

Genetics and Epigenetic in Mental Health

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ABSTRACT

Genetics and epigenetics play critical roles in mental health, offering insights into the complex interplay between biological predisposition and environmental influences in the development and progression of mental disorders. Genetic studies have identified numerous risk loci associated with conditions such as schizophrenia, bipolar disorder, and depression, highlighting the polygenic nature of these illnesses. However, the presence of genetic risk factors alone does not fully account for the variability in disease onset, severity, or response to treatment. This gap is increasingly understood through the lens of epigenetics, which involves heritable changes in gene expression that do not alter the DNA sequence itself but are influenced by environmental factors, such as stress, diet, and exposure to toxins. Epigenetic mechanisms, including DNA methylation, histone modification, and non-coding RNAs, can modulate gene activity in response to external stimuli, leading to long-lasting effects on brain function and behavior. These processes are particularly important during critical periods of brain development, where epigenetic modifications can shape neural circuits involved in emotion regulation, cognition, and stress response. Emerging research suggests that the interaction between genetic predisposition and epigenetic changes contributes to the heterogeneity observed in mental health disorders, explaining why individuals with similar genetic risks can have different outcomes. Understanding these intricate genetic and epigenetic

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networks is essential for developing personalized therapeutic strategies, which could revolutionize the prevention, diagnosis, and treatment of mental health conditions. Advances in this field hold the promise of identifying biomarkers for early intervention and creating targeted interventions that consider an individual's unique genetic and epigenetic profile, ultimately improving mental health outcomes on a global scale.

Keywords: Genetics and epigenetics; mental health disorders; depression.

1. INTRODUCTION

Mental health disorders, including depression, anxiety, bipolar disorder, and schizophrenia, are major contributors to the global burden of disease. Understanding the causes of these disorders is critical for developing effective treatments and preventive strategies [1]. Traditionally, the focus has been on genetic factors, but more recent research has highlighted the importance of epigenetics—the study of heritable changes in gene expression that do not involve changes to the underlying DNA sequence [2]. Mental health disorders represent a complex interplay between genetic predispositions and environmental influences, forming the basis of an intricate biological and psychological matrix that determines an individual's mental well-being. The exploration of genetics in mental health seeks to understand how inherited variations in DNA contribute to the risk of developing psychiatric conditions such as depression, anxiety, schizophrenia, and bipolar disorder. Epigenetics, on the other hand, delves into how environmental factors, including stress, diet, and exposure to toxins, can modify gene expression without altering the underlying DNA sequence. Together, these fields provide a comprehensive view of the biological underpinnings of mental health, offering insights into potential therapeutic interventions and personalized treatment strategies [3]. Mental health is a complex and multifaceted domain influenced by an intricate interplay of genetic, epigenetic, and environmental factors. Understanding the biological underpinnings of mental health disorders has been a pivotal focus of psychiatric research, leading to significant advancements in the identification of genetic contributors to these conditions [4]. The advent of genome-wide association studies (GWAS), whole-genome sequencing, and other genomic technologies has enabled researchers to unravel the genetic architecture of various psychiatric disorders, such as schizophrenia, bipolar disorder, major depressive disorder, and autism spectrum disorders [5,6]. However, while genetic predisposition plays a critical role, it is not the

sole determinant of mental health outcomes. Epigenetic mechanisms, which regulate gene expression without altering the underlying DNA sequence, have emerged as vital modulators that mediate the effects of environmental factors on the genome, thus bridging the gap between genetic susceptibility and environmental influences [7, 8].

The genetic component of mental health disorders is underscored by the identification of numerous risk genes and genetic variants that contribute to the susceptibility to psychiatric conditions. These genetic variations can range from single nucleotide polymorphisms (SNPs) to copy number variations (CNVs) and rare mutations, each contributing to the heritability of mental health disorders. For instance, large-scale GWAS have identified several loci associated with schizophrenia, implicating genes involved in neurotransmission, synaptic function, and immune response. However, the effect sizes of individual genetic variants are often small, suggesting that the genetic architecture of mental health disorders is highly polygenic, with the cumulative effect of many genes contributing to the overall risk. Moreover, genetic heterogeneity, where different genetic factors may lead to similar clinical phenotypes, adds another layer of complexity to understanding the genetic basis of mental health disorders [9-11].

While genetic research has provided valuable insights into the heritability of mental health disorders, it has also highlighted the limitations of focusing solely on genetic factors. The relatively low penetrance of most psychiatric risk variants and the observation that identical genetic variants can result in different outcomes in different individuals suggest that other factors are at play [12]. This has led to the growing recognition of the role of epigenetics in mental health. Epigenetic modifications, such as DNA methylation, histone modification, and non-coding RNA regulation, are key mechanisms that control gene expression and can be influenced by various environmental factors, including stress, diet, and exposure to toxins. These modifications can alter the transcriptional

potential of genes, leading to changes in cellular function and, ultimately, behavior and mental health[13]. Epigenetic mechanisms are particularly relevant in the context of mental health because they provide a molecular link between environmental exposures and the genome. For example, early-life stress has been shown to lead to long-lasting changes in DNA methylation patterns in genes involved in stress response pathways, which can predispose individuals to mental health disorders later in life[14]. Similarly, exposure to adverse environmental factors, such as maternal stress during pregnancy or childhood trauma, has been associated with epigenetic changes that increase the risk of developing conditions like depression and anxiety. These findings underscore the dynamic nature of the epigenome, which can be shaped by experiences across the lifespan, contributing to the development and progression of mental health disorders[15]. The interplay between genetics and epigenetics in mental health is further complicated by the concept of gene-environment interactions. These interactions occur when the effect of an environmental exposure on mental health is influenced by an individual's genetic makeup. For instance, individuals with a genetic predisposition to depression may be more sensitive to the effects of chronic stress, leading to epigenetic changes that exacerbate their risk of developing the disorder. Conversely, protective genetic variants may buffer against the negative impact of environmental stressors. Understanding these gene-environment interactions is crucial for identifying individuals who are at the highest risk for mental health disorders and for developing personalized interventions that target both genetic and environmental factors [16].

The concept of transgenerational epigenetic inheritance has added a new dimension to our understanding of how genetic and epigenetic factors contribute to mental health. This phenomenon refers to the transmission of epigenetic marks from one generation to the next, potentially influencing the mental health of offspring based on the experiences of their parents or even grandparents[17]. Animal studies have provided evidence that epigenetic changes induced by stress or trauma can be passed down to subsequent generations, affecting their behavior and susceptibility to mental health disorders. While the evidence for transgenerational epigenetic inheritance in humans is still emerging, it raises important questions about the long-term impact of environmental exposures on mental health and the potential for epigenetic interventions to break the cycle of inherited vulnerability[18]. In recent years, there has been growing interest in the potential of epigenetic therapies for the treatment of mental health disorders. Epigenetic drugs, such as DNA methyltransferase inhibitors and histone deacetylase inhibitors, have shown promise in preclinical studies for their ability to reverse aberrant epigenetic modifications associated with psychiatric conditions[19]. These therapies offer a novel approach to treating mental health disorders by targeting the underlying epigenetic dysregulation rather than simply alleviating symptoms. However, the development of epigenetic therapies for mental health is still in its early stages, and there are significant challenges to be addressed, including the need for greater specificity in targeting epigenetic modifications and the potential for unintended effects on other genes and biological processes [20].

