



Overcoming antibiotic-resistant *Helicobacter pylori* infection: Current challenges and emerging approaches

Gabriel Reis Rocha, Fabian Felipe Bueno Lemos, Luis Guilherme de Oliveira Silva, Marcel Silva Luz, Gabriel Lima Correa Santos, Samuel Luca Rocha Pinheiro, Mariana Santos Calmon, Fabrício Freire de Melo

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Gabriel Reis Rocha, Fabian Felipe Bueno Lemos, Luis Guilherme de Oliveira Silva, Marcel Silva Luz, Gabriel Lima Correa Santos, Samuel Luca Rocha Pinheiro, Mariana Santos Calmon, Fabrício Freire de Melo, Instituto Multidisciplinar em Saúde, Universidade Federal da Bahia, Vitória da Conquista 45029-094, Bahia, Brazil

Corresponding author: Fabrício Freire de Melo, PhD, Professor, Instituto Multidisciplinar em Saúde, Universidade Federal da Bahia, Rua Hormindo Barros, 58, Quadra 17, Lote 58, Vitória da Conquista 45029-094, Bahia, Brazil. freiremeloufba@gmail.com

Abstract

Recent studies have shown a noticeable increase in global *Helicobacter pylori* (*H. pylori*) resistance, with clarithromycin resistance surpassing 15% in various areas. However, inadequate epidemiological monitoring, especially in developing countries, and the absence of uniform testing methods lead to discrepancies between regions and a possible underestimation of resistance levels. The complexity of treating *H. pylori* is driven by its highly dynamic genome, which is prone to frequent mutations contributing to phenotypical resistance. The usual course of action in empirical treatment involves using a combination of various drugs simultaneously, leading to significant resistance selection pressure and potential side effects. The emergence of *H. pylori* strains resistant to multiple drugs is closely tied to failures in first-line treatment, highlighting the need to prevent further resistance by using optimal initial empirical therapy or regimens guided by antibiotic susceptibility testing, requiring a collection of mixed samples and multiple isolates for accurate assessment. The emergence of new treatments like potassium-competitive acid blockers offers a hopeful approach to decrease antimicrobial usage while still ensuring effectiveness in comparison to traditional therapies with proton pump inhibitors. Additionally, the use of probiotics is under investigation to identify specific strains and formulations that may mitigate therapy-associated adverse effects.

Key Words: *Helicobacter pylori*; Antibiotic resistance; Multidrug resistance; Heteroresistance; Empirical treatment; Antimicrobial susceptibility testing

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Core Tip: The rise of antibiotic resistance in *Helicobacter pylori* (*H. pylori*) has become a global concern and led to the reduction of efficacy of conventional therapies. Resistant *H. pylori* strains, often inadequately mapped by regional surveillance, frequently demand multiple eradication attempts, imposing considerable financial burdens and adverse effects and contributing to secondary resistance development. This study aimed to provide a comprehensive review of the current landscape of mechanisms and prevalence of *H. pylori* resistance and to summarize promising therapeutic alternatives under evaluation. These strategies might improve treatment efficacy, enhancing patient outcomes in this challenging scenario.

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INTRODUCTION

Helicobacter pylori (*H. pylori*) is a microaerophilic, gram-negative bacterium that commonly colonizes the human gastric mucosa with an estimated prevalence of approximately 44% of adults and 35% of children and adolescents worldwide [1]. The discovery of *H. pylori* in 1983 by Warren and Marshall [2] and their subsequent research revealing its association with chronic gastritis and peptic ulcer disease [3] profoundly impacted the gastroduodenal pathology field and revolutionized clinical management of these conditions.

Although most *H. pylori*-positive individuals are asymptomatic, the presence of the bacterium invariably leads to persistent inflammation of the gastric mucosa (chronic gastritis), which raises the risk of developing functional and structural abnormalities as well as neoplasms [4]. Thus, *H. pylori* infection can culminate in conditions such as peptic ulcer disease, atrophic gastritis [5], gastric adenocarcinoma [6,7], and gastric mucosa-associated lymphoid tissue lymphoma [8]. Since the eradication of *H. pylori* can reduce dyspeptic symptoms [9], halt the progression of preneoplastic lesions [10], lower the risk of cancer [11,12], and induce regression of early-stage mucosa-associated lymphoid tissue lymphoma [13], treatment of the infection is beneficial and therefore recommended for both symptomatic and asymptomatic individuals [4].

The activity of hydrogenase, catalase, superoxide dismutase, and urease enzymes allow the bacteria to survive and thrive in the stomach [14,15]. While *H. pylori* can elicit a robust immune response with lymphocytes, eosinophils, macrophages, and dendritic cells being the most identified cell types [16], the bacterium has also developed mechanisms to evade immune detection and maintain its colonization. For instance, vacuolating cytotoxin A, a pore-forming toxin present in many bacterial strains and a major determinant of *H. pylori* pathogenicity [17], has been demonstrated to inhibit macrophage maturation, T cell proliferation, and the antigen presentation process [18,19]. This immunomodulatory activity combined with a significant arsenal of enzymes essential for its successful colonization of the gastric mucosa, may contribute significantly to the evasion of host defenses and long-term persistence of the infection.

Thus, once adults are *H. pylori*-positive, the infection usually persists throughout life unless approached with specific therapy or until severe atrophic gastritis [20-22]. Indeed, the capacity of *H. pylori* to not only be in gastric mucus attached to gastric epithelial cells but also inhabit the intracellular environment (and being inaccessible to many antibiotics) provides the bacteria an intrinsic mechanism of relative antimicrobial resistance [23,24]. Thus, eradicating *H. pylori* generally demands the combination of different antibiotics and adjunctive drugs that are conventionally administered in 14 days [4]. Additionally, while its high genetic plasticity is often examined to explain the ability of *H. pylori* to successfully infect hosts and cause disease [25,26], it also plays a critical role in the development of highly resistant strains [27]. This adaptability enables the bacteria to efficiently acquire developing resistance to antimicrobials, even when other factors such as horizontal gene transferring are considered [28].

Clarithromycin, amoxicillin, tetracycline, nitroimidazoles, levofloxacin, rifabutin, and furazolidone are among the antibiotics that may be effective against *H. pylori*. To prevent excessive use of antibiotics, strategies for empirically eradicating *H. pylori* are categorized into first-line, second-line, and rescue approaches, which must consider the local antimicrobial resistance profile [4,29]. When aiming for rational medication usage, antimicrobial susceptibility testing (AST) is a reasonable strategy that enables tailored therapy when feasible [4]. However, the limited availability of these methods hinders their widespread adoption, necessitating cost-effectiveness evaluations in different areas.

Indeed, from 2006 to 2016, resistance rates to clarithromycin, metronidazole, and levofloxacin have increased across all World Health Organization (WHO) regions [30]. Several studies are currently being carried out to evaluate different approaches for optimizing empirical treatment in this context. For example, alternative options may include the use of new antisecretory drugs to enhance treatment efficacy and reduce the need for multiple antibiotic usage [31,32], shortening the duration of well-established therapy regimens [33,34] and decreasing the concomitant administration of drugs [35]. Ultimately, the objectives are to improve effectiveness, enhance patient adherence (by streamlining therapeutic regimens or minimizing adverse events), and mitigate the selection pressure of antibiotics.

FUNDAMENTALS OF *H. PYLORI* TREATMENT

Therapeutic regimens for *H. pylori* infection consist of a combination of antibiotics with a strong acid suppressant[20]. To ensure the bactericidal efficacy of antimicrobials, it is important to raise gastric pH with antisecretory drugs, such as proton pump inhibitors (PPIs), like omeprazole and lansoprazole, or potassium-competitive acid blockers (P-CABs), like vonoprazan and tegoprazan[24]. Additionally, first-line therapy often includes bismuth. Although the mechanisms of bismuth salts are not fully understood, they offer advantages including antibacterial properties through the inhibition of different enzymes (like urease, fumarase, alcohol dehydrogenase, and phospholipase) and a cytoprotective effect on the gastric mucosa, facilitating ulcer healing and impeding *H. pylori* from attaching to gastric epithelial cells[36].

