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Genetic Factors in the Etiology of Autism: A Case Study in Buena Fé Canton

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ABSTRACT
Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition marked by enduring impairments in social reciprocity, pragmatic communication, and behavioral flexibility. Despite an estimated global prevalence of approximately 1% of children, little is known about the ASD burden and its determinants in Ecuador's rural settings, particularly in under-researched regions where healthcare infrastructure is often minimal. This study aimed to quantify ASD prevalence and delineate key aetiological factors among 70 children aged 3–10 years enrolled in two early childhood programmes in Buena Fé Canton, a geographically and socioeconomically diverse rural area. Between January and March 2023–2024, participants were screened using the Denver II and the Modified Checklist for Autism in Toddlers (MCHAT), with diagnoses confirmed through ICD 11 criteria and multidisciplinary clinical assessment to ensure accuracy and diagnostic reliability. Caregiver interviews and health records provided data on familial aggregation, maternal metabolic health, hypertensive disorders, environmental exposures, and antenatal care access, offering a comprehensive perspective on potential contributing factors. All 70 screened children met ASD criteria, revealing a substantial local caseload that may reflect broader, unaddressed trends. Familial history was reported in 60% of cases; 40% of mothers had lived in areas of intensive pesticide use or elevated particulate pollution during gestation; 30% experienced gestational diabetes or obesity; and 70% faced limited prenatal care access, which is a significant barrier in early detection and intervention. These findings underscore a multifactorial aetiology in which inherited susceptibility converges with modifiable gestational and socio-economic stressors. Tailored interventions should prioritise rural antenatal metabolic and environmental screening, environmental health safeguards, and the deployment of integrated, family-centred diagnostic and support services in primary care settings.

Keywords: *autism spectrum disorder; organophosphate pesticides; gestational diabetes; environmental neurotoxicology.*

INTRODUCTION
Autism Spectrum Disorder (ASD, Trastorno del Espectro Autista—TEA) is a heterogeneous neurodevelopmental syndrome characterised by persistent deficits in social reciprocity, pragmatic communication, and behavioural flexibility (Alcalá & Ochoa Madrigal, 2022). Affected children frequently demonstrate echolalic speech, circumscribed interests, and marked sensory reactivity (e.g., tactile defensiveness, auditory hypersensitivity). Such phenotypic breadth mandates highly individualised diagnostic formulations and intervention plans.

Although the World Health Organization (WHO) estimates a global point prevalence of approximately one percent (World Health Organization, 2024), the expression and detection of ASD are strongly conditioned by contextual variables. In Ecuador, structural barriers—including sub-optimal prenatal care, maternal under-nutrition, and limited developmental-screening infrastructure—exacerbate diagnostic delays, particularly in peri-urban and rural cantons (World Health Organization, 2024). Buena Fé, an agrarian district in Los Ríos Province, epitomises these challenges, yet epidemiological data on prevalence or risk architecture remain conspicuously absent. Health-system inequities, compounded by workforce shortages in developmental pae-diatrics, attenuate early-identification rates and defer entry into evidence-based services.

Caregiver knowledge gaps and culturally mediated misconceptions further impede timely referral to specialists. Elucidating salient prenatal and perinatal risk vectors is therefore essential for precision-prevention strategies and the deployment of family-centred psycho-education (Lautarescu et al., 2021). Against this backdrop, the present study undertakes a granular exploration of ASD risk determinants in Buena Fé, with the overarching aim of informing multidisciplinary service design and optimising developmental outcomes.

LITERATURE REVIEW

ASD is conceptualised as the emergent phenotype of polygenic liability interacting with context-specific environmental stressors (Styles et al., 2020). Genome-wide association studies implicate variants in synaptic-scaffolding genes (e.g., SHANK3) and neurexin super-family members (e.g., CNTNAP2) in aberrant synaptogenesis and cortical network formation. Gene penetrance, however, is modulated by epigenetic plasticity and by exposures across sensitive developmental windows.

Current neurodevelopmental models of ASD suggest that disruptions in the expression of genes involved in synaptic organization affect functional connectivity between cortical regions. Specifically, dysfunctions in genes such as NRXN1, NLGN3, and SYNGAP1 have been associated with impairments in the stabilization of excitatory and inhibitory synapses, leading to imbalances in the architecture of neural networks. These early anomalies may compromise the development of social, cognitive, and sensorimotor abilities—core components of the autistic phenotype.

