

A Review of Research on the Protection of Traditional Settlements in China Based on the Theory of "Gene Mapping" Construction

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Abstract: Under the current wave of globalization and modernization, the conservation of traditional settlements in China faces unprecedented challenges and opportunities. With the acceleration of urbanization, many traditional settlements are under the threat of destruction or disappearance, imperiling both cultural diversity and the continuity of national heritage. The "gene mapping" theory borrows the concept of genes from biology, decomposing the material forms and cultural connotations of traditional settlements into identifiable and inheritable basic units, thereby providing a new analytical framework for settlement conservation. This paper first reviews the basic concepts and development of the "gene mapping" theory, and then systematically sorts out the research results of domestic scholars in gene identification, extraction and mapping construction from three aspects: "landscape genes", "cultural genes" and "spatial genes". On this basis, this paper identifies the principal limitations of current research and proposes future research directions, aiming to offer theoretical insights and practical guidance for the conservation and transmission of traditional settlements in China.

Keywords: Gene Mapping; Traditional settlements; Conservation of historical and cultural heritage; Research review

1. Introduction

Traditional settlements in China are products of the long-term accumulation of regional culture. They document the natural conditions, lifeways, and social transformations of specific localities, serving as vital carriers for the continuity of Chinese civilization. However, with China's urbanization rate exceeding 66% by 2023, many traditional settlements are being eroded—some have vanished entirely. Against this backdrop, the scientific conservation and transmission of traditional settlements has become a pressing practical concern. In recent years, Chinese scholars have begun to introduce the biological concept of the "gene" into settlement studies. The central premise of this approach is that, much as biological organisms transmit hereditary information through genes, traditional settlements harbor core elements that determine their defining characteristics; these elements can be conceptualized as settlement "genes." Building on this foundation, researchers have further developed methods for constructing "gene mapping"—systematic, visual frameworks designed to document and represent the characteristic information of settlements.

2. Overview of the Localization of Gene Mapping Theory in Domestic Research

2.1. The Introduction of Gene Theory

The term "gene" originated in biology. In 1909, Danish botanist Wilhelm Johannsen first coined the word "gene" to denote the fundamental unit carrying hereditary information in living organisms^[1]. Subsequently, British scholar Richard Dawkins, in his landmark 1976 work *The Selfish Gene*, introduced the concept of the "meme", proposing that the transmission and evolution of culture operate through mechanisms analogous to those of biological genes^[2]. This idea opened an intellectual doorway for the subsequent application of genetic concepts to the study of culture and space.

In China, the earliest efforts to integrate genetic concepts with cultural research can be traced to the

late 1980s. At that time, the rapid pace of urbanization gave rise to the erosion of urban memory and the rupture of cultural continuity—phenomena that prompted certain scholars to explore these issues through the lens of "cultural genes." As early as 1990, Liu Changlin proposed that the deep-seated modes of thought and psychological structures characteristic of an ethnic group could be understood as a form of "cultural gene," exerting a profound influence on societal development^[3]. The systematic application of gene theory to the study of traditional settlements did not emerge until the early twenty-first century. From the outset of the twenty-first century, scholarly inquiry in China into the application of gene theory to urban development and the transformation of traditional settlements has grown steadily in both breadth and depth.

In the field of urban morphology abroad, it is worth noting that British geographer M. R. G. Conzen had already advanced the concept of morphogenetic regions as early as 1960, through his meticulous plan analysis of the English market town of Alnwick. Conzen emphasized that urban space preserves stratified layers of cultural memory accumulated across successive historical periods^[4]. Building upon this foundation, J. W. R. Whitehand subsequently elaborated and extended Conzenian theory, consolidating what has since become known as the "Conzenian tradition" in British urban morphology^[5]. These international contributions provided a significant academic reference point for the later development of landscape gene theory in China. In addition, the Italian school of urban morphology, represented by Muratori and Caniggia, developed a typological-processual approach that examines how building types evolve within their urban contexts—a perspective that offers further parallels with the gene-based analytical framework adopted by Chinese scholars. Moreover, UNESCO's Historic Urban Landscape (HUL) approach, formally adopted in 2011, similarly emphasizes the layered, inherited character of urban environments, reinforcing the conceptual affinity between international heritage discourse and domestic gene mapping theory.

2.2. The Emergence and Development of Research on Gene Map Construction

Following introduction of the landscape gene concept, Chinese scholars have conducted extensive research on the construction of gene mapping. A "gene map," in essence, is a systematic, diagrammatic representation of the various genetic elements present within a settlement. Its function is broadly analogous to that of a genomic map in biology, offering a comprehensive means of capturing and conveying the "hereditary information" of a given settlement.

