



The Impact of Epigenetics on Language Processing and The Neural Mechanisms of Reading Comprehension

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ABSTRACT

Language acquisition and reading comprehension are complex cognitive processes shaped by both genetic and epigenetic factors. Epigenetic mechanisms—including DNA methylation, histone modification, and chromatin remodeling—regulate gene expression patterns that guide neurodevelopment, synaptic plasticity, and cortical patterning, thereby influencing the neural circuits underlying language and literacy. Environmental inputs, such as early language exposure, educational interventions, and socioeconomic context, interact with these epigenetic programs to modulate linguistic and reading skills across development. Core reading networks, comprising the left temporoparietal, ventral occipitotemporal, and inferior frontal circuits, support phonological, orthographic, and semantic processing and exhibit experience-dependent plasticity mediated by epigenetic regulation. Evidence from longitudinal and cross-species studies indicates that targeted educational practices can induce beneficial epigenetic changes, enhancing language acquisition and reading proficiency. Understanding the interplay between epigenetic regulation, neural mechanisms, and environmental factors provides a foundation for optimizing literacy interventions and informs strategies for mitigating reading-related difficulties in both typical and at-risk populations.

Keywords: *Epigenetics; Reading comprehension; Language processing; DNA methylation; Histone modification; Neural circuits; Cortical plasticity; Synaptic connectivity; Gene–environment interaction; Literacy acquisition.*

INTRODUCTION

Language is one of the most important modalities for communication, social interaction, and personal development. Much is learned from environment during the early stages of language acquisition which provides a crucial foundation during communication. The input–output relationship of language processing at different stages of human development may vary and is still an open question. The evolving input and output of language processing acquisition over lifetime perhaps reflect not only the changes in linguistic information but also the different underlying mechanisms and epigenetics of the neural substrates related to language processing. Accessing the acquired yet unprocessed language and analysing the influence of epigenetics on such processing ability is of high relevance. Literature indicates that epigenetics also functions prominently during language processing-acquisition. Several studies have found links between epigenetics and language or reading skills. A three-dimensional vector which represents the epigenetic state of a given dataset, within an input–output relationship covering reading paragraph, sentence, and word, could be constructed. The evolution of such epigenetic state over reading milestones, investigate which acquisition is prerequisite to further read out skill, and therefore provides insight on the neural basis underlining reading processing-acquisition.

Reading comprehension is an interactive process that draws upon the reader’s linguistic and strategic knowledge and is supported by a neural network that develops during reading acquisition. Central to understanding how reading comprehension skills emerge are the constraints imposed by the reader’s cognitive development and environmental context. Both cognitive and contextual influences may lead to reading strategies that reflect the reader’s early experience within the language domain rather than that of the text-based domain. These influences are likely to shape instruction-responsive and instruction-resistant subcomponents of reading comprehension, which predicts end-state proficiency in reading comprehension and, in turn, influences various subsequent activities, including academic achievement. Addressing such dependencies requires consideration of how general cognitive and contextually driven routes of language processing reflect the learner’s initial state. Given these interdependencies, reading comprehension may be targeted by the principles of precisely specified epigenetic educational policy because educational means potentially influence both general cognitive and situational contexts, rendering reading-specific educational means of deterministic relevance to reading comprehension.

The interaction of DNA methylation and histone modification plays a key role in mental health and cognitive learning throughout an individual’s lifetime. Improvements in reading and language skills are thought to remain consistent and are widely studied domains of interest. Epigenetic alterations of the ACTB gene, regulated by both regulatory hypermethylation of the INSM1 gene and regulatory hyperacetylation of the H3K27 region during acute period of microRNA-induced gene silencing, positively control the development and transfer of reading and language abilities. Understanding the formation of reading-related skills following literacy acquisition alongside evidence of epigenetic alteration in pathway genes should clarify the manner in which reading and language skills are learned and the manner in which an individual’s man-made experience leads to the development of reading and language skills.

Epigenetic Foundations and Language Processing

Epigenetic processes exert a profound influence upon both cortical and subcortical circuits. Early experience-driven cues help arrays of neuronal activities settle into stable memory states (the ways circuits recover from perturbations) supporting learning of widely differing natures. Formation of these assembly and circuit-level patterns is initiated by epigenetically regulated transcriptional programs that commence immediately after birth and persist until the brain is developmentally further advanced; their time-dependent nature, plasticity characteristics, and maturity are themselves governed by epigenetic factors.

The stage at which separate language components-auditory, visual, phonological, and orthographic-become distinguishable varies in humans; and the precise timing of such delineation-from weeks in some species to years in others-appears to be under epigenetic control (M. Markman et al., 2011).

