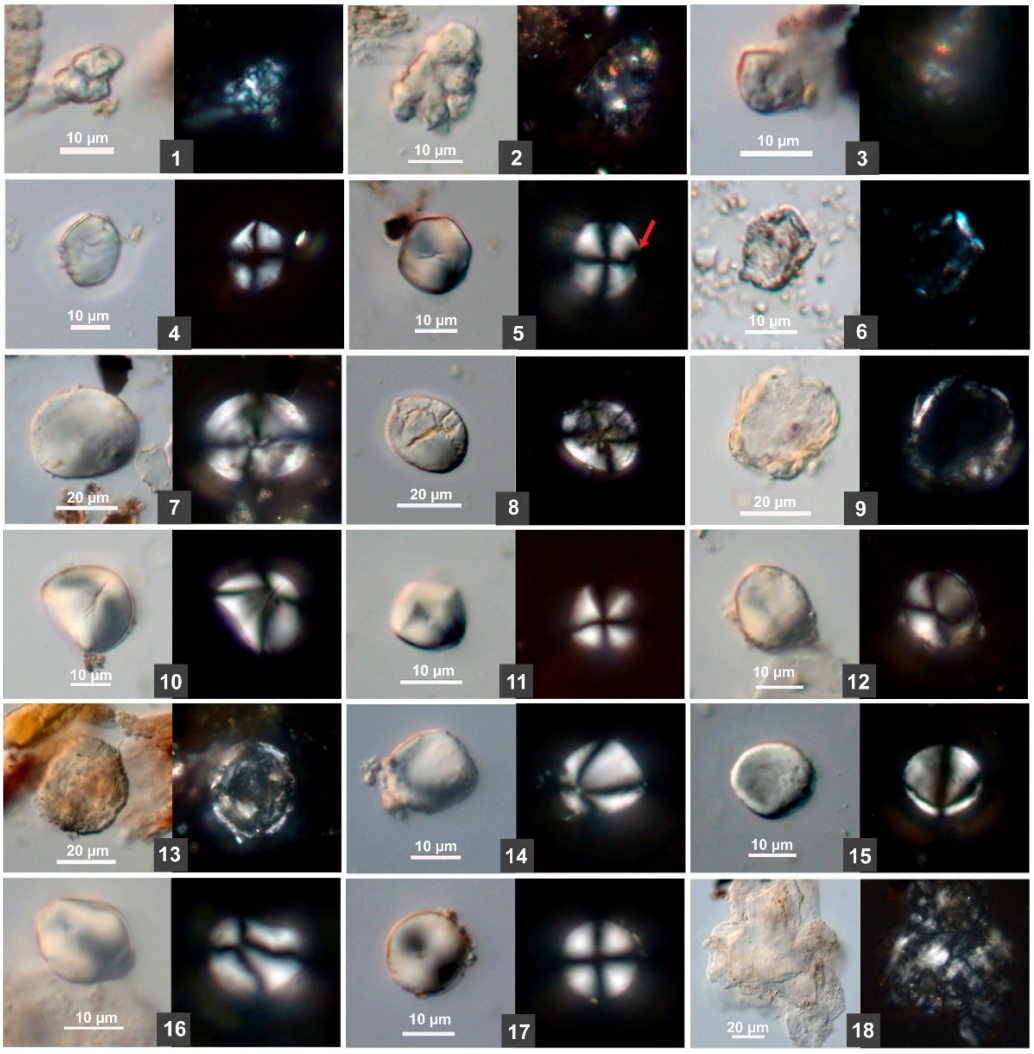


Figure 5. Representative starch morphotypes from Jiahu pottery samples. (1–3) Type I, rice compounds and single granule, showing weak birefringence and hollowed center related to enzymatic

hydrolysis; (4) Type II, Panicoideae; (5) Type III, Job's tears showing a zig-zag arm on the extinction cross (pointed by arrow); (6) Type II, damaged Panicoideae starch, consistent with mashing; (7) Type IV, Triticeae; (8) Type IV, damaged Triticeae starch, showing deep channels, broken edge related to enzymatic hydrolysis; (9) Type IV, Triticeae mildly gelatinized starch, consistent with mashing; (10–12) Type V, snake gourd root, bell-shaped, polygonal, and round; (13) Type VI, foxnut; (14) Type VII, yam; (15) Type VIII, ginger; (16) Type IX, tuber; (17) UNID; (18) gelatinized mass.

