

Pathogenesis of Inflammatory Bowel Disease

Süleyman Dolu^{ID}, Hale Akpinar^{ID}

Department of Gastroenterology, Faculty of Medicine, Dokuz Eylül University, İzmir, Türkiye

Cite this article as: Dolu S, Akpinar H. Pathogenesis of Inflammatory Bowel Disease. *J Enterocolitis*. 2025;4(Suppl 1):S4-S7.

Corresponding author: Süleyman Dolu, e-mail: dr.sdolu@gmail.com

Received: February 03, 2025 **Accepted:** March 12, 2025

DOI: 10.14744/Jenterocolitis.2025.15570



Content of this journal is licensed under a Creative Commons Attribution-NonCommercial 4.0 International License.

Abstract

Inflammatory bowel disease (IBD) is a multifactorial condition characterized by chronic inflammation of the gastrointestinal mucosa. Despite extensive research, its precise etiology remains unknown. However, significant progress has been made in understanding its complex pathogenesis, which involves a combination of genetic predisposition, environmental influences, microbial dysbiosis, and immune dysregulation. Numerous genetic loci are associated with Crohn's disease. Environmental factors such as smoking, dietary habits, physical activity, antibiotic exposure, and early-life influences play crucial roles in disease initiation and progression. Dysbiosis disrupts intestinal homeostasis and exacerbates inflammation. Immune dysregulation, particularly involving the Th1, Th2, and Th17 pathways, results in an imbalance between proinflammatory and regulatory responses, perpetuating chronic inflammation.

Keywords: Crohn's disease, microbiota, ulcerative colitis

INTRODUCTION

Inflammatory bowel disease (IBD) is a chronic, relapsing inflammatory disorder of the gastrointestinal tract that primarily includes Crohn's disease (CD) and ulcerative colitis (UC). The pathogenesis of IBD is multifactorial, involving a complex interplay of genetic predisposition, immune dysregulation, environmental factors, and gut microbiota. Although the precise etiology remains unclear, it is well established that multiple contributing factors collectively influence disease onset, progression, and severity (Figure 1).

Genetic susceptibility plays a crucial role in IBD pathogenesis, as evidenced by the identification of multiple risk loci associated with immune response regulation, epithelial barrier function, and microbial interactions. Genome-wide association studies have highlighted key genetic variations, such as mutations in *NOD2*, *ATG16L1*, and *IL23R*, which significantly contribute to disease susceptibility, particularly in Crohn's disease. However, genetic predisposition alone is insufficient to trigger IBD, indicating the necessity of additional environmental and immunological factors.

Environmental factors, including diet, smoking, antibiotic exposure, and alterations in the gut microbiome, have been implicated in disease pathogenesis. Smoking has been found to exert differential effects on IBD subtypes, exacerbating Crohn's disease while providing a protective effect against ulcerative colitis. Emerging evidence suggests that early-life antibiotic exposure and altered gut microbial composition may disrupt intestinal immune homeostasis, further contributing to IBD development.

Immune dysregulation is a hallmark of IBD, characterized by an imbalance between proinflammatory and anti-inflammatory responses. In patients with IBD, an exaggerated immune reaction to commensal gut microbiota leads to persistent intestinal inflammation. Dysregulation of key immune pathways, including the Th1/Th17 axis in Crohn's disease and the Th2/Th9 response in ulcerative colitis, plays a central role in disease pathogenesis. Additionally, cytokine networks, such as tumor necrosis factor-alpha (TNF- α), interleukin-12 (IL-12), and interleukin-23 (IL-23), have been identified as pivotal mediators of inflammation, paving the way for the development of targeted biological therapies.

Given the complexity of IBD pathogenesis, ongoing research continues to explore novel mechanisms underlying disease development. Understanding the intricate interactions among genetic, environmental, and immune-related factors is essential for identifying new therapeutic targets and improving disease management. This review aims to provide an updated overview of the key pathogenic mechanisms driving IBD, with a focus on emerging insights that may shape future treatment strategies.

