

RESEARCH ARTICLE

Ancient Genomes Illuminate the Demographic History of Southwest China

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Abstract

Southwest China, at the crossroads of East Asia, Southeast Asia, and the Tibetan Plateau, is pivotal for understanding human migration and population history. Recent ancient DNA (aDNA) studies, integrated with archaeological, ethnological, and linguistic evidence, reveal deep diversity among Paleolithic hunter-gatherers, shaped by both divergence and long-distance exchange. With the advent of agriculture, interactions between Yellow River farmers and local foragers produced varied outcomes, ranging from replacement to admixture across subregions. In the historical period, intensified gene flow from multiple parts of East Asia further transformed the region, contributing to today's extraordinary ethnolinguistic diversity. Despite progress, major challenges remain, including limited samples, poor DNA preservation in subtropical settings, and uneven spatiotemporal coverage. Expanding genomic datasets and strengthening interdisciplinary integration will be critical to reconstructing a comprehensive picture of demographic and cultural evolution in this key region.

Keywords: Southwest China, Ancient DNA, Hunter-gatherers, Agricultural Transition, Historical Period.

1. Introduction

Southwest China, positioned at the nexus of East Asia, Southeast Asia, and the Tibetan Plateau, represents a pivotal crossroads in shaping the genetic landscape and cultural networks of southern East Asia. Geographically, the region encompasses the Yunnan–Guizhou Plateau, the Sichuan Basin, the southern margins of the Tibetan Plateau, and the western Guangxi–Guangdong Hills. In archaeological contexts, however, the scope of “Southwest China” is often defined more broadly, extending from the Tibetan Plateau to the transitional zone leading into the low-altitude hills of central China [1]. The Tibetan Plateau stands apart for its extreme elevation,

distinctive ecological conditions, and unique cultural trajectories, particularly in its central and western areas. Accordingly, here we define “Southwest China” primarily as the Yunnan–Guizhou Plateau, the Sichuan Basin, and the western Guangxi–Guangdong Hills, encompassing the modern provinces of Sichuan, Chongqing, Yunnan, Guizhou, and Guangxi of southern China. This area is notable for its complex topography and ecological diversity, and is among the most ethnolinguistically diverse regions of China, home to populations speaking branches of the Sino-Tibetan, Hmong-Mien, Tai-Kadai, and Austroasiatic language families. Southwest China played a central role not only in the origins and dispersal of

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agriculture, but also in subsequent cultural exchanges and population movements, making it a key region for reconstructing both Chinese and broader East Asian demographic history.

Archaeological evidence demonstrates that human occupation in Southwest China extends back to the Early Paleolithic [2]. Lithic artifacts from sites such as Guanyindong in Guizhou and Tianhe Cave in Yunnan (170,000–30,000 BP) exhibit Levallois [3,4] and Keilmesser [5] techniques, commonly associated with Neanderthals, suggesting their possible dispersal into the region by the Middle Paleolithic [6]. By the Late Paleolithic, modern humans from Southeast Asia expanded northward into Southwest China [7], with widespread microlithic assemblages indicating that they replaced or absorbed earlier populations and became dominant lithic producers [8]. At the Paleolithic–Neolithic transition, assemblages from the Lancang River basin in Yunnan display unifacial pebble tool production characteristic of the Hòabìnhian tradition, a Southeast Asian technological complex marking a shift toward more sedentary hunter-gatherer lifeways [9]. Its northernmost extension reached into southwestern Yunnan (e.g., Xiaodong rockshelter in Cangyuan), and its distribution along river valleys highlights the role of rivers as both subsistence bases and corridors of movement [10,11].

With the onset of the Neolithic, population interaction and cultural exchange in Southwest China intensified. Around 6,000 years ago, migrants associated with the Yangshao culture reached the northwestern Sichuan Plateau, where they interacted with local foragers, adopting mixed subsistence strategies that combined millet cultivation with the gathering of wild plant resources [12]. Archaeobotanical evidence from Yingpanshan and Haimenkou in Sichuan and Yunnan confirms the coexistence of millet and

rice cultivation, underscoring the region's highly diversified subsistence economy shaped by the admixture of distinct agricultural traditions [13–15]. In the historical era, patterns of migration and exchange were closely tied to shifts in political authority, trade networks, and state frontier policies. Archaeological and textual records indicate the emergence of polities such as Ba, Shu, and Dian during the Xia, Shang, and Zhou periods [16], which maintained close ties with Southeast Asia [17]. With imperial expansion into the southwest, Han cultural influences increasingly integrated with local Yi, Miao, Tibetan, Zhuang, and other traditions, fostering enduring ethnic and cultural diversity.

