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Integrating Epigenetics and Genomic Psychology to Explain the Development and Maintenance of Complex Mental States

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ABSTRACT

This paper explores the intersection of genomic psychology and epigenetics in shaping complex mental states. Genomic approaches illuminate the role of genetic variation in individual differences and the stability of psychobiological traits, while epigenetic mechanisms mediate environmentally induced modifications without altering DNA sequences. Evidence indicates that epigenetic processes influence neural circuit formation, synaptic plasticity, and personality traits, bridging environmental inputs and behavioral outcomes. Genomic psychology provides a framework to integrate genetic, epigenetic, and environmental factors, elucidating developmental trajectories, resilience, and vulnerability in mental states. By combining insights from epigenetic regulation and genomic variation, this approach clarifies the formation, maintenance, and variability of psychological characteristics across the lifespan, highlighting the dynamic interplay between biology and experience in mental-state development.

Keywords: *Genomic Psychology, Epigenetics, Mental States, Neurodevelopment, Gene–Environment Interaction, Personality Traits, Synaptic Plasticity, Psychobiological Stability, Developmental Trajectories, Psychological Variation.*

INTRODUCTION

The recent emergence of genomic approaches to psychology has focused attention on the precise genetic mechanisms through which biological predispositions influence both individual differences and the stability of psychobiological states over time. On a parallel track, growing evidence indicates that epigenetic modifications, which govern gene expression without altering the underlying DNA sequence, play a central role in developmental processes and have profound effects on both an organism's phenotype and its ability to respond flexibly to environmental perturbations (Martino Coda & Gräff, 2020). Detailed exploration of

these two fields has uncovered substantial evidence that environment-sensitive epigenetic modifications influence the genesis and maintenance of complex mental states at the level of neural circuit formation, synaptic plasticity, and fundamental personality dimensions (Ptak & Petronis, 2010). The respective roles of genomic and epigenomic mechanisms thus warrant concerted consideration.

A core mission of modern psychology is to articulate how complex mental states, such as moods, thoughts, perceptions, and memories, arise from biological constituents. Efforts to integrate epigenetics and genomic psychology with respect to mental states face distinct hurdles, which are systematically addressed. The core concepts of epigenetics, genomic psychology, and mental states are first clearly defined. A wide-ranging overview of evidence for epigenetic influence on developmentally delayed mental states, such as personality and psychopathology, follows, as does a complementary review of genomic and epigenetic factors regulating stereotyped mental-state dimensions.

Episodic experiences play a vital role in shaping life trajectories yet are typically not monitored. Elements of ongoing experience, however, can be recorded through neural activity around the time of these experiences. Such activity can contribute to a developmental cascade, whereby neural features of particular experiences regulate the architecture of subsequent experience, helping shape life trajectories at a larger temporal scale. Experimental studies have examined different aspects of experience architecture across both the genomic and epigenomic domains; integration of findings from these studies has yet to occur (P. Jiménez et al., 2018) [table 1].

Table 1: Epigenetic Mechanisms and Developmental Impact

Epigenetic Mechanism	Role in Neurodevelopment	Evidence / Studies	Behavioral / Mental State Outcome
DNA methylation	Regulates gene expression during neuronal differentiation, migration, and synaptogenesis	Rodent studies (Belén Barreto Zarza & Freijó, 2022); longitudinal human data (ALSPAC, Generation R)	Anxiety, stress response, social reward, behavioral resilience
Histone modifications	Influences chromatin accessibility for gene transcription	Animal models; CNS studies (Kuehner et al., 2020)	Neural circuit formation, cognitive flexibility
Chromatin remodeling	Maintains long-term changes in gene expression	Animal and human studies	Persistence of developmental trajectories in behavior and cognition
Non-coding RNAs	Modulates gene expression post-transcriptionally	CNS models; epigenetic research	Emotional regulation, neuropsychiatric phenotypes
Critical windows / plasticity periods	Heightened sensitivity to environmental inputs; establishes long-term epigenetic signatures	Rodent and human developmental studies (Broekman, 2011; Murgatroyd & Spengler, 2011)	Vulnerability/resilience to stress, adaptation of social and emotional responses
Prenatal/postnatal environmental exposure	Impacts gene regulation and neurodevelopment	Maternal stress models, early-life interventions	Lifelong behavioral trajectories, risk for psychopathology

Theoretical Foundations

The brain is an extraordinarily malleable organ, particularly in early development, when environmental exposures can guide the formation of neural circuits in a manner that corresponds to phylogenetically conserved neurobiological programs. While epigenetic mechanisms have a limited role in establishing these circuits, the epigenome within specifiable brain regions nevertheless sustains longitudinal modifications that correlate with behavioral outcomes. Once-theoretical linkages between epigenetic processes and personality traits now find some empirical support; far more work, however, remains necessary before sound models can be articulated that describe, specify, and elucidate such connections. Such models could help clarify the emergence of complex mental phenomena, including the risk or resilience associated with specific genotypes, the associability of stressors and stress responses, and the role of epigenetic regulatory processes in shaping those meta-features of behavior.

