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Review

Genetic and Environmental Contributions to Antisocial Personality Disorder

Hannah Soojeong Oh

Purdue University Northwest, Hammond, IN 46323, USA; oh413@pnw.edu; Tel.: + 1 (219) 368-4262

Abstract

Antisocial personality disorder (ASPD) is a clinically heterogeneous psychiatric condition marked by persistent violations of social norms, impulsivity, aggression, and impaired interpersonal functioning. With an estimated prevalence of 1–4% in the general population and substantially higher rates in forensic contexts, ASPD contributes to considerable public health and societal burden. This review synthesizes evidence on the developmental risk architecture of ASPD across genetic, environmental, and epigenetic domains. Behavioral genetic research (twin, family, and adoption studies) indicates moderate heritability for antisocial behavior and ASPD-related traits, with genetic influences tending to increase from childhood into adolescence and varying by sex and behavioral phenotype. Molecular studies support a polygenic liability model in which many variants of small effect—implicating dopaminergic and serotonergic signaling, neurodevelopmental processes, and immune-related pathways—contribute to externalizing risk, although ASPD-specific associations remain limited. Longitudinal evidence identifies robust environmental predictors, including childhood maltreatment, adverse family climates, deviant peer affiliation, socioeconomic disadvantage, and community violence, which shape trajectories from early conduct problems to adult antisocial outcomes. Emerging work suggests that epigenetic processes, particularly DNA methylation, may help explain how early adversity becomes biologically embedded by altering gene regulation in neural systems relevant to impulse control and emotion regulation. Overall, the literature supports a developmental framework in which ASPD reflects cumulative, context-dependent risk arising from genetic liability interacting with environmental exposures, highlighting prevention-focused implications and the importance of early intervention on modifiable pathways.

Keywords: antisocial personality disorder; externalizing behavior; conduct disorder; behavioral genetics; gene–environment interaction; epigenetics

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1. Introduction

Antisocial personality disorder (ASPD) is a psychiatric condition affecting approximately 1–4% of the general population [1]. Prevalence is substantially higher in certain settings: up to 18% in clinical samples, averaging around 47% in forensic samples, and as high as 60–78% among incarcerated men [2]. Individuals with ASPD typically exhibit a persistent pattern of disregard for societal norms and the rights of others, often expressed as manipulative, deceitful, or criminal behaviors [3,4]. ASPD is strongly associated with adverse social and public health outcomes, including elevated rates of criminal activity, substance use disorders, and significant societal and economic burden [5]. Given the severity and persistence of these consequences, there is a pressing need to better understand the factors that contribute to the development and maintenance of ASPD at both the individual and societal levels [6].

This review synthesizes existing literature on the multifactorial origins of ASPD, with a specific focus on genetic vulnerability, environmental risk factors, and their interaction across development [1]. Drawing on evidence from behavioral genetics, molecular studies, and social and developmental research, it evaluates how inherited predispositions may interact with exposures such as early-life adversity, family environment, peer influences, and socioeconomic context to shape antisocial outcomes. By integrating findings across these domains, it identifies potentially modifiable pathways that can inform targeted prevention and intervention strategies and contribute to a more comprehensive framework for understanding and addressing the societal impact of ASPD. Overall, this review is intended to provide researchers, clinicians, and policymakers with an evidence-based foundation for reducing the negative social consequences associated with ASPD by clarifying its underlying risk architecture.

2. Diagnostic Framework and Clinical Heterogeneity of ASPD

2.1. Diagnostic Criteria of ASPD

2.1.1. Diagnostic and Statistical Manual of Mental Disorders, 5th Edition (DSM-5)

DSM-5 classifies ASPD as a Cluster B personality disorder marked by persistent patterns of irresponsible, exploitative, and remorseless behavior. Key diagnostic criteria include failure to conform to legal and social norms, deceitfulness, such as lying or conning others, impulsivity and aggression, and lack of remorse for harming others. The disorder is deeply ingrained, often persisting into adulthood [7]. Given its clinical complexity and heterogeneous presentation, ASPD requires nuanced assessment approaches that account for both subtypes and comorbidities [6]. More broadly, while DSM-5 criteria provide a diagnostic foundation, emerging research advocates for dimensional models to guide targeted interventions [7]. In particular, future studies should prioritize identifying biological and cognitive markers to enhance diagnostic accuracy.