In recent years, the application of whole-genome sequencing in ancient DNA (aDNA) research has opened new opportunities for investigating the demographic history of prehistoric populations. While northern China has been the primary focus—owing to more favorable preservation conditions that have enabled systematic reconstruction of genetic lineages from ~40,000 years ago through the historical period [18]—research in Southwest China has lagged, constrained by subtropical climates, acidic soils, and limited sample availability. Consequently, major gaps remain in our understanding of population origins, migrations, and admixture in this region. Nevertheless, the analysis of the limited datasets available has already provided valuable insights into its complex demographic history (Figure 1 and Table 2). Building on these findings, this study synthesizes recent aDNA research from Southwest China and integrates evidence from archaeology, ethnology, and linguistics to investigate population origins, migration dynamics, and admixture processes, offering new perspectives for reconstructing the demographic and cultural trajectories of this critical region.

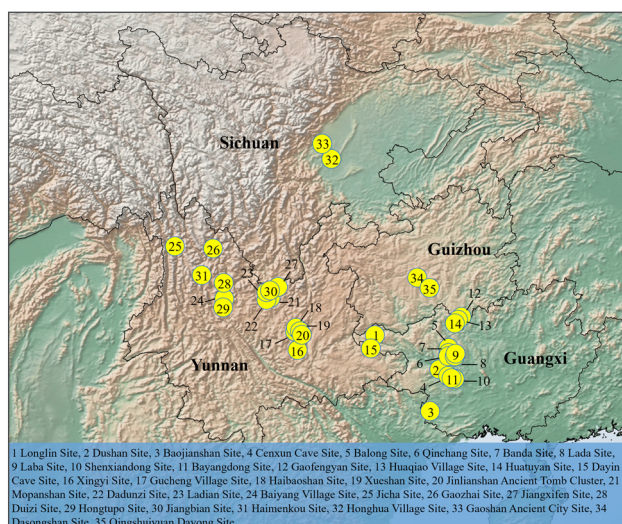


Figure 1. Distribution of Ancient Sites in Southwest China with Published Ancient DNA Analyses

Table 1. Glossary of Terms Used in This Study

Term	Definition
Ancient Southern East Asians (SEA)	Represented by individuals from Neolithic sites such as Liangdao in Fujian and Qihe Cave, distributed along the southeastern coast of East Asia, showing close genetic affinity with present-day southern populations.
Ancient Northern East Asians (NEA)	Primarily refers to Neolithic to Bronze Age agricultural populations from the Yellow River Basin, Heilongjiang, and Shandong regions; they constitute a major ancestral source for modern Sino-Tibetan language speakers.
Southeast Asian Hòabìnhian Population (Hòabìnhian)	Hunter-gatherer groups distributed across mainland Southeast Asia from the Late Paleolithic to Early Neolithic, exemplified by individuals such as La368 from Laos, carrying distinctive early Southeast Asian genetic components.

Table 2. Summary of Major Ancient Populations in Southwest China and Their Ancient Genomic Samples Discussed in This Study

