Understanding bacterial virulence and combating multidrug resistance in tropical Southeast Asia

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ABSTRACT

This study aimed to 1) investigate the factors contributing to bacterial pathogenicity and 2) identify evidence-based strategies for prevention and control, with a focus on tropical environments like Thailand. A systematic review was conducted using peer-reviewed journals, government reports, and publicly available datasets published between 2000 and 2024. Key databases included PubMed, SpringerLink, and ScienceDirect. Studies were selected based on relevance to bacterial virulence, environmental impacts, and regional health strategies. Data were synthesized thematically around core concepts such as adhesion, invasion, toxin production, and antimicrobial resistance. Virulence in bacteria is driven by molecular factors and significantly influenced by environmental conditions such as climate change, pollution, and antibiotic misuse. Case studies from Thailand demonstrated both successful interventions (e.g., antibiotic stewardship, photodynamic therapy) and challenges in controlling bacterial spread. Regional insights emphasized the role of public health infrastructure and environmental management. Addressing bacterial pathogenicity requires a multidisciplinary approach that integrates microbiological knowledge, environmental science, and public health policy. Tailored strategies are essential for reducing bacterial threats in tropical and resource-constrained regions, and further research should bridge the gap between scientific discovery and practical implementation.

Key words: Bacterial Virulence Factors, Multidrug-Resistant Bacteria (MDR), Pathogenicity in Tropical Climates, Antibiotic Resistance Strategies, Environmental Impacts on Bacterial Infections

Introduction

Infectious diseases caused by pathogenic bacteria continue to rank among the leading causes of morbidity and mortality worldwide. According to the World Health Organization (2021), bacterial infections remain a significant public health burden, particularly in low- and middle-income countries. The growing emergence of multidrug-resistant (MDR) bacterial strains—exacerbated by inappropriate antibiotic use in both healthcare and agriculture—has intensified this global crisis, leading to infections that are increasingly difficult to treat (CDC, 2022; Koh et al., 2019).

Tropical regions, such as those in Southeast Asia, face unique challenges in bacterial infection control due to high humidity, rising temperatures, environmental pollution, urbanization, and weak public health infrastructure. These conditions not only foster the growth and transmission of pathogenic bacteria but also create hotspots for the emergence of antimicrobial resistance. Recent studies suggest that climate variability and pollution—especially from microplastics—contribute to enhanced bacterial virulence by promoting biofilm formation and resistance mechanisms (Soni et al., 2024; Zhang et al., 2023). However, the influence of these environmental factors remains underexplored in the context of molecular pathogenesis.

While a considerable body of research exists on the molecular biology of bacterial virulence—such as adhesion factors, toxins, and immune evasion mechanisms—there is a disconnect between these scientific insights and their practical application in public health strategy. Furthermore, Southeast Asia lacks region-specific reviews that integrate molecular data with local environmental and policy frameworks.

Objectives

This review addresses these gaps by synthesizing current evidence on bacterial virulence mechanisms alongside environmental and human behavioral factors, with a focus on tropical settings like Thailand. By bridging molecular microbiology and public health, the study aimed to inform more context-sensitive prevention and control strategies in resource-limited environments.

Methods

This review synthesized peer-reviewed literature, government reports, and publicly accessible datasets to explore bacterial virulence factors and related prevention strategies. Key methods included:

1. Literature Search: Databases such as PubMed, SpringerLink, and ScienceDirect were searched for studies published between 2000 and 2024 using keywords like "bacterial virulence factors," "environmental impact on pathogenicity," "antibiotic resistance," and "infection prevention in tropical regions."

2. Criteria for Inclusion and Exclusion:
   - Relevant studies with empirical data or systematic reviews were prioritized.
   - Non-pathogenic studies or those with insufficient methodological details were excluded, while foundational pre-2000 studies were included selectively.

3. Data Synthesis: Extracted data were categorized into themes (e.g., adhesion, invasion, toxins, environmental impact, antibiotic resistance) and analyzed to identify trends and gaps.