GENETIC FACTORS

Recent advancements in genetic research, driven by initiatives such as the *Human Genome Project* and the advent of genome-wide association studies (GWAS), have uncovered various genetic risk factors for IBD. These breakthroughs have significantly enhanced our understanding of the hereditary aspects of this disease and its molecular foundations.^{1,2}

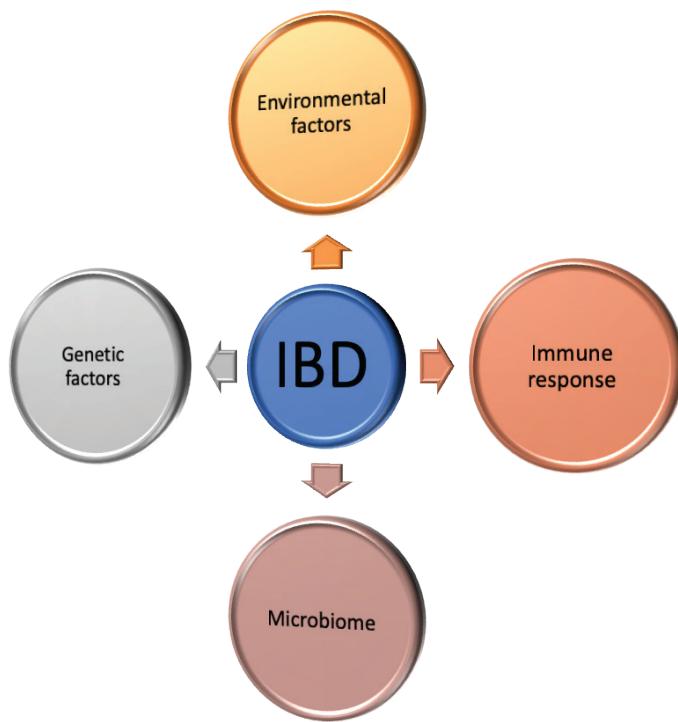


Figure 1. Factors affecting IBD pathogenesis.

Family studies have reported a family history in 1.5%–28% of CD cases and 1.5%–24% of UC cases.^{3–5} In CD, the risk is approximately eightfold higher, whereas in UC, the risk is fourfold higher.⁶ However, the incomplete concordance rates among twins suggest that genetic factors alone are insufficient to explain disease occurrence, highlighting the role of environmental influences.^{7,8}

To date, over 240 genetic loci have been implicated in IBD susceptibility, with at least 30 loci shared between CD and UC. *NOD2* is a key player in CD, as variants of *NOD2* are frequently observed in affected patients. Studies have reported a mutation prevalence of up to one-third in certain populations.^{9,10} For example, a 2006 study conducted in Turkey found a mutation frequency of 10.7% among patients with CD.¹¹

ENVIRONMENTAL FACTORS

Environmental factors play a significant role in the progression of IBD by interacting with an individual's genetic predisposition, ul-

MAIN POINTS

- **Complex Pathogenesis:** IBD arises from genetic predisposition, environmental factors, microbial dysbiosis, and immune dysregulation.
- **Genetic and Environmental Influences:** Key mutations (*NOD2*, *ATG16L1*, *IL23R*) increase susceptibility, while smoking, diet, and antibiotics affect disease risk.
- **Gut Microbiota Imbalance:** IBD is linked to reduced beneficial bacteria (*Faecalibacterium*, *Roseburia*) and increased proinflammatory taxa (*Enterobacteriaceae*, *Fusobacterium*).
- **Immune Dysregulation:** Crohn's disease is driven by Th1/Th17 pathways, ulcerative colitis by a Th2 response, leading to chronic inflammation.
- **Targeted Therapies:** Anti-TNF agents and IL-23 inhibitors help modulate immune pathways and improve patient outcomes.

timately influencing both disease susceptibility and clinical presentation.