In addition to structural genetic variants, epigenetic modifications induced by environmental factors—such as DNA methylation and histone acetylation—play a critical regulatory role in gene expression during key stages of embryonic and postnatal development. Factors such as prenatal exposure to pollutants, maternal infections, or nutritional deficiencies can trigger persistent epigenetic changes that either enhance or mitigate ASD risk, even in individuals with genetic susceptibility. This integrative perspective underscores the need to consider the dynamic interplay between the genome and the exposome in understanding the etiology of autism.

ICD-11 Dimensional Framework

The 11th Revision of the International Classification of Diseases (ICD-11) abandons former subtype taxonomies and instead stratifies ASD by current support needs (World Health Organization, 2024). Table 1 operationalises these specifiers and Table 2 summarises key epidemiological estimates linked to each level.

Table 1. ICD-11 support-need specifiers[1]

ICD-11 Level	Core description	Illustrative Ecuadorian scenario
Level 1	Mild social-pragmatic difficulties; functional language intact	Child in a mainstream classroom requiring occasional social skills coaching

Level 2	Marked communication deficits; limited functional language	Pupil needing structured language intervention and visual supports
Level 3	Severe social-communication impairment; often co-occurring intellectual disability	Individual requiring augmentative communication and 1:1 assistance

[1] Adapted from WHO ICD-11 Clinical Descriptions and Diagnostic Guidelines.

Meta-analytic evidence indicates that ~50 % of school-age autistic children are minimally verbal, while ~25 % exhibit persistent receptive–expressive language discordance, both factors that potentiate social exclusion and academic underachievement (Styles et al., 2020). Multimodal assessment—triangulating caregiver reports, naturalistic observation and standardized metrics—is therefore indispensable.

Table 2. Indicative prevalence and service intensity by ICD-11 level[2]

Level	Approximate global proportion	Typical service intensity
1	40 – 45 %	Out-patient behavioural therapy, parent training
2	35 – 40 %	Special-education placement, multidisciplinary clinics
3	15 – 20 %	Continuous support, respite care, specialised schooling

[2] Synthesized from recent meta-analyses of school-aged cohorts.

Meta-analytic evidence indicates that about fifty percent of school-age autistic children are minimally verbal, while roughly twenty-five percent exhibit persistent receptive–expressive language discordance—factors that potentiate social exclusion and academic underachievement (Styles et al., 2020). Multimodal assessment—triangulating caregiver reports, naturalistic observation, and standardised metrics—is therefore indispensable.

\Genetic and Environmental Aetiology

Contemporary models posit ASD as the product of gene–environment interplay (Costa et al., 2019; El-Baz et al., 2023). Germ-line variants confer neurobiological susceptibility, yet phenotypic expression hinges on prenatal and perinatal exposures that perturb neuro-ontogeny. Table 3 outlines environmental determinants particularly salient for the Ecuadorian context.

Table 3. Primary environmental risk factors potentially associated with ASD in Ecuador[3]

Risk factor	Mechanistic synopsis	Contextual relevance to Buena Fé
Air pollution	Fine particulate matter induces fetal neuro-inflammation and oxidative stress, elevating ASD odds [6, 7]	Cane-field burning and diesel transport increase $PM_{2.5}$ burden
Pesticide exposure	Organophosphates cross the placenta, disrupt neurogenesis, and double ASD risk [9]	Intensive cacao and banana cultivation relies on these compounds
Maternal metabolic disorders	Obesity and gestational diabetes create chronic inflammation and epigenetic dysregulation [22, 28]	Limited antenatal screening allows hyperglycaemia to go undetected
Hypertensive pregnancy	Preeclampsia restricts uteroplacental perfusion, leading to fetal hypoxia and later neurodevelopmental deficits [30]	Rural clinics lack routine Doppler monitoring
Prenatal substance exposure	Valproate, SSRIs, acetaminophen, and alcohol each demonstrate dose-dependent neuro-teratogenicity [11–21]	Over-the-counter medication use is common, often without medical supervision

[3]Summaries compiled from Lautarescu et al. (2021), Costa et al. (2019), El-Baz et al. (2023), Ye et al. (2022), and Rahman et al. (2022). Study objective. The present investigation quantifies ASD prevalence among children aged 3 – 10 years in Buena Fé and delineates associated genetic and environmental risk factors. By clarifying these determinants, we aim to propose feasible psycho-educational pathways and emphasise the critical role of multidisciplinary teams in diagnosis and management, thereby improving the quality of life of affected children and their families. Subsequent sections detail the methodology employed to measure prevalence and correlate risk variables, followed by results, discussion, and recommendations for strengthening early-identification systems in comparable low-resource settings.

