Advances in Humanities Research Vol.13 Issue 1 EWA Publishing
Available Online: 8 January 2026 DOI: 10.54254/2753-7080/2026.31246

From cultural symbiosis to civilizational integration: archaeological and ancient DNA evidence from the Dasongshan cemetery in central Guizhou from a community perspective

Maoying Wang

School of History and Ethnic Culture, Guizhou University, Guiyang, China

1586542209@qq.com

Abstract. Taking the Dasongshan cemetery in the Guian New Area as a core case study, this paper integrates mortuary archaeological evidence with ancient DNA results within a "community" analytical framework to examine the transition in central Guizhou from pluralistic cultural symbiosis to institutionalized civilizational integration. Archaeological evidence indicates that since the Han–Jin period, external institutions and material cultures were continuously introduced and long coexisted with local burial customs. Ancient genomic data reveal a population structure dominated by Yellow River–related ancestry, stably overlaid with components from South China–Southwest China and Southeast Asia, alongside a small number of outlier individuals, reflecting patterns of intermarriage and regional interaction. The findings demonstrate that central Guizhou functioned as a key node where multi-source populations converged and were incorporated into state governance networks.

Keywords: Guizhou, Dasongshan cemetery, ancient DNA, community

1. Introduction

The central Guizhou region is located at the intersection of mountainous and river-valley corridors on the eastern Yunnan–Guizhou Plateau. It possesses the dual attributes of a transportation corridor and a resource node, and its historical trajectory can be understood within a long-term sequence of "the advancement of state governance → intensified population mobility → reorganization of local societies". Existing regional studies indicate that since the Han dynasty, the establishment of commanderies and counties, the expansion of transportation networks, resource exploitation, and patterns of settlement distribution exhibit observable coupling relationships. These findings suggest that the institutional penetration of early central authorities continuously reshaped local social structures and material cultural landscapes [1]. From an archaeological perspective, the introduction of Central Plains elements into Guizhou is not an abstract notion but is marked by concrete material indicators. For example, Han-style roof tiles and brick building materials bearing inscriptions such as "Changle Weiyang" found among Han-period architectural components at the Ninggu site in Anshun provide identifiable archaeological evidence for the entry of institutions, technologies, and populations [2].

Within this long-term context, this paper defines "cultural symbiosis" as the prolonged coexistence of populations and cultural elements from different origins within the same social space, accompanied by sustained interaction and reorganization driven by intermarriage, migration, trade, and governance networks. "Civilizational integration", by contrast, refers to a condition in which, under strengthened institutionalized governance and cross-regional circulation systems, material culture and social practices exhibit greater regulation and convergence [1]. The Dasongshan cemetery provides a critical material window through which to examine these processes. According to publicly released information and reports by the excavation team, the cemetery is located in the Machang Town area of the Guian New Area and was uncovered through rescue excavations conducted in conjunction with infrastructure development. Within a short period, the excavation revealed a cemetery of considerable scale, with a chronological span extending from the Two Jin period through the Ming dynasty, and with the highest concentration of burials dating to the Song, Yuan, and Ming periods. Its continuity and complexity endow it with strong potential for investigating the material dynamics of "pluralistic coexistence to gradual integration" [3].

The central questions addressed in this study are as follows: In the historical periods of central Guizhou, did "cultural symbiosis/civilizational integration" primarily manifest as cultural diffusion driven by the transmission of institutions and artifacts, or was it accompanied by substantial population influx and sustained interethnic interaction? Furthermore, how should population differences between Guizhou and neighboring regions (such as Guangxi and areas oriented toward Southeast Asia) be identified at the genetic level, and how can such evidence be integrated with process-oriented archaeological interpretations (see Figure 1) [4-6].