Tracing the trajectory of this field, research on gene mapping has broadly unfolded across three developmental phases. The first phase, spanning approximately 2003 to 2010, was one of conceptual formulation and theoretical construction, with the primary focus on defining what landscape genes are and establishing procedures for their identification and extraction. The second phase, covering roughly 2010 to 2020, was characterized by methodological diversification and practical application: research methods became increasingly varied, digital technologies such as GIS were widely adopted, and the corpus of case studies expanded considerably. The third phase, extending from 2020 to the present, has seen the field move toward multidisciplinary integration and intelligent analytical approaches^[6].

In terms of research content, current domestic scholarship on gene mapping is organized around three principal directions. The first is the landscape gene map—the earliest-established and most prolific direction, represented above all by the work of a pioneering research team. The second is the spatial gene map, represented by the research of Duan Jin's team at Southeast University and Huang Zongsheng's team at Guizhou University^[7]. The third direction concerns cultural gene mapping, a strand of inquiry that, while relatively fragmented in scope, has nonetheless generated a substantial body of valuable scholarship. Beyond these three principal directions, certain researchers have proposed additional genetic constructs—most notably the concept of the "institutional gene"^[8], although work in these areas remains nascent and comparatively limited in scale systematically synthesize the aforementioned developmental phases, the three principal gene dimensions, and the emerging methodological trends, a comprehensive conceptual framework is constructed (Figure 1).

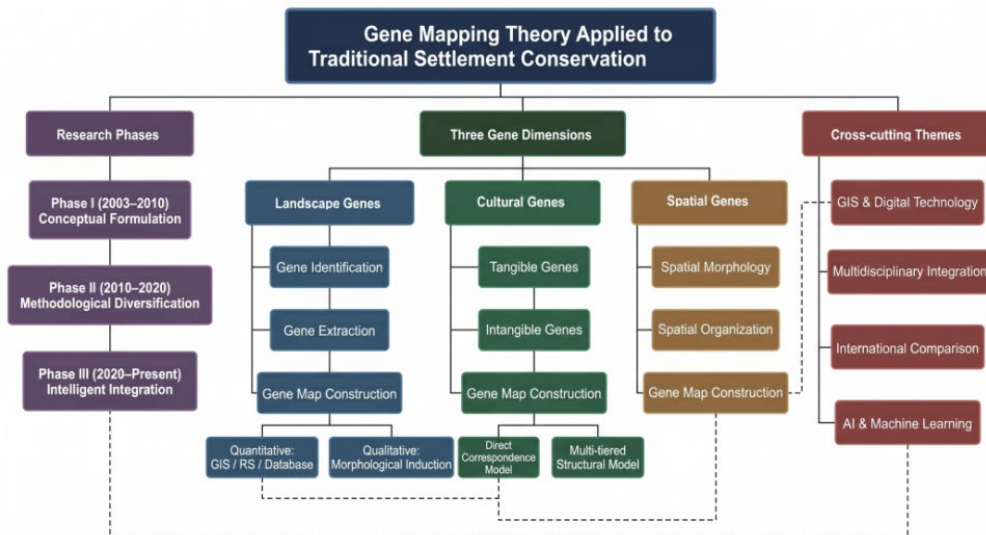


Figure 1. Conceptual Framework of Gene Mapping Theory Applied to Traditional Settlement Conservation.

3. Research Progress in the Application of Gene Map Theory to the Conservation of Traditional Settlements

A keyword search for "gene map" in the China National Knowledge Infrastructure (CNKI) database reveals that, since 1980, the ten most frequently occurring co-keywords in this body of literature are: landscape gene, map construction, cultural gene, traditional village, DNA, traditional settlement, gene identification, genome, and traditional settlement landscape (Figure 2). This distribution indicates that gene map theory has achieved considerable depth of development within the field of traditional settlement conservation, with its principal orientations centering on landscape restoration in the context of rural revitalization and heritage protection, as well as the transmission of regional culture. A systematic review of the relevant CNKI literature further confirms that current domestic research on gene map theory is primarily organized around three analytical dimensions: landscape genes, cultural genes, and spatial genes.

