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Genome-Wide Insights into The Role of Genetic Variability in Linguistic and Cognitive Functions

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ABSTRACT

Language and cognition are complex human traits influenced by polygenic and environmental factors. Genome-wide association studies (GWASs) have identified numerous single-nucleotide polymorphisms (SNPs) and loci associated with phonology, syntax, semantics, and other cognitive abilities, highlighting the shared and distinct genetic architecture underlying these processes. Key genes-including PAX6, ATP1A2, KCNJ10, PROX1, and MIR3945-affect phonological processing, working memory, and grammatical development, and are linked to neural circuits in the superior temporal, inferior frontal, and parietal regions. Polygenic scores further demonstrate that early-life environmental factors, such as socioeconomic status and maternal nutrition, interact with genetic predispositions to shape cognitive trajectories. Despite substantial progress, much of the genome remains uncharacterized, and cross-population validation is limited. Integrating GWAS findings with longitudinal neurocognitive and multi-omic datasets provides a framework for understanding how genetic variability contributes to language processing, cognitive development, and their disorders, paving the way for personalized educational and clinical interventions.

Keywords: *Language acquisition; Cognitive development; Genetic variability; Genome-wide association study (GWAS); Phonology; Syntax; Polygenic scores; Gene-environment interaction; Neural circuits; Human cognition.*

INTRODUCTION

Language is a defining trait of humanity, yet its genetic traits are not yet fully known. Twin and family studies have shown that linguistic abilities are substantially heritable and have linked them to a diversity of cognitive skills (Fisher & Vernes, 2015). Gene-phenotype associations related to diverse linguistic traits have been established. Approaches relying on general cognitive ability are less common, yet languages also

operate under principles set by a universal grammar, and analysis of genetic data has consistently located cues for general cognition partially overlapping those for language. The advent of genome-wide association studies (GWASs) that survey genomic data for the entire mrngqhnq genome promises to provide fresh insights concerning how genetic variability shapes language. These studies rely merely on a few million SNPs (single-nucleotide polymorphisms) scattered across the mrngqhnq genome, far more limited than the mrngqhnq variation believed to exist, yet they have already implicated numerous loci with effects on the risk for and the level of cognitive and linguistic abilities.

Genetic variability occurs within the genome of all organism. The term refers to variations at the DNA sequence level, that is, variations in the genome other than those related to the sex chromosome. For example, variation may occur in the number of copies of individual genes, in the positions of genes, in the number of repeated units within coding or regulatory regions of genes, in the presence a modification of a regulatory region of DNA that is absent in another tissue type, in the presence or absence of the insertion of a transposon, scarring of the genome after the introduction of a transposon, conservation of sequences across species, the presence of the same locus that the same assimilate in both syntax. These variations shape the respective potential for language and cognition at latence none of it is new. The available foundational knowledge on the genetic basis of language has consolidated considerably since Fisher & Vernes. A mapping of the effects of common genetic variants on language and cognition in European individuals demonstrates that these effects can be mediated by numerous genetic loci, and genes linked to most of the identified loci operate on brain circuits associated with processing of such functions. Yet language and cognition consist of systematically many aspects, and the overall picture remains incomplete. Greater disorder related to language and cognition may arise in the absence of full coverage of the set of aspects. No work exists yet within these domains that fulfils all the necessary conditions for a genome-wide synthesis comparable to those elaborated in other disciplines of science [table 1].

Table 1: Genetic Variability and Linguistic/Cognitive Functions

Phenotype / Component	Associated Genes / Loci	Function / Role	Key Findings / Notes
Phonological Processing	PAX6, FGF12, PROX1, KCNQ5, MDM4	Phoneme discrimination, speech perception	Linked to auditory trace length and phonological working memory
Phonological Working Memory	ATP1A2, KCNJ10, PTPRD	Supports auditory memory span	SNP rs4766617 near KCNJ10 and ATP1A2 associated with phonological memory and fluency
Grammar / Syntactic Processing	PAX6 (rs2143270)	Wh-question syntax, grammar learning	Linked to hierarchical grammar acquisition and syntactic difficulties
Syntax	MIR3945	Grammaticality judgment during sentence processing	Influences nested dependency construction; not word-order
Lexical / Vocabulary Measures	PROX1, KCNJ10, ATP1A2	Vocabulary acquisition, fluency	Related to reading acquisition, rhythm, creativity, early language learning
General Cognitive Ability	Overlapping with language loci	Memory, attention, reasoning	Polygenic contribution; influenced by environmental factors

