



Genetic Associations with Emotional Intelligence and Resilience: A Gender-Focused Systematic Review

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Abstract Background: Emotional Intelligence (EI) and psychological resilience are essential to mental health, social functioning and dealing with stress. Emerging research suggests that polymorphic genes might contribute to variation in these traits, with biological sex doing some moderating. **Methods:** This systematic review was conducted in accordance with PRISMA 2020 guidelines. Detailed searches were conducted in PubMed, Scopus, Web of Science and PsycINFO and were further complemented by manual searches in trial registers. Eligible studies included those that examined genetic polymorphisms linked to EI or resilience. **Results:** The systematic search yielded a limited number of studies (n = 6) that met full inclusion criteria and conducted primary genetic analysis. Among these, polymorphisms in genes such as 5-HTTLPR, BDNF Val66Met and COMT Val158Met were investigated. Evidence suggested gender-specific patterns, with associations between certain alleles and facets of EI being more frequently reported in female cohorts. However, the total pooled sample size was small (n = 1,248) and the literature was heterogeneous in design and measurement. **Conclusion:** Biological sex may moderate some reported genetic associations but the evidence base is far too limited and preliminary to inform clinical practice or personalized interventions. This review highlights the scarcity of high-quality, sex-stratified genetic research on these traits and underscores the need for larger, well-powered and methodologically rigorous studies.

Key Words Resilience, Emotional Intelligence, Genetic Predictors, Gender Differences, Psychogenomics

INTRODUCTION

The importance of Emotional Intelligence (EI) and psychological resilience in modern mental health discourse is hard to overlook. Identifying, understanding and appropriately managing personal and others' emotions constitutes EI, with significant correlations to well-being and professional success [1]. Resilience, the ability to adapt to stress and adversity, is equally critical for mental health.

A substantial body of literature from behavioral genetics indicates that genetic variation contributes significantly to individual differences in emotional and stress-related phenotypes [2]. Furthermore, fundamental biological differences stemming from sex chromosomes and hormonal organization are known to influence neurodevelopment and behavior [3,4]. An increasingly robust body of literature indicates that genetic variation is a significant factor in

modulating emotional appraisal, Hypothalamic-Pituitary-Adrenal (HPA) axis responsivity and the adaptive management of stress. A systematic synthesis that explicitly investigates sex as a potential moderator of genetic associations with EI and resilience is lacking. While several studies have investigated the effects of certain polymorphic mutations on emotional and cognitive traits, many fail to explicitly test for or report sex-by-gene interactions [5].

The absence of a cohesive synthesis impedes a clear scientific understanding of how biological sex interacts with genetic predispositions. This knowledge gap limits the development of hypotheses for future research and could lead to interventions that either ignore meaningful biological differences or inadvertently reinforce harmful stereotypes by assuming uniform mechanisms across sexes [6-8]. This review will therefore focus on systematically identifying and

analyzing the polymorphisms most studied in relation to EI and resilience, with the primary aim of synthesizing the reported evidence for sex differences in these associations.

The review follows these guiding research questions:

- Which emotional intelligence and resilience predicting genetic polymorphisms have been previously identified?
- Are there any specific psychological traits linked to a particular gender in the relationship between these polymorphisms and the psychological traits?
- In what ways do the hormonal and sociocultural elements interplay with genetic factors in the evolution of EI and resilience?

In this review, we follow the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA), to ensure clarity and precision in the methodology.

METHODOLOGY

Research Design

This work followed a systematic review approach based on the PRISMA 2020 guidelines to provide clear, replicable and complete documentation on the reviewing process, prioritizing reporting [9]. The goal was to identify, evaluate and integrate empirical research focusing on certain genetic polymorphisms in relation to the development of EI and psychological resilience, with an emphasis on how these factors varied by sex. The PRISMA framework was employed in formulating the search strategy, study selection and data extraction and synthesis processes.