According to the Maastricht VI/Florence consensus (2022)[4], the bismuth-containing quadruple therapy (BQT), which includes a PPI, bismuth, tetracycline, and metronidazole, is recommended as a first-line empirical therapy globally. In regions where clarithromycin resistance is below 15%, another first-line option is the clarithromycin triple therapy, consisting of a PPI, clarithromycin, and amoxicillin. However, in areas with high ($\geq 15\%$) or unknown clarithromycin resistance, if BQT is not available, the preferred first-line treatment is the non-bismuth concomitant quadruple therapy (non-BQT), which includes a PPI, clarithromycin, amoxicillin, and metronidazole administered concomitantly. After the failure of first-line therapies, second-line and rescue treatments should be guided by local resistance patterns. Alternative options include levofloxacin-based therapies (comprising a PPI, levofloxacin, amoxicillin, with or without bismuth), high-dose PPI-amoxicillin dual therapy, and rifabutin-based therapies[4].

Regarding AST-based therapy, traditional culture-based methods are limited by technical constraints, subjective interpretation, prolonged execution time, and the necessity for invasive procedures (prior endoscopy), which is not always required for diagnosis except in high cancer-risk cases[4]. Molecular methods, such as PCR, provide reliability in identifying particular mutations that cause resistance, but they usually rely on endoscopic procedures. Emerging non-invasive AST methods, such as real-time PCR on fecal samples, are being investigated as alternatives[37,38]. Further evaluation is needed to determine the overall advantages and cost-effectiveness of AST-guided tailored treatment compared to empirical treatments before issuing widespread clinical advice.

FACTORS DRIVING ERADICATION THERAPY FAILURE

Genetic mechanisms of antibiotic resistance

H. pylori inherently possesses a highly dynamic genome, characterized by extensively repetitive chromosomal sequences that facilitate frequent mutations, even in the absence of multiple coexisting lineages within a single host[28]. Additionally, this genetic fluidity is closely linked to the high correlation between phenotypical and genotypical resistance within different strains of the bacteria[39]. Understanding the genetic basis of *H. pylori* resistance can lead to more effective treatments as the targeted identification of resistance-associated genes enables a tailored therapy of resistant strains of the bacteria that could optimize outcomes and reduce antibiotic resistance development[40,41].

Resistance to clarithromycin in *H. pylori* is linked to the structures through which macrolides operate, namely the ribosomal 50S subunit[42]. A2142G, A2143G, and A2142C are the main nucleotide substitutions in the 23S rRNA molecule, accounting for more than 90% of clarithromycin-resistant *H. pylori*[43]. These point mutations are located in the peptidyl transferase loop, a critical area for the binding of macrolide antibiotics, and their alterations compromise the ability of the drug to operate effectively, leading to a less effective treatment of the bacteria[44]. Despite this, A2115G, G2212A, G2141A, A2144T, and T2289C point mutations are also currently known to impede clarithromycin action against the bacteria[45]. Furthermore, it is believed that efflux pump systems, specifically the HP0605-HP0607 gene cluster, also may worsen *H. pylori* resistance when the bacteria already present 23S rRNA alterations[46].

Regarding fluoroquinolones, *H. pylori* primarily develops resistance through mutations in the genes encoding bacterial type II topoisomerases, specifically DNA gyrase, which is crucial for DNA replication and serves as the target of these drugs[47]. Resistance typically arises from alterations in the A subunits of DNA gyrase, encoded by the *gyrA* gene[48]. The quinolone resistance-determining region within this gene is particularly susceptible to mutations that alter the target protein structure and binding affinity to the enzyme, especially in codons 91 and 87[49]. Nevertheless, quinolone resistance can also develop through mutations in the B subunits of DNA gyrase, encoded by the *gyrB* gene[50].

Resistance to metronidazole in *H. pylori* primarily arises from disruptions in the activation of the drug, which occurs through redox reactions inside the bacteria carried out by enzymes, such as oxygen-insensitive NADPH nitroreductase [51]. This interaction triggers the production of reactive oxygen species and other reductive intermediates that lead to severe DNA damage and cytotoxicity. Despite impairing the survival of the bacteria, it also heightens the mutation rate, resulting in higher resistance of *H. pylori* to metronidazole compared to other antibiotics[52,53]. *RdxA* is one of the genes responsible for encoding reductase enzymes and is a primary site for mutations, which can lead to the inactivation of these enzymes and the disruption of metronidazole activation within the bacterial cell[54]. However, several mutations in *rdxA* are developmental signals rather than being associated with resistance, limiting the reliability of molecular methods for detecting metronidazole resistance[53]. Another gene, *frxA*, also plays a similar role in metronidazole resistance, particularly when combined with other mutations, although its specific contribution to resistance is not as clearly agreed upon as *rdxA*[55,56].

Concerning beta-lactams, *H. pylori* resistance mechanisms hinge on mutations in a few critical genes. Amoxicillin and other drugs in this class target penicillin-binding proteins in the bacterial periplasm, forming a stable complex that disrupts the cross-linking of peptidoglycan in the cell wall[57]. Unlike many other gram-negative pathogens where beta-lactamase production is central to resistance development, *H. pylori* primarily relies on mutations in the *pbb1A* gene that

may occur at multiple sites[58]. These mutations reduce the affinity of penicillin-binding proteins for beta-lactams, significantly diminishing antibiotic effectiveness[59]. Additionally, genetic alterations in porin proteins, particularly *hopB* and *hopC*, are also believed to contribute to resistance to multiple beta-lactams, especially when they occur in synergy with each other and with *pbp1A* mutations[60,61].

Tetracycline is a broad-spectrum antibiotic that inhibits bacterial protein synthesis by binding to the 30S subunit of ribosomes and blocking aminoacyl-tRNA attachment[62]. Resistance mechanisms to tetracycline have been documented in other bacteria, typically involving specific antibiotic efflux pumps[63]. In *H. pylori*, however, efflux pumps specific to tetracycline are rarely reported, with references only to a homolog of the *tetA*(P) efflux pump and other multidrug efflux systems as potential resistance mechanisms[64,65]. Tetracycline resistance in *H. pylori* is more commonly associated with mutations in the 16S rRNA-encoding genes, particularly at positions 926-928 and 965-967, which disrupt the binding site of the antibiotic and decrease its efficiency[63,66].

Lastly, furazolidone and rifampicin are considered alternative antibiotics for rescue treatment[67]. Furazolidone is a nitrofurantoin and shares similarities with metronidazole, dealing damage to the DNA of the bacteria but also requiring activation by reductase reactions within the bacteria[68,69], such as flavodoxin pyruvate oxidoreductase, encoded by the *porD* gene[70]. Mutations in this gene are thought to be the main contributors to increased resistance to furazolidone by *H. pylori*, although most research on this mechanism is dated and scarce[71]. Rifampicin functions by binding to the β subunit of DNA-dependent RNA polymerase, encoded by the *rpoB* gene, thereby severely disrupting RNA transcription and protein synthesis[72]. Resistance to rifampicin is typically associated with mutations in the rifampicin resistance-determining region of the *rpoB* gene, though resistance can also arise from mutations outside this region[73,74].

Multidrug resistance and heteroresistance mechanisms

Multidrug resistance (MDR) (*i.e.* resistance to three or more antibiotics of different classes) in *H. pylori* presents a significant challenge in clinical management. Boyanova *et al*[75] reported that the most common patterns of MDR in *H. pylori* may be resistance to clarithromycin, metronidazole, and fluoroquinolone. MDR can be developed through the accumulation of gene mutations that confer single-drug resistance. However, other direct contributors are intrinsically related to MDR manifestation, including the upregulation of multidrug efflux pump systems and biofilm formation.

The expression of several genes is associated with active efflux phenotypes that lead to MDR in *H. pylori* by protecting the bacteria from toxic antibiotic effects. Key genes involved include HP0605 (*hefA*), HP1174 (*gluP*), HP1181, and HP1184 [76-79]. Specifically, the upregulation of *gluP* by the activity of *spoT* enzyme can stimulate biofilm formation in *H. pylori* [78]. Notably, when compared to planktonic (freely existing) cells, biofilm-forming cells also exhibit significantly higher expression of other efflux pump proteins genes, including *hefA*, HP1181 (both related to MDR), and HP1165 (related to tetracycline resistance) and those coding for transmembrane ABC transporters[76,78,80].