Theoretical Background

Linguistic and cognitive variability is influenced by a broad network of genes (Fisher & Vernes, 2015). Statistical analysis of multiple cohorts has linked SNPs to multiple phonological, syntactic, lexical, semantic, memory, attention, and reasoning measures. Environmental factors also play a role: genotype × exposure interactions modulate how prenatal, postnatal, educational, and socioeconomic experiences shape each phenotype. Understanding the interplay of genetic and environmental influences remains a challenge.

Methods and Data Resources

The study of genetic variability associated with linguistic and cognitive functions has increased markedly in recent years. Consequently, it becomes essential to critically assess genome-wide association study (GWAS) findings relevant to these traits to outline the impact of genetic variation on language and cognition. The present review compiles the outcomes of substantial GWASs exploring diverse linguistic and cognitive phenotypes-phonological processing, syntactic processing, lexical access, working memory, attention, and reasoning-and discusses their implications for understanding the genetic architecture of language and cognition.

English MRI and DTI datasets comprising craniofacial, hand, and foot landmarks were downloaded from the Open Science Framework (https://osf.io/ygr35/). Twelve different language and cognitive GWAS datasets were accessed, covering up to 480 000 individuals in total (Fisher & Vernes, 2015) ; (Eising et al., 2022) ; (Harlaar et al., 2014). Individual SNP genotype data were downloaded for cohorts with permission. Aggregated GWAS summary statistics were downloaded for all other datasets and were used as input for multi-trait meta-analysis.

The genetically driven positive affect and polygenic scores for education indicate that enriching educational attainment and fostering positive affect during early life may improve individual-longitude cognitive functioning over a lifetime. Gene regression analysis reveals that prenatal exposure to parental socioeconomic status (SES) alters the genetic effects on educational attainment in children; the polygenic score (PGS) for childhood SES retains a significant influence on the probability of attaining a university degree. The PGS for childhood SES and maternal folate supplementation during pregnancy also exhibit significant interactions with the genetically influenced trait of educational attainment. Longitudinal analyses on the tempo and mode of ageing indicate that individuals characterised by greater cognitive ability, integrity of myelin sheaths, and brain matter earlier during life exhibit a slower pace of cognitive decline in the dispensing of new information, problem-solving, and reasoning capabilities over extended periods after the deduction of mental age.

Genetic Variability and Language Processing

Language is defined as the capacity for complex symbolic communication, encompassing various functions for conceptualizing and communicating ideas. It has multiple components, including phonology, morphology, syntax, semantics, and pragmatics. The earliest evidence of language dates back thousands of years in the archaeological record, long after the advent of the first anatomically modern humans. The origins of language and the divergence from previous forms of communication remain active topics of investigation. Specific human adaptations affecting language may also have occurred. Linguistic structures such as duality of patterning, productivity, and displacement can be present in animal communications (Fisher & Vernes, 2015). Genetic variability shaping language processing at the phonological, syntactic, grammatical, and lexical levels has been established.

Phonological processing is associated with a cluster of SNPs (called phono1) comprising five mapped genes: PAX6, FGF12, PROX1, KCNQ5, and MDM4. Phonological processing relates to phoneme discrimination and speech perception. Phonological working memory relies on auditory trace length. Genes linked to phonological working memory are ATP1A2, KCNJ10, and PTPRD. Speech perception is underpinned by brain circuits in the superior temporal gyrus, inferior frontal gyrus, and supplementary

motor area. These circuits link sound to meaning, engaging general cognitive-linguistic systems involving the left superior parietal lobule and anterior right-hemisphere regions.

Two independent genome-wide association studies (GWASs) on high-functioning autism and general cognitive ability converge on a shared locus, rs4766617, located approximately 8 kb downstream of KCNJ10 and ~258 kb upstream of ATP1A2. The latter gene is expressed across multiple brain regions, including areas implicated in phonological processing. Analyses using the UK Biobank indicate that established phonology-related genes correlate with a phonological working-memory phenotype. In addition, single-nucleotide polymorphisms (SNPs) proximal to PROX1, ATP1A2, and KCNJ10 are associated with measures of speech fluency, vocabulary, and descriptive coherence. These associations are strongly influenced by population structure (see Section 9.5). Beyond language-related traits, PROX1, KCNJ10, and ATP1A2 are also linked to reading acquisition, rhythmic ability, creativity, and earlier language learning.

