International Journal of Innovative Technologies in Social Science

e-ISSN: 2544-9435

Operating Publisher
SciFormat Publishing Inc.
ISNI: 0000 0005 1449 8214

2734 17 Avenue SW,
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ARTICLE TITLE	THE NEW UNDERSTANDING OF AUTISM - A LITERATURE REVIEW
DOI	https://doi.org/10.31435/ijitss.2(50).2026.5694
RECEIVED	22 March 2026
ACCEPTED	27 June 2026
PUBLISHED	30 June 2026
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THE NEW UNDERSTANDING OF AUTISM - A LITERATURE REVIEW

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ABSTRACT

Introduction: Autism spectrum disorder (ASD) is a neurodevelopmental condition characterized by marked heterogeneity in clinical presentation, genetic architecture, and developmental trajectories. Traditional models conceptualizing ASD as a single disorder have increasingly failed to explain the broad variability observed among affected individuals. Recent advances in genomics, epidemiology, and developmental neuroscience suggest that ASD comprises multiple biologically distinct phenotypes shaped by complex interactions between genetic susceptibility, environmental exposures, and developmental timing.

The aim of this review was to synthesize current evidence on the most probable genetic, epigenetic, and environmental mechanisms underlying the development and manifestation of ASD, with particular emphasis on recent large-scale studies identifying distinct autism phenotypes and their associated risk factors.

Materials and Methods: A narrative review of the literature was conducted using structured searches of PubMed and Google Scholar. Peer-reviewed articles published in English up to January 1, 2026 were included. Priority was given to large-scale genomic studies, meta-analyses, and population-based epidemiological investigations examining genetic architecture, phenotypic stratification, developmental timing, and environmental risk factors associated with ASD.

Results: The reviewed evidence indicates that ASD is best conceptualized as a group of related but biologically heterogeneous neurodevelopmental conditions rather than a single disorder. Data-driven analyses have identified four major autism phenotypes supported by distinct patterns of common and rare genetic variation and class-specific developmental gene expression profiles. ASD risk is highly polygenic, involving cumulative effects of numerous common variants alongside rare inherited and de novo mutations. Environmental factors, including maternal metabolic and endocrine disorders, infections, and exposure to environmental pollutants, contribute to ASD risk, although many associations are substantially influenced by familial confounding. Additionally, developmental timing plays a critical role, as genetic liability influences not only ASD risk but also age at diagnosis and clinical presentation across the lifespan.

Conclusions: Current evidence supports a multidimensional and developmental model of ASD in which genetic susceptibility, environmental exposures, and developmental processes interact to produce diverse phenotypic outcomes. The identification of distinct autism phenotypes enables a more personalized approach to patient care and provides a foundation for the development of phenotype-specific diagnostic, personalized risk assessment and therapeutic strategies. Advances in research methodologies and diagnostic technologies allow for earlier and more accurate identification of individuals at risk, facilitating timely intervention. Furthermore, continued discovery of novel genetic variants and their functional consequences may enable targeted treatments aimed at improving outcomes for individuals affected by ASD. These findings underscore the importance of enhanced prenatal care, including monitoring and management of maternal risk factors, to support optimal neurodevelopment. Future research should prioritize integrative, genetically informed approaches to further elucidate causal mechanisms and advance precision medicine in autism.

KEYWORDS

Autism Spectrum Disorder, ASD, Neurodevelopmental Disorders, Autism Phenotypes, Genetics

CITATION

Butkowska, Z., Tadulewicz, I., Kocik, A., Komisarczyk, Ł., Nowak, N., Drozd, M., Kozłowska, A., Kornela, T., & Góralska, A. (2026). The new understanding of autism - a literature review. *International Journal of Innovative Technologies in Social Science*, 2(50). https://doi.org/10.31435/ijitss.2(50).2026.5694

Introduction

Autism spectrum disorder (ASD) is a neurodevelopmental condition primarily characterized by persistent difficulties in social communication and interaction, accompanied by restricted, repetitive patterns of behavior, interests, or activities [2]. Historically, autism was conceptualized as a single diagnostic entity encompassing a broad range of clinical phenotypes—from individuals with profound intellectual disability and minimal verbal communication to cognitively able adults with subtle social difficulties and high educational attainment [3].

Over recent decades, the prevalence of ASD diagnoses has increased markedly. In the 1980s, autism was estimated to affect approximately 1 in 2,000 children, whereas contemporary surveillance data from several high-income countries report prevalence estimates as high as 1 in 36 children [21]. This increase is largely attributed to broadened diagnostic criteria, improved awareness, enhanced screening tools, and changes in service access rather than a true rise in incidence. Nevertheless, ASD remains a major public health concern,

associated with substantial lifelong disability, increased psychiatric comorbidity, and significant psychosocial and economic burden for individuals, families, and healthcare systems [10].