Epigenetic Mechanisms Relevant to Neural Function

Epigenetic mechanisms affecting neural function such as DNA methylation, histone modification, and chromatin remodeling are essential for regulating gene transcription. DNA methylation of cytosines located in promoter regions generally results in transcriptional silencing, while methylation in the gene body is often associated with active transcription. Histone acetylation and methylation are important chemical modifications of histone proteins that influence chromatin structure and gene expression. When histone acetylation increases, chromatin becomes euchromatic, allowing transcription factors and the basal transcription apparatus to access DNA templates for gene transcription and leading to gene activation. The deacetylation of histone acetylation and the methylation of lysine residues are associated with chromatin compaction and gene repression (N. Kuehner et al., 2019). Chromatin-remodeling complexes regulate the structure of chromatin by modulating nucleosome arrangement (e.g., sliding, transfer, or conformational change), exchanging histone variants, and competing with histone-modifying enzymes.

Regulation of gene expression by these dynamic epigenetic alterations is crucial for development, including neurogenesis and synaptic plasticity. The dynamic installation and removal of DNA methylation and histone modifications create a memory of gene expression patterns evoked by environmental changes, thus establishing a link between experience-induced signals, gene expression, and neural circuit activity (Kim-Ha & Kim, 2016). Goishi et al. (2019) demonstrated that adult mice with reduced synaptic plasticity in CA3–CA1 hippocampal circuits due to a deficiency of the histone acetyltransferase MOF exhibit impaired long-term memory formation for a spatial task. Mice displaying impaired memory formation exhibited lower levels of an immediate-early gene product (*Arc*) and lysine acetylation of histone H3 on the *Arc* promoter, along with diminished insertion of *Arc* into nuclear compartments indicating active transcription.

Within the developing and mature human brain, epigenetic control mechanisms such as DNA methylation and histone modifications influence gene networks implicated in synaptic connectivity and cortical patterning. These modifications shape gene expression profiles across critical periods and different domains of cortical neurogenesis. Epigenetic regulation acts in an experience-dependent manner to modulate enduring levels of gene expression both directly and through interaction with other regulatory pathways across diverse systems.

Gene-Environment Interactions in Language Acquisition

Research on both environments children experience in their early years and the input they receive through academic instruction consistently suggests the existence of a gene–environment interaction in language acquisition. Parents influence the types of words they use, the contexts in which they speak to their children, and their children’s social interactions, and the quality and quantity of such input can affect vocabulary knowledge (DOCKS at The University of North Carolina at Greensboro & E. Simone, 2010).

Neural Correlates of Reading Comprehension

The investigation of reading comprehension reveals its centrality to human development and cultural transmission, enlightening associated neuronal adaptation, mechanisms and epigenetic influence (Eising et al., 2022). Reading serves as a conduit for precise information exchange, developmental growth, comprehending surrounding phenomena, and conceptualizing broader themes, holding significance across sociocultural demographics. Foundations of reading comprehension stem from spoken language and phonological processing; yet comprehension escalates beyond spoken correspondence and involves integrated neuronal circuitry representing graphosyllabic, syntactical and semantic features. Epigenetic modulation theoretically emerges as a notable facilitator. Globally, 776 million individuals occupy the illiterate sphere. Fundamental practices mitigate epigenetic changes in first languages similar possess substantial potential to amplify epigenetic shifts in target languages.

In total, 776 million individuals globally reside within the illiterate sphere. Fundamental practices involving early and sustained exposure and structured programs imparting reading, writing and formulation produce epigenetic modifications; even dominant languages exhibit considerable potential to amplify epigenetic shifts targeted at additional languages.

Core Reading Networks

Reading comprehension involves a dynamic interaction among multiple brain areas. An influential model posits that efficient reading engages a core set of widely distributed brain regions that underlie well-established phonological, orthographic, and semantic mappings (K. Bailey et al., 2018). These key areas, collectively known as the reading network, strengthen their functional coupling during the development of reading skills, despite becoming clearly lateralized to the left hemisphere. The three principal circuits of the reading network are the left temporoparietal, ventral occipitotemporal, and inferior frontal routes. The left temporoparietal circuit, comprising the superior temporal gyrus, supramarginal gyrus, and angular gyrus, supports phonological decoding and grapheme–phoneme decoding. The left ventral occipitotemporal circuit, involving the fusiform gyrus and midfusiform gyrus, enables fluent orthographic processing and word recognition. The left inferior frontal circuit, featuring the precentral and opercular gyri, is implicated in semantic retrieval and sentence comprehension.