Main Population	Sampling Region	Number of Ancient Genomic Samples	Calibrated Age (cal a BP)	Sample Period	Genetic Characteristics	References
Longlin	Guangxi	1	10686-10439	Late Paleolithic	Carrying Basal Asian Xingyi ancestry and Ancient Southern East Asian components, representing a deep lineage predating the north-south differentiation in East Asia, with no genetic contribution to modern populations.	[24]
Dushan	Guangxi	1	8974-8593	Early Neolithic	Genetic admixture of Longlin ancestry and Ancient Southern East Asian populations.	[24]
Baojianshan	Guangxi	2	8335-6400	Early Neolithic	Genetic admixture of three ancestral sources: Basal Asian Xingyi ancestry, Ancient Southern East Asians, and Hòabìnhian populations.	[24]
Historical Guangxi Populations (Laba, LaCen, BaBanQin-Cen, etc.)	Guangxi	26	1688-294	Historical Period	Genetic admixture of Ancient Southern East Asians and Ancient Northern East Asians, forming the genetic foundation of modern Zhuang-Dong and Miao-Yao language families.	[24]
Xingyi_EN	Yunnan	1	7158-6888	Early Neolithic	Carrying Basal Asian Xingyi ancestry, representing one of the sources of the Tibetan Plateau’s ghost ancestry.	[26]
Xingyi_LN	Yunnan	9	5435-4296	Late Neolithic	Forming a novel genetic lineage characterized by Central Yunnan ancestry, which serves as a primary ancestral source for modern South Asian language-speaking populations.	[26]
Xingyi_BA	Yunnan	10	3894-3385	Bronze Age	Exhibiting genetic continuity of the Central Yunnan ancestry component.	[26]
Haimenkou	Yunnan	6	3200-2900 ^a	Bronze Age	Exhibiting close genetic affinity with Ancient Northern East Asian populations.	[26,45]
Baiyangcun	Yunnan	16	3569-3366 ^b	Bronze Age		[26]
Gaozhai	Yunnan	14	2490-2121 ^b	Bronze Age		[26]
Dayindong	Yunnan	5	3444-3180 ^b	Bronze Age	Genetic admixture of Ancient Southern East Asian components and Central Yunnan ancestry.	[26]

Gaoshan	Sichuan	5	4500-3720 ^a	Late Neolithic	Predominantly carries millet-farming genetic components associated with the Yellow River Basin populations, with minor admixture from Hòabínhian ancestry.	[45]
HHC_cliff	Sichuan	4	~1800 ^c	Historical Period	Genetic structure clusters closely with Bronze-to-Iron Age northern populations from the Yellow River Basin.	[57]
Qingshuiyuan Dadong(QSYDD)	Guizhou	1	11201-11079	Late Paleolithic	Shares mitochondrial haplogroup M71d with Longlin individuals.	[60]
Dasongshan	Guizhou	106	960-301 ^b	Historical Period	Predominantly carries genetic components from Yellow River Basin agricultural populations, admixed with Hòabínhian ancestry and Longlin ancestry from Guangxi.	[62,63]

Note: ^aOnly a subset of samples within the population underwent direct radiocarbon dating; the ages of the remaining samples are inferred from archaeological context. ^bOnly a subset of samples within the population underwent direct radiocarbon dating. ^cSamples were not directly radiocarbon dated; the ages are based solely on archaeological context.

2. The Guangxi Region of Southwest China

Guangxi, bordering the South China Sea and Vietnam, has long served as a critical corridor linking East and Southeast Asia. The western part of Guangxi lies on the southeastern margin of the Yunnan–Guizhou Plateau, with a general northwest-to-southeast slope, while the Zuo and You River basins host dense concentrations of prehistoric cultural sites. Ancient DNA studies in this region have so far focused on the Longlin, Dushan, and Baojianshan individuals, together with several groups from the historical period (Fig. 1, Table 2). The human cranium from Laomucuo Cave (“Longlin individual,” ~11 ka) has been debated morphologically, with early cranial assessments proposing archaic–modern admixture [19,20], and subsequent inner ear labyrinth analyses favouring affinity with early modern humans [21]. Genomic data are consistent with a modern human classification: the Longlin genome does not show excess Neanderthal or Denisovan ancestry beyond levels typical of Holocene East Asians. Critically, Longlin harbours a previously unrecognised “deep East Asian” lineage that, together with Ancient Southern East Asians (ASEA) [22] and Southeast Asian Hòabínhian foragers, delineates three early southern lineages [23]. This deep lineage predates the north–south differentiation within East Asia [22] and leaves little or no direct trace in present-day populations.

Subsequent work identified a 7.1 ka individual from Xingyi, Yunnan (Xingyi_EN), carrying an even more basal, deeply divergent ancestry. The “deep East Asian” component in Longlin corresponds to the ancestral stratum of Xingyi_EN—termed Basal Asian Xingyi ancestry [24]. Mixture modelling

indicates that Longlin comprises ~48.8–71.5% Basal Asian Xingyi ancestry with the remainder related to ASEA, implying Paleolithic gene flow between Southwest China and regions to the south mediated by mountain corridors and river valleys [24]. By ~9 ka, the Dushan genome shows ~17% Longlin-related ancestry and ~83% ASEA, signalling sustained connectivity between inland Southwest China and the southeastern seaboard [25]. Later, individuals from Baojianshan (8.3–6.4 ka) carry an additional ~28% Hòabínhian ancestry on a Dushan-like background, yielding a three-source composite and indicating that Southeast Asian foragers had dispersed into Guangxi by the Early Neolithic [23,24].

