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EARLY-LIFE ANTIBIOTIC EXPOSURE AND THE RISK OF ATOPIC DERMATITIS IN CHILDREN: A NARRATIVE REVIEW OF GUT MICROBIOTA-RELATED MECHANISMS

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ABSTRACT

Background: Atopic dermatitis is one of the most common chronic inflammatory diseases in childhood, and its prevalence has markedly increased in industrialized countries over recent decades. Increasing attention has been directed toward the role of the gut microbiota in immune system development and in the pathogenesis of allergic diseases. Early-life antibiotic exposure is considered one of the major environmental factors capable of disrupting the normal maturation of the intestinal microbiome.
Aim: The aim of this literature review was to analyze current evidence regarding the association between prenatal and early childhood antibiotic exposure and the risk of atopic dermatitis in children, with particular emphasis on mechanisms related to gut microbiota dysbiosis and the gut–skin axis.
Methods: A narrative literature review was conducted based on currently available cohort studies, observational studies, and meta-analyses investigating the relationship between prenatal and early-life antibiotic exposure, alterations in gut microbiota composition, and the development of atopic dermatitis in children.
Results: Available studies indicate that antibiotic therapy during infancy may reduce bacterial diversity, impair short-chain fatty acid production, and dysregulate immune responses mediated by T helper 2 (Th2) lymphocytes. These alterations may contribute to increased intestinal permeability and chronic inflammatory processes involved in the development of atopic dermatitis. Several cohort studies and meta-analyses suggest a positive association between early antibiotic exposure and an elevated risk of atopic dermatitis, although the strength of this relationship varies depending on exposure timing, antibiotic class, outcome definition, and control for confounding factors.
Conclusions: Current evidence supports a potential link between prenatal and early childhood antibiotic exposure and an increased risk of atopic dermatitis through mechanisms associated with gut microbiota dysbiosis and the gut–skin axis. However, further prospective studies are required to establish causal relationships more precisely.

KEYWORDS

Atopic Dermatitis, Gut Microbiota, Antibiotics, Dysbiosis, Gut–Skin Axis, Children

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1. Introduction

Atopic dermatitis is a chronic, relapsing inflammatory skin disease characterized by pruritus, skin dryness, and impaired epidermal barrier function. The disease most commonly begins in early childhood and affects approximately 15–20% of children in industrialized countries (Nutten, 2015). The increasing prevalence of atopic dermatitis observed over recent decades suggests a substantial contribution of environmental factors to the pathogenesis of the disease (Weidinger & Novak, 2016).

Contemporary research increasingly highlights the importance of the gut microbiota in immune regulation and the development of allergic and atopic diseases (Petersen et al., 2019). Microorganisms colonizing the gastrointestinal tract participate in immune system maturation, maintenance of intestinal barrier integrity, and production of anti-inflammatory metabolites (Belkaid & Hand, 2014). Alterations in gut microbiota composition, commonly referred to as dysbiosis, may lead to excessive immune activation and contribute to the development of atopic disorders (Lee et al., 2018).

One of the most significant factors influencing gut microbiota composition during early life is antibiotic use. Although antibiotics remain essential in the treatment of bacterial infections, they may also cause long-term disturbances of the intestinal microbiome by eliminating beneficial commensal bacteria and reducing microbial diversity. Numerous studies have suggested an association between prenatal or infancy antibiotic exposure and an increased risk of atopic dermatitis (Tsakok et al., 2013).

The aim of this review is to present current knowledge regarding the impact of early childhood antibiotic exposure on the risk of atopic dermatitis in children, with particular emphasis on mechanisms related to gut microbiota alterations.

2. Literature Review Methodology

This study was conducted as a narrative literature review aimed at summarizing current evidence on the relationship between prenatal and early-life antibiotic exposure, gut microbiota dysbiosis, and the risk of atopic dermatitis in children. The review focused on both epidemiological evidence and biologically plausible mechanisms related to the gut–skin axis.