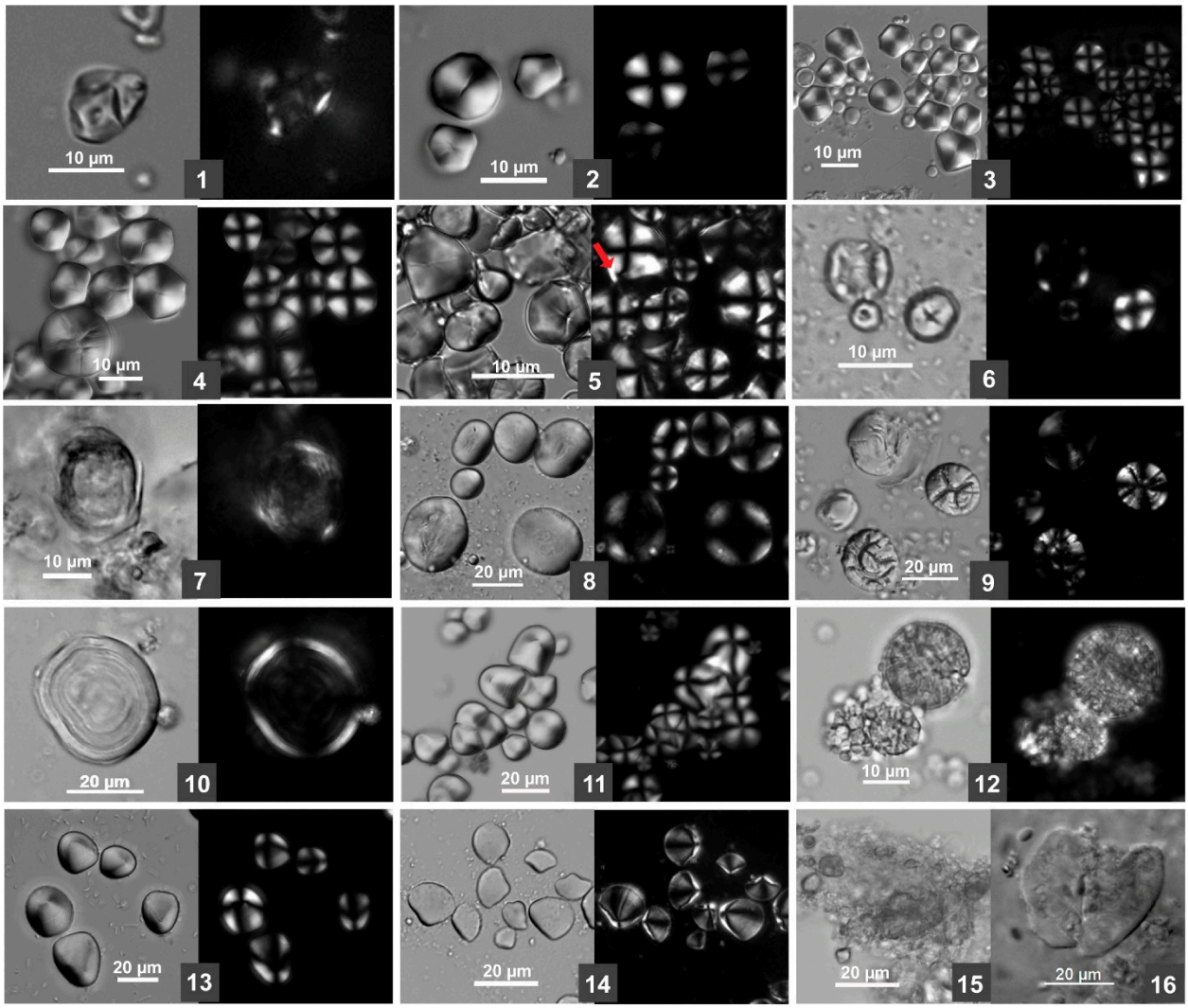


Figure 6. Modern starch comparative references. (1) rice *Oryza sativa*, fermented; (2) barnyard grass *Echinochloa colonum*; (3) broomcorn millet *Panicum miliaceum*; (4) foxtail millet *Setaria italica*; (5) Job's tears *Coix lacryma-jobi* (arrow pointing to the zig-zag arm); (6) sprouted broomcorn millet, showing enzymatic hydrolysis; (7) fermented millet, showing hollowed center with better preserved periphery and mild gelatinization; (8) wheat grass *Agropyron cristatum*; (9) wheat *Triticum aestivum* starch in *qu* starter, showing enzymatic hydrolysis; (10) mashed wheat grass *Agropyron* sp., showing mild gelatinization and more damaged center; (11) snake gourd *Trichosanthes cucumerina*; (12) foxnut *Euryale ferox*; (13) yam *Dioscorea polystachya*; (14) ginger *Zingiber officinale*; (15) fermented, gelatinized rice; (16) fermented, gelatinized broomcorn millet.

Type I rice starches (*Oryza* sp.) were identified in 13 vessels, making them the most ubiquitous starch type in the assemblage (86.7% ubiquity). They typically occurred as compound starches composed of multiple small polygonal granules. A total of 94 rice compound starches and isolated single granules were recorded, accounting for 20.8% of the total assemblage. Measurements of 142 individual granules yielded sizes ranging from 2.9 to 7.04 µm (mean = 4.72 µm), consistent with those of modern reference rice starches

(Figure 7). Most granules exhibited weak or blurred birefringence and lacked distinct extinction crosses, consistent with brewing-related damage in our experimental reference (Figure 5: 1–3; cf. Figure 6: 1).