These lines of inquiry have motivated several conceptual and empirical extensions of genomic analysis within psychology, culminating in a framework termed Genomic Psychology. Psychobiological science seeks to specify, by reference to observable behavior, the psychogenic conditions under which a given genotype, through agency and plasticity, detaches from modes of interactive development that might otherwise lead to widespread vulnerability and instead aligns towards safety and resilience. Two routes merit particular focus. First, the existing theoretical apparatus allows for the identification of the systems-level genomic configurations that determine the specific behavioral traits through which gene-environment interactions operate and that generate measurable developmental trajectories. Second, a well-established, partly theoretical relationship links these trajectories to molecular and epigenetic modifications spanning the course of interaction and exerting distinct influence on detailed behavioral execution; Gene-environment-neurodevelopment and epigenomic-process/behavior relationships can then be described, penetrated, tested, documented, and augmented exclusively at the level of behavior (P. Jiménez et al., 2018).

Epigenetic Mechanisms and Neurodevelopment

Ella Kuehner, Nicolas Kuehner, and Thomas Gräff emphasize the critical role of epigenetic regulation in the mammalian central nervous system (CNS) and its implications for neuropsychiatric disorders. Proper gene expression regulation is essential for brain development, including neuronal differentiation, migration, synaptogenesis, and circuit formation. DNA methylation, histone modifications, chromatin remodelling, and non-coding RNAs constitute key epigenetic mechanisms that influence gene expression across the lifespan. Perturbation of epigenetic regulation in animal models drives alterations in animal behaviour and disease-related phenotypes, underscoring the link between epigenetic processes and complex mental states. [table 2].

Table 2: Genomic Psychology and Mental State Development

Concept / Factor	Definition / Mechanism	Impact on Mental States
Genomic Psychology	Study of genetic and epigenetic variation shaping psychological traits	Individual differences in cognition, emotional regulation, and risk-taking
Gene-environment interactions	Genes interact with environmental experiences to shape neurodevelopment	Stress responses, resilience, personality traits
Epigenetic regulation within genomic framework	Environmental influences produce lasting modifications on gene expression	Adaptive/maladaptive behavior, vulnerability to mental disorders
Developmental trajectories	Longitudinal patterns of neurodevelopment shaped by genomic and epigenetic processes	Stability or change in emotional-behavioral profiles over lifespan

Critical periods & plasticity	Time windows during which environmental inputs have maximal impact on gene expression and neural circuits	Formation of long-term coping strategies, behavioral resilience or susceptibility
Multiomic integration	Combining genomic, epigenomic, transcriptomic, and behavioral data	Precise mapping of trait expression and individual mental state variation

A growing body of evidence indicates that epigenetic modification constitutes a crucial mechanism bridging environmental influences and mental states. Such structural genome alterations extend beyond classical gene expression to affect mental state trajectories. Genomic Psychology-an integrative approach linking gene, environment, and mental state-emphasizes epigenetic processes and their interactions with genomic variants to elucidate developmental trajectories and corresponding behavioural consequences.

Genomic Psychology: A Framework for Individual Differences

Evolutionary systems theory provides a framework for understanding how species adapt to ever-changing environments through variation and selection processes at different hierarchical levels. The darwinian process of variation and selection also applies to the evolution of mental states in individuals. An important avenue of genomic-psychological research focuses on dissecting these evolutionary processes. Genomic psychology is the systematic study of variation and selection related to psychological attributes (behaviours, abilities, and so forth) and their neural underpinnings at the genomic level. It is founded on the understanding of the genome as an arena where genetic, epigenetic, and other forms of variation compete for inheritance and that the major forces shaping any trait during a species' or individual's evolution can also serve it during an adaptation episode.

Genomic psychology is a construct that encapsulates the theoretical and empirical work related to genomic variation and its function in systematically and ontogenetically shaping psychological traits (P. Jiménez et al., 2018). Even though the specific genetic variants that constitute the genomic system of an individual at conception are already fully defined when the first epigenetic changes take place during early embryonic development, the competition for inheritance in the genome does not cease at conception. A genomic overview of psychological attributes is thus possible, which integrates genomic, epigenomic, and psychological data. Genomic psychology focuses on factors that enable an organism to keep operating in advantageous domains: the formulation of individual traits (the psychological attributes that strive to remain active during an adaptation episode) and their innate expression and modulation (the precise conditions to which these attributes are to be tailored). Genomic-psychological research on the genomic conditioning of mental states that have been affected or shaped by epigenetic modifications, either at the organismal or intercellular (network) level, has been particularly fruitful. The systemic gathering of epigenomic, multiomic, transcriptomic, and other types of information makes more precise genomic-psychological inquiries into how largely epigenetically controlled mental states are variated and selected during life possible.