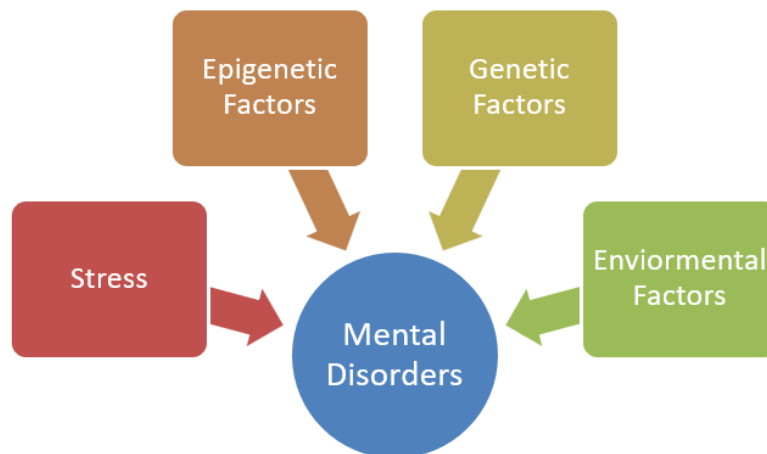


Fig. 1. Factors involved in mental disorder

2. GENETICS AND MENTAL HEALTH

Genetics plays a pivotal role in mental health, offering profound insights into the biological underpinnings of various psychiatric disorders. The field of psychiatric genetics has evolved significantly over the past few decades, driven by advancements in genomic technologies and the increasing recognition of the complex interplay between genes and the environment. Mental health disorders, including schizophrenia, bipolar disorder, major depressive disorder, and anxiety disorders, are among the most debilitating conditions worldwide. Understanding the genetic basis of these disorders is crucial for developing more effective treatments, personalized medicine approaches, and potentially preventive strategies [21,22]. The heritability of many psychiatric disorders is well-established. Twin, family, and adoption studies have consistently demonstrated that these disorders tend to run in families, suggesting a strong genetic component. For instance, schizophrenia has a heritability estimate of around 80%, indicating that genetic factors contribute significantly to the risk of developing the disorder. Similarly, bipolar disorder and major depressive disorder have heritability estimates ranging from 60% to 80%, underscoring the substantial genetic influence. However, the identification of specific genetic variants associated with these disorders has been challenging due to their polygenic nature, meaning that many genes, each with a small effect, contribute to the overall risk [23, 24].

One of the major breakthroughs in psychiatric genetics has been the advent of genome-wide association studies (GWAS). These studies have allowed researchers to scan the entire genome for common genetic variants associated with mental health disorders [25, 26]. GWAS have identified numerous single nucleotide polymorphisms (SNPs) that are associated with an increased risk of psychiatric disorders. However, each of these variants typically contributes only a small increase in risk, highlighting the complexity of the genetic architecture of mental health. Despite this, the identification of these variants has provided valuable insights into the biological pathways involved in these disorders. For example, many of the risk variants for schizophrenia are located in genes involved in synaptic function and neurotransmitter signaling, which are critical processes in brain function and cognition [27, 28]. Beyond common genetic variants, rare genetic

mutations have also been implicated in mental health disorders. Copy number variations (CNVs), which involve large deletions or duplications of DNA segments, have been associated with a range of psychiatric conditions, including schizophrenia and autism spectrum disorder. These rare variants often have a larger effect size compared to common SNPs, meaning they confer a greater risk of developing the disorder. For instance, CNVs at several loci, such as 22q11.2 and 16p11.2, have been strongly linked to schizophrenia. These findings suggest that while common variants contribute to the overall genetic risk, rare mutations can have a significant impact on an individual's susceptibility to mental health disorders [29, 30].

Epigenetics, which refers to changes in gene expression that do not involve alterations in the DNA sequence, also plays a critical role in mental health. Epigenetic modifications, such as DNA methylation and histone modification, can be influenced by environmental factors, such as stress, diet, and exposure to toxins, and can affect gene expression in the brain. These changes can alter neural development and function, potentially leading to the onset of psychiatric disorders. Importantly, epigenetic changes are reversible, offering potential avenues for therapeutic intervention. For example, research has shown that antidepressant treatments can reverse some of the epigenetic changes associated with depression, suggesting that targeting epigenetic mechanisms could be a promising strategy for treating mental health disorders [31, 32]. Gene-environment interactions are another crucial aspect of the genetics of mental health. While genetic predisposition plays a significant role, environmental factors can influence the expression of these genetic risks. For instance, individuals with a genetic predisposition to depression may only develop the disorder when exposed to significant stress or trauma. Similarly, the onset of schizophrenia may be triggered by a combination of genetic risk factors and environmental stressors, such as prenatal exposure to infections or substance abuse during adolescence. Understanding these interactions is essential for developing prevention strategies and identifying individuals at high risk for mental health disorders [33].

The concept of polygenic risk scores (PRS) has emerged as a tool for quantifying an individual's genetic risk for mental health disorders. PRS are

calculated by summing the effects of multiple genetic variants associated with a disorder, providing an estimate of an individual's genetic predisposition. While PRS are not yet used in clinical practice, they hold promise for identifying individuals at high risk for psychiatric disorders, who may benefit from early intervention or targeted prevention strategies. However, there are still significant challenges to be addressed, including the need for more accurate and comprehensive risk models and the ethical considerations of using genetic information in mental health care [34, 35].

2.1 Heritability of Mental Health Disorders

Many mental health disorders have a significant genetic component. Twin, family, and adoption studies have shown that disorders such as schizophrenia, bipolar disorder, and major depressive disorder have high heritability estimates, often ranging between 40-80%. These studies suggest that genetics play a substantial role in the susceptibility to these disorders. Mental health disorders represent a significant public health challenge, affecting millions of people worldwide[36]. These disorders, which include conditions such as depression, anxiety, bipolar disorder, schizophrenia, and autism

spectrum disorder, are characterized by a complex interplay of genetic, environmental, and psychological factors. One of the critical aspects of understanding these disorders is the concept of heritability, which refers to the proportion of variation in a population that can be attributed to genetic differences among individuals. Heritability is a central focus in psychiatric genetics as it provides insights into the biological underpinnings of mental health disorders and informs the development of personalized treatment approaches[37, 38]. The study of heritability in mental health disorders has a long and complex history, tracing back to early twin and family studies in the early 20th century. These studies provided the first empirical evidence that mental health disorders tend to run in families, suggesting a genetic component. Twin studies, in particular, have been instrumental in quantifying the heritability of these disorders by comparing the concordance rates between monozygotic (identical) and dizygotic (fraternal) twins. Monozygotic twins share 100% of their genes, while dizygotic twins share, on average, 50% of their segregating genes. By comparing the similarity in mental health outcomes between these two groups, researchers can estimate the heritability of various mental health conditions [39, 40].



Fig. 2. The connection between genetics and mental health, with a DNA helix intertwined with a human brain

However, heritability estimates for mental health disorders are not static or definitive. They can vary significantly depending on the population studied, the methods used to measure the disorder, and the specific definition of the disorder itself. For example, heritability estimates for major depressive disorder typically range from 30% to 40%, indicating that genetic factors play a moderate role in the risk for this condition. In contrast, the heritability of bipolar disorder is estimated to be as high as 70% to 80%, suggesting a more substantial genetic influence. Schizophrenia also has a high heritability, with estimates ranging from 60% to 80%, indicating that genetic factors are a major contributor to the risk of developing this disorder[41-43]. Despite the clear evidence for genetic contributions to mental health disorders, it is essential to recognize that heritability does not equate to genetic determinism. Heritability estimates do not imply that a disorder is entirely genetic or that environmental factors are unimportant. Rather, heritability reflects the relative contribution of genetic differences to the variation in a trait within a specific population at a specific time. Environmental factors, such as early-life stress, trauma, socioeconomic status, and lifestyle, also play crucial roles in the development and expression of mental health disorders. The interaction between genetic and environmental factors is complex and multifaceted, with some individuals being more genetically predisposed to mental health disorders but only developing them in the presence of specific environmental triggers[44, 45].