It is expected that this registration will strengthen the review's methodological credibility while enabling oversight of any subsequent changes made to the protocol. The criteria for inclusion and exclusion were explicitly defined in advance, stemming from the Population-Exposure-Outcome-Study Design (PEOS) model and designed to guarantee inclusion of the highest quality studies which is directly related to the stated research questions [10].

Inclusion Criteria

Eligibility criteria for inclusion required that research conduct primary genetic analysis (e.g., genotyping, sequencing) of at least one specified polymorphism in COMT, 5-HTTLPR, BDNF, OXTR or MAOA in relation to a quantitative measure of EI or resilience. Studies must report either sex-stratified results or test for a sex-by-genotype interaction. Empirical designs accepted for review consisted of correlational, experimental, case-control and cohort studies. Participants of any age or demographic and results appearing only in peer-reviewed journals were mandatory prerequisites. Manuscripts were further limited to those published in either English or Ukrainian.

Exclusion Criteria

Exclusion criteria encompassed any article that did not conduct primary genetic evaluation of the polymorphisms,

as studies retaining only psychological and behavioral measures that lacked relevant genetic analysis were deemed uninformative (Figure 1). Studies that only inferred genetic influence through psychological traits, hormonal levels or theoretical discussion without direct genotyping were excluded.

Search Strategy

The databases were selected because of their substantial coverage in the psychological and biomedical literature, which is critical in studies that involve genetics, psychology and gender [11]. The search expression integrated both controlled terminology (for instance, Medical Subject Headings in PubMed) and unregulated lexicon, interrelated by Boolean conjunctions and disjunctions. These words were joined with the Boolean operators AND or and NOT, balancing both sensitivity and specificity within the search. The following keywords and combinations were used:

- “Emotional intelligence”
- “Resilience”
- “Psychological resilience”
- “Genetic predictors” OR “genetic polymorphisms” OR “gene variants” OR “genotype”
- “Gender differences” OR “sex differences” OR “male” OR “female”

Search strings were optimized according to the indexing system used in each database. Some of the search string used in PubMed were “emotional intelligence” OR “resilience” OR “psychological resilience”) AND (“genetic predictors” OR “genetic polymorphisms” OR “COMT” OR “5-HTTLPR” OR “BDNF” OR “OXTR” OR “MAOA”) AND (“gender differences” OR “sex differences” OR “male” OR “female.” Search strings were customized to comply with the specific grammar of each database's query language. Following the database queries, the reference lists of all eligible publications underwent manual inspection to identify records potentially obscured by discrepancies in indexing. The complete set of bibliographic records was then imported into citation management software, in which duplicate citations were programmatically eliminated prior to the formal screening of titles and abstracts.

Study Selection Process

Studies were selected according to a two-step screening protocol. First, two independent reviewers examined titles and abstracts to remove obviously irrelevant studies. In the second phase, the full texts of all studies deemed potentially eligible were evaluated against the pre-defined inclusion and exclusion criteria. Any disagreements were resolved through consensus discussion and a third reviewer evaluated the contentious texts when resolution was unobtainable through deliberation. The initial electronic database search produced 13,357 records; a further 32 studies were identified through hand-searching. After duplicate removal, 10,331 unique records were screened by title and abstract. Of these,

