

Intricacies of the enigmatic gastric pathogen *Helicobacter pylori* in the context of One Health Approach

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ABSTRACT

Background: *Helicobacter pylori* (*H. pylori*) infection is a global health concern, causing chronic inflammation that can lead to gastritis, peptic ulcer, and gastric adenocarcinoma. While *H. pylori* primarily colonizes the human stomach, evidence suggests potential zoonotic transmission and its presence in various animal species. This highlights the need for a One Health approach to understand its epidemiology and control. **Objective:** This study aims to explore the role of animals as reservoirs for *H. pylori*, examine interspecies transmission dynamics, and assess the interconnectedness of human, animal, and environmental health in the context of *H. pylori* infection. Additionally, it evaluates the implications of antimicrobial resistance and proposes strategies for surveillance and management. **Method:** A comprehensive review of recent studies was conducted, focusing on zoonotic pathways, environmental factors influencing *H. pylori* transmission, and the emergence of antimicrobial resistance. The study integrates findings from human medicine, veterinary science, and environmental health under the One Health framework. **Result:** Humans remain the primary reservoir for *H. pylori*, but evidence of zoonotic transmission underscores the importance of animals as potential secondary hosts. Environmental factors, including contaminated water and poor sanitation, contribute to transmission. The misuse of antibiotics in human medicine and agriculture accelerates antimicrobial resistance, complicating treatment strategies. **Conclusion:** Understanding *H. pylori* within the One Health framework is essential to address its multifaceted transmission dynamics and control challenges. Collaborative efforts across human, veterinary, and environmental health sectors are vital for effective surveillance, prevention, and antimicrobial stewardship. Integrating these strategies can promote the health and welfare of individuals and ecosystems globally.

Keywords: *Helicobacter pylori*, One Health, Zoonotic transmission, Antimicrobial resistance, Environmental health.

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INTRODUCTION

Helicobacter pylori (*H. pylori*), a Gram-negative microaerophilic microbe, settles in the stomach of humans and associates with various gastrointestinal disorders, including gastritis, peptic ulcers, and even stomach cancer.^{1,2} In 1982, the discovery of *H. pylori* as a gastric pathogen for the first time by Barry Marshall and Robin Warren revolutionized the understanding and treatment of gastrointestinal diseases.³ *H. pylori* colonizes the stomach lining, where it can cause inflammation and disrupt the stomach's protective mucus layer. This can lead to various conditions, ranging from asymptomatic gastritis to peptic ulcers and gastric malignancies. While many individuals with *H. pylori* infection remain asymptomatic, it can manifest as abdominal discomfort, bloating, nausea, and in severe cases, bloody vomit or stools. Long-term infection promotes the probability of instigating peptic ulcers and gastric cancer.⁴ Diagnosis often includes a combination of methods, including rapid urease test, stool antigen tests, serological tests, urea breath tests, and endoscopic biopsy followed by histology and culture for *H. pylori*. Accurate diagnosis is crucial for appropriate management. A combination of proton pump inhibitors (PPIs) and antibiotics (such as clarithromycin, amoxicillin, levofloxacin, or metronidazole) is needed to eradicate *H. pylori*.⁵ However, antibiotic resistance is a growing concern, emphasizing the need for tailored treatment regimens based on local resistance patterns. Strategies for prevention and control primarily focus on

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reducing transmission, improving sanitation, and addressing risk factors such as overcrowding and poor socioeconomic conditions. Public health interventions may include health education, screening programs, and antibiotic stewardship. The One Health study identifies the integrating approach of human, animal, and environmental health, underscoring cooperation across disciplines to mitigate complex health challenges. This collaborative approach is essential for understanding the ecology and transmission dynamics of infectious agents like *H. pylori*, which may have reservoirs in animals and the environment. One Health promotes integrated surveillance systems that monitor infectious diseases across human, animal, and environmental sectors. Early detection of emerging pathogens or antimicrobial resistance patterns in animals or environmental reservoirs can inform proactive public health responses.⁶ The One Health framework recognizes the interconnected nature