Smoking

Smoking has a paradoxical effect on IBD. While it worsens Crohn's disease, it appears to protect against ulcerative colitis. The mechanisms underlying these effects include alterations in immune responses, increased mucus production, and inhibition of autophagy, a process critical for maintaining cellular homeostasis.^{9,12–14}

Physical Activity

Regular physical activity is associated with a reduced incidence of Crohn's disease. In patients with established Crohn's disease, physical activity has been linked to decreased disease activity and improved overall well-being. However, the relationship between physical activity and ulcerative colitis remains less clear.¹⁵

Dietary Factors

Studies suggest that a diet rich in fiber and fruits is associated with a lower risk of Crohn's disease, while high vegetable consumption appears to have a protective effect against ulcerative colitis. In contrast, diets high in animal fat, polyunsaturated fatty acids, and refined carbohydrates have been linked to an increased risk of IBD. Although elimination diets and specific dietary interventions, such as the Mediterranean and specific carbohydrate diets, may help alleviate symptoms, their impact on objective inflammatory markers remains uncertain due to methodological limitations in current research.^{16,17}

Antibiotic Use

Antibiotic use has been associated with an increased risk of IBD. A large case-control study involving 24,000 patients demonstrated a correlation between the frequency of antibiotic use and an increased risk of developing ulcerative colitis and Crohn's disease. Antibiotics are thought to disrupt gut microbiota composition, contributing to dysbiosis and intestinal inflammation.¹⁸

Nonsteroidal Anti-Inflammatory Drugs (NSAIDs)

NSAIDs are known to have adverse effects on the gastrointestinal system. Regular use of high-dose NSAIDs has been associated with an increased risk of IBD.¹⁹

Hormonal Factors

Oral contraceptives and hormone replacement therapies have been linked to an increased risk of IBD in women, highlighting the potential influence of hormonal modulation on disease onset and progression. This association suggests that exogenous hormonal factors may contribute to alterations in immune responses, gut microbiota composition, and intestinal barrier function, all of which play critical roles in IBD pathogenesis.^{20,21}

Appendectomy

Appendectomy has been recognized as a risk factor for Crohn's disease, potentially due to immune system alterations. However, it appears to have a protective effect against ulcerative colitis, suggesting a complex relationship between the appendix, gut immunity, and IBD pathogenesis.²²

Psychological Factors

A study suggested that individuals experiencing lower levels of stress had a decreased likelihood of developing IBD, indicating a potential link between psychological well-being and disease risk.²³

Exposures During Infancy

Early postnatal factors, such as breastfeeding, mode of delivery (vaginal vs. cesarean), and antibiotic exposure, influence gut microbiota development and immune system maturation. These factors have been associated with an altered risk of developing IBD later in life. Breastfeeding, in particular, promotes intestinal barrier integrity and immune tolerance.²⁴⁻²⁷

Other Factors

The rising prevalence of IBD in developing countries correlates with increasing industrialization and urbanization.¹⁹ Air pollution, dietary changes, and environmental toxins are believed to contribute to this trend.

MICROBIOME

Over the past two decades, the microbiome has become a central focus of research on IBD.²⁸ The gut microbiota plays a crucial role in maintaining the balance between T helper cells (Th cells) and regulatory T cells (Tregs), ensuring equilibrium between proinflammatory and anti-inflammatory responses. This highlights the essential role of gut microbiota in preserving host health and metabolic balance. Disruptions in the composition or function of these microorganisms disturb microbial homeostasis, leading to intestinal inflammation. This imbalance is further exacerbated in IBD, promoting dysbiosis and altering the regulation of key metabolic pathways.²⁹

Dysbiosis is characterized by a reduction in the number, diversity, and stability of bacterial populations within the microbiome, and these imbalances are closely linked to the onset and progression of IBD. In individuals with IBD, a notable depletion of beneficial commensal bacteria and essential microbial metabolites is frequently observed, further contributing to disease pathogenesis and intestinal inflammation.³⁰