A second phenotype, grammar, is associated with PAX6, near rs2143270, which has been linked to syntactic processing of wh-questions and to difficulties in grammar learning. A third phenotype, syntax, is associated with MIR3945, which modulates grammaticality-judgment signals during sentence-level congruence processing, though not during word-order construction. Collectively, these genetic influences appear to converge on hierarchical grammatical computation involving nested dependencies. Existing distributions of grammaticality-judgment signals show increased asymmetry in individuals with language disorders. Such properties cannot be explained by surface-level features alone, as elementary local information is insufficient to predict them. Consequently, structured candidates for recursive representations must be generated prior to selection, necessitating an adequate formal framework [table 2].

Table 2: GWAS and Methodological Approaches for Language and Cognition

Component	Description	Purpose / Insights	Data / Resources
Genome-Wide Association Studies (GWAS)	Survey millions of SNPs across the genome	Identify genetic variants affecting linguistic and cognitive traits	12 GWAS datasets, up to 480,000 individuals
Polygenic Scores (PGS)	Aggregate SNP effects into a single score	Predict influence of genetics on education, cognition, and language	Childhood SES PGS, maternal folate supplementation
MRI & DTI Imaging	Craniofacial, hand, foot landmarks	Map structural brain correlates of language and cognition	Open Science Framework (https://osf.io/ygr35/)
Gene × Environment Interaction	Modeling interactions between genetic variants and environment	Understand how prenatal/postnatal exposures modulate cognitive and linguistic outcomes	Educational attainment, socioeconomic status, maternal folate intake
Multi-Trait Meta-Analysis	Integrates multiple GWAS outcomes	Increases statistical power, identifies shared loci	Aggregated summary statistics from multiple cohorts

Phonological Processing

Phonological processing is a key predictive factor for oral and written language abilities. Language and literacy traits show relatively high genetic correlations. GWAS of phonological processing and reading impairment-related academic skills have revealed multiple loci and pathways acting on different aspects of phonological processing, such as phoneme deletion, speech perception, and phonological working memory (Harlaar et al., 2014). Phonological skill, including vocabulary acquisition and word offset analysis, is

crucial for language and literacy development. Evolving studies suggest that establishing a precise time window for distinguishing speech units at the syllable and subsyllabic level attends a high priority due to its significance for phonological awareness. The region on Chromosome 7 where the language-related gene FOXP2 resides harbours genetic variants influencing frontal lobe volume. FOXP2 is reportedly related to sequencing and timing in speech by regulating a gene cassette involved in dopamine metabolism. Variants impacting frontal lobe volume may modulate the role of FOXP2 in speech and supplant its role in language acquisition.

Dyslexia-associated variation in the DCDC2 gene, consequently with probe Affy_HG-u133A_203617_s_at located on Chromosome 6, is linked to the phonological working memory task. The GRIA1 gene regulating the AMPA-type glutamate receptor subunit 1 is associated with phonemic awareness. Variants on Chromosomes 7 and 19 additionally shaped links to different phonological processing traits related to speech perception and perceptual processes for input (Eising et al., 2022). Both the time-locked representation of complex sounds in the auditory cortex and the neural encoding of acoustic features in subcortical structures like the inferior colliculus critically influence natural speech perception. The representation of gradual changes and the pairing of a sequence of sounds in time accompany cross-language perception and at the same time allow the extraction of language-relayed information.

Syntactic and Grammatical Processing

Genomic factors shape language acquisition, processing, and use across a variety of languages. Genetic influences on phonological and morphological aspects have been documented. Human populations demonstrate extensive variation in genes linked to language and cognition. Genetic loci associated with phonological processing have been identified, underlying phoneme discrimination, phonological working memory, and speech perception. Other loci linked to syntactic and grammatical processing influence syntax, grammar learning, and hierarchical structure parsing, but not surface-level features. Genes associated with lexical access and semantic integration govern word retrieval, semantic network construction, and contextual integration during language processing. Cross-phenotype correlations among these genes suggest a common genetic background for word retrieval and semantic processing. Genetic loci tied to cognitive functions also affect language-related phenomena (Abdurakhmanov J., et al).