of antimicrobial use and resistance in human medicine, veterinary medicine, and agriculture. Strategies to combat AMR include prudent antimicrobial use, surveillance of resistance patterns, and promoting substitute strategies to prevent and control the disease. Environmental factors, like water quality and sanitation, can influence the transmission of gastrointestinal pathogens such as *H. pylori*. One Health advocates for sustainable environmental management practices that mitigate the transmission of infectious diseases and protect human and animal health. One Health promotes public awareness and education on the links between human, animal, and environmental health. Empowering communities to understand these connections can foster behavior changes that reduce the risk of infectious diseases, including those caused by *H. pylori*. *H. pylori* remains an important public health concern, particularly in its association with gastrointestinal diseases. Addressing this challenge effectively requires a multifaceted approach that encompasses diagnosis, treatment, prevention, and control measures. The One Health framework offers a valuable perspective for understanding and combating infectious diseases like *H. pylori* by addressing all these components. Collaborative effort across disciplines is essential for developing holistic strategies that promote health and well-being for both humans and ecosystems.

METHODOLOGY

To review the importance of a One Health program, we searched “NCBI-PubMed” using the keywords “One Health approach” and “*Helicobacter pylori*,” resulting in a total of 125 articles. Additionally, to explore the significance of potential zoonotic transmission pathways, we searched “NCBI-PubMed” using the keywords “zoonotic transmission” and “*Helicobacter pylori*,” identifying a total of 42 articles. In this review, we summarize the results of relevant studies and discuss the crucial role of interspecies transmission dynamics within the One Health approach. Finally, this review highlights the significance of sustainable environmental management practices that mitigate the transmission of infectious diseases and protect human and animal health, including advocating for behavior changes that may reduce the risk of infectious diseases, including those caused by *H. pylori*.

Thematic Analysis and Representation

A systematic review of peer-reviewed literature and databases collected from the “NCBI-PubMed” search was conducted to identify relevant studies on *H. pylori* transmission, AMR, and environmental determinants. Data were extracted using predefined criteria focusing on zoonotic transmission, antimicrobial susceptibility, and public health interventions. A thematic analysis approach was employed to synthesize findings and present actionable insights.

Helicobacter pylori and Pathogenesis

H. pylori, one of the most diverse bacterial species, infects 50% of the population around the world. While *H. pylori*

infection often remains asymptomatic, it may cause several gastrointestinal disorders, like gastritis, peptic ulcer, also even gastric cancer. It was an enigma how *H. pylori* thrives in the stomach’s acidic environment. It colonizes the gastric mucosa, particularly the antrum and corpus regions, where it attaches to the epithelial cells using adhesins and other surface molecules. *H. pylori* secretes various virulence factors that help it to colonize and persist in the stomach. One of the key virulence factors is urease, an enzyme that hydrolyzes urea to produce ammonia, which neutralizes the acidic environment surrounding the bacterium. This allows *H. pylori* to escape the brunt of the stomach environment and colonize the gastric mucosa. Bacteria’s pathogenicity and persistence have been found to be largely dependent on blood group antigen-binding protein A (BabA), which is stimulated through the pH-sensitive binding mechanism. In order to avoid the harmful effects of acid in the gastric environment, *H. pylori* adheres to the stomach’s cell lining and the mucus that covers it. The constant replacement of the stomach lining, however, creates an obstacle for the bacteria because it causes them to shed into the lumen, where they are eliminated. *H. pylori* can quickly separate from the old cells before they are affected by the gastric acid because of to the pH-sensitive BabA protein. The pathogen then returns to the new stomach lining cells to proceed with the infection process.⁷ The infection by *H. pylori* activates an inflammatory response in the gastric mucosa, which results in the infiltration of different immune cells. The bacterium secretes proteins, like cytotoxin-associated gene A (CagA) and vacuolating cytotoxin A (VacA), which play an important role in activating host immune responses and causing tissue damage. Figure 1 shows the schematic representation depicting the role of different virulence factors of *H. pylori* in the development of gastroduodenal diseases. Several studies also demonstrated that the plasticity region genes, located outside the *cag* pathogenicity island, are some of the contributors to *H. pylori* pathogenesis for causing gastroduodenal diseases.^{8,9} Inflammation of the gastric mucosa is a hallmark of *H. pylori* infection. The progression of chronic gastritis to atrophic gastritis is characterized by the loss of gastric glandular cells. The infection by *H. pylori*

