



Investigating the Role of Epigenetics in The Evolution of Language and Speech Patterns Across Different Cultures

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ABSTRACT

Language and speech patterns evolve through a dynamic interplay of cultural transmission and biological mechanisms. Emerging evidence suggests that epigenetic processes-including DNA methylation, histone modification, and non-coding RNA activity-mediate the relationship between environmental inputs and neural pathways underlying language acquisition and phonological development. Epigenetic marks laid down during prenatal, early childhood, and adolescent stages modulate neural circuits governing articulation, auditory processing, and speech motor control, shaping individual and population-level variation in phonology, syntax, and prosody. These processes interact with sociocultural factors such as caregiver input, community structure, and social stressors, influencing both the acquisition and diversification of language. Cross-cultural studies indicate that epigenetic regulation contributes to systematic phonological and linguistic variation while preserving universal constraints, suggesting a biologically mediated pathway for the evolution of language and speech. Integrating epigenetic, neurodevelopmental, and cultural perspectives provides a framework to understand how biological predispositions and social environments co-direct the emergence, transmission, and evolution of human languages across populations.

Keywords: *Language evolution; Epigenetics; Phonology; Speech acquisition; Gene-environment interaction; Cultural transmission; Neural plasticity; DNA methylation; Histone modification; Cross-cultural linguistics.*

INTRODUCTION

Language and speech patterns are fundamental components of human behavior and are thus subject to evolution (Chopoorian et al., 2021). Although this evolution primarily occurs through cultural transmission,

some theoretical models posit a biological component to ensure the phenotypic emergence of language (Devanna et al., 2019). Epigenetics may constitute a bridge between the biological and cultural components of language evolution. Epstein and Pothos hypothesize that epigenetic mechanisms from the prenatal period onward could influence the development of language-related phenotypes, establish culturally invariant critical periods for first-language acquisition, and modulate phonetic variation across different learning environments and languages. To test this hypothesis, the researchers construct an integrated framework based on the mechanisms of epigenetics and prior theoretical models of language evolution. The emergence, transmission, and many of the basic structural features of human language cannot be fully explained by genetic evolution, indicating the need for further exploration into the factors that shape its development over cultural time.

Theoretical Foundations

Epigenetics describes mechanisms that modify gene activity without altering the underlying DNA sequence. These modifications include chemical changes to DNA, such as methylation, and to histones, the proteins around which DNA is packaged. They also involve the production of non-coding RNAs that affect chromatin structure or direct other factors to specific genes (Devanna et al., 2019). Epigenetic alterations alter the timing and level of gene expression during development and can remain stable for long periods, yet they still exhibit greater plasticity than mutations, making them more likely to have a role in the evolution of language and related traits.

The evolution of language is sometimes framed in the areas of cultural evolution, which addresses the transfer of information between individuals, and biological evolution, which examines innate neurological predispositions. Descriptions of cultural evolution emphasize the processes by which languages change over time, including phonetic variation, grammatical structure, and even writing systems (Fisher & Vernes, 2015). Biological approaches investigate the shared molecular features of languages around the world and the corresponding regional patterns found in genes involved in neurodevelopment and learning (Ruzibaeva N., et al). Understanding how cultural and biological processes interact offers insights into how environmental factors may exert long-term influence on genes associated with language across different languages and cultures [table 1].

Table 1: Key Concepts and Mechanisms of Epigenetics and Language Evolution

Concept	Description	Relevance to Language Evolution
Epigenetics	Modifications to gene activity without altering DNA sequence (e.g., DNA methylation, histone modification, ncRNA)	Regulates timing and level of gene expression; contributes to neurodevelopment and learning critical for language
Cultural Evolution	Transfer of information between individuals (social learning, imitation, peer influence)	Explains changes in phonetics, grammar, and writing systems across populations
Biological Evolution	Innate neurological and genetic predispositions	Influences shared molecular features of language and brain development
Coevolution	Interaction of biological and cultural processes	Environmental factors can shape gene expression, affecting language traits
Critical Periods	Developmental windows for first-language acquisition	May be regulated by epigenetic mechanisms ensuring language learning efficiency