Despite advances in diagnosis, the biological mechanisms underlying ASD remain incompletely understood. Traditional case–control approaches have struggled to identify singular causal pathways, highlighting the need for models that better capture clinical and biological heterogeneity. Recent large-scale genetic and epidemiological studies now provide compelling evidence that ASD comprises multiple phenotypic and biological subtypes, each influenced by distinct combinations of genetic and environmental risk factors [18]. This review synthesizes current findings on ASD etiology, with a focus on genetic architecture, developmental timing, and modifiable environmental influences.

Materials and Methods

This narrative review was conducted using a structured literature search of major scientific databases, including PubMed and Google Scholar. Peer-reviewed articles published in English up to January 1, 2026 were considered. Search terms included combinations of "autism," "autism spectrum disorder," "ASD," "genetics," "environmental risk factors," and "phenotypes." Priority was given to large-scale genomic studies, meta-analyses, and population-based epidemiological investigations published in high-impact journals. Reference lists of relevant articles were manually screened to identify additional key publications.

Discussion

Recent advances in autism research, particularly large-scale studies, have fundamentally reshaped the understanding of ASD as a complex, multidimensional condition rather than a single disorder. Using data-driven generative mixture modeling approaches, researchers have identified four autism phenotypes characterized by distinct constellations of behavioral traits, cognitive profiles, and psychiatric comorbidities [14]. Importantly, these phenotypic classes are underpinned by divergent genetic architectures, providing biological validation for clinically observed heterogeneity. The study used a generative finite mixture modelling framework to parse broad phenotypic and genetic heterogeneity across a large cohort of autistic individuals and identifying four latent phenotypic classes of ASD [3].

Characteristic of a Four Autism Phenotypes

1. Social/Behavioral Class

This class is characterized by pronounced difficulties in core autism domains, including impaired social communication and increased restricted, repetitive behaviors relative to other groups. Individuals in this class also exhibit elevated levels of disruptive behavior, attention deficit, anxiety and mood symptoms, but do not show significant developmental delays compared to their autistic peers. Co-occurring diagnoses such as ADHD and major depression are enriched in this class, reflecting the convergence of behavioural and psychiatric features [3].

2. Mixed ASD with Developmental Delay (Mixed ASD with DD)

Individuals in this class demonstrate significant enrichment in developmental delays, including language delays, intellectual disability, and motor coordination disorders. Although core autism features (social communication and repetitive behaviors) vary across individuals in this class, the dominant characteristic is strong developmental impairment. These individuals show lower rates of ADHD, anxiety, and depressive symptoms than those in the Social/Behavioral or Broadly Affected classes [3].

3. Moderate Challenges Class

Members of this class exhibit intermediate severity across the evaluated phenotypic domains, scoring consistently below other autistic classes (i.e., fewer difficulties) across measures such as social communication, repetitive behavior, attention deficit, disruptive behavior, anxiety/mood, developmental delay, and self-injury. However, compared to nonautistic siblings, individuals in this class still meet diagnostic criteria for ASD, indicating a subclinical yet persistent profile of autism-related traits [3].

4. Broadly Affected Class

This class encompasses individuals with the most pervasive and severe profile across multiple phenotype categories. Individuals classified as Broadly Affected exhibit high difficulties across all seven defined domains — including social communication deficits, restricted and repetitive behaviors, attention problems, disruptive behavior, anxiety/mood symptoms, developmental delays, and self-injury. They also display the highest burden of co-occurring conditions, including intellectual disability and cognitive impairment, and show distinct genetic signatures such as elevated de novo variant loads in high-constraint genes [3].

Genetic Architecture

The genetic architecture underlying ASD is markedly complex and multifactorial [5]. Analyses of common genetic variation demonstrate that ASD risk is highly polygenic, with thousands of single nucleotide polymorphisms exerting small but additive effects across genes involved in synaptic signaling, neuronal development, metabolic regulation, and immune function. These findings support an aggregate liability model in which cumulative genetic burden, rather than single high-impact variants, confers susceptibility to ASD [8].

Beyond common variants, rare inherited and de novo mutations play a critical role in shaping phenotypic diversity. Phenotypic classes characterized by global developmental impairment—particularly the Mixed ASD with Developmental Delay and Broadly Affected groups—exhibit substantial enrichment of rare and de novo variants in genes under strong evolutionary constraint. These variants frequently affect genes involved in chromatin remodeling, transcriptional regulation, and early neurodevelopmental processes, providing a plausible biological basis for the more severe and pervasive clinical presentations observed in these groups. In contrast, phenotypes dominated by behavioral and psychiatric features show stronger associations with polygenic risk, suggesting distinct etiological mechanisms across ASD subtypes [9].