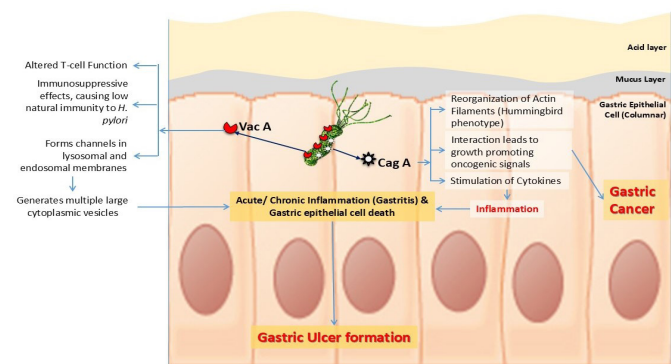


Figure 1: Schematic representation describing how *Helicobacter pylori* infection is linked to the development of gastroduodenal diseases

is an important probable factor for developing peptic ulcers. The disruption of the gastric mucosal barrier and the inflammatory response contribute to ulcer formation. Long-term *H. pylori* infection significantly enhances the possibility of developing gastric adenocarcinoma, particularly intestinal-type gastric cancer. The various events by which *H. pylori* triggers carcinogenesis include chronic inflammation, genomic instability, and the direct effects of bacterial virulence factors on host cells. The severity of *H. pylori*-related diseases can vary based on different host factors like genetic susceptibility, host immune response, and environmental factors. Host genetic polymorphisms, particularly in genes related to the host immune response and inflammation, might influence the chance of experiencing serious *H. pylori* infection consequences.

Diagnostics Laboratory Capacity Building

If someone experiences symptoms like abdominal pain, nausea, bloating, or signs of an ulcer, the doctor may suggest one or more of the diagnostic tests. Building laboratory capacity for *H. pylori* diagnostics involves a multi-faceted approach aimed at enhancing the capabilities of diagnostic laboratories to detect and characterize *H. pylori* infections accurately.

Firstly, the detection of an organism is the key event to initiate the proper treatment against the same. To date, the majority of the available tests for *H. pylori* detection are rapid urease test (RUT), histological examination, bacterial culture, DNA probe, and PCR base detection. The problem with these many detections is their dependency on the invasive method, endoscopy. The non-invasive procedures involve urea breath test, serology testing, and examination of ^{15}N Ammonia excreted in urine.

A urea Breath Test (UBT) involves swallowing a substance containing urea. If *H. pylori* is present, the bacteria break down the urea, releasing carbon dioxide that can be detected in the patient's breath. This test is reliable, non-invasive, and commonly used.¹⁰ Stool Antigen Test detects *H. pylori* antigens (proteins) in a stool sample, indicating an active infection.¹¹ It is also non-invasive and widely used. Antibodies against *H. pylori* can be detected through a blood test (serology). However, since antibodies can remain after the infection has cleared, this test is less commonly used to confirm an active infection. In cases where further examination is needed, an endoscopy may be performed. A small pinch of tissue (biopsy) is taken from the stomach lining for testing, usually through histology, culture, or rapid urease testing. This is more invasive but provides detailed information. Additionally, PCR tests can detect *H. pylori* DNA from stool or biopsy samples and are sometimes used to check for antibiotic resistance.¹² Doctors initially start with non-invasive tests like breath or stool tests for many patients. Dental plaque and saliva are the rich source of microorganisms. Studies demonstrated that the *H. pylori* DNA can be found in saliva and tooth plaque, which may lead to oral transmission.¹³

The choice of test is dictated by the patient's clinical situation. For obtaining a gastric tissue sample for urease, the most cost-effective test or performing biopsy testing (if extra tissues can be managed) when a RUT test gives a negative result is justified for a patient who will be undergoing an endoscopic procedure. Generally, the initial choice of test is the simple, non-invasive serologic tests.