Healthy gut microbiota is predominantly composed of *Firmicutes* and *Bacteroidetes*, which together constitute approximately 90% of the bacterial population. In patients with IBD, there is a marked reduction in beneficial bacteria such as *Faecalibacterium* and *Roseburia*, alongside an increase in proinflammatory taxa such as *Enterobacteriaceae* and *Fusobacterium*. Dysbiosis is also characterized by a decline in microbial diversity and stability, leading to impaired production of short-chain fatty acids and other essential metabolites that play crucial roles in maintaining intestinal health and immune regulation.^{28,31-36}

Numerous studies have investigated changes in the microbiome and/or metabolome in IBD. However, environmental factors such as nutrition, medications, ethnicity, and geographic location can influence the gut microbiome. It remains uncertain whether these microbial alterations are a driving factor in the development of inflammation or a consequence of the inflammatory process itself. Therefore, the association between the microbiome and IBD is not yet fully understood.

IMMUNE SYSTEM

Dysregulation of the immune system plays a pivotal role in the pathogenesis of IBD, involving complex interactions between innate and adaptive immune responses. The intestinal immune system is finely tuned to maintain a balance between tolerating commensal microbiota and mounting an effective defense against harmful pathogens. Disruptions in this equilibrium can lead to excessive immune activation, chronic inflammation, and the development of IBD. This persistent immune imbalance contributes to ongoing inflammation in affected individuals.

The key immune changes observed in patients with IBD include:

- Dysregulation of the Epithelial Barrier
- Dysregulation of Immune Cells
- Dysregulation of Secreted Mediators

Innate Immune System

The innate immune system serves as the body's first line of defense against microbial invaders, with Toll-like receptors (TLRs) and NOD-like receptors (NLRs) playing essential roles in detecting microbial components and initiating immune responses. In IBD, dysregulated expression and function of these receptors contribute to an impaired innate immune response, leading to excessive inflammation, disrupted microbial tolerance, and increased intestinal barrier dysfunction.¹⁹

Adaptive Immune System

The adaptive immune system, primarily mediated by T and B cells, is highly specific but requires more time to become fully activated. In Crohn's disease, a Th1-dominant immune response drives inflammation through excessive production of proinflammatory cytokines such as interferon-gamma (IFN- γ) and TNF- α . In contrast, ulcerative colitis is characterized by a Th2-skewed response, marked by elevated levels of interleukin-4 (IL-4) and IL-13, which contribute to mucosal inflammation. Additionally, Th17 cells, known to produce IL-17, IL-22, and other proinflammatory cytokines, are increased in both conditions, playing a crucial role in maintaining chronic inflammation and mucosal damage.^{9,19}

Cytokine-targeted therapies, such as anti-TNF agents and IL-23 inhibitors, have demonstrated efficacy in modulating immune pathways and improving clinical outcomes.

Peer-review: Internally peer-reviewed.

Author Contributions: Concept – S.D.; Design – H.A.; Supervision – H.A.; Resources – S.D.; Materials – S.D.; Data Collection and/or Processing - S.D.; Analysis and/or Interpretation – H.A.; Literature Review – S.D.; Writing - S.D.; Critical Review – H.A.

Use of AI for Writing Assistance: AI-assisted technologies were not used in this study.

Conflict of Interest: The authors have no conflicts of interest to declare.

Funding: The authors declared that this study received no financial support.

