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Gene–Environment Interplay in Psychiatric Risk as a Framework for Clinical Psychology

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ABSTRACT

Psychiatric disorders are complex conditions influenced by both genetic and environmental factors. Gene–environment interplay—including gene–environment correlations (rGE) and gene–environment interactions (G×E)—offers a framework for understanding individual variability in susceptibility, resilience, and risk. rGE processes highlight how genotypes influence exposure to environmental conditions, whereas G×E emphasizes how environmental contexts shape the expression of genetic predispositions. Transactional and dynamic models further capture how genetic susceptibility and environmental selection interact iteratively across development. Integrating genomic, environmental, and longitudinal data enhances risk prediction and informs precision approaches in clinical assessment and intervention. This framework underscores the potential of gene–environment research to refine preventive and therapeutic strategies in psychiatry.

Keywords: *gene–environment interplay, psychiatric risk, gene–environment correlation, gene–environment interaction, differential susceptibility, polygenic risk, longitudinal studies, clinical psychology, preventive intervention, precision psychiatry.*

INTRODUCTION

Psychiatric disorders are a leading cause of disease burden worldwide. Understanding risk for these complex conditions is a national and global health priority. Psychiatric risk modelling can illuminate the aetiology, trajectories, manifestations, and interventions for these disorders. Recently, gene–environment interplay has emerged as a promising area of psychiatric risk research. Over a century of empirical work highlights widely studied mechanisms, conceptual frameworks, and predictive factors linking gene–environment interplay to psychiatric risk. These insights greatly add to the understanding of risk modelling. The current framework distills these insights into key principles relevant to clinical psychology. The first section details the theoretical foundations underpinning gene–environment interplay. Subsequently, the

methodological approaches employed to connect gene-environment interplay with psychiatric risk are summarized. Next, the evidence documenting connections between gene-environment interplay and psychiatric risk across a range of conditions is presented. The final section outlines the clinical implications of these insights for assessment and intervention, highlighting the potential to refine precision medicine and enhance preventive and therapeutic approaches.

Psychiatric disorders are among the most disabling conditions worldwide, accounting for approximately 60 million years of life lost and disability adjusted life years (DALY). Understanding risk for these complex conditions is nationally and globally prioritized. Modelling risk can illuminate the aetiology, trajectories, manifestations, and interventions of many psychiatric disorders. Gene-environment interplay has emerged as a promising area of enquiry when studying this topic. The last century of empirical work has identified widely studied mechanisms, conceptual frameworks, and predictive factors connecting gene-environment interplay to psychiatric risk (Belsky et al., 2009). These capabilities greatly enrich the understanding of risk modelling and the systematic exploration of candidate avenues. A framework synthesising these insights into core principles relevant to clinical psychology was thus formulated. Developed by the Canadian Psychological Association's International Expert Task Force on the Future of Professional Practice, this framework was conceived, refined, and mapped through a collaborative process involving experts from diverse professional and disciplinary fields.

2. Theoretical Foundations of Gene–Environment Interplay

Recent advances in molecular genetics and the emergence of a psychobiological model of developmental psychopathology have provided a robust framework for understanding gene-environment interplay in psychiatric risk. Gene-environment interplay refers collectively to gene-environment correlations (rGE) and gene-environment interactions (G×E), both of which impact how the environment shapes individual development (Belsky et al., 2009). Transdisciplinary research has documented extensive evidence linking gene-environment interplay to risk for depression and anxiety disorders, psychotic disorders, and neurodevelopmental and behavioral conditions.

Some individuals are more sensitive to both positive and negative environmental influences, thereby exhibiting greater plasticity in their development and behavior. Nevertheless, because the pathways connecting genetic and environmental influences to psychopathology are still not well understood, the emphasis is on differential susceptibility rather than on direct effects of genes or environment on disorder. Likewise, the term “interactive” is preferred to “modifying” to underscore the idea that genetic and environmental influences come into play in concert rather than sequentially [table 1].