Zoonotic Potential and Animal Reservoirs of *H. pylori*

H. pylori is primarily considered a human pathogen due to its strong association with human gastric mucosa. However, evidence demonstrates that the infection by *H. pylori* may have zoonotic potential, meaning it can be transmitted between animals and humans. Additionally, certain animal species have been declared as potential reservoirs for *H. pylori*. While *H. pylori* is primarily adapted to colonize the human stomach, cases of infection by *H. pylori* in non-human hosts have been reported.

In developed countries, around 20%–50% of the population is infected with *H. pylori*, whereas it reaches 60-70% in Asia and 90% in Africa.¹⁴ This high incidence is probably linked to the exercises taken to escalate the food production from animals to meet the gradually increasing population, ignoring hygienic necessities.^{15, 16} *H. pylori* inhabits the gut of both humans and animals.^{17, 18} *H. pylori* was found in the milk of several agricultural animals, according to earlier research.^{19, 20} *H. pylori* infections have been discovered in a number of animal species, serving as potential reservoirs for human infection. Studies have also demonstrated the isolation of *H. pylori* from domestic animals such as dogs, cats, pigs, and sheep.²¹ Transmission between humans and these animals could occur through close contact or shared environments. Handlers managing animals and food of animal origin displayed higher levels of antibodies (Ab) against *H. pylori*. This proposes that domestic and farming animals can be the cradle of infection in humans.^{15, 22, 23}

Humans, especially children, drink milk of animal origin. Therefore, drinking milk signifies the probable projected theory for the transmission of *H. pylori* from animals to humans. The presence of *H. pylori* was detected in raw as well as pasteurized milk along with milk products of animal origin using both conventional methods and molecular techniques^{24, 25}. These cases raise the possibility of zoonotic transmission, although the frequency and significance of such transmission events are still debated. Transmission of *H. pylori* between humans and animals could occur through direct contact, such as close contact with infected animals or consumption of contaminated food or water. However, the exact mechanisms and frequency of zoonotic transmission remain unclear and may vary depending on factors such as host specificity and strain diversity. *H. pylori* infection has been documented in non-human primates, including chimpanzees, gorillas, and macaques.²⁶ Given the close genetic relatedness between humans and non-human primates, zoonotic transmission between these species is plausible. Some wild animals, such

as rodents, birds, and certain carnivores, have also been found to carry *H. pylori* infections. The role of these animals as potential reservoirs for human infection requires further investigation. Genetic studies of *H. pylori* humans and animal isolates have revealed considerable genetic diversity within the species. Some strains isolated from animals exhibit genetic similarities to human-adapted strains, suggesting potential cross-species transmission.

Transmission dynamics between humans and animals are likely influenced by factors such as host specificity, ecological interactions, and geographic distribution. Understanding the genetic and epidemiological links between human and animal *H. pylori* strains is crucial for elucidating the zoonotic potential of *H. pylori*. *H. pylori* is primarily a human pathogen; evidence suggests that it may have zoonotic potential, with certain animal species serving as potential reservoirs for infection.^{15, 22-26} Further research is needed to better understand the dynamics of *H. pylori* transmission between humans and animals and the implications for public health.

Antimicrobial Resistance (AMR) Concerns of *H. pylori*

The emergence of antibiotic resistance, a natural phenotype, downregulates the efficacy of the commonly used antibiotics. Releasing residual antibiotics into the surroundings from food processing industries and rigorous use in health and clinical sectors stands out as a definite reason for the resistant bacterial pathogens to propagate in the environment. Besides the heterogeneity of the *H. pylori* genome, the antimicrobial susceptibility profile, and virulent factors are also highly variable as per the geographical locations and, most importantly, the isolation time. *H. pylori* is highly resilient to the changing environment by virtue of spontaneous mutations and accumulating genetic recombination. With the diagnosis of *H. pylori* infection, the implementation of empirical treatment for its eradication without prior susceptibility assay is definitely not a wise decision, yet unfortunately, done in most developing countries. The *H. pylori* isolation from biopsy samples to antibiotic susceptibility profiling is highly tedious, and its cost-effectiveness poses the reasons behind these issues. As a result, the treatment efficacy drops down. Henceforth, monitoring of antimicrobial susceptibility patterns both spatiotemporally and locally is of utmost necessity to rule out the resistant bacterial population from out-competing the sensitive ones in our surroundings. Antimicrobial resistance (AMR) is a growing concern in the management of *H. pylori* infections.^{27, 28} The bacterium's ability to develop resistance to antibiotics complicates treatment and may lead to treatment failure. Increasing antimicrobial resistance of *H. pylori* against traditionally used antibiotics is creating tension in the scientific community to such an extent that WHO has placed *H. pylori* among the 6 high-priority bacteria due to its high clarithromycin resistance, which poses a challenge to human health.²⁹ The primary antibiotics used against *H. pylori* include clarithromycin, metronidazole, amoxicillin, and levofloxacin.

