Research

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Mapping Trauma-Related Psychiatric Genetics: A Bibliometric Study on Gene, Epigenetic and Resilience

Travma ile İlişkili Psikiyatrik Genetik Haritalama: Gen, Epigenetik ve Dayanıklılık Üzerine Bibliyometrik bir Çalışma

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ABSTRACT

Objective: This study explored the development of research in the genetics and epigenetics of trauma-related psychiatric outcomes, delineating the journals, institutions, countries and research themes that have characterized the literature.

Method: We performed a search in the Web of Science Core Collection for publications with search terms related to chosen hypothalamic-pituitary-adrenal (HPA)-axis genes, genetic and epigenetic mechanisms, and trauma-related outcomes. The final dataset consisted of 863 publications. Biblioshiny was used to characterize publication patterns and research performance; VOSviewer was used to visualize co-citation relationships, international collaboration, keyword co-occurrence, and influential sources.

Results: The USA had the highest number of publications followed by Germany, China and the Netherlands. The number of citations increased significantly after 2015 The analysis of collaboration revealed strong ties between European countries, with more recent input from Asia. Changes in keyword patterns also pointed to a broader thematic change. Recent work has increasingly incorporated epigenetics, resilience, and social support.

Conclusion: The literature on psychiatric outcomes of trauma has expanded from a narrow focus on genetic susceptibility to include epigenetic regulation, neurobiological processes, and resilience.

Keywords: Post traumatic stress disorder, resilience, epigenetics, HPA-axis genes, bibliometric analysis

ÖZ

Amaç: Bu çalışma, travmayla ilişkili psikiyatrik sonuçların genetiği ve epigenetiğine yönelik araştırmaların kapsamlı bir bibliyometrik analizini gerçekleştirmeyi; temel dergiler, kurumlar, ülkeler ve güncel araştırma konularına odaklanmayı amaçlamıştır.

Yöntem: Veriler, seçilmiş hipotalamus-hipofiz-adrenal (HPA) ekseni genleri, genetik ve epigenetik mekanizmalar ve travmayla ilişkili sonuçlarla ilgili anahtar kelimeler kullanılarak Web of Science Core Collection veri tabanından elde edilmiştir. Toplam 863 yayın analiz edilmiştir. Tanımlayıcı analizler için Biblioshiny kullanılırken, ortak atıf örüntüleri, iş birlikleri, anahtar kelime eş-oluşumları ve temel kaynaklara ilişkin ağ görselleştirmelerinin oluşturulmasında VOSviewer kullanılmıştır.

Bulgular: Yayınların ülkelere göre dağılımı incelendiğinde, Amerika Birleşik Devletleri ilk sırada yer alırken Almanya, Çin ve Hollanda onu izlemektedir. Atıf sayılarında özellikle 2015 sonrasında belirgin bir yükseliş gözlenmiştir. Ülkeler arası iş birliği açısından Avrupa'daki güçlü bağlantılar dikkat çekerken, Asya kaynaklı bilimsel katkının daha yakın dönemde arttığı görülmektedir. Anahtar kelimelerdeki değişim de araştırma gündemindeki dönüşümü yansıtmaktadır. Son dönemde epigenetik ve psikolojik sağlamlığın yanı sıra sosyal desteği de içeren daha geniş temalara doğru bir yönelim gözlenmiştir.

Sonuç: Bulgular, travmayla ilişkili psikiyatrik sonuçlar üzerine gelişen literatürün genetik yatkınlıkla sınırlı kalmadığını; epigenetik düzenleme, nörobiyolojik süreçler ve psikolojik sağlamlık gibi farklı araştırma eksenlerini de kapsadığını göstermektedir.

Anahtar sözcükler: Travma sonrası stres bozukluğu, dayanıklılık, epigenetik; HPA-ekseni genleri

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Introduction

Responses to severe psychological trauma can vary widely between individuals, dependent upon a combination of environmental exposures, genetic susceptibility and epigenetic regulation (Yehuda and Daskalakis 2016). One of the major neuroendocrine systems that mediates the body's response to prolonged or severe stress is the hypothalamic-pituitary-adrenal (HPA)-axis (Heim 2001, Nemeroff 2001, McEwen 2007). Prolonged dysregulation of the HPA-axis can lead to alterations in brain structure and neurochemistry, potentially increasing the risk of anxiety, major depression, and post traumatic stress disorder (PTSD) (Yehuda and Daskalakis 2013, McEwen 2015). However, responses to trauma are heterogeneous, and some individuals may exhibit resilience or even post-traumatic growth (Yehuda 2002, Feder 2009, Yehuda 2004).

Over the past two decades, psychiatric genetics has progressed from early candidate gene association studies to an integrative framework encompassing dynamic chromatin and DNA modifications, genome-wide association studies (GWAS), and gene-by-environment (G×E) interactions (Klengel 2015, Binder 2015; Zannas 2014, West 2014). Within this framework, a core set of candidate genes has been identified as key biological factors involved in neural plasticity, recovery, and responses to trauma.

The most important molecular regulators of the stress response include the nuclear receptor subfamily 3 group C member 1 gene (NR3C1), which encodes the glucocorticoid receptor, and FK506 binding protein 5 (FKBP5), which is involved in the ultra-short negative feedback regulation of glucocorticoid sensitivity (Binder 2009). Early-life adversity and trauma may recalibrate long-term stress reactivity and contribute to potential intergenerational effects through epigenetic modifications, such as allele-specific DNA demethylation of FKBP5 and altered promoter methylation of NR3C1 (Klengel 2013, Yehuda 2016). Adult neurogenesis, synaptic consolidation, hippocampal integrity, fear conditioning, and fear extinction learning are influenced by brain-derived neurotrophic factor (BDNF), particularly by its functional Val66Met polymorphism (Bramham 2005, Messaoudi 2005, Mahan 2012, Ressler 2012).