Epigenetics: Mechanisms and Core Concepts

Epigenetics encompasses processes that alter gene expression without modifying the underlying DNA sequence. It includes mechanisms such as DNA methylation, histone modification, and the activity of non-coding RNA (ncRNA) molecules. These processes can have profound effects on neurodevelopment and learning, both of which are tightly linked with the acquisition of language and speech, and there is evidence that epigenetic modification may be widespread within the language-associated neurodevelopmental, learning, and phonological variations across languages and dialects, both within and between populations (Devanna et al., 2019).

Although language is a unique feature of human beings, historical and cross-cultural evidence shows that, like other biological and cultural traits, languages evolve over time. On one hand, models of cultural transmission, which include social learning, imitation, and the influence of peers, play a significant role in transforming language (including basic syllables) into a wide variety of forms. On the other hand, humans are born with diverse biological traits governed by genes, and biological predispositions have also been posited to play a role in shaping language and language development.

Language Evolution: Historical and Cross-cultural Perspectives

Language has been shaped by cultural evolution to be as learnable as possible given children's cognitive limitations. Different developmental abilities such as turn taking, intention reading, comprehension, syntax, and phonology appear at different times and may have distinct developmental trajectories. Hence, the evolution of language likely involved coevolution with biological factors, especially in early stages, involving the vocal tract and brain, though these biological bases are neither universal nor fixed. Language also adapts to the brains, vocal tracts, and hands of speakers, and it influences cultural evolution, which can in turn affect biological evolution; differences in vocal tract anatomy between groups, for example, influence language structure (Dediu et al., 2013).

Epigenetic Influences on Language-Related Traits

Humans share a remarkable ability to absorb and develop language, yet there is substantial cross-population diversity in language and speech. The transmission of language across generations combines a learned, cultural component with an innate, biological one; the former varies widely among human populations, but the latter remains less characterized. Accordingly, epigenetic biological mechanisms that shape language-related traits are considered to influence human language independently of the culture-wide, learned aspects of language acquisition.

Language acquisition unfolds along a predictable and rapid trajectory governed by biological, neural, and epigenetic processes, even though the specific language learned and individual differences vary widely. To enhance phonetic and phonological development during the early years of language acquisition, first languages are increasingly transmitted through bilingualism and gesture. Epigenetic modifications appear to form the regulatory basis for observed individual variation in phonetic input, conditioned as much by social environment and early exposure as by genetic predisposition. Such modifications make development resilient to minor variations but sensitive to prolonged stresses that may induce maladaptive outcomes.

Neurodevelopmental Pathways and Speech Acquisition

Neurodevelopmental pathways from epigenetic marks laid down during early morphogenetic and neurogenic events ultimately direct patterns of articulation, sound, and symbol acquisition. During pre- and peri-natal development, environmental interactions engage genes that regulate pathways involved in vocal tract morphology, central auditory processing, and the establishment of speech motor circuits. Epigenomic investigations of gene regulatory networks linking such pathways to environmental inputs may therefore reveal when and where populations diverge in their susceptibility to phonological variation, rhythmic and prosodic properties, or symbol-oriented versus substrate-offloading modalities. Plasticity remains high during infancy and early childhood (M. Markman et al., 2011), when cultivation by parents, caregivers, and

peers directs acquisition along trajectories consonant with population norms. The timing of exposure to a given modality can influence the choice of that modality (Fisher & Vernes, 2015) (Fisher & Vernes, 2015). Foundational, regulatory, and feedback components of the gene regulatory networks involved in the first language establish further epigenomic marks that tune neural developments ongoing during school years and intonation during adulthood. During adolescence, a secondary wave of epigenomic marks orchestrates the maturation of a multi-level and communicative speech situation; a top-light declarative phase of the first language gives way to a bottom-light driven-situation phase of new languages. Sensory affinities, frequency of exposure, cultural perspectives, the unschooled influence of peers, and even direct experiences also cross-interact with earlier-deployed and still-active marks on the regulatory networks of foundational genes, thus participating in the very constitution of the language adopted [table 2].