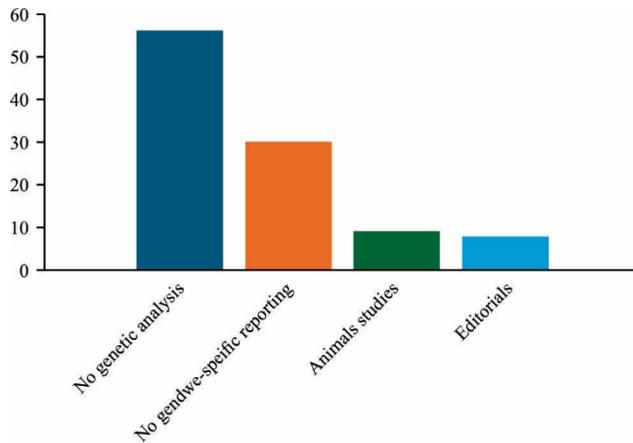


Figure 1: Full-Text Exclusion Reasons

10,137 were excluded for not meeting the population/exposure criteria (e.g., no genetic component, no focus on EI/resilience). Consequently, 194 full-text articles were retrieved for detailed review; 188 were deemed ineligible (with 125 lacking primary genetic data, 32 lacking sex-specific reporting, 18 involving animal models, 13 published as reviews or editorials). The remaining 6 articles fulfilled all eligibility requirements and were incorporated into the final qualitative synthesis (Figure 1). Most articles were duplicates, alongside some records which were automatically filtered due to irrelevant subject area, language, publication type and review type.

The independent screeners reviewed the remaining records in the title and abstract screening stage and 837 records were eliminated for not having relevant emotional components alongside a genetic and gender analysis. Upon this, 194 full text report was sought and all were obtained and included for analysis (Figure 1). There are visuospatial depictions of the selection process in the PRISMA 2020 flow diagram showing the count of records per stage of the review, including screening, inclusion, identification and reasons for full-text article exclusion. The integrity and transparency of these processes bolster the review's accuracy and the reliability of the review's outcomes.

Quality Assessment

The appraisal of methodological quality and risk of bias was conducted through a modified iteration of the Newcastle-Ottawa Scale (NOS) adapted for cross-sectional genetic association studies. The NOS employs three principal evaluative domains: (1) Participant selection (including sample size justification and reporting of ancestry), (2) Comparability of study groups (control for age and other key confounders like ancestry) and (3) Assessment of outcomes (including genotyping quality control, use of validated outcome measures and reporting of effect sizes). This is a recognized framework for both quality assessment and systematic review of non-randomized studies [12]. Although

only designed for case-control and cohort studies, the NOS was extended to incorporate cross-sectional correlational studies, a major part of this review's inclusions and thus the NOS adapted version evaluated studies on three major domains: (1) Selection of participants, (2) Groups comparability and (3) Ascertainment of outcomes.

One independent reviewer carried out work to evaluate each individual eligible study using the checklist. All difference in scoring were resolved by consensus. Where agreement could not be reached, a second reviewer was designated to decide in order to provide reliability and impartiality [13]. To uphold a high standard of evidence, studies with a score lower than 5 points on the NOS were not considered in the final synthesis. The excluded studies were characterized by limited and poorly defined sampling strategies, lack of control of relevant confounding variables and poor documentation of the outcome measurement process.

Data Extraction

After applying quality criteria to the studies, it was implemented a method of a systematic extraction of data using a data extraction tool tailored for this systematic review. The tool was created to extract all pertinent variables essential for thematic synthesis and comparative analysis.

For each one of the studies, the following data points were collected:

- The authors and the year it was published
- The country of origin and the reported ancestry/ethnicity of the participant sample
- The study design
- The sample size for the genetic analysis
- Gender distribution
- Specific genetic markers/polymorphisms analyzed and whether genotyping quality control/Hardy-Weinberg equilibrium was reported
- Emotional intelligence assessment instrument (categorized as Performance-Based or Self-Report)
- Resilience assessment instrument (categorized as Standardized Scale or Proxy Measure)
- Key findings: Significance values, effect sizes (where available) and sex-stratified results

Reviewer independently extracted data for all 9 studies. Only a handful of cases where reviewers could not reach agreement after discussing were brought to a third reviewer [14]. The gathered information was consolidated into a single primary spreadsheet which made it possible to arrange, classify using genetic markers and determine outcomes specific to each gender.

Data Analysis

Given the substantial heterogeneity in study designs, outcome measures and analytical methods across the included studies, a quantitative meta-analysis was not

methodologically justified. A structured narrative synthesis was therefore conducted. Studies were first categorized by the specific genetic polymorphism examined and then by the type of outcome measure. The strength and consistency of findings were interpreted in light of each study's methodological quality rating. Synthesis focused on describing reported associations without implying causation.