REFERENCES

1. Baig ZA, Majeed A. An insight into genetic landscape of inflammatory bowel disease. *J Pak Med Assoc*. 2023;73(12):2415-2422. [\[CrossRef\]](#)
2. El Hadad J, Schreiner P, Vavricka SR, Greuter T. The Genetics of Inflammatory Bowel Disease. *Mol Diagn Ther*. 2024;28(1):27-35. [\[CrossRef\]](#)
3. Tysk C, Lindberg E, Järnerot G, Flodérus-Myrhed B. Ulcerative colitis and Crohn's disease in an unselected population of monozygotic and dizygotic twins. A study of heritability and the influence of smoking. *Gut*. 1988;29(7):990-996. [\[CrossRef\]](#)
4. Halme L, Paavola-Sakki P, Turunen U, Lappalainen M, Farkkila M, Konstula K. Family and twin studies in inflammatory bowel disease. *World J Gastroenterol*. 2006;12(23):3668-3672. [\[CrossRef\]](#)
5. Santos MPC, Gomes C, Torres J. Familial and ethnic risk in inflammatory bowel disease. *Ann Gastroenterol*. 2018;31(1):14-23.
6. Moller FT, Andersen V, Wohlfahrt J, Jess T. Familial risk of inflammatory bowel disease: a population-based cohort study 1977-2011. *Am J Gastroenterol*. 2015;110(4):564-571. [\[CrossRef\]](#)
7. Ørholm M, Binder V, Sørensen TI, Rasmussen LP, Kyvik KO. Concordance of inflammatory bowel disease among Danish twins. Results of a nationwide study. *Scand J Gastroenterol*. 2000;35(10):1075-1081. [\[CrossRef\]](#)
8. Can G, Tezel HA. İnflamatuvar barsak hastalıkları ve genetik. *Anatolian Curr Med J*. 2020;2(3):80-6. [\[CrossRef\]](#)