Both risk-enhancing and protective variants have been identified, emphasizing the importance of effect directionality and gene–gene interactions. These findings confirm that no single genetic variant is sufficient to explain ASD risk and support an aggregate liability model [9, 14].

Beyond common variation, rare inherited and de novo mutations further contribute to phenotypic diversity. Class-specific enrichment of rare variants within biologically meaningful gene sets and pathways suggests that distinct neurodevelopmental mechanisms may converge on partially overlapping clinical manifestations. Moreover, these genetic differences align with class-specific gene expression patterns during critical developmental windows, linking molecular variation to observable developmental milestones [17].

Most Frequently Studied and Statistically Significant Genetic Variants Associated with ASD

Several genes have been consistently implicated in ASD susceptibility across populations and study designs [13]. Variants in *CNTNAP2* are associated with altered neuronal connectivity and have been linked to impairments in language development and social communication. Polymorphisms in *MTHFR*, which plays a central role in folate metabolism and DNA methylation, highlight the importance of epigenetic regulation in neurodevelopment. Similarly, variation in *OXTR* underscores the contribution of oxytocin-mediated social and emotional processes to ASD phenotypes, while *VDR* polymorphisms suggest a role for vitamin D signaling in brain development, with evidence for both risk-enhancing and potentially protective effects depending on the specific variant [6].

Importantly, these genes do not operate in isolation but interact within broader biological networks. Their effects are modulated by developmental timing, epigenetic mechanisms, and environmental exposures, reinforcing the notion that ASD arises from dynamic, multilayered biological interactions rather than discrete genetic causes [11].

Differences Between Earlier- and Later-Diagnosed Autism

According to Zhang et al. (2025), individuals with autism diagnosed at earlier ages and those diagnosed later in childhood or adolescence differ in both developmental trajectories and genetic profiles. Earlier–diagnosed autism is associated with distinct socioemotional and behavioural developmental trajectories that emerge at younger ages. These trajectories are characterized by lower social and communication abilities in early childhood, which may lead to clear, observable autistic features and earlier clinical referral [1].

In contrast, later–diagnosed autism tends to involve developmental profiles in which socioemotional and behavioural difficulties become more apparent later in childhood or adolescence, rather than in the earliest years. Such features may not meet diagnostic thresholds until environmental or developmental demands increase with age [1].

The polygenic factor associated with earlier diagnosis corresponds to genetic variants that contribute to classic early-emerging autistic traits, and has only moderate genetic correlations with conditions such as ADHD and other mental–health disorders [16].

Conversely, the polygenic factor associated with later diagnosis exhibits higher genetic correlations with ADHD and a range of mental–health conditions, including depression and PTSD. This suggests that individuals with later diagnoses may carry genetic liabilities that predispose them to broader neuropsychiatric profiles, which may obscure or delay recognition of autism until later developmental stages [4].

Maternal Health, Environmental Exposures, and Familial Confounding

Epidemiological research has consistently reported associations between maternal health conditions—such as metabolic disorders, infections, endocrine dysfunction, and exposure to environmental pollutants—and increased ASD risk in offspring [19,20]. However, genetically informed family-based analyses indicate that many of these associations are substantially attenuated after accounting for shared familial genetic and environmental factors. This suggests that observed correlations often reflect underlying genetic liability or shared environmental exposures rather than direct causal effects of prenatal insults [12].

These findings highlight the importance of caution in interpreting observational prenatal risk factors and underscore the need for study designs that explicitly address familial confounding [7]. While maternal health remains a critical component of prenatal care, disentangling causal environmental effects from inherited susceptibility is essential for accurate risk assessment and effective prevention strategies.

Conclusions

The synthesis of recent genetic, developmental, and epidemiological research leads to several key conclusions. Autism spectrum disorder is not a single disorder but comprises multiple phenotypic and biological subtypes with partially distinct genetic architectures. Genetic liability for ASD is highly polygenic and multifactorial, involving both common and rare variants acting across diverse neurodevelopmental pathways. Phenotypic subtypes and age at diagnosis capture meaningful biological differences, supporting a developmental and dimensional model of ASD. Many associations between maternal health factors and ASD risk are influenced by familial confounding, emphasizing the need for cautious causal interpretation. Future research and clinical practice should prioritize stratified, personalized approaches integrating genetic, developmental, and environmental data.