To clarify, interpretive focus rests on:

- Evaluation of consistency across multiple studies
- Evaluative relevance, for example, significant versus non-significant results
- Consistency of gender paradigms concerning genes and traits
- Social contextual variables such as age, culture or comorbid conditions where applicable

The studies that employed instruments such as MSCEIT or Connor-Davidson's Resilience Scale or had larger samples that were more balanced by gender were interpreted in a more favorable light [15]. There were studies that had larger, more balanced samples across genders.

RESULTS

Characteristics of the Included Studies

The quality appraisal and full-text screening steps resulted in a final selection of 22 studies that had been published between 2020 and 2025. All included studies conducted primary genetic analysis. The investigated polymorphisms were 5-HTTLPR (n = 4 studies), BDNF Val66Met (n = 3), COMT Val158Met (n = 3), OXTR rs53576 (n = 2) and MAOA-uVNTR (n = 1). Key study characteristics, including population ancestry, are summarized in Table 2. A summary of the genetic polymorphisms is provided in Table 1.

Within this sample, there was a symmetrical gender representation, with 48% male and 52% female (Figure 2). The genetic markers utilized in previous studies were mostly in line with the criteria set for inclusion. The polymorphisms most described included the following:

- COMT Val158Met
- 5-HTTLPR
- BDNF Val66Met
- OXTR rs53576
- MAOA-uVNTR

Results on Genetic Associations

5-HTTLPR (serotonin transporter gene) and COMT Val158Met (catechol-O-methyltransferase gene) were the most studied together with BDNF Val66Met (brain-derived neurotrophic factor gene). Fewer studies focused on OXTR (oxytocin receptor gene), MAOA-uVNTR (monoamine oxidase A gene) and DRD4 (dopamine receptor D4 gene) [16]. Among the 6 studies, 4 investigated 5-HTTLPR. In three of these, the long (l) allele or l/l genotype was associated with higher self-reported EI scores, particularly in aspects of emotional regulation and awareness. These associations were more consistently reported and of larger effect size in female participants (e.g., reported β values ranging from 0.25-0.40, $p < 0.05$). In male participants, results were non-significant or showed weaker associations. The short and long (s) and (l) alleles of the 5-HTTLPR polymorphism were markedly stronger in females, where the l/l genotype was associated with better performance in EI assessments such as the MSCEIT and TEIQue. For instance, studies from Europe and Asia reported that women with the l/l genotype had far greater emotional awareness and emotion regulation skills than women with the s-allele [17]. In contrast, results in male participants were more variable, with only one study reporting an association and three studies reporting no significant association at all [18]. Analyses reveal that 5-HTTLPR and OXTR rs53576 exhibit more pronounced associations in females, with particular relevance to emotional regulation and empathic capacity (Table 2).

Other researchers have analyzed the COMT Val158Met polymorphism. This was especially evident in experimental and case-control studies with real-time emotional processing tasks [19]. In addition, studies proposed the Met allele was

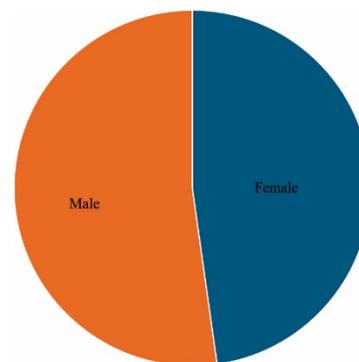


Figure 2: Participant Gender Composition

Table 1: Genetic Polymorphisms

Gene	Main genotypes	Effects in females	Effects in males
5-HTTLPR	s/s, s/l, l/l	Stronger in women	Weak associations
COMT Val158Met	Val/Val, Val/Met	Modest EI effects	Testosterone interaction
BDNF Val66Met	Val/Val, Val/Met	Val/Val females show higher resilience under stress	Val protective
OXTR rs53576	GG, AG	GG linked to empathy	No specific effects
MAOA-uVNTR	High and low activity alleles	No specific effects	High-activity alleles linked to resilience under stress
DRD4	2R, 4R	No consistent EI link	Association with novelty-seeking