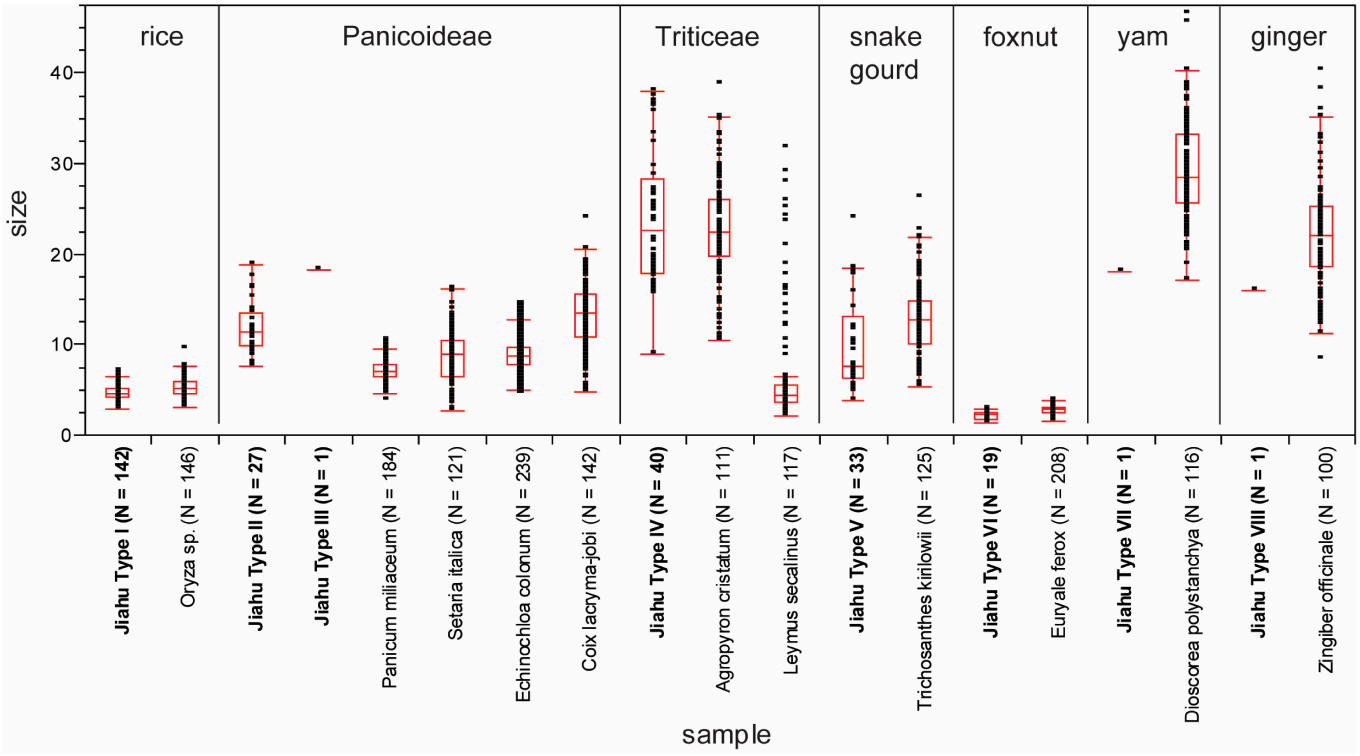


Figure 7. Boxplot comparison of starch granule size distributions for Jiahu starch morphotypes and corresponding modern reference taxa.

Type II Panicoideae taxa starches were recovered in seven vessels (n = 31; 6.9% of the total assemblage; 46.7% ubiquity). The granules are small and predominantly polygonal, with a few spherical forms, ranging in size from 7.65 to 18.88 μm (mean = 12.10 μm). Their morphology and size range are consistent with several Panicoideae taxa, including foxtail millet (*Setaria italica*), broomcorn millet (*Panicum miliaceum*), barnyard grass (*Echinochloa* sp.), and small granules of Job's tears (*Coix lacryma-jobi*) (Figure 5: 4; cf. Figure 6: 2–5; Figure 7). Consequently, individual granules cannot be assigned confidently to a more specific taxon based on starch morphology alone. However, phytolith analysis provides complementary information that permits more confident taxonomic interpretation (see below).

Carbonized barnyard grass seeds have previously been recovered from Jiahu [62], and Job's tears starches have been identified at the nearby Lingjing (ca. 14,000–11,000 cal. BP) and Shunshanji (ca. 8500–7000 cal. BP) sites in the Ying River region [63]. Although millet micro- and macrobotanical remains have been reported from several Peiligang culture sites (ca. 8000–7000 cal. BP), including Tanghu [64] and Peiligang [65], this study provides the first evidence for millet starch remains at Jiahu.

Type III Job's tears starch (*Coix lacryma-jobi*) was recorded in one vessel (n = 1; 0.2% of the total assemblage; 6.7% ubiquity). The granule is polygonal, with a linear fissure, and exhibits a zigzag-shaped extinction cross, a diagnostic characteristic of Job's tears starch. Its size (18.41 μm) also falls within the range of modern reference Job's tears starches (Figure 5: 5; cf. Figure 6: 5; Figure 7).

Type IV starches, attributed to wild grasses of the Triticeae tribe, were identified in seven vessels (n = 41; 9.1% of the total assemblage; 46.7% ubiquity). Some granules exhibit evidence of enzymatic hydrolysis and mild gelatinization (Figure 5: 7–9; cf. Figure 6:

8–10). Several Triticeae genera, including *Agropyron*, *Elymus*, and *Leymus*, are widely distributed across North China [66]. The Type IV granules range in size from 8.98 to 38.16 μm (mean = 23.96 μm), consistent with modern reference starches of these wild Triticeae taxa (Figure 7). Starches attributed to wild Triticeae grasses have also been reported from multiple Early and Middle Holocene sites in the Huai River region [63].

Type V starches, identified as snake gourd root (*Trichosanthes kirilowii*), were documented from three vessels (n = 33; 7.3% of the total assemblage; 20.0% ubiquity). The starch granules range in size from 3.97 to 24.04 μm (mean = 10.01 μm) and exhibit diverse morphologies, including bell-shaped, spherical, oval, and polygonal forms. The hilum is typically eccentric, and the extinction cross often displays bent arms. These characteristics are consistent in both morphology and size with modern reference starches from snake gourd roots (Figure 5: 10–12; cf. Figure 6: 11; Figure 7). Snake gourd is widely distributed across North China, and its root starches have been identified at Lingjing (ca. 14,000–11,000 cal. BP) and Shunshanji (ca. 8500–7000 cal. BP) sites in the Huai River valley [63], suggesting a long history of use as a food resource.

Type VI starches, identified as foxnut, the seed of prickly water lily (*Euryale ferox*), were observed in a single vessel (n = 4; 0.9% of the total assemblage; 6.7% ubiquity). These occur as round compound starch aggregates ranging in size from 16.97 to 34.14 μm (mean = 22.86 μm), composed of tightly packed small polygonal granules measuring 1.5–2.97 μm (mean = 2.25 μm) and enclosed within a distinct outer boundary. Their morphology and size are consistent with modern reference foxnut starches (Figure 5: 13; cf. Figure 6: 12; Figure 7). Prickly water lily is a freshwater plant widely distributed in China [67] (p. 118), and its seed starches have also been identified in fermentation-related pottery residues from the Peiligang site [8], located north of Jiahu.

Type VII starch, tentatively identified as yam (*Dioscorea polystachya*), was recovered from a single vessel (n = 1; 0.2% of the total assemblage; 6.7% ubiquity). The granule is triangular in shape and measures 18.24 μm. Its morphology and size are consistent with modern reference yam starches (Figure 5: 14; cf. Figure 6: 13; Figure 7). Yam is widely distributed across China, and its starches have been identified in fermentation-related pottery residues from multiple Neolithic Yangshao culture sites in the Yellow River valley [10]. Because this identification is based on a single starch granule, it should be regarded as tentative.