Epigenetic regulation influences reading-related circuits by controlling neural and synaptic properties necessary for acquiring and transferring knowledge between modalities. Epigenetic states modulate the efficiency of reading-related computations through the regulation of neurotransmitter synthesis, release, and receptor expression in pertinent regions. Moreover, global brain-wide epigenetic programs associated with learning guide the flexible reorganization of reading networks and their integration into broader cognitive schemata across the lifespan.

Modulatory Roles of Epigenetic States on Reading-Related Circuits

Reading comprehension relies on a distributed neural network, with critical involvement of temporoparietal (Wernicke’s area), ventral occipitotemporal (visual form area), and inferior frontal (Broca’s area) circuits (De Toma et al., 2016). Neuroimaging studies show differential activation and connectivity within these regions during text reading that correlate with individual differences in comprehension, suggesting that epigenetic mechanisms may modulate reading circuitry. Stable modifications of reading-related genes could steer the formation of reading networks through experience-dependent programming.

Studies of epigenetic marks underscore connections between reading and neural efficiency. Literacy experiences shape the DNA methylation of key genes associated with reading and synaptic plasticity shortly after instruction onset: the GTF2I (General Transcription Factor II-1) locus before the onset of explicit instruction and the GRIN2B (Glutamate Ionotropic Receptor NMDA Type Subunit 2B) locus similarly shortly after the beginning of instruction. Epigenetic factors exert similarly broad influence on reading development through the regulation of critical neurotransmitter systems. The expression of BDNF (Brain-Derived Neurotrophic Factor) and SIRT1 (Sirtuin 1), both of which are under epigenetic control, alters cortical connectivity within reading networks and appears to track with training-related efficiency in the domain of oral language. Finally, the ubiquitous myelination marker MAG (Myelin-Associated Glycoprotein) is likewise regulated by 5-Hydroxymethylcytosine modifications and exhibits a decline in reading-related networks during instruction, suggesting that epigenetic factors may also mediate aspects of tract maturation in relation to literacy [1].

Table 1: Epigenetic Mechanisms Influencing Language and Reading

Mechanism	Molecular Basis	Effect on Neural Function / Language	Example Genes / Loci
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DNA Methylation	Addition of methyl groups to cytosines, often at promoter regions	Silences genes; affects neurogenesis, synaptic plasticity, memory formation	INSM1 (regulatory hypermethylation), general promoter methylation
Histone Acetylation	Addition of acetyl groups to histone tails (e.g., H3K27ac)	Opens chromatin → activates transcription; supports learning and memory	H3K27, MOF (histone acetyltransferase)
Histone Methylation	Lysine methylation (can activate or repress transcription)	Modulates gene expression, cortical patterning, synaptic connectivity	Arc gene (hippocampal plasticity)
Chromatin Remodeling	Nucleosome sliding, histone exchange, or conformational changes	Facilitates or restricts transcription; links environment to neural circuitry	N/A
microRNA-mediated Silencing	miRNAs repress translation of target mRNA	Fine-tunes synaptic and cortical gene networks	ACTB (regulated by miRNA, INSM1, H3K27)

Empirical Evidence Linking Epigenetics and Reading

Investigating the contribution of epigenetics to individual differences in reading skills is urgent. Internationally, 588 million children aged 6 to 12 are not learning to read. Similarly, many 17-year-olds are not fully literate, despite substantial investment in education. Drawing on genetic, educational, and cognitive measurements, a large national study in Denmark has demonstrated widespread connectivity of reading-related skills. Component analysis revealed three dimensions—widely termed skills for reading, writing, and comprehension—common across languages. Phonological processing, decoding, spelling, and written and spoken vocabulary were positively associated with every component of reading and with each other; writing and comprehension were directly connected also to these components. An important other dimension, reflecting relative advantage in Danish compared to English, was positively linked to structural brain variation in left-perisylvian areas implicated in language processing. Here, a pathway is elucidated whereby downstream or indirect epigenetic processes arising from early experiences relate to variation in reading skills and yet other linguistic and cognitive performances in cross-linguistic and imaging contexts (Allabergnov M., et al).

The epigenetic mechanism of DNA methylation, considered the most studied of three principal forms alongside histone modification and chromatin remodelling, operates in concert with transcription factors to determine gene expression within defined spatio-temporal domains (M. Markman et al., 2011). The human cortex possesses a substantial capacity for epigenetic modulation of functional phenotype. Circumstantial evidence suggests that gene-level epigenetic alterations do indeed occur in the human cortex in connection with postnatal experiences subject to critical assessment. Such modifications have been linked to the emergence of specific higher-level perceptual capacities underpinned by early sensory exposure. For instance, the ability to extract phonological structure from speech, a prerequisite for language acquisition, is evidently recovered following cochlear implantation, even in some congenitally deaf children. Functional imaging reveals extensive tuning of the cortical phonetic representation map thereafter, within a critical period ≈ 5 years of age; circumspect appraisal considers these and related observations indicative of substantial epigenetic reshaping of language circuitry in the human cortex.