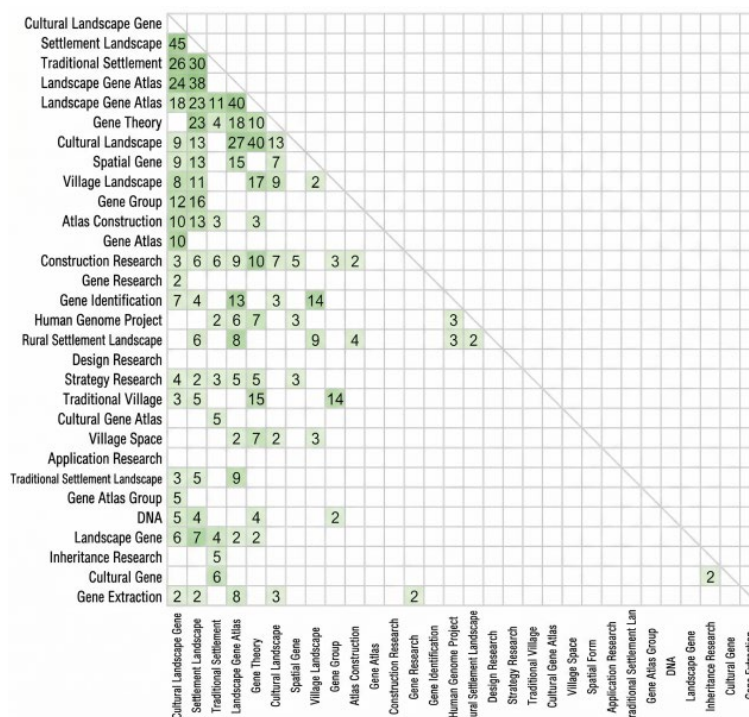


Figure 2. Co-occurrence Matrix Analysis of Gene Mapping Themes in CNKI.

3.1. Landscape genes

The landscape genes constitute the most extensively researched and theoretically consolidated direction within this field. It focuses on the visually perceptible and experientially tangible landscape elements of traditional settlements, encompassing architectural forms, spatial layouts, and the characteristics of the natural environment.

3.1.1. Identification and Extraction of Landscape Genes

The identification and extraction of landscape genes represents both the first and the most fundamental step in the entire research process. With regard to identification criteria, a broad consensus has emerged among scholars that landscape genes should possess several defining characteristics: temporal stability, meaning that they resist casual alteration over time; spatial distinctiveness, meaning that they serve to differentiate one settlement from another; and continuity, meaning that they can be consistently traced across different settlements^[9](Table 1).

Table 1. Principal Classification Criteria for Landscape Genes of Traditional Settlements

Classification Criterion	Classification Outcomes	Applicable Context
Significance and composition	Dominant genes, attached genes, hybrid genes, variant genes	In-depth settlement studies
External manifestation	Dominal genes, invisible genes	Comprehensive classification research
Characteristic deconstruction	Architectural genes, cultural genes, environmental genes, layout genes	Tangible/Intangible distinction
Spatial analytical scale	Vernacular dwelling genes, block genes, single-settlement genes, local settlement genes, regional settlement genes, settlement cluster genes	Multi-scalar analysis
Cultural connotation	Single-element genes, composite-element genes	Analysis of cultural complexity
Morphology of individual settlements	Two-dimensional plan genes, three-dimensional front elevation genes, three-dimensional side elevation genes	Morphological documentation
Mode of expression and description	Symbolic genes, graphic genes, textual genes	Gene map representation
Ease of extraction	Directly extractable genes, indirectly extractable genes	Operational guidance

On the technical front, recent years have witnessed a number of innovative methodological developments in gene identification. Some scholars have proposed a "characteristic deconstruction and extraction method," which disaggregates settlement characteristics into four foundational categories—architectural attributes, cultural symbols, environmental responses, and spatial organization—and proceeds to identify landscape genes through four corresponding analytical procedures: planar morphological analysis, three-dimensional spatial derivation, imageability perception interpretation, and systemic structural dissection. Yang Xiaojun and his research team, meanwhile, have introduced a DNA double-helix bionic model, employing a coupling algorithm that integrates a morphological chain with a semantic chain to achieve intelligent parsing of landscape genes^[6]. The emergence of these new approaches signals a broader methodological transition in landscape gene identification—one moving away from subjective qualitative judgment and toward objective quantitative analysis.

In the international arena, Karl Kropf has approached the question from the perspective of urban morphology, examining how the constituent elements of urban spatial form may be systematically analyzed and described. The multi-tiered morphological analytical framework he proposed offers meaningful points of reference for domestic research on gene identification^[10].

3.1.2. Construction of Landscape Gene Maps

Once landscape genes have been identified and extracted, the subsequent step involves organizing this genetic information into a coherent and systematic map. Current approaches to constructing landscape gene mapping are broadly divisible into quantitative and qualitative methods.