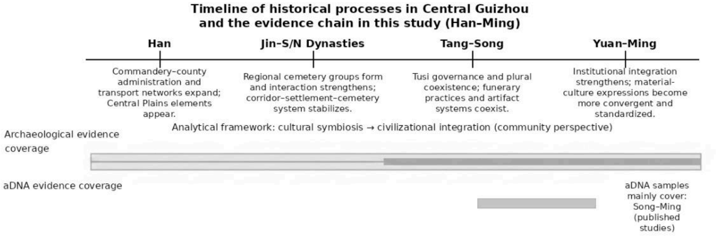

Figure 1. Timeline of historical processes and evidence chains in central Guizhou (Han dynasty–Ming dynasty). Drawn by the author

2. Archaeological overview of the Dasongshan cemetery

The Dasongshan cemetery is located in the Machang Town area of the Guian New Area, situated on a relatively gentle terrace within a karst landscape [3, 6]. At present, a comprehensive and systematically published excavation report has yet to be released. Accordingly, this paper does not attempt a detailed typological description of burial forms or artifact assemblages; instead, it approaches the site as a large-scale, long-term cemetery system dating to historical periods. Two points are particularly salient. First, the chronological span of the burials—from the Two Jin period through the Ming dynasty, with extensions into the Song and Yuan periods—indicates that this area maintained a stable settlement–cemetery configuration and a continuous burial tradition over an extended duration. Second, the complexity of the material record suggests that the populations represented and the associated social networks cannot be adequately explained through a single ethnic attribution or a unidirectional model of cultural transmission [3]. On this basis, the Dasongshan cemetery is interpreted within a framework of "community formation in corridor spaces." The patterns of continuous interment and the coexistence of diverse cultural elements revealed by the cemetery more plausibly reflect a processual outcome in which multi-source populations converged at a nodal point in central Guizhou, interacted, and were gradually incorporated into institutional networks, rather than an isolated local burial phenomenon [1, 3].

3. Ancient DNA analysis and results

3.1. Data sources and analytical pipeline: sampling, library construction, sequencing, and data integration

Research published in recent years on the Dasongshan cemetery in Machang Town, Guian New Area (referred to in the literature as Dasongshan/DSS/Songshan), has produced two complementary datasets that can be mutually cross-validated. The first consists of low-coverage whole-genome data centered on historical-period individuals from Dasongshan, designed to situate the cemetery population within the broader East Asian genetic landscape. The second treats "Songshan" as a composite population, generating panel-based data (Human Origins/1240k) spanning a long temporal range from the Song to the Ming dynasties, enabling cross-dynastic comparisons and admixture model fitting [4-6].

In studies focusing on individual-level data from Dasongshan, samples entered population genetic analyses through a stepwise filtering process of "initial screening → deeper sequencing → downstream statistical analysis". Of the 11 individuals initially screened, 7 were retained for further analysis based on endogenous DNA content exceeding threshold levels and controllable contamination rates. These genomes achieved an average coverage of approximately 0.32× (ranging from ~0.07× to 0.82×), with 77,000–429,000 effective SNPs overlapping the 1240k panel. Such data density is sufficient to support population genetic inference under low-coverage conditions using PCA, ADMIXTURE, f-statistics, and qpAdm [4].

At a larger sample scale, the "Songshan" population-level study generated panel-based data for individuals from multiple burial areas dating to historical periods. After quality control, these samples—covering approximately AD 990–1649—formed a dataset suitable for diachronic comparison, providing temporal depth for assessing the stability of population structure during the Song–Ming period, as well as the frequency and directional patterns of outlier individuals [5].

In terms of cross-study integration, existing research consistently merges newly generated data with reference datasets such as AADR/1240k and Human Origins. Projected PCA is conducted using smartpca, while f-statistics and qpAdm modeling are performed with ADMIXTOOLS. Pseudo-haploid genotype calling at 1240k loci is employed to enhance comparability across datasets with differing sequencing depths. Methodologically, these practices ensure consistency in comparative frameworks and the reproducibility of statistical inferences [4-6].

3.2. Data quality control and authentication: damage patterns, fragment lengths, and contamination control

With respect to authenticity assessment, the Dasongshan samples exhibit canonical ancient DNA terminal damage patterns and short fragment characteristics (mean fragment length approximately 47–55 bp), consistent with expected "chemical damage–fragmentation" signatures of ancient DNA sequences [6]. In terms of contamination control, published datasets report mitochondrial contamination rates largely in the range of ~1%–2%, while X-chromosome contamination estimates for male individuals are also low (approximately

0.2%–3%). Overall, these metrics meet the reliability standards required for comparative analyses of historical-period populations [6].