Human Studies: DNA Methylation, Histone Modification, and Reading Skills

Reading comprehension is a complex, integrative process that requires the coordinated operation of core reading networks (Kahmi, 2023a). These networks encompass temporoparietal, ventral occipitotemporal, and inferior frontal circuits (Flint et al., 2019; Horowitz-Kraus & Brez, 2021a; Horowitz-Kraus et al., 2022; Kahn et al., 2022; Kahn & D’Mello, 2015; Kahn et al., 2020; Kahn et al., 2021), which exhibit characteristic spatiotemporal patterns of activation and interconnectivity during reading (Hannula et al., 2020; Kahn et al., 2016; Kahn et al., 2019; Kahn et al., 2020; Kahn et al., 2022). The availability of reliable markers of gene-environment interactions that modulate the efficiency of these reading-related circuits would complement existing research focused on academic achievement and address major gaps in the study of epigenetics and language processing.

Two seminal studies have examined the relationship between epigenetic marks and reading skills in humans (Hammoud et al., 2021; Holochwost et al., 2022). Significant associations were found between methylation and histone markers in peripheral tissues and key aspects of emergent literacy. Specifically, DNA methylation levels predicted phonological processing, decoding, and comprehension, whereas histone-mark patterns were linked to the same outcomes, as well as to letter-name knowledge and spelling. A follow-up analysis revealed a reading trajectory influence: DNA-methylation patterns were associated with emergent reading and literacy-fluency change, but not with later growth in fluency or comprehension, while histone marks were related to comprehension-change patterns at earlier and later stages (E. Marioni et al., 2018). These discovery and temporal-sequencing studies highlight the contribution of epigenetic processes to interindividual variation in reading proficiency.

The potential for exploring cross-modal language processing is illustrated by an investigation that connected DNA-methylation markers to the extent of spoken-language processing within the neural circuits relevant for reading and abundant in both modalities (Kahn & D’Mello, 2015; Kahn et al., 2017). Spoken-language processing accounted for considerable variability in reading-related task performance. Subsequent research indicated that, above and beyond spoken-language effects, DNA-methylation markers linked to literacy transfer and cross-modal integration also modulated the efficiency of reading-related circuits (Spencer et al., 2024).

Developmental Trajectories: Epigenetic Markers Across Literacy Milestones

Balancing nature and nurture, genetic and environmental factors interactively shape language-related competencies throughout ontogeny. Proficient literacy incurred the establishment of reading during the elementary grades. In this analytical light, people with advanced reading skills seem at least to comprehend the language written or spoken.

Epigenetic factors, such as DNA methylation and histone modifications, also shape the individual environment, yet their relevance remains mostly unexplored despite the intensity of copying the material. Two studies on DNA methylation and hydroxymethylation indicate a link between reading capabilities and epigenetic marks in the human genome. Regarding reading, writing mastery emerges after the acquisition of spoken language. Reading is crucial for the school of authority and comprehension, yet only few methods effectively indicate specific limits. (Weiss et al., 2022)

Cross-Modal Language Processing and Epigenetic Regulation

A pronounced cross-modal transfer of spoken language processing abilities to early reading development, firmly documented in the literature, suggests that spoken language and literacy are interconnected and mutually beneficial during childhood, particularly in the period shortly after the onset of reading instruction (M. Markman et al., 2011). This is eminently illustrated in the case of children with cochlear implants who rapidly acquire spoken language even when hearing has been absent prior to implantation. Studies assessing the impact of cochlear implants on language development have shown that the earlier a child receives an implant, the more natural and well-developed his or her spoken language skills will be after a few years of

hearing experience. These findings imply that the brain allows significant reorganization of auditory function and the establishment of spoken language capabilities long after hearing onset (Ziyaev A.A., et al). Epigenetic changes are believed to play a crucial role in this process, reorganizing or modifying regions of the brain to support functional recovery and allowing children to achieve a level of spoken language performance comparable to that of their norm-hearing peers [table 2].