Table 2: Gene-Environment and Neurodevelopmental Influences on Language Acquisition

Factor	Mechanism/Pathway	Impact on Language Development	Notes / Observations
Neurodevelopmental Pathways	Epigenetic marks during prenatal and early postnatal periods	Shape articulation, phonetics, rhythm, prosody, and symbol acquisition	Early plasticity is high; timing of exposure influences modality selection
Environmental Input	Interaction with caregivers, peers, community norms	Critical for phonetic, grammatical, and communicative milestones	Adverse childhood experiences can modulate epigenetic regulation
Gene-Environment Interaction	Epigenetic modulation in response to social and environmental factors	Affects cognitive, emotional, and linguistic behaviors	Community organization influences phonetic variation and availability of input
Epigenetic Plasticity	Chemical DNA/histone modifications and ncRNA activity	Provides resilience to minor stressors but sensitivity to prolonged stress	Shapes population-level differences in language and phonology
Multilingualism & Gesture	Early exposure to multiple languages or gestures	Enhances phonetic and phonological development	Cross-interacts with epigenomic marks to tune neural development

Gene-Environment Interactions in Language Learning

Varied environmental conditions and practices underpin different processes in language development. Evidence suggests that interaction with caregivers is vital for healthy language learning (Ziyaev A.A., et al). Children who lack such communication do not reach communicative milestones and develop speech patterns. Such differences can be observed across individuals within a society, dialect groups, or entire communities with different heritage languages (L, 2017). The literature indicates three relevant factors.

First, precisely when language-external factors exert their maximal influence differs among communities; ongoing distributional studies survey both cross-temporal and cross-spatial variation (DOCKS at The University of North Carolina at Greensboro & E. Simone, 2010). Second, a considerable variation in linguistic and para-linguistic input is well-established as a function of parental concern. Third, regulations control whether parental input is reliably available; the ongoing effects of adverse childhood experiences operate through epigenetic modulation.

Gene-sociocultural interaction has direct consequences for language development; differences in community organisation determine how these factors are correlated on average. Epigenetic modulation of cognitive and emotional systems strongly influences the regulation of language-external behaviour and the selection of communities. It remains unclear whether gene-regulation patterns differ across communities, but phonetic variation exhibits stable cross-societal structures.

Epigenetic Regulation and Phonological Variation

A corpus of languages and dialects reveals systematic phonological variation shaped by genomic and epigenomic regulation. Statistical associations between the abundance of language-related epigenetic marks and phonological trait typology confirm that contemporary patterns of cultural transmission reflect densely interweaved biological histories. Research exploring common mechanisms by which diverse cultures modulate epigenetic states relevant for language associated with fundamental tenets of evolutionary theory. Variation and diversification emerge from universal templates, balanced by governing principles or preferences that delimit freedom of expression to preserve an overarching unity.

Plastically acquired patterns may either crystallize, transition into fixed biological makeup, and become susceptible to evolution, or establish an interplay among generationally fixed forms that vary within both universal guidelines and cultural specification. Specifics of these interactions are dictated by genome assembly downloaded during evolution and safeguarded by its exploration through development. Languages influence acquisition and the epigenetic environment, with social status granting privileged access. By systematically transforming the epigenetic state, literature anticipates the widespread adoption of diverse languages, enriching per capita scientific discovery amid pressures that continually promote convergence.

Cultural Transmission and Epigenetic Modulation

Language-related traits are sensitive to epigenetic modulation by various environmental inputs, which may depend on the nature of cross-generation transmission. Patterns of commonly spoken languages tend to be associated with modifications in epigenetic marks, suggesting that such marks participate in their evolution. The neurobiological systems subserving learning and speech development exhibit marked distinctions across human populations. These findings imply that genetically encoded biological predispositions facilitate the acquisition of language, dialects, and other sociolinguistic phenomena, and that removable but potentially lasting marks on the epigenetic genome participate in their cultural evolution (Chopoorian et al., 2021).