Type VIII starch, tentatively identified as ginger (*Zingiber officinale*), was recovered from a single vessel (n = 1; 0.2% of the total assemblage; 6.7% ubiquity). The granule measures 16.07 μm and is nearly fan-shaped, with the hilum positioned close to the margin and exhibiting pronounced relief under differential interference contrast (DIC) microscopy. These features are among the most diagnostic characteristics of starches from many *Zingiber* species [68] (Plate 27). The specimen is also consistent in both morphology and size with reference starches of *Zingiber officinale* in our comparative collection (Figure 5: 15; cf. Figure 6: 14; Figure 7). Ginger starches have been reported in fermentation-related pottery residues from multiple Neolithic sites in the Yellow River valley [10], suggesting their possible role in early fermentation practices. Because this identification is likewise based on a single starch granule, it should also be regarded as tentative.

Type IX starches, attributed to underground storage organs (USOs), were recovered from three vessels (n = 3; 0.7% of the total assemblage; 20% ubiquity). These granules are relatively large, oval in shape, and possess an eccentric hilum, characteristics typical of many USOs. However, they lack sufficient diagnostic features for assignment to a more specific taxonomic level (Figure 5: 16).

In summary, the starch assemblage is dominated by cereals in both abundance and ubiquity. Rice compounds were by far the most abundant and ubiquitous starch type

(86.7% ubiquity), followed by Panicoideae and Triticeae grasses. USOs and seeds comprise a much smaller component of the assemblage and include snake gourd, foxnut, and tentatively identified yam and ginger. Most starches recovered from the 15 residue-bearing vessels exhibit damage consistent with enzymatic hydrolysis and thermal processing, suggesting that these vessels were associated with both brewing- and cooking-related processing. In particular, some Panicoideae and Triticeae starch granules exhibited a combination of enzymatic hydrolysis and mild gelatinization, a pattern consistent with starch damage produced during mashing of malted cereals.

4.2. Fungal Remains

Fungal remains were identified in 15 vessels (n = 1–23 per sample). A total of 189 fungal particles were recorded, including cleistothecia, hyphae, mycelia, and yeast cells, of which cleistothecia are morphologically most consistent with *Monascus* sp.

The morphology of *Monascus* has been documented extensively for more than a century [55,56,69–71]. The diagnostic characteristics described in these studies have been widely adopted for the taxonomic identification of *Monascus* in food science and fermentation research [3,57,72]. Our identification is based on these published descriptions, together with modern reference collections curated at the Stanford Archaeology Center and comparative materials generated through experimental fermentation studies.

In the residue samples, cleistothecia are the most abundant fungal component (n = 124; 65.6% of the total assemblage; 93.3% ubiquity). These structures are purple, red, or orange, spherical to oval in shape, and composed of asci containing numerous small ascospores (Figure 8: 1–3; cf. Figure 8: 11). In one instance, a cleistothecium connected to a hypha appears to originate from plant epidermal cells in an early developmental stage (Figure 8: 4; cf. Figure 8: 10). Hyphae and mycelia are also common (n = 49 and 8, respectively, representing 25.9% and 4.2% of the total assemblage, with ubiquities of 80% and 33.3%, respectively). Most hyphae are hyaline, with a few appearing brown, and some exhibit branching and septation, morphological characteristics consistent with those of *Monascus* (Figure 8: 4–7; cf. Figure 8: 10, 12).

In contrast to the abundant filamentous fungal remains recovered from the interior residues, no fungal elements were identified in the control soil sample (P7), which instead contained numerous microcharcoal particles. Likewise, the pottery exterior controls yielded only one or two fungal elements per sample (Table 4). These marked differences indicate that the abundant fungal remains recovered from the vessel interiors are unlikely to reflect general environmental contamination. Furthermore, the extensive growth of *Monascus* requires nutrient-rich substrates together with appropriate temperature and moisture conditions, conditions that could not persist in surrounding burial soils following vessel deposition. Taken together, these observations suggest that the abundant *Monascus* remains preserved within the pottery residues have not resulted from post-depositional colonization.

Nevertheless, because molecular analyses were not conducted, the taxonomic assignment is based on morphology and should be interpreted within the broader context of the associated microfossil assemblage.

Yeast cells were identified in five vessels (n = 8; 4.2% of the total fungal assemblage; 33.3% ubiquity). Despite being present in relatively low abundance, they occur in multiple vessels and co-occur with *Monascus* remains and fermentation-related starch damage. Notably, in the P2 bottle and P6 basin, yeast cells are attached to tracheary elements and epidermal tissues, respectively. The cells are round to oval in shape (7–11.61 μm) and are morphologically consistent with *Saccharomyces cerevisiae* in our reference collection;

however, species-level identification cannot be confirmed based on morphology alone (Figure 8: 8, 9; cf. Figure 8: 13).