Table 1: Key Components of Gene-Environment Interplay in Psychiatric Risk

Domain	Key Concepts	Mechanisms / Examples	Implications for Psychiatric Risk
Gene–Environment Correlation (rGE)	Genetic influence on environmental exposure	- Passive: inherited genes + parental environment- Evocative: genetically influenced traits evoke environmental responses- Active: individuals select environments aligned with genetic tendencies (e.g., musical interests)	Shapes differential exposure to risk/protective factors; contributes to trait development and susceptibility
Gene–Environment Interaction (G×E)	Genetic modulation of environmental effects	Certain traits expressed only under specific environmental conditions; e.g., serotonin transporter variation × early-life adversity → depression risk	Explains why genetic risk manifests differently depending on environment; highlights differential susceptibility
Transactional / Dynamic Models	Continuous feedback between genes, environment, and behavior	- MAOA × childhood adversity → antisocial behavior- Differential susceptibility: ‘for better or worse’ response to environments- Probabilistic epigenesis	Supports understanding of plasticity, lifelong gene-environment interplay, and individual variation in psychiatric outcomes
Genetic Methods	GWAS, polygenic risk scores	Identify loci associated with depression, schizophrenia, psychosis; interact with environmental exposures	Refines risk assessment; informs preventive and therapeutic strategies
Environmental Assessment	Evaluation of exposures and their effects	Measures differential exposure vs differential sensitivity; accounts for moderating effects	Differentiates diathesis–stress vs differential susceptibility; informs context-specific interventions
Longitudinal / Causal Approaches	Temporal and causal inference methods	Longitudinal studies, natural experiments, RCTs where possible	Helps establish directionality and causality; reduces bias in environmental and gene-environment analyses

2.1. Gene–Environment Correlation

A central tenet of gene–environment interplay posits that genetic predispositions can shape an individual’s susceptibility to environmental influence (Belsky et al., 2009). Accordingly, the term ‘gene–environment correlation’ describes processes through which an individual’s genotypes influence the exposure and sensitivity to specific environmental conditions. These processes can be classified into three broad types: passive, evocative, and active. In passive gene–environment correlation, children inherit both genetic and environmental parental influences, such as parentally transmitted genotypes simultaneously affecting cognitive or temperament development as well as the parental environment. Evocative gene–environment correlation occurs through the expression of genetically influenced characteristics (e.g., temperament, appearance) that evoke specific responses from the environment (e.g., parenting style). Finally, active gene–environment correlation describes the tendency of individuals to select or create environments related to

their genetically influenced characteristics. An interest in music, for example, might lead a person to pursue specific schools, friends, or events that develop musical abilities further (A. E. Vinkhuyzen & R. Wray, 2014)

2.2. Gene–Environment Interaction

Gene \times environment ($G \times E$) interaction constitutes an important category of gene–environment interplay. An individual's genetic constitution interacts with his or her environment in such a way that certain traits or behaviors are expressed only in the context of a particular environment or set of environmental conditions or experiences. Activity of genes can be positively and negatively modulated by the environments an individual encounters throughout life, which in turn influences behavioral development and expression (Belsky et al., 2009).

The $G \times E$ interaction framework considers not only the effects of genetic predispositions and pre-environmental biological makeups on individual responses or propensities to external stressors but also the influences others have on specific individual–environment transactions, and the multitude of effects one biosocial distributed exposure might have on another influential biological event, become plastic throughout the lifespan, and continue to vary over time. The framework encompasses independent $G \times E$ interactions, $G \times E$ cascades in which an initial environmental experience alters the expression of a gene leading to such further psychosocial change that the pre-environmental disposition loses its relevance, and $G \times E$ mediations a pre-existing genomic property determines the predisposition to experience certain environmental events early in life thus directly following up on Belsky et al. An extensive $G \times E$ interaction that is fully consistent with the aforementioned guidelines and requirements is the interaction of variation in a pleiotropic gene for the serotonin transporter and early life adversity in determining depression and related problems (A. E. Vinkhuyzen & R. Wray, 2014) [table 2].

Table 2: Conceptual Framework for Clinical Application

Framework Component	Clinical Relevance	Mechanistic Insights	Applications
Differential Susceptibility	Recognizes variability in sensitivity to positive/negative environments	High plasticity \rightarrow stronger response to interventions	Tailored prevention and treatment based on individual susceptibility profiles
rGE Awareness	Genetic predispositions shape environmental exposure	Guides understanding of risk accumulation and protective contexts	Early identification of high-risk environments; preventive environmental modification
$G \times E$ Modeling	Interaction between genotype and environment	Explains heterogeneity in psychiatric disorder expression	Precision medicine: selecting interventions suited to patient-specific gene-environment profiles
Transactional / Dynamic Perspective	Genes and environment continually influence behavior	Accounts for cascading effects of early experiences on later outcomes	Long-term monitoring and adaptive interventions across lifespan
Integration of Genetic & Environmental Data	Combines polygenic risk scores with environmental exposure	Enhances predictive accuracy for psychiatric outcomes	Supports clinical risk stratification, early intervention, and personalized therapy