Exposure to language is a prerequisite for learning it, yet language itself is not learned, omnibenevolence notwithstanding. Human beings worldwide manifest proclivities for language acquisition. Some are remarkably proficient at it, while others are less so, but the proclivity itself remains ubiquitous. Furthermore, language is an entity composed of multiple distinct but interrelated components. People learn specific languages, dialects, stylistic registers, and other sociolinguistic variants. Except for marginal instances, such learning is constrained to critical and sensitive epochs.

Social Environment, Stress, and Language Development

The social environment influences the acquisition of language and its underlying neurobiological mechanisms throughout the lifespan. Climate, social structures, daily rhythms, and the nature of stressors vary widely across the globe and can modulate neurodevelopment, even in species with well-defined language capabilities (Bergelson et al., 2023). Children who grow up in environments different from those typical of their parents may therefore exhibit distinct language-relevant behaviors, propelling the evolution and diversification of culturally transmitted languages (M. Markman et al., 2011).

Epigenetic marks associated with language-related genes, and their physiological effects on syntax, phonology, and word use, are sensitive to social stresses and cultural influences (Azimova S., et al). As neurobiological pathways from epigenetic modification to language output were mapped, it became clear that these marks would likely vary across populations, following patterns comparable to those of language traits themselves. The ability of early-life experiences to impact these epigenetic marks, and the long-term impact of such experiences on linguistic behaviors, remain only partly understood (Ziyaev A.A., et al). Yet it is already evident that communication deprivation-whether caused by physical impediments such as hearing loss, by chronic social stress, or by culturally driven abrupt changes in the target language-can induce regulatory modifications predisposing towards distinctive neurodevelopmental trajectories (Tung & Gilad, 2013).

Diet, Toxins, and Epigenetic Marks Across Populations

Epigenetic modifications, including DNA methylation, histone machinery changes, and non-coding RNA activity can be influenced by an individual's diet at conception, gestation, breastfeeding, and throughout the lifespan. Anchors can also be moulded by environmental contaminants, such as heavy metals, pesticides, and hydrocarbons, child abuse, and stress during critical neurodevelopmental windows. Accordingly, dietary patterns and exposure to toxins that vary across environments depending upon local vegetation, fauna, dirt composition, agrarian practices, and socio-political conditions can also contribute to cross-population differences in language and speech-related learning. Several epigenetically responsive genes are involved in languages and related capacities (Giuliani et al., 2016); (Meloni & Müller, 2018); (Vineis et al., 2017).

Literacy, Education Systems, and Epigenetic Plasticity

Literacy and education systems influence epigenetic plasticity, shaping how individuals learn and adapt. Varied communication genres, social contexts, and cross-cultural practices impact literacy development and schooling. Integrated social supports, equity, and technology remain critical to educational quality and inclusivity. Formal education fosters linguistic skills from infancy onward (Finnegan, 2003). Global diversity in teaching, learning, and evaluation modes may interact with population-specific epigenetic patterns that guide locally relevant literacy acquisition. Careful analysis of curricula, pedagogies, and terminologies within communities and between countries could elucidate these connections. Knowledge of frequent errors or alongside language varieties amenable to adjustment may further tailor instruction and materials (Allabergenov M., et al). Cognitive plasticity reflects macroepigenetic variation and ongoing modulation by external stimuli (Chopoorian et al., 2021). Social environment and stress shape epigenetic states influencing language development, susceptibility, and resilience to adverse economic shocks and extreme weather events. Amplification of shocks, climate change, and urbanisation raise the stakes for safeguarding social networks, intergenerationally transmitted knowledge, and related trajectories of epigenetic change.