Resistance to these antibiotics can develop through mechanisms such as target site alterations, enzymatic inactivation, or decreased drug accumulation. Clarithromycin resistance is a significant concern as it is a key component of many first-line therapy regimens for *H. pylori* eradication. Resistance to clarithromycin is often associated with point mutations in the 23S rRNA gene of *H. pylori*, which reduces the binding affinity of the antibiotic to its target (Table 1).³⁰ By exploiting this point mutation, a low-cost nested PCR assay directly from the biopsy samples has been developed for the rapid detection of clarithromycin-resistant *H. pylori* strains, providing rapid initiation of effective antibiotic treatment and avoiding empirical therapy.³¹

Metronidazole is another commonly used antibiotic in *H. pylori* treatment regimens. Resistance to metronidazole can arise due to mutations in genes encoding nitroreductases, which are involved in activating the drug (Table 1).⁵ Cross-resistance between metronidazole and other nitroimidazole antibiotics may also occur. While less common, resistance to amoxicillin and levofloxacin can also occur in *H. pylori* strains. Amoxicillin resistance may arise due to alterations in penicillin-binding proteins, while levofloxacin resistance is often associated with mutations in genes encoding DNA gyrase and topoisomerase IV. The presence of antibiotic resistance in *H. pylori* strains can significantly impact treatment outcomes. It can lead to treatment failure, persistent infection, and increased risk of recurrent disease. Inadequate eradication of *H. pylori* due to antibiotic resistance may also contribute to the development of more severe complications, such as peptic ulcers and gastric cancer. *H. pylori* strains resistant to multiple antibiotics, known as multidrug-resistant (MDR) strains, have been reported.²⁹ MDR strains pose a particularly challenging problem for treatment, as they limit the effectiveness of standard eradication therapies and require alternative treatment approaches.

Rational use of antibiotics is necessary to minimize selective pressure for resistance development. So, research into new antimicrobial agents and therapeutic approaches for *H. pylori* eradication is the pressing priority to mitigate the rising concerns of antimicrobial resistance. In conclusion, antimicrobial resistance in *H. pylori* is a significant concern that requires ongoing surveillance, research, and the development of innovative strategies to improve treatment outcomes and minimize resistance's detrimental impact on public health.

Environmental Determinants of *H. pylori* Infection

H. pylori infection, a common bacterial infection of the stomach, is influenced by various environmental determinants. *H. pylori* is primarily spread through oral-oral or fecal-oral routes. Poor hygiene practices, inadequate sanitation facilities, and crowded living conditions increase the risk of transmission. In developing countries with lower standards of hygiene, the prevalence of *H. pylori* infection tends to be higher. Individuals from lower socioeconomic

Table 1: Summary of *H. pylori* AMR patterns and associated genetic mechanisms

Antibiotic	Resistance mechanism	Clinical impact
Clarithromycin	Point mutations in 23S rRNA gene	Reduced binding, leading to treatment failure
Metronidazole	Mutations in nitroreductase-encoding genes	Drug activation inhibited
Levofloxacin	Mutations in DNA gyrase and topoisomerase IV	Reduced drug efficacy

backgrounds are more prone to be infected with *H. pylori*. This could be due to factors such as limited access to healthcare, poor living conditions, and higher rates of exposure to contaminated environments.³²