Conceptual Integration: Epigenetics, Genomics, and Mental States

Since conception, genes interact with the environment to shape human functioning in the short and long term. This represents a major shift in perspective, from environmental influences affecting genetic expression, to both genetic and environmental factors exerting independent effects on neurodevelopment, complex psychological characteristics, and psychopathological risk (A. M. Cecil et al., 2022). Genomic psychology provides a framework for organizing knowledge on how genetic influences translate into differential functioning, which can clarify the links between epigenetics, biological factors, and mental states. Substantial evidence documents genome-wide genetic influences on a range of human characteristics-emotional stability, intelligence, sociality, and risk-taking-which, aspects associated with the

development and maintenance of normal and abnormal mental states. Individual differences across complex missing organizational layers, such as the large knowledge base on traits, thus does not preclude the possibility of systematic and functionally relevant mapping of genomic information, via network links, to higher order configurations and differential functioning challenges concerning genomic psychology can then be addressed through a systems approach, formal and probabilistic modeling, and empirical research at relevant developmental stages.

Epigenetics and genomic psychology together articulate how environmental inputs interact with specific genetic variants, at both the level of individual genes and genome-wide, to shape the formation of neurobiological, cognitive, and affective systems responsible for complex psychological characteristics. During gestation these processes lay down a set of distinct long-lasting trajectories that frame subsequent experience-dependent change, relevant for the construction of potential behavioral states.

Epigenetic Regulation Across Developmental Trajectories

The impact of both the prenatal and early postnatal environments on epigenetic regulation and individual differences in mental states is well documented. In rodents, alterations to the maternal environment during pregnancy induce pronounced epigenetic and behavioral changes that persist into adulthood, indicating global plasticity in the epigenome during this early period (Schuebel et al., 2016). The establishment of the neural circuitry underlying core mental states occurs rapidly after birth in both rodents and humans, suggesting that early postnatal conditions are likewise crucial (Broekman, 2011). Specific perturbations to maternal–fetal and mother–offspring interactions in mice elicit longitudinal changes in DNA methylation and hydroxymethylation which correlate with variation in anxiety, social reward, and stress response (Belén Barreto Zarza & Bernardino Arranz Freijó, 2022). Within the first few weeks of life, perturbation of maternal care affects lineage specification and cerebral development, resulting in a pattern of DNA methylation associated with behavioral resilience to juvenile stress.

Development also involves sensitive and critical windows during which environmental exposures exert heightened influence, engendering significant individual differences and substantial reductions in plasticity thereafter (Froukje Philippien Broekman, 2011). Such windows have been extensively studied in the context of stress, with volatile early-life systems selected to coordinate with other major environmental shifts such as weaning, independence, and social role acquisition (Broekman, 2011). In rodent models, both pre- and postnatal stressors induce widespread epigenetic changes and determine overall behavioral resilience. Longitudinal epigenomic analyses indicate that these alterations engender characteristic signatures, aligning with the notion of common developmental trajectories connecting early experience with adulthood. These signatures vary according to timing, stress severity, and species, revealing substantial but organized epigenetic diversity across the timeline of pre- and postnatal stress.

Prenatal and Early Postnatal Environments

Prenatal and early postnatal exposures exert critical influences on development. Experiences during these periods shape not only neurobiological systems but also the epigenome itself, engendering persistent changes in gene regulation that in turn contribute to brain formation and emotional-behavioral functioning. The early-life environment is therefore fundamentally predictive of future mental state profiles (Murgatroyd & Spengler, 2011). The neural substrates affected and the specific biological processes engaged by distinct experiences are not yet fully characterized. A better understanding of the complex interplay between exposure and outcome—collectively termed “epigenetic programming”—promises to elucidate the nature of environmental impact during critical development windows (Froukje Philippien Broekman, 2011). Desired insights include the identities of epigenetically regulated genes, the modes of upstream control over these genes, and the broader arrays of available functional states. To summarize the above perspective, only select neurobiologically relevant exposures during formative epochs appear to establish longitudinal epigenetic signatures implicated in the lifelong regulation of emotional-behavioral dynamics.

Critical Windows and Plasticity

Critical windows for plasticity in independent gene regulatory systems influence the genome's response to distinct environmental stimuli throughout development. In the neural system, when a critical window opens for a specific experience, the genes in that regulatory system selectively and simultaneously respond and “write in” the associated social experience (P. Jiménez et al., 2018). For example, plasticity mechanisms that transform stress or trauma experiences into enduring threat profiles constitute a critical evolutionary adaptation. Such experiences shape the epigenome, thereby influencing which social experiences impact the neural system and the individual's subsequent behavior (Murgatroyd & Spengler, 2011).

Development is characterized by distinctive critical periods during which the deleterious effects of challenging environments on mental states are especially pronounced. Longitudinal studies have confirmed that in both humans and model organisms, early adverse exposure leads to persistent epigenetic marks that functionally modulate circuit-level neuronal activity and signaling cascades long after the cessation of exposure. Importantly, the establishment of such enduring and extensive epigenetic changes need not imply that sensitivity to the corresponding experience is permanently impaired. During a subsequent re-exposure event, for instance, even circuits subjected to early adverse exposition may still reshape the epigenome yet retain the capacity to organize an appropriate adaptive response. Notably, the long-lasting epigenetic effects of early adversity uncovered in various studies are widely believed to typify standard plasticity and retention rather than establish a new, nonplastic state.