MATERIALS AND METHODS

A cross-sectional study was carried out in the Buena Fe canton, during the period from January to March 2023. The main objective of this research was to establish the prevalence of autism spectrum disorder (ASD) in children between the ages of 3 and 10 years, as well as to identify the risk factors associated with this condition, the methodology allowed to obtain a snapshot of the current status of ASD in this child population, facilitating the analysis of relevant clinical and contextual variables.

The study population consisted of a total of 70 children, who were selected from institutional records corresponding to two programs aimed at child care: the “Creciendo con Nuestros Hijos” (CNI) program and the “Cuidado Integral de Niños” (CNH) program. These programs provide early stimulation and child development follow-up services, which allowed access to a sample with previous basic records. Specific exclusion criteria were applied, leaving out of the study those children who presented genetic syndromes unrelated to ASD or who already had established neurological diagnoses, in order to avoid clinical bias in the identification of cases.

As part of the initial screening for possible developmental delays, the Denver Developmental Screening Test II (DENVER II) was used. This tool is widely recognized internationally and assesses four key areas of child development: gross motor, fine motor, language and social behavior. In the context of this study, the application of the test was adapted to simplify the interpretation of the results, classifying them into three categories: normal development, doubtful development and abnormal development. This categorization made it possible to more clearly identify children with possible developmental disturbances.

Once the screening phase with the DENVER II was completed, a second specific tool for autism screening was applied: the Modified Questionnaire for the Detection of Autism in Toddlers (M-CHAT). The purpose of this instrument is to detect early risk indicators of ASD by means of structured questions addressed to parents or caregivers. Based on the answers obtained, participants were classified into two groups: “NO”, corresponding to children with a low probability of presenting ASD, and “YES”, which grouped those with signs suggesting a potential risk.

Children classified in the “YES” group were referred to a more rigorous clinical evaluation phase, which included direct observation of behavior and a detailed clinical interview with parents or caregivers, to confirm or rule out the presence of characteristics compatible with the diagnosis of ASD, based on the observed behavior, the child's developmental history and the information provided by the family. Additionally, relevant data were collected on possible risk factors associated with ASD. Among these were considered family history of ASD and the presence of genetic variants previously documented in clinical records, when available, demographic factors such as advanced parental age, defined in this study as mothers older than 35 years and fathers older than 40 years at the time of the child's birth.

A number of maternal conditions during pregnancy, such as gestational diabetes, hypertension, obesity, anxiety, and depression, were also considered because of their possible implication on fetal neurodevelopment. These variables were collected through interviews with the mothers and review of medical records. Finally, perinatal factors were taken into account, including preterm birth (less than 37

weeks of gestation), birth complications (such as neonatal asphyxia or emergency cesarean section), and low birth weight, defined as a birth weight of less than 2,500 grams.

This methodology combined developmental screening techniques and specific detection of ASD with the collection of clinical and perinatal history, thus allowing a comprehensive approach to the phenomenon studied. The structure of the study facilitated the identification not only of suspected cases of ASD, but also of the contextual and biological conditions that could be related to its occurrence, contributing to a broader understanding of the clinical and epidemiological profile of this condition in the infant population evaluated. The questionnaire described in Table 3 was used in the development of this research as the main tool for the collection of information. This instrument was applied with the purpose of exploring various factors associated with autism spectrum disorder (ASD), allowing an organized and coherent data collection. Its implementation responded to the need to have a validated means that would facilitate the rigorous analysis of the variables contemplated in the study.

For its construction, different categories and subcategories relevant to the research context were taken into account, which allowed structuring the questionnaire in a logical and functional manner. The validity of the instrument was supported by the review of health professionals, who evaluated the clarity, objectivity, pertinence and organization of each item; this previous validation ensured the adequacy of the content of the questionnaire and its usefulness as a methodological tool within the study.

The application of the instrument made it possible to obtain specific information on relevant dimensions of the phenomenon under investigation, facilitating its analysis in a systematic manner. Thanks to the organized structure of the questionnaire, it is possible to identify patterns and recurrent characteristics in the data collected, this process contributed to the development of a clear and grounded methodological approach, which allowed a more precise and deeper understanding of the factors associated with Autism Spectrum Disorder (ASD) in the context studied.

Table 3. The questionnaire applied in the research was previously validated.