The prevalence of *H. pylori* infection varies widely across different geographic regions. In general, developing countries have higher rates of infection compared to developed countries. Factors such as climate, dietary habits, and cultural practices may contribute to these differences. Contaminated water sources and food items, particularly those prepared under unhygienic conditions, can serve as reservoirs for *H. pylori*. Consuming raw or undercooked shellfish and vegetables irrigated with contaminated water are potential sources of infection.³³ Close contact with infected individuals, such as within households or in crowded institutional settings like prisons or military barracks, increases the likelihood of *H. pylori* transmission. The significance of intra-familial transmission is demonstrated by studies that reveal the presence of infected family members considerably raises the probability of *H. pylori* infection among household contacts. *H. pylori* infections are more prevalent in children and may persist into adulthood if neglected. Younger age groups, especially children living in developing countries, are particularly susceptible to infection. Cultural practices such as sharing utensils or communal eating habits can facilitate the spread of *H. pylori* within communities. Smoking has been associated with an increased risk of *H. pylori* infection and may exacerbate the severity of associated diseases such as peptic ulcer disease and gastric cancer. While the role of specific dietary factors in *H. pylori* transmission is not fully understood, certain dietary habits, such as consuming spicy foods or foods with high salt content, may influence the risk of infection or disease progression. Understanding these environmental determinants is crucial for implementing effective strategies for the prevention and control of *H. pylori* infection, particularly in high-risk populations. Public health interventions focusing on improving sanitation, promoting hygiene practices, and raising awareness about the transmission routes of *H. pylori* can help reduce the burden of this infection.

Public Health Interventions and Education to control *H. pylori* infection

Education and public health initiatives are essential for preventing and managing *H. pylori* infection. Public health authorities might launch educational initiatives to increase public awareness of *H. pylori* infection, its transmission pathways, and related health hazards. These programs, which stress the value of good hygiene habits, handling food safely, and getting medical attention for symptoms, can be directed at both the general public and high-risk populations. The spread of *H. pylori* can be decreased by promoting good handwashing with soap and water, particularly before meals and after using the restroom.³⁴ Hygienic habits can be promoted in homes, schools, and healthcare facilities through educational materials and community outreach initiatives. Stopping the spread of *H. pylori* requires having access to clean water and sufficient sanitary facilities. Enhancing community sanitation infrastructure should be the main goal of public health initiatives, especially in low-resource environments where access to sanitary facilities and clean water is restricted. The burden of disease can be decreased by putting screening systems in place to find people who have an *H. pylori* infection, especially those who are more likely to experience consequences like stomach cancer. Treatment with antibiotics and acid-suppressing medications can effectively eradicate *H. pylori* infection and prevent associated health problems.³⁵ Certain populations, such as children living in overcrowded households or individuals from low socioeconomic backgrounds, may be at higher risk of *H. pylori* infection. Targeted interventions, such as school-based education programs or community outreach initiatives, can be tailored to address the specific needs of these high-risk groups. Public health initiatives to encourage smoking cessation can help avoid diseases linked to *H. pylori* because smoking has been linked to an elevated risk of *H. pylori* infection and related consequences. Although the exact function of nutrition in the spread of *H. pylori* is unknown, encouraging a nutritious diet full of fruits, vegetables, and whole grains may help lower the chance of *H. pylori* infection and the problems that come with it. Addressing *H. pylori* infection requires a multi-sectoral approach involving collaboration between healthcare providers, public health agencies, policymakers, and community organizations.³⁶ By working together, stakeholders can develop and implement comprehensive strategies to prevent and control *H. pylori* infection effectively. By implementing these public health

Table 2: Public health interventions and their anticipated outcomes.

Intervention	Target audience	Outcome
Hygiene education programs	General public	Reduced person-to-person transmission
Improved water sanitation	Communities in need	Lower contamination of water sources
Screening and early treatment	High-risk populations	Prevention of gastric complications

interventions and education programs, it is possible to reduce the prevalence of *H. pylori* infection and mitigate its impact on population health (Table 2). Regular monitoring and evaluation of these initiatives are essential to ensure their effectiveness and identify areas for improvement.³⁷