Longitudinal Epigenetic Signatures and Behavioral Correlates

Longitudinal epigenetic data extending from prebirth to adulthood provide insights into developmental timing effects on neurodevelopmental outcomes. These trajectories, derived from prospective studies such as ALSPAC and Generation R, enable estimation of deviations from normative patterns and examination of DNAm stability across time. In humans, DNAm patterns can vary within a day due to circadian rhythms, potentially influencing mental health. Further exploration of these cyclic epigenetic oscillations represents an intriguing avenue for future investigation (A. M. Cecil et al., 2022).

Epidemiological studies indicate that childhood adversity is associated with anxiety and depression, yet not all experience lifelong psychological damage. Instead, resilient individuals often engage in active behaviours to cope with stress, maintaining good mental health; even in their lifetime, some experience change to maladaptive resilient behaviour, lessening their quality of life and moving on to opportunistic depressive state (A. Cory-Slechta et al., 2017) ; (Schuebel et al., 2016).

Genomic Variation and Mental State Phenotypes

Development and maintenance of complex mental states are influenced by processes of epigenetic regulation in some way. A systematic review of research on the epigenetic regulation of behavior and its relationship with genome variation across the human lifespan provides multiple independent lines of evidence connecting such regulation across developmental time with genomic variation and genomic mental state phenotypes. Genomic mental state phenotypes associating with gene expression, cellular signaling, and neural architecture shape behavior; epigenetic regulation, in turn, explains why individuals within a population develop and retain different genome-wide mental state phenotypes (P Quinn et al., 2019).

Epigenetic regulation across the lifespan is progressively outlined, detailing when and how acquired experience of external environmental factors, such as exposure to physical and emotional stressors or quality of affection and care, is internalized and incorporated into normative biological functioning. The emergence of such “meta-instructions” from the environment modulates the neurodevelopmental processes that construct the human brain, enabling a spectrum of neuronal circuit articulation and connectivity choices through which individual genome-wide mental state phenotyping transpires.

Polygenic Influences on Affect, Cognition, and Resilience

Various genome-wide association studies (GWAS) have identified hundreds of genomic regions associated with measures of psychological well-being, psychiatric disorders, cognitive and perceptual abilities, personality traits, and creativity (Talarowska, 2020). Investigation of a multi-phenotype GWAS in a large sample of individuals revealed 63 loci influencing emotional well-being, 172 loci influencing a broader range of factors including psychoticism, 48 loci influencing attention, and 12 loci influencing creative cognition. These findings highlight the extensive influence of genetic factors on mental states in human populations, although specific genes, molecular mechanisms, and causal relationships remain to be established.

More generally, individual differences in these mental state-affecting variables influence susceptibility to clinical disorders, and polygenic scores derived from GWAS aggregate the component genotypes contributing to such variation across the population. Such scores exhibit significant predictive validity for many common DSM-5 disorders, integrating pleiotropic information from causal variants influencing liability to each disorder. Genomic influence on discursive attention appears to extend to a wide range of behavioral correlates relevant to pre-psychotic developmental periods, as indicated by significant mediation of the effect from parental attention problems to offspring psychosis risk via offspring attention problems. These insights are consistent with developmental models linking attention to diverse cognitive, affective, and motivational constructs.

Gene-Environment Interactions in Real-World Contexts

Gene \times environment interactions play a pivotal role in shaping the architecture of individuals over time. Genetic predispositions specify a behavioural or psychobiological potential that, when expressed, constitutes a phenotype that emerges within an environmental context (P. Jiménez et al., 2018). For instance, although serotonin transporter (SLC6A4)-related polymorphisms are associated with increased vulnerability to depression after negative life events, stressful experiences remain a precondition for the development of the disorder. Furthermore, the same polymorphisms have been linked to upward polygenic score shifts driven by positive experiences. In formal terms, the epigenetic and genomic dimensions can be described as environmental and genetic determinants, respectively, of temporal patterns; thus, the two spheres can be analysed using methodologies suited to their nature.

Gene-environment interactions can occur at multiple levels of analysis. In genomic psychology, behaviours in response to real-world stimuli may be regarded as transdiagnostic mental-state precedents and outcomes encompassed within an overarching developmental epigenetic architecture. Employing a transdiagnostic scheme with publicly available datasets, analyses of meta-epigenetic transgenerational trajectories, and the identification of functionally validated epigenetic genetic variants, the epigenome-wide association of a polygenic composite corresponding to the Schizophrenia-Illness spectrum has been mapped; it integrates three-dimensional structural indices, intercellular transcriptional states, and time-course neurobehavioural features. Shifts along this meta-epigenetic trajectory have been statistically modelled, accommodating both effector and environmental variables.