4. Regional Focus: Emphasis was placed on Southeast Asian studies, especially Thailand, for context-specific insights into tropical climates and local public health strategies.

5. Validation: Sources were cross verified with credible organizations such as WHO, CDC, and national health agencies to ensure reliability.

Virulence Factors in Bacteria

The pathogenicity of bacteria is attributed to various virulence factors, each contributing to their ability to infect and persist within hosts:

1. Adhesion Factors: Adhesins, such as Type-1 pili and MSCRAMMs (Microbial Surface Component Recognizing Adhesive Matrix Molecules), facilitate bacterial attachment to host cells, initiating infection. These molecules bind to host receptors, exploiting complementary shapes to secure attachment (Sharma AK et al., 2016; Kaiser G, 2023). Adhesion is often the first step in bacterial colonization, providing a foundation for subsequent invasion and immune evasion. Some bacteria exhibit host specificity due to unique receptor-binding interactions.

2. Invasion Factors: Pathogens utilize enzymes and toxins to breach host barriers and disseminate into tissues. Enzymes such as hyaluronidase and

collagenase break down connective tissues, enabling bacteria to spread. Toxins can disrupt cellular junctions, facilitating invasion and systemic infection. (Sharma AK et al., 2016). The ability to invade host tissues allows pathogens to access nutrients and evade localized immune responses.

3. Evasion Mechanisms: Capsules, surface proteins, and antigenic variation are employed by bacteria to evade recognition and phagocytosis by the host immune system. For example, polysaccharide capsules prevent opsonization, while surface protein alterations help bacteria avoid antibody binding. (Sharma AK et al., 2016). Some bacteria, such as *Neisseria gonorrhoeae*, change their surface antigens to stay one step ahead of the host's adaptive immunity.

4. Toxins: Bacteria produce a wide array of toxins that harm host cells. Endotoxins, integral to Gram-negative bacterial membranes, trigger systemic inflammation by activating Toll-like receptor 4 (TLR4) pathways. Exotoxins, secreted by both Gram-positive and Gram-negative bacteria, target specific host cellular processes, such as inhibiting protein synthesis (e.g., diphtheria toxin) or disrupting cell membranes (e.g., hemolysins). (Leitão JH, 2008).

5. Immune Modulation: Some bacteria produce proteins, like superantigens and IgA proteases, which impair immune cell function, disrupting host defenses. (Fraser JD and Proft T, 2008) Superantigens, such as those produced by *Staphylococcus aureus,* cause excessive T-cell activation, leading to immune dysregulation and tissue damage.

6. Nutrient Acquisition: Bacteria secrete enzymes to break down host tissues, releasing nutrients essential for their survival and growth. Siderophores, for example, are molecules secreted by bacteria to scavenge iron from host proteins like transferrin and lactoferrin. This process is vital for bacterial metabolism and virulence in iron-limited environments such as the human body.

Impact of Environmental and Human Activities

Environmental changes and human behaviors play a critical role in shaping the virulence and transmission of pathogenic bacteria. In tropical regions, such as Southeast Asia, these factors exacerbate the spread of infections and contribute to the emergence of antimicrobial resistance.

1) Climate Change:

Rising temperatures and humidity levels directly influence bacterial survival, growth, and transmission dynamics. Warmer aquatic environments, for example, enhance the proliferation of *Vibrio cholerae*, increasing the risk of cholera outbreaks. Temperature shifts also facilitate the expansion of thermophilic pathogens into previously temperate zones, altering local disease patterns and increasing public health vulnerability (Soni et al., 2024).

2) Pollution and Microplastics:

Microplastics in aquatic ecosystems serve as substrates for bacterial attachment and biofilm formation. These biofilms protect bacteria from environmental stressors, including UV radiation and chemical disinfectants, thereby increasing bacterial persistence and resistance. Moreover, industrial pollutants can create selective pressure that accelerates the development of antibiotic-resistant strains (Zhang et al., 2023; Soni et al., 2024).