ITEMS	
Category A: Etiological Factors of Autism	
Subcategory 1: Child Demographic Factors	
N°	**Genre**
1	Male
2	Female
Subcategory 1.1: Demographic Factors of the mother	
N°	**Age**
1	Under 25 years of age.
2	Between 25 and 35 years old.
3	Older than 35 years old.
Subcategory 2: Genetic Factors	
N°	**Family history of neurological disorders:**
1	Autism Spectrum Disorder (ASD).
2	Epilepsy.
3	Attention Deficit Hyperactivity Disorder (ADHD).
4	Intellectual Disability.
Subcategory 3: Environmental Factors	
N°	**Prenatal exposure to toxic substances:**
1	Pesticides for crop pest control.
2	Insecticides (Baygon, etc).
N°	**Ingestion of toxic substances during pregnancy:**
1	Drugs
2	Alcohol
3	Both
4	None

Subcategory 4: Biological Factors

N°	**Prenatal Treatments:**
1	Prenatal infections.
2	Threatened Preterm Labor (PTB).
3	Neonatal Hypoxia.

N°	**Newborn classification according to gestational age:**
1	Preterm: Between 22- and 37-weeks gestational age.
2	Term: Between 37- and 42-weeks gestational age.
3	Post-term: 42 completed weeks or more gestation.

N°	**Weight of the newborn:**
1	Low birth weight: Less than 2500gr.
2	Normal weight: Between 2500gr to 3800gr.
3	Macrosomic: Greater than 3800gr.

ITEMS	
Category B: Psychological Factors Related to the Mother	
Subcategory 1: Mental health during pregnancy	
N°	**Emotional impact during gestation:**
1	High levels of stress during gestation.
2	Persistent anxiety during gestation.
3	Transient sadness during gestation.
4	Difficulty managing emotions during pregnancy.
N°	**Social Support and Interpersonal Relationships:**
1	Little interaction with family or friends during gestation.
2	Conflicting relationships during pregnancy.
3	Emotional impact of family loss.
4	Physical or psychological violence during pregnancy.
N°	**Perception of Pregnancy:**
1	Feelings of ambivalence about motherhood.
2	Concern about the likelihood of your child having any health problems.
3	Concern about lifestyle modifications.

ITEMS	
Category C: Lifestyle During Pregnancy	
N°	**Health and nutrition practices**
1	Adequate nutrition during gestation.
2	Poor nutrition during gestation.
N°	**Medical check-ups during pregnancy:**
1	Less than 5 medical checkups.
2	Between 5 and more medical controls.
3	No medical control.
N°	**Adequate intake of folic acid:**
1	Before 6 months from conception of pregnancy
2	During the first 3 months of pregnancy
3	After 3 months of pregnancy
N°	**Physical activity as recommended by the physician:**
1	Moderate physical activity (walking, etc)
2	High intensity physical activity (running, weight lifting, etc).
3	I do not engage in any physical activity.

RESULTS

The cross-sectional survey carried out in Buena Fé Canton made it possible to establish the prevalence of Autism Spectrum Disorder (ASD) among children aged 3 to 10 years and to identify a range of aetiological factors that shape its development. Analysis of the 70 confirmed cases showed that ASD cannot be ascribed to a single cause; rather, it results from multiple interacting determinants.

ASD is recognised as a neurodevelopmental disorder with a multifactorial aetiology. According to the World Health Organization (2023), roughly one in every 100 children is affected. Risk factors include genetic predisposition, prenatal exposure to infections and adverse socioeconomic conditions (Alcalá & Ochoa Madrigal, 2022; World Health Organization, 2024). In the present study, maternal conditions during pregnancy—chiefly gestational diabetes and obesity—were corroborated as being associated with a higher incidence of ASD (Ye et al., 2022; Zhang et al., 2022).

Analysis of Aetiological Factors

- Family history: A high prevalence of families with an ASD background was ob-served, supporting the hypothesis of genetic predisposition (Styles et al., 2020).
- Prenatal conditions: Exposure to harmful substances—such as pesticides and air pollution—correlated with an increased risk of ASD (Allen et al., 2017; Costa et al., 2019).
- Socio-economic factors: Limited access to prenatal care emerged as a significant moderating factor in the community studied (ALDIA, 2021).

Systematisation of Variables

To summarise the findings, Table 4 presents the key variables analysed in the cross-sectional survey.

Table 4. Main variables, their definition and observed outcomes.

Variable	Definition	Findings
Family history	Presence of ASD in first-degree relatives	60 % of cases reported a positive family history
Prenatal conditions	Exposure to pesticides and air pollution	40 % of mothers lived in areas with high contamination
Socio-economic status	Access to prenatal healthcare services	70 % reported limited access to health services
Maternal health	Gestational diabetes and obesity	30 % of mothers presented gestational diabetes

Percentages are derived from the 2023 cross-sectional survey of 70 children in Buena Fé; the patterns observed align with previously reported risk factors by Styles et al. (2020) for family history, Rahman et al. (2022) for air-pollution exposure, and Ye et al. (2022) together with Zhang et al. (2022) for gestational diabetes and maternal obesity.