Epistasis and Network-Level Effects on Mental States

Biological research is increasingly shifting away from narrow genetic determinism, which posited that a small set of genes is necessary and sufficient for explaining the majority of human behaviours, towards an emphasis on epigenetics and genomic interactions. This transition provides an ideal context for promoting a broader understanding of genomic psychology that embraces and integrates the epigenetic paradigm. Epigenetic regulatory mechanisms influence the genome and gene expression without altering the core DNA sequence and respond continuously throughout the life course to a wide array of environmental conditions. Such ‘multi-level’ exposure histories trigger activity-dependent epigenetic modifications that leave longitudinal and temporally-structured signatures on the genome, reconnecting structure, function, and development (Martino Coda & Gräff, 2020). Such processes shape how the genome remains functional

across the shifting developmental states of the neurobiological system throughout the life course, and thereby enhance and refine the epigenetic foundations for contemporary, genome-wide psychological support for the polygenic genetic basic of more complex mental states. Historically, genomically-grounded psychology has concentrated heavily on the nature of the individual mental states or their immediate phenotypic manifestations, neglecting the analysis of the contemporary antecedents of such states, the richness and variety of polygenic traits simultaneously influencing individual mental states, and the ways by which their detailed examination might illuminate the evolution and social regulation of human psychology and behaviour.

The contemporary notion of mental states or of mentally-based traits is informed by genomic analysis of the manner in which (variable) polygenic ensembles influence the regulation or the ultimate expression of such states. The more general field of psychological science tends to define mental states as “relatively enduring and stable patterns of thought, emotion and behaviour”. Such states responses, by a variety of names (mood, affect, affective state, affective personality), as well as candid, atypical, spontaneous, positive, and negative, lie frequently in the foreground of public and private discourse. They receive worldwide attention in informal communications and in the more formal and regulated arenas of study, analysis, and treatment by management sciences and techniques, by social humane sciences, and by clinical sciences. Contemporary genome–psychology attention begins to centre on the distinctive parliamentary epistasis of mental states and upon their widespread social and political regulation.

Mechanisms Linking Epigenetics to Mental States

Complex mental states take form during critical periods of development, when the circuitry that underpins human thought, feeling, and behaviour is being constructed. Epigenetic changes drive early programming of neurodevelopmental trajectories that establish vulnerability or resilience to later-life stressors (Alameda et al., 2022) ; and this programming may be involved in their ongoing maintenance (Schuebel et al., 2016). At the molecular level, genome-scale epigenetic analyses of blood, bilateral dorsolateral prefrontal cortex, and medial temporal lobe in young adults have revealed longitudinal changes that track with affective dysregulation. These studies also demonstrate that such epigenetic trajectories can explain residual heritability otherwise unaccounted for by polygenic-risk scores, consistent with a model whereby epigenetic variation marks early-life exposures that shape developmental-course pathways involved in the emergence of individual differences in affective states (P. Jiménez et al., 2018).

Neuroendosomal systems influence psychological change by modulating the strength and nature of representations of the social world that the developing brain encodes. Longitudinal blood-derived epigenetic programmes specific to the amygdala have been linked to five-dimensional frameworks of social-affective behaviour two years later in youth. mRNA transcriptomic analyses in prefrontal cortex also have revealed restricted neurotransmitter signalling-systems programmes whose developmental evolutions explain variation in depressive and sociability dimensions at the same age. Epigenetic architectures are therefore integrated with both early-life (adverse and plastic) and current (social, metabolic, and physical) influences.

Neurodevelopmental Circuit Formation

Neurodevelopmental circuit formation involves epigenetic mechanisms such as DNA methylation and post-translational histone modifications that dynamically influence gene expression during brain development. Aberrant methylation patterns of gene promoters, such as Reelin hypermethylation, have been implicated in neuropsychiatric disorders like schizophrenia. Early-life stress and trauma can shape neurodevelopment through alterations in these epigenetic marks, leading to disrupted cortisol regulation and reduced stress resilience. Empirical evidence indicates that diverse environmental factors and interventions-including enrichment, exercise, and dietary modifications-can affect neural mechanisms targetable by genomic and epigenomic tools, thereby counteracting risk factors or promoting favorable behaviors. Genetic and

epigenetic influences jointly govern the emergence of neurodevelopmental conditions; yet some epigenetic modifications either persist or occur later in ontogeny, fundamentally affecting the formation and operation of developmental circuits (Martino Coda & Gräff, 2020).

Synaptic and Epigenetic Plasticity

Formation of complex circuits during brain development establishes the rich repertoire of mental states available later in life. Epigenetic regulation orchestrates networks of gene expression crucial for the emergence of such circuits. Perturbations in epigenetic control during critical windows of development influence the genetic programs activated by environmental experiences, altering the ability to channel exposure into the formation of mental states. Over the long term, the focus and pleasure derived from experiences of diverse complexity become an epigenetically driven dimension of personality, contributing to the maintenance of mental states (De Toma et al., 2016). The integration of circuits supporting developmental processes such as social behavior introduces a further degree of regulatory complexity. Environmental experiences may reinforce pretrained patterns whenever they match the threshold of the respective subnetwork. Additionally, independent and orthogonal elements reflected by patterns of distinct mental states may saturate the flexibility enabled by such pre-established routes. In these instances, the epigenome remains continuously open to the integration of exposure across different circuitry. The mechanisms illustrated combine resilience and flexibility without compromising individual specificity and pre-establishing organization (P. Jiménez et al., 2018).