Expanded-sample studies further employ a composite filtering strategy combining damage patterns, mitochondrial/sex-chromosome contamination estimates, and sequencing coverage, with explicit contamination thresholds (e.g., < 5%) to define samples eligible for downstream analyses. In addition, kinship detection and the exclusion of close relatives are applied to reduce potential biases introduced by family structure, particularly in PCA clustering and qpAdm admixture proportion estimation [6].

3.3. Population structure: PCA and ADMIXTURE reveal a stable "north–south admixture zone"

Within a PCA framework, historical-period individuals from Dasongshan/Songshan consistently fall between the northern and southern East Asian genetic gradients and within the Han Chinese cline, showing closer affinity to geographically proximate central–southwestern Han populations. This spatial positioning indicates that the Dasongshan population cannot be characterized as purely "northern" or "southern"; rather, it occupied a long-term admixture zone with overlapping northern and southern components, a pattern that aligns well with the corridor-like role of southwestern China during historical periods [4, 5].

ADMIXTURE results corroborate the PCA-based inference. The core Songshan population is dominated by Yellow River–related ancestry, with a stable overlay of local South China–Southwest components and more broadly defined Southeast Asian–related components. A small number of individuals display elevated proportions of southern-related ancestry, indicating discernible genetic heterogeneity within the cemetery system. Importantly, this heterogeneity does not represent stochastic noise but rather a reproducible "outlier signal" observed across multiple structure analyses [5, 6].

3.4. Quantitative tests and admixture models: f-statistics and qpAdm support a lineage pattern of "yellow river dominance with southern admixture"

At a quantitative level, qpAdm modeling provides an operational admixture framework for the core Songshan population, which can be adequately explained as predominantly Yellow River–related ancestry with additional southern inputs. Outlier individuals consistently exhibit higher proportions of southern ancestry, translating the observed pattern of "relative homogeneity at the group level versus marked individual variation" into reportable admixture parameters [5, 6].

More critically, relevant studies juxtapose the dominance of Yellow River–related ancestry—shared with Han Chinese populations—with processes of Han cultural expansion in historical periods. The genetic evidence is interpreted as being more consistent with a model of demic diffusion, involving substantial population movement, rather than a purely cultural diffusion driven solely by the transmission of artifacts, institutions, or ideas [6].

3.5. Haplogroups, kinship, and ROH: genetic clues to multi-source origins and marriage structure

Haplogroup analyses provide individual-level corroboration for "multi-source integration". Published samples from Dasongshan show relatively diverse maternal lineages but a more concentrated set of paternal lineages, producing a pattern of "greater paternal concentration and more dispersed maternal diversity". This configuration is more compatible with open marriage systems and intergroup intermarriage, and it suggests that the burial community was not a highly closed, lineage-based group [4].

Kinship and Runs of Homozygosity (ROH) analyses further illuminate aspects of social structure. Existing studies reveal no pronounced close-kin clustering, with ROH profiles dominated by short segments, collectively indicating a population background without strong signals of close inbreeding. Expanded datasets also identify kinship links across different burial areas, implying that these zones may have been embedded within a broader burial community network rather than representing several isolated small groups [4, 6].

3.6. Summary: genetic evidence for a combined process of "immigration, local continuity, and sustained interaction"

Synthesizing results from PCA, ADMIXTURE, qpAdm, and related analyses, the genetic composition of the historical Dasongshan/Songshan population can be summarized in three key points:

(1) Directionality and stability of the core lineage. The core Songshan population consistently occupies a position within the Han genetic cline and is modeled as predominantly Yellow River–related ancestry. This conclusion is robust across different studies and statistical frameworks, indicating a structural association between the principal population component of historical-period communities in central Guizhou and northern/Central Plains–related lineages [4, 5].

(2) Persistent overlay of southern sources. Under conditions of Yellow River–related dominance, components associated with local South China–Southwest populations and more broadly defined Southeast Asian sources are stably present. Rather than being incidental features of a few samples, these components constitute a population-level "background constant", implying that community formation involved not unilateral replacement of local lineages but gradual reorganization through sustained intermarriage and interaction [5, 6].

(3) Individual heterogeneity and community openness. A small number of outlier individuals show stronger southern inputs and systematic deviations in structure analyses. When combined with kinship and ROH evidence for the absence of strict endogamy, these patterns can be interpreted as a genetic projection of continued influx from multiple source populations into corridor spaces, followed by incorporation into the community through marriage networks [4, 6].