Quantitative methods rely principally on digital technologies and mathematical modeling. GIS technology has been applied to the processing and analysis of satellite remote sensing data, generating a range of maps depicting the spatial morphology and landscape gene characteristics of traditional settlements, including spatial configuration maps and spatial arrangement maps^[11]. Li Xiaoying and colleagues, taking traditional villages in Gaochun District, Nanjing as their subject, constructed a landscape spatial database using database technology and a GIS platform, presenting genetic information through cartographic visualization^[12]. The principal advantages of these quantitative approaches lie in the relative objectivity of their outputs and their suitability for large-scale comparative analysis. Analogous work has been pursued internationally: Howey and Burg, for instance, evaluated the current state of GIS application in landscape analysis, arguing that GIS can effectively support the construction of dynamic models of landscape evolution and assist researchers in understanding processes of cultural landscape change methods, by contrast, focus on the inductive synthesis and diagrammatic representation of shared characteristics among landscape genes^[13]. A further approach draws on molecular biology theory to guide the identification and extraction process, enabling the construction of landscape gene mapping organized around three dimensions: layout, architecture, and cultural markers.

It is worth noting that the construction of landscape gene mapping has yet to converge on a unified set of standards or procedures. The maps produced by different scholars vary considerably in their hierarchical structures, classification schemes, and modes of representation. Some adopt a multi-tiered system structured as "genome—gene—basic factor," while others place genes and factors within a single undifferentiated level. This diversity reflects, on the one hand, the continued exploratory character of the field, and on the other, the practical difficulties it poses for cross-study comparison and integration.

Beyond questions of construction methodology, research on landscape gene mapping also engages with the analysis of genetic information structures. The core framework for landscape gene information structure comprises three nested levels: the "landscape information unit", the "landscape information point", and the "landscape information corridor". The landscape information unit constitutes the most fundamental level, encoding the historical and cultural memory of a given region; the landscape information point represents the external manifestation of the information unit within a specific landscape context; and the landscape information corridor is the structure formed by arranging multiple information points according to a defined organizational logic. This progressively layered analytical approach facilitates a more systematic understanding of the compositional structure of traditional settlement landscapes.

3.2. Cultural genes

In the conservation of traditional settlements in China, the concept of "cultural gene" may be understood as a core cultural factor transmitted across generations, one that plays a decisive role in shaping particular cultural landscapes. The cultural gene functions not only as a marker of cultural identity but also as a key mechanism for differentiating and recognizing distinct cultures. Since the turn of the twenty-first century, theoretical inquiry into cultural genes has exhibited an increasingly diversified character, opening up new perspectives and methodological pathways for the translation of theory into practice^[14].

3.2.1. Identification and Extraction of Cultural Genes

Dong Yu, Fei Yue, and their colleagues have proposed a "tangible—intangible" classificatory framework, dividing cultural genes into two broad categories—visible, material genes and invisible, intangible genes—and developing separate identification and extraction procedures for each^[15]. This classificatory approach is relatively intuitive and lends itself to practical application. Huo Yanhong's research offers a complementary perspective: she treats water cultural heritage as a form of cultural gene subject to identification and extraction, and, on the basis of delineated cultural zones, formulates differentiated conservation strategies for distinct regions^[16]. This case demonstrates that cultural gene identification need not be confined to the domain of architecture and settlements, but may be extended to encompass the broader field of cultural heritage.

With respect to the identification of intangible cultural genes, He Feng and colleagues have observed that recent scholarship has expanded its focus from material forms to the analysis of cultural genealogies, now encompassing the identification of a diverse range of living cultural genes—including tea ceremony transmission, folk craftsmanship, festival activities, and ethnic music. Nevertheless, the identification of intangible cultural genes remains a significant challenge, as such genes are often difficult to express and document in visually explicit terms.

3.2.2. Construction of Cultural Gene Maps

The methodological approaches to constructing cultural gene mapping may be broadly organized into two categories. The first is the direct correspondence model, in which identified cultural factors are organized into a map either directly or through a two-tiered structure. Liu Bo extracted constituent elements and defining characteristics from urban spatial morphologies across different historical periods, establishing a relational map between cultural genes and urban spatial form^[17]. Liu Zongming and Zhang Hongliang classified genes according to their attributes and constructed a two-tiered gene map^[18].