2.1.2. Structured Clinical Interview for DSM-IV Axis II Personality Disorders (SCID-II)

The most commonly used method to assess ASPD in clinical settings is the SCID-II. This semi-structured, clinician-rated interview evaluates DSM-IV criteria for ASPD and rates symptoms on a three-point scale (absent, subthreshold, or present) based on clinical judgment and patient history [8,9]. Another frequently used approach involves self-report questionnaires such as the Personality Diagnostic Questionnaire-4 and the Personality Assessment Inventory [10]. These tools moderately align with SCID-II assessments but differ in categorical diagnostic thresholds, highlighting the challenges of consistent ASPD classification. The choice between clinician-administered interviews and self-report tools depends on clinical context and practical considerations. Interviews are typically preferred for formal diagnosis because they incorporate collateral information and clinical judgment, thereby mitigating reporting biases and symptom overlap [11].

In terms of measurement, SCID-II conceptualizes ASPD as a dimensional construct representing severity on a continuum rather than discrete categories. This view is supported by item response theory analyses and evidence showing that adult-onset ASPD shares similar latent antisocial traits with childhood-onset cases, raising questions about strictly categorical diagnostic criteria. This dimensional perspective also helps contextualize variations in symptom expression across individuals. Sex differences in ASPD assessment via SCID-II are minimal: men may endorse more overt behavioral symptoms such as aggression, while women show slightly higher rates of impulsivity or relational manipulation; however, these differences do not substantially bias overall severity scores [8]. Epidemiologically, ASPD remains more prevalent in males than females in the general population, although clinical populations present more complex comorbidity patterns that can obscure clear sex differences [12]. Beyond traditional interviews and questionnaires, emerging approaches to ASPD assessment, including computerized adaptive testing and the integration of multi-informant data, aim to further enhance reliability and objectivity; these methods still require additional validation before widespread clinical adoption.

2.2. Subtypes of ASPD

Research highlights considerable heterogeneity within ASPD, identifying several distinct subtypes that differ in adaptive functioning, familial background, and comorbidity patterns [1]. The psychopathic-like subtype is characterized by callousness, superficial charm, and predatory behaviors [13]. The socially withdrawn subtype is marked by avoidance of social interactions and engagement in covert antisocial acts. The impulsive-histrionic subtype displays thrill-seeking tendencies and emotional volatility. The emotionally dysregulated subtype presents intense anger, mood swings, and frequent interpersonal conflicts. The attentionally dysregulated subtype is associated with poor focus and hyperactivity [14].

2.3. ASPD vs. Psychopathy

ASPD and psychopathy are frequently conflated due to overlapping behavioral features, such as impulsivity and persistent violation of social norms [15]. However, research indicates that only about one third of individuals diagnosed with ASPD meet criteria for psychopathy, highlighting substantial heterogeneity within ASPD populations. ASPD is primarily defined by observable behaviors such as rule-breaking, deceitfulness, and disregard for the rights of others, and is often associated with higher anxiety and mood disorder burden among individuals with the emotionally dysregulated subtype [16]. In contrast, psychopathy represents a more severe and specific phenotype characterized by prominent affective and interpersonal traits, including emotional detachment, superficial charm, manipulativeness, grandiosity, boldness, and low anxiety [16]. The Psychopathy Checklist–Revised is a widely used instrument for assessing psychopathy and emphasizes these affective and interpersonal features [17]. Clinically, this distinction is consequential, as psychopathy is associated with approximately threefold higher rates of violent and nonviolent criminal recidivism compared with ASPD alone [10,18].

3. Genetic Risk Factors in ASPD

3.1. Heritability of ASPD

Genetic factors are a well-established component of ASPD etiology. Evidence from twin, family, and adoption studies indicates that genetic influences account for approximately 30–50% of the variance in antisocial behavior and ASPD risk [19]. Rhee and Waldman (2002) reported heritability estimates of ~50% for antisocial behaviors in childhood and adolescence, with genetic contributions increasing from childhood into adolescence, particularly in males [19]. Pezzoli et al. (2025) synthesized genetically informed studies and reported heritability estimates for ASPD ranging from 31% to 46% across populations and age groups [20]. Rautiainen et al. (2016) supported a polygenic architecture for ASPD by identifying suggestive risk loci in a genome-wide association study (GWAS), building on prior twin and adoption studies that estimated heritability at up to ~50% [21]. Reichborn-Kjennerud et al. (2015) estimated that 31–46% of the variance in ASPD traits was attributable to genetic factors, which largely accounted for stability in antisocial traits over time, in a longitudinal Norwegian twin cohort [22]. Key heritability estimates across major study designs are summarized in Table 1.