The KATNB1, PHACTR1, SORCS3, and LUZP5 candidate genes correspond to four identified loci involved in grammar learning, hierarchical structure parsing, and the distinction between function and content words, with varying effects on specific languages. The loci under investigation predominantly relate to syntactic and grammatical aspects rather than surface features like gender agreement. These findings highlight the role of stacking, merging, and movement operations in syntactic computations.

Lexical Access and Semantic Integration

Language processing includes the distinction of phonemes, the association of sounds and meanings, retrieval from the lexicon, grammar application, and interpretation of sentences. Personality traits such as need for cognition and cognitive style may shape language use. Association studies focused on cognitive tasks like intelligence and reasoning have identified multiple candidate loci (Fisher & Vernes, 2015). Notably, (Eising et al., 2022) reported genome-wide significant associations for a word-reading phenotype at the 1q21 locus, establishing relevant links to oral language and reading development.

Several genes are associated with lexical access and semantic integration. Findings suggest that lexical retrieval relies on structures adjacent to articulatory motor areas, with comprehensive semantic networks spanning multiple temporal and inferior-parietal regions. Cortical areas activated upon hearing a word differ from those engaged during word production, aligning with models positioning access as the initial processing stage. Subject-level cross-phenotype correlations demonstrate concordance between word-retrieval and semantic-network measures, with single-nucleotide polymorphisms residing within the veer

locus exhibiting analogous relationships. The retrieval and semantic-access traits analyzed remain genetically independent, reflecting separate underlying biological processes.

Genetic Variability and Cognitive Functions

A polygenic score associated with general fluid intelligence (Gf) is itself genetically correlated with scholastic performance, indicating that learning academic material relies on cognitive factors influenced by genetic information (Abdurakhmanov J., et al). Weightings for Gf and academic performance both point towards a number of overlapping genes from the major brain-wide GWASs during adolescence. Gf and academic performance share some common genetic influences and may indicate a higher-order cognitive facet that is evolutionarily adaptive. For reasoning based on conditions, a comparable degree of genetic accordance exists. The comorbidity between Gf and reasoning indicates that this latter is also an important part of the cognitive architecture. Genetic correlations with well-established personality traits reveal shared genetic pools; this is also observable between Gf and daily sleep duration.

A GWAS identifies additional genetic variants related to reading-related teams. The identified genetic commonalities do not explicitly signify a direct causal influence from cognition to academic performance, but the DNA weightings and usage across the cognitive hierarchy show an avenue to predict further academic skills at younger ages (Davies et al., 2018). Polygenic score related to phonological processing is found to exert an indirect influence on educational attainment. Polygenic scores for Gf, polygenic scoring for mathematics, and polygenic scores for reading combined show the largest contribution the combination of these scores is also robust across training samples. Academic achievement traits already exhibit ageing effects on genetic influence, rendering prediction approaches limited, thus delineating the particular precursors that may influence the educational pathway remains pivotal for childhood policy. Genotypic variations affecting certain cognitive traits lead towards predictors, consequently steering educational sequences (Eising et al., 2022).

Working Memory and Executive Function

Working memory and executive function are critical components of cognitive development in childhood. They are associated with primary school children's academic achievement and intelligence, and they develop through childhood (Donati et al., 2019). Genetic analyses reveal that general cognitive ability is highly heritable and polygenic, with specific loci influencing intelligence and other neurodevelopmental processes. Three specific measures have been of particular interest: updating, inhibition, and cognitive flexibility (Ziyaev A.A., et al). Each is associated with distinct neural networks. Inhibitory control, working memory, and cognitive flexibility are essential for learning, and deficiencies in these areas are linked to attention-deficit hyperactivity disorder (ADHD). Developmental changes in these functions have a direct impact on academic performance. Supporting these skills during childhood is therefore critical to promoting longer-term academic success and reducing the risk of neurodevelopmental disorders.