Methodological Approaches and Evidence

Increasing appreciation of language diversity across cultures has revived interest in its evolutionary origins. Two explanatory frameworks have emerged: biological approaches invoke pre-existing genetic or epigenetic endowments, whereas cultural accounts posit that language is predominantly an artefact of social transmission and learning. These perspectives need not be mutually exclusive; epigenetic mechanisms, which modify phenotype without altering genetic sequence, are increasingly recognised for their role in evolution. Furthermore, cultural transmission itself may modulate epigenetic profiles (Azimova S., et al).

Individuals acquire language in a manner similar to the learning of motor skills, suggesting that traits supporting acquisition are subject to selection. By mapping epigenetically regulated neurodevelopmental trajectories that influence the rate and manner of language acquisition, a framework emerges for

understanding inter- and intra-population variation in language. Available evidence indicates that epigenetic marks associated with language-related traits can be identified through bioinformatic approaches, opening avenues for targeted experimental investigation.

Comparative Genomics and Epigenomic Profiling

A critical step in investigating the role of epigenetics in language evolution is to identify specific marks that are both language-associated and exhibit population variation. Comparative genomics and epigenomic profiling contribute to this goal by providing strategies for the detection of population-specific epigenetic signatures associated with language ability (Mozzi et al., 2016) and information on the epigenome that may be relevant to the study of speech and other language-related traits (Devanna et al., 2019).

Language-associated epialleles could be investigated across language-related traits and species. An alternative is to focus on epialleles associated with specific language-related genes across populations or species. Many studies have identified genetic variants that are associated with language-related phenotypes, including FOXP2 and related genes (Dediu, 2011). Language-related epigenetic marks are likely to be concentrated in regulatory regions of existing language-related genes. Epigenomic data sets would thus aid the discovery of language-related regulatory regions, which may themselves exhibit population specificity. Identification of population-specific epiallelic variants can then direct efforts toward the characterization of population-specific marks in those regulatory regions and of the population and language-specific features that they influence.

Longitudinal and Cross-Cultural Cohort Studies

Although the human capacity for language is largely fixed and universal, languages themselves exhibit a staggering amount of diversity. This diversity poses an abiding enigma: how can and have such radically different systems of expressive sound evolved and been maintained, generation by generation, in different populations? Evolutionary anthropologists and linguists have separately approached the question using distinct yet overlapping frameworks, with linguistic variation understood either in evolutionary terms as a product of cultural transmission or as differences between populations shaped by von Neumann-type selection due to differential fixation of features, replication biases, or patterns of borrowing. These separate lines of inquiry can and should be integrated (Sasmakov S.A., et al.).

One striking parallel between biological and cultural systems and rich ground for exploration of greater theoretical integration is epigenetics. Epigenetic marks can influence traits associated with both speech (i.e., the physical realization of phonological contrast) and language (i.e., variation in phonological inventory) and, to a yet more considerable degree, diet. Cross-population patterns regarding certain languages yet more strikingly corroborate the link between epigenetics in dietary and other cultural correlates. Epigenetics therefore connects social environments with culturally selected aspects of phonological system. Continuous development of mothertongue patterns during early life is a critical window for proper and efficient absorption of any language while greater flexibility persists on the other factors even can hardly exist during the formation of critical period for each language. Yet, too late or too early exposure diverse between and within population and hence direct connection to those rich population correlations and also connection to many of world languages still preserved yet gone language among certain population styles and many other tendencies toward harmonic patterns. (Dediu, 2011)

Experimental Models and Ethical Considerations

Language-associated traits are visible in cultural products that employ signed, spoken, and written modalities for communication. How cultures shape language-related traits remains unclear. Experimental models clarify how traits evolve in a culture, yet measuring traits- their presence, absence, or surface appearance- across geographical scales in human populations remains neglected. Epigenetic marks are candidates for tracing variations across cultures and populations (Chopoorian et al., 2021). An estimated

23,000 genes comprise the human genome. Disentangling the regulatory landscape of language-related traits is crucial for understanding their geographical diffusion.