A literature search was conducted in May 2026 using PubMed, Scopus, and Web of Science databases. The search covered publications released between January 2015 and December 2025. Earlier publications were included only when they were considered landmark studies or provided essential background information on gut microbiota development, intestinal barrier function, immune regulation, or atopic dermatitis pathophysiology.

The following keywords and Medical Subject Headings (MeSH), where applicable, were used in different combinations: “atopic dermatitis,” “eczema,” “gut microbiota,” “gut microbiome,” “microbiome,” “antibiotics,” “antibacterial agents,” “dysbiosis,” “children,” “infants,” “prenatal exposure,” “early-life exposure,” “short-chain fatty acids,” and “gut–skin axis.” Boolean operators were used to combine search terms. Examples of search strategies included: “atopic dermatitis” AND “antibiotics” AND “children”; “eczema” AND “early-life antibiotic exposure” AND “microbiota”; and “gut microbiome” AND “gut–skin axis” AND “atopic dermatitis.”

The inclusion criteria were as follows: original cohort studies, case-control studies, observational studies, systematic reviews, meta-analyses, randomized controlled trials, and mechanistic or experimental studies addressing at least one of the following issues: early-life or prenatal antibiotic exposure, gut microbiota alterations, immune mechanisms associated with dysbiosis, atopic dermatitis in children, or microbiota-targeted interventions. Publications were included if they were written in English and available in full text.

The exclusion criteria included publications not directly related to atopic dermatitis, gut microbiota, antibiotic exposure, or pediatric populations; studies focusing exclusively on adult populations; conference abstracts without full-text availability; editorials, letters, and opinion articles without original data or substantial review content; and studies with insufficient methodological detail. Duplicate records were removed before screening.

The initial screening was based on titles and abstracts. Publications considered potentially relevant were then assessed in full text. The final selection prioritized studies with clear exposure definitions, clinically relevant outcomes, appropriate population characteristics, and discussion of potential confounding factors such as delivery mode, breastfeeding, infection history, genetic predisposition, and environmental exposures. Particular attention was given to studies that distinguished between prenatal antibiotic exposure, antibiotic exposure during the first year of life, and later childhood exposure.

Because this article was designed as a narrative review rather than a systematic review, no formal meta-analysis or quantitative risk-of-bias assessment was performed. The findings were synthesized descriptively and organized into thematic sections covering gut microbiota development, antibiotic-induced dysbiosis, immunological mechanisms, epidemiological associations, skin microbiota, probiotic-based interventions, and clinical implications. A total of 39 scientific publications meeting the inclusion criteria and thematic relevance requirements were analyzed.

3. Development of the Gut Microbiota in Early Childhood

Colonization of the gastrointestinal tract begins during the perinatal period and represents one of the key stages in immune system development (Tamburini et al., 2016). Multiple factors influence gut microbiota composition, including delivery mode, feeding type, gestational age, environmental exposure, and pharmacotherapy (Arrieta et al., 2014). Infants born vaginally are primarily colonized by microorganisms originating from the maternal vaginal and intestinal microbiota, whereas children delivered by cesarean section exhibit reduced microbial diversity and delayed colonization by beneficial bacteria such as *Bifidobacterium* and *Lactobacillus* species (Dominguez-Bello et al., 2010).

Breastfeeding plays a crucial role in shaping a healthy intestinal microbiome. Human milk contains oligosaccharides promoting the growth of probiotic bacteria and numerous immunomodulatory compounds

(Walker, 2013). Properly developed gut microbiota contributes to regulatory T-cell maturation, immunoglobulin A production, and maintenance of intestinal barrier integrity (West et al., 2017).

The first two years of life are considered a critical period for microbiota development. Disturbances occurring during this period may result in long-term immunological and metabolic consequences (Korpela & de Vos, 2018). Antibiotic therapy remains one of the most important factors disrupting normal gut colonization.

4. Effects of Antibiotics on the Gut Microbiota

Antibiotics are among the most commonly prescribed medications in pediatric populations, particularly during the first years of life (Hersh et al., 2013).