Over subsequent millennia these ancient ancestries declined and, in most groups, disappeared. Historical populations dated to ~1.5 ka (e.g., Laba, LaCen, BaBanQinCen, Shenxiandong, Bayangdong) form a tight cluster overlapping present-day Tai–Kadai speakers (notably the Zhuang), whereas the ~0.5 ka Gao Huahua group clusters separately and is closer to Hmong–Mien speakers. qpAdm models Guangxi groups from ~1.5–0.5 ka as ~58.2–90.6% ASEA plus ~9.4–41.8% Ancient Northern East Asian (ANEA) ancestry related to Neolithic Yellow River farmers (e.g., Yangshao). f4 statistics detect a Dushan-related deep signal only in BaBanQinCen [23], pointing to substantial population turnover between ~6.4 and 1.5 ka, with incoming Yellow River–related ancestry reshaping local gene pools and contributing to the genetic foundations of present-day Tai–Kadai and Hmong–Mien populations in the region.

3. The Yunnan Region of Southwest China

Yunnan lies at the interface between the Tibetan Plateau and the Southeast Asian lowlands, characterized

by rugged topography and exceptional ecological diversity. Since prehistory it has served as a vital corridor for human migration and cultural exchange. Archaeological records document a continuous cultural sequence from the Paleolithic through the Bronze Age, with the Dian culture standing out as a regional hallmark of the Bronze Age. Recent ancient DNA studies in Yunnan have focused on key populations including the Xingyi, Haimenkou, Baiyangcun, and Gaozhai individuals. Integrating geographic and genomic evidence, Yunnan can be broadly subdivided into three zones—Central, Eastern, and Western Yunnan—providing a framework to investigate the genetic structure of ancient populations and their interactions with adjacent regions.

3.1 Central Yunnan

The Xingyi site in Tonghai County, located in the central Yunnan Basin, spans ~3,800 years from the Early Neolithic to the historical period and represents the most informative sequence in Central Yunnan. Ancient DNA reveals that the earliest individual—dated to ~7.1 ka (Xingyi_EN)—harbors a previously undescribed, deeply divergent Asian ancestry, termed Basal Asian Xingyi ancestry [24]. Genetic analyses show that Xingyi_EN, the ~40 ka Tianyuan individual from northern China, and the ~8 ka Hòabìnhàn individual La368 from Laos are genetically equidistant [24,26], indicating that Basal Asian Xingyi ancestry diverged from other Asian lineages at least 40,000 years ago. This ancestry admixed with Ancient Southern East Asians in the ~11 ka Longlin genome from Guangxi but subsequently disappeared from later Yunnan and Guangxi populations. Remarkably, it persisted on the Tibetan Plateau, where it contributes to the “ghost ancestry” that today accounts for ~20% of the genetic makeup of highland populations, alongside ~80% ancestry from Ancient Northern East Asians since ~5.1 ka [27]. Ancient Tibetan individuals dated to ~2.5 ka share ~25% of their genome with Xingyi_EN, identifying Xingyi-related groups as one source of this ghost ancestry [24]. However, Xingyi_EN lacked the EPAS1 high-altitude adaptation allele, implying admixture with additional, as yet unidentified groups [24]. From a maternal perspective, Xingyi_EN carried the rare haplogroup M61, whose subclade A5582c is present in modern Yi, Tibetans, and populations of northeastern India, suggesting continuity in maternal lineages [28].

By the Late Neolithic (~5.5 ka), the Xingyi population had undergone a major genetic shift, marked by the rise of a distinct Central Yunnan ancestry (Xingyi_

LN). This component is differentiated from both Ancient Northern and Southern East Asians and represents the primary ancestral source of present-day speakers of Tibeto-Burman and other South Asian-related language families [28]. From the Late Neolithic to Early Bronze Age (~5.5–3.3 ka), Central Yunnan ancestry remained dominant, indicating strong genetic continuity [24]. Isotopic evidence shows that around 4.9 ka the Xingyi population transitioned from foraging to millet agriculture [29]. Importantly, genome-wide data suggest this transition occurred without major external influx, reflecting a shift through local continuity rather than large-scale population replacement [24].