Table 1. Genetic evidence for ASPD across study designs

Study Design	Sample Characteristics	Key Findings	Interpretation	Key References
Twin studies	Large population-based twin cohorts (>10,000 twin pairs)	Heritability estimates ~40–55% for antisocial traits	Substantial genetic influence with environmental moderation	[19,51]
Family studies	National registry-based and clinical family samples	Elevated antisocial risk among first-degree relatives	Familial aggregation supports inherited liability	[1,52]

Adoption studies	Longitudinal adoptee cohorts (n ≈ 1,000)	Biological parental antisociality predicts outcomes despite adoption	Genetic risk independent of rearing environment	[36,53]
GWAS	Large population cohorts (tens of thousands)	Polygenic risk distributed across externalizing traits	Many variants of small effect; modest variance explained	[21,54]

Importantly, the magnitude of genetic influence varies by behavioral phenotype, age, and sex. Heritability tends to increase from childhood to adolescence, particularly for aggressive and non-aggressive antisocial behaviors in males, suggesting a developmental escalation in genetic effects [19]. In females, genetic effects are also evident but may manifest differently and may be more contingent on environmental context [20]. These patterns underscore the heterogeneous and developmentally dynamic nature of genetic contributions to ASPD. Gard et al. (2019) similarly concluded that genetic influences remain substantial across studies, although estimates vary depending on the antisocial phenotype assessed and demographic characteristics [19,23]. Taken together, these findings support a model in which genetic liability is robust but moderated by developmental stage and individual differences.

3.2. Candidate Common Genetic Variants Associated with ASPD

Recent advances in psychiatric genetics support a polygenic model of ASPD risk, in which many common genetic variants of small effect contribute to liability for antisocial and externalizing traits. Rather than being determinative, these variants are most informative as entry points into biological pathways relevant to ASPD, including dopaminergic and serotonergic signaling, synaptic function, neurodevelopmental processes, and immune-related mechanisms. Representative genes discussed in this section are summarized in Table 2.

Table 2. Genetic risk factors contributing to antisocial and externalizing phenotypes

Gene	Variant / Locus	Biological Function	Phenotype Studied	Key Empirical Findings	Interpretation & Limits	Key References
MAOA	uVNTR (3R/4R), rs6323	Monoamine degradation	Aggression, antisocial behavior	Low-activity MAOA interacts with childhood maltreatment to predict aggression	Gene–environment interaction; not deterministic; strongest for aggression	[29,46]
SLC6A4	5-HTTLPR (S/L, rs25531)	Serotonin reuptake	Emotional reactivity, impulsivity	S allele linked to stress sensitivity and amygdala reactivity	Context-dependent; not ASPD-specific	[28,55]
DRD4	Exon 3 VNTR (7R)	Dopamine D4 receptor	Novelty seeking, externalizing traits	7R allele modestly associated with novelty seeking	Small effects; temperament-level risk	[56]
DRD2	rs1800497 (Taq1A)	Reward processing	Substance use, antisocial traits	A1 allele associated with reduced D2 availability	Indirect pathway via reward sensitivity	[57]
COMT	Val158Met (rs4680)	Prefrontal dopamine metabolism	Executive control, impulsivity	Met allele alters PFC dopamine signaling	Inconsistent behavioral effects	[58]

TPH2	Multiple ss (e.g., rs4570625)	Serotonin synthesis	Impulsive aggression	Variants linked to aggression-related traits	Mixed findings; small samples	[59]
DAT1 (SLC6A3)	40-bp VNTR (9R/10R)	Dopamine reuptake	Impulsivity, ADHD traits	Associations with impulsivity reported	No consistent ASPD link	[60]
HLA region	Chr6p21.3 (multiple loci)	Immune regulation	Externalizing risk	GWAS suggests immune involvement	No specific ASPD allele identified	[21,33]
LINC00951–LRFN2	rs4714329 (chr6)	Synaptic organization	Antisocial behavior	Suggestive GWAS association moderated by adversity	Did not reach genome-wide significance	[61]
SNAP25	Various SNPs	Synaptic vesicle fusion	Impulsivity, executive dysfunction	Linked to impulsivity in neurodevelopmental studies	Indirect contribution only	[62]

3.2.1. Dopaminergic Signaling Pathways

Several candidate genes involved in dopaminergic signaling have been examined in relation to antisocial and externalizing traits. The dopamine transporter gene SLC6A3 (also known as DAT1), located on chromosome 5p15.3, encodes the dopamine transporter and plays a key role in dopamine reuptake at the synapse. A frequently studied variant is a variable number tandem repeat (VNTR) polymorphism in the 3′ untranslated region, commonly described as the 9-repeat (9R) and 10-repeat (10R) alleles (rs28363170). Variation in this VNTR has been examined in relation to impulsivity and other externalizing traits, consistent with its role in dopaminergic signaling.