Neuroendocrine Modulation and Stress Responsivity

Allostasis is a process of active adaptation to stress. In the systems of the brain involved in the stress response, allostatic change implies epigenetic modulation because several minutes are required before new protein synthesis is initiated. Within the first hour after an acute stressor, genome-wide surveys indicate that 5–15% of transcribed genes are destined for irreversible change in expression, many exhibiting a temporary response profile. The initial pattern of transcription permits other genes to enter delayed response segments and many of the first-response genes belong to neural homeostatic and regenerative pathways, permitting rapid recovery to baseline states. During repeated or prolonged stress, epigenetic change can reinforce the initial transcriptomic shift. The proteins that catalyze such changes are altered during transient stress, suggesting that environmental and hormonal signals can influence epigenetic modulation. Specific attention should be directed to the role of different stress hormones such as glucocorticoid, catecholamine, and arginine vasopressin within their respective stress systems (G. Hunter, 2012). Animal studies corroborate gene expression changes due to the early stress exposure and the emergence of anxiety-like behaviors that correlate with epigenetic fixation of stress-response genes (Matosin et al., 2017).

Methodological Approaches

The human epigenome is subject to a complex interplay of changes throughout the life course. External factors, the development of tissues and organs, and individual experiences generate inherent dynamics in the regulation of genes through epigenetic marks. Understanding the impact of these marks on individual differences in behaviour, and in particular complex mental states, therefore requires consideration of trajectories of mental development and behaviour over time. Genomic variation also contributes significantly to phenotypic differences, including individual differences associated with complex mental states and psychiatric conditions. Genetic variants, including single nucleotide polymorphisms (SNPs), modify biological systems from neurodevelopment to behaviour, thereby contributing to an individual's unique configuration and, consequently, their personality, cognition, social interaction styles, emotionality, psychopathology, and other socially relevant dimensions (P. Jiménez et al., 2018). Polygenic risk scores (PRS) derived from large-scale genome-wide association studies (GWAS) predicting general cognitive ability, educational attainment, and psychiatric disorders such as major depression have been demonstrated to be associated with educational performance, academic life stage, and literacy skill trajectories. Genome-wide genetic variants also modify how people respond to environmental influences that in turn affect

behaviours relevant to mental states; for example, genetic profiles can render children more or less susceptible to the detrimental effects of severe hostility or neglect in childhood.

The scientific literature increasingly reflects a tendential shift towards understanding the interrelationships between epigenetic factors and genomic variation or other environmentally imprinted biological modifications as a route to deeper insights into personality and psychopathology. The growing volume of literature on these interrelationships provides an opportunity to broaden the scope of mainstream genomic psychology and to include complex mental states associated with transdiagnostic concepts and theories into its subject matter. Ultimately, coupling the development of integrative knowledge about epigenetic and genomic processes with an experimentally accessible formalism such as genomic psychology could enable mechanistic models of complex mental states to be framed in terms of their biological underpinnings and developmental dynamics. An appraisal of the interplay between epigenetic and genomic methods, questions, findings, and hypotheses in this context will help identify cross-fertilization opportunities and consequential theoretical avenues for future research.

Epigenome-Wide Association Studies and Neuroimaging

Growing interest in epigenetic regulation of gene expression opens new avenues for understanding the genesis of complex mental states and delineating their genetic and environmental determinants. Three interrelated methodological approaches are particularly promising. First, epigenome-wide association studies (EWAS) leverage year-to-year stability of DNA-methylation signatures to link personally experienced environmental exposures to individual differences in mood, cognition, and personality (A. M. Cecil et al., 2022). Such an approach holds potential for advancing knowledge about the timing and buffering effects of prenatal, perinatal, and postnatal environments, as well as estate features undergirding mental resilience. Second, combining genome-wide association studies (GWAS) with top-down, high-dimensional neuroimaging data connects genetic variants, both polygenic and single-nucleotide, pertaining to major mood disorders, psychiatric treatments, and cognitive performance with brain-activity patterns predictive of mood, attention, impulsivity, and structural properties relevant to complex mental states (Hatcher et al., 2019). Such integration clarifies individual tendencies and the cumulative impact of multiple variants. Third, bringing together genomic, epigenomic, transcriptomic, proteomic, and neuroimaging data enables investigation of fine-grained and potentially causative biological mechanisms connecting the genome and epigenome to the emergence of complex mental states and neurodevelopmental disorders.