3) Antibiotic Use and Misuse:

Excessive and inappropriate use of antibiotics in human medicine and animal husbandry remains a major driver of multidrug resistance. Practices such as non-prescription antibiotic use, prophylactic use in livestock, and incomplete treatment courses contribute to the selection and spread of resistant strains like Methicillin-resistant *Staphylococcus aureus* (MRSA) and carbapenem-resistant Enterobacteriaceae (CDC, 2022; Koh et al., 2019).

4) Urbanization and Habitat Disruption:

Rapid urban expansion and deforestation increase human exposure to zoonotic bacteria. Wildlife forced into closer contact with human settlements can transmit pathogens such as Leptospira or Burkholderia pseudomallei. At the same time, poor sanitation in overcrowded urban areas fosters bacterial transmission through contaminated water and surfaces (Soni et al., 2024).

4) Globalization and Human Mobility:

The increased movement of people, goods, and animals across borders facilitates the global spread of pathogenic bacteria. International travel and trade have been implicated in the introduction of antibiotic-resistant strains of *Salmonella* and *Klebsiella pneumoniae* into new regions, often outpacing public health containment strategies (WHO, 2021).

These environmental and anthropogenic factors do not act in isolation; rather, they create synergistic effects that amplify bacterial virulence and complicate infection control. Understanding these complex interactions is essential for developing targeted, context-specific interventions to reduce the global burden of bacterial diseases.

Common Virulent Bacteria and Their Impact

The article examines various bacteria that contribute significantly to infections:

• *Staphylococcus aureus*: Known for its ability to cause a range of infections, including skin infections, toxic shock syndrome, and sepsis, this bacterium employs numerous virulence mechanisms. Toxins such as enterotoxins and toxic shock syndrome toxins, enzymes like coagulase and hyaluronidase, and its capacity to form biofilms contribute to its persistence and resistance to treatments. In hospital settings, *S. aureus* is a major concern due to its multidrug-resistant strains, such as MRSA (Methicillin-resistant *Staphylococcus aureus*) (Britannica, 2024).

• *Escherichia coli*: Although commonly found in the human gut as a harmless commensal, Pathogenic *E. coli* are classified into several types, such as Enterohemorrhagic *E. coli* (EHEC), most notably *E. coli* O157:H7. This strain causes bloody diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome (HUS). The pathotype responsible for urinary tract infections is Uropathogenic *E. coli* (UPEC) cause severe diseases, including urinary tract infections, gastroenteritis, and hemolytic uremic syndrome. These strains employ Shiga toxins and adhesins to colonize and damage host tissues. Additionally, *E. coli* is a frequent cause of hospital-acquired infections, particularly in immuno-compromised individuals. (Sato A et al., 2019).

• *Pseudomonas aeruginosa*: This opportunistic pathogen primarily affects individuals with compromised immune systems, such as those with cystic fibrosis or burn wounds. Its virulence factors include biofilm formation, the production of exotoxins, and the secretion of enzymes like elastase. These mechanisms enable *P. aeruginosa* to resist antibiotics and disinfectants, making it a significant challenge in healthcare environments. (Leitão JH, 2020).

• *Streptococcus pyogenes* (Group A Streptococcus): Responsible for diseases such as strep throat, scarlet fever, and necrotizing fasciitis, *S. pyogenes* utilizes M protein, streptolysins, and hyaluronic acid capsules to evade immune responses and cause severe tissue damage. Its ability to produce superantigens contributes to systemic immune activation and toxic shock syndrome. (Patterson MJ, 1996).

• *Mycobacterium tuberculosis*: The causative agent of *tuberculosis* primarily affects the lungs but can also spread to other organs. Its cell wall contains mycolic acids, which confer resistance to many antibiotics and allow the bacterium to survive within macrophages. This resilience makes *tuberculosis* a persistent public health challenge. (Rohde K et al., 2007).

Clostridioides difficile (formerly *Clostridium difficile*) is a major cause of antibiotic-associated diarrhea and pseudomembranous colitis. It produces toxins A and B, which damage the intestinal epithelium and trigger inflammation. These infections frequently arise after broad-spectrum antibiotic use, which disrupts the gut microbiota and permits *C. difficile* overgrowth (Bartlett, 2002).