2.3. Transactional and Dynamic Models

Genes influence behavior not only through direct effects but also via gene–environment interactions. Genetic vulnerabilities may moderate environmental effects rather than acting directly; for instance, the MAOA gene interacts with childhood adversity in identifying risk for antisocial behavior. The diathesis–stress model describes vulnerability as an elevated risk linked to adversity, but this interpretation may distort understanding of gene–environment interplay. An alternative perspective emphasizes variation in susceptibility to environmental influences, describing differential response to circumstances in a ‘for better and for worse’ manner. The differential-susceptibility model underscores individual differences in sensitivity that engage plasticity and responsiveness to both positive and negative conditions.

Significant evidence demonstrates gene–environment interaction and differential susceptibility across diverse behavioral dimensions and psychiatric outcomes; major depressive disorder exemplifies sensitivity to both positive and adverse contexts (Belsky et al., 2009). Transactions between genetic predisposition and environmental choice constitute an equally important yet less explored dimension of gene–environment interplay, with the potential to enrich conceptualization of gene–environment interactions and advance understanding of their role in psychiatric risk (P. Jiménez et al., 2018). As under the differential-susceptibility model, probabilistic epigenesis recognizes gene–environment interplay in the emergence of behavior. Moreover, the transactional process through which genetic risk shapes environmental selection and choice further elucidates gene–environment interplay.

Expressive, receptive, and relational capacities critically influence the selection and construction of environments and may moderate their impact; accordingly, genes contribute not only to selective pressures and the associational structure of experience but also to the functional interpretation of selected experiences.

3. Methodological Approaches in Psychiatric Risk Research

Genome-wide association studies (GWAS) have identified over a hundred loci associated with psychiatric disorders, yet this genetic risk is only informative when integrated with environmental data (A. E. Vinkhuyzen & R. Wray, 2014). Because of overlapping risk pathways, convergence on neurobiological targets, and clinical comorbidity, disorders such as major depression and psychosis represent an informative dimension on which to probe gene–environment interplay (Meller et al., 2020). GWAS-informed genetic scores for major depression and polygenic risk scores for schizophrenia robustly interact with environmental exposures to predict clinically relevant measures of severity for subclinical variants of these conditions. Such variants comprise stepping-stones on the path to full-blown syndromes and entail distinct but overlapping risk profiles (Akhmedova N., et al).

3.1. Genetic Methods

Gene–environment interplay plays an important role in the aetiology of psychiatric disorders, with the potential to refine risk assessment and guide preventive intervention. Genetic methods are a core component of this research area and involve either gene–environment correlation (rGE) or gene–environment interaction (G×E). The former refers to a systematic association between an individual's genetic make-up and their exposure to environmental risk factors, which can result in biased estimates of the effect of a given environment on disorder liability. The latter concerns the conditional influence of genetic liability on the expression of a given environmental risk, offering a nuanced understanding of the interplay between nature and nurture. Three novel approaches to the study of G×E in psychiatric disorders now complement established methods for the investigation of rGE (A. E. Vinkhuyzen & R. Wray, 2014).

3.2. Environmental Assessment

Environmental assessment examines the role of environmental exposures in psychiatric disorders and explores whether the influence of such exposures results from main effects or from gene–environment interaction (Belsky et al., 2009). Investigations addressed whether individual differences in psychological functioning entail differentiated exposure to adverse influences, or an alteration in the effect of the same environmental dose on disorder risk (Ruzibaeva N., et al). The classic diathesis–stress model assumes

genetic vulnerability elevates risk only under unfavourable conditions, implying that individuals no-prone to psychiatric disorder remain unperturbed by adversity. An alternative, differential susceptibility model postulates that some individuals manifest heightened sensitivity to both negative and positive environments, remaining susceptible to psychiatric disorder even when exposure levels to risk remain low (A. E. Vinkhuyzen & R. Wray, 2014).

3.3. Longitudinal Designs and Causal Inference

Longitudinal studies are often regarded as essential for examining the determinants of psychopathology, as they help determine the directionality of exposure (Thapar & Rutter, 2019). Nevertheless, correlation does not imply causation. Observational studies typically attempt to answer causal questions by relying on the premise that correlation equals causation. This assumption is flawed, particularly with respect to environmental exposures, largely due to the involvement of common causes or time-invariant disturbance variables that can simultaneously affect exposure and outcome. Consequently, longitudinal studies run the risk of circumventing, rather than addressing, bias and may thus inadvertently dilute the value of the data collected. Randomized controlled trials (RCTs) are considered the gold standard for causal association; however, many environmental exposures cannot be or are not ethically justified to be manipulated through RCTs. Natural experiments exploit settings in which certain exposures are separated from other known or unknown confounding variables, thus aiding in causal inference without researcher manipulation.