Implications for Theories of Language Evolution

Epigenetic processes contributing to language and speech evolution across populations and cultures may enrich existing theoretical frameworks and suggest policy-relevant implications. Initial hypotheses framed specific cultural and biological models of language evolution in terms of culture-driven and biology-driven trajectories for language-relevant traits across human populations (Dediu et al., 2013). Epigenetic contributions encompassing both language evolutionary factors continue to warrant exploration. Language evolution has long intrigued scholars. Early characterizations of the phenomenon portrayed languages as monolithic unities, or as instances of discrete deviations from such unities, whereas more recent approaches revisit the nature of language variation and change, framing language evolution as a multilevel, multi-temporal process. Cultural evolution models proposed for diverse phenomenon similarly emphasize capacity for uneven change across levels conferring dynamic invariance on evolution. Regardless of perspective, the range of variation exhibited by groups across multiple and distinctive dimensions, despite shared ancestry and gene frequencies yielding genome sameness, remains an open question.

Integrating Epigenetics into Biological and Cultural Models

In the past decade, scientists from geneticists through anthropologists have collaborated to investigate the evolution of human language and the processes it continues to undergo. Geneticists provide evidence of considerable temporal variability in the genetic make-up of human populations and how this variability shapes neural circuitry, cognitive processes, and language in profound ways. Anthropologists provide insights into the socio-cultural environment in which language evolves, diversifies, and dies out (Dediu & Christiansen, 2016). An adequate theory of language evolution must embrace both of these perspectives (Sasmakov S.A., et al).

Epigenetics can transmit information within an organism and across generations without changes in DNA sequence. Chemical marks like methylation or acetylation alter gene expression by affecting how genetic messages are read, therefore shaping phenotypes. Most epigenetic marks acquired during life are reset during gametogenesis, preventing transmission from one generation to the next, but some epigenetic marks, such as imprints and stress-related changes, escape resetting and can be inherited. Current models of language evolution reject the idea that a single mutation created language. Instead, they emphasise that complex regulatory networks operate in gene spaces involved in language and that these networks remain modifiable throughout life in response to experience.

Implications for Language Diversity and Vulnerable Populations

Diversity is a hallmark of human languages; however, some populations remain vulnerable to significant loss of language. Population genetics, historical linguistics, and anthropology have investigated the coevolution of languages and human beings. Further attention to the role of epigenetics is warranted, because this additional explanatory factor may yield insights into the mechanisms that induce language diversity among vernaculars and communicative systems. Interventions can then be designed to ensure language transmission across generations

Future Directions and Policy Considerations

Some questions about the role of epigenetics in the evolution of language and speech patterns across cultures remain unanswered and important for future research, methodology, and interdisciplinary cooperation. Three gaps emerge. First, population genomic scans have yet to discover shared epigenomic or sequence variants that would facilitate cohort comparisons across population pairs. Second, longitudinal studies addressing critical periods, early-life experiences, or intervention effects have not yet been

implemented in a cross-cultural framework (Sasmakov S.A., et al). Third, molecular and behavioural markers enabling projections about early-life language exposure and associated epigenomic states are still being identified. Establishing reliable and arboreal classifiers for such markers would open opportunities to probe the impact of oral, signed, or written communication on language-independent phenotypes.

Conclusion

Eight million years ago, human ancestors diverged from the common ancestor shared with chimpanzees and bonobos (Novelli, 2013). With the emergence of early hominids, a gradual process began, leading to the appearance of modern *Homo sapiens* in Africa about 200,000 years ago. Although biology and culture have acted together throughout this period, the cultural phase or system of language development has accelerated and extended remarkably (Chopoorian et al., 2021). Arguably, this extended system of cultural language development appears much more pronounced across human populations than that of neighbouring primates today, and the field of Language Evolution is witnessing renewed interest against the background of an increased multidisciplinary engagement with, and a strengthening of, the links between Biology and Cultural/Theoretical Issues (Dediu, 2011).

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