The human immune response includes neutrophil recruitment and cytokine release to contain the infection, but in severe cases, immune dysregulation contributes to tissue damage. Effective management strategies include antibiotic therapy (e.g., vancomycin, fidaxomicin), fecal microbiota transplantation (FMT), and supportive care. Understanding both host defenses and therapeutic interventions is key to mitigating *C. difficile* pathogenicity.

Prevention and Management

The article underscores strategies for combating bacterial pathogenicity:

1. Vaccination: Vaccines targeting specific bacterial antigens are particularly relevant in tropical climates like Thailand, where diseases such as cholera and typhoid fever are prevalent. Ensuring wide vaccine coverage in endemic regions reduces outbreaks and prevents severe cases. (CDC, 2024).

2. Improved Hygiene: In tropical climates, humidity facilitates the survival and spread of bacteria. Measures such as frequent handwashing, ensuring safe drinking water, and promoting sanitation are essential. In Thailand, initiatives to improve access to clean water and public hygiene in rural and urban areas significantly reduce diarrheal diseases. (Butt T and Von Seidlein L, 2015).

3. Environmental Management: Stagnant water and improper waste management in tropical environments can become breeding grounds for bacteria. Public health programs focused on reducing waterborne diseases in Thailand include efforts to improve drainage systems and community education. (WHO, 2024).

4. Antibiotics and Alternatives: Judicious use of antibiotics is critical to prevent the emergence of resistance. In Thailand, implementing antibiotic stewardship programs in hospitals and educating the public about the dangers of self-medication are key strategies.

Alternatives such as phage therapy and probiotics show promise in combating resistant strains. (Rappuoli R et al., 2014).

5. Community Engagement: Local education campaigns in Thailand, focusing on the prevention of bacterial infections through food safety practices and vaccination awareness, empower communities to take proactive measures against infections. (ASEAN Agrifood, 2021).

Summary of Case Studies from Thailand (Based on Critical Analysis)

1. Antibiotic Resistance:

- At Siriraj Hospital, 78.1% of patients treated for Gram-negative bacterial infections with Polymyxin B showed positive clinical outcomes. (Ngamprasertchai T et al., 2018).
- This study underscores the effectiveness of targeted antibiotic therapy for multidrug-resistant bacterial infections and highlights the need for alternative treatments to combat resistance.

2. Innovative Therapies:

- Research into Methylene Blue-mediated photodynamic therapy demonstrated its potential to treat extensively drug-resistant bacteria in nosocomial settings. (Songsantiphap C et al., 2022)
- This therapy, by activating Methylene Blue with specific light wavelengths, effectively reduces bacterial loads, providing a novel approach in antibiotic-resistant cases.

3. Environmental and Zoonotic Risks:

- Deforestation in Thailand has led to increased zoonotic bacterial infections. Wildlife reservoirs like *Leptospira* and *Burkholderia pseudomallei* have caused diseases such as leptospirosis and melioidosis due to closer human-wildlife contact. (Soni J et al., 2024)
- These findings highlight the impact of environmental disruption on bacterial pathogenicity and public health.

4. Public Health Policies:

- Thailand's National Strategic Plan for Antimicrobial Resistance exemplifies effective regional strategies to manage resistance. (Husada D et al., 2020).
- Predictive models for bacterial late-onset neonatal sepsis, achieving 95.5% diagnostic accuracy, offer scalable solutions for resource-limited settings and early interventions.

5. Hospital-Based Interventions:

- At Ramathibodi Hospital, an integrated approach combining infection control measures with environmental decontamination reduced outbreaks of carbapenem-resistant *Klebsiella pneumoniae*. (Chotiprasitsakul D et al., 2019).
- This case underscores the importance of multi-faceted strategies in managing nosocomial infections effectively.

These case studies reflect Thailand's proactive measures and challenges in combating bacterial virulence and antibiotic resistance, providing valuable insights into addressing similar issues in tropical regions globally.

