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Clinical Microbiology of Common Bacterial Infections: Diagnosis Treatment and Antimicrobial Resistance

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Abstract
Bacterial infections are still a major health issue worldwide due to their high prevalence, clinical significance and rising antimicrobial resistance. The clinical microbiology of common bacterial infections will be discussed, with emphasis on how to make the diagnosis, as well as on the antibiotics options for treatment, the mechanisms of antibiotic resistance and on new developments in antibiotic therapy. Conventional microbiological methods will remain important for pathogen identification and antimicrobial susceptibility testing for the purposes of guiding therapy and selection of pathogens. New molecular diagnosis, genome sequencing and rapid detection technologies can help increase the accuracy of diagnosis and help to implement timely clinical interventions. However, with the increase in the prevalence of multidrug resistant (MDR) organisms, the choice of antibiotic is becoming more challenging and the need for treatment failure and the burden of care is increasing. Antimicrobial stewardship, evidence-based prescribing, infection prevention and resistance surveillance are important in reducing the use of inappropriate antibiotics, and bacterial transmission. Newly developed techniques such as artificial intelligence, precision medicine, new antimicrobials and bacteriophage therapy are likely to add to the robustness of infection management. Increased diagnostics, susceptibility data, and integrated public health response efforts are essential to enable a more robust clinical response and address AMR.

Keywords: Clinical microbiology, Bacterial infections, Antimicrobial resistance, Molecular diagnostics, Antimicrobial stewardship

Introduction

Despite the ever-changing nature of microbiology and the approval of many antibiotics in recent years, bacterial infections continue to pose a significant clinical threat due to the significant morbidity they cause, their impact on health care visits and the complications that result from them. Bacterial infections are common in multiple organ systems: respiratory tract, urinary tract, gastrointestinal tract, blood stream, and skin and soft tissues. They present either as relatively mild, self-limiting infections, or as more severe systemic infections, hospitalizable, and requiring intensive antimicrobial therapy. The advent of diagnostic microbial and antimicrobial therapeutic techniques has been a tremendous improvement; however, the problems of bacterial infections are still severe because of the location of pathogens, clinical presentation, and emergence of antimicrobial resistance. Obviously, the management of bacterial diseases is growing increasingly challenging, and a proper microbiological identification, together with the clinical evaluation and therapeutic decision-making, is more important than ever for better patients' outcomes (Kolář, 2022).

Clinical microbiology plays a crucial role in the identification of bacterial pathogens, interpretation of the clinical significance of these pathogens and in selecting the correct antimicrobial treatment. The traditional methods of microbiological diagnosis (i.e. specimen collection, bacterial growth, Gram staining, biochemical identification, and antimicrobial susceptibility testing) are still fundamental in day-to-day diagnosis. The techniques can provide some information on the characteristics of the bacteria and the pattern of antibiotic resistance, aiding the separation of bacterial colonization from clinically significant infections. But, the common methods have the disadvantages of needing long incubation periods, necessitating the requirement that the organism be alive, and are not as sensitive following antibiotic

treatment. The limitations could be partly responsible for delayed decisions for treatment particularly in patients with severe infections requiring immediate clinical intervention. Therefore, there is a need for better microbiological diagnosis in terms of timeliness and reliability in today's management of infectious diseases (Gillespie & Bamford, 2022).
Recent advances in molecular diagnosis have expanded the scope of opportunities for quick and accurate identification of bacterial pathogens. A range of new molecular methods like polymerase chain reaction (PCR), multiplex molecular assays and nucleic acid-based detection platforms can detect microbial genetic material without the need for lengthy culture processes. The approaches have the potential of rapid diagnostic, high sensitivity and identification of multiple pathogens simultaneously. Molecular techniques can also be used to help identify specific antimicrobial resistance genes, and this could help to make more timely decisions about therapy. Their clinical application should be taken into account, however, for the accuracy of the diagnosis, interpretation of positive results, infrastructure requirements, and cost-effectiveness. This combination of molecular methods and traditional microbiological methods could thus be used as an aid for more comprehensive diagnostic approaches, rather than an alternative to them (Gerace *et al*., 2022).
Whole genome sequencing is another biotechnological breakthrough in clinical microbiology that provides a global view of the genetic material of bacteria when involved in an identification, their level of resistance and their possible connection to other bacteria. Genomic characterization can aid in the investigation of resistant organisms and further understanding of the molecular mechanisms involved in antimicrobial resistance. But the cost of sequencing, bioinformatics requirements, data analysis challenges and the lack of a uniform analysis pipeline present technological obstacles to the implementation of these technologies. Resistance and susceptibility associations between antimicrobial resistance markers and genomic data are also critical to the translation of genomic data to clinically actionable data and must be trusted. The above points suggest that, to achieve meaningful improvements in diagnostic performance, technological advances need to be supported by strong laboratory validation and clinical interpretation.
Antimicrobial resistance is one of the biggest hurdles of the diagnosis and treatment of bacterial infections. There are many different ways resistance can develop, including: inactivation of antibiotics by enzymes; change in antibiotic targets; lessening of membrane permeability; active efflux of antibiotic from the cell. These can reduce the effectiveness of the most frequently used antibiotics and increase the demand for the use of other medicines. The appearance and spread of multidrug-resistant bacterial pathogens have made empirical antibiotic therapy more complicated and helped to cause the challenge in the management of both community-acquired and healthcare-associated infections. Other causes of the emergence of resistant bacterial populations include inappropriate antibiotic use, unnecessary antibiotic exposure and suboptimal infection control. Therefore, understanding the clinical implications of resistance is crucial, because upon this, effective development of antimicrobial treatment strategies would be based. (Zhu *et al*., 2022)
The relationship between antimicrobial resistance and treatment response is more important in situations where rapid treatment action is required. Empirical antibiotic therapy is frequently commenced before a microbiological diagnosis is made as a delay in appropriate antibiotic prescribing may be correlated with complications. Appropriate first-line antibiotics can result in an under- or over-cover of the pathogen, while inappropriate antibiotics use can result in the use of broad-spectrum antibiotics. The value of AIMT is thus an invaluable asset to aid the decision-making process after laboratory results. Also, local resistance patterns, pharmacological properties, anatomical site and severity of infection should be taken into account when choosing the appropriate agent. Considering these factors in clinical decisions could enhance the success of treatment and help guide responsible antimicrobial prescribing (AMP) (Flynn & Guarner, 2023).
Diagnosis and treatment of specific bacterial infections varies, too. Since the aetiology of UTIs is becoming more complex, UTIs highlight the importance of considering ASBPs and highlight the challenges of empirical antibiotic treatment. It is important to differentiate uncomplicated from complicated clinical presentations, in addition to taking into account patient characteristics, previous antimicrobial exposures, and the potential for resistant organisms in order to manage appropriately. These differences in infections make a one-size-fits-all approach to antibiotic treatments inappropriate for all bacterial diseases, and highlight the need for personalized microbiological-based antibiotic treatment (Frimodt-Møller & Bjerrum, 2023).
The field of clinical microbiology is progressing but there are substantial shortcomings in the coordination of technology and integration of diagnostics, antimicrobial susceptibility testing and antibiotic usage decisions. Besides laboratory-level innovations, innovations in antimicrobial stewardship and clinical interpretation and infection prevention are necessary to address resistance-related problems. An integrated approach to the study of common bacterial infections is therefore essential to understand the value and contribution of traditional and novel diagnostic approaches, and to evaluate therapeutic options and strategies to improve resistance-informed clinical management (Hassall *et al*., 2024). The objectives of this study are as follows:

1. To examine the clinical microbiological characteristics and diagnostic approaches used for identifying common bacterial infections.
2. To evaluate conventional and emerging antimicrobial treatment strategies for common bacterial infections in contemporary clinical practice.
3. To assess antimicrobial resistance mechanisms, diagnostic challenges, and their implications for effective antibiotic selection and management.

2. Clinical Microbiology of Common Bacterial Infections

2.1. Classification of Clinically Important Bacterial Pathogens

Bacterial pathogens that have clinical relevance are classified on a fairly standard basis based on their gram-staining, cell morphology, virulence factors, and susceptibility to antimicrobial agents. *Staphylococcus aureus, Streptococcus*

pneumoniae, Escherichia coli, and *Klebsiella pneumoniae* are major contributors of human infectious diseases among Gram-positive organisms and among Gram-negative bacteria, respectively. They are becoming more clinically relevant due to the increasing antimicrobial resistance that affects their therapeutic management and control of infection (Baciu *et al*., 2024). Correct identification and susceptibility testing of pathogens enables targeted choice of antimicrobials and aids in clinical decision making (Gajic *et al*., 2022).

2.2. Infections of the Respiratory Tract Due to Bacteria

Bacterial infection of the respiratory tract is still a major source of morbidity, especially in children, elderly, and those with underlying respiratory diseases. The most common pathogens are *Streptococcus pneumoniae, Haemophilus influenzae* and *Staphylococcus aureus* and clinical manifestations depend on the severity of the infection and individual susceptibility. Traditional diagnostic approaches can fail to achieve optimal pathogen recoveries and test results may be delayed after antimicrobial exposure (Alnimr, 2023). Targeted next-generation sequencing allows for the rapid detection of a wider range of respiratory pathogens and a selected set of resistance genes, which could help enhance the diagnostic accuracy and provide guidance for antimicrobial therapy decisions (Lin *et al*., 2023).

2.3. Treatment of Urinary Tract Bacterial Infections

Gram negative organisms, particularly *Escherichia coli*, are common cause of UTIs, while *Klebsiella pneumoniae* and other opportunistic pathogens are responsible for complicated UTIs. Empirical antibiotic selection and effective clinical management are challenging due to the increasing resistance of urinary microorganisms (Baciu *et al*., 2024). Urine culture and antimicrobial susceptibility testing are still key to the diagnosis of causative organisms and selection of treatment options. Standardized susceptibility assessment will enable information about the response of bacteria to antimicrobials to guide directed therapy in order to avoid exposure to ineffective antimicrobials (Gajic *et al*., 2022).

2.4. Gastrointestinal Bacterial Infections

Bacterial infection of the gastrointestinal tract refers to various microorganisms such as *Salmonella, Shigella, Campylobacter* or pathogenic *Escherichia coli* that can lead to inflammatory diarrhea, gastrointestinal tract infection and systemic complications. Clinical outcomes depend on the pathogen virulence, host characteristics and antimicrobial resistance patterns (Ansari & Yamaoka, 2022). More resistance among the clinically relevant bacterial organisms makes the therapeutic approach more complicated, especially if the use of antimicrobial agents is clinically warranted (Baciu *et al*., 2024). Molecular diagnostic technologies provide potential to detect resistance-associated genetic