In summary, ASD is best conceptualized as a spectrum of interrelated but biologically distinct neurodevelopmental pathways. Embracing this complexity is essential for advancing precision diagnostics, improving prognostic accuracy, and developing targeted interventions that address individual risk profiles across the lifespan.

Future research should prioritize multidimensional approaches that integrate genetic data, longitudinal developmental trajectories, and detailed phenotypic characterization. Embracing the biological and clinical diversity of ASD will be essential for advancing precision medicine approaches and ultimately improving outcomes for autistic individuals across the lifespan.

Authors' Contribution:
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Łucja Komisarczyk – Editing, supervision
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All authors have read and agreed with the published version of the manuscript.
Funding Statement: The study did not receive special funding.
Conflict Of Interest: The author declare no conflict of interest.

REFERENCES

1. Maenner, M. J., Warren, Z., Williams, A. R., Amoakohene, E., Bakian, A. V., Bilder, D. A., Durkin, M. S., Fitzgerald, R. T., Furnier, S. M., Hughes, M. M., Ladd-Acosta, C. M., McArthur, D., Pas, E. T., Salinas, A., Vehorn, A., Williams, S., Esler, A., Grzybowski, A., Hall-Lande, J., … Shaw, K. A. (2023). Prevalence and characteristics of autism spectrum disorder among children aged 8 years - Autism and Developmental Disabilities Monitoring Network, 11 sites, United States, 2020. MMWR Surveill Summ., 72(2), 1–14. https://doi.org/10.15585/mmwr.ss7202a1

2. Lord, C., Brugha, T. S., Charman, T., Cusack, J., Dumas, G., Frazier, T., Jones, E. J. H., Jones, R. M., Pickles, A., State, M. W., Taylor, J. L., & Veenstra-VanderWeele, J. (2020). Autism spectrum disorder. Nat Rev Dis Primers., 6(1), 5. https://doi.org/10.1038/s41572-019-0138-4

3. Litman, A., Sauerwald, N., Green Snyder, L., Foss-Feig, J., Park, C. Y., Hao, Y., Dinstein, I., Theesfeld, C. L., & Troyanskaya, O. G. (2025). Decomposition of phenotypic heterogeneity in autism reveals underlying genetic programs. Nat Genet., 57(7), 1611–1619. https://doi.org/10.1038/s41588-025-02224-z

4. Zhang, X., Grove, J., Gu, Y., Buus, C. K., Nielsen, L. K., Neufeld, S. A. S., Koko, M., Malawsky, D. S., Wade, E. M., Verhoef, E., Gui, A., Hegemann, L., APEX Consortium, iPSYCH Autism Consortium, PGC-PTSD Consortium, Geschwind, D. H., Wray, N. R., Havdahl, A., Ronald, A., … Warrier, V. (2025). Polygenic and developmental profiles of autism differ by age at diagnosis. Nature, 646(8087), 1146–1155. https://doi.org/10.1038/s41586-025-09542-6

5. Geschwind, D. H., & State, M. W. (2015). Gene hunting in autism spectrum disorder: On the path to precision medicine. Lancet Neurol., 14(11), 1109–1120. https://doi.org/10.1016/S1474-4422(15)00044-7

6. Grove, J., Ripke, S., Als, T. D., Mattheisen, M., Walters, R. K., Won, H., Pallesen, J., Agerbo, E., Andreassen, O. A., Anney, R., Awashti, S., Belliveau, R., Bettella, F., Buxbaum, J. D., Bybjerg-Grauholm, J., Bækvad-Hansen, M., Cerrato, F., Chambert, K., Christensen, J. H., … Børglum, A. D. (2019). Identification of common genetic risk variants for autism spectrum disorder. Nat Genet., 51(3), 431–444. https://doi.org/10.1038/s41588-019-0344-8

7. Khachadourian, V., Arildskov, E. S., Grove, J., O'Reilly, P. F., Buxbaum, J. D., Reichenberg, A., Sandin, S., Croen, L. A., Schendel, D., Hansen, S. N., & Janecka, M. (2025). Familial confounding in the associations between maternal health and autism. Nat Med., 31(3), 996–1007. https://doi.org/10.1038/s41591-024-03479-5

8. Wang, M., Zhang, X., Zhong, L., Zeng, L., Li, L., & Yao, P. (2025). Understanding autism: Causes, diagnosis, and advancing therapies. Brain Res Bull., 227, 111411. https://doi.org/10.1016/j.brainresbull.2025.111411