Discussion

The findings of this review highlight the multifaceted nature of bacterial virulence and underscore the pressing need for integrated approaches to address pathogenicity in tropical climates. The interplay between bacterial virulence factors and environmental influences, such as climate change, pollution, and urbanization, reveals a complex network of factors exacerbating bacterial infections, particularly in resource-constrained settings like Southeast Asia. (Fraser JD and Proft T, 2008) These insights emphasize that bacterial pathogenicity cannot be effectively tackled in isolation but requires coordinated efforts across molecular research, public health, and environmental management. (Soni J et al., 2024)

Key interventions, such as antibiotic stewardship programs. (Britannica, 2024). vaccination campaigns, (Sato A et al., 2019). and public hygiene initiatives, (Patterson MJ, 1996). demonstrate significant promise in mitigating the impact of bacterial infections. However, the emergence of multidrug-resistant strains, fueled by antibiotic misuse and overuse, remains a critical challenge. (Rohde K et al., 2007) Innovative therapies, such as photodynamic antimicrobial strategies, (Bartlett JG, 2002). present a viable alternative, but their scalability and accessibility in low-resource settings need further exploration.

Region-specific factors, particularly in Thailand, add another layer of complexity. For example, the high prevalence of zoonotic infections linked to deforestation and habitat destruction underscores the need for tailored public health strategies that address both environmental and social determinants of health. (CDC, 2024). Case studies from Thailand demonstrate the effectiveness of localized interventions but also highlight gaps in widespread implementation and monitoring. (Butt T and Von Seidlein L, 2015).

Despite these advances, significant knowledge gaps persist. For instance, the impact of microplastics as vectors for bacterial virulence in aquatic ecosystems and the long-term effects of climate change on bacterial pathogenicity warrant deeper investigation. (WHO, 2024). Additionally, there is a need to bridge the gap between molecular research and practical applications in public health policies, ensuring that scientific advancements translate into tangible outcomes for affected populations. (Rappuoli R et al., 2014).

Limitation

While this review provides a comprehensive overview of bacterial virulence factors and their interaction with environmental and human influences, several limitations should be acknowledged:

1. Data Availability: The focus on Southeast Asian studies, particularly Thailand, may limit the generalizability of findings to other regions. Comparative analyses with non-tropical settings were not extensively conducted.

2. Bias in Literature Selection: The reliance on peer-reviewed literature and government reports may have introduced selection bias, potentially overlooking unpublished or non-English studies that could provide additional insights.

3. Scope of Innovative Therapies: While promising therapies like photodynamic antimicrobial strategies were discussed, their clinical applicability and cost-effectiveness in diverse healthcare settings remain uncertain.

4. Limited Discussion on Long-Term Impacts: The long-term implications of interventions, such as vaccination and antibiotic stewardship, on bacterial evolution and resistance patterns were not thoroughly explored.

5. Environmental Factors: Although environmental impacts were discussed, detailed quantitative analyses of factors such as pollution levels or specific climate variables influencing bacterial virulence were beyond the scope of this review.

Addressing these limitations in future research could enhance the understanding of bacterial pathogenicity and inform the development of more effective, globally applicable strategies.

Conclusion

This review emphasizes the critical need for integrated approaches to combat bacterial pathogenicity, particularly in tropical and resource-limited settings. Key interventions, such as antibiotic stewardship, vaccination, and innovative therapies like photodynamic strategies, offer promising solutions but require further research and adaptation for low-resource contexts. Addressing knowledge gaps and enhancing the integration of molecular insights with public health strategies will be essential in mitigating bacterial infections and quality care.

References

ASEAN Agrifood. (2021).*Consumer education and awareness campaigning guidelines* https://www.asean-agrifood.org

Bartlett JG. (2002). Antibiotic-Associated Diarrhea. *N Engl J Med. 346*(5):334–9. doi:10.1056/NEJMcp011603.