Advances in molecular genetics have significantly enhanced our understanding of the genetic basis of mental health disorders. Genome-wide association studies (GWAS) have identified numerous genetic variants associated with various mental health conditions, providing new insights into the biological pathways involved. However, the genetic architecture of mental health disorders is highly polygenic, meaning that many genetic variants, each contributing a small effect, combine to influence the risk of developing a disorder. This polygenic nature makes it challenging to identify specific genes or genetic variants that can be used as reliable biomarkers for diagnosis or treatment[46, 47]. The concept of "missing heritability" also presents a challenge in the study of mental health disorders. While twin and family studies suggest a substantial genetic component, the genetic variants identified through GWAS and other molecular methods account for only a small

fraction of the heritability. This discrepancy has led researchers to explore other potential sources of heritability, such as rare genetic variants, gene-environment interactions, and epigenetic mechanisms. Epigenetics, in particular, has emerged as a promising area of research, focusing on how environmental factors can influence gene expression without altering the underlying DNA sequence. Epigenetic changes, such as DNA methylation and histone modification, may help explain how environmental factors contribute to the development of mental health disorders in genetically predisposed individuals[48, 49].

The implications of heritability research for mental health treatment and prevention are profound. Understanding the genetic basis of mental health disorders can lead to more personalized approaches to treatment, where interventions are tailored to an individual's genetic profile. For example, pharmacogenetics, which studies how genetic differences influence an individual's response to medications, holds promise for optimizing the treatment of mental health disorders by identifying the most effective drugs with the fewest side effects for each patient. Additionally, knowledge of genetic risk factors can inform preventive strategies, allowing for early identification and intervention in individuals at high risk for developing mental health disorders[50, 51]. However, the translation of heritability research into clinical practice is not without challenges. Ethical considerations, such as genetic privacy, the potential for genetic discrimination, and the psychological impact of genetic information on patients, must be carefully navigated. Moreover, the complexity of mental health disorders, with their intricate interplay of genetic and environmental factors, means that genetic information alone is unlikely to provide a complete picture of an individual's risk or prognosis. A holistic approach that integrates genetic, environmental, and psychological factors is essential for the effective management of mental health disorders[52, 53].

2.2 Genetic Risk Factors

Advances in genomic technologies, such as genome-wide association studies (GWAS), have identified numerous genetic variants associated with mental health disorders. For example, variants in the *COMT*, *BDNF*, and *5-HTTLPR* genes have been linked to psychiatric conditions. However, these variants often have small effect sizes, indicating that mental health disorders are

polygenic, involving the cumulative effect of many genes. Genetic risk factors play a significant role in mental health, contributing to the susceptibility of various psychiatric disorders. These factors involve inherited variations in genes that influence brain development, neurotransmitter systems, and stress response mechanisms[54]. Conditions such as schizophrenia, bipolar disorder, depression, and anxiety have all been linked to genetic predispositions. For instance, specific gene variants like those in the serotonin transporter gene (5-HTTLPR) are associated with an increased risk of depression, particularly when combined with environmental stressors. Similarly, genes like DISC1 and COMT have

been implicated in schizophrenia[55]. However, the relationship between genetics and mental health is complex and multifactorial; it is influenced by gene-environment interactions, where environmental factors like trauma, stress, and lifestyle can either mitigate or exacerbate the genetic risks. While genetic predispositions do not guarantee the development of mental illness, they highlight the importance of understanding individual vulnerabilities, potentially guiding personalized treatment and prevention strategies. Advances in genetics and genomics continue to shed light on these intricate relationships, paving the way for more targeted interventions in mental health care[56].

Table 1. various genetic risk factors associated with different mental health conditions[57-61]

Genetic Marker	Gene(s) Involved	Mental Health Condition(s)	Type of Mutation	Risk Factor Description
5-HTTLPR	SLC6A4	Depression, Anxiety	Polymorphism	Variants in the serotonin transporter gene can influence susceptibility to stress-related disorders.
COMT Val158Met	COMT	Schizophrenia, Bipolar Disorder	SNP (Single Nucleotide Polymorphism)	This polymorphism affects dopamine metabolism, influencing cognitive function and emotional regulation.
BDNF Val66Met	BDNF	Depression, Anxiety, Schizophrenia	SNP	Affects brain-derived neurotrophic factor, which is crucial for brain plasticity and mood regulation.
CACNA1C	CACNA1C	Bipolar Disorder, Schizophrenia	SNP	Involved in calcium channel regulation, this gene impacts neural activity and mood stabilization.
NRG1	NRG1	Schizophrenia	SNP, CNV (Copy Number Variation)	Neuregulin 1 plays a role in neural development and synaptic plasticity, associated with schizophrenia risk.
DISC1	DISC1	Schizophrenia, Bipolar Disorder, Major Depression	Translocation, SNP	Disrupted-in-Schizophrenia 1 is crucial for brain development and connectivity; mutations linked to major psychiatric conditions.
ANK3	ANK3	Bipolar Disorder	SNP	Ankyrin G, involved in the stability of neuronal connections, is associated with mood disorders.
MTHFR C677T	MTHFR	Depression, Anxiety, Schizophrenia	SNP	Affects folate metabolism, leading to elevated homocysteine levels, which are linked to various psychiatric disorders.
GRIN2B	GRIN2B	Autism Spectrum Disorders, Schizophrenia	SNP, Deletions	Encodes a subunit of NMDA receptors, crucial for synaptic plasticity; mutations may affect cognitive function.
FKBP5	FKBP5	PTSD, Depression, Anxiety	SNP	Modulates glucocorticoid receptor sensitivity, influencing stress response and vulnerability to PTSD.
TSC1/TSC2	TSC1, TSC2	Autism Spectrum Disorders, Cognitive Impairments	Deletions, Mutations	Tuberous sclerosis complex genes, when mutated, can lead to neurodevelopmental disorders.

Table 2. Gene-environment interactions for mental health[64-66]

Gene	Environmental Factor	Mental Outcome	Health Mechanism
5-HTTLPR (serotonin transporter gene)	Childhood trauma	Depression, anxiety	Alters serotonin regulation, affecting mood and stress response
COMT (Catechol-O-methyltransferase gene)	Cannabis use during adolescence	Increased risk of psychosis	Affects dopamine metabolism, influencing psychotic symptoms
BDNF (Brain-Derived Neurotrophic Factor)	Early-life stress	Depression	Modifies neuroplasticity and stress response pathways
MAOA (Monoamine oxidase A)	Childhood maltreatment	Aggressive behavior, antisocial personality	Influences neurotransmitter breakdown, affecting aggression and impulse control
DRD4 (Dopamine receptor D4)	Low parental care	ADHD symptoms, risky behavior	Modifies dopamine signaling, affecting attention and reward processing

2.3 Gene-Environment Interactions

The relationship between genetics and mental health is not straightforward. Environmental factors, such as stress, trauma, and substance use, can interact with genetic predispositions to increase the risk of developing mental health disorders. For instance, individuals with a specific variant of the *5-HTTLPR* gene are more likely to develop depression following stressful life events [62]. Gene-environment interactions play a critical role in shaping mental health outcomes, highlighting the complex interplay between genetic predispositions and environmental influences [63].

Genes can influence how an individual responds to environmental factors, such as stress, trauma, or social conditions, which in turn can trigger or exacerbate mental health issues. For instance, individuals with certain genetic variants may be more susceptible to depression when exposed to chronic stress or adverse life events. Conversely, supportive environments can mitigate the impact of genetic vulnerabilities, promoting resilience even in those at genetic risk[66]. The diathesis-stress model is a key framework for understanding these interactions, positing that mental health disorders arise from the interaction of a predisposed vulnerability (diathesis) and stressful life events. Recent research in epigenetics further complicates this picture by showing that environmental factors can alter gene expression through mechanisms like DNA methylation, leading to changes in brain function and behavior that persist over time. This means that gene-environment interactions are not only dynamic but can have long-lasting effects, influencing mental health across the lifespan. Understanding these interactions is crucial for developing personalized interventions that consider both genetic makeup and environmental

context, paving the way for more effective prevention and treatment strategies in mental health care[67, 68].