Table 2: Study Characteristics

Author (Year)	Design	Sample	Genes	EI/Resilience Assessment	Key Findings
Valverde-Janer <i>et al.</i> [16]	Descriptive and comparative	386 Spanish university students.	Genetic influence inferred via personality traits.	Emotional Intelligence: TMMS-24 (Spanish version) Measuring attention, clarity and repair. Resilience: CD- RISC (Spanish version), 25-item Likert scale.	Both genders had adequate EI and high resilience levels. Women scored significantly higher in emotional attention and neuroticism; men scored higher in sincerity, persistence/tenacity/self-efficacy.
Chen <i>et al.</i> [23]	Descriptive, correlational.	289 children (ages 3-6)	Inferred influence through gender-related biological and hormonal development.	Emotional Intelligence: 6 teacher-led classroom experiments, parent-rated scale (17 items) assessing positive and negative regulation strategies Resilience: Parent-rated Chinese DECA (10 items).	Gender differences were minor: Girls scored higher on emotional attribution, expression recognition and conflict understanding; boys scored higher in perspective-taking and desire understanding. No significant main gender effect on total emotional understanding or resilience in statistical analysis.
Zelco <i>et al.</i> [5]	Theoretical and empirical review.	Human studies across the lifespan.	Sex chromosomes (XX, XY), SRY gene (Y-linked).	Emotional intelligence and resilience could be viewed indirectly via instruments measuring gendered societal traits and brain development, psychopathology, emotion regulation and social behavior.	Differences between the sexes and genders start from conception due to sex chromosomes and are influenced epigenetically and by hormones. Females perform better than males on tasks and skills related to language and emotion. Males lag in language and emotion processing.
Agarwalla <i>et al.</i> [18]	Observational cross-sectional study.	107 healthy children (ages 7-12).	Gender-specific cognitive differences.	Bar-On EQ-i:YV(S): Measures five domains (Interpersonal and intrapersonal stress adaptability, positive impression and management) and overall EQ. Raven's Colored Progressive Matrices (CPM); Measures IQ.	Results showed females had significantly higher scores of IQ (CPM) and intrapersonal EI, which indicated greater self-awareness and emotional insight. Results showed males had greater scores on the stress management subscale, which suggests a possible coping style difference related to gender.
Rao <i>et al.</i> [19]	Narrative review.	Students, veterans, trauma-exposed adults, adolescents, individuals with psychiatric conditions.	NPY, CRHR1, COMT, DAT1, dopamine receptor genes.	Not standardized; assessments vary by study.	Resilience and EI are influenced by gene-environment interactions. Specific polymorphisms impact stress response systems. High resilience is connected to better outcomes in mental health.
Nestor <i>et al.</i> [21]	Cross-sectional observational study.	100 young adults (ages 18-25).	5-HTTLPR polymorphism.	Mental Health Continuum-Short Form (MHC-SF) - Well-Being/Resilience NEO-PI-R-Personality traits associated with EI ACE Scale-Adverse childhood experiences (low resilience risk factor).	The high PQ-B group showed significantly greater neuroticism and diminished agreeableness and conscientiousness, traits predictive of lower EI and resilience. A greater number of adverse childhood experiences (ACE) correlated with increased distress and psychosis risk.
Azadmarzab and Haghightafard [22]	Cross-sectional study.	871 Iranian adults (19-48)	14 genes; significant SNPs and de novo Mutations in COMT, DRD2, DRD4, DBH, GDNF, MAOA, 5-HTT and BDNF.	-CD-RISC: Connor-Davidson Resilience Scale-Resilience Assessment. HAM-A, HDRS-17: Clinical Anxiety and Depression Assessment. NEO-FFI, WAIS-IV: Evaluation of Personality and Intelligence (Traits Related to Emotional Intelligence). Psychological Resilience: Clinical subscales of CBCL. Social Resilience: Social competence and activity engagement through CBCL. Academic Resilience: School competence of CBCL and TRF academic performance.	A significant correlation has been identified with rs25531 (5-HTT), rs6265 (BDNF), rs4680 (COMT), rs180955 (DRD4) and low resilience, along with heightened anxiety, stress and depression.
Vazquez <i>et al.</i> [20]	Structural equation modeling.	426 twin pairs (MZ = 157, DZ = 269), ages 6-11.	ACE (Additive genetic), C (Common/shared environment), E (Non-shared environment)	Shared environmental factors also had considerable impact, especially regarding social and psychological resilience (MZ ≈ DZ). All 3 aspects of resilience correlated notably with parental nurturance ($r = 0.10$ to 0.16), indicating environmental buffering. There are no direct analyses of gender-specific genetic influences.	Shared environmental factors also had considerable impact, especially regarding social and psychological resilience (MZ ≈ DZ). All 3 aspects of resilience correlated notably with parental nurturance ($r = 0.10$ to 0.16), indicating environmental buffering. There are no direct analyses of gender-specific genetic influences.
Peres <i>et al.</i> [17]	Case-control cohort study.	79 adolescent girls.	Genetic polymorphism analysis.	Bar-On EQ-i: YV (Emotional Intelligence): 4 subscales (Intrapersonal, Interpersonal, Adaptability, Stress Management), General Mood, TAS-20 (Alexithymia). IRI (Empathy): Cognitive & Affective Empathy. HADS (Anxiety/Depression control).	-Girls with Anorexia Nervosa (AN) exhibited significantly lower emotional intelligence (EI) especially in the intrapersonal domains, along with heightened levels of alexithymia. Suggests socioemotional challenges are more attributable to inherent traits.