9. Fang, Y., Cui, Y., Yin, Z., Hou, M., Guo, P., Wang, H., Liu, N., Cai, C., & Wang, M. (2023). Comprehensive systematic review and meta-analysis of the association between common genetic variants and autism spectrum disorder. Gene, 887, 147723. https://doi.org/10.1016/j.gene.2023.147723

10. Chiarotti, F., & Venerosi, A. (2020). Epidemiology of autism spectrum disorders: A review of worldwide prevalence estimates since 2014. Brain Sci., 10(5), 274. https://doi.org/10.3390/brainsci10050274

11. Fang, Y., Cui, Y., Yin, Z., Hou, M., Guo, P., Wang, H., Liu, N., Cai, C., & Wang, M. (2023). Comprehensive systematic review and meta-analysis of the association between common genetic variants and autism spectrum disorder. Gene, 887, 147723. https://doi.org/10.1016/j.gene.2023.147723

12. Kodesh, A., Levine, S. Z., Khachadourian, V., Rahman, R., Schlessinger, A., O'Reilly, P. F., Grove, J., Schendel, D., Buxbaum, J. D., Croen, L., Reichenberg, A., Sandin, S., & Janecka, M. (2021). Maternal health around pregnancy and autism risk: A diagnosis-wide, population-based study. Psychol Med., 1–9. https://doi.org/10.1017/S0033291721001021

13. Qiu, S., Qiu, Y., Li, Y., & Cong, X. (2022). Genetics of autism spectrum disorder: An umbrella review of systematic reviews and meta-analyses. Transl Psychiatry., 12(1), 249. https://doi.org/10.1038/s41398-022-02009-6

14. Hashem, S., Nisar, S., Bhat, A. A., Yadav, S. K., Azeem, M. W., Bagga, P., Fakhro, K., Reddy, R., Frenneaux, M. P., & Haris, M. (2020). Genetics of structural and functional brain changes in autism spectrum disorder. Transl Psychiatry., 10(1), 229. https://doi.org/10.1038/s41398-020-00921-3

15. Warrier, V., Zhang, X., Reed, P., Havdahl, A., Moore, T. M., Cliquet, F., Leblond, C. S., Rolland, T., Rosengren, A., EU-AIMS LEAP, iPSYCH-Autism Working Group, Spectrum 10K and APEX Consortia, Rowitch, D. H., Hurles, M. E., Geschwind, D. H., Børglum, A. D., Robinson, E. B., Grove, J., Martin, H. C., … Baron-Cohen, S. (2022). Genetic correlates of phenotypic heterogeneity in autism. Nat Genet., 54(9), 1293–1304. https://doi.org/10.1038/s41588-022-01072-5

16. Mandelli, V., Landi, I., Busuoli, E. M., et al. (2023). Prognostic early snapshot stratification of autism based on adaptive functioning. Nat. Mental Health, 1, 327–336. https://doi.org/10.1038/s44220-023-00056-6

17. Antaki, D., Guevara, J., Maihofer, A. X., et al. (2022). A phenotypic spectrum of autism is attributable to the combined effects of rare variants, polygenic risk and sex. Nat Genet, 54, 1284–1292. https://doi.org/10.1038/s41588-022-01064-5

18. Aviel-Shekler, K., Hamshawi, Y., Sirhan, W., et al. (2020). Gestational diabetes induces behavioral and brain gene transcription dysregulation in adult offspring. Transl Psychiatry, 10, 412. https://doi.org/10.1038/s41398-020-01096-7

19. Brignell, A., Marraffa, C., Williams, K., & May, T. (2022). Memantine for autism spectrum disorder. Cochrane Database of Systematic Reviews, (8), CD013845. https://doi.org/10.1002/14651858.CD013845.pub2

20. Careaga, M., Murai, T., & Bauman, M. D. (2017). Maternal immune activation and autism spectrum disorder: From rodents to nonhuman and human primates. Biol Psychiatry., 81(5), 391–401. https://doi.org/10.1016/j.biopsych.2016.10.020

21. Elgueta, D., Murgas, P., Riquelme, E., Yang, G., & Cancino, G. I. (2022). Consequences of viral infection and cytokine production during pregnancy on brain development in offspring. Front Immunol., 13, 816619. https://doi.org/10.3389/fimmu.2022.816619

22. Elsabbagh, M., Divan, G., Koh, Y. J., Kim, Y. S., Kauchali, S., Marcín, C., Montiel-Nava, C., Patel, V., Paula, C. S., Wang, C., Yasamy, M. T., & Fombonne, E. (2012). Global prevalence of autism and other pervasive developmental disorders. Autism Res., 5(3), 160–179. https://doi.org/10.1002/aur.239