During the Bronze Age, Xingyi subsistence strategies were fully agricultural. Although Central Yunnan ancestry continued to dominate, maternal lineages show clear turnover. Northern East Asian haplogroups such as A19 and D4 disappeared, local Southwest China haplogroups like F1a3 persisted, and the introduction of haplogroup M75—linked to Southeast Asian groups—points to female-mediated gene flow from the south. The M61 lineage detected in the Early Neolithic was no longer present, suggesting its local extinction or dilution [28]. In present-day populations, Central Yunnan ancestry remains widely distributed among Tibeto-Burman and other language families of Yunnan. Genomic data further demonstrate that most ethnic minorities in the region carry both Central Yunnan ancestry and admixture from Ancient Northern East Asians, reflecting multiple waves of interaction since the Late Neolithic [24].

3.2 Western Yunnan

Western Yunnan is represented by sites such as Mopanshan, Dadunzi, Ladian, Baiyangcun, Haimenkou, Jicha, Gaozhai, Jiangxifen, Duizi, Hongtupo, and Jiangbian (Fig. 1; figure 2), which together provide the foundation for reconstructing the population genetic history of this region. Principal component analysis shows that individuals from western Yunnan cluster with Tibetan groups, indicating shared affinities, yet notably lack the Plateau-specific “ghost ancestry” (Basal Asian Xingyi ancestry) that characterizes ancient highland populations [24]. Between ~3,800 and 1,700 BCE, populations in western Yunnan display strong genetic ties to Ancient Northern East Asians. At Haimenkou (~3,200–2,900 BP), individuals derive ~96% of their ancestry from Yellow River Basin northern populations [30]. Similarly, individuals from Baiyangcun (~3,569–3,366 BP) are overwhelmingly of Ancient Northern East Asian ancestry, with direct genetic continuity

to Yellow River farmers. Later, at Gaozhai (~2,500–2,100 BP), individuals likewise inherited Yellow River ancestry, while burial organization reveals

multi-generational family lineages spanning 3–10 generations, pointing to highly stable local social structures [28].

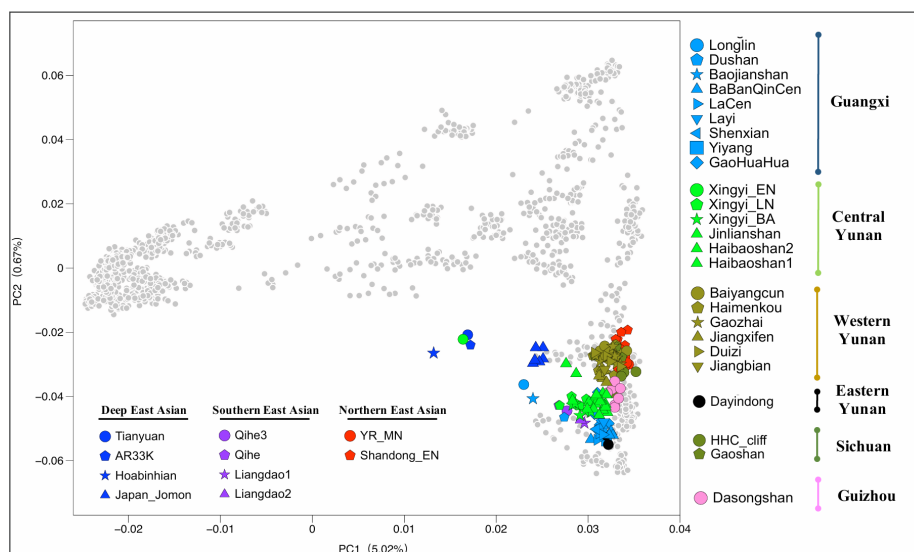


Figure 2. Principal Component Analysis (PCA) of Ancient Individuals from Southwest China

Although Ancient Northern East Asian ancestry dominates in western Yunnan, a component of Central Yunnan ancestry is also detectable, demonstrating gene flow from central into western Yunnan during the Late Neolithic and Bronze Age. By contrast, gene flow in the reverse direction—from western into central Yunnan—was weak and statistically insignificant, suggesting that the demographic influence of central Yunnan groups on western Yunnan populations was substantially stronger than vice versa [24]. The prevalence of Ancient Northern East Asian ancestry in western Yunnan aligns with the southward expansion of Proto-Sino-Tibetan languages. Today, Sino-Tibetan speakers in northwestern Yunnan (e.g., Pumi and Bai) retain high proportions of Ancient Northern East Asian ancestry, whereas southern groups such as the Hani show a greater contribution from Central Yunnan ancestry [24].