Britannica. (2024). *Staphylococcus aureus* bacterium https://www.britannica.com/science/bacterial-disease

Butt T and Von Seidlein L. A (2015). systematic review of the impact of improved housing interventions on health in low and middle income tropical settings. *Value in Health.;18*(7), A564. https://www.valueinhealthjournal.com/article/S1098-3015(15)03921-2/fulltext.

Chotiprasitsakul D, Srichatrapimuk S, Kirdlarp S, Pyden AD, Santanirand P. (2019). Epidemiology of carbapenem-resistant Enterobacteriaceae: a 5-year experience at a tertiary care hospital. *Dovepress.com.12*, 461-468.

Fraser JD and Proft T.(2008). The bacterial superantigen and superantigen-like proteins. *Immunol Rev*. 225:226–43. doi:10.1111/j.1600-065X.2008.00681.x.

Husada D, Chanthavanich P, Chotigeat U, Sunttarattiwong P, Sirivichayakul C, Pengsaa K, et al. (2020). Predictive model for bacterial late-onset neonatal sepsis in a tertiary care hospital in Thailand. *BMC Pediatrics. 20*, 151. doi: 10.1186/s12887-020-01940-9.

Kaiser G. (2023). The Ability to Adhere to Host Cells and Resist Physical Removal. In: Kaiser A, editor. Microbiology. LibreTexts. https://bio.libretexts.org/Bookshelves/Microbiology/Microbiology_(Kaiser)/Unit_3%3A_Bacterial_Pathogenesis/5%3A_Virulence_Factors_that_Promote_Colonization/5.2%3A_The_Ability_to_Adhere_to_Host_Cells_and_Resist_Physical_Removal

Koh TH, Tan TY, Liang S, Wong W, Lin RT, Lee S. (2019). Antibiotic resistance in bacteria isolated from blood cultures in Southeast Asia. *Southeast Asian J Trop Med Public Health.;50*(4), 657–66.

Ngamprasertchai T, Boonyasiri A, Charoenpong L, Nimitvilai S, Lorchirachoonkul N, Wattanamongkonsil L, (2018). Effectiveness and safety of polymyxin B for the treatment of infections caused by extensively drug-resistant Gram-negative bacteria in Thailand. *Infect Drug Resist*.;11:1219-24. doi:10.2147/IDR.S167019.

Rappuoli R, Pizza M, Del Giudice G, De Gregorio E (2014). Vaccines, new opportunities for a new society. *Proc Natl Acad Sci. 111*(34) doi: 10.1073/pnas.1402981111.

Rohde K, Yates RM, Purdy GE, Russell DG. (2007). Mycobacterium tuberculosis and the environment within the phagosome. *Immunol Rev. 160*(0), 65–77.

Sharma AK, Dhasmana N, Dubey N, Kumar N, Gangwal A, Gupta M, (2016). Bacterial Virulence Factors: Secreted for Survival. *Indian J Microbiol. 57*(1),1-10. doi: 10.1007/s12088-016-0625-1. PMCID: PMC5243249, PMID: 28148975.

Songsantiphap C, Vanichanan J, Chatsuwan T, Asawanonda P, Boontaveeyuwat E. (2022). Methylene blue–mediated antimicrobial photodynamic therapy against clinical isolates of extensively drug-resistant Gram-negative bacteria causing nosocomial infections in Thailand: an in vitro study. *Front Cell Infect Microbiol*.; 12:929242. doi:10.3389/fcimb.2022.929242.

Soni J, Sinha S, Pandey R. (2024). Understanding bacterial pathogenicity: a closer look at the journey of harmful microbes. *Front Microbiol.; 15*: doi:10.3389/fmicb.2024.1370818.

World Health Organization. (2021). Global health estimates: Leading causes of death. Cause-specific mortality, https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates/ghe-leading-causes-of-death.

World Health Organization. (2024). *WHO Southeast Asia*. https://www.who.int/southeastasia.

Zhang XX, Jin YZ, Lu YH, Huang LL, Wu CX, Lv S, (2023). *Infectious disease control: from health security strengthening to health systems improvement at global level. Glob Health Res Policy*. doi: 10.1186/s41256-023-00319-w.