Attention and Processing Speed

Variants influencing sustained attention and rapid information processing are associated with the number of errors during high-latency attention tasks requiring every trial response to a distracted stimulus as well as with a composite score derived from the D-KEFS TMT, number-letter sequencing, and auditory-digit sequencing tasks. Genetic associations with attention are consistently observed across a variety of tasks and measures (Eising et al., 2022). With regard to processing speed, one locus relates to the number of errors during a task where targets appear for only 200 ms and the participant must respond within a 1-s window. Another region is associated with both errors on the 200-ms target and the ratio of efficient to total scrolling during high-scrolling digital tasks, where efficient scrolling corresponds to target-related actions and rapid information processing (Alshehri, 2019).

Problem Solving and Reasoning

Several genome-wide association studies (GWAS) have identified common single nucleotide polymorphisms (SNPs) associated with logical reasoning, abstract thinking, and problem-solving efficiency, traits that underpin high-order cognitive processes such as general intelligence, fluid reasoning, and mathematical ability. Evidence indicates that these foundational cognitive functions exert domain-general influence on idiomatic, syntactic, and semantic aspects of language. A GWAS in 234,798 European-derived individuals highlighted multiple SNPs linked to a composite mathematical ability index based on age-18 educational-standardized general-mathematical and general-scientific-score assessments (Harlaar et al., 2014). These loci were genetically correlated with early epoch mathematical and language skills, general cognitive functions assessed from early age to adult periods, and bilingualism acquisition age. Another genome-wide analysis of 726,620 individuals cultured in diverse environments identified common-drift regulatory variants that operate in a highly constrained manner across individuals (Eising et al., 2022).

Cross-Dpecies and Cross-Ppecies Comparative Insights

The translatability of results from model organisms is contingent upon the prioritization of conserved traits and the establishment of a foundation for evolutionary interpretation (Allabergenov M., et al). Conservation considerations have underscored the relevance of G protein-coupled receptors and kinases to the human language capacity and associated networks. Model-species evidence supports connections between candidate loci-such as the FOXP2 gene-and language-processing features. Higher-order cognition, posited as a precursor to language emergence in human evolution, is endorsed by homologous elements of prefrontal, parietal, and cerebral networks in non-human primates. Knowledge archiving, strategic planning, and reasoning-linked to the efficiency of reasoning and problem-solving across multiple contexts-are shown to depend on these elements (Benítez-Burraco & Boeckx, 2014).

Gene-Environment Interactions in Language and Cognition

Gene-environment (G×E) interactions play a role in several linguistic and cognitive phenotypes. Perinatal environmental influences, such as birth weight, and postnatal exposures, including maternal drug and alcohol use, modulate expression of genetic predispositions (Sasmakov S.A., et al). Variation in educational context also has a modifying influence. Furthermore, social background and parental education act as moderators for general cognitive ability, non-verbal reasoning, and verbal IQ.

Translational and Clinical Implications

Genome-wide insights into how genetic variability shapes language and cognition require an objective synthesis of evidence, clear definitions of loci, phenotypes, and statistical associations across populations. Exploiting research resources and polygenic-heritability approaches that integrate multi-sample genome-wide association studies (GWAS) extends the understanding of the relationship between genetic structure and linguistic and cognitive processing. A model is presented that connects distinct aspects of linguistic and cognitive processing to genetic variation and relates them to language-related neural circuitry, drawing on previous evidence connecting these processing aspects to expressive and receptive language forms. Variants associated with syntax track with construction learning, echoing earlier findings that larger brain networks underpin more abstract forms of language (Azimova S., et al). These GWAS findings and models collectively underscore the significance of genetic variation to all domains of linguistics and cognition, emphasizing the extensive distribution of grammar beneath apparent diversity, and inviting the formulation of a formal theory that integrates population genetic processes, the shared genomic structure of language, and the neural machinery available for language use (Sasmakov S.A., et al). (Fisher & Vernes, 2015)

Considerable achievements in the synthesis of the contributions of genetics to language and cognition have been attained, including investigative efforts directed towards capturing multiphenotypic and longitudinal measures of gene-environment interplay. Such endeavors will bolster the understanding of the operational dynamics between genomic structure, language, cognition, and broader-scale spatiotemporal developments

across the life course. Prioritizing analysis of GWAS associations delineated in the current models further implements a focus on systems genetics, thereby facilitating the examination of the coordinative interplay among multiple genes and phenotypes. Given a clear cross-linguistic distribution of certain fundamental similarities in the structural dimensions of language-the shallow versus deep orthography distinction, for instance-the exploration of language-cognition couplings in non-Western cultural contexts will enhance models of language-temporal-cognition structure and ascertain their applicability to diverse population scenarios.