3.3 Eastern Yunnan

Eastern Yunnan is represented primarily by the Dayindong site, dated to ~3,400 BP. Genomic evidence shows that Dayindong individuals carried a mixed ancestry profile composed of Ancient Southern East Asian and Central Yunnan components [24], a pattern further supported by mitochondrial data [28]. This admixture likely reflects the role of the Pearl River system in facilitating connectivity. The Nanpanjiang River, a major upper tributary of the Pearl River, links eastern Yunnan with Guangxi and Guangdong, providing a natural corridor for human movement and cultural interaction. Through this network, eastern Yunnan populations engaged

directly with southern East Asian groups [24]. The genetic legacy of Dayindong persists today among Tai–Kadai-speaking populations of the Pearl River Basin, such as the Zhuang and Dai, whose ancestry derives ~60% from Ancient Southern East Asians and ~40% from Central Yunnan ancestry [24]. This pattern supports the scenario of westward migration of Bronze Age coastal populations along river systems. Compared with contemporaneous populations in central Yunnan (dominated by local Central Yunnan ancestry) and western Yunnan (dominated by Yellow River–related ancestry), eastern Yunnan groups exhibit greater admixture and openness, underscoring their transitional role and Yunnan’s broader function as a corridor of multiethnic convergence.

4. The Sichuan Region of Southwest China

Sichuan lies at the transitional zone between the Tibetan Plateau and the middle–lower Yangtze River plains. The region is dominated by the Sichuan Basin, enclosed by mountains yet traversed by a dense river network. This unique geography—combining enclosure with connectivity—has long positioned Sichuan as a strategic corridor linking northwest, southwest, and central China. Archaeological discoveries in the region are abundant, including the Late Neolithic Baodun culture centered on the Chengdu Plain and the Bronze Age Sanxingdui and Jinsha sites. Ancient DNA research on Sichuan populations has expanded in recent years, providing new perspectives on their origins and interactions. The Late Neolithic Gaoshan site (Dayi County, ~4.5 ka), part of Phase I of the Baodun culture, is among the

earliest with genomic data. Ancient DNA reveals that Gaoshan individuals derived ~92% of their ancestry from Yellow River Neolithic millet farmers and ~8% from Southeast Asian hunter-gatherers represented by the Hòabínhian tradition [30]. Notably, although the northernmost known Hòabínhian sites are confined to Yunnan [10], this ancestry is present in Gaoshan individuals, implying northward genetic input through migration or gene flow. Archaeobotanical data further show that Gaoshan communities practiced mixed rice–millet cultivation [31]. Yet, genomic evidence indicates that millet agriculture was associated with migration and population replacement from the north, whereas rice agriculture was adopted primarily through cultural transmission without substantial accompanying gene flow [30].

Later evidence comes from the Honghua Village cliff tombs (Eastern Han period, Meishan City), dated by associated grave goods such as *jianlun wuzhu* coins [32]. Ancient DNA from four individuals excavated in 2024 reveals close affinity to Bronze- and Iron-Age Yellow River populations, with clear differentiation from contemporaneous southern groups [32]. Kinship analysis identified these individuals as a nuclear family (a father and three children). This co-burial pattern centered on the nuclear family mirrors practices documented in the Central Plains during the Han–Jin periods. Together, archaeological and genomic evidence support the view that the cliff-tomb tradition in Sichuan originated from the Central Plains, highlighting continuing gene flow between the Sichuan Basin and northern China during the Eastern Han.

5. The Guizhou Region of Southwest China

Guizhou, situated on the eastern margin of the Yunnan–Guizhou Plateau, is dominated by mountainous terrain, extensive karst landscapes, and abundant caves that provided key habitats for Paleolithic populations [33]. Its dense river systems facilitated long-range cultural connections, and by the Warring States period the region was home to the distinctive Yelang culture. In later historical times, Han cultural influence coexisted and intertwined with indigenous traditions. Ancient DNA studies in Guizhou remain limited, but include the ~11 ka Qingshuiyuan Dadong individual and the multi-phase Dasongshan cemetery population.