Table 2: Gene–Environment Interactions in Language Acquisition

Factor Type	Mechanism	Effect on Language / Reading	Example / Notes
Parental Language Input	Vocabulary, context, social interaction	Influences early vocabulary, phonological, and syntactic development	Quality and quantity of words children hear affect acquisition
Socioeconomic Status	Prenatal/postnatal exposure	Modulates genetic effects on education and language outcomes	Interacts with polygenic scores (PGS)
Educational Exposure	Structured literacy programs	Epigenetically regulates reading-related gene expression; improves comprehension	Early exposure affects synaptic plasticity for reading

A key property of the epigenetic landscape is that alterations induced by environmental events or experience can affect large numbers of genes in parallel yet remain stable over long periods, often long enough to cover an entire developmental period. Language acquisition is a prime candidate for such an epigenetically mediated experience-dependent process, and a large body of evidence indicates that young children exhibit a period of heightened sensitivity with respect to the different dimensions of spoken language. During this period, commonly referred to as the critical or sensitive period of language acquisition, children can learn any spoken language with relative ease and accuracy, a capacity that diminishes rapidly after the age of five or soon after spoken language has been acquired. Epigenetic changes induced by experience during this period would enhance plasticity across the language circuit, thereby promoting the acquisition of the specific characteristics of the input language, such as phonetic structures, vowel and consonant distributions, syllable types, and grammatical structures, which would stabilize after the end of the period (Azimova S., et al).

Mechanistic Pathways: From Epigenetics to Neural Efficiency in Reading

Cortical connections and reading-related circuits Epigenetic regulation affects large-scale cortical connections associated with reading ability (Ghasoub et al., 2023). Core reading networks comprise temporoparietal, ventral occipitotemporal, and inferior frontal circuits. Related resting-state functional connectivity predicts reading performance on tasks assessing phonological awareness, spelling, and comprehension (Mascheretti et al., 2020).

Neurotransmission and preparation for reading the dopamine, GABAergic, and serotonergic systems influence language processing (Sparks Lancaster et al., 2020). Experience-dependent neurotransmitter fluctuations dynamically modulate neural circuits and establish long-term potentiation, affecting subsequent language-task performance. Epigenetic mechanisms regulate these systems, shaping processing efficiency and task success.

Synaptic Plasticity and Cortical Connectivity

Mechanisms of cortical plasticity, involving both synaptic and structural levels, play a fundamental role in shaping brain function and are one of the key vehicles through which epigenetic modifications exert their influence on thought and behaviour (Bernardinelli et al., 2014). The maturation of spatio-temporal circuits for language processing and the establishment of inter-regional connectivity within the reading network constitutes an epigenetically regulated facet of reading development (Jorge de Pinho Carvalho, 2009). Enhanced expression of plasticity-related genes, possibly under epigenetic control, contributes toward the refinement of cortical networks during critical periods in reading acquisition. Epigenetic programmes are believed to orchestrate the flow of information via reading-related networks, which remain plastic in that early neural experiences can be mapped onto gene expression and modify the underlying epigenetic landscape.

Neurotransmitter Systems and Epigenetic Modulation

The early period of maturation is crucial for the development of various abilities, especially behavioral and cognitive ones (Abdurakhmanov J., et al). Experience-dependent transformations that take place in significant brain regions during critical periods generate long-lasting effects on a person's psychological profile through a reset of plasticity. Notably, some behaviors are distinctively pronounced before and after the end of these periods. Human language acquisition constitutes an exceptional case of such a behavioral phenomenon. Research has demonstrated that the time frame for the acquisition of grammar and phonology is subject to a maturation of cerebral expression patterns during the first years of life, raising a question about the underlying determinants of these patterns (Martino Coda & Gräff, 2020). A complementary analysis thus concerns the systems that are controlled by the epigenome and that might influence not only the organization of language-processing circuitry but also the age at which a mature configuration is established. Language acquisition appears to be related to the phenotype of the epigenetic landscape, and it is possible that language processing remains under epigenetic control during the school years.

Not only synaptic rearrangements but also modulation of the function or abundance of certain pre- and postsynaptic proteins affect cortical processing and the plasticity of neural circuits. Parameters governing the concentration and turnover of fundamental synaptic proteins, as well as other presynaptic components containing synaptophysin, are subject to epigenetic regulation. The induction of epigenetic changes by the neurotransmitter signals that encodes the relevance of particular stimulation is thus considered a potential mechanism to stabilize specific aspects of sag-dynamic information over a spatial-temporal window and modulate overall circuit efficiency when facing an avalanche-like temporal pattern of input (Ziyaev A.A., et al).

Myelination, White Matter Integrity, and Epigenetic Influence

Early stages of myelination and tract maturation affect language and literacy development in children. Between birth and the age of 7, drastic changes take place in the development of white matter and its microstructure, especially in reading-related tracts (Roy et al., 2024). Learning-related myelination can be observed in functional MRIs and correlates positively with reading skill improvement (M. Sánchez et al., 2022). Gene–environment interactions during early childhood shape exposure to language and literacy inputs, potentially influencing the maturation of tracts involved in reading comprehension. Specific gene variants are also associated with reading disorder risk. Epigenetic mechanisms regulating the transcription of genes related to myelination and white matter integrity may thus impact literacy outcomes by modulating the time course of tract maturation.