Studies have demonstrated that antibiotics may reduce the abundance of commensal bacteria, decrease microbial diversity, and promote overgrowth of potentially pathogenic microorganisms (Dethlefsen & Relman, 2011). Broad-spectrum antibiotics are considered particularly harmful because they induce profound alterations in gut microbiome structure (Francino, 2016).

Korpela et al. (2016) demonstrated that even short-term antibiotic therapy during infancy may cause long-lasting alterations in gut microbiota composition persisting for several months. Similar observations were reported by Langdon et al. (2016), who emphasized that antibiotics may interfere with immune development by eliminating bacteria involved in immune tolerance induction.

Antibiotic use is also associated with reduced production of short-chain fatty acids such as butyrate, propionate, and acetate, which exert anti-inflammatory effects and support intestinal barrier integrity (Koh et al., 2016). Deficiency of these metabolites may increase intestinal permeability and promote inflammatory processes.

5. The Gut–Skin Axis and Immunological Mechanisms

In recent years, increasing attention has been directed toward the concept of the gut–skin axis, which describes interactions between intestinal microbiota and skin health (Salem et al., 2018). Gut microorganisms influence immune system function by modulating dendritic cells, regulatory T lymphocytes, and the production of pro-inflammatory and anti-inflammatory cytokines (Rooks & Garrett, 2016).

Gut dysbiosis may contribute to dominance of the T helper type 2 immune response, which is characteristic of atopic diseases (Zheng et al., 2016). Atopic dermatitis is associated with increased production of interleukin-4, interleukin-5, and interleukin-13, which intensify inflammation and epidermal barrier dysfunction (Brunner et al., 2017).

Increased intestinal permeability also appears to play an important role. Damage to the intestinal epithelial barrier enables translocation of antigens and bacterial toxins into systemic circulation, potentially resulting in chronic immune activation (Bischoff et al., 2014). This phenomenon, commonly referred to as “leaky gut,” has increasingly been linked to immune-mediated disease development (Mu et al., 2017).

Studies further indicate that children with atopic dermatitis exhibit altered gut microbiota composition compared with healthy individuals. Patients with atopic disorders often demonstrate reduced abundance of *Bifidobacterium* species and increased prevalence of potentially pro-inflammatory bacteria (Wang et al., 2008).

6. Association Between Antibiotic Exposure and Atopic Dermatitis

Numerous epidemiological studies have investigated the relationship between early-life antibiotic exposure and the risk of atopic dermatitis.

One of the most recent studies, conducted by Hoskinson et al. (2024), demonstrated that antibiotic use during the first year of life was associated with increased risk of atopic dermatitis and significant disturbances in gut microbiota composition. The authors observed reduced bacterial diversity and decreased abundance of short-chain fatty acid-producing bacteria.

Similar findings were reported by Chiesa Fuxench et al. (2024), who analyzed prenatal and early childhood antibiotic exposure in relation to atopic dermatitis development. Their study revealed a significantly increased disease risk among children exposed to multiple antibiotic courses.

An important methodological limitation observed across many cohort studies is the possibility of confounding by indication. Children receiving antibiotics early in life are often affected by recurrent respiratory or gastrointestinal infections, which themselves may influence immune system maturation and increase susceptibility to allergic diseases. Therefore, it remains difficult to fully distinguish the effects of antibiotic exposure from the effects of underlying infections.

Metsälä et al. (2015) reported that both prenatal antibiotic exposure and antibiotic use during the first year of life were associated with increased risk of atopic diseases. The risk appeared to increase with the number of antibiotic courses administered.

Despite the growing body of evidence, not all studies confirm a direct causal relationship between antibiotic exposure and atopic dermatitis. Some authors have emphasized the potential role of environmental, genetic, and infectious factors (Flohr & Yeo, 2011).

7. Skin Microbiota and Its Role in Atopic Dermatitis

In addition to gut microbiota, the skin microbiome also plays a crucial role in the pathogenesis of atopic dermatitis (Kong & Segre, 2012). Patients with atopic dermatitis frequently demonstrate excessive colonization by *Staphylococcus aureus*, which correlates with disease severity (Totté et al., 2016).