The Qingshuiyuan Dadong individual, dated to ~11 ka, represents the earliest known genome from Guizhou. Mitochondrial analysis shows it carried haplogroup M71, also observed in the Longlin individual from

Guangxi, but with two unique mutations (6257A and 11518A). These mutations are absent in East Asians yet occur at high frequency among present-day mainland Southeast Asian groups, including populations in Thailand, Laos, and Myanmar [34]. Based on this signature, Fu Qiaomei’s team defined a novel subclade, M71d, with an estimated origin ~22 ka. This finding suggests that by the Late Paleolithic, Guizhou acted as a key corridor linking populations across East and Southeast Asia [34]. The Dasongshan cemetery spans from the Western/Eastern Jin dynasties to the Song, Yuan, and Ming periods. Genomic data from the Song–Yuan–Ming phases reveal a composite ancestry: ~63.6–65.7% from Yellow River agricultural populations, ~25.2–34.3% from Southeast Asian Hòabínhian-related groups, and up to 26.1% from Guangxi (Longlin-related) lineages [35]. Among seven Ming individuals, four distinct mitochondrial haplogroups—B4c2, M32’56, R9b1a3, and M—were detected, all common in southern China and Southeast Asia, indicating enduring affinities with southern populations [36]. These genetic results, combined with the presence of Han cultural artifacts in the burials, show that the spread of Han culture into the southwest during the Song–Yuan–Ming periods was accompanied by substantial population migration. These migrants admixed extensively with local groups, further enriching the genetic diversity of the region [35].

6. Summary and Outlook

As a pivotal nexus linking East Asia, Southeast Asia, and the Tibetan Plateau, Southwest China has emerged as a key region for understanding long-term population dynamics. The application of ancient DNA has greatly advanced our knowledge of this region, offering unprecedented insights into the evolutionary history and cultural interaction networks of its populations from the Paleolithic through the historical periods. Genomic data now illuminate deep divergences among early hunter-gatherer groups, the emergence of distinct regional ancestries during the Neolithic, the impact of agricultural expansions from the Yellow River Basin, and the complex admixture processes that shaped Bronze and Iron Age societies.

These findings reveal Southwest China not as a peripheral zone but as an active crossroads where diverse lineages converged, interacted, and transformed. Ancient genomes from Guangxi, Yunnan, Sichuan, and Guizhou highlight repeated episodes of migration and admixture, from the persistence of deeply divergent Paleolithic lineages such as Basal

Asian Xingyi, to the influx of Yellow River farmers and the incorporation of Southeast Asian ancestries. By the historical period, intensified demographic exchanges across imperial frontiers and trade routes further reshaped the region's genetic structure, laying the foundation for its enduring ethnolinguistic diversity.

6.1 Genetic Diversity of Early Hunter-Gatherer Populations

The principal component analysis (PCA; Fig. 2) reveals marked genetic differentiation among hunter-gatherer groups in Southwest China during the Late Paleolithic to Early Neolithic. Three highly divergent Asian ancestries are represented: Basal Asian Xingyi ancestry, Southeast Asian Hòabínhian ancestry, and Ancient Southern East Asian ancestry. The Basal Asian Xingyi lineage constitutes a newly identified genetic branch unique to Southwest China, predating the north–south differentiation of East Asians. The Longlin individual from Guangxi (~11 ka) carried ~50% Basal Asian Xingyi ancestry and shares a common origin with the Early Neolithic Xingyi_EN individual from Yunnan (~7.1 ka). Unlike Xingyi_EN, however, Longlin also incorporated Ancient Southern East Asian ancestry, while later Baojianshan individuals (~8.3–6.4 ka) carried an additional Hòabínhian component, showing that Southeast Asian hunter-gatherer lineages had dispersed into Guangxi and admixed locally by the Early Neolithic. Complementary evidence from Guizhou's Qingshuiyuan Dadong individual (~11 ka), who carried the distinct Southeast Asian haplogroup M71d also found in Longlin, highlights the role of Southwest China as a Late Paleolithic migration corridor bridging East and Southeast Asia. Taken together, these results demonstrate that Southwest China harbored exceptional genetic diversity in the Late Paleolithic–Early Neolithic, reflecting both deep population divergence and extensive gene flow among early foraging groups.