Mechanistically, these three points converge on a "composite process". On the one hand, the dominance of Yellow River–related ancestry and the relative stability of the core population structure during the Song–Ming period support an interpretation that links Han cultural expansion with population movement—that is, a coupled process of "institutional advance–population mobility–reweaving of social structure" consistent with demic diffusion. On the other hand, the persistent presence of southern-related components and the appearance of outlier individuals emphasize that local lineages and peripheral interactions were not interrupted but instead became embedded within the community in more subtle yet quantifiable ways [4-6].

Accordingly, the transition in central Guizhou from "cultural symbiosis" to "civilizational integration" should not be understood as a linear trajectory of "cultural input followed by local assimilation". Rather, it represents a long-term integrative process in which population migration served as a major driving force, accompanied by the sustained participation of local and neighboring lineages. The outcome was a community-level structure dominated by Yellow River–related ancestry while retaining a southern genetic substrate, alongside substantial and observable individual-level heterogeneity [4-6].

4. From "cultural symbiosis" to "civilizational integration": mutual corroboration between archaeological manifestations and genetic evidence

4.1. Pluralistic coexistence and symbiotic patterns during the Song–Yuan period

From the perspective of regional archaeological materials, the mortuary landscape of central Guizhou since the Tang–Song period cannot be subsumed under a single institutional system. Multiple burial traditions—such as earthen pit graves, stone-chamber tombs, brick-chamber tombs, and cave burials—coexisted in parallel, indicating the long-term presence of different cultural traditions and social groups within the same region during a single period [7]. Accompanying this plurality of burial forms is the "co-presence" and "differentiated coexistence" of artifact assemblages. Objects with transregional attributes, including currencies and certain artifact types, entered local society, while localized operational traditions and modes of identity expression retained discernible continuity [7]. This configuration more closely resembles "plural cohabitation within a community" than a unidirectional process of cultural replacement.

4.2. Institutionalized integration and material convergence since the Ming Dynasty

Regional studies suggest that, with the strengthening of institutionalized governance and the expansion of transportation, military, and corvée–taxation networks, central Guizhou became more tightly embedded within state structures. Under these conditions, material culture and social practices tended to exhibit stronger regulation and replicability [1]. With respect to the Dasongshan cemetery, publicly available information emphasizes that its rescue excavations conducted over a short period established a cultural sequence and chronological framework spanning from the Two Jin period to the Ming dynasty, underscoring its benchmark significance [3]. When considered alongside the ancient DNA evidence for a "stable core population structure", the period since the Ming dynasty may be understood as a phase characterized by "reinforced institutional networks and relatively stabilized community boundaries". This was not an instantaneous assimilation that erased differences, but rather a convergence at the level of practice facilitated by more robust systems of governance and circulation.

4.3. Mechanisms of population movement and intergroup interaction

The driving forces behind "cultural symbiosis/civilizational integration" in central Guizhou hinge not on the mere presence of external cultural elements, but on the pathways through which these elements entered and were absorbed by local society. The critical question is whether these processes were dominated by "cultural diffusion" centered on the transmission of artifacts and institutions, or by a coupled "demic–cultural diffusion" involving substantial population influx and sustained intermarriage. Equally important is whether population differences between Guizhou and neighboring regions (such as Guangxi and areas oriented toward Southeast Asia) can be consistently identified at the genetic level and integrated with historical processes [4-6].

Ancient DNA results provide testable answers to these questions. First, the core Songshan population consistently occupies a position between the northern and southern East Asian genetic gradients in PCA and falls within the Han genetic cline, while qpAdm modeling indicates dominance of Yellow River–related ancestry. This combination of "structural position plus proportional dominance" is difficult to account for through artifact transmission alone [5]. Second, a small number of outlier individuals display elevated proportions of southern ancestry in structure analyses and admixture modeling, and show quantifiable genetic affinities with South China–Southwest populations. These patterns indicate that local lineages were not unidirectionally replaced, but rather remained actively involved in community networks over the long term, leaving differentiated genetic signals at the individual level [5, 6].