3. EPIGENETICS AND MENTAL HEALTH

Epigenetics, the study of changes in gene expression that do not involve alterations to the underlying DNA sequence, has increasingly been recognized as a crucial factor in understanding mental health. These changes are often triggered by environmental factors, such as stress, diet, and exposure to toxins, which can influence the way genes are turned on or off. Unlike genetic mutations, which are permanent changes to the DNA sequence, epigenetic modifications can be reversible, adding a layer of complexity to how we understand the interaction between genes and the environment in the context of mental health[69, 70]. One of the key mechanisms of epigenetic regulation is DNA methylation, where a methyl group is added to the DNA molecule, typically at cytosine bases that precede a guanine (CpG sites). This modification can suppress gene expression, effectively "silencing" certain genes. In the brain, DNA methylation plays a significant role in neurodevelopment and synaptic plasticity, both of which are critical processes in the maintenance of mental health. Abnormal methylation patterns have been linked to various mental health disorders, including depression, anxiety, schizophrenia, and bipolar disorder. For instance, hypermethylation of genes involved in serotonin production, a neurotransmitter that regulates mood, has been observed in individuals with depression, leading to reduced serotonin levels and contributing to depressive symptoms[71, 72]. Histone modification is another important epigenetic mechanism. Histones are proteins around which DNA is wrapped, and chemical changes to these

proteins can either loosen or tighten their grip on DNA, thereby regulating gene expression. Acetylation of histones generally enhances gene expression by relaxing the DNA structure, making it more accessible to transcription factors. Conversely, deacetylation tends to repress gene expression. In the context of mental health, disruptions in histone modification have been associated with several psychiatric conditions. For example, alterations in histone acetylation have been implicated in the pathology of schizophrenia, where they may contribute to the dysregulation of genes involved in synaptic function and neural connectivity[73, 74].

Non-coding RNAs, particularly microRNAs, are also crucial players in the epigenetic regulation of mental health. MicroRNAs can bind to messenger RNAs (mRNAs) and prevent them from being translated into proteins, effectively downregulating gene expression. Dysregulation of microRNAs has been associated with a variety of mental health disorders. For instance, changes in specific microRNAs have been linked to the pathophysiology of anxiety and post-traumatic stress disorder (PTSD), where they may modulate the expression of genes involved in the stress response and emotional regulation[75, 76]. The impact of epigenetics on mental health is further complicated by the bidirectional relationship between the two. While epigenetic modifications can influence mental health outcomes, mental health conditions can also lead to changes in epigenetic patterns. For example, chronic stress, a common feature in many mental health disorders, has been shown to induce epigenetic changes that alter the expression of genes involved in the hypothalamic-pituitary-adrenal (HPA) axis, a central component of the body's stress response system. These changes can perpetuate a cycle

of stress and epigenetic alterations, potentially exacerbating mental health issues[77, 78].

3.1 Epigenetic Mechanisms

Epigenetic modifications, such as DNA methylation, histone modification, and non-coding RNA expression, regulate gene expression without altering the DNA sequence[79, 80]. These modifications are dynamic and can be influenced by environmental factors, including stress, diet, and exposure to toxins. Epigenetics provides a potential mechanism by which environmental factors can leave a lasting impact on gene expression and contribute to the development of mental health disorders. Epigenetic mechanisms play a crucial role in mental health by influencing gene expression without altering the underlying DNA sequence[81, 82]. These mechanisms include DNA methylation, histone modification, and non-coding RNAs, all of which can affect how genes are turned on or off in response to environmental factors. For example, DNA methylation involves the addition of methyl groups to DNA molecules, which can suppress gene activity and has been linked to various mental health disorders such as depression and schizophrenia. Histone modifications, which involve chemical changes to the proteins around which DNA is wrapped, can also impact gene expression by altering the accessibility of DNA for transcription. Non-coding RNAs, which are RNA molecules that do not encode proteins but can regulate gene expression, have been implicated in the regulation of genes associated with mental health conditions[83]. These epigenetic changes can be triggered by environmental stressors, traumatic experiences, and other external factors, potentially leading to alterations in brain function and behavior[84, 85].

Table 3. Some key epigenetic changes associated with various mental health disorders[86-88]

Mental Health Disorder	Epigenetic Changes	Description
Depression	DNA Methylation	Altered methylation patterns in genes like BDNF and NR3C1; can affect stress response and neuroplasticity.
Schizophrenia	Histone Modification	Changes in histone acetylation and methylation in genes such as DISC1 and COMT; influences gene expression and neuronal function.
Bipolar Disorder	Non-Coding RNA	Altered expression of microRNAs like miR-34 and miR-132; affects mood regulation and synaptic plasticity.
Autism Spectrum Disorder	DNA Methylation & Histone Modification	Abnormal DNA methylation in genes such as MECP2 and changes in histone modifications; impacts brain development and synaptic function.
Post-Traumatic Stress Disorder (PTSD)	DNA Methylation & Non-Coding RNA	Changes in methylation patterns in stress response genes like FKBP5; altered expression of miRNAs involved in stress and emotional regulation.

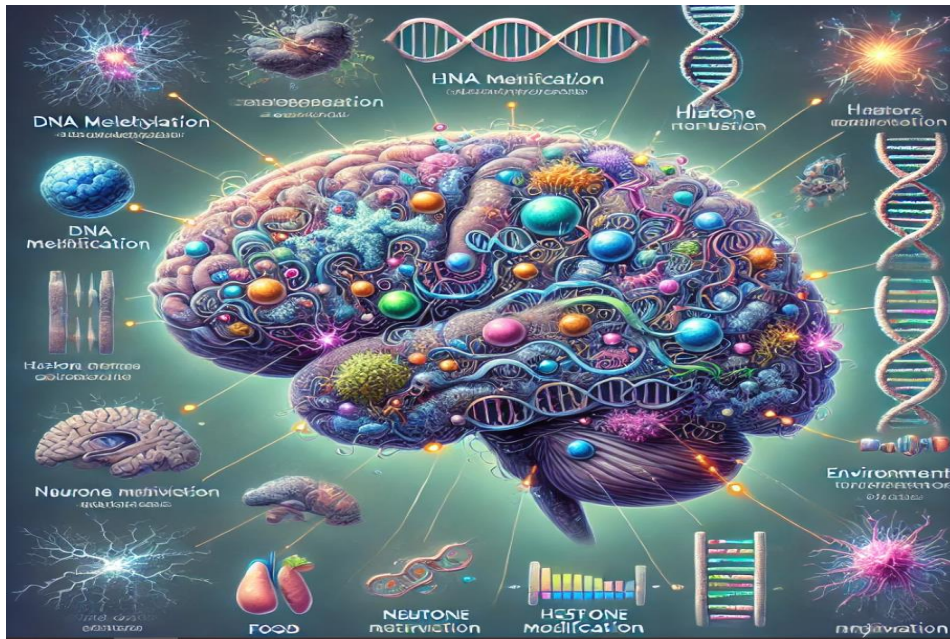


Fig. 3. Epigenetic changes in mental health disorders

Furthermore, the dynamic nature of epigenetic regulation means that these changes can be reversible, offering potential avenues for therapeutic intervention in mental health disorders. Understanding these mechanisms provides valuable insights into the complex interplay between genetics, environment, and mental health, highlighting the importance of considering both genetic predispositions and environmental influences in the development and treatment of mental health conditions [89].

3.2 Epigenetic Changes in Mental Health Disorders

Numerous studies have identified epigenetic changes associated with mental health disorders. For example, increased DNA methylation at the *SLC6A4* gene, which encodes the serotonin transporter, has been observed in individuals with depression [90, 91]. Similarly, altered histone acetylation patterns have been linked to schizophrenia and bipolar disorder. These findings suggest that epigenetic modifications may play a key role in the pathophysiology of mental health disorders. Epigenetic changes play a crucial role in the development and progression of mental health disorders by influencing gene expression without altering the underlying DNA sequence [92].