One Health Program for *H. pylori* infection

Implementing a One Health program for *H. pylori* infection would involve a collaborative approach that integrates efforts across human health, animal health, and environmental sectors to address the complex factors influencing the transmission and control of the bacterium. A surveillance system must be put in place to keep an eye on the distribution and frequency of *H. pylori* infections in people, animals, and the environment. This would involve collecting data from clinical settings, veterinary clinics, and environmental samples to track patterns of transmission and identify emerging hotspots. Necessary steps may be taken to conduct research to better understand the transmission dynamics of *H. pylori* across different host species and environmental reservoirs. Epidemiological studies can help identify risk factors associated with infection and inform the development of targeted interventions. It is essential to launch public awareness campaigns that emphasize the One Health approach to *H. pylori* infection. These campaigns would educate healthcare professionals, veterinarians, policymakers, and the general public about the interconnectedness of human, animal, and environmental health in the context of *H. pylori* transmission and control. It is indispensable to strengthen diagnostic capabilities for detecting *H. pylori* infection in humans and animals. This could involve standardizing laboratory protocols, sharing diagnostic resources between human and veterinary health sectors, and training personnel in One Health diagnostics. Investigate the role of animal reservoirs, such as domestic pets and livestock, in the human transmission of *H. pylori*. In order to lower the frequency of *H. pylori* in animal populations and lower the risk of zoonotic transmission, interventions like vaccination or antibiotic stewardship programs may be implemented. Addressing environmental variables that lead to *H. pylori* transmission is crucial, such as contaminated water sources and poor sanitation practices. Implementing measures like improvement of water quality, sanitation infrastructure, and food safety standards may play a crucial role in reducing environmental reservoirs of *H. pylori*.³⁸ The development of policies and guidelines will promote the One Health approach to *H. pylori* infection control (Table 3). Fostering collaboration between human health, animal health, and environmental agencies at the local, national, and international levels will facilitate information sharing, resource allocation, and joint decision-making. It is necessary to provide training opportunities for healthcare professionals, veterinarians, environmental scientists, and other stakeholders involved in *H. pylori* control efforts. This could include workshops, seminars, and online courses focused on One Health principles, epidemiology, diagnostics,

Table 3: Policy priorities for combating *H. pylori*

Policy area	Recommended action
AMR Monitoring	Establish regional AMR surveillance
Diagnostic Improvement	Promote use of rapid PCR diagnostics
Research Funding	Develop alternative antimicrobial agents

and intervention strategies. By integrating efforts across multiple sectors and disciplines, a One Health program for *H. pylori* infection can enhance the effectiveness of control measures and aid in reducing the morbidity and mortality rates associated with *H. pylori* in both human and animal populations (Table 3).

Limitation

Detecting *H. pylori* in environmental samples such as water and soil presents significant challenges. The bacterium often loses viability outside the human host, making it difficult to culture and identify using conventional microbiological methods. This limitation hampers efforts to trace environmental sources of *H. pylori* infections effectively. The exact transmission routes of *H. pylori* remain poorly understood, although person-to-person contact, contaminated water, and food are suspected pathways. However, pinpointing specific environmental transmission routes is complicated by the reliance on indirect evidence, as direct detection of *H. pylori* in environmental contexts is rare and technically demanding.

Additionally, genetic predisposition and socioeconomic conditions play critical roles in determining infection rates. Factors such as genetic variability in immune responses and disparities in access to sanitation and clean water can influence susceptibility to *H. pylori*. These intertwined influences make it difficult to isolate the role of environmental factors from genetic and socioeconomic contributors, further complicating the understanding of *H. pylori* transmission dynamics³⁹.

CONCLUSION

H. pylori remains a significant public health concern, particularly in its association with gastrointestinal diseases. Addressing this challenge effectively requires a multifaceted approach that encompasses diagnosis, treatment, prevention, and control measures. The One Health framework offers a valuable perspective for understanding and combating infectious diseases like *H. pylori* by recognizing the coordinated efforts in human, animal, and environmental health sectors. Collaboration across disciplines is essential for developing holistic strategies that promote health and well-being for both humans and ecosystems.

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PEER-REVIEWED CERTIFICATION

During the review of this manuscript, a double-blind peer-review policy has been followed. The author(s) of this manuscript received review comments from a minimum of two peer-reviewers. Author(s) submitted revised manuscript as per the comments of the assigned reviewers. On the basis of revision(s) done by the author(s) and compliance to the Reviewers' comments on the manuscript, Editor(s) has approved the revised manuscript for final publication.