Longitudinal Designs and Causal Inference

Longitudinal measurement is prominent in health research and supports the understanding of disease and trait progression over time. It enables the prospective study of time-varying covariates and contributes to elucidating pathogeneses. Statistical methods such as linear mixed-effect models, generalized estimating equations, and quadratic inference functions are widely applied to longitudinal data to account for within-family correlation and repeated measurements (C. Strickland et al., 2018). Approaches involving related subjects must address both familial and measurement correlations.

Longitudinal studies have revealed temporally regulated epigenetic processes that influence neurodevelopmental outcomes, underscoring the need for timing considerations in epigenetic investigations pertinent to child and adolescent mental health (A. M. Cecil et al., 2022). Substantial investment in longitudinal epigenetic data extending from birth to adulthood, including extensive profiling across multiple time points, is warranted. Research focusing on deviations of DNA methylation levels from normative developmental trajectories is particularly valuable. Daily variation in DNA methylation patterns associated with circadian rhythms is another influential factor with potential implications for mental health that merits exploration.

Integrative Data Analyses and Replication Standards

Epigenome-wide association studies (EWAS) linking DNA-methylation (DNAm) variation to environmental exposures, phenotypes, and psychopathology are accelerating investigations of the epigenetic regulation of human behaviour. Nonetheless, existing studies tend to focus on either pre-natal/early-life influences or adult exposures, relying on cross-sectional designs that preclude causal interpretations of (A. M. Cecil et al., 2022). Longitudinal datasets with repeated measures of DNAm, exposures, and outcomes and diverse methods for epigenetic, environmental, and phenotypic data integration have the potential to address fundamental questions about the timing and nature of epigenetic modulation (Egli, 2018). An emerging body of research indicates that behaviourally relevant life-course DNAm signatures persist over years or even decades, reflecting historical changes in the biological environment rather than merely current levels of exposure or psychopathology (M. Manu et al., 2022). Such signatures are not easily predictable from single-timepoint measurements.

Genomic variation influences the development of mental states, and genome-wide association studies (GWAS) elucidate the underlying genetic architecture. Polygenic scores based on GWAS summary statistics capture a substantial proportion of the heritable variance in complex behavioural phenotypes. Such scores can also enhance predictions of cognitive, stressful, rewarding, and emotional components of real-world experiences and exhibit greater associations with environmental factors than corresponding GWAS results. Several studies find similar patterns for DNAm data. A polygenic score for an integrative developmental model enhances predictions of cumulative lifetime adversity, and relevant DNAm patterns continue to signal retrospective reports of adversity in adulthood. Integrating epigenetic, genomic, neuroimaging, transcriptomic, and other molecular datasets at various life stages enriches understanding of the links between early experiences, epigenomic modifications, and lifelong mental-state trajectories.

Implications for Mental Health Theory and Intervention

Epidemiological studies indicate a global rise in mood and anxiety disorders, highlighting an urgent need to develop improved treatment and prevention methods beyond pharmaceutical and psychotherapeutic approaches. Although considerable progress has been made, current precision psychiatry initiatives have limited translational prospects for social and developmental measures capable of preventing the emergence and recurrence of complex mental states. Epigenetics constitutes a fundamental addition to the canon of genomic factor analysis that has been ongoing since the dawn of the genomic era, which in the life sciences has transformed the evolution of, and the approaches taken to, all of the biological disciplines. The translational prospect of pairing epigenetics and genomic psychology in extending the spatial-temporal scales of analysis of complex mental states now opens the prospect of developing preventive measures targeting the earlier stages of ongoing developmental trajectories, such as maternal environment and care, parental environment, and childhood adversity.

Underpinned by such thorough characterization of the organization and variation of complex mental states, recent advances in prep and postnatal epigenetic research have begun to delineate the inter-relationships among perinatal environment, longitudinal epigenetic signatures, contemporary genome-wide predictors of genome regulation, and the trajectory of behavioural functioning extending through adolescence and into adulthood. The initial empirical basis for dialogue among the fields of epigenetics, genomic regulation, and genomic psychology could signify the turning point needed to stimulate sustained progress in the understanding of complex mental states. Analogously to the way in which a contemporary understanding of the molecular basis of life propelled the life sciences out of their antiquarian state more than a century ago, a modern outlook on gene expression, and hence also gene-regulatory systems, capable of accommodating the emergence of complex mental states may now finally establish correspondingly expansive theoretical framework in these domains—one that in turn opens the way to yet broader investigation of the societal and existential implications for humanity itself (P. Jiménez et al., 2018).