4. Evidence Linking Gene–Environment Interplay to Psychiatric Risk

Gene–environment interplay helps explain why psychiatric disorders develop in some individuals and not others despite similar exposures. Clinical findings suggest that gene–environment correlation, gene–environment interaction, and dynamic effects are key to understanding environmental risk. Insight into gene–environment interplay assists in risk stratification, precision medicine, preventive and early intervention strategies, identification of therapeutically modifiable targets, and enhancement of resilience (Belsky et al., 2009).

4.1. Depression and Anxiety Disorders

Depression and anxiety disorders represent the most widely studied clinical conditions with gene–environment interplay. Gene–environment interaction, specifically, has emerged as a prominent explanation for why stressful experiences, especially in childhood, are associated with elevated risk. The interaction of the serotonin transporter gene (5-HTTLPR) with childhood adversity in predicting depression illustrates the concept. One meta-analysis of 54 studies reported that individuals with one or two short-allele copies of 5-HTTLPR are at increased risk for depression following childhood abuse or neglect. An alternative meta-analysis including 24 studies found no gene–environment interaction, yet the environmental exposure remained a strong predictor of depression. Other candidate genetic variants also appear to interact with environmental exposures in predicting depression, but less consistently.

4.2. Psychotic Disorders

Gene–environment interplay likewise represents a substantial mechanism for the development of psychotic disorders. Early family environment moderates the association between polygenic risk score and adult psychosis, and a gene–environment interaction involving the COMT polymorphism and stressful life events defines a population at risk for psychotic delusions. Gene–environment interaction explains 9% of the variance in this risk, and another candidate gene involved in oligodendrocyte differentiation modulates the relationship between childhood maltreatment and adult psychotic experiences.

4.3. Neurodevelopmental and Behavioral Conditions

Gene–environment interaction is also pertinent to neurodevelopmental and behavioral conditions. At least 60 gene variants in pathways related to neural development and function interact with prenatal exposure to smoking in predicting childhood attention-deficit/hyperactivity disorder (A. E. Vinkhuyzen & R. Wray,

2014). Likewise, polygenic risk associated with autism spectrum disorder and attention-deficit/hyperactivity disorder interacts with paternal age in the transmission of de novo mutations.

4.1. Depression and Anxiety Disorders

Gene–environment interplay influences the development of anxiety and depressive symptoms across childhood and adolescence. Genetic variants explain approximately 10–15% of symptom severity variance, with multiple genome-wide association studies identifying risk single-nucleotide polymorphisms (SNPs) associated with these phenotypes. Many of these SNPs reside in non-coding regions of the genome and appear to regulate gene expression, particularly in the brain. Genome-wide heritability estimates for depression are between 31% and 42%, both in the general population and in clinically ascertained samples. Genetic correlations between panic disorder, major depressive disorder (MDD), and neuroticism have been observed, yet identifying specific genes involved in adolescent depression and anxiety remains challenging.

Environmental factors from personal, neighbourhood, and regional levels influence anxiety and depression. These factors shape both exposure and vulnerability to adverse events, impact normative development, and interact with family and individual characteristics. A cross-continental analysis based on 171,557 children and adolescents pinpointed 20 risk SNPs linked to anxiety, depression, or both, illustrating the importance of both genetic and environmental influences on these widespread disorders (Thapaliya et al., 2024).

Gene–environment interactions determine risk for stress- and anxiety-related conditions. Research on individual genes, including the serotonin transporter, brain-derived neurotrophic factor, monoamine oxidase A, catechol-O-methyltransferase, and arginine vasopressin, demonstrates that some genotypes increase susceptibility following stressful exposures. Interactions are also evident at the polygenic level. Common variants in the serotonin transporter loci modulate depression risk in genetically vulnerable individuals exposed to stressful life events during childhood. Exposure to stressful experiences during adolescence alters brain function and behaviour, enhancing susceptibility to anxiety and depression. Experience-dependent maturation of emotional systems during this period positions genetic factors as crucial for determining risk (Gonda et al., 2018).