These changes are mediated through mechanisms such as DNA methylation, histone

modification, and non-coding RNA molecules. In mental health disorders like depression, bipolar disorder, and schizophrenia, epigenetic modifications can affect the expression of genes involved in neurodevelopment, synaptic plasticity, and stress responses. For instance, DNA methylation can lead to the silencing of genes that are crucial for neuronal function, while histone modifications can alter chromatin structure, thereby influencing gene accessibility and expression. Environmental factors such as stress, trauma, and lifestyle choices can induce these epigenetic changes, potentially leading to maladaptive neural circuits and contributing to the onset or exacerbation of mental health conditions. Research into epigenetic mechanisms offers promising avenues for understanding the complex interplay between genetics and environment in mental health, and may lead to novel therapeutic strategies that target these epigenetic modifications to ameliorate symptoms and improve outcomes for individuals with mental health disorders [93-95].

3.3 Transgenerational Epigenetics

Emerging evidence suggests that epigenetic changes can be transmitted across generations, potentially contributing to the heritability of mental health disorders. For instance, studies in rodents have shown that exposure to stress can result in epigenetic modifications that are passed on to offspring, affecting their behavior and

stress responses. While more research is needed in humans, these findings raise the possibility that the effects of environmental stressors can be inherited, contributing to the familial risk of mental health disorders[96-98].

Transgenerational epigenetics is a fascinating and complex field. It explores how epigenetic modifications—changes in gene expression that do not involve alterations to the DNA sequence itself—can be passed down from one generation to the next. This can impact mental health disorders in several ways[99-102]:

- **Inheritance of Epigenetic Marks:** Certain epigenetic modifications, such as DNA methylation or histone modification, can be inherited. These marks may influence the expression of genes associated with mental health conditions, potentially predisposing offspring to similar disorders.
- **Environmental Influences:** Environmental factors, such as stress, diet, and toxins, can lead to epigenetic changes. If a parent experiences significant environmental stressors, these epigenetic changes can be passed down, potentially affecting the mental health of their children and subsequent generations.
- **Gene-Environment Interactions:** Transgenerational epigenetic effects may involve complex interactions between genetic predispositions and environmental factors. This interaction can shape mental health outcomes in ways that are not solely attributable to genetic inheritance.
- **Potential for Interventions:** Understanding transgenerational epigenetics offers potential for developing interventions that could address mental health issues across generations. For example, early interventions or changes in environmental factors could potentially modify epigenetic marks and improve mental health outcomes.

4. CLINICAL IMPLICATIONS

4.1 Biomarkers for Diagnosis and Prognosis

The identification of genetic and epigenetic biomarkers holds promise for improving the diagnosis and prognosis of mental health disorders. For example, specific DNA methylation patterns may serve as biomarkers for early detection of schizophrenia or for

predicting treatment response in depression. However, the translation of these findings into clinical practice remains challenging, and further validation studies are needed[103]. Biomarkers for diagnosis and prognosis in mental health disorders are crucial in advancing our understanding and treatment of these conditions. These biomarkers can be genetic, proteomic, neuroimaging-based, or derived from other biological samples, such as blood or cerebrospinal fluid. For diagnosis, biomarkers can help in identifying the presence of a disorder more accurately and at an earlier stage than traditional methods. For instance, specific genetic variations or alterations in brain structure observed through neuroimaging can indicate susceptibility to conditions like schizophrenia or bipolar disorder. In terms of prognosis, biomarkers can provide insights into the likely course of the disorder, including potential responses to treatment and long-term outcomes. For example, alterations in levels of certain proteins or neurochemical markers can suggest how well a patient might respond to specific medications or therapies. The integration of biomarkers into clinical practice holds the promise of more personalized and effective treatment strategies, allowing for tailored interventions based on individual biological profiles, thereby improving overall patient outcomes and advancing the field of mental health research[104, 105].

4.2 Personalized Medicine

Understanding the genetic and epigenetic underpinnings of mental health disorders can inform the development of personalized treatment strategies[109]. For instance, pharmacogenetic testing can identify individuals who are more likely to respond to certain medications based on their genetic makeup. Additionally, epigenetic therapies, such as drugs that target DNA methylation or histone modification, are being explored as potential treatments for psychiatric conditions. Personalized medicine in mental health represents a transformative approach that tailors treatment strategies to the individual characteristics of each patient, rather than relying on a one-size-fits-all model. This approach integrates a comprehensive understanding of genetic, environmental, and lifestyle factors to provide more precise and effective interventions. By analyzing genetic markers, clinicians can identify individuals who are at higher risk for certain mental health conditions or who might respond differently to various

Table 4. Biomarkers for Diagnosis and Prognosis [106-108]

Disorder	Biomarkers	Purpose
Major Depressive Disorder (MDD)	- C-Reactive Protein (CRP): Elevated levels associated with inflammation. - Brain-Derived Neurotrophic Factor (BDNF): Reduced levels linked to depression. - Cortisol: High levels related to stress and depression.	- Diagnose and monitor disease progression. - Guide treatment options.
Bipolar Disorder	- BDNF: Altered levels during manic and depressive episodes. - Genetic Markers: Variants in genes like BDNF, CACNA1C. - Neuroimaging: Changes in brain structure and function.	- Differentiate from unipolar depression. - Predict response to treatment.
Schizophrenia	- Dopamine: Dysregulation of dopamine pathways. - Neuroimaging: Structural and functional brain abnormalities. - Genetic Markers: Variants in genes like COMT, DISC1.	- Aid in early diagnosis. - Assess severity and treatment response.
Anxiety Disorders	- Cortisol: Elevated levels linked to anxiety. - Neuroimaging: Altered brain activity patterns. - Genetic Markers: Variants in genes related to stress response.	- Diagnose and evaluate treatment efficacy. - Identify underlying biological mechanisms.
Post-Traumatic Stress Disorder (PTSD)	- Cortisol: Altered levels related to stress response. - Neuroimaging: Changes in brain areas involved in stress. - Genetic Markers: Variants related to stress sensitivity.	- Diagnose and track disease progression. - Predict treatment response.
Obsessive-Compulsive Disorder (OCD)	- Neuroimaging: Abnormalities in brain circuits related to anxiety and control. - Genetic Markers: Variants in genes associated with serotonin and neurodevelopment.	- Support diagnosis. - Assess treatment response.

Table 5. Prevention strategies in mental health [114-120]

Category	Strategy	Description	Target Population
Primary Prevention	Promotion of Mental Health Awareness	Educating the public about mental health, reducing stigma, and encouraging help-seeking behavior.	General population, schools, workplaces.
Primary Prevention	Stress Management Programs	Providing resources and training to help individuals manage stress effectively.	General population, particularly high-stress environments.
Primary Prevention	Parenting and Family Support	Offering parenting classes and family counseling to improve family dynamics.	Families, new parents, at-risk families.
Secondary Prevention	Early Screening and Intervention	Identifying and addressing mental health issues early through regular screenings and interventions.	Individuals at risk, schools, healthcare settings.
Secondary Prevention	Crisis Intervention Services	Providing immediate support and resources during mental health crises.	Individuals experiencing acute mental health issues.
Secondary Prevention	Support Groups and Peer Support	Facilitating group meetings and peer support for those experiencing mental health challenges.	Individuals with emerging mental health concerns.
Tertiary Prevention	Rehabilitation and Therapy Programs	Offering long-term support, therapy, and rehabilitation for individuals with chronic mental health conditions.	Individuals with diagnosed mental health conditions.
Tertiary Prevention	Medication Management	Ensuring proper medication management and adherence for individuals with mental health disorders.	Individuals under psychiatric care.
Tertiary Prevention	Community Reintegration Programs	Assisting individuals in reintegrating into the community after treatment.	Individuals recovering from severe mental health conditions.

medications. Additionally, personalized medicine takes into account personal history, such as past treatment responses and co-occurring conditions, to optimize therapeutic responses and co-occurring conditions.

strategies[110]. This method also leverages advancements in neuroimaging and biomarkers to gain insights into brain function and structure, further guiding treatment decisions. Ultimately, personalized medicine aims to enhance the efficacy of mental health treatments, reduce adverse effects, and improve overall patient outcomes by ensuring that each intervention is as closely aligned with the individual's unique biological and psychological profile as possible[111].