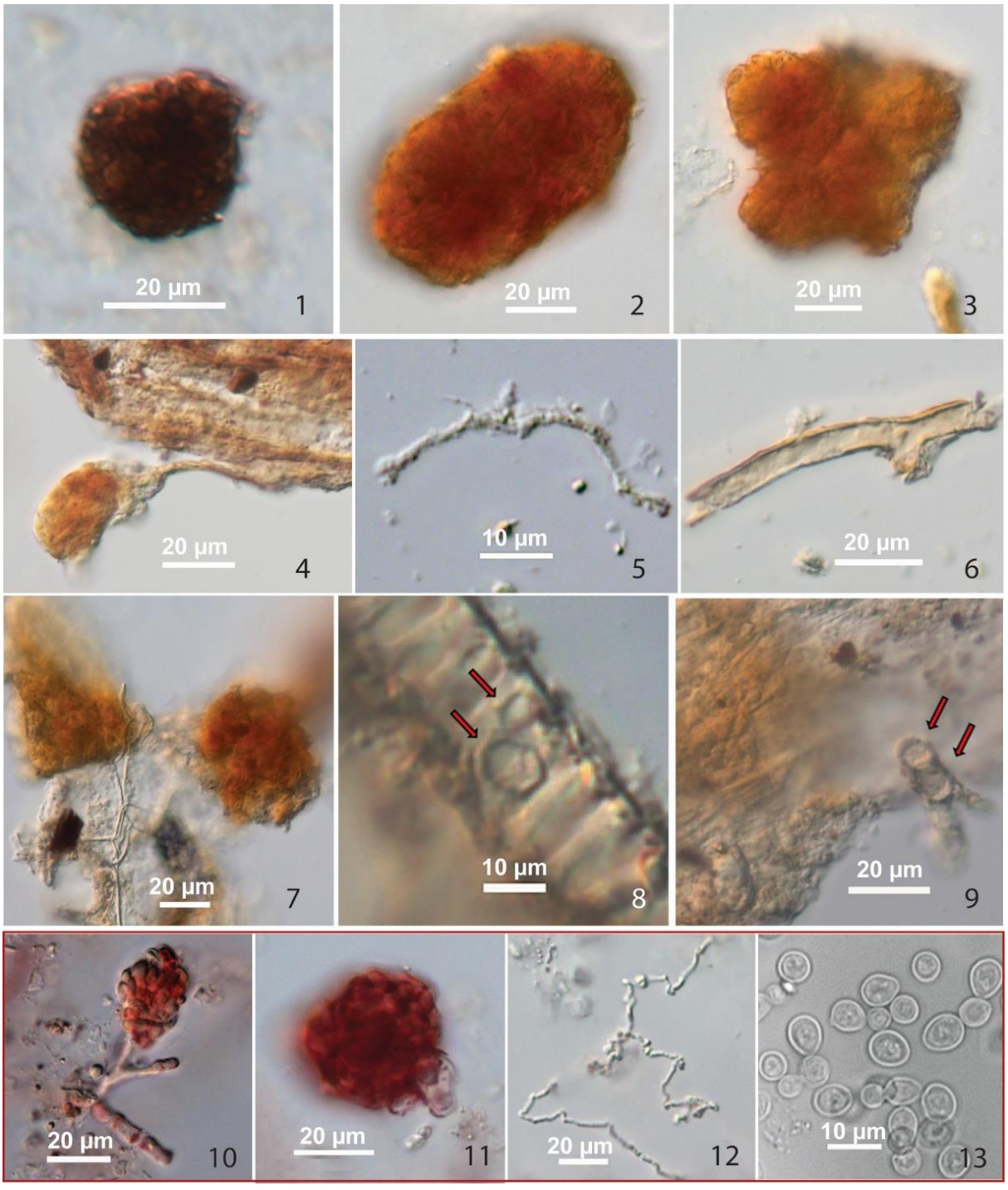


Figure 8. Representative fungal remains from Jiahu pottery compared with modern samples. *Jiahu fungi (1–9)*: (1) *Monascus* cleistothecum, round and oval shapes; (2) *Monascus* cleistothecum, appearing oval in shape, possibly resulting from the overlap of two adjacent round cleistothecia; (3) a cluster of four round *Monascus* cleistothecia; (4) *Monascus* hypha connected with cleistothecium growing from plant epidermis; (5) hypha, septate; (6) hypha, brown color; (7) two cleistothecia with mycelium; (8) connected yeast cells (arrows pointing) attached to plant tracheary; (9) two connected yeast cells (arrows pointing) attached to plant epidermis. *Modern fungi (10–13)*: (10) *Monascus* in the development stage; (11) *Monascus* cleistothecium in the mature stage; (12) *Monascus* hyphae; (13) yeast *Saccharomyces cerevisiae*.

Table 4. Jiahu fungi record.

Sample	Yeast Cell	*Monascus* Cleistothecium	Hypha	Mycelium	Fungi Total
P2 bottle	2	18	2	1	23
P3 bottle		10	3		13
P4 bottle	2	5	1		8
P7 jar	1				1
P8 jar		1			1
P9 jar		7	1		8
P10 jar		6	5	1	12
P11 jar		13	6	1	20
P12 jar		5	1		6
P13 jar		4	5		9
P14 jar		4	2		6
P15 jar	1	5	1		7
P16 jar		22	18	4	44
P6 basin	2	8		1	11
P5 cauldron		16	4		20
Total N.	8	124	49	8	189
Total %	4.2	65.6	25.9	4.2	100.0
Ubiquity N.	5	14	12	5	15
Ubiquity %	33.3	93.3	80.0	33.3	100.0
Size (μm)	7–11.61				
Control samples					
P1 incised basin	0	0	0	0	0
P2 EX			2		2
P7 Soil			0		0
P11 EX		1	1		2
P14 EX		1			1
P15 EX		1	1		2
P16 EX			2		2

In summary, *Monascus* remains were the dominant fungal component and occurred in nearly all residue samples. The co-occurrence of abundant *Monascus* remains, associated hyphae, yeast cells, and fermentation-related starch damage demonstrates a consistent association among these microfossil remains across multiple vessels.

4.3. Phytolith Remains

A total of 337 phytoliths were recovered from 15 vessels. Most phytoliths were concentrated in two vessels, P4 bottle (n = 204) and P8 jar (n = 62), whereas each of the remaining vessels contained only 1–12 phytoliths.

The phytolith assemblage is dominated by morphotypes associated with Poaceae. The phytolith assemblage from P4 bottle is morphologically diverse and includes elongate forms, bilobates, saddles, common bulliforms, *Phragmites* bulliforms, hair cells, and opaque perforated platelets. In contrast, P8 jar contains primarily husk phytoliths, most of which are highly fragmentary and can therefore only be broadly assigned to the Paniceae tribe. However, a few specimens can be tentatively identified as broomcorn millet η-type (n = 4), foxtail millet Ω-type (n = 1), possible barnyard grass β-type (n = 3), and Triticeae dendriform phytoliths (n = 1). In addition, crenate or columellate phytoliths derived from grass seed husks or inflorescences were also identified (n = 9) (Table 5; Figure 9). The presence of husk phytoliths from two millet taxa and possibly barnyard grass is consistent with the identification of Panicoideae starch granules that may have derived from these taxa. The P8 jar sample also contained abundant microcharcoal fragments, indicating repeated exposure to high-temperature heating.