Additional dopaminergic candidates include DRD4 and DRD2, which encode dopamine receptor D4 and dopamine receptor D2, respectively. DRD4, located on chromosome 11p15.5, contains a 48-base pair VNTR in exon 3, with the 7-repeat (7R) allele being the most extensively studied. Variation in the DRD4 exon 3 VNTR has been examined in relation to novelty seeking and risk-taking tendencies, with meta-analytic evidence suggesting a modest association with these traits. DRD2, located on chromosome 11q23, encodes a key regulator of reward processing and reinforcement learning. The Taq1A polymorphism (rs1800497) has been linked to differences in dopamine receptor availability and reward sensitivity, factors associated with susceptibility to substance use and other externalizing behaviors. Together, these findings support altered reward-related processing as a plausible pathway through which dopaminergic genetic variation may contribute to antisocial and externalizing tendencies [24].

The catechol-O-methyltransferase gene COMT further implicates dopaminergic regulation within prefrontal circuitry. COMT plays a central role in dopamine metabolism in the prefrontal cortex, a brain region critical for executive control and decision-making. A well-characterized functional polymorphism, Val158Met (rs4680), influences enzymatic activity, with the Met allele associated with reduced catechol-O-methyltransferase activity and altered prefrontal dopamine signaling [25]. Behavioral associations involving this variant with impulsivity or aggression appear to be context-dependent, consistent with the role of prefrontal dopamine in cognitive and behavioral regulation [26].

3.2.2. Serotonergic and Monoaminergic Signaling Pathways

The serotonergic system also plays a central role in behavioral regulation relevant to antisocial outcomes. The serotonin transporter gene SLC6A4 contains a polymorphic promoter region known as 5-HTTLPR, which includes short (S) and long (L) alleles that influence transcriptional efficiency. The S allele of 5-HTTLPR, particularly within the triallelic framework that includes rs25531, has been

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examined in relation to functional variation in serotonin transporter regulation and emotional processing [27]. Evidence suggests that this allele is associated with increased neural emotional reactivity, especially in the context of environmental stressors [28]. Genes involved in serotonin synthesis, including TPH1 and TPH2, have also been explored as contributors to affective and behavioral regulation.

The monoamine oxidase A gene MAOA, located on Xp11.3, encodes an enzyme responsible for the breakdown of serotonin, dopamine, and norepinephrine. A commonly studied functional variant is a VNTR polymorphism in the promoter region (MAOA-uVNTR), with low-activity alleles—most notably the 3-repeat variant—associated with reduced enzymatic activity and higher monoamine availability. These variants have been examined in relation to aggression, impulsivity, and antisocial behavior, particularly in males, with evidence indicating that behavioral effects are moderated by environmental exposures such as childhood maltreatment. In addition, the coding single nucleotide polymorphism (SNP) rs6323 in exon 8 of MAOA influences enzyme activity and has been associated with impulsivity [29].

3.2.3. Synaptic and Neurodevelopmental Pathways

The synaptosomal-associated protein 25 gene SNAP25 is involved in synaptic vesicle fusion and neurotransmitter release and has been investigated as a candidate gene for impulsivity and other externalizing behaviors, particularly in the context of attention-deficit/hyperactivity disorder [30]. Although some SNAP25 variants have been associated with neurodevelopmental and executive function differences, direct associations with ASPD remain limited, suggesting that SNAP25 may contribute indirectly to antisocial traits through broader effects on cognitive and behavioral regulation [31].

The LINC00951–LRFN2 gene cluster on chromosome 6 has been examined as a candidate locus relevant to antisocial and externalizing traits because of its involvement in neurodevelopmental processes and synaptic organization, with enriched expression in cortical regions, including the prefrontal cortex. This locus spans approximately chr6:135,000,000–135,200,000 and contains the SNP rs4714329, which has shown suggestive evidence of association with antisocial behavior and related externalizing traits in a GWAS, although it does not reach conventional genome-wide significance thresholds [32]. Notably, reported associations involving rs4714329 appear to be moderated by environmental factors, with stronger effects among individuals exposed to significant early-life adversity, consistent with gene–environment interaction models, although direct evidence remains limited. Based on its genomic context and the known functions of nearby genes such as LRFN2, rs4714329 has been hypothesized to influence pathways related to synaptic organization and plasticity [21].