4.3 Prevention Strategies

Insights into gene-environment interactions and epigenetic modifications can inform prevention strategies for mental health disorders. For example, interventions that reduce exposure to environmental risk factors, such as stress management programs or early-life interventions, may mitigate the epigenetic changes associated with mental health disorders. Additionally, public health strategies that promote healthy environments and reduce social inequalities may help prevent the onset of mental health disorders in vulnerable populations[112, 113].

5. FUTURE DIRECTIONS

The future of mental health is poised to be shaped by a confluence of technological advancements, personalized care approaches, and a deeper understanding of mental health's intersection with overall well-being[121-123]. The integration of artificial intelligence and machine learning is set to revolutionize diagnostics and treatment, offering more precise and individualized interventions. For instance, AI could enhance early detection of mental health issues through analysis of behavioral patterns and biometrics. Telehealth and virtual therapy are likely to become more sophisticated, providing greater access to mental health services and reducing the stigma associated with seeking help. Additionally, there's a growing emphasis on preventative care and holistic approaches, acknowledging that mental health is deeply intertwined with physical health, lifestyle, and social factors. Personalized medicine, driven by genetic and environmental factors, could lead to tailored treatment plans that address the unique needs of each individual. Furthermore, the expansion of mental health education and awareness initiatives aims to foster a more supportive and informed society, encouraging early intervention and reducing barriers to care[124]. As research continues to unveil the

complexities of mental health, the future promises a more integrated, accessible, and empathetic approach to supporting mental well-being. The field of psychiatric genetics and epigenetics is rapidly evolving, with several promising avenues for future research. These include:

- **Integrative Approaches:** Combining genetic, epigenetic, transcriptomic, and proteomic data to gain a comprehensive understanding of the molecular mechanisms underlying mental health disorders.
- **Longitudinal Studies:** Conducting long-term studies to track epigenetic changes over time and their relationship to the onset and progression of mental health disorders.
- **Ethical Considerations:** Addressing the ethical implications of genetic and epigenetic research, particularly concerning privacy, stigma, and the potential for discrimination based on genetic or epigenetic information.

6. CONCLUSION

The study of genetics and epigenetics in mental health has the potential to revolutionize our understanding of psychiatric disorders and pave the way for more effective treatments and preventive measures. While significant progress has been made, many challenges remain, including the need for larger and more diverse study populations, the integration of multi-omics data, and the translation of research findings into clinical practice. By continuing to explore the complex interplay between genetics, epigenetics, and the environment, we can move closer to a future where mental health care is more personalized, precise, and effective.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Author has declared that no competing interests exist.

REFERENCES

1. Bakusic J, Godderis L, Claes M, Schaufeli W. Epigenetic changes in burnout and depression; 2021b.
2. Bianchi M, Renzini A, Adamo S, Moresi V. Coordinated actions of MicroRNAs with other epigenetic factors regulate skeletal muscle development and adaptation. *Int J Mol Sci.* 2017;18(4). Available:<https://doi.org/10.3390/ijms18040840>.
3. Matosin N, Cruceanu C, Binder EB. Preclinical and clinical evidence of DNA methylation changes in response to trauma and chronic stress. *Chronic Stress (Thousand Oaks).* 2017;1. Available:<https://doi.org/10.1177/2470547017710764>.
4. Miyaki K, Suzuki T, Song Y, Tsutsumi A, Kawakami N, Takahashi M, Shimazu A, Inoue A, Kurioka S, Kan C, Sasaki Y, Shimbo T. Epigenetic changes caused by occupational stress in humans revealed through noninvasive assessment of DNA methylation of the tyrosine hydroxylase gene. *J Neurol Neurol Disord.* 2015;2(2). Available:<https://doi.org/10.15744/2454-4981.2.201>.
5. Abarghouei MR, et al. A study of job stress and burnout and related factors in the hospital personnel of Iran. *Electron Physician.* 2016;8.
6. Ahola K, et al. Relationship between burnout and depressive symptoms: a study using the person-centred approach. *Burn Res.* 2014;1.
7. Alasaari JS, et al. Environmental stress affects DNA methylation of a CpG rich promoter region of serotonin transporter gene in a nurse cohort. *Plos One.* 2012;7.
8. Bakusic J, et al. Epigenetic perspective on the role of brain-derived neurotrophic factor in burnout. *Transl Psychiatry.* 2020;10.
9. Bakusic J, et al. Role of NR3C1 and SLC6A4 methylation in the HPA axis regulation in burnout. *J Affect Disord.* 2021;295.
10. Bakusic J, et al. Stress, burnout and depression: A systematic review on DNA methylation mechanisms. *J Psychosom Res.* 2017;92.
11. Bakusic J, et al. Increased methylation of NR3C1 and SLC6A4 is associated with blunted cortisol reactivity to stress in major depression. *Neurobiol Stress.* 2020;13.
12. Bear MF, Connors BW, Paradiso MA. *Neuroscience : Exploring the brain.* Jones and Bartlett Publishers, Inc; 2015.
13. Blom V, et al. Genetic susceptibility to burnout in a Swedish twin cohort. *Eur J Epidemiol.* 2012;27.
14. Butler S. The impact of advanced capitalism on well-being: An evidence-informed model. *Human Arenas.* 2019;2.
15. Cao Z, et al. Serotonin transporter gene (5-HTT) rs6354 polymorphism, job-related stress, and their interaction in burnout in healthcare workers in a Chinese hospital. *Psychopharmacology.* 2018;235.
16. Chirico F. Job stress models for predicting burnout syndrome: A review. *Ann Ist Super Sanita.* 2016;52.
17. Chou, L.P., C.Y. Li, and S.C. Hu, Job stress and burnout in hospital employees: Comparisons of different medical professions in a regional hospital in Taiwan. *BMJ Open,* 2014. 4.
18. Choudhury SR, et al. CRISPR-dCas9 mediated TET1 targeting for selective DNA demethylation at BRCA1 promoter. *Oncotarget.* 2016;7.
19. Chrousos GP, Gold PW. The concepts of stress and stress system disorders. Overview of physical and behavioral homeostasis. *JAMA.* 1992;267.
20. Deligkaris P, et al. Job burnout and cognitive functioning: A systematic review. *Work Stress.* 2014;28.
21. Duman RS. Depression: A case of neuronal life and death? *Biol Psychiatry.* 2004;56.
22. Duval F, et al. Interaction between the serotonergic system and HPA and HPT axes in patients with major depression: Implications for pathogenesis of suicidal behavior. *Dialogues Clin Neurosci.* 2002;4.
23. Egan MF, et al. The BDNF val66met polymorphism affects activity-dependent secretion of BDNF and human memory and hippocampal function. *Cell.* 2003;112.
24. Fabbri, M., et al., MicroRNA-29 family reverts aberrant methylation in lung cancer by targeting DNA methyltransferases 3A and 3B. *Proc Natl Acad Sci U S A,* 2007. 104.