Certain *H. pylori* strains can form biofilms on gastric mucosa, consisting of dead cells and extracellular polymeric substances, including mannose-related proteoglycans and extracellular DNA[81-83]. In various pathogens and situations, the biofilm matrix serves as a robust, non-specific barrier that shields bacterial communities from direct antimicrobial effects, aiding horizontal gene transfer and promoting the overexpression of resistance mechanisms[84,85]. Conceivably, studies have shown that biofilm-forming *H. pylori* exhibit increased levels of minimum bactericidal concentration for amoxicillin, metronidazole, tetracycline, and erythromycin than planktonic counterparts[76,86]. Moreover, when biofilm cells are subjected to the same antimicrobial concentration as planktonic cells, they present decreased susceptibility to clarithromycin[86]. Although the mechanisms are not fully understood, biofilm formation appears to significantly contribute to the MDR observed in *H. pylori* strains. Hence, targeting biofilm inhibition could be a promising strategy in combating these resistant infections.

The coexistence of subpopulations with different levels of antibiotic resistance within a single patient is termed heteroresistance[87]. In *H. pylori* infection, this phenomenon can be perceived within a single biopsy (intraniche heteroresistance) or across different biopsy sites (interniche heteroresistance)[88]. Heteroresistance can arise from simultaneous infection with multiple *H. pylori* strains with distinct resistance profiles or within a single monoclonal strain due to antibiotic pressure or spontaneous mutations[89].

Due to variations in heteroresistance frequency among diverse populations and geographic areas[90], the overall prevalence of this phenomenon in *H. pylori* is not well defined, with reported rates ranging from 7%-60% for clarithromycin and 14%-61% for metronidazole[91,92]. Given the significance of these frequencies, it is both cost-effective and recommended that endoscopic procedures aimed at AST include the collection of combined samples from both the antrum and corpus as well as the retrieval of multiple isolates from each biopsy site[90,93]. Consequently, a more precise drug-susceptibility profile is achieved, leading to more precise antibiotic regimen adjustments[90].

Host factors contributing to therapeutic failure

Sustaining intragastric acid suppression in *H. pylori*-positive patients is essential for relieving peptic ulcer symptoms and enhancing antibiotic efficacy. Since cytochrome P450 2C19 (CYP2C19) is responsible for around 80% of the biotransformation of first-generation PPIs such as omeprazole, lansoprazole, and pantoprazole[94], CYP2C19 polymorphisms significantly impact the pharmacokinetics, bioavailability, and clinical efficacy of these drugs[95]. The phenotype manifestations of CYP2C19 polymorphisms include ultrarapid metabolizer (UM), normal (NM) (previously referred to as extensive), intermediate, and poor metabolizers (PM)[96].

The distribution of CYP2C19 phenotypes shows significant ethnic and geographic differences, with nearly one-third of the global population exhibiting a significant variation, *i.e.* being either PM or UM[96,97]. Notably, a recent meta-analysis concluded that patients with CYP2C19 UM or NM phenotypes undergoing eradication regimens containing first-generation PPIs (omeprazole, pantoprazole, or lansoprazole) have a 2.14-fold significantly higher likelihood of *H. pylori* eradication failure compared to those with intermediate or PM phenotypes[98]. Thus, pharmacogenetic guidelines

recommend considering a 50%-100% increase in the dosage of these PPIs to optimize therapeutic efficacy in both CYP2C19 UM and NM[99]. Regarding the impact of CYP2C19 polymorphisms on the *H. pylori* eradication rate using new-generation PPIs, such as rabeprazole and esomeprazole, some studies indicate less interference, but the available evidence is inconsistent and graded as moderate or weak[99].

There are no well-established international guidelines regarding the use of CYP2C19 genetic testing in the pretreatment setting. CYP2C19 genetic tests have significant limitations in terms of sensitivity, as they are not designed to detect all possible variants of the CYP2C19 gene, including rare alleles with deletions in the gene locus[99]. Additionally, according to randomized controlled trials (RCTs), CYP2C19 phenotypes do not impact the acid suppression effect of P-CABs like vonoprazan and tegoprazan[100,101], which are predominantly metabolized by CYP3A4 according to *in vitro* evaluation [102]. Consequently, given that these drugs are currently recommended as alternatives to PPIs in first-line pharmacological regimens, the clinical utility of CYP2C19 testing before treatment is uncertain, requiring further cost-effectiveness evaluation across diverse patient populations.

Furthermore, poor compliance with therapeutic regimens conceivably increases the risk of unsuccessful *H. pylori* eradication. Adverse drug events, such as nausea, diarrhea, fatigue, and abdominal pain, although generally mild, are common, reported by 26%-74% of patients[103,104], and must be considered due to their impact on therapeutic adherence and patient well-being. Reinforcing medication adherence might importantly improve *H. pylori* eradication rates in developing countries[105]. Lastly, treatment compliance is impacted by cost and complexity[104], emphasizing the critical need for more affordable and streamlined therapeutic regimens.

GLOBAL AND REGIONAL RESISTANCE PATTERNS

The rising resistance of *H. pylori* to antibiotics poses a significant global health challenge, with resistance patterns differing markedly across regions[106]. Meta-analyses have documented a substantial increase in antibiotic resistance worldwide. A 2018 meta-analysis[30] indicated metronidazole resistance as the most common resistance pattern, surpassing 15% in all regions WHO regions, while clarithromycin resistance exceeded 15% in most WHO regions, except in the Americas. A more recent meta-analysis from 2024[107] indicated that pooled primary resistance to clarithromycin (from 2013 to 2023) surpassed 15% in all regions, ranging from 16.0% [95% confidence interval (CI): 11.7%-20.8%]) in the Americas to 28.9% (95% CI: 26.6%-31.2%) in Asia (Figure 1A). Remarkably, in children, clarithromycin resistance is the predominant pattern of resistance with a global prevalence of 38.2%, which is significantly higher than that observed in adults (25.6%)[107]. Nonetheless, recent findings show substantial variability regarding resistance in *H. pylori*-infected children[107-110].

Amoxicillin and tetracycline generally show lower resistance rates (< 10%) across most regions, making them more reliable options in treatment protocols within these areas[30]. However, amoxicillin resistance is considerably higher in Africa at 70.4% (95% CI: 64%-76.4%), where metronidazole resistance is also remarkably frequent at 84.2% (95% CI: 78.9%-88.9%)[107] (Figure 1B). Despite being highly heterogeneous, these findings align with past research[111] and highlight the ongoing need to improve efforts in antibiotic stewardship and monitoring antibiotic resistance trends in Africa.

In India, a recent meta-analysis encompassing studies from 2000 to 2023 identified the prevalence of resistance to clarithromycin at 35.6% (with a downward trend), to metronidazole at 77.7% (stable), and to levofloxacin at 32.8% of patients (with an upward trend)[112]. Thus, metronidazole-containing regimens are inadequate as a first-line treatment in most regions of India, and amoxicillin, tetracycline, and furazolidone are being considered as options[112]. Similarly, in China, antimicrobial resistance is 36.7%, 69%, 29.4%, and 1.4% for clarithromycin, metronidazole, levofloxacin and amoxicillin, respectively. This shows that amoxicillin may be important for treatment[113] and that bismuth is essential for regimens containing metronidazole and clarithromycin in China, given its ability to overcome resistance[114].

In Australia, the prevalence of clarithromycin resistance has been over 20.0% since 2010, with an average increase of 3.7% per year, while stable trends have been seen for metronidazole resistance (35.3%)[115]. In Portugal, a 2018 meta-analysis identified resistance to clarithromycin in 42% and metronidazole in 25% of patients[116]. Resistance rates to clarithromycin and levofloxacin are higher than 25% in Turkey[117] and 30% in the United States[118]. In the studies cited, resistance to tetracycline and amoxicillin showed low rates[115-118].