3.2.4. Immune-Related Pathways

The human leukocyte antigen (HLA) gene region on chromosome 6p21.3 has drawn interest in psychiatric genetics because of its central role in immune function and its potential relevance to neurodevelopment and neuroimmune signaling. This region is highly polymorphic and has been implicated across multiple neuropsychiatric GWAS, supporting the broader view that immune-related genetic variation can influence brain development, emotional regulation, and behavior through neuroimmune pathways [33]. However, to date, no specific HLA alleles or SNPs have been robustly or consistently associated with ASPD. HLA-region variation may therefore be more relevant to broader externalizing liability through neuroimmune and neurodevelopmental mechanisms than to ASPD-specific risk [21].

3.2.5. Copy Number Variants (CNVs)

In addition to candidate SNPs, recent research has examined whether CNVs, which are submicroscopic deletions or duplications that alter gene dosage and regulation, contribute to antisocial and externalizing phenotypes. Although evidence on CNVs specific to ASPD is limited, findings from related neurodevelopmental and psychiatric disorders suggest that rare CNVs affecting genes involved in synaptic function and brain development may influence traits relevant to antisocial behavior.

For example, deletions at 16p11.2 and 22q11.2, which encompass multiple genes important for neurodevelopment, have been associated with behavioral dysregulation, impulsivity, and executive function deficits in schizophrenia and autism spectrum disorders [34]. CNVs affecting NRXN1 at 2p16.3, encoding a synaptic adhesion molecule critical for neuronal connectivity, have also been linked to social impairments and broader behavioral dysregulation [35]. While these findings cannot be attributed directly to ASPD, they highlight neurodevelopmental mechanisms that may increase vulnerability to antisocial traits.

4. Environmental and Social Risk Factors in ASPD

A substantial body of research has highlighted the influence of environmental and social factors on the development and persistence of ASPD. Among these, the family environment is a particularly influential risk factor. More broadly, adverse experiences across family, peer, and community contexts can increase the risk of persistent antisocial behaviors, as summarized in Table 3.

Table 3. Environmental and social risk factors contributing to antisocial and externalizing phenotypes

Environmental Factor	Developmental Timing	Exposure Characteristics	Primary Evidence Type	Key Findings (Direction & Magnitude)	Mechanistic Pathways	Behavioral Outcomes	Strength & Replication	Key References
Childhood maltreatment	Early–mid childhood	Physical, emotional, sexual abuse; neglect	Longitudinal cohorts; meta-analyses	Robust association with conduct disorder and later ASPD; risk increases with cumulative trauma	HPA-axis dysregulation; epigenetic modification; emotion regulation deficits	Aggression, impulsivity, chronic antisocial behavior	Strong, highly replicated	[63,64]
Family conflict / dysfunction	Childhood – adolescence	Chronic conflict, harsh or inconsistent parenting	Prospective longitudinal studies	Elevated risk for persistent antisocial trajectories	Social learning; impaired attachment; stress reactivity	Rule-breaking, aggression	Strong, replicated	[36,65]
Deviant peer affiliation	Adolescence	Association with delinquent or antisocial peers	Longitudinal developmental studies	Peer antisocial behavior predicts escalation beyond childhood	Peer reinforcement; social reward sensitivity	Delinquency, violence	Strong, replicated	[40,66]

				conduct problems				
Low socioeconomic status	Childhood–adolescence	Poverty, parental unemployment, material deprivation	Population-based cohort studies	Modest but consistent increase in antisocial risk	Chronic stress; limited access to resources	Externalizing behavior	Moderate, consistent	[67,68]
High-crime neighborhood	Childhood–adolescence	Exposure to violence and community disorder	Neighborhood-level longitudinal analyses	Independent contribution beyond family socioeconomic status	Normative reinforcement of aggression; stress exposure	Aggression, antisocial traits	Moderate, replicated	[42]
Prenatal / early-life stress	Prenatal–early childhood	Maternal stress, obstetric complications	Prospective birth cohorts	Small-to-moderate associations with later behavioral dysregulation	Neurodevelopmental vulnerability; stress-response programming	Impulsivity, emotional dysregulation	Moderate, biologically plausible	[69]

4.1. Family Environment

Children raised in family environments characterized by chronic conflict, emotional neglect, or inconsistent and harsh discipline show a substantially increased risk of developing externalizing behavior problems during childhood and adolescence. Large-scale longitudinal studies consistently demonstrate that exposure to adverse family environments is associated with an increased likelihood of conduct disorder. For example, children exposed to chronic family adversity have approximately 1.55 times greater odds of receiving a conduct disorder diagnosis compared with those raised in more stable environments, indicating that serious behavioral problems occur more frequently in persistently stressful or neglectful family contexts [36].