25. Fraser, R. and C.J. Lin, Epigenetic reprogramming of the zygote in mice and men: on your marks, get set, go! *Reproduction*, 2016. 152.
26. Freni-Sterrantino A, et al. Work-related stress and well-being in association with epigenetic age acceleration: A Northern Finland birth cohort 1966 study. *Aging (Albany NY)*. 2022;14.
27. Godderis L, Boone A, Bakusic J. COVID-19: A new work-related disease threatening healthcare workers. *Occup Med (Lond)*. 2020;70.
28. Goldstein DS. Adrenal responses to stress. *Cell Mol Neurobiol*. 2010;30.
29. Han L, et al. DNA methylation regulates MicroRNA expression. *Cancer Biol Ther*. 2007;6.
30. He SC, et al. Interactive effects of corticotropin-releasing hormone receptor 1 gene and work stress on burnout in medical professionals in a Chinese Han population. *J Affect Disord*. 2019; 252.
31. He SC, et al. Interaction between job stress, serum BDNF level and the BDNF rs2049046 polymorphism in job burnout. *J Affect Disord*. 2020;266.
32. Holoch D, Moazed D. RNA-mediated epigenetic regulation of gene expression. *Nat Rev Genet*. 2015;16.
33. Holtzheimer PE, Nemeroff CB. Future prospects in depression research. *Dialogues Clin Neurosci*. 2006;8.
34. Jablonka E, Lamb MJ. The changing concept of epigenetics. *Ann N Y Acad Sci*. 2002;981.
35. Janusek LW, Tell D, Mathews HL. Epigenetic perpetuation of the impact of early life stress on behavior. *Curr Opin Behav Sci*. 2019;28.
36. Jia H, et al. The relationship between job stress and job burnout moderated by BDNF rs6265 polymorphism. *Psychopharmacology*. 2021;238.
37. Karsli-Ceppioglu S. Epigenetic mechanisms in psychiatric diseases and epigenetic therapy. *Drug Dev Res*. 2016;77.
38. Kerr JL, et al. The effects of acute work stress and appraisal on psychobiological stress responses in a group office environment. *Psychoneuroendocrinology*. 2020;121.
39. Kohli RM, Zhang Y. TET enzymes, TDG and the dynamics of DNA demethylation. *Nature*. 2013;502.
40. Kouzarides, T., Chromatin modifications and their function. *Cell*. 2007;128.
41. Kuehner JN, et al. Epigenetic regulations in neuropsychiatric disorders. *Front Genet*. 2019;10.
42. Kular L, Kular S. Epigenetics applied to psychiatry: Clinical opportunities and future challenges. *Psychiatry Clin Neurosci*. 2018;72.
43. Lee RS, Sawa A. Environmental stressors and epigenetic control of the hypothalamic-pituitary-adrenal axis. *Neuroendocrinology*. 2014;100.
44. Li M, et al. What do DNA methylation studies tell us about depression? A systematic review. *Transl Psychiatry*. 2019;9.
45. Li Y, et al. Interaction between the BDNF gene rs16917237 polymorphism and job stress on job burnout of Chinese university teachers. *J Affect Disord*. 2022;309.
46. Liu XS, et al. Editing DNA methylation in the mammalian genome. *Cell*. 2016;167.
47. Lu CT, et al. Current approaches to enhance CNS delivery of drugs across the brain barriers. *Int J Nanomedicine*. 2014;9.
48. Mahgoub M, Monteggia LM. Epigenetics and psychiatry. *Neurotherapeutics*. 2013;10.
49. McEwen BS. Protective and damaging effects of stress mediators. *N Engl J Med*. 1998;338.
50. McEwen BS, Stellar E. Stress and the individual: Mechanisms leading to disease. *Arch Intern Med*. 1993;153.
51. Middeldorp CM, Cath DC, Boomsma DI. A twin-family study of the association between employment, burnout and anxious depression. *J Affect Disord*. 2006;90.
52. Middeldorp CM, et al. Familial clustering in burnout: A twin-family study. *Psychol Med*. 2005;35.
53. Moore SR, Kobor MS. Variability in DNA methylation at the serotonin transporter gene promoter: epigenetic mechanism or cell-type artifact? *Mol Psychiatry*. 2020;25.
54. Oakley RH, Cidlowski JA. The biology of the glucocorticoid receptor: New signaling mechanisms in health and disease. *J Allergy Clin Immunol*. 2013;132.
55. Peterson CL, Laniel MA. Histones and histone modifications. *Curr Biol*. 2004;14.
56. Petitpierre M, Stenz L, Paoloni-Giacobino A. Epigenomic changes after acupuncture treatment in patients suffering from burnout. *Complement Med Res*. 2022;29.

57. Pruunsild P, et al. Identification of cis-elements and transcription factors regulating neuronal activity-dependent transcription of human BDNF gene. *J Neurosci.* 2011;31.
58. Ratman D, et al. How glucocorticoid receptors modulate the activity of other transcription factors: a scope beyond tethering. *Mol Cell Endocrinol.* 2013;380.
59. Roberts S, et al. DNA methylation of FKBP5 and response to exposure-based psychological therapy. *Am J Med Genet B Neuropsychiatr Genet.* 2019;180.
60. Russell PJ. *iGenetics.* Pearson; 2014.
61. Saaltink DJ, Vreugdenhil E. Stress, glucocorticoid receptors, and adult neurogenesis: A balance between excitation and inhibition? *Cell Mol Life Sci.* 2014;71.
62. Schaaf MJ, Kloet ER, Vreugdenhil E. Corticosterone effects on BDNF expression in the hippocampus. Implications for memory formation. *Stress.* 2000;3.
63. Schneiderman N, Ironson G, Siegel SD. Stress and health: Psychological, behavioral, and biological determinants. *Annu Rev Clin Psychol.* 2005;1.
64. Smith SM, Vale WW. The role of the hypothalamic-pituitary-adrenal axis in neuroendocrine responses to stress. *Dialogues Clin Neurosci.* 2006;8.
65. Smith ZD, Meissner A. DNA methylation: Roles in mammalian development. *Nat Rev Genet.* 2013;14.
66. Song Y, et al. Altered DNA methylation status of human brain derived neurotrophin factor gene could be useful as biomarker of depression. *Am J Med Genet B Neuropsychiatr Genet.* 2014;165B.
67. Thomas M, et al. Increased BDNF methylation in saliva, but not blood, of patients with borderline personality disorder. *Clin Epigenetics.* 2018;10.
68. Vinkers CH, et al. Successful treatment of post-traumatic stress disorder reverses DNA methylation marks. *Mol Psychiatry.* 2021;26.
69. Vojta A, et al. Repurposing the CRISPR-Cas9 system for targeted DNA methylation. *Nucleic Acids Res.* 2016;44.
70. Weber A, Jaekel-Reinhard A. Burnout syndrome: A disease of modern societies? *Occup Med (Lond).* 2000;50.
71. Wei H, et al. The prevalence of nurse burnout and its association with telomere length pre and during the COVID-19 pandemic. *Plos One.* 2022;17.
72. Winter J, Jurek B. The interplay between oxytocin and the CRF system: Regulation of the stress response. *Cell Tissue Res.* 2019;375.
73. Yehuda R, et al. Lower methylation of glucocorticoid receptor gene promoter 1F in peripheral blood of veterans with posttraumatic stress disorder. *Biol Psychiatry.* 2015;77.
74. Quednow BB, Ejebe K, Wagner M, Giakoumaki SG, Bitsios P, Kumari V, et al. Meta-analysis on the association between genetic polymorphisms and prepulse inhibition of the acoustic startle response. *Schizophr Res.* 2017. Available:<https://doi.org/10.1016/j.schres.2017.12.011>.
75. Dobbyn A, Huckins LM, Boocock J, Sloofman LG, Glicksberg BS, Giambartolomei C, et al. Co-localization of Conditional eQTL and GWAS Signatures in Schizophrenia. *bioRxiv.* 2017. Available:<https://doi.org/10.1101/129429>.
76. Giambartolomei C, Zhenli Liu J, Zhang W, Hauberg M, Shi H, Boocock J, et al. A Bayesian framework for multiple trait Colocalization from summary association statistics. *Cold Spring Harbor. Laboratory.* 2017.
77. Mancuso N, Shi H, Goddard P, Kichaev G, Gusev A, Pasaniuc B. Integrating gene expression with summary association statistics to identify susceptibility genes for 30 complex traits. *Cold Spring Harbor Laboratory.* 2016.
78. Huckins LM, Dobbyn A, Ruderfer D, Hoffman G, Wang W, Pardinas AF, et al. Gene expression imputation across multiple brain regions reveals schizophrenia risk throughout development. *bioRxiv.* 2017. Available:<https://doi.org/10.1101/222596>.
79. Gusev A, Mancuso N, Finucane HK, Reshef Y, Song L, Safi A, et al. Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. *Cold Spring Harbor. Laboratory.* 2016.
80. Barbeira AN, Dickinson SP, Torres JM, Bonazzola R, Zheng J, Torstenson ES, et al. MetaXcan: Summary statistics based gene-level association method infers accurate PrediXcan results. *bioRxiv.* 2017. Available:<https://doi.org/10.1101/045260>