In the Americas, steady upward trends in resistance to clarithromycin (1.85%-32.20%) and levofloxacin (9.20%-58.10%) were seen in Mexico between 1997 and 2017[119]. In Brazil, a multicenter study identified resistance to clarithromycin in 16.9% and metronidazole in 13.5% of patients admitted between 2012 and 2015[120]. In subsequent studies in northeastern Brazil, the prevalence of resistance to clarithromycin detected was 14.4%-14.5%[120,121], while in the southern region resistance to clarithromycin ranged from 8.7%-19.1% and to levofloxacin from 16.4%-22.5%[120,122]. However, the recent evaluation of resistance in *H. pylori* is scarce in Latin America[107], which limits a representative determination of the profile in these territories. For example, resistance in *H. pylori* has not been investigated in Brazil since 2020, a period marked by the severe acute respiratory syndrome coronavirus 2 pandemic, in which there was indiscriminate consumption of antibiotics, including macrolides[123]. In 2022, a study in Ecuador found resistance to clarithromycin in 33.6% of cases[124]. Furthermore, on the African continent, studies conducted in Egypt reported rates of resistance to clarithromycin ranging from 28.7% to 52.8% among *H. pylori*-positive patients between 2021 and 2022[125, 126]. Still, there are significant gaps in the profile of recent resistance in other African countries.

The economic unavailability of resources for detecting resistance profiles and underlying mechanisms leads to several limitations regarding epidemiological surveillance in developing countries. Additionally, the lack of standardized testing protocols and follow-up data in some regions further complicates the accurate assessment of antibiotic resistance, leading to potential underestimation or regional disparities in reported resistance levels[116]. Moreover, most studies present

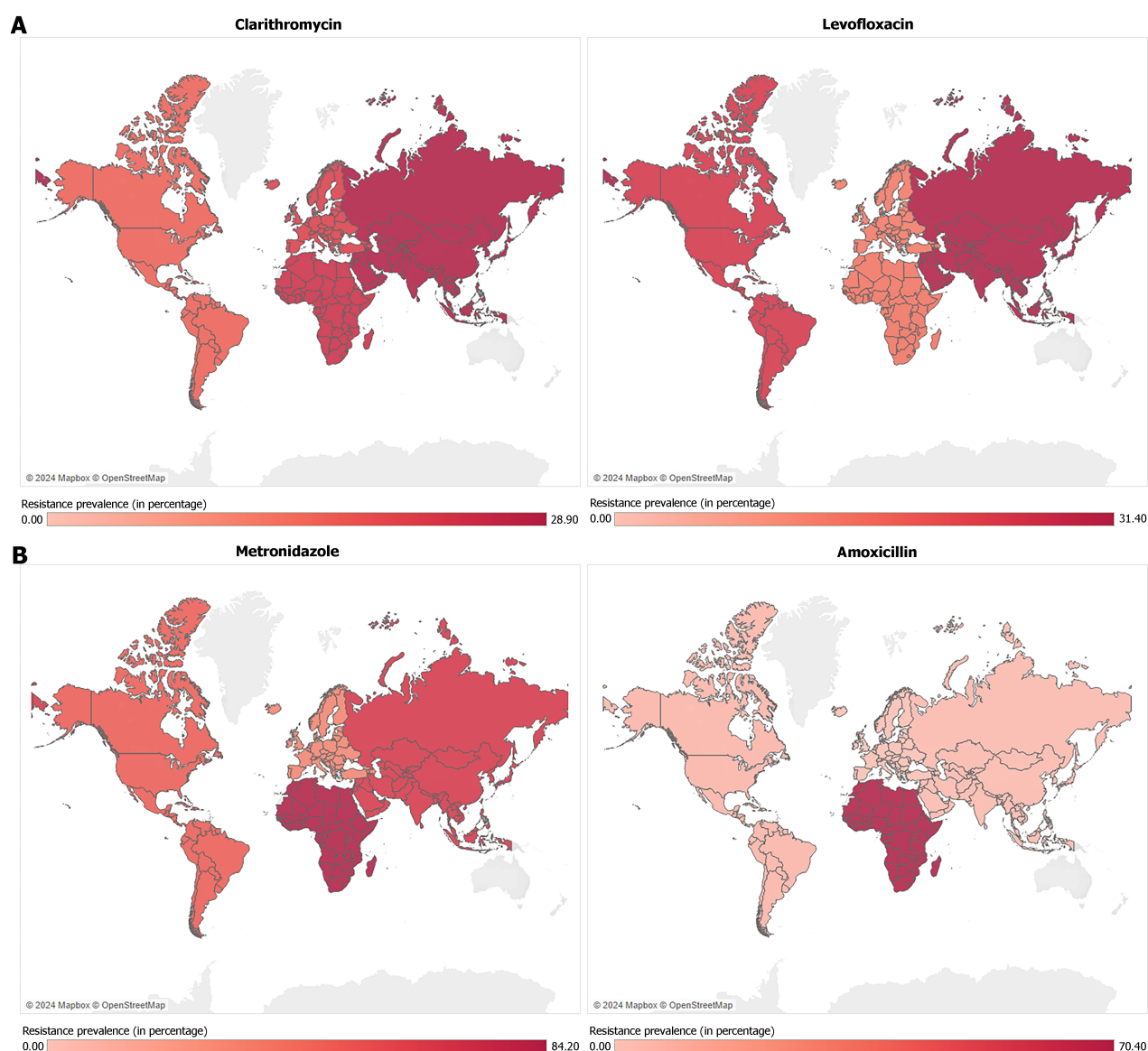


Figure 1 Distribution of primary resistance to clarithromycin and levofloxacin, metronidazole and amoxicillin by continent (2013-2023). A: Distribution of primary resistance to clarithromycin and levofloxacin by continent (2013-2023), according to a meta-analysis by Yu *et al* [107]; B: Distribution of primary resistance to metronidazole and amoxicillin by continent (2013-2023), according to a meta-analysis by Yu *et al* [107].

high levels of heterogeneity, complicating the accurate assessment of antibiotic resistance and potentially contributing to the underestimation of regional disparities in resistance rates [30,107,111]. The currently available data concerning the mechanisms and the prevalence of *H. pylori* resistance to clarithromycin, metronidazole, levofloxacin, tetracycline, amoxicillin, rifampicin, and MDR patterns, at global and continental levels, are summarized in Table 1.

IMPROVING EMPIRICAL PHARMACOLOGICAL APPROACHES

With increasing antibiotic resistance leading to *H. pylori* eradication failure, evaluating the most effective treatment approaches is essential. According to the Taipei global consensus [127], a highly effective empiric regimen is generally preferred over a susceptibility-guided approach due to cost and convenience. However, AST-guided therapy can be used as a first-line option when available [20]. This approach might be particularly beneficial in settings where data on local resistance patterns lacks an update. Hence, a more in-depth evaluation is required to compare the efficacy and cost-effectiveness of AST-guided therapies *vs* empirical approaches from a broader public health perspective. Furthermore, to prevent eradication failure it is essential to consider including medications that improve effectiveness and adherence if they are accessible.