This elevated risk is observed across diverse populations, with multiple studies reporting similar effect sizes, underscoring the robustness and reproducibility of the association between family adversity and conduct disorder [36]. Longitudinal cohort research further shows that behavior problems emerging early in life often persist over time. Children who exhibit severe or chronic conduct problems are more likely to experience adverse outcomes in adolescence and early adulthood, including continued antisocial behavior, substance misuse, legal difficulties, and impaired social functioning.

Importantly, childhood disruptive behaviors are widely recognized as a developmental precursor to antisocial personality disorder in adulthood. Although not all individuals with early externalizing problems progress to ASPD, the risk of persistent antisocial outcomes is substantially higher when behavioral difficulties begin early and occur in the context of chronic family adversity. Collectively, these findings highlight the central role of the early family environment in shaping long-term trajectories of antisocial behavior.

4.2. Childhood Trauma

Childhood trauma represents a major environmental risk factor for ASPD. Experiences such as physical, sexual, or emotional abuse, neglect, and exposure to domestic violence can exert lasting adverse effects on psychological development. Early trauma has been associated with dysregulation of stress-response systems, including altered functioning of the hypothalamic–pituitary–adrenal (HPA) axis, which may contribute to heightened emotional reactivity and impaired stress regulation [37].

Neuroimaging studies further indicate that individuals with histories of childhood abuse or neglect often exhibit structural and functional alterations in brain regions involved in emotional regulation and behavioral control, particularly the hippocampus and prefrontal cortex [38]. These neural alterations have been linked to increased impulsivity and difficulties in emotion regulation, which are core features of antisocial personality disorder.

At the population level, epidemiological research shows that exposure to multiple forms of childhood trauma is associated with a substantially elevated risk of antisocial and other externalizing outcomes in adulthood [39]. Conduct problems that emerge in the context of early trauma are widely recognized as a developmental precursor to ASPD. Although some trauma-related behaviors may initially function as adaptive responses to threatening environments, their persistence and reinforcement across development can render them maladaptive, contributing to the enduring behavioral patterns characteristic of ASPD.

4.3. Peer Influence

Peer influence during adolescence is a well-established predictor of antisocial behavior. Longitudinal studies consistently show that adolescents who affiliate with deviant or antisocial peers exhibit higher levels of antisocial and delinquent behavior over time. For example, data from a large community sample of more than 1,300 youths followed from middle adolescence into young adulthood demonstrated that affiliation with peers engaged in antisocial conduct was associated with increases in individuals' own antisocial behavior across adolescence [40].

Evidence from diverse populations further indicates that greater involvement with antisocial peers is consistently linked to more severe antisocial and delinquent outcomes, supporting the generalizability of this risk factor. Although the magnitude of these associations varies across samples and measurement approaches, longitudinal patterns suggest that deviant peer affiliation contributes to the escalation and persistence of antisocial behavior beyond early adolescence.

Mechanistically, peer socialization processes can reinforce maladaptive norms and behaviors within adolescent networks. Repeated exposure to peers who model aggression, rule-breaking, or delinquency increases the likelihood that individuals will adopt similar behaviors [41]. These processes are particularly influential during developmental periods marked by heightened sensitivity to social reward, underscoring the robust role of deviant peer associations in shaping antisocial trajectories from adolescence into adulthood, even when accounting for earlier conduct problems and family background.

4.4. Socioeconomic Status

Socioeconomic disadvantage and community context further contribute to the risk of antisocial outcomes. Growing up in impoverished or high-poverty neighborhoods can expose children and adolescents to chronic stress, instability, and higher levels of community violence, which have been associated with elevated conduct problems and antisocial behavior. Longitudinal research indicates that lower family income and neighborhood disadvantage predict an increased likelihood of later antisocial behavior, even after controlling for individual and family characteristics. Neighborhood-level analyses similarly highlight the role of structural disadvantage, with greater neighborhood poverty associated with higher rates of behavioral dysregulation and externalizing problems among youth [42]. These patterns may reflect a combination of limited access to supportive resources, increased exposure to violence or disorder, and reduced community cohesion, all of which can undermine prosocial development.