Table 5. Jiahu phytolith record.

	Residue Samples																	Control Samples					
	P2 bottle	P3 bottle	P4 bottle	P7 jar	P8 jar	P9 jar	P 10 jar	P 11 jar	P 12 jar	P 13 jar	P 14 jar	P 15 jar	P 16 jar	P6 basin	P5 cauldron	totl N.	totl %	P1 ba-sin	P 2 ex	P 7 soil	P 11 ex	P 14 ex	P 15 ex	P 16 ex
η-type broomcorn millet husk					4											4	1.2							
Ω-type foxtail millet husk					1											1	0.3							
β-type barnyard grass husk					3											3	0.9							
Paniceae husk					30											30	8.9							
Dendriform husk				1	1									1		3	0.9							
UNID husk					4						1					5	1.5							
Crenate/crenate/ Columellate					6			1		1		1				9	2.7							
Rice double-peaked	1															1	0.3							
Phragmite bulliform			7	1					1			2		1		12	3.6	5						
Common bulliform			45													45	13.4	25				2	2	1
Elongates/square		3	105		13					1					5	127	37.7	81	1			1		
Rondel			35													35	10.4							
Bilobate			3													3	0.9							
Cross			1								1					2	0.6							
Opaque perforated platelets			3	1							1					5	1.5							
Hair cell		1	5													6	1.8							
Epidermal	9	2		1		3	1	2		6	2	1	3	9		39	11.6							
Tracheary	2	1				1					1		2			7	2.1							
Sponge spicule																		1						
Total	12	7	204	4	62	4	1	3	1	8	6	4	5	11	5	337	100	111	1	0	0	3	2	1

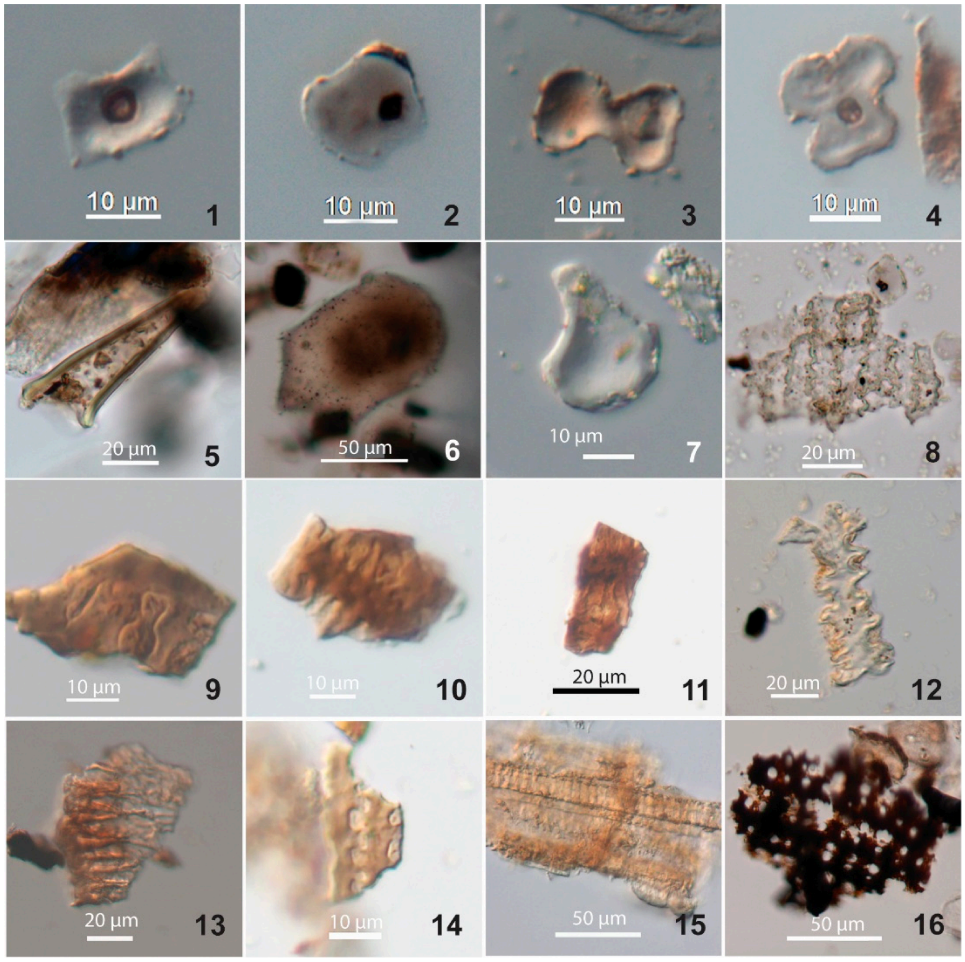


Figure 9. Representative phytolith morphotypes from Jiahu pottery. (1) Rodel; (2) saddle; (3) bilobate; (4) cross; (5) hair cell; (6) Phragmites bulliform; (7) common bulliform; (8) elongate sinuate; (9) Ω-type millet husk; (10) η-type broomcorn millet husk; (11) possible β-type barnyard grass husk; (12) dendriform Triticeae husk; (13) rice double-peaked; (14) elongate crenate; (15) tracheary; (16) Opaque perforated platelets.

These contrasting phytolith assemblages indicate that different categories of plant materials were probably processed in these two vessels. P4 bottle appears to have contained leafy plant materials, whereas P8 jar was more directly associated with cereal processing. Notably, most phytoliths recovered from P8 jar exhibit varying degrees of discoloration, ranging from light brown to dark brown or black (Figure 9: 9–11, 14), most likely resulting from heat-induced alteration [73,74]. The sand-tempered fabric of the P8 jar (Supplementary Materials Table S2), together with the abundant microcharcoal fragments and heat-altered phytoliths, is consistent with repeated exposure to high temperatures.