6.2 Neolithic Agricultural Spread and Genetic Mechanisms

With the onset of the Neolithic, the genetic landscape of Southwest China was reshaped by the spread of agriculture. Ancient DNA evidence demonstrates that this process involved not only the transmission of subsistence technologies but also complex demographic interactions between Yellow River Basin farmers and indigenous foragers. These interactions are captured by two contrasting models: population replacement and local continuity. The population replacement model is evident in Sichuan and western Yunnan. Individuals

from Gaoshan in Sichuan and from Baiyangcun and Haimenkou in western Yunnan derive more than 90% of their ancestry from Neolithic millet-farming populations of the Yellow River Basin. This indicates that the spread of millet agriculture into these regions was accompanied by large-scale migrations and the genetic replacement of local groups. By contrast, the local continuity model characterizes central Yunnan, represented by the Xingyi population. Around 4.9 ka, communities in this region adopted millet cultivation, yet their nuclear genomes remained stable and distinct from northern groups, with no evidence for substantial external influx. In PCA space (Fig. 2), they consistently form a separate cluster from Yellow River farmers, highlighting continuity of indigenous lineages. These results suggest that in central Yunnan the transition to agriculture occurred primarily through cultural diffusion, rather than through demographic replacement.

6.3 Genetic Diversity in the Historical Period

During the historical period, populations across Southwest China exhibited complex but regionally distinctive genetic patterns. Overall, their genetic structure was shaped by extensive admixture between northern and southern East Asian ancestries, yet with notable heterogeneity among provinces. In Guangxi, historical groups such as those from Laba and BaBanQinCen were dominated by southern East Asian ancestry (~58.2–90.6%) but incorporated substantial northern East Asian components. Yunnan populations displayed more intricate compositions, combining local Central Yunnan ancestry with northern and southern East Asian inputs. In contrast, populations in Sichuan and Guizhou were more strongly influenced by northern East Asian ancestry. For instance, individuals from Honghua Village (Eastern Han, Sichuan) clustered closely with Bronze–Iron Age populations of the Yellow River Basin, while those from Dasongshan (Song–Yuan–Ming, Guizhou) were primarily northern-derived but retained Southeast Asian Hòabínhian ancestry. Principal component analysis (Fig. 2) highlights this regional differentiation, with Guangxi, Yunnan, Sichuan, and Guizhou forming distinct clusters along major axes of variation. These results indicate that cultural expansion and demographic migrations from the Central Plains profoundly restructured the genetic makeup of Southwest China. Such transformations were likely driven by state-led colonization policies, including the Qin–Han implementation of the commandery–county system and the establishment of military–agricultural colonies, which facilitated

large-scale north-to-south migration and reshaped the demographic fabric of the southwest through admixture with local populations.

Despite important initial progress, ancient DNA research in Southwest China still faces major challenges. Temporal gaps remain severe—for instance, in Guangxi no genetic data are yet available between ~6,000 and 1,500 cal BP, limiting our understanding of continuity and transitions from prehistoric to historic periods. Sample sizes are also small, and in many cases single individuals have been used to infer regional genetic structures, providing only limited statistical power to characterize the diversity of early hunter-gatherer groups. Spatially, key regions along the upper Yangtze River—including Sichuan, Chongqing, and Yunnan—form crucial corridors linking Central China and Southeast Asia, yet remain underexplored. Moreover, the warm, humid climate and acidic soils of Southwest China pose persistent challenges to DNA preservation. Collectively, these issues result in significant gaps in temporal, spatial, and population coverage, constraining attempts to reconstruct the region's complex demographic history.

Future progress will depend on expanding sample sizes and filling chronological and geographic gaps, while also deepening integration with archaeology, ethnology, linguistics, and related disciplines. Such cross-disciplinary approaches will allow a more comprehensive and fine-grained reconstruction of population migrations and cultural transformations in Southwest China, providing a firmer foundation for understanding the region's historical trajectories and enduring ethnolinguistic diversity.

Author Contributions

Conceptualization, F.Z. and R.F.Z.; validation, M.J.R. and J.T.C.; formal analysis, M.J.R. and F.Z.; investigation, R.F.Z.; data curation, J.T.C.; writing—original draft preparation, M.J.R. and J.T.C.; writing—review and editing, F.Z. and R.F.Z.; visualization, M.J.R.; supervision, F.Z. and R.F.Z.; project administration, F.Z. and R.F.Z.; funding acquisition, F.Z. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest

The authors declare no conflicts of interest.

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