Adverse social environments can interact with individual predispositions to shape antisocial trajectories across development. Gene–environment research suggests that vulnerability related to impulsivity or poor self-regulation may be amplified under conditions of cumulative adversity, while neighborhood-level factors such as collective efficacy and social cohesion can moderate the impact of socioeconomic disadvantage on violent and antisocial behavior [43]. Together, these findings support a multilevel model in which environmental exposures and social context shape risk in concert with underlying susceptibilities, motivating closer consideration of the gene–environment interactions that may link these experiences to persistent antisocial behavior in the next section.

5. Gene–Environment Interactions in ASPD

ASPD is increasingly conceptualized as the downstream outcome of a developmentally embedded interaction between genetic liability and environmental exposure. Genetic factors establish a baseline vulnerability for antisocial and externalizing traits; however, this vulnerability does not translate into stable behavioral pathology in the absence of relevant environmental input. Epigenetic mechanisms provide a biologically plausible and theoretically powerful framework for understanding how inherited genetic susceptibility becomes functionally instantiated through experience-dependent regulation of gene expression across development. Human studies indicate that early-life stress can induce stable epigenetic modifications that persist across development and influence later psychopathology, supporting the concept of epigenetic programming by early adversity [44].

Rather than functioning as an independent "third factor," epigenetic regulation operates as a biological interface linking genotype and environment, allowing environmental signals to modulate transcriptional activity within neural systems governing impulse control, emotional regulation, and social behavior. This framework moves beyond simplistic additive models and situates ASPD within a biologically grounded developmental process in which genetic susceptibility and environmental exposure interact dynamically across development [45].

5.1. Mechanistic Bridge

Genetic variation within monoaminergic and dopaminergic systems, including MAOA, SLC6A4, and DRD4, has been consistently associated with individual differences in impulsivity, aggression, and broader externalizing tendencies. Importantly, these variants do not exert deterministic effects; instead, their behavioral relevance emerges most clearly under conditions of environmental adversity such as childhood maltreatment, emotional neglect, family conflict, and chronic psychosocial stress [46].

Epigenetic mechanisms provide a biologically plausible framework for understanding this contingency. Processes such as DNA methylation and histone modification regulate chromatin accessibility and transcriptional activity in response to environmental signals, thereby shaping neural development without altering the underlying DNA sequence. A systematic review of human studies demonstrates consistent associations between childhood maltreatment and altered DNA methylation of stress-related genes, providing direct empirical support for epigenetic mediation of early adversity [47]. Converging experimental and human evidence further indicates that exposure to stress-related environments is associated with epigenetic alterations in serotonergic, dopaminergic, and stress-response pathways that influence neurobiological systems critical for behavioral regulation [45].

Gene–environment interactions involving MAOA variation illustrate this principle in a concrete manner. Empirical evidence indicates that DNA methylation of the MAOA gene, in conjunction with MAOA genotype, moderates the association between childhood maltreatment and aggressive behavior, linking early adversity to externalizing outcomes through an epigenetic mechanism [48]. Low-activity MAOA variants alone do not predict antisocial outcomes; however, individuals carrying these variants who are exposed to severe early adversity exhibit elevated levels of aggression and externalizing behavior. Notably, these effects are most robust for intermediate phenotypes—such as impulsivity, emotional dysregulation, and aggressive behavior—rather than for categorical ASPD diagnosis. This pattern underscores the importance of conceptualizing ASPD as the endpoint of developmental trajectories shaped by interacting biological and environmental processes, rather than as the direct consequence of single genetic effects. Representative epigenetic mechanisms linking genetic susceptibility, environmental adversity, and externalizing phenotypes are summarized in Table 4.

Table 4. Epigenetic mechanisms associated with antisocial or externalizing phenotypes

Gene / Pathway	Epigenetic Mark	Environmental Exposure (Timing)	Tissue / Sample	Direction of Change	Neurobiological System Affected	Behavioral Phenotype	Strength & Replication	Key References
MAOA	DNA methylation (promoter)	Childhood maltreatment (early–mid childhood)	Peripheral blood; brain inference	↑ Methylation moderates low-activity genotype effects	Monoamine degradation; prefrontal–limbic regulation	Aggression, impulsivity, externalizing behavior	Replicated G×E; strongest evidence among candidates	[29,48]
SLC6A4	Promoter methylation (5-HTTLPR-linked)	Chronic stress / adversity (childhood–adolescence)	Peripheral blood	↑ or ↓ methylation depending on context	Serotonergic signaling; amygdala reactivity	Stress sensitivity, emotional reactivity	Moderate evidence; context-dependent	[47]
NR3C1 (GR)	Promoter methylation (exon 1F)	Family violence / early adversity (early childhood)	Peripheral blood; postmortem brain (other studies)	↑Methylation → reduced GR expression	HPA-axis negative feedback	Impulsivity, stress dysregulation	Highly replicated across disorders	[37,70]
OXTR	CpG methylation	Low parental warmth / neglect (childhood)	Peripheral blood	↑Methylation (context-dependent)	Social bonding and affiliative processing	Reduced empathy, social dysfunction	Emerging evidence; limited samples	[71]
BDNF	Promoter methylation (exon IV)	Severe or repeated trauma (childhood–adolescence)	Peripheral blood	↑Methylation → ↓expression	Synaptic plasticity and learning	Emotion regulation deficits	Moderate evidence; replicated in mood disorders	[70]
CRHR1	Stress-related regulatory methylation	Early neglect / chronic stress	Peripheral blood	Altered regulation (direction varies)	Corticotropin-releasing hormone signaling	Emotional instability, fear reactivity	Limited but biologically plausible	[72]