81. Huckins LM, Breen MS, Girdhar K, Van Rooij SJH. CommonMind Consortium et al. Genetically predicted gene expression in the brain and peripheral tissues associated with PTSD. In Preparation.
82. Cortes A, Dendrou C, Motyer A, Jostins L, Vukcevic D, Dilthey A et al. Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Cold Spring Harbor Laboratory; 2017.
83. Akashi M, Takumi T. The orphan nuclear receptor RORalpha regulates circadian transcription of the mammalian core-clock Bmal1. *Nat Struct Mol Biol.* 2005;12.
84. Albert FW, Kruglyak L. The role of regulatory variation in complex traits and disease. *Nat Rev Genet.* 2015;16.
85. Almli LM, et al. A genome-wide identified risk variant for PTSD is a methylation quantitative trait locus and confers decreased cortical activation to fearful faces. *Am J Med Genet B Neuropsychiatr Genet.* 2015;168B.
86. Ashley-Koch AE, et al., Genome-wide association study of posttraumatic stress disorder in a cohort of Iraq-Afghanistan era veterans. *J Affect Disord.* 2015;184.
87. Bell CG, et al. Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *Plos One.* 2010;5.
88. Bharadwaj RA, et al. Genetic risk mechanisms of posttraumatic stress disorder in the human brain. *J Neurosci Res.* 2018;96.
89. Binder EB. The role of FKBP5, a co-chaperone of the glucocorticoid receptor in the pathogenesis and therapy of affective and anxiety disorders. *Psychoneuroendocrinology.* 2009;34.
90. Binder EB, et al. Association of FKBP5 polymorphisms and childhood abuse with risk of posttraumatic stress disorder symptoms in adults. *JAMA.* 2008;299.
91. Boland EM, Ross RJ. Recent advances in the study of sleep in the anxiety disorders, obsessive-compulsive disorder, and posttraumatic stress disorder. *Psychiatr Clin North Am.* 2015;38.
92. Breslau N, et al. Trauma and posttraumatic stress disorder in the community: The 1996 Detroit area survey of trauma. *Arch Gen Psychiatry.* 1998;55.
93. Bonanno GA. Loss, trauma, and human resilience: Have we underestimated the human capacity to thrive after extremely aversive events? *Am Psychol.* 2004; 59.
94. Boscarino JA. Posttraumatic stress disorder and physical illness: Results from clinical and epidemiologic studies. *Ann N Y Acad Sci.* 2004;1032.
95. Breen MS, et al. Gene networks specific for innate immunity define post-traumatic stress disorder. *Mol Psychiatry.* 2015; 20.
96. Burchard EG. Medical research: Missing patients. *Nature.* 2014;513.
97. Carroll RJ, Bastarache L, Denny JC. R PheWAS: Data analysis and plotting tools for phenome-wide association studies in the R environment. *Bioinformatics.* 2014;30.
98. Charney AW, et al. Evidence for genetic heterogeneity between clinical subtypes of bipolar disorder. *Transl Psychiatry.* 2017;7.
99. Consortium GT. Human genomics. The genotype-tissue expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science.* 2015;348.
100. Cookson W, et al. Mapping complex disease traits with global gene expression. *Nat Rev Genet.* 2009;10.
101. Cosgrove VE, Suppes T. Informing DSM-5: biological boundaries between bipolar I disorder, schizoaffective disorder, and schizophrenia. *BMC Med.* 2013;11.
102. Daskalakis NP, et al. Expression profiling associates blood and brain glucocorticoid receptor signaling with trauma-related individual differences in both sexes. *Proc Natl Acad Sci U S A.* 2014;111.
103. Daskalakis NP, et al. New translational perspectives for blood-based biomarkers of PTSD: From glucocorticoid to immune mediators of stress susceptibility. *Exp Neurol.* 2016;284.
104. Daskalakis NP, Lehrner A, Yehuda R. Endocrine aspects of post-traumatic stress disorder and implications for diagnosis and treatment. *Endocrinol Metab Clin N Am.* 2013;42.
105. Denny JC, et al. Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. *Nat Biotechnol.* 2013;31.
106. Denny JC, et al. PheWAS: Demonstrating the feasibility of a phenome-wide scan to discover gene-disease associations. *Bioinformatics.* 2010;26.

107. Dias BG, et al. Epigenetic mechanisms underlying learning and the inheritance of learned behaviors. Trends Neurosci. 2015;38.
108. Edmondson D, Kanel R. Post-traumatic stress disorder and cardiovascular disease. Lancet Psychiat. 2017;4.
109. Edmondson D, et al. Posttraumatic stress disorder and risk for coronary heart disease: A meta-analytic review. Am Heart J. 2013;166.
110. Eraly SA, et al. Assessment of plasma C-reactive protein as a biomarker of posttraumatic stress disorder risk. JAMA Psychiatry. 2014;71.
111. Flint J, Munafò MR. The endophenotype concept in psychiatric genetics. Psychol Med. 2007;37.
112. Fromer M, et al. Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nat Neurosci. 2016;19.
113. Gamazon ER, et al. A gene-based association method for mapping traits using reference transcriptome data. Nat Genet. 2015;47.
114. Jones MJ, Goodman SJ, Kobor MS. DNA methylation and healthy human aging. Aging Cell. 2015;14.
115. Klimek V, et al. Dopaminergic abnormalities in amygdaloid nuclei in major depression: A postmortem study. Biol Psychiatry. 2002;52.
116. Larsen NY, et al. Layer III pyramidal cells in the prefrontal cortex reveal morphological changes in subjects with depression, schizophrenia, and suicide. Transl Psychiatry. 2022;12.
117. Lessel D, Kubisch C. Hereditary syndromes with signs of premature aging. Dtsch Arztebl Int. 2019;116.
118. Levine ME, et al. An epigenetic biomarker of aging for lifespan and healthspan. Aging (Albany NY). 2018;10.
119. Li Z, et al. Epigenetic age analysis of brain in major depressive disorder. Psychiatry Res. 2018;269.
120. Lipps HJ, Postberg J, Jackson DA. Epigenetics, disease and behaviour. London: Portland Press; 2010.
121. Liu C, et al. DNA Methylation and psychiatric disorders. Prog Mol Biol Transl Sci. 2018;157.
122. Lopez-Otin C, et al. The hallmarks of aging. Cell. 2013;153.
123. Ly K, et al. Telomere length in early childhood is associated with sex and ethnicity. Sci Rep. 2019;9.
124. McGowan PO, Szyf M. Environmental epigenomics: Understanding the effects of parental care on the epigenome. Essays Biochem. 2010;48.

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