As shown in the table, family history constitutes a significant factor, supporting the hypothesis of genetic predisposition (Styles et al., 2020). Prenatal conditions—particularly pesticide ex-posure—were likewise correlated with an increased incidence of ASD (Allen et al., 2017; Costa et al., 2019). An unfa-vourable socio-economic profile (limited access to prenatal healthcare) also acted as a moderating element. Finally, maternal health (gestational diabetes and obesity) showed a significant association with ASD development (World Health Organization, 2024; Lautarescu et al., 2021).

DISCUSSION

Research on genetic factors in the etiology of autism spectrum disorder (ASD) has gained significant relevance in recent years, especially as studies continue to reveal the complex interaction between genetics

and environmental factors. Understanding these elements is key to advancing early diagnostic strategies, individualized interventions, and more effective preventive approaches. One of the main research approaches focuses on identifying how inherited genetic variations contribute to the development of the disorder. Through genome-wide association studies (GWAS) and sequencing techniques, multiple genes involved in neurological, synaptic, and brain development processes have been discovered, which helps explain the broad clinical heterogeneity of ASD.

In the context of case studies conducted in Buena Fé Canton, several key points arise that deserve detailed analysis. These cases allow the observation of clinical patterns and family histories that may reflect a strong genetic contribution, which must be studied with meticulous attention to detail. Scientific evidence indicates that genetic predisposition plays a crucial role in the development of autism. Twin and family studies have shown high heritability, suggesting that genetic factors are highly significant in the onset of the disorder and can be inherited from one generation to another. Various studies have identified numerous genes associated with increased risk, reinforcing the notion that hereditary factors significantly contribute to ASD incidence. These include genes involved in synaptic regulation, neuronal organization, and brain plasticity—essential functions during neurodevelopment.

In the cases analyzed in Buena Fé Canton, familial patterns of ASD were observed, strongly supporting the hypothesis of genetic influence. The presence of more than one case per family suggests possible hereditary aggregation, which should be considered a biological risk factor, and efforts should be made to implement control measures aimed at reducing ASD cases. The identification of specific genetic markers could enable more effective screening and early intervention strategies. These markers could help detect children at high risk early on, facilitating targeted interventions during critical stages of neurological development. While genetic factors are indeed crucial, it is essential to consider the context in which these predispositions are expressed. Genetics alone does not explain all cases; environmental factors may act as triggers or modulators of these vulnerabilities.

The interaction between genetic vulnerabilities and environmental triggers—such as prenatal exposure to toxins, nutritional deficiencies, or psychosocial stressors—can significantly influence the expression of autism. This interaction, known as gene–environment interplay, represents an emerging field of high scientific value. In the cases presented in Buena Fé Canton, it would be pertinent to conduct a thorough analysis of potential environmental factors that may be interacting with genetic predispositions. This would help build a more comprehensive understanding of the disorder's origins and identify opportunities for targeted, contextualized interventions that could contribute to a reduction in ASD incidence.

Findings from the various ASD cases in Buena Fé Canton highlight the importance of examining genetic factors in autism's etiology, while acknowledging the complex network of elements that interact to give rise to the observed phenotype. Only through an integrative approach will it be possible to advance toward more precise and effective clinical solutions. Future research should delve deeper into these interactions by integrating genetic analyses with environmental assessments to develop a more holistic understanding of autism. This multidimensional approach could drive progress in the prevention, diagnosis, and treatment of ASD, directly benefiting affected individuals and their families.

CONCLUSION

The study highlights the need for a multidisciplinary approach to ASD research, one that considers not only genetic factors but also the child's developmental environment. It is therefore crucial to foster early interventions and psycho-educational programmes that address the needs of both children and their families, as these measures could substantially enhance the quality of life of the individuals involved. In conclusion, the exploration of genetic factors in the etiology of autism, particularly as illustrated by case studies in Buena Fé Canton, underscores the complexity of this disorder. While genetic predispositions significantly contribute to the risk of developing autism, it is imperative to consider the intricate interactions with environmental factors that may influence its manifestation. This multifaceted understanding not only

enhances our knowledge of the underlying mechanisms of autism but also has practical implications for early diagnosis and intervention strategies. By integrating genetic insights with environmental assessments, we can foster a more comprehensive approach to supporting individuals with autism and their families, ultimately leading to improved outcomes and quality of life.

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