Novel antisecretory agents

PPIs have been employed for the treatment of dyspepsia since the 1980s, with the first-generation including omeprazole, lansoprazole, and pantoprazole [128]. However, limitations in the effects of PPIs on *H. pylori* eradication highlighted the

Table 1 Summary of antibiotic resistance mechanisms and their global distribution

Resistance pattern	Main resistance mechanisms	Resistance prevalence by region (2013-2023)				
		Africa	Americas	Asia	Europe	General
Clarithromycin	Nucleotide substitutions disrupting the antibiotic binding site in the 23S rRNA (A2142G, A2143G, A2142C, A2115G, G2212A, G2141A, A2144T, and T2289C mutations); efflux pump systems (HP0605-HP0607)	24.6% (16.4-33.9) ¹	16.0% (11.7-20.8) ¹	28.9% (26.6-31.2) ¹	21.3% (18.1-24.6) ¹	26.7% (24.7-28.8) ¹
Metronidazole	Partial inactivation of reductase enzymes required for metronidazole activity (mutations mainly in <i>rdxA</i> and possibly in <i>frxA</i> gene)	84.2% (78.9-88.9) ¹	48.1% (43.2-53.1) ¹	66.1% (62.1-69.9) ¹	29.9% (24.0-36.1) ¹	59.6% (55.2-63.9) ¹
Levofloxacin	Disrupted antibiotic binding site in the DNA gyrase (mainly <i>gyrA</i> but also <i>gyrB</i> gene mutations)	14.3% (0-49.9) ¹	25.0% (5.2-52.8) ¹	31.4% (28.3-34.6) ¹	13.3% (10.4-16.4) ¹	26.2% (23.5-28.9) ¹
Amoxicillin	Reduced affinity to PBPs (<i>pbp1A</i> gene mutations); porin protein alterations (<i>hopB</i> and <i>hopC</i>)	70.4% (64.0-76.4) ¹	4.8% (2.8-7.3) ¹	2.8% (2.0-3.7) ¹	0% (0-0.2) ¹	2.6% (1.8-3.5) ¹
Tetracycline	Disrupted antibiotic binding site in rRNA (mutations in 16S rRNA-encoding genes); efflux pump tetA[P] (HP1165), and other multidrug efflux systems	1% (0.1-2.5) ¹	1.1% (0-4.2) ¹	2.2% (1.3-3.2) ¹	0% (0-0) ¹	1.5% (0.9-2.3) ¹
Rifampicin	Amino acid exchanges disrupting antibiotic binding site in the β subunit of DNA-dependent RNA polymerase (mutations in <i>rpoB</i> gene)	0% ³ (Algeria) [234,235]	0%-23.0% ³ (Colombia)[236, 237], 7.0%-19.0% ³ (New York, United States)[238]	14.4% ³ (Iran) [239], 5.4%-73.2% ³ (China)[240]	11.4% ³ (Belgium) [241], 8.3% ³ (Bulgaria)[242], 1.2% ³ (France) [243], 33.3% ³ (Spain)[244]	Unavailable
Multi-drug resistance patterns	Accumulation of single-drug resistance genes; upregulation of multidrug efflux pump systems (<i>hefA</i> , <i>gluP</i> , HP1181 and HP1184); biofilm formation	1.6% ³ (Egypt) [245], 15.7% ³ (Cameroon) [246]	12.5% ³ (Chile)[247]	10.0% (7-14) ² (children in East Asia)[248], 14.7% ² (India)[112], 24.9% ³ (China) [249]	1.4% ² (Portugal) [116], 0.8% ³ (Austria)[250], 2.4% ³ (Spain)[251]	6.0% ² (children) [252]

¹Pooled primary resistance prevalence from 2013-2023 according to a meta-analysis by Yu *et al*[107].

²Prevalence of multiple antibiotic resistance according to meta-analyses conducted between 2013 and 2023.

³Rates derived from primary studies conducted between 2013 and 2023 (unavailable data from metanalyses). PBPs: Penicillin-binding proteins.

need for more efficacious therapeutic approaches, driving the development of newer generations of PPIs and additional pharmaceutical agents aimed at improving therapeutic outcomes[128].

Subsequent generations of PPIs, such as rabeprazole, esomeprazole, ilaprazole, anaprazole, tenatoprazole, and dexlansoprazole, were introduced as alternative options for the treatment of *H. pylori*[128,129]. McNicholl *et al*[130] performed a meta-analysis to compare the efficacy of esomeprazole and rabeprazole to first-generation PPIs (omeprazole, lansoprazole, and pantoprazole) in *H. pylori* treatment effectiveness. The analysis indicated that regimens containing esomeprazole and rabeprazole achieved higher eradication rates compared to those with first-generation PPIs[130]. However, the authors cautioned that these findings should not be generalized due to variations in therapeutic regimens and differences in patient metabolism related to *CYP2C19* polymorphisms. Notably, the efficacy differences were minimal in poor metabolizers and significant in normal metabolizers[130].

These findings underscore that identifying a single PPI as the most effective for eradication regimens may not be appropriate, and the choice of PPI should be tailored to individual clinical circumstances[130,131]. It is important to note that the overall efficacy of newer generations of PPIs remains comparable in *H. pylori* eradication, as demonstrated by Zhu *et al*[132] and Jin *et al*[133], that found no significant differences between anaprazole and rabeprazole and ilaprazole and esomeprazole, respectively.

Advances in pharmacotherapy have also introduced vonoprazan, a P-CAB, as a new option in *H. pylori* eradication therapy[134]. Vonoprazan acts by ionically, reversibly, and competitively binding to the H⁺/K⁺-ATPase pump, which is responsible for gastric acid secretion[134]. This mechanism inhibits acid secretion more efficiently and for a longer time than PPIs, due to the high pKa of vonoprazan, which promotes increased drug accumulation in the gastric environment [134,135].

In this context, an RCT conducted by Bunchorntavakul and Buranathawornsom[136], involving 118 patients, evaluated two treatment groups: One received vonoprazan 20 mg, amoxicillin 1 g, and clarithromycin 500 mg, while the other received omeprazole 20 mg, amoxicillin 1 g, and clarithromycin 500 mg. The study concluded that the vonoprazan group was not inferior to the omeprazole group and demonstrated slightly superior eradication rates[136].

Further, Chey *et al*[137] conducted a RCT involving 1046 patients and concluded that vonoprazan-containing regimens, including both triple (vonoprazan/amoxicillin/clarithromycin) and dual (vonoprazan/amoxicillin) therapies, achieved superior outcomes in the overall study population compared to the PPI-containing triple therapy, regardless of clarithromycin resistance. The intention-to-treat (ITT) eradication rates were 80.8% for vonoprazan in triple therapy, 77.2% for vonoprazan in dual therapy, and 68.5% for lansoprazole in triple therapy[137].

In the context of quadruple therapy, a recent RCT conducted by Yang *et al*[32], including 600 patients, found that vonoprazan-dual therapy, either administered for 14 or 10 days, achieved better eradication rates than a 14-day quadruple therapy (rabeprazole/bismuth/tinidazole/clarithromycin) according to per-protocol (PP) analysis. Additionally, 10-day vonoprazan-dual therapy exhibited lower incidence of adverse events than the 14-day treatments[32]. Furthermore, when incorporated in quadruple therapies, vonoprazan demonstrated significant results. A randomized study led by Lu *et al*[138] in China, involving 234 patients, compared three treatment groups: Vonoprazan 20 mg, amoxicillin 1 g, furazolidone 100 mg, and colloidal bismuth 200 mg for either 10 or 14 days; or esomeprazole 20 mg, amoxicillin 1 g, furazolidone 100 mg, and colloidal bismuth 200 mg for 14 days. The study concluded that vonoprazan-based regimens were as effective as the esomeprazole regimen and provided lower costs[139]. Table 2 summarizes the findings related to vonoprazan eradication rates from the clinical studies cited.

Meta-analyses also highlight the promise of vonoprazan as a first-line treatment for *H. pylori* compared to PPIs. A recent meta-analysis conducted by Liu *et al*[140], which included 27 studies comparing vonoprazan-containing therapies among themselves or with PPI-containing therapies, indicated that vonoprazan-based BQT achieved the highest pooled eradication rate among the therapies. Also, vonoprazan dual therapy (vonoprazan-amoxicillin) did not present a significant difference in eradication rates *vs* PPI-containing BQT in both ITT [odds ratio (OR) = 1.02, 95%CI: 0.70-1.47] and PP analyses (OR = 0.82, 95%CI: 0.41-1.62), but it did demonstrate a significantly reduced risk of adverse events (OR = 0.40, 95%CI: 0.24-0.68)[140]. Similarly, previous meta-analyses have indicated the general superiority of vonoprazan-based regimens compared to those based on PPIs[139,141] and that vonoprazan dual therapy is as effective as PPI-containing BQT[142]. Thus, RCTs and meta-analyses performed so far underscore the promise of P-CABs in *H. pylori* treatment, positioning it as a feasible option with both efficacy and safety. Once more evidence is collected from various regions, these drugs may be included in future guidelines in first-line regimens, as they appear to enable less use of antimicrobials without compromising effectiveness.