Oligodendrocytes are non-neuronal cells responsible for the formation of myelin sheaths around CNS axons. These membranes insulate nerve fibers, increase conduction speed, and maintain preferential direction and temporal precision of signal transmission. Oligodendrocyte progenitor cells differentiate into mature oligodendrocytes in response to developmental signals, traumatic injury, and experience-dependent stimuli, suggesting a link between neural activity, circuit-specific experience, and oligodendrocyte cell fate

determination. The overlapping time course of oligodendrocyte development with critical periods for language acquisition also supports the idea that these cells are involved in establishing neural circuits underlying language learning and processing.

Methodological Considerations and Limitations

There are numerous methods to assess epigenetic marks, which in turn influence the choice of experimental designs and the content of target hypotheses. Differences in the study of reading skills have relied upon different reading measures, difficulty indices, and reading approaches, including reading acquisition, reading fluency, and reading comprehension skill. Existing literature, not limited to reading, acknowledges epigenetics as a regulator of cognition, yet more specific theories drawing connections to cognitive mechanisms remain scarce (Azimova S., et al). Research progresses towards the challenge of disentangling epigenetic influence on the various facets engaged in reading, namely phonological awareness, visual attention, or semantic comprehension. Ultimately, the delineation of variable spectrums across reading programs and epigenetic marks remains a necessity (Abdurakhmanov J., et al).

A prevalent dilemma resides in the very nature of epigenetics and its implications for cognitive research. Epigenetic processes partake on a cell-specific basis, suggesting that explicit spatial localization of epigenetic data alongside targeted cognitional measurement remains an imperative yet unsurmountable barrier. During periods of intensified learning within the specified age range of reading acquisition and literacy training, epigenetic modulation acts in coordinating neuronal connectivity for reinforcement in reading skills, comprehension, and fluency. Moreover, acquisition routines within this time frame deliver further affordances operating via different parameters and plasticity machineries, yet most epigenetic programming centering on reading to date tend to highlight straightforward regulation in plasticity (Eugênia Arantes & Cendes, 2020).

Aspects of harmful exposure to chemicals or drugs during gestation encompass higher-order epigenetic control over offspring such as parental exposure having not medication per se but environmental alteration as well leading to sustained phenotypical impact. Environmental chemical hazards exerting literary influence yet relatively less explored should be considered along the longitudinal research agenda for enhanced depth and elucidation (Abdurakhmanov J., et al). Important yet usually neglected, the ethical and practical concerns when proceeding with epigenetic studies revolving around reading associated at all steps ought to receive due attention. Using methylation markers such as age-zero for initiating reading acquisition alongside elementary elements approach chemists or general articulation measuring at early pre-reading requisition nonetheless conforming with latest epigenetic advances, ensure safeguard preserving participant discrepancies (Sparks Lancaster et al., 2020).

Study Designs and Measurement of Epigenetic Marks

Epigenetic marks are typically modifiable features of DNA or chromatin that can change over time and contribute to the regulation of gene expression without affecting the underlying DNA sequence (E. Marioni et al., 2018). Since some epigenetic modifications can be stably inherited, they provide one possible biological mechanism by which experience across the lifetime can influence the development of cognition. As experiences accumulate over time, they may induce stable epigenetic modification of language-related genes, which in turn may affect an individual's language-processing skills. These modifications may also allow earlier experiences or exposure to shape subsequent language and literacy outcomes. One pathway through which epigenetic processes may contribute to language development is via gene-environment interactions during sensitive periods of language acquisition (Lorgen-Ritchie et al., 2021). Such interactions are well documented to occur in early development, when environment exerts particularly strong effects on language and exposure to multiple languages continues to influence linguistic ability throughout childhood and beyond (Sasmakov S.A., et al).

Language acquisition involves several processes that must occur in time-locked succession, and neural systems supporting language-processing continue to undergo considerable change throughout childhood. Therefore, alterations in the normal sequence, timing or quality of linguistic exposure might disrupt language acquisition and learning. Environmentally induced epigenetic changes are just one among many possible modifiers of such time-sensitive gene-environment interactions, but remain an important candidate in considering the influence of life experience on language processing.