4.2. Psychotic Disorders

Schizophrenia is a chronic psychiatric disorder affecting nearly 20 million people worldwide, typically manifesting in early adulthood. The positive (delusions, hallucinations), negative (emotional flatness, poverty of speech), and cognitive (attention, working memory, executive function impairments) symptoms often severely compromise social and occupational functioning. Concurrent depression, substance use, and elevated suicide risk occur in about 25% of patients. Schizophrenia development results from a complex interplay of genetic and environmental factors. Heritability is approximately 80%, with contributions from rare damaging variants and common variants exerting small to moderate influence. Genomic variation interacts with perinatal, adolescent, and adult exogenous factors—many operating additively—to drive risk. Evidence now points to interconnected gene \times environment processes governing transmission from multifactorial liability to the disorder. Understanding these interactions is critical for identifying at-risk individuals and developing personalized prevention and treatment strategies.

Gene \times environment interactions have not been reliably established concerning the etiology of psychotic disorders. Associations have been observed between polygenic risk scores for schizophrenia and early-life adversities, migration status, and urban upbringing—additive effects further supporting a continuum between psychotic experiences and disease liability. Analogous links exist for attention-deficit/hyperactivity disorder, autism, and other neurodevelopmental conditions. These findings challenge the traditional nature-versus-nurture framework and underscore the need for a broader definition of gene–environment interplay that encompasses correlated exposure and polygenic influences. (Pignon et al., 2022)

4.3. Neurodevelopmental and Behavioral Conditions

Epigenetic mechanisms, modulating the interplay between genes and environment, have garnered increased attention in the context of diverse neurodevelopmental and behavioral conditions. Evidence suggests that alterations in the epigenome are related to stress regulation and the emergence of psychopathology (Murgatroyd & Spengler, 2011). Genes influencing neurodevelopmental outcomes and their vulnerability to psychosocial adversities can directly shape behaviour; for instance, the relationship between methylation of the Reelin gene and the psychopathological trajectory of individuals prenatally exposed to opiates. Gene–environment interplay, in conjunction with an enriched environment, has been associated with altered hypothalamo-pituitary-adrenal axis development and protects against alcohol exposure in utero.

Gene–environment mechanisms are thought to participate in the onset of other disorders, including Attention Deficit Hyperactivity Disorder; links have been reported between Dopamine Transporter gene polymorphisms and parenting style (Belsky et al., 2009). Gene–environment studies of Autism Spectrum Disorders mostly consider direct gene–environment interactions or the impact of rare variants.

5. Clinical Implications for Assessment and Intervention

Phenotypic expression emerges from an interaction of environmental, biological, and psychological factors. Interaction between genetic factors and the environment stress the multifaceted nature of psychiatric risk. At the level of gene-environment correlation (r_{GE}), the individual's genetic make-up influences the environment to which they are exposed. At the level of gene-environment interaction ($G \times E$), environmental exposures differentially affect individuals on the basis of their genetically influenced characteristics (Belsky et al., 2009). A growing body of research links gene-environment interplay to the risk of depression and anxiety disorders, psychotic disorders, and neurodevelopmental and behavioural conditions (A. E. Vinkhuyzen & R. Wray, 2014). Identifying psychiatric trajectories through the lens of gene-environment interplay can enhance clinical utility by improving risk stratification, guiding precision medicine, informing the design of preventive and early intervention strategies, and spurring research on the efficacy of psychotherapeutic approaches targeting modifiable environmental factors (Fox & G Beevers, 2016).

5.1. Risk Stratification and Precision Medicine

Increased understanding of gene–environment interplay supports stratified approaches in psychiatric risk assessment and intervention. The complexity of psychiatric disorders arises from their polygenicity, with an average of 100 risk variants per disorder, together with extensive pleiotropy across disorders. The cumulative effect of these risk variants is quantified using a polygenic risk score (PRS). Elevated PRS associates with greater likelihood of developing a disorder, as well as younger age-at-onset and more severe courses, and thus assists in risk prediction (Rees & J. Owen, 2020). Gene–environment interplay shapes psychiatric risk throughout the life course, necessitating longitudinal designs for comprehensive analysis of critical periods. Even so, genetic influences remain substantial throughout life; for example, 70% of genetic influences on schizophrenia risk persist even after stress-inducing events. Such insights align with precision medicine by informing timely intervention for individuals at risk or suspected to already experience early symptoms or atypical trajectories.

5.2. Preventive and Early Intervention Strategies

Psychiatric disorders represent a significant and diverse social problem. As such, many preventive and early-intervention strategies for individuals showing early signs of mental health deterioration—such as those exhibiting risk symptoms and/or traits—are emerging (G O'Connor & E Spagnola, 2009). Integrating research on the interplay of psychosocial and biological factors raises awareness of when preventive and early intervention approaches would be most appropriate, especially for classical high- and moderate-risk groups, as well as for extension populations identified by both traditional and recent frameworks (Oliver et al., 2019).