Optimized empirical antibiotic regimens

Enhancing first-line empirical therapy is essential to prevent the development of secondary MDR in *H. pylori* strains, as first-line treatment failure plays a significant role in the emergence of MDR in *H. pylori*[143,144]. However, the rising levels of antibiotic resistance hinder the selection of therapies that effectively balance efficacy, a low incidence of adverse effects, and high patient adherence. In this context, greater efforts are required to develop treatment options that cost-effectively meet these criteria[145].

Since evidence suggests that clarithromycin resistance has likely exceeded 15% on all continents[30,107,146], BQT is widely recommended as the preferred empirical treatment on a global scale. Thus, clarithromycin triple therapy should be reserved for areas with reliably updated surveillance confirming resistance rates below 15%, as outdated data risks compromising treatment efficacy. In a meta-analysis from 2021, Rokkas *et al*[147] found that vonoprazan triple therapy and reverse-hybrid therapies consisting of a PPI and amoxicillin for 14 days, with clarithromycin plus metronidazole in the initial 7 days were the most effective among eight first-line regimens, while standard (PPI) triple therapy was the least effective[147].

Additionally, more recent RCTs following the Maastricht VI/Florence Consensus Report have provided stronger evidence for different therapeutic approaches and alternatives in light of the high levels of current antibiotic resistance. In China, a recent RCT found that 10-day vonoprazan-amoxicillin dual therapy with vonoprazan 20 mg twice/day provided lower adverse events and a non-inferior efficacy compared to 14-day BQT[31]. Further, poor compliance (less than 80% of prescribed drugs taken) was significantly linked to treatment failure in the vonoprazan-amoxicillin dual therapy group but not in the BQT group, which indicates that the extended 14-day duration of BQT may be redundant[31]. Indeed, recent research in China and Taiwan has found that 10-day BQT has non-inferior efficacy to the 14-day BQT as a first-line therapy and presents a lower incidence and severity of adverse effects, such as dizziness and vomiting[34,148,149].

Recently, the LEGACy consortium, which included patients from European and Latin American countries, demonstrated that BQT was the only regimen to achieve a cure rate exceeding 90.0% (compared to 88.7% for non-BQT regimens and 75.2% for triple therapy)[150]. Additionally, the 2024-Hp-EuReg trial, involving 49690 patients, provided a comprehensive analysis further confirming that BQT consistently achieves eradication rates above 90% across all European regions[151]. Notably, the 10-day single-capsule BQT proved to be the regimen most reliably associated with optimal effectiveness[151].

Regarding second-line therapy for *H. pylori* infection after failure of clarithromycin triple therapy[152], an RCT conducted in Taiwan reported that both levofloxacin-based quadruple therapy and BQT have shown comparable rates of effectiveness (88%) in a scenario with increased trends in resistance[153]. In the context of rescue treatment regimens, rifabutin-containing triple therapy and high-dose amoxicillin dual therapy demonstrate similar efficacy to BQT but with fewer side effects[154,155]. Furthermore, a recent multicenter trial[156] found that a BQT regimen containing amoxicillin and tetracycline achieved optimal eradication rates as a rescue therapy[156]. Notably, administering tetracycline three times daily instead of four reduced adverse events without compromising efficacy[156].

Table 2 Cited clinical studies conducted to analyze the effectiveness of vonoprazan

No. of patients	Group with vonoprazan (days)	Eradication	Control group (days)	Eradication	Identification	Ref.
1046	Vonoprazan 20 mg + amoxicillin 1 g + clarithromycin 500 mg (14 days)	80.8% ¹	Lansoprazole 30 mg + amoxicillin 1 g + clarithromycin 500 mg (14 days)	68.5% ¹	NCT04167670	[135]
118	Vonoprazan 20 mg + amoxicillin 1 g + clarithromycin 500 mg (7 days)	96.7% ¹	Omeprazole 20 mg + amoxicillin 1 g + clarithromycin 500 mg (14 days)	88.5% ¹	TCTR20210219007	[134]
600	Vonoprazan 20 mg + amoxicillin 1 g (14 days)	92.5% ²	Rabeprazole 20 mg + bismuth potassium citrate/tinidazole/clarithromycin, combined packet 4.2 g (14 days)	81.5% ²	NCT05469685	[32]
234	Vonoprazan 20 mg + amoxicillin 1 g + furazolidone 100 mg + bismuth 200 mg (10 days)	96.2% ¹	Esomeprazole 20 mg + amoxicillin 1000 mg + furazolidone 100 mg + bismuth 200 mg (14 days)	93.6% ¹	NCT04907747	[136]

¹Eradication rate by intention-to-treat.²Eradication rate per-protocol.

TAILORED THERAPIES AND FUTURE DIRECTIONS

AST

AST is essential to ensure effective tailored bacterial eradication therapies. AST can be conducted through both culture-dependent methods, mostly performed to determine the minimum inhibitory concentration (MIC) of antibiotics, and molecular assays[157-159].

Culture-dependent AST: Given the possibility of interniche heteroresistance, culture-dependent techniques require the collection of at least two biopsy samples from both the antrum and the corpus and involve time-consuming and labor-intensive *H. pylori* isolation[93]. Among these, phenotypical methods [*e.g.*, Agar dilution (AD), disk diffusion (DD), broth microdilution (BD), and gradient E-tests (GET)] are commonly used for AST, though each method has its own limitations [160].

AD comprises the incorporation of different antibiotic concentrations into agar plates, inoculation of *H. pylori* strains, and observation of the growth for MIC determination[161,162]. Despite being fastidious, this technique is regarded as the golden standard to assess the MIC of antimicrobial agents and as the reference method to compare other AST approaches [4]. However, widely accepted clinical MIC breakpoints have not yet been established for antibiotics other than clarithromycin, including amoxicillin, metronidazole, levofloxacin, and furazolidone[163]. The current cutoff points established under the European Committee on Antimicrobial Susceptibility Testing are based on epidemiological thresholds, which constrain their applicability in clinical practice[163]. This limitation affects the interpretation of AD results as well as other MIC-oriented techniques, such as BD and GET.

Notwithstanding, BD and GET offer less fastidious methods for MIC determination. BD consists in the inoculation of *H. pylori* into a range of serially diluted antibiotics within a liquid medium[164]. Despite the challenges associated with the growth of *H. pylori* in broth, the development of supplemented media, automation, and the possibility of simultaneous testing of multiple antibiotics have made BD a promising technique[165,166]. Meanwhile, GET utilizes a plastic strip with a stable, exponential gradient of antibiotics, which is applied to agar plates inoculated with bacteria. The MIC is determined through the examination of a visible ellipse of inhibited bacterial growth around the strip after an incubation period[167,168]. However, despite its practicality and capability to test a broad spectrum of antibiotics (*e.g.*, amoxicillin, clarithromycin, levofloxacin, and metronidazole), GET encounter financial constraints that limit their application in clinical settings, especially in developing countries[169].

Although quantitative methods such as AD, BD, and GET are valuable for assessing *H. pylori* susceptibility, DD remains a widely used qualitative AST method for *H. pylori*[170]. In this technique, paper disks saturated with antibiotics are placed on an agar plate inoculated with the target bacteria. Upon incubation, the zone of inhibition around each disk is measured to assess the effectiveness of the antibiotic in impeding bacterial growth[171,172]. Despite its simplicity and ease of execution, DD does not provide precise MIC values, thereby limiting its ability to offer detailed information about bacterial sensitivity[173]. Collectively, all these techniques highlight the need for continued development and standardization in susceptibility testing methods to improve their clinical utility and accessibility.

Molecular-based AST: In contrast to phenotypic techniques, molecular-based antibiotic susceptibility tests are designed to detect specific genetic mutations or markers in the *H. pylori* genome that are associated with resistance to particular antibacterial agents[174]. Currently, the most commonly employed molecular-based techniques are PCR and next-generation sequencing[163]. PCR is particularly effective for detecting specific mutations within the *H. pylori* genome, whereas next-generation sequencing offers a more comprehensive overview of resistance determinants and is increasingly used to profile antibiotic resistance in clinical isolates of the bacterium[175-178]. Although these techniques

usually require gastric biopsy, isolation of viable specimens is not necessary, which streamlines the process and reduces the time and labor involved in susceptibility testing. Furthermore, results from molecular-based ASTs using fecal samples have shown a close correlation with those obtained from gastric biopsies, suggesting that non-invasive testing is a viable alternative[179,180].