The second is the multi-tiered structural model, which introduces additional hierarchical levels between genes and factors. A comparatively comprehensive example is provided by the research of Liu Chang and Lei Qing, who analyzed the structural relationships between expressed and recessive factors and, drawing on eight constituent elements—form, color, pattern, material, craftsmanship, environment, behavior, and semantics—constructed a cultural genealogical map of the Mongolian yurt. They further established a cultural gene evaluation model organized around five analytical perspectives: people, events, objects, settings, and scenes^[19]. Luo Sixi, taking traditional villages in Hanzhong City as the research subject, classified cultural genes into four types—dominant, attached, hybrid, and variant—as the basis for map construction, and subsequently proposed conservation and transmission strategies grounded in the resulting map^[20]. Wang Yinxia, meanwhile, employed GIS technology to determine the spatial distribution characteristics of villages in southern Fujian, using this foundation to identify both material and intangible cultural genes and to construct a comprehensive cultural gene map^[21].

3.3. Spatial Genes

The spatial gene represents the most recently established of the three research directions, yet it has gained momentum rapidly. Its focus lies on the stable and representative organizational patterns and structural relationships embedded within the spatial morphology of settlements. Compared with the landscape gene approach, spatial gene research places greater emphasis on the combinatorial relationships between elements rather than on the characteristics of individual elements in isolation.

3.3.1. Identification and Extraction of Spatial Genes

Scholarly research on spatial genes has largely proceeded by constructing analytical frameworks based on the varying combinatorial relationships between elements, predominantly through qualitative inquiry. The foundational procedural framework for spatial gene research was proposed by Academician Duan Jin, comprising three sequential steps: identification and extraction, analytical evaluation, and heritage guidance and control. The Duan Jin research team subsequently elaborated and expanded upon the conceptual content of spatial genes^[7].

In terms of specific identification methods, scholars have adopted a variety of approaches. One line of inquiry begins with the combinatory relationships between elements. Shao Runqing traced the relationships among natural landscape features, historical culture, and physical spatial morphology in order to identify stable and representative spatial combination patterns, subsequently conducting gene identification and extraction on the basis of elemental relationships^[22]. Cheng Junjie and colleagues examined the relationships between villages and their natural surroundings, as well as the relationship between road network configurations and environmental conditions, thereby describing and extracting the spatial morphological regularities and spatial gene characteristics of traditional villages^[23]. An alternative approach conducts identification directly at the level of individual elements. Song Yuying classified settlement spatial genes into four categories—plots, settlements, roads, and buildings—as the basis for identification and extraction^[24]. Liu Suyi, in studying the spatial genes of historic urban districts and small towns, drew on the five urban structural elements proposed by Academician Qi Kang, synthesizing morphological elements into spatial genes designated as "framework, cluster, axis, core, and boundary"^[25].

3.3.2. Construction of Spatial Gene Maps

In the construction of spatial gene mapping, domestic researchers have largely drawn on the theoretical framework of biological gene mapping and integrated it with typological methods to produce multi-tiered map systems. Du Sen and Qin Yu selected Zhagana Village as their research subject and completed the construction of a spatial gene map using "tripartite spatial relationship" graphics in conjunction with a "geographic information element classification" coding method^[26]. Li Bingxue, Dong Yanping, and their colleagues, taking traditional villages along the middle reaches of the Fen River as their specific research subject, constructed an evaluation mechanism to systematically assess the spatial

genes of traditional villages, extracting characteristic factors across three dimensions—natural environment, settlement spatial layout, and architectural space—to establish a spatial gene map for traditional villages. It is acknowledged, however, that domestic research on spatial gene mapping still retains considerable room for further development^[27].

Taken as a whole, although spatial gene map research is a relative latecomer to the field, it has already produced a number of comparatively mature methodological approaches. Nevertheless, when measured against landscape gene map research, the number of documented case studies remains limited, the degree of methodological standardization is still insufficient, and substantial scope for future development remains.

4. Conclusion

Through a systematic review, this paper examines research progress in the conservation of traditional settlements in China under the "gene map" theoretical framework. Scholars both domestically and internationally have achieved notable results in this area, contributing diverse innovative methods for the identification, extraction, and map construction of landscape genes, cultural genes, and spatial genes. These methods fall broadly into qualitative and quantitative categories. Qualitative approaches analyze the connotations and characteristics of the three gene types, providing conceptual depth for map construction, while quantitative methods—particularly GIS technology—offer robust technical support for the digitization and visualization of gene mapping. Despite meaningful advances, the field retains certain limitations and its technical instruments remain underdeveloped. Future progress will depend substantially on deeper interdisciplinary engagement, and the effective integration of biological and typological theories into gene map construction and analysis represents a central challenge for researchers in this field.

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