5.3. Therapeutic Approaches Targeting Environmental Modifiability

The gene–environment framework offers new insights into how gene–environment interplay shapes psychiatric risk. Accordingly, mental disorders often develop following exposure to environmental stressors, which better predict symptom onset than other risk factors such as genetic or family history. Gene–environment intersection mechanisms critically inform the nature of psychiatric treatment in three ways: (1) they bolster efforts at precision risk stratification; (2) knowledge of when disorders manifest under specific exposure conditions aids in designing appropriate preventive and early-intervention strategies; and (3) tailored therapeutic approaches targeting modifiable environmental or secondary features may yield greater clinical benefits (P. Jiménez et al., 2018). Support for such treatment models, which address patient-specific vulnerability and developmental timing characteristics, is beginning to accumulate (Allabergenov M., et al).

6. Ethical, Legal, and Social Considerations

Caution is warranted when discussing gene–environment interplay in relation to psychiatric disorders. Polygenic risk scores (PRS) predict disease liability based on aggregate genetic information, presenting ethical concerns when communicated to patients (C Palk et al., 2019). Clinical real-world evidence suggests that polygenic analysis for psychiatric illness informs high-risk individuals; nevertheless, the countervailing risk of stigma must be managed (Marques Filipe et al., 2021). Similar tensions arise with environmental epigenetics, providing diagnostic and prognostic insight into neurodevelopmental trajectories across diverse contexts. When risk factors are purportedly established, transparency about partial and probabilistic findings is crucial (Mannonov A., et al).

7. Practical Challenges and Future Directions

Gene–environment interplay is crucial for explaining psychiatric risk, yet several barriers obscure its clinical significance. First, the gap between evidence and practice remains problematic after ten years of deliberation—especially with regard to its application in personalized medicine. Second, the usual approach to plasticity genes complicates anticipation of developmental outcomes of exposure to cumulative risk, undermining its relevance for prevention, intervention, or early assistance. Plasticity indicators may instead inform the timing of environmental action, but do not capture broader gene–environment interactions pertinent to aetiological processes. Finally, a neglect of cognition constrains understanding of longitudinal risk progression, particularly across the sensitive period. Generalist genes differentially influence the ability to acquire risk-conducive cognitions, such as attentional biases and irrational beliefs, which subsequently shape emotional disturbance and maladaptive behaviour. A more elaborate articulations of gene–environment interplay would enhance its clinical salience and retention within personalised-medicine agendas (A. E. Vinkhuyzen & R. Wray, 2014) ; (Belsky et al., 2009) ; (Fox & G Beevers, 2016).

8. Conclusion

Gene–environment interplay advanced and established the study of how genetic and environmental factors interact to increase or decrease risk for psychiatric symptoms and disorders, from conception onward (Belsky et al., 2009). This research also informed frameworks for assessing and mitigating psychiatric risk. The framework developed and adapted for the present exposition distinguishes between two aspects of gene–environment interplay: (1) gene–environment correlation, wherein genetically influenced characteristics determine exposure to environmental experiences; and (2) gene–environment interaction, whereby genetic susceptibility influences the effects of environmental exposure.

Gene–environment interplay has considerable implications for mainstream clinical psychology (A. E. Vinkhuyzen & R. Wray, 2014). Despite the important role of the environment in shaping mental health across the lifespan and direct efforts by clinical psychologists, psychology has been slow to establish the necessary developmental, environmental, methodological, and conceptual frameworks to incorporate insights on gene–environment interplay and psychiatric risk. Attention to the modulation of exposure to,

treatment of, and phenomenological response to environmental factors within the individual, family, and societal contexts of psychiatric disorders can strengthen clinical assessment and intervention.

Major advances in genetic research ability to identify individual and population risk and protective factors have not fully transformed psychiatric assessment, intervention, and treatment decisions. Biological pathways through which genetic risk predicts psychiatric outcome, the ontogenetic timing of risk factors, epigenomic mechanisms, the distinction between risk, preventive, and therapeutic factors, and recognition of the absence of or presence of high resilience-indicating protective factors all powerfully shape clinical formulation and guide decision-making regarding additional assessment and intervention. A substantial opportunity therefore exists to further refine clinical frameworks integrating genetic research with the individual–family–societal triad.

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