Despite these advantages, several factors still limit the widespread use of molecular-based methods. Notably, there is variability in the concordance between genotype and phenotype across different antibiotics[181]. For example, determining susceptibility to metronidazole can be highly complex, whereas studies have shown excellent concordance for clarithromycin and levofloxacin[39,182,183]. Additionally, the high costs and the need for advanced technological infrastructure, which is often unavailable in certain regions, further restrict the widespread adoption of these methods. Consequently, there are still constraints preventing molecular-based AST from reaching its full potential.

AST-guided therapy results

The extensive variation in susceptibility among *H. pylori* strains and the differing availability of AST in different regions make it difficult to achieve universally applicable results from AST-based treatments, which demand specific analysis under different populations and clinical contexts. Previous meta-analyses indicated that AST-guided therapy could provide higher eradication rates when compared to unspecified first-line empirical therapies[184,185]. While some analyses suggested the superior effectiveness of AST-guided therapy over BQT[185,186], the substantial heterogeneity identified precluded a significant conclusion. Still, no significant differences were found in second-line or third-line treatment scenarios[185], which might occur since subsequent empirical therapies culminate in progressively broader spectrum coverage of resistant strains.

Presently, there is a specific focus on the effectiveness and feasibility of genotypic (molecular-based) tailored therapies in eradicating *H. pylori*. They have shown similar eradication outcomes to culture (phenotypic)-guided therapies in first-line treatment and non-inferiority in third-line therapy, as reported by a recent multicenter RCT[187]. While molecular-guided therapies consistently have better eradication rates than standard triple therapy[188,189], a meta-analysis by Li *et al*[188] showed lower efficacy when compared to empirical quadruple therapy (either BQT or non-BQT), but the authors emphasized the limited number of RCTs (only five) focusing on this comparison at the time, avoiding unwarranted conclusions[188]. Yet, the pooled eradication rates of genotypic-tailored therapy reported in the study were notably lower than those presented in a single-arm meta-analysis (79.0% *vs* 86.9% and 86.0% *vs* 91.5% by ITT and PP analyses, respectively)[190]. Further, the addition of bismuth in genotypic-guided tailored treatment can potentially enhance its eradication rate[190,191].

Aside from effectiveness, choosing between tailored or empirical therapy includes considering local factors such as the background rate of antimicrobial resistance, availability of resources (especially ASTs and bismuth), and cost-effectiveness of ASTs[186,192]. Due to the unavoidable variability in cost-effectiveness evaluation across different periods, locations, and sample constraints, it is not feasible to make broad generalizations.

In France, a recent multicenter RCT (presenting an 18.7% rate of clarithromycin resistance) reported that 14-day PCR-guided triple therapy (consisting of esomeprazole, amoxicillin plus clarithromycin or levofloxacin) was non-inferior and less expensive than 14-day non-BQT in ITT analysis[193]. In South Korea, numerous studies have been carried out to assess the cost-effectiveness of dual priming oligonucleotide-based multiplex PCR, which can be used to detect point 23S ribosomal RNA gene mutations related to clarithromycin resistance. Although these studies were confined to a single country and focused on the same analytical tool, the results were inconsistent, with some reporting that tailored therapy reduced average costs for successful eradication[194,195], while others showed higher average medical costs[196,197].

Nevertheless, as *H. pylori* infection can be accurately diagnosed with non-invasive methods (such as stool antigen test and urea breath test), the need for endoscopy and biopsy, generally required for AST, is often avoidable in a “test-and-treat” approach that employs empirical regimens, ultimately preventing additional costs. Changing this paradigm, the development of non-invasive methods that accurately identify antibiotic resistance can be convenient alternatives in tailored treatment compared to conventional biopsy-ASTs. Genotypic testing of clarithromycin resistance in stool samples is a promising alternative, presenting a pooled sensitivity of 93% (95%CI: 90%-96%) and specificity of 98% (95%CI: 93%-100%), according to a meta-analysis by Ren *et al*[41].

Despite often showing enhanced outcomes, according to current evidence, tailored treatments achieve high cure rates (> 90%) in only 40% to 63% of cases[198,199]. While robust trials have demonstrated the consistency of BQT in achieving > 90% eradication rates, suggesting that routine AST-guided therapy may not significantly improve overall therapeutic success[151]. However, the unavailability of bismuth in some regions and the complexity of its traditional regimen, requiring multiple pills daily, pose challenges to adherence in real-world settings. Furthermore, a retrospective cohort study in Thailand involving 1080 patients concluded that AST-guided therapy offered higher efficacy and could be a cost-effective strategy if initiated immediately after first-line treatment failure[200]. Notably, this approach was linked to reduced costs for subsequent medication, post-treatment urea breath test, and hospital visits in a real-world scenario [200]. In the context of pediatric *H. pylori* infection, recent clinical guidelines recommend AST to assess clarithromycin susceptibility as a first-line strategy, highlighting its importance in improving treatment outcomes and reducing antimicrobial resistance[201].

Antibiofilm agents

Due to growing concerns about antimicrobial resistance, there is an increased emphasis on developing new treatments for *H. pylori*. Adjuvant therapies are designed to boost the effectiveness of antibiotic treatments, either by countering bacterial resistance mechanisms or by altering the response of the host[202]. While ongoing enhancements to antibacterial drug combinations may offer short-term effectiveness, their impact often diminishes over time[203]. Thus, research into

complementary approaches, including antibiofilm agents and the use of probiotics, is still in progress.

The formation of *H. pylori* biofilms decreases the efficacy of conventional treatments[81]. In this sense, several studies are being developed to investigate the use of antibiofilm agents as adjuvants[204]. Most antibiofilm agents originate from natural products, with many being secondary metabolites produced by microorganisms, including phytochemicals, biosurfactants, antimicrobial peptides, and microbial enzymes[205]. Additionally, certain quorum-sensing inhibitors and probiotics have been identified to exhibit anti-biofilm properties[206,207]. These natural products demonstrate strong anti-biofilm and antibacterial properties *in vitro*. Notably, some, like *Pistacia vera* L. oleoresin, *Casearia sylvestris* leaf derivatives, Amu-ru 7, and dihydrotanshinone I, have shown effectiveness against *H. pylori*-resistant strains in both *in vitro* and *in vivo* studies[208-212], suggesting the potential to mitigate *H. pylori* MDR and creating a complementary effect against it. For instance, *Pistacia vera* L. oleoresin boosts the effectiveness of levofloxacin, aiding in the suppression of drug resistance in *H. pylori* strains. Armeniaspirol A is another antibiofilm agent that may exhibit significant antibacterial activity against *H. pylori*, including strain resistant to multiple drugs[204]. Furthermore, the combination of armeniaspirol A with omeprazole was more successful in eliminating *H. pylori* *in vivo* than standard triple therapy in a mouse model of MDR infection[213].

In recent years, nanomaterials have been utilized to eliminate *H. pylori* biofilms and reduce drug resistance[214-216]. A recent study reported that combining antibiotics with rhamnolipid, a glycolipid biosurfactant that can disrupt biofilms and potentially inhibit bacterial adhesion, effectively prevented biofilm formation *in vitro*[217]. Also, nanodrugs formulated with berberine derivatives and rhamnolipids successfully penetrated the mucus layer and effectively eradicated *H. pylori* biofilms in both *in vitro* and *in vivo* studies[218]. Moreover, the data presented in a study demonstrated that New Synthesized Silver Ultra-NanoClusters could represent a novel strategy for the treatment of *H. pylori* infections either alone or in combination with metronidazole[219]. Previous studies have indicated that N-acetylcysteine, an antioxidant that helps to break down mucus, decreases bacterial load and improves eradication rates[220, 221]. It is currently the only molecule in clinical trials that has shown effectiveness against *H. pylori* biofilms[222-224].