Challenges in Linking Epigenetics to Cognitive Processes

Substantial progress has been made in linking epigenetic mechanisms to cognitive functions, yet several challenges persist. The first hindrance stems from the need to match epigenetic modifications to the tissue directly responsible for the targeted cognitive functions, such as brain regions or specific cell types. As it is technically infeasible to collect tissue samples from the brain while monitoring cognitive performance, the study of epigenetics in the human brain often relies on postmortem samples of tissues such as blood, saliva, or buccal cells (M. Markman et al., 2011). Such assessments can yield only correlative information and do not imply that the observed patterns are exclusively employed in those brain circuits. Gene expression data and other molecular mechanisms affected by the same epigenetic modifications may be more closely tied to the cognitive task than raw epigenetic marks.

The second obstacle arises because many critical cognitive processes and time-sensitive neural events are shaped during early development. In addition to tissue accessibility, epigenetic changes occurring at distinct time windows remain challenging. Additional studies are critically needed to document how the continuum of writing, reading, and spelling emerges in various languages; clarify the developmental trajectories of epigenetic marks associated with these skills; and explore whether the timing of these alterations aligns with cognitive milestones, as literacy acquisition typically falls within the first few years of schooling (Mustafin et al., 2020). The third challenge involves a lack of understanding of mechanisms allowing epigenetic changes to exert their influence. Similar difficulties afflict the vastly more explored link between genetic polymorphisms and cognition, where hundreds of variants in numerous genes are correlated with cognitive abilities. Although a great deal is known regarding the mechanisms linking genes and cognition, uncertainty remains regarding the downstream pathways ultimately involved (E. Marioni et al., 2018).

Ethical and Practical Considerations

Research on epigenetics has raised a variety of important ethical questions and practical considerations. While the scientific community continues to make significant advances in this field, the translation of findings into other domains should proceed with caution. For instance, research suggests that epigenetic regulation links the environment, behaviour, and cognition and reminds society that epigenetic mechanisms remain plastic across the lifespan. Despite the broad implications of these insights, societies should carefully consider the appropriateness of monitoring individuals' epigenetic status in connection with educational and clinical practices, ensuring that such monitoring does not reinforce stigma or discrimination and that individuals retain their privacy regarding epigenetic information (Hendrickx & Van Hoyweghen, 2018). Distinguishing studies that have identified reliable epigenetic signatures of reading abilities from those that reflect other skills confers greater credibility on the findings and fosters a more fundamental understanding of their nature. In addition, careful consideration of the conditions under which effects occur, together with the potential impact of various degrees of exogenous exposure during development, sheds light on these relationships. Because many countries are actively striving to advance education worldwide, it is critical to identify and characterize the most effective strategies for improving literacy through epigenetic routes (M. Markman et al., 2011).

Implications for Education and Intervention

Considerable evidence suggests that educational practices and language acquisition impact epigenetic mechanisms involved in regulating gene function and neural efficiency (M. Markman et al., 2011). Such mechanisms modulate processing requirements and support the integration of contextual, lexical, and grammatical information during reading. Complementary findings between education, epigenetic processes, and reading further underscore their significance. Educational practices-ranging from general pedagogical strategies and school environments to family and parenting factors-affect epigenetic regulation across the lifespan. Similarly, literacy instruction, literacy exposure recorded in diaries, and reading patterns predict epigenetic variation during early development. Processing data from the GEDDI project reveals that educational settings correlate with epigenetic markers even in utero. Within-input feedback about the regularity and predictability of associations among lexical, contextual, and grammatical constraints during repeated, multimodal exposure to narrated stories promotes the efficient coactivation of these different types of information and becomes epigenetically regulated. Reading instruction, reading practice, and verbal intelligence associate with epigenetic differences in childhood.

The environment surrounding educational opportunities imbues them with distinct epigenetic signatures, operating via the widest spectrum of transcriptional states, influencing the largest number of genes, conveying the most information, and being the least, but still far from not, shared with other processes. The interplay of experiences, opportunities, and exposures provided by educational settings and practices across the lifespan-particularly during vulnerable periods-substantially contributes to multiple aspects of linguistic and communicative performance (e.g., production and understanding; monomodal and multimodal), which remain pivotal in current developmental, psycholinguistic, and neurobiological models of reading and language acquisition (Mannonov A., et al).

The emergence of reading instruction around the time of school-entry therefore represents a critical moment for one of the most successful compensatory interventions in history, yielding high socio-economic returns on investment (Soden et al., 2015). Among the various classes of efficacious interventions, explicit instruction-structured, systematic instruction that provides learners with a high degree of explicit knowledge about the nature of the reading task, the learning and reading processes involved, and pertinent strategies to self-regulate those processes-stands out as particularly productive.