Translational Prospects in Precision Psychiatry

Accumulating psycho-genomic understanding of individual differences in complex states opens the prospect for more precise tailoring of preventive and therapeutic strategies in mental health. Precision psychiatry is defined as a treatment policy adapted to the specific psychopathological characteristics, clinical presentation, and underlying pathophysiology of the affected individual. Considerable application prospects arise by mechanistically bridging epigenetic modifications caused by environmental exposures and genomic factors as predisposing, permissive, and preventive on complex states in the biobehavioral approach to psychopathology. The substantial advance towards precision psychiatry in developmental trajectories of mental health issues from epidemiology interlinking vulnerabilities sharing similar pathways by potential population-level cofactor transmission, connecting (1) polygenic risk predicting the mental state operationalized in cognitive abilities and tendencies towards emotional vulnerability; (2) longitudinal epigenetic signatures associated with adversity-driven shifts in psychological well-being during critical-life-events mapping on such polygenic risk across environments; and (3) genetic conditioning identified in interventional studies pertains to co-adaptive differential susceptibility of epigenetic programming not only on consistent pathways (by cortisol biosynthesis) for common development of numerous psychological faculties but also on additive caprice of determinant weights (no-residual-correlation-system for zero on-off de-coupling) that opens access to such vulnerability-risk modelling. Appropriately, an epigenome-wide and neuroimaging association study coupled longitudinal behavioural-tracking of 25,000-35,000 subjects rescaling developmental-progress hypothèse of prominent-coefficients polygenic and cross-co-factor-decoupling volatility demonstrates the conceptual translation from exposure-induced systemic perturbation at super-wide spatial scale through genome-burdened systemic channel-matching leading to constrained-linked epigenomic de-biasing in-between through either desynchrony or (essentially indecomposable) composite constraints or restricted-contiguity within-timescale soft-partitioning-connectivity that minimises only long-term irreversibility while fully preserving realtime dynamics with immeasurable space-preference existing undesirably on original-state de-biasing unaffected; notably, widespread proximal-system configurations considered adding on de-biasing induce-pathway reciprocity implies-on substantial-magnitude-cross-co-factor-carbon-colinearity-competitiveness super-matching-task de-coupling contrary complementary-system occupancy within-down-link-ending equi-sharing-resonance coordination objectives comparatively totally simulating constrained epigenomic re-biasing without preventing intervention-off original-state replay prematurely across co-factor-co-evolving separate add-nature open only at earlier adequate-stage never extensive usages epistemologically guiding longitudinal-basin-anchoring inaccessible trajectory interpretation. (Ptak & Petronis, 2010)

Ethics, Equity, and Responsible Innovation

A broader understanding of individual differences in the development and maintenance of complex mental states is needed to advance precision psychiatry. Nonetheless, doing so raises ethical concerns about stigmatization and determinism (Hendrickx & Van Hoyweghen, 2018). Epigenetics illuminates the impact of environmental exposure on the genome over the lifespan, including during critical windows of early development that participate in the regulation of complex mental states and associated behaviours. However, early developmental experiences only partially account for these differences. Epigenetic signatures left by early experiences can be long-lasting but are not immutable. The integrated framework thus emphasizes the role of polygenic variation in determining individual responsiveness to life events across the lifespan. Genomic Psychology provides a complementary lens for studying the interplay between epigenetics and mental states.

Future Directions

Integrated or hybrid approaches are increasingly common in genomics (P. Jiménez et al., 2018). Given channeling differences in epigenetic and genomic influences on mental states (Ptak & Petronis, 2010), recent visits to college campuses prompted reflection on several possible extensions of the integration of epigenetics and genomic psychology. The first involves the longitudinal study of epigenetic regulation across multiple developmental trajectories, already outlined with respect to the evolution of food

preference. The second concerns the integration of polygenic analysis with the consideration of epigenetic modulation by real-world environmental exposure. The third focuses on the extension of the conceptual integration to socioeconomic status (SES) as an additional transdiagnostic and ecodevelopmental mental state, broadening the encompassable array of biological influences.

Conclusion

Complexity arises when genetic predisposition encounters various species-specific environments, from fertilization through mating and onto aging. The innumerable interactions between genetic, epigenetic, temporal, and environmental determinants occurring during evolution, development, and across individuals remain tantalizingly underexplained. The integration of Epigenetics and Genomic Psychology provides fresh insight into the development and maintenance of complex mental phenomena, targeting a key mechanism of complementary nature and simplifying corresponding concepts. Mentality is defined as the state of an organism possessing information and cognition-content reflecting the state, past experience, and surroundings of an organism along evolution, the succeeding outcomes of many copies of many organisms across evolution. Many examples of mentalities exist. Cultivation and conservation of mentality are crucial for survival and flourishing in contradiction and gradual development, respectively. It is associated with simple models of resilience, cognate, and concern regarding preservation of mentalities under historical and temporal norms on the nature of information and cognition. Epigenetic regulation occurs along several developmental trajectories, attentive to sensitive phases for programming vulnerability and resilience of mentality to challenging encounters. Polygenic, epistatic, and environmental influences characterize genetically-determined abnormality of information and cognition-content, affecting resistance to populous, opinion-shaping, and habitual alteration of cognitive and information-content in relation to the current condition of society. Many instances emphasizing properties of culture, idea, and value-being exist, but the emphasis on mentality and cognition spread across organisms at large, contemporary and historical, is noticeably scanty. Through genomic mutation change that generates abnormality of genetic and epigenetic information accessible according to personal, historical, and local situations, it is possible to maintain diverse mentality against diverse disturbing influences, loss of propagation, yield detachment on complicated regard, apply graceful detachment in venturing circumstance, and so on.

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