Probiotics and adjuvant therapies

Recent research is focused on the impact of adding probiotics to *H. pylori* eradication therapy. Probiotics are believed to potentially influence treatment primarily by reducing drug-associated side effects, competing at microbial adhesion sites, and enhancing the immune response[225]. Clinical study results, however, have been inconsistent[225].

For instance, a double-blind RCT by Ismail *et al*[226] found that the use of *Lactobacillus reuteri* after standard triple therapy was significantly associated with a higher eradication rate (22.2% and 24.3% differences in ITT and PP analyses, respectively) and mitigation of adverse effects. However, regarding the quadruple therapy scenario, while certain research reported enhanced treatment efficacy by probiotics supplementation[227], several double-blind RCTs[228,229] did not find a statistically significant improvement in eradication rates with *Lactobacillus reuteri* strains, despite a general agreement in their ability to reduce the frequency of side effects.

Some meta-analyses have suggested that the addition of probiotics in *H. pylori* treatment may be beneficial in standard triple therapy since they are associated with enhanced eradication rates and reduced risk of treatment adverse effects[230, 231]. Notably, Lau *et al*[230] indicated possible benefits through *Lactobacillus* and *Saccharomyces* incorporation in standard triple therapy. However, these findings have not been universally accepted, as other studies did not find an improvement in the eradication rate with probiotics[232].

In this context, Yang *et al*[233] recently conducted an umbrella review of systematic reviews with meta-analyses, which suggested that therapies incorporating probiotics were significantly associated with improved eradication rates and a lower risk of side effects compared to standard therapy alone. Nevertheless, as reported by the authors, methodological aspects regarding low-quality studies and heterogeneity constrain the applicability of these findings as general clinical recommendations[233]. Despite the promising potential of probiotic supplementation, there is still a critical need for high-quality, multicenter RCTs that focus on specific formulations to comprehensively evaluate their effects in clinical settings. Therefore, reliable and evidence-based data can be used to update treatment guidelines and recommendations concerning the use of probiotics in *H. pylori* therapy. Table 3 provides an integrated summary of the *Helicobacter pylori* treatment strategies discussed, encompassing empirical and AST-guided antimicrobial regimens, probiotics, and antibiofilm agents, while outlining emerging alternatives and future research directions for optimizing therapeutic outcomes.

CONCLUSION

Given the increasing global trends in *H. pylori* resistance, particularly against clarithromycin, metronidazole, and levofloxacin, it is essential to enhance regional and local resistance surveillance efforts, especially in developing countries where data are sparse and empirical regimens might be inappropriate. Furthermore, the validation of current PCR-based AST methods across diverse populations should be prioritized by establishing correlations between identified mutations and confirmed resistance phenotypes. Whole-genome sequencing can also play a pivotal role in identifying novel mutations and resistance determinants, particularly in regions outside Europe and Asia, where research remains limited and robust data are lacking. While BQT is generally recommended as the first-line treatment, except in regions with clarithromycin resistance rates below 15%, an evaluation of the cost-effectiveness of empirical *vs* AST-guided strategies should be conducted through RCTs and prospective real-world studies.

In parallel, improved treatments can be potentially attained by introducing emergent drugs, including P-CABs. Region-specific studies assessing their efficacy and cost-effectiveness will be essential to determine their applicability and

Table 3 Overview of current treatments, potential approaches, and future directions in overcoming antibiotic resistance in *Helicobacter pylori*

	AST-guided therapy		Empirical therapy						Antibiofilm agents	Probiotics
	By phenotypic determination	By molecular determination	BQT	Non-BQT	CLA-TT	LEV-TT or LEV-QT	AMX-DT	RIF-TT		
Advantages	Antimicrobial stewardship; AST can be done for all recommended antibiotics (<i>vs</i> molecular-AST)	Antimicrobial stewardship; reliable to detect CLA resistance; does not require the isolation of viable species; non-inferior efficacy <i>vs</i> BQT; less cost <i>vs</i> non-BQT in some RCTs	Optimal reliability (> 90% cure rate) regardless of resistance profile in Europe and some Latin American countries	Possible option when bismuth is not available	Reduced costs; fewer antibiotics	In second-line therapy, LEV-QT is comparable to BQT in areas with increased trends in resistance	Good reliability in general	Good reliability in general	May improve eradication rates in biofilm-forming multidrug-resistant strains	May improve eradication rates and lower the risk of side effects
Limitations	Highly time-consuming; affected by collection, transport, and techniques; availability	Limited number of antimicrobial agents; limited correlation with MET resistance; availability	Complex dosing in conventional regimens; availability	Not indicated in regions with dual resistance > 15%	Indicated only if CLA resistance < 15% in updated data	High trends in resistance compromise LEV-TT efficacy	High resistance rates in Africa and some areas in Asia	Potential adverse events; costs	Currently, only NAC has been shown effective in clinical trials	Methodological aspects regarding low-quality studies; heterogeneity of strains
Emerging approaches	Vonoprazan-containing AST-guided therapies; non-invasive AST, including CLA resistance in stool samples		Sc-BQT; 10-day BQT (non-inferior efficacy and lower adverse events <i>vs</i> 14-day BQT); vonoprazan-containing BQT and TT; vonoprazan-amoxicillin; BQT with amoxicillin-tetracycline						NAC; rhamnolipids; SUNCs; <i>Pistacia vera</i> L. oleoresin; <i>Casearia sylvestris</i> leaf derivative; ARM1	<i>Lactobacillus reuteri</i> ; <i>Saccharomyces spp.</i>
Future steps	Update regional and local resistance surveillance, especially in developing countries; validation of PCR-AST in diverse populations by correlating detected mutations with actual resistance profiles; identification of novel mutations and determinants of resistance through WGS; development and validation of non-invasive molecular-AST		Cost-effectiveness evaluation between empirical and AST-guided therapies in both RCTs and real-world data; evaluation of vonoprazan-containing therapies through multicenter RCTs in different regions and populations; evaluation of the impact of different antimicrobial therapies on the gut microbiota resistome through multicenter RCTs						Further evaluation of potential agents in high-quality clinical trials	Determination of specific strains and formulations through high-quality and multicenter RCTs

AMX: Amoxicillin; ARM1: Armeniaspirol A; AST: Antimicrobial susceptibility testing; BQT: Bismuth-containing quadruple therapy; CLA: Clarithromycin; DT: Dual therapy; LEV: Levofloxacin; MET: Metronidazole; NAC: N-acetylcysteine; Non-BQT: Non-bismuth-containing quadruple therapy; QT: Quadruple therapy; RCT: Randomized controlled trial; RIF: Rifabutin; Sc-BQT: Single-capsule bismuth-containing quadruple therapy; SUNCs: Silver Ultra-NanoClusters; TT: Triple therapy; WGS: Whole-genome sequencing.

future recommendations in guidelines, as they seem to allow for reduced antimicrobial usage without sacrificing efficacy. Additionally, P-CAB-containing regimens could be further explored within the context of AST-guided therapies. Furthermore, ongoing research is assessing the potential benefits of anti-biofilm agents and probiotics in clinical settings, with an emphasis on identifying specific beneficial strains and formulations.

Post-treatment evaluation remains crucial in clinical management, and confirming *H. pylori* eradication can be achieved using non-invasive tests like the urea breath test and stool antigen test. In light of the challenges associated with the cost and availability of AST and P-CABs, alongside the significant limitations of antibiotic resistance data due to insufficient surveillance, routine post-treatment assessment is indispensable for informed clinical decision-making.

FOOTNOTES

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Country of origin: Brazil

ORCID number: Gabriel Reis Rocha 0000-0002-3090-0726; Fabian Felipe Bueno Lemos 0000-0002-4686-7086; Luis Guilherme de Oliveira Silva 0000-0001-7275-7182; Marcel Silva Luz 0000-0003-1650-5807; Gabriel Lima Correa Santos 0000-0003-3673-9889; Samuel Luca Rocha Pinheiro 0000-0002-8877-892X; Mariana Santos Calmon 0000-0002-3871-7408; Fabrício Freire de Melo 0000-0002-5680-2753.

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