In addition, hair cells, epidermal tissues, and tracheary elements were recovered from 11 vessels (73.7%). Yeast cells and *Monascus* remains were observed attached to these plant tissues, suggesting that the tissues formed part of the fermented residue matrix (Figure 8: 4, 8, 9).

Among the control samples, the interior of the P1 basin yielded 111 phytoliths, whereas the absence of starch granules and fungal elements. The remaining control samples from pottery exteriors and adhering soil contained only negligible numbers of phytoliths (0–3 per sample) (Table 5).

Phytoliths occur in low numbers in most residue and control samples, with the exception of the P4 bottle, P8 jar, and the interior of the P1 basin, where they are considerably more abundant. Such high phytolith concentrations likely reflect vessel-specific

plant processing activities rather than background contamination. The phytolith assemblages further indicate that different plant tissues and taxa were processed in different vessel types.

Overall, in all three types of microfossil assemblages, the marked contrast between archaeological residues and control samples suggests that the observed microfossils cannot be explained by post-excavation contamination.

5. Discussion

The coexistence of starch granules, fungal remains, and phytoliths identified in the pottery residues provides multiple complementary lines of microfossil evidence for reconstructing the roles of Jiahu pottery vessels in alcoholic brewing. The following discussion addresses the three research questions outlined in the Introduction.

5.1. Brewing Ingredients and Techniques at Jiahu

Starch and phytolith analyses indicate the presence of both wild and domesticated plant taxa, including rice, broomcorn millet, foxtail millet, Job's tears, possible barnyard grass, Triticeae grasses, snake gourd root, foxnut, and possible yam and ginger. The exploitation of such a wide range of cereals, seeds, and USOs indicates a broad-spectrum subsistence strategy.

A large proportion of cereal starches exhibits enzymatic hydrolysis, brewing-related alteration (including mashing), and cooking-induced gelatinization, patterns consistent with the processing of starchy food materials for alcoholic brewing. These results suggest that these plants were used not only as daily food resources but also as brewing ingredients at Jiahu.

The strongest evidence for alcoholic production associated with the analyzed pottery vessels is the co-occurrence of brewing-related fungi, characteristic starch damage, and plant tissues bearing attached fungal elements. Collectively, these independent observations are most consistent with a *qu*-based brewing system involving saccharification and fermentation.

Given that rice starches and *Monascus* cleistothecia exhibit the highest ubiquity and abundance within their respective assemblages, rice and *Monascus* were probably the most important cereal components of the *qu*-based brewing system, whereas multiple cereals and USOs probably served as additional ingredients.

In addition, some Panicoideae and Triticeae starch granules displayed the combined pattern of enzymatic hydrolysis and mild gelatinization, consistent with starch alteration produced by the mashing of malted cereals, suggesting the possible practice of malt-based brewing.

Importantly, no single line of evidence is sufficient to identify ancient brewing practices; rather, the interpretation presented here is based on the convergence of starch, fungal, and phytolith evidence recovered from the same pottery residues.

Honey and fruits may also have been incorporated into the fermentation process, as suggested by McGovern et al. [7]. However, their presence in these starch-rich residue samples does not explain how saccharification—the process by which starches are converted into fermentable sugars—was achieved within the vessels. Instead, the abundant *Monascus* remains identified in this study suggest that enzymes secreted by this filamentous fungus may have played an important role in saccharification, although malted cereals may also have contributed to this process.

5.2. Pottery Vessels Associated with Fermented Beverages and Foods

Previous residue studies across Early Neolithic China indicate that globular vessels were commonly used for brewing and storing fermented alcoholic beverages (Figure 1; Supplementary Materials Table S1 for detailed site record). The globular jars and bottles from Jiahu appear to have served similar functions, as indicated by their residues, which contain starches exhibiting brewing-related damage together with fungal elements, including molds and yeast cells. Rice starches were identified in all jars and bottles, whereas *Monascus* remains occur in 92% of these vessels (Tables 3 and 4). Compared with rice, other starchy plant taxa exhibit lower frequencies and more limited distributions across the residue samples, suggesting that rice played the predominant role in fermentation activities at Jiahu (Figure 10). Although the jars are generally larger than the bottles, the preserved microfossil remains suggest that their functions were similar.