On this basis, the historical evolution of central Guizhou can be interpreted as a composite mechanism. At the macro level, the dominance of Yellow River–related ancestry and its stability through the Song–Ming period align with a framework of demic diffusion, in which directional population movement accompanied Han cultural expansion. At the same time, the persistent presence of southern-related components and the recurrent appearance of outlier individuals demonstrate that sustained intermarriage and regional interaction within corridor spaces did not cease; instead, local and peripheral lineages were continuously incorporated and reorganized through community networks [4-6]. This provides a population-level explanation for the archaeological pattern of "coexisting burial systems followed by convergence in practice": symbiosis was not a static coexistence, but a dynamic process in which shared institutions and practices gradually emerged through prolonged interaction.

4.4. Summary

By integrating the archaeologically observable patterns of pluralistic coexistence and subsequent institutionalized convergence with the genetic structure characterized by "dominant Yellow River–related ancestry, superimposed southern sources, and pronounced individual heterogeneity", it can be argued that the transition in central Guizhou from "cultural symbiosis" during the Song–Yuan period to more pronounced "civilizational integration" after the Ming dynasty was not a linear process of replacement. Rather, it represents a gradual fusion and institutional convergence of multi-source populations under the sustained influence of state structures and regional networks.

5. Conclusion

First, the social evolution of central Guizhou during historical periods can be summarized as a processual chain of "pluralistic cohabitation → interactive reorganization → institutionalized convergence". Since the Tang–Song period, the coexistence of multiple burial systems and artifact assemblages reflects the long-term presence of diverse cultural traditions within a single community. From the Ming dynasty onward, under conditions of strengthened institutional networks, social practices increasingly tended toward regulation and convergence [1, 7].

Second, ancient DNA evidence from Dasongshan/Songshan converges on consistent conclusions at both the level of population structure and admixture modeling. Historical-period populations were dominated by Yellow River–related ancestry, while stably incorporating components associated with local South China–Southwest populations and more broadly defined Southeast Asian sources. A small number of outlier individuals retained stronger signals of southern ancestry, pointing to sustained intergroup interaction and differentiated modes of integration [4-6].

Third, the mutual corroboration of archaeological and genetic evidence supports an interpretation of central Guizhou as a "community node within corridor spaces". The introduction of external institutions and cultural elements was not accomplished solely through the transmission of artifacts, but occurred in tandem with substantial population movement, marriage networks, and the continuity of local lineages. Accordingly, "civilizational integration" is better understood as a gradual process of institutionalized convergence rather than the wholesale erasure of local traditions [1, 4, 5].

Fourth, from a materials-based perspective, the significance of the Dasongshan cemetery lies not only in its scale and chronological breadth, but also in its capacity to provide a continuously traceable observational window into how multi-source populations occupying the same space were incorporated into state structures. Future work—once formal excavation reports become available—can further refine burial phasing, inter-area variation, and artifact genealogies, and integrate these data with higher-coverage genomic evidence. Such efforts will help anchor explanations of "symbiosis–integration" mechanisms at finer temporal resolutions and within more specific social units [3, 6, 7].

References

[1] Zhou, B., & Zhang, H. (2022). The historical development of Guizhou as reflected by archaeological remains. *Guizhou Cultural History Review*, (3), 95–101. https: //doi.org/10.14040/j.cnki.52-1004/k.2022.03.003

[2] Liu, E., & Guo, B. (2004). Excavation of the Ninggu Han-dynasty site and tombs in Anshun City, Guizhou Province. *Archaeology,* (6), 50–58, 104.

[3] Shu, C. (2023). The archaeological excavation team of the Dasongshan burial complex explores Guizhou's long-slumbering cultural heritage. *Contemporary Guizhou,* (Z4), 11–12.

[4] Zhang F., Zhang X., Bai B., et al.: "Ancient Genomes Provide Insights into the Genetic History in the Historical Era of Southwest China", *Archaeological and Anthropological Sciences, 16*(8), 120, 2024.

[5] Zhu K., Hu C., Yang M., et al.: "The Demic Diffusion of Han Culture into the Yunnan–Guizhou Plateau Inferred from Ancient Genomes", *National Science Review, 11*(12), nwae387, 2024.

[6] Wan W., Wu S., Zhang H., et al.: "Ancient Genomes in Southwest China Revealed Genetic Interactions among Diverse Populations in the Historical Period", *BMC Biology, 23*, 174, 2025.

[7] Ye, C. (2016). An exploration of archaeological remains from the Tang–Song jimi period in central Guizhou. *Local Culture Research,* (6), 60–70.