Catechol-O-methyltransferase (COMT) and the serotonin transporter-linked polymorphic region (5-HTTLPR/SLC6A4) may contribute to individual differences in emotional reactivity, threat processing, prefrontal executive function and cognitive flexibility under traumatic stress (Caspi 2003). OXTR signaling adds a social component to this biological framework as it is associated with social cognition, affiliative behavior and attachment, and the modulation of psychological stress .

Thus, we examined six genes that are often mentioned in the trauma literature: COMT, BDNF, FKBP5, NR3C1, OXTR and SLC6A4/5-HTTLPR. They were chosen based on the extent of their study and their relevance to biological processes implicated in stress and trauma responses. In total, these genes encompass several interacting systems including neuroendocrine feedback, neuroplasticity, monoaminergic regulation and neuropeptidergic mechanisms that have been linked to social responses to stress (Daskalakis 2013). This well defined group allowed us to explore different complementary aspects of the neurobiological response to trauma in a common bibliometric framework.

There is a lot of primary research and review literature on the genetics and epigenetics of trauma, but it is difficult to see how the field has progressed overall. The usual type of review will focus on particular genes, molecular mechanisms and/or clinical phenotypes. This means less transparency of bigger trends, e.g. in publication activity, international and institutional collaborations, and research topics. Bibliometric analysis and science mapping offer a way to examine these features across a large body of literature and to trace how the structure and focus of a research field change over time (Aria 2017, Cuccurullo 2017, Donthu 2021).

Against this background, we addressed four questions. First, how did publication output and citation patterns in trauma-related genetics and epigenetics change between 2004 and July 2026? Second, which countries, institutions, and core journals contributed most prominently to the literature and its intellectual structure? Third, what do co-citation patterns and international collaboration networks reveal about the intellectual and collaborative organization of the field? Finally, how did thematic clusters and keyword patterns change over time, particularly as research attention expanded from symptom-focused genetic

markers toward epigenetic regulation and resilience-related concepts? Accordingly, this study focused on a defined set of frequently investigated candidate genes relevant to HPA-axis and stress-related pathways, with the broader aim of mapping the development of this literature and identifying directions for future translational research.

Method

Data Source and Search Strategy

We searched the Web of Science Core Collection (WoSCC; Clarivate Analytics), including SCI-EXPANDED, SSCI, A&HCI, and ESCI, for publications relevant to the study. WoSCC was chosen because of the standardized reference metadata, established indexing criteria and multidisciplinary coverage of research in psychiatry and neurobiology. All searches and data extraction were performed on 29 July 2026 to ensure consistency of the dataset and to minimize variation due to database updates or indexing lags. The search terms were combined using Boolean operators in the Topic (TS) field, which comprises titles, abstracts, author keywords and Keywords Plus.

TS = ("COMT" OR "BDNF" OR "FKBP5" OR "NR3C1" OR "OXTR" OR "SLC6A4" OR "5-HTTLPR" OR "HPA-axis genes") AND ("genetic" OR "epigenetic" OR "polymorphism" OR "SNP" OR "methylation" OR "gene expression") AND ("resilience" OR "post-traumatic growth" OR "post-traumatic stress disorder" OR "PTSD" OR "trauma").

Because the search was conducted on July 29, 2026, publication data for 2026 represent only a partial year.

Eligibility Criteria and Screening Process

Retrieved bibliographic records were screened according to predefined eligibility criteria:

Inclusion criteria were (1) Peer-reviewed original research articles (Article, n=679; 78.2%) and review articles (Review, n=189; 21.7%); (2) studies published between 2004 and July 29, 2026; and (3) studies directly examining relationships among the targeted HPA-axis/stress-related genes, epigenetic mechanisms, and trauma-related clinical outcomes or resilience. Exclusion criteria were (1) Non-peer-reviewed or other publication types, including conference proceedings, meeting abstracts, book chapters, editorials, letters, early access documents, and errata/corrigenda; (2) duplicate records; and (3) publications outside the scope of trauma-related psychiatric genetics (e.g., studies investigating candidate genes exclusively in oncological, cardiovascular, or other somatic contexts without relevance to psychological trauma).

Although no language restrictions were applied during the initial search, the vast majority of records were published in English (n=856), with a small number published in Russian (n=2), Spanish (n=2), French (n=2), and Chinese (n=1), resulting in a final curated dataset of 863 publications. Complete bibliographic records, including citation information and cited references, were exported as tab-delimited text files for subsequent computational analysis.

Computational Software and Statistical Analysis

A dual-software approach was used for data analysis. The bibliometrix package (version 4.1.2), implemented through the Biblioshiny interface in R (version 4.3.0), was used to generate descriptive statistics, calculate the compound annual growth rate (CAGR), assess source-level impact (H-index and Bradford's law), and evaluate institutional and country contributions. VOSviewer (version 1.6.19; Leiden University) was used for science mapping, network analysis, clustering, and overlay visualization.

Network Mapping Parameters and Threshold Settings

To ensure methodological transparency and reproducibility, specific threshold values and clustering parameters were defined in VOSviewer (Van Eck 2010, Waltman 2010).

Co-Citation Network (Cited References): The minimum citation threshold for each cited reference was set at 20 citations.

Country Collaboration Network: The minimum document threshold for each country was set at five documents.

Keyword Co-Occurrence Network: For the combined Author Keywords and Keywords Plus, we required a minimum of 10 occurrences for a keyword to enter the network. This threshold provided a good trade off between detail and readability, as lower values produced maps that were too dense and higher values removed nodes that were conceptually relevant to the analysis.

Clustering and Normalization: The network was clustered and analyzed for modularity using the default algorithms LinLog/Modularity Optimization in VOSviewer. We used association strength normalization to determine proximity of nodes.

Methodological Limitations Related to Database Coverage

The Web of Science Core Collection does not cover all scholarly journals, so its indexing may be biased toward English-language, Western, and higher-impact publications. Therefore, this limitation in coverage was taken into account when interpreting the differences in research output and collaboration between countries.

Ethical Statement

No ethical approval was needed for this study because only publicly available secondary data were used for the analysis.

Results

Descriptive Performance and Growth Dynamic

The final dataset includes 863 publications published between 2004 and July 2026, where 2026 is a partial publication year. Over this period, publication output grew at a compound annual growth rate (CAGR) of 8.9%. The publication and citation trends have increased significantly after 2011, with the publication output reaching the highest level in 2021 (74 articles, 3,365 citations). Research activity remained high through 2025, and substantial activity was also seen in the partial 2026 data (65 articles, 3,380 citations) (Figure 1).

The 863 publications have received a total of 33,480 citations, with an average of 38.80 citations per publication (Table 1).

Table 1. Descriptive statistics of the bibliometric dataset (2004–2026)

Category	Indicator / Parameter	Value / Distribution
Timespan	Publication Years (Range; Median)	2004–2026; Median: 2017
Document Types	Original Research Articles	679 (78.2%)
	Review Articles	189 (21.7%)
Language Distribution	Primary / Secondary Languages	English: 856; Russian: 2; Spanish: 2; French: 2; Chinese: 1
Dataset Volume	Total Publications (N)	863
Citation Impact	Total Citations	33,480
	Average Citations per Document	38.80
Annual Growth Rate	Compound Annual Growth Rate (CAGR)	8.92%

Detailed information on the 10 most-cited papers, including authors, titles, publication years, journals, and citation counts (e.g., Krishnan 2007, 1,875 citations; Perroud 2011, 374 citations), is presented in Table 2.

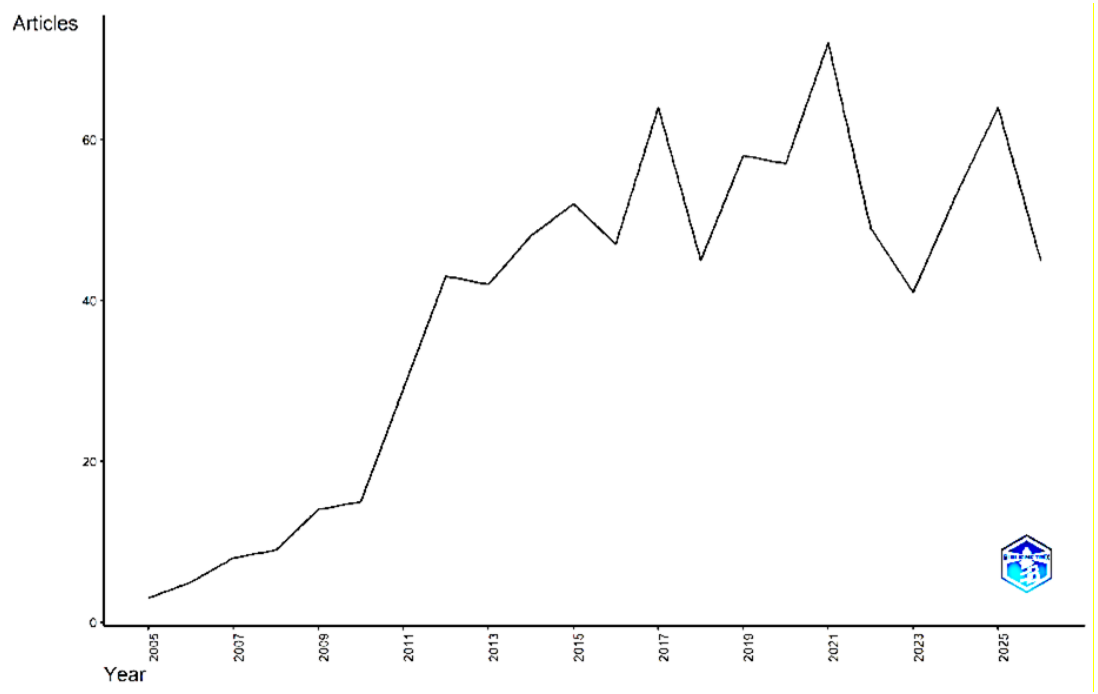


Figure 1. Annual scientific production and citation dynamics (2004–July 2026; partial year)

*T*he figure shows annual publication counts on a single y-axis. Citation totals are reported in the text but are not displayed on a separate axis.

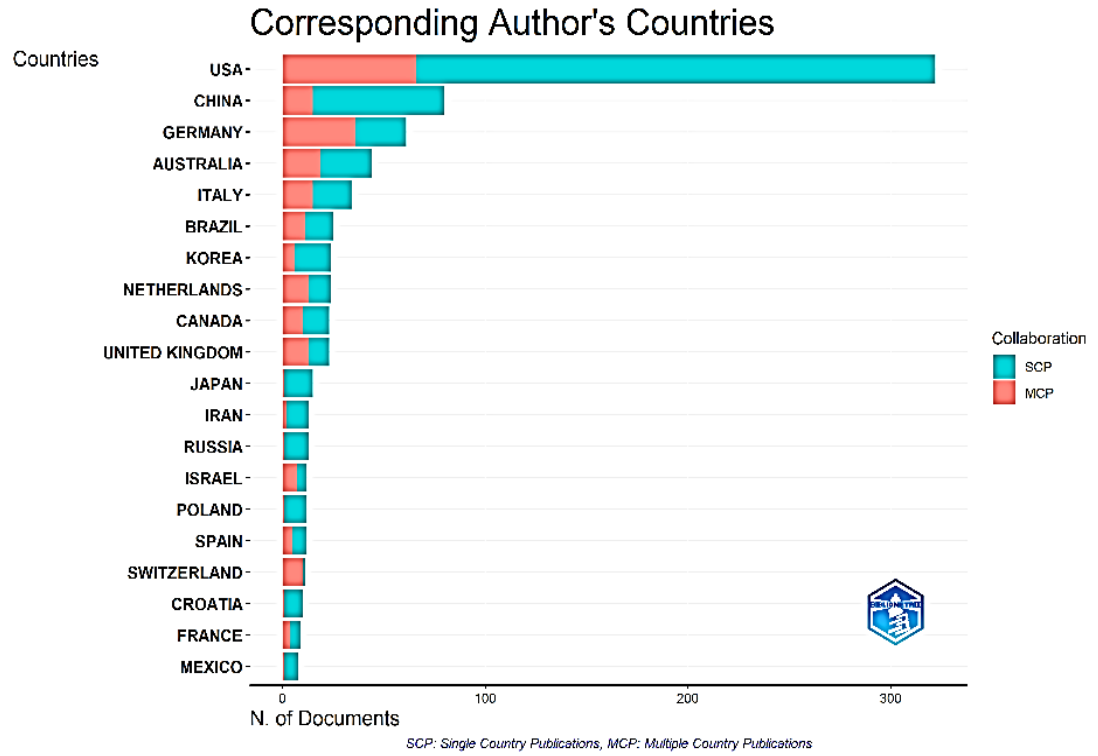


Figure 2. Global scientific production by corresponding author country.

The horizontal bar chart shows the 20 most productive countries based on the corresponding authors' affiliations. Publication output is stratified into single-country publications (SCPs) and multiple-country publications (MCPs), as calculated using the bibliometrix package in R. The United States had the highest publication output (n=406), followed by Germany and China

Table 2. Top 10 most cited publications in trauma genetics and epigenetics

Rank	Title	Authors	Journal	Year	Total Citations
1	Molecular adaptations underlying susceptibility and resistance to social defeat in brain reward regions	Krishnan V, Nestler EJ, et al.	Cell	2007	1,875
2	Mechanisms of stress in the brain	McEwen BS, Nasca C, et al.	Nature Neuroscience	2015	1,068
3	Association of FKBP5* polymorphisms and childhood abuse with risk of PTSD* symptoms in adults	Binder EB, Ressler KJ, et al.	JAMA	2008	1,067
4	BDNF* function in adult synaptic plasticity: The synaptic consolidation hypothesis	Bramham CR, Messaoudi E.	Progress in Neurobiology	2005	964
5	Psychobiology and molecular genetics of resilience	Feder A, Charney DS, Nestler EJ.	Nature Reviews Neuroscience	2009	895
6	Understanding resilience	Wu G, Feder A, Charney DS, et al.	Frontiers in Behavioral Neuroscience	2013	517
7	Holocaust exposure induced intergenerational effects on FKBP5 methylation	Yehuda R, Binder EB, Klengel T, et al.	Biological Psychiatry	2016	483
8	Fear conditioning, synaptic plasticity and the amygdala: implications for PTSD	Mahan AL, Ressler KJ.	Trends in Neurosciences	2012	464
9	Vantage sensitivity: Individual differences in response to positive experiences	Pluess M, Belsky J.	Psychological Bulletin	2013	436
10	Increased methylation of glucocorticoid receptor gene (NR3C1)* in adults with childhood maltreatmen	Perroud N, Courtet P, et al.	Translational Psychiatry	2011	374

*FKBP5: FK506 binding protein 5; PTSD: Post-traumatic stress disorder; BDNF: Brain-derived neurotrophic factor; NR3C1 : nuclear receptor subfamily 3, group C, member 1

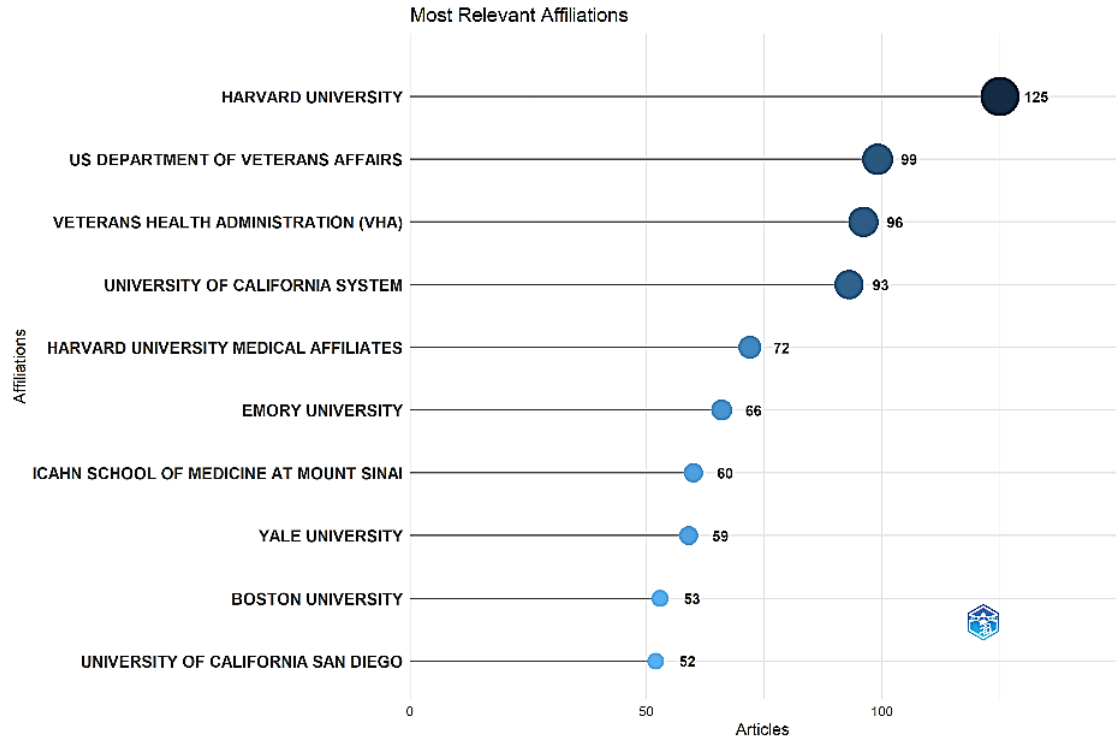


Figure 3. Institutional output of leading affiliations.

The lollipop chart shows the 10 most productive academic and governmental research institutions. Larger nodes and longer horizontal bars represent higher numbers of publications. Harvard University (125 publications) had the highest publication output, followed by the U.S. Department of Veterans Affairs (99 publications) and the Veterans Health Administration (96 publications)

Productivity by Country and Institution

The United States accounted for the largest share of publications based on corresponding author country, contributing 406 papers (46.7% of the total). Germany ranked second with 105 publications (12.1%), followed by China (n=87, 10.0%) and Australia (n=52, 6.0%). The Netherlands and Italy contributed 41 publications each (4.7%) (Figure 2).

An analysis of single-country publications (SCPs) and multiple-country publications (MCPs) showed that, although the United States had the highest number of SCPs, European countries, including Germany, the Netherlands, and the United Kingdom (UK), had notably high MCP proportions exceeding 35%.

At the institutional level, Harvard University had the highest publication output, with 125 publications, followed by the U.S. Department of Veterans Affairs (n=99), the Veterans Health Administration (n=96), the University of California System (n=93), Harvard University Medical Affiliates (n=72), and Emory University (n=66) (Figure 3). Major U.S. institutions together contributed more than half of the total institutional research output, indicating a strong academic and governmental presence in this research area.

Core Journals and Local Source Impact

Local source impact was evaluated using local H-index scores and citation counts (Figure 4). Translational Psychiatry ranked highest, with a local H-index of 18 and 642 local citations. It was followed by the Journal of Affective Disorders (local H-index=16; 588 local citations), Psychoneuroendocrinology (local H-index=16; 574 local citations), Biological Psychiatry (local H-index=15; 512 local citations), and Frontiers in Psychiatry (local H-index=15; 480 local citations). Local citation patterns also identified Biological Psychiatry, Translational Psychiatry, and Psychoneuroendocrinology as some of the most dominant sources in the dataset, mirroring their prominent representation in the literature on trauma-related psychiatric genetics and epigenetics.

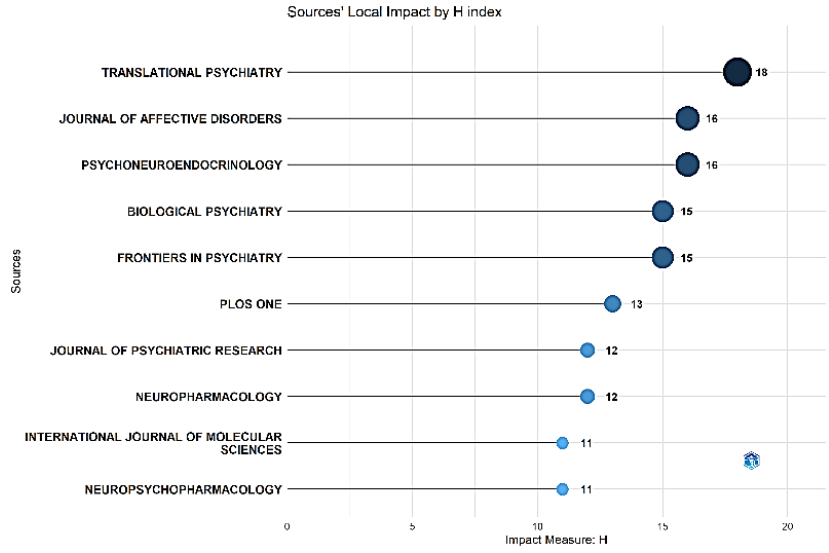


Figure 4. Local source impact by local h-index.

The lollipop chart shows the 10 journals with the highest local H-index values within the dataset of 863 publications, as calculated using the bibliometrix package in R. Translational Psychiatry (H-index=18), Journal of Affective Disorders (H-index=16), and Psychoneuroendocrinology (H-index=16) showed the highest local H-index values.

Co-Citation Network and Intellectual Structure

The co-citation network was built with a minimum threshold of 20 citations and included 112 interconnected nodes grouped in three main thematic clusters (Figure 5). The red cluster is centered on HPA-axis and epigenetic research and includes key studies of FKBP5 genetic variation (Binder 2008), allele-specific DNA demethylation (Klengel 2013), and glucocorticoid receptor reprogramming (McGowan

2009, Yehuda 2013). The green cluster was characterized by the study of neuroplasticity, BDNF and fear extinction including the study of BDNF Val66Met polymorphism (Egan 2003; Hariri 2003) and amygdala-related synaptic plasticity (Ressler 2011). The yellow/blue cluster was illustrative of earlier gene-by-environment models and serotonergic sensitivity, especially the area of research concerning the 5-HTTLPR polymorphism (Caspi 2003, Risch 2009). Together, these clusters offer a map of the field's intellectual structure and show how multiple biological pathways are represented in the literature on trauma-related psychiatric genetics.

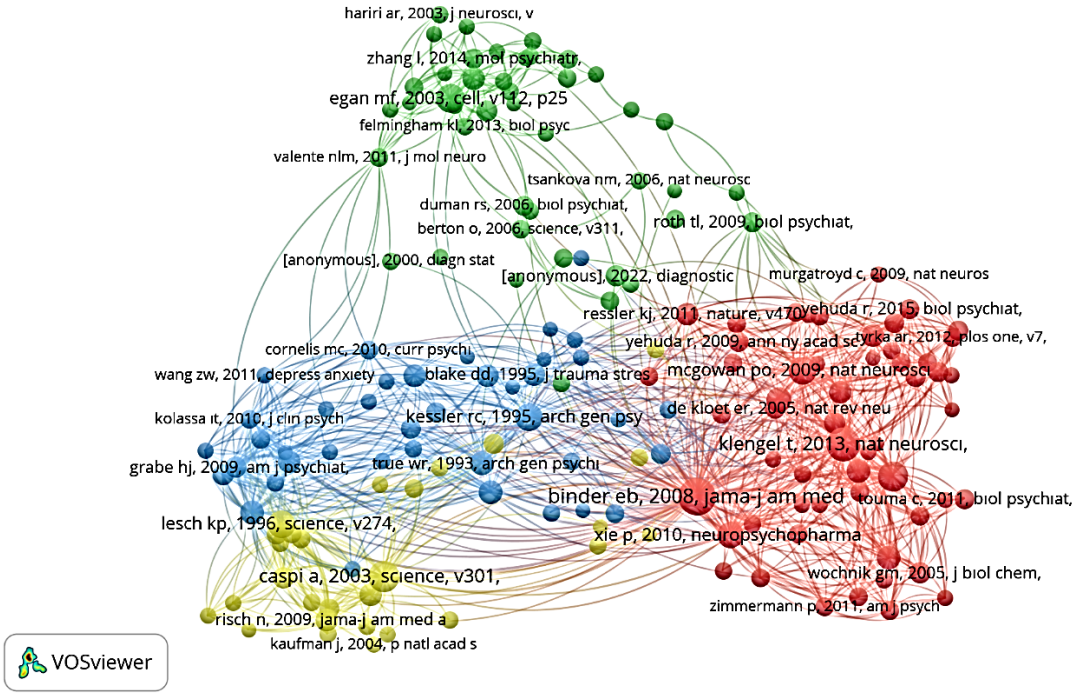


Figure 5. Co-citation network of landmark publications.

The VOSviewer co-citation network of cited references was constructed using a minimum co-citation threshold of 20 citations, resulting in 112 visualized nodes. Co-citation intensity normalization and LinLog/modularity clustering were applied. Node size represents the overall number of co-citations, whereas link thickness indicates co-citation intensity. Node colors represent different intellectual clusters: red, HPA-axis and epigenetics (FKBP5, NR3C1); green, neuroplasticity and fear extinction (BDNF); and yellow/blue, early gene-by-environment (G×E) models and monoaminergic vulnerability (5-HTTLPR, COMT).

Cross-National Collaboration Networks

The cross-national collaboration network was established with a minimum threshold of five articles per country and includes 28 nations (Figure 6). The United States was the most central country in the network with the highest total link strength (TLS > 320) and close collaborative linkages with Germany, China, the Netherlands and Australia. The European countries were linked together in a complex but largely decentralized regional network, with notably strong ties between Germany, the Netherlands, the United Kingdom (UK) and Switzerland. A more recent collaborative activity trend was seen for East Asia, especially for China and South Korea, whose typical publication years in the overlay visualization were between 2020 and 2022.

Keyword Co-Occurrence and Thematic Evolution

The keyword co-occurrence overlay showed shifts in thematic emphasis throughout time and contained 134 terms that met the minimum criterion of 10 occurrences (Figure 7). Candidate gene variations and diagnostic concepts dominated the network during the earlier period (2004–2014; blue/purple nodes), with phrases like 5-HTTLPR, serotonin transporter, COMT, PTSD, depression, and anxiety showing up frequently. The later time frame (2015–2026; green/yellow nodes) was distinguished by a stronger focus on positive

adaptation and epigenetic mechanisms. Terms including epigenetics, DNA methylation, histone acetylation, neuroplasticity, resilience, stress resilience, and social support were frequently used. Taken together, the keyword patterns suggest that the literature has broadened from an earlier emphasis on symptom-related genetic markers to include epigenetic, neurobiological, and psychosocial perspectives.

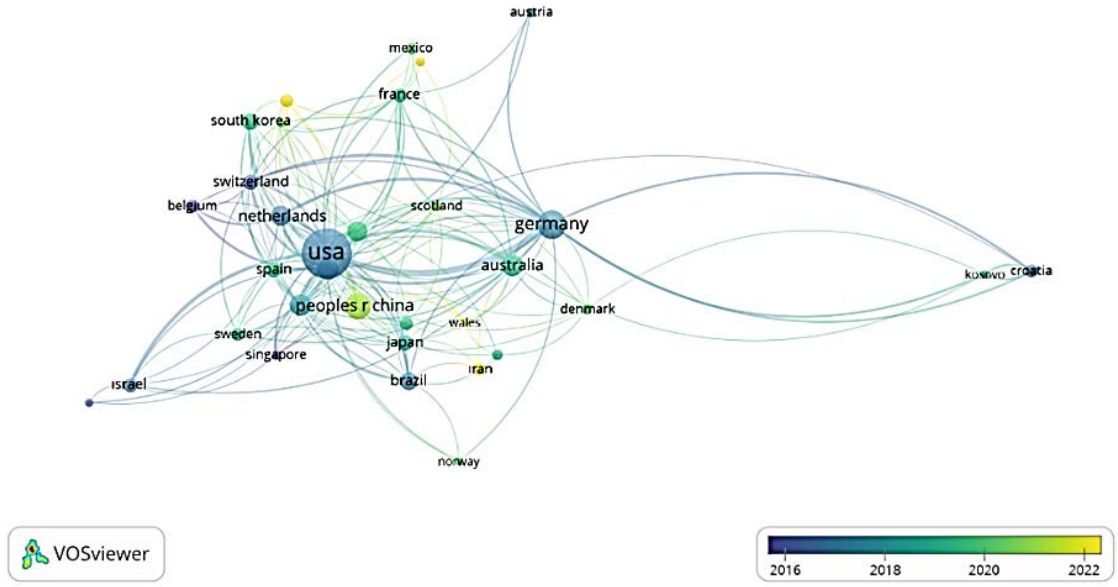


Figure 6. Cross-national collaboration network overlay.

The VOSviewer country co-authorship overlay network was constructed using a minimum threshold of five documents per country, with 28 countries displayed. Node size represents country-level publication output, and link thickness indicates the strength of collaboration between countries. Node color represents the average publication year according to the overlay color gradient (dark blue, 2016; yellow, 2022), illustrating temporal patterns in international collaboration, including more recent research activity in China and South Korea.

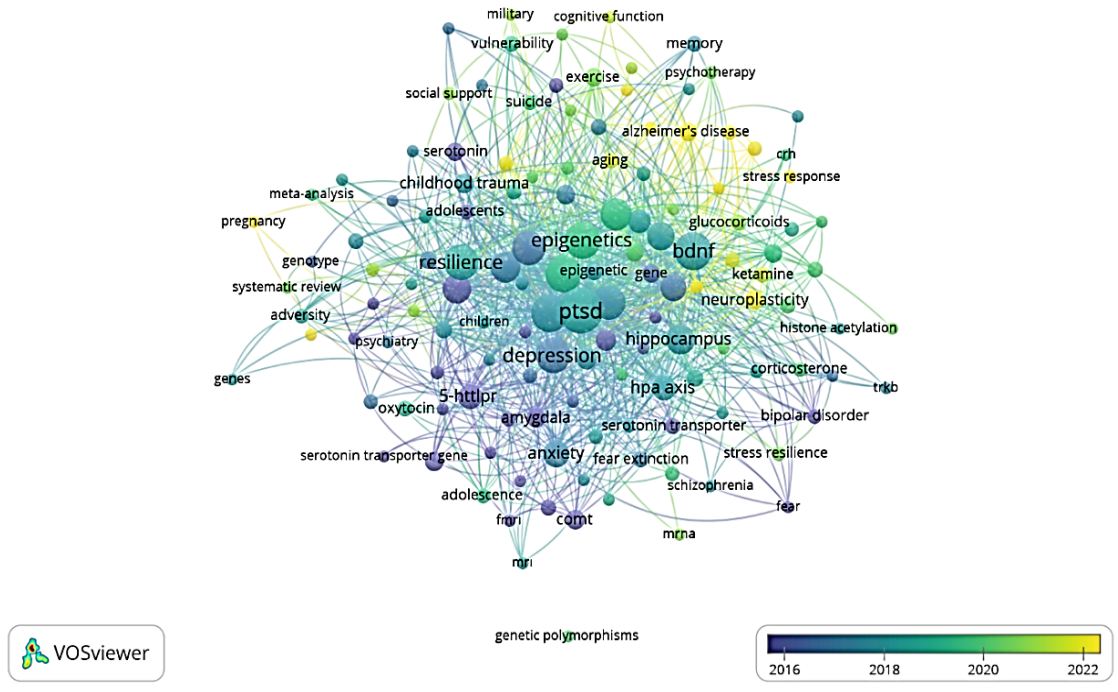


Figure 7. Keyword co-occurrence network and thematic trend overlay

The VOSviewer keyword co-occurrence overlay visualization was generated using a minimum threshold of 10 occurrences, with 134 keywords mapped. Node size represents keyword occurrence frequency, whereas links indicate co-occurrence strength. Node color represents the average publication year according to the overlay color gradient, with earlier themes shown in blue and more recent themes in green/yellow. The visualization indicates a thematic shift from candidate gene and symptom-focused research toward epigenetics, neuroplasticity, resilience, and related psychosocial themes

Local citation patterns placed Biological Psychiatry, Translational Psychiatry, and the Journal of Affective Disorders among the most frequently cited journals in the dataset.Their prominence indicates their substantial contribution to the literature on genetic and epigenetic mechanisms related to trauma (Figure 8).

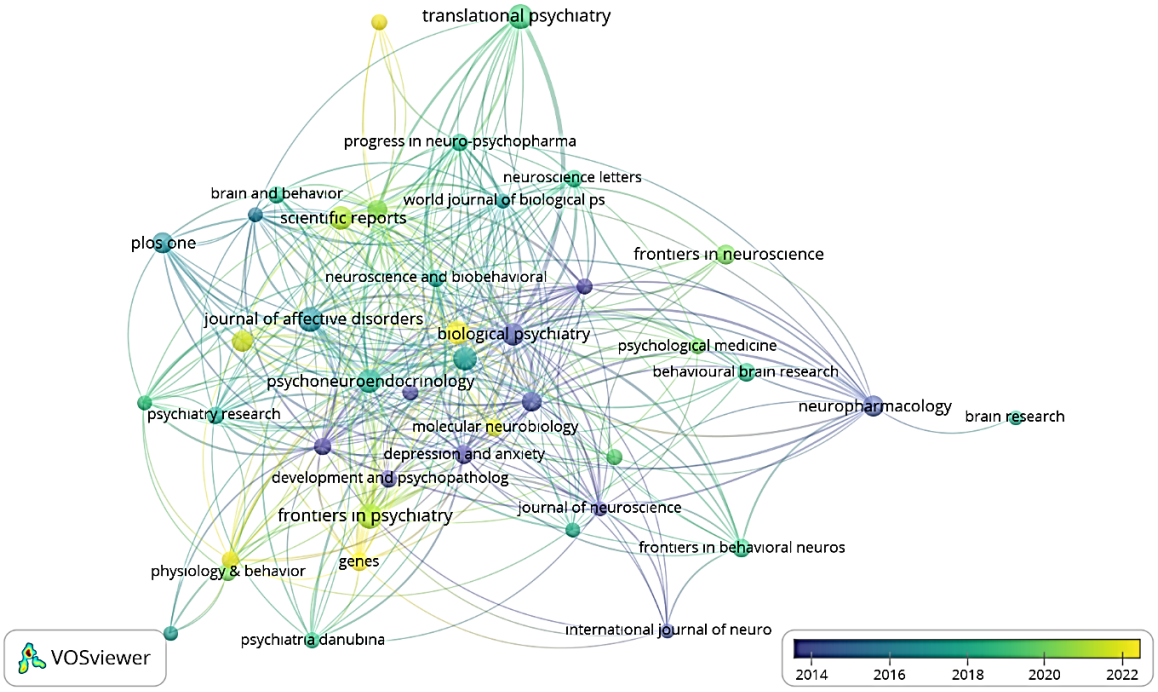


Figure 8. Most locally cited sources in the intellectual base

The VOSviewer journal co-citation overlay map includes 42 sources meeting a minimum citation threshold of 20. Node size represents the total number of local citations, whereas link thickness indicates the strength of co-citation relationships between sources. Node color represents temporal patterns in source activity according to the overlay color gradient, with earlier sources shown in blue and more recent sources shown in yellow.

Discussion

This bibliometric analysis provides a systematic, data-driven overview of global research on trauma-related psychiatric genetics and epigenetics from 2004 through July 2026. Because data collection for 2026 was completed on July 29, publication counts for that year reflect only partial-year output and should therefore be interpreted with caution when compared with those of previous years. By integrating performance indicators with network visualizations, this study provides insights into the collaborative structures, conceptual shifts, and intellectual evolution of this rapidly developing field.

Thematic evolution was clearly reflected in keyword co-occurrence patterns (Figure 7) and co-citation clustering (Figure 5). During the earlier period (2004–2013), research was dominated by candidate gene approaches, particularly those focusing on the serotonin transporter (5-HTTLPR/SLC6A4) and COMT, with the influential gene-by-environment (G×E) model introduced by Caspi (2003) playing a prominent role. However, extensive methodological critiques and difficulties in replicating findings from candidate gene G×E studies (Risch 2009) appear to have contributed to a broader conceptual shift in the field.

Our overlay mapping shows that research after 2015 was more directed to systemic neuroplasticity and molecular epigenetics. Allele-specific FKBP5 DNA demethylation (Klengel 2013) and NR3C1 hypermethylation associated with early-life adversity (McGowan 2009, Perroud 2011) have helped shed light on molecular mechanisms by which severe psychological trauma can be biologically embedded. Also the keyword patterns showed a similar change. Earlier emphasis on pathology-oriented categories including PTSD and major depression was increasingly supplemented by concepts of positive adaptation such as resilience, vantage sensitivity and the potential buffering role of social support (Feder 2009, Wu 2013,

Kalisch 2015). This more overarching thematic development may be indicative of a change in clinical perspective, where genetic and epigenetic mechanisms are being considered not only in connection to vulnerability, but also to recovery, treatment response, and long-term adaptation (Yehuda 2016).

The geographical distribution of publications was heavily biased toward the United States, which accounted for 46.7% of the total output. Germany, China and Netherlands also made substantial contributions to the literature (Figure 2). Part of the high U.S. contribution may reflect the size of the research funding and infrastructure, including that of the National Institutes of Health (NIH) and the Department of Veterans Affairs (VA). In this research environment, the VA has opportunities to study large veteran populations and to do genomic research on trauma-related conditions such as PTSD, which may help explain the strong U.S. presence in this field.

European countries like Germany, the Netherlands and the United Kingdom had stronger international collaboration with MCP proportions above 35%, compared with the more centralized U.S. structure. This pattern could be partially explained by a multinational research framework and funding structure that promotes collaboration across national borders. The collaboration network (Figure 6) also indicated more recent research activity in East Asia, particularly in China and South Korea, with publication activity clustered in the 2020–2026 period.

Analysis of local citations and H-index (Figure 4) indicated that Translational Psychiatry, Journal of Affective Disorders, Psychoneuroendocrinology and Biological Psychiatry were some of the most influential journals in the field. Their high profile in molecular neurobiology and in clinical psychiatry is a reflection of the translational orientation of the field, in particular the rising interest in understanding the potential clinical relevance of genetic and epigenetic markers in trauma-related psychiatric outcomes.

There are several limitations to keep in mind when interpreting these results. Only the Web of Science Core Collection was searched. Though WoSCC offers standardized metadata and quality citation information, it may not be as representative for non-English language publications, regional journals and monographs, and thus could favor English language and Western scholarships. The search was conducted on six candidate genes with a large number of studies (COMT, BDNF, FKBP5, NR3C1, OXTR and SLC6A4). This choice mirrors their well-established presence in stress and trauma-related research but excludes other emerging candidates, including CRHR1 and ADCYAP1R1, and more general polygenic approaches based on genome-wide association studies (GWAS). Therefore, our results should be interpreted as a bibliometric map of studies on chosen candidate genes instead of a full picture of trauma-related psychiatric genetics. Citation-based measures also have the additional limitation of reflecting scholarly attention, not clinical utility . Thus, a highly cited study is not necessarily the most clinically relevant or impactful. Finally, local H-index values and co-citation patterns may still be influenced by institutional or author self-citations, which standard bibliometric algorithms may not fully account for.

Conclusion

This study provides a comprehensive bibliometric mapping of research on selected key candidate genes in trauma-related psychiatric genetics and epigenetics. Over the past two decades, the field has evolved from a predominant focus on candidate gene association studies toward a more integrative neurobiological framework encompassing epigenetic regulation (FKBP5 and NR3C1 DNA methylation), synaptic plasticity (BDNF), and psychosocial resilience (Džaferović and Ašić 2026). The United States remains the leading contributor to research output, while European countries demonstrate strong international collaboration and East Asian countries show increasing research activity.

Future research should extend beyond targeted candidate-gene approaches to include large-scale, cell-type-specific epigenome-wide association studies (EWAS) aimed at identifying novel chromatin and transcriptomic pathways associated with vulnerability to trauma. Prospective longitudinal cohort studies may provide valuable insights into how epigenetic modifications change in relation to psychotherapy, pharmacotherapy, and lifestyle-based interventions. Strengthening international collaboration, particularly by including genetically diverse and historically underrepresented populations from Africa,

Latin America, and Asia, may improve the generalizability and clinical relevance of emerging psychiatric epigenetic biomarkers.

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