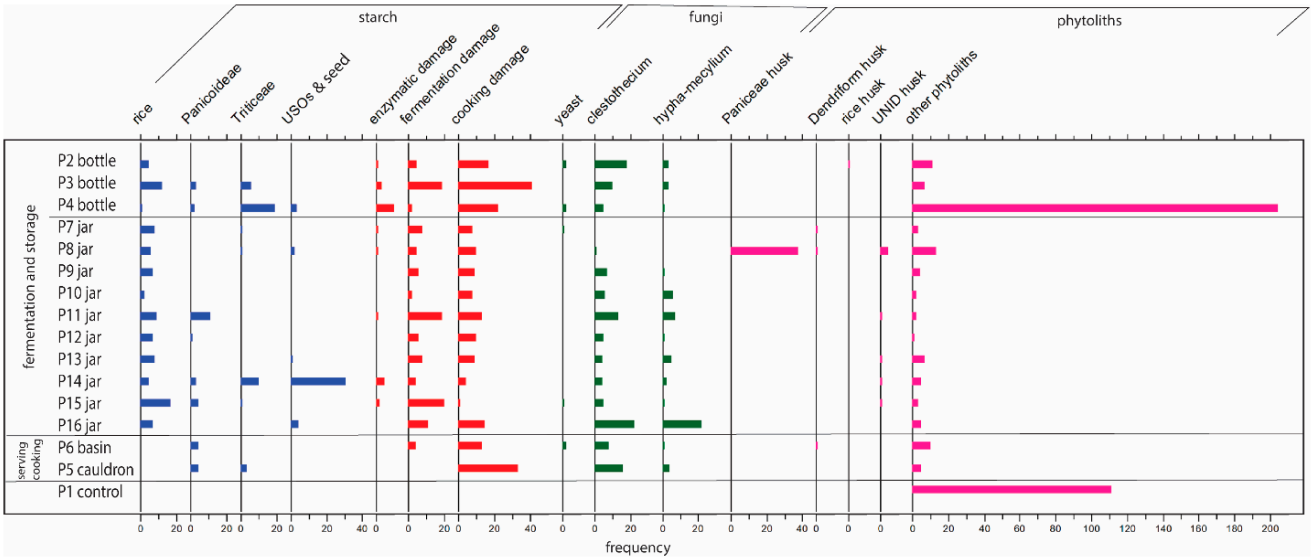


Figure 10. Comparison of major components of microfossil assemblages.

In contrast, rice was not identified in the basin and cauldron, although other starch types exhibiting fermentation- and cooking-related damage, together with *Monascus* cleistothecia, were present (Figure 10). This combination indicates that these two vessels were also associated with fermented foodstuffs. However, because of their open-mouth forms, they were not to have served as the primary fermentation containers. Instead, they were more likely used for heating, preparing, or serving fermented foods and beverages.

When the two functional categories of vessels are compared (Figure 10), most globular jars and bottles contain abundant fermentation-related microorganisms together with starch granules exhibiting all three types of damage associated with brewing, indicating that they served as the primary vessels for fermentation and storage. By contrast, although the basin and cauldron also yielded fermentation-related microorganisms, the damaged starch granules are dominated by cooking-induced gelatinization, suggesting that these vessels were primarily used for heating, preparing, or serving fermented foods and beverages rather than for primary fermentation.

Similar patterns have been reported from multiple sites, including Shangshan, Xiaohuangshan, and Peiligang, where not only globular jars but also basins, plates, and cooking cauldrons yielded fermentation-related starch and fungal remains [4,5,8].

Ethnographic and historical sources indicate that fermentation residues remaining after red rice beer production were commonly reused in cooking, such as in the preparation of meat dishes and preserved vegetables [3] (pp. 104–110), [60]. In addition, the heating of

alcoholic beverages prior to consumption, documented archaeologically in the Longshan culture, may also have contributed to the presence of fermented food residues in cooking vessels [75].

The interpretation of vessel function is based on the combined evidence from vessel morphology and residue composition rather than on either line of evidence alone. Overall, multiple vessel types at Jiahu were associated with fermented food remains, although globular jars and bottles appear to have been the principal vessels used for the production and storage of fermented beverages. This pattern is consistent with that observed at other Early Neolithic sites in China and suggests that fermentation formed an integral component of Early Neolithic culinary practices.

5.3. Spreading of Qu-Based Brewing and Development of Malt-Based Saccharification

Previous studies have established a broad chronological framework for the development of the *qu*-based, multi-ingredient brewing. This technique first emerged in the Shangshan culture of the lower Yangzi River region around 10,000–8500 years ago [4–6], reached the Yellow River region by 8000–7000 years ago [8], and became widespread across North China during the Middle Neolithic period (7000–3800 BP) [10] (Table 6.1). Across these sites, the *qu*-based method appears to have been characterized by a recurring association between *Monascus* and rice, suggesting that this combination formed the core of the brewing system. However, this apparent technical continuity has been interrupted by a temporal gap of several hundred years and a geographical gap in the Huai River region, where Jiahu is situated.

The results of the present study help bridge this temporal and geographic gap by demonstrating that fermentation practices in the Huai River region between 9000 and 7500 BP closely resemble those documented in both the lower Yangzi and Yellow River regions. These findings indicate that Jiahu may have occupied an important intermediary position in the spread of *qu*-based brewing technology from the lower Yangzi into North China (Figure 1).

The present study also provides what is currently the earliest archaeological evidence suggesting the use of malt-based brewing in China, which later became widespread in the Yellow River Valley and emerged as one of the principal traditions of alcoholic beverage production in China. Further research is needed to clarify its origins and developmental trajectory.

6. Conclusions

The present study employed microfossil analysis to investigate the functions of pottery vessels from Jiahu and evaluate their association with alcoholic production. The conclusions are derived from the convergence of multiple independent lines of evidence, not from any single proxy. The results indicate that residues preserved in Jiahu pottery contain evidence consistent with both *qu*-based and malt-based brewing, and relevant microfossil remains include *Monascus* fungal elements, yeast cells, multiple cereal taxa, and starch-rich USOs.

This interpretation differs from the previous identification of Jiahu residues as representing a mixed fermented beverage composed of rice, honey, and fruits. However, honey and fruits may also have been incorporated into the Jiahu fermentation process. When considered together, the previous chemical analyses and the present microfossil evidence provide complementary lines of evidence, indicating that rice was one of the most important brewing ingredients, that saccharification was achieved primarily through a *qu*-based method with contributions from malted cereals, and that honey and fruits may have supplied additional fermentable sugars.

Jiahu therefore appears to have served as an important transmission node in the spread of *qu*-based brewing from the lower Yangzi region into North China, while also preserving the earliest currently documented evidence suggesting the use of malt-based saccharification in China during the ninth millennium BP. Together, these findings substantially revise current understanding of Jiahu brewing practices and provide important new insights into the technological diversity and early development of alcoholic brewing traditions in Neolithic China.

Methodologically, this study demonstrates that microfossil analysis provides a robust framework for reconstructing ancient brewing ingredients and technologies, while integration with chemical residue analysis can further strengthen archaeological interpretations where complementary molecular evidence is available.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/heritage9080335/s1, Table S1. Neolithic and early Bronze Age sites revealed alcohol remains in China (ca. 10,000–3100 cal. BP; n = 38); Table S2. Jiahu pottery samples analyzed. References [76–97] are cited in Supplementary Materials.

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