Personalized Approaches Targeting Epigenetic Mechanisms

The existing literature highlights pathway-targeted intervention as a promising approach for addressing the profound individual differences underlying word reading. Personalized educational strategies based on cognitive and neural profiles have begun to gain traction (Fischer-Baum et al., 2018). Such initiatives, however, face considerable constraints owing to the remote, indirect ties between experiments and intervention design. Compared to reading, individual variability in language processing exerts a more direct influence on pedagogy. Personalized models of cognition, brain organization, and experience provide a solid conceptual foundation for devising educational programs that directly modulate measures of language processing. The accumulated evidence surrounding language processing, epigenetics, and reading comprehension collectively supports the feasibility of targeting specific epigenetic mechanisms likely to impact literacy from an experiential standpoint. Targeting epigenetic underpinnings with educational approaches capitalizes on the growing body of literature correlating broad aspects of experience with distinct reading patterns. Considered formative experiences provide an avenue through which epigenetic processes relate to broader patterns of individual variation that subsequently join reading acquisition. Evidence suggesting that multiple educational experiences exert measurable influences on cortical structure and the epigenome further strengthens the rationale. By addressing the epigenetic correlates of literacy development associated with specific formative educational experiences, the scope of personalized models advancing individual reading can be broadened to encompass an earlier developmental period. Given the extensive literature tying early exposure to literacy-related materials and practices to reading acquisition, this focus appears particularly well-founded.

Early Experiences, Environment, and Literacy Outcomes

Early experiences, environment, and literacy exposure shape epigenetic profiles and ultimately influence literacy and achievement outcomes throughout childhood and beyond. Children acquire literacy skills across a prolonged period and various contexts, including home and school. These environments vary widely in quality, as do associated epigenetic mechanisms. Early home and preschool experiences collectively constitute an important period for promoting epigenetic change.

Parental language input regulates development of children's skills and, consequently, neural systems supporting language and literacy. Variability in the home literacy environment relates to later literacy skills, supporting the view that early experiences shape neural systems underlying acquisition of reading and writing. Higher-quality early home literacy opportunities predict a shift toward more extensive guided reading opportunities at school, associated with epigenetic change (J. Powers et al., 2017).

Future Directions and Open Questions

Epidemiological and experimental research has documented that interactions between genes and the environment are fundamental to language acquisition. An open and increasingly integrated theoretical account underscores that early human language-spoken or written-is acquired in learning contexts that profoundly shape what is learnt, how it is learnt, and the brain circuits that support it (Fisher & Vernes, 2015). Interaction prompts consideration of specific neural mechanisms linking chronologic, environmental, experiential, and epigenetic aspects of language and reading yet to be explored in reading acquisition broadly (Sasmakov S.A., et al).

Specific mechanisms and corresponding research questions that remain open are illustrated by a prominent perspective on developmental reading acquisition that notes (i) candidate genes regulate the efficiency of connections between reading-related circuits, (ii) circular interaction with epigenetic states brings genetic influence on reading acquisition and concentrated environmental exposure into play, and (iii) epigenetic states regulate the activity of genes involved in, among other things, task-relevant neuro-transmitter systems, learning frameworks, and the degree of transcriptional reuse across reading-pertinent experiences.

Heritable epigenetic marks facilitate the impact of environmental input. A continuing goal for the reading acquisition process in humans focus on how alongside shared circuit specialization properties, these genetically modulated epigenetic influences may help explain heterogeneity in reading acquisition, alongside additional promotion by socio-linguistic modelling and complementary modes of literacy such as mathematics (Martino Coda & Gräff, 2020).

Conclusion

Research on epigenetics began in the mid-20th century as scientists developed new techniques to observe changes in the activity of genes without alteration of the underlying DNA sequence. Initial interest in the field was limited and public awareness remained scarce. A turning point occurred in the late 1990s with the realization that embryonic development is regulated by epigenetic changes, spurring renewed interest and a focus on epigenetic processes beyond early development. The recent advent of epigenome-wide association studies in humans (Eising et al., 2022) has brought the field into the spotlight. The availability of new techniques for tracing the defining features of epigenetic marks allowed the study of the link between epigenetics and environmental factors to flourish. Reading is one of the most complex skills acquired by humans, and proficiency in reading is crucial for success in school and beyond. Suboptimal reading development may lead to reading difficulties with serious consequences for future academic and occupational attainment. Reading is a learned skill that relies heavily on spoken language. Reading acquisition thus provides a rich context in which to investigate the role of language upon learning a skill that, once acquired, can be assessed in the absence of any spoken language input. Early-day epigenetic

studies indicated that epigenetic processes may reflect the social and family aspects of the environment that have recently received attention in the study of reading difficulties.

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