9. Guan Q. A Comprehensive Review and Update on the Pathogenesis of Inflammatory Bowel Disease. *J Immunol Res.* 2019;2019:7247238. [\[CrossRef\]](#)
10. Jarmakiewicz-Czaja S, Zielińska M, Sokal A, Filip R. Genetic and Epigenetic Etiology of Inflammatory Bowel Disease: An Update. *Genes (Basel).* 2022;13(12):2388. [\[CrossRef\]](#)
11. Uyar FA, Over-Hamzaoglu H, Türe F, Güll A, Tözün N, Saruhan-Direskeneli G. Distribution of common CARD15 variants in patients with sporadic Crohn's disease: cases from Turkey. *Dig Dis Sci.* 2006;51(4):706-710. [\[CrossRef\]](#)
12. Pullan RD. Colonic mucus, smoking and ulcerative colitis. *Ann R Coll Surg Engl.* 1996;78(2):85-91.
13. Lakatos PL, Szamosi T, Lakatos L. Smoking in inflammatory bowel diseases: good, bad or ugly? *World J Gastroenterol.* 2007;13(46):6134-6139. [\[CrossRef\]](#)
14. Monick MM, Powers LS, Walters K, et al. Identification of an autophagy defect in smokers' alveolar macrophages. *J Immunol.* 2010;185(9):5425-5435. [\[CrossRef\]](#)
15. Jones PD, Kappelman MD, Martin CF, Chen W, Sandler RS, Long MD. Exercise decreases risk of future active disease in patients with inflammatory bowel disease in remission. *Inflamm Bowel Dis.* 2015;21(5):1063-1071. [\[CrossRef\]](#)
16. Gubatan J, Kulkarni CV, Talamantes SM, Temby M, Fardeen T, Sinha SR. Dietary Exposures and Interventions in Inflammatory Bowel Disease: Current Evidence and Emerging Concepts. *Nutrients.* 2023;15(3):579. [\[CrossRef\]](#)
17. Hou JK, Abraham B, El-Serag H. Dietary intake and risk of developing inflammatory bowel disease: a systematic review of the literature. *Am J Gastroenterol.* 2011;106(4):563-573. [\[CrossRef\]](#)
18. Nguyen LH, Örtqvist AK, Cao Y, et al. Antibiotic use and the development of inflammatory bowel disease: a national case-control study in Sweden. *Lancet Gastroenterol Hepatol.* 2020;5(11):986-995. [\[CrossRef\]](#)
19. Zhang YZ, Li YY. Inflammatory bowel disease: pathogenesis. *World J Gastroenterol.* 2014;20(1):91-99. [\[CrossRef\]](#)
20. Khalili H, Higuchi LM, Ananthakrishnan AN, et al. Oral contraceptives, reproductive factors and risk of inflammatory bowel disease. *Gut.* 2013;62(8):1153-1159. [\[CrossRef\]](#)
21. Khalili H, Higuchi LM, Ananthakrishnan AN, et al. Hormone therapy increases risk of ulcerative colitis but not Crohn's disease. *Gastroenterology.* 2012;143(5):1199-1206. [\[CrossRef\]](#)
22. Reif S, Lavy A, Keter D, et al. Appendectomy is more frequent but not a risk factor in Crohn's disease while being protective in ulcerative colitis: a comparison of surgical procedures in inflammatory bowel disease. *Am J Gastroenterol.* 2001;96(3):829-832. [\[CrossRef\]](#)
23. Bitton A, Dobkin PL, Edwardes MD, et al. Predicting relapse in Crohn's disease: a biopsychosocial model. *Gut.* 2008;57(10):1386-1392. [\[CrossRef\]](#)
24. Bertin B, Foligné B, Ley D, et al. An Overview of the Influence of Breast-feeding on the Development of Inflammatory Bowel Disease. *Nutrients.* 2023;15(24):5103. [\[CrossRef\]](#)
25. Wells JM, Gao Y, de Groot N, Vonk MM, Ulfman L, van Neerven RJJ. Babies, Bugs, and Barriers: Dietary Modulation of Intestinal Barrier Function in Early Life. *Annu Rev Nutr.* 2022;42:165-200. [\[CrossRef\]](#)
26. Ames SR, Lotoski LC, Azad MB. Comparing early life nutritional sources and human milk feeding practices: personalized and dynamic nutrition supports infant gut microbiome development and immune system maturation. *Gut Microbes.* 2023;15(1):2190305. [\[CrossRef\]](#)
27. Sosna B, Aebisher D, Myśliwiec A, et al. Selected Cytokines and Metalloproteinases in Inflammatory Bowel Disease. *Int J Mol Sci.* 2023;25(1):202. [\[CrossRef\]](#)
28. Santana PT, Rosas SLB, Ribeiro BE, Marinho Y, de Souza HSP. Dysbiosis in Inflammatory Bowel Disease: Pathogenic Role and Potential Therapeutic Targets. *Int J Mol Sci.* 2022;23(7):3464. [\[CrossRef\]](#)
29. Upadhyay KG, Desai DC, Ashavaid TF, Dherai AJ. Microbiome and metabolome in inflammatory bowel disease. *J Gastroenterol Hepatol.* 2023;38(1):34-43. [\[CrossRef\]](#)
30. Yu J. Gut microbiome and metabolome: The crucial players in inflammatory bowel disease. *J Gastroenterol Hepatol.* 2023;38(1):5-6. [\[CrossRef\]](#)
31. Wang W, Chen L, Zhou R, et al. Increased proportions of Bifidobacterium and the Lactobacillus group and loss of butyrate-producing bacteria in inflammatory bowel disease. *J Clin Microbiol.* 2014;52(2):398-406. [\[CrossRef\]](#)
32. Zheng J, Sun Q, Zhang J, Ng SC. The role of gut microbiome in inflammatory bowel disease diagnosis and prognosis. *United European Gastroenterol J.* 2022;10(10):1091-1102. Erratum in: *United European Gastroenterol J.* 2023;11(3):313. [\[CrossRef\]](#)
33. Mah C, Jayawardana T, Leong G, et al. Assessing the Relationship between the Gut Microbiota and Inflammatory Bowel Disease Therapeutics: A Systematic Review. *Pathogens.* 2023;12(2):262. [\[CrossRef\]](#)
34. Schirmer M, Garner A, Vlamakis H, Xavier RJ. Microbial genes and pathways in inflammatory bowel disease. *Nat Rev Microbiol.* 2019;17(8):497-511. [\[CrossRef\]](#)
35. Manichanh C, Borruel N, Casellas F, Guarner F. The gut microbiota in IBD. *Nat Rev Gastroenterol Hepatol.* 2012;9(10):599-608. [\[CrossRef\]](#)
36. Metwaly A, Reitmeier S, Haller D. Microbiome risk profiles as biomarkers for inflammatory and metabolic disorders. *Nat Rev Gastroenterol Hepatol.* 2022;19(6):383-397. [\[CrossRef\]](#)