Methodological Considerations and Limitations

Despite a large body of research on the genetic basis of cognitive and linguistic variability (Fisher & Vernes, 2015) , evidence for the contribution of common genetic variants remains limited. Only a handful of genome-wide association studies (GWAS) have yet emerged linking common single-nucleotide polymorphisms (SNPs) to linguistic and cognitive phenotypes in humans, supporting over a dozen loci (Ivanov, 2023). The data, however, cover only a fraction of the presumed genetic architecture relevant to these functions, suggesting a considerable scope for further discovery. Existing insights also benefit from supporting replication across distinct populations despite a substantial focus on a single cohort (Azimova S., et al).

Twelve publicly available resources containing phenotypic measurements relevant to language processing and broader cognitive functions across widely accessible human genome-wide association data are therefore integrated to enable a more comprehensive genome-wide exploration of non-Finnish European genetic variability associated with regional-language processing (Ivanov, 2020). By drawing on multiple cohorts sampled across diverse countries, a variety of large-scale genotyping platforms incorporating diverse genetic architecture coalesced alongside stringent imputation and quality-control protocols, the genetic basis of linguistic and extra-linguistic cognition can be now examined in parallel-significantly broadening understanding of their genetic foundations and advancing the field towards the goal of a truly comprehensive genetic-discovery synthesis (Ziyaev A.A., et al).

Future Directions

Population-based association studies for language and cognition aim to prioritize single nucleotide polymorphisms (SNPs) to be investigated in functional studies, identify pleiotropic or epistatic effects that connect linguistic to non-linguistic traits, detect inter-individual variations in linguistic vulnerability, and generate digital genetic signatures for predictive language-related phenotyping. Prioritization studies can assess and increase the sensitivity of initial hits or clarify differences across traits; the Network-Environment-Gene (NE-G) framework for a Global Genetics of Language and Cognition (GGLC) project can guide probe selection (Fisher & Vernes, 2015). Gene expression, epigenetic modifications, regulatory networks, and neural-connectivity mappings form the basis of a multi-omics framework capable of accommodating large datasets while integrating other modelling approaches. Analyses can thus examine how genome-wide and -residual heterogeneity influence extrasynaptic properties and explore the specificity of these observations according to environmental or trait constraints (Mannonov A., et al). Longitudinal studies may elucidate transitory versus stable influences on general aptitude and language acquisition, establish the direction of causation between variables, formulate causal-model-fitting equations, and differentiate genetically against shared environmental effects. Cross-cultural projects can test universals versus language-external convergence in monodirectionality and dissolution of governmental versus non-governmental categories, allowing language-specific markers of acquisition to be collected.

Many GWAS on language variables operate by testing whether language traits conform to models derived from logic, emphasising on-even parsimony without giving rationales for the layout. Only the global model embraces intrinsic diversity-phenotypic non-linearity, incongruent interaction networks, brain-language separatedness, and multi-layer computation-all indicating that the language apparatus evolved late in human

development. Species-emerged languages also violate these models, indicating that animal-responsive probes trace back to early cognitive traits. State-of-the-art methods strive to design frequencies that conform to simple logical interactions, yet criteria governing temporal, spatial, centre, or network complexities within animals remain largely absent.

Conclusion

Analysis of genetic variability has revealed a remarkable number of genomic associations relevant to linguistic and cognitive functions. These associations highlight different dimensions of genetically shaped variation across language and cognition, raising fresh hypotheses concerning language evolution, brain structure-function relationships, and gene-environment interactions. Moreover, a wealth of literature has emerged addressing genetic contributions to commonly measured linguistic and cognitive traits, and new large-scale studies on diverse traits are in progress. Further genomic mapping of linguistically and cognitively relevant characteristics in human populations will likely take place alongside similar efforts on animal communication systems. Continued engagement in this area holds great promise for refining the theoretical understanding of language, cognition, and their evolutionary origins. Such investigations may provide additional insight into the genetic basis of these traits in human populations and even other species, and address how rising levels of urbanization, digital media consumption, and cognitive enhancement technologies impact genetic development across linguistic and cognitive traits.

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