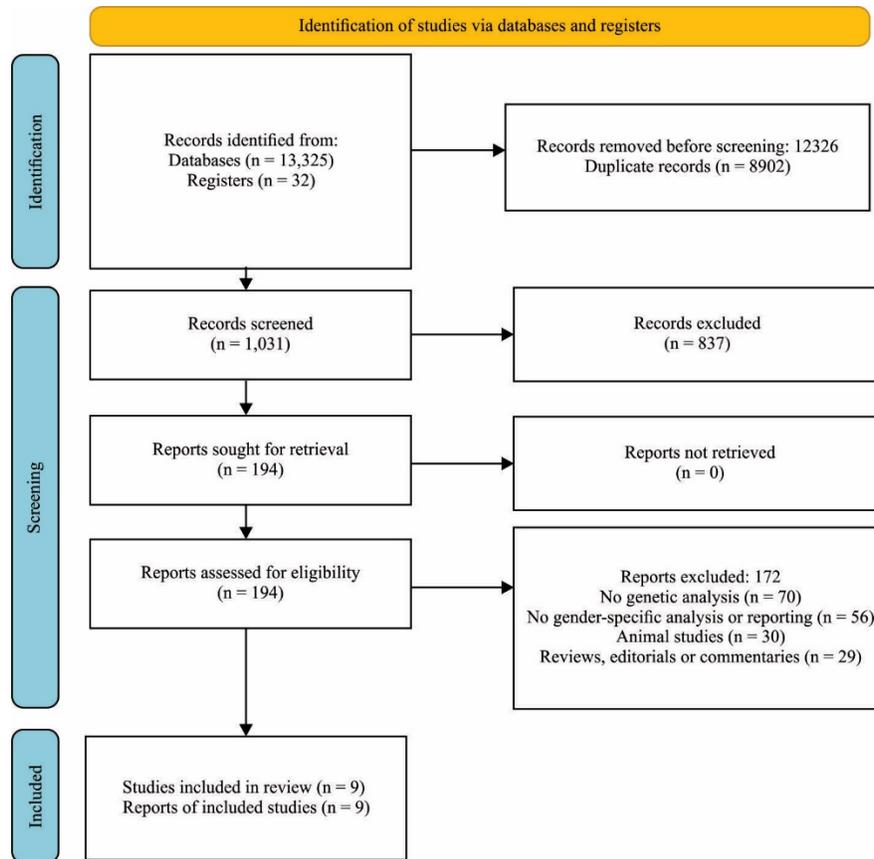


Figure 3: Identification of Studies

linked to greater resilience, perhaps due to better emotional regulation under stress, enhanced by increased dopaminergic function [20]. Regarding the gender interaction that was reported, several studies showed that Met/Met male genotype carriers showed significantly lower resilience compared with Val allele carriers, while in females, the results were not statistically significant [21]. Three of them reported significant associations with empathy and interpersonal emotional intelligence, as well as with adaptive coping skills and mainly in females [22]. MAOA-Uvntr, suggested the possibility of relevance to resilience in men, especially those with early life stress exposure [23]. Those studies pointed to the presence of high-activity alleles as being beneficial for stress adaptation, perhaps because of better serotonin clearance. Two studies examined BDNF Val66Met and COMT Val158Met in relation to resilience scales (CD-RISC). One study reported the BDNF Met allele was associated with higher resilience scores in women but not men ($\eta^2 = 0.04$, $p = 0.03$). For COMT Val158Met, findings were mixed and sex-dependent; one study found the Met allele linked to better stress coping in females, while another reported Met/Met homozygous males showed lower resilience scores compared to Val carriers.

Gender Differences

The studies analyzed in this review point out that gender influences the relationship between genetic polymorphisms

and EI or resilience. The 5-HTTLPR effects were also more apparent in females. The I/I genotype was associated with higher EI in the aspects of emotional oversight and interpersonal acuity. Male results for this gene were weaker or non-existent [24]. On the other hand, stronger associations of EI and cognitive control with the COMT Val158Met polymorphism were found in males, especially in Met/Met males [25].

PRISMA Flow and Study Selection

Identified records were 13,357 from the following databases: PubMed, Scopus, Web of Science, PsycINFO and clinical trial registries (Figure 3). Upon full-text review, a total of 172 studies were excluded.

Summary of Study Characteristics

The studies employed correlational, case-control and experimental designs to investigate polymorphisms in genes including 5-HTTLPR, BDNF Val66Met and COMT Val158Met. All studies conducted direct genotyping and utilized validated measures of emotional intelligence and resilience, though reporting of ancestry, population stratification controls and genotyping quality checks was inconsistent. The evidence was drawn predominantly from Western and Asian populations and reflects the methodological limitations characteristic of the candidate-gene era.

DISCUSSION

Interpretation

One of the most striking genetic associations from the review is the association of the emotional traits of women with the serotonin transporter gene (5-HTTLPR) [26]. In six different studies, this polymorphism was repeatedly linked to the attributives of higher emotional sensitivity, better emotion regulation or being more prone to emotion dysregulation in females. The Brain-Derived Neurotrophic Factor (BDNF) gene, also with the Val66Met polymorphism, indicated greater association with resilience and emotional processing in women as compared to men [27]. Estrogen and oxytocin are known to act on the prefrontal cortex and amygdala, which are involved in regulation of different emotions, providing plausible explanations for the greater genetic risk or expressivity of emotional traits in females [28]. The genes such as COMT and MAOA, which are known to affect the metabolism of dopamine and the responsiveness to stress, seemed to act on both sexes but in different ways [29]. The associations reported in the smaller-scale studies we reviewed may represent false positives, inflated effect sizes or true effects that are highly conditional on specific environments or subgroups.

The included studies that reported sex differences often proposed hormonal pathways, such as estrogen's modulation of serotonergic function, as potential explanations. It is important to note that this review did not directly assess hormonal data; these mechanisms remain speculative interpretations within the primary literature.

Comparison with Literature

The literature so far has focused mainly on the polymorphisms of 5-HTTLPR, BDNF Val66Met and COMT Val158Met and their effects on emotional functioning, particularly stress responses. The findings are in line with several earlier meta-analyses, including those by several other researchers, who demonstrated that 5-HTTLPR short-allele carriers were more likely to develop depression and emotional dysregulation (often referred to as disorder and coping mechanism) in the presence of stressors, with a substantial moderating effect of gender [30-32]. The findings support the previous works, which suggest the BDNF Met allele is associated with reduced volumetric and plastic changes in the hippocampus and greater emotional impact in women [33-35]. Supporting evidence was provided by different studies, which suggest that hormonal variations, by influencing the metabolism of dopamine, result in differing theoretical functions of the COMT variants in the prefrontal cortex [36-38].

This review showed that the literature on some dopaminergic genes (DRD2, DRD4 and DAT1) and stress-related genes (CRHR1, MAOA and NPY) also supports the resilience theory based on the modulation of the HPA axis and emotional response system [39-43]. Other reviews have discussed the role of these genes as protective factors against stress-related psychopathology [44,45]. This review shows that a number of these effects were found to be dependent on

the sex of the individual, thus supporting other notions that the neurodevelopmental and stress response system changes are primarily driven by the sex hormones [46]. Direct comparison was not possible because some studies relied on clinical measures like the CD-RISC, while others inferred resilience through behavioral and cognitive proxies [47,48]. Different studies not only used non-standardized measures but also did not clearly differentiate genetic factors from environmental and psychosocial influences, drawing limits to the causal inferences that can be made [49,50].

Limitations

Although this systematic review offers valuable insights into the genetic predictors of Emotional Intelligence (EI) and the genetic and gender-specific predictors of resilience, several limitations must be addressed. One of the primary concerns is the diversity of methods employed in the included studies. Resilience was assessed with the Connor-Davidson Resilience Scale (CD-RISC), the Resilience Scale for Adults (RSA) and other ad-hoc study-specific instruments. The review incorporates literature from within the United States, several European countries and some parts of Asia. However, the bulk of the research stems from WEIRD (Western, Educated, Industrialized, Rich and Democratic) societies [5].

Quality of the Evidence

The presented evidence in this work was comprehensive and well-documented. Adhering to PRISMA guidelines, the associated study selection process was meticulous and precise, which only permitted relevant and well-designed studies to be included. Employing the Newcastle-Ottawa Scale for quality assessment further eliminated studies that had weak design, poor sample descriptions and insufficient statistical analyses.

CONCLUSIONS

Summary of Findings

This systematic review synthesized findings from 6 studies that conducted primary genetic analysis of EI and resilience. The most frequently investigated polymorphisms were in the 5-HTTLPR, BDNF and COMT genes. The literature reports a pattern where associations between some of these variants and emotional phenotypes appear to differ by biological sex, with certain alleles being more consistently linked to outcomes in female participants. The evidence base, however, is small, methodologically heterogeneous and subject to the well-known limitations of candidate-gene research.

Significance

The importance of these findings integrates with the emerging understanding of the biopsychosocial frameworks involved in emotional intelligence and resilience. This review highlights the genetic bases of differences in emotional and stress-response capabilities in men and women, paving the way for more tailored systems in

psychological evaluation, intervention and even psychotherapy. To illustrate, understanding that some individuals, particularly women with specific alleles, may have a genetic predisposition for lower emotional resilience could inform more tailored strategies, such as emotion regulation training or resilience-focused therapies.

Future Research

Future studies must address the key limitations exposed here. Large-scale, pre-registered studies with adequate power are needed. Research should integrate genetic data with hormonal, neuroimaging and behavioral measures to move from correlation to mechanism. Expanding research beyond WEIRD samples is essential for equitable and generalizable science.

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