Byrd et al. (2018) demonstrated that exacerbations of atopic dermatitis were associated with reduced skin microbiota diversity and dominance of *Staphylococcus aureus* strains. Impaired skin barrier function facilitates colonization by pathogenic microorganisms and intensifies inflammatory responses.

Growing evidence indicates close interactions between gut microbiota and skin microbiota. Metabolites produced by intestinal bacteria may influence cutaneous immune responses and epidermal barrier integrity (Rios-Covian et al., 2016).

8. Probiotic-Based Therapeutic Approaches in Atopic Dermatitis

The role of the gut microbiota in atopic dermatitis has attracted increasing scientific interest, particularly regarding the potential therapeutic effects of microbiome modulation. Current evidence suggests that probiotics may influence immune system maturation, support immune tolerance, and contribute to the prevention and management of allergic diseases. Kim and Kim (2019) demonstrated that probiotic supplementation may improve skin symptoms and modulate immunological parameters in children with atopic dermatitis. Pärtty et al. (2015) highlighted the importance of early microbiota-targeted interventions in immune-related disorders. Similarly, West et al. (2016) emphasized the potential role of probiotics in both the treatment and primary prevention of allergic diseases, including atopic conditions. Although available findings remain promising, further studies are required to determine the most effective probiotic strains, treatment duration, and clinical indications for microbiota-based therapies in atopic dermatitis prevention and management.

9. Limitations of Current Research

Interpretation of studies investigating the relationship between antibiotic exposure and atopic dermatitis requires consideration of multiple methodological limitations. In many studies, it remains difficult to distinguish the effects of antibiotics themselves from the effects of infections that necessitated treatment. This issue is particularly important because sibling-control and family-based analyses have shown that some associations may be attenuated after adjustment for shared familial and environmental factors (Mubanga et al., 2021).

Additional limitations include heterogeneous definitions of atopic dermatitis and lack of standardized methods for gut microbiota assessment (Chiu et al., 2019). Environmental factors, genetic predisposition, diet, delivery mode, and breastfeeding practices may also significantly influence study outcomes (Abrahamsson et al., 2012).

Most currently available studies are observational in nature, limiting the possibility of establishing definitive causal relationships. Publication bias may also contribute to overestimation of positive findings, as studies demonstrating significant associations are more likely to be published. Nevertheless, findings from numerous studies remain consistent and support a potentially important role of antibiotic exposure in the development of atopic diseases.

10. Clinical Implications

The growing number of studies concerning gut microbiota highlights the need for more rational antibiotic prescribing practices among pregnant women and young children. Excessive and unnecessary antibiotic therapy may result in persistent disturbances of the intestinal microbiome and increased risk of allergic disease development.

Development of preventive strategies targeting gut microbiota modulation may also prove clinically significant. Potential preventive interventions include promotion of breastfeeding, reduction of unnecessary antibiotic exposure, probiotic supplementation, and support of natural microbial colonization following birth.

In clinical practice, increasing attention has also been directed toward the potential use of microbiological biomarkers to identify children at high risk of developing atopic dermatitis.

11. Conclusions

Current evidence supports a possible association between early-life antibiotic exposure and increased risk of atopic dermatitis; however, causality has not yet been definitively established. One of the most important mechanisms responsible for this association appears to be gut microbiota dysbiosis leading to impaired immune regulation and intestinal barrier dysfunction.

Antibiotic therapy may reduce bacterial diversity, decrease the abundance of beneficial commensal microorganisms, and limit production of anti-inflammatory metabolites. These changes may promote immune responses characteristic of allergic diseases.

Despite the growing number of studies, further prospective investigations are necessary to better understand the relationship between gut microbiota and atopic dermatitis. Rational antibiotic use in pregnant women and young children, as well as development of microbiota-targeted therapeutic approaches, may become important elements in preventing allergic diseases.

Declaration of the Use of Generative AI and AI-Assisted Technologies in the Writing Process. In preparing this work, the authors used ChatGPT for the purpose of improving language and readability. After using this tool, the authors reviewed and edited the content as needed and accept full responsibility for the substantive content of the publication.

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