5.2. Temporal Bridge

The developmental timing of environmental exposure plays a decisive role in shaping the magnitude and persistence of epigenetic modification. Early childhood and adolescence represent sensitive periods of heightened neural and epigenomic plasticity, during which environmental experiences exert especially strong and lasting effects on biological and behavioral outcomes. Adverse exposures during these windows, including abuse, neglect, and sustained psychosocial stress, can induce epigenetic alterations in genes regulating stress responsivity and emotional control, with consequences that extend into adulthood.

Evidence from animal models demonstrates that early-life stress produces enduring epigenetic changes in stress-regulatory systems, accompanied by persistent alterations in aggression, anxiety-like behavior, and social functioning [49]. Converging human studies similarly indicate that epigenetic signatures associated with early adversity remain detectable years later and are linked to externalizing and antisocial behavioral trajectories across the lifespan [45]. At the same time, residual epigenetic plasticity during adolescence suggests that maladaptive developmental trajectories are not fully fixed, underscoring the importance of developmental timing for both risk exposure and intervention.

5.3. Clinical Bridge

The experience-dependent and partially reversible nature of epigenetic regulation carries important implications for prevention and intervention. Psychosocial interventions, including trauma-informed therapies, enriched caregiving environments, and sustained social support, have been shown to influence stress-related biological systems and improve emotional and behavioral regulation, particularly when implemented during sensitive developmental periods. These findings suggest that epigenetic processes may represent a modifiable pathway through which environmental interventions exert lasting effects on antisocial behavior.

Advances in behavioral genetics and epigenetics have also motivated interest in precision-oriented frameworks that integrate genetic liability, environmental history, and developmental timing. Although the clinical application of polygenic risk scores and epigenetic biomarkers in ASPD is not yet established, such approaches may ultimately prove valuable for stratifying developmental risk trajectories and tailoring preventive strategies, rather than guiding diagnosis or pharmacological treatment [49]. At present, the primary contribution of this research lies in refining etiological models and identifying biologically informed windows for intervention.

Taken together, epigenetic plasticity provides both a conceptual and biological bridge linking genetic vulnerability, environmental exposure, and developmental timing. This framework supports a shift away from static models of ASPD toward a dynamic understanding of risk, resilience, and intervention grounded in developmental neuroscience [50].

6. Conclusion

In conclusion, ASPD arises through a sequential and interactive developmental pathway in which genetic liability confers sensitivity, environmental exposures shape risk expression, and epigenetic mechanisms may help mediate the effects of adversity by altering gene regulation. These influences likely operate most strongly during critical developmental windows, contributing to enduring changes in neural systems relevant to impulse control, emotion regulation, and social behavior. Framing epigenetic regulation as a biologically plausible bridge between genetic susceptibility and environmental stressors offers a coherent lens for understanding ASPD heterogeneity and for prioritizing prevention-oriented research. Addressing key knowledge gaps—including brain-relevant epigenetic signatures, longitudinal developmental trajectories, and the extent to which interventions can modify these pathways—will be essential for translating this model into more effective prevention and early intervention strategies, with the longer-term goal of reducing the burden of ASPD for individuals and society.

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Abbreviations

The following abbreviations are used in this manuscript:

ASPD	Antisocial Personality Disorder
DSM-5	Diagnostic and Statistical Manual of Mental Disorders, 5th Edition
SCID-II	Structured Clinical Interview for DSM-IV Axis II Personality Disorders
GWAS	Genome-Wide Association Study
SNPs	Single Nucleotide Polymorphisms
HLA	Human Leukocyte Antigens
CNVs	Copy Number Variants
VNTR	Variable Number Tandem Repeat
HPA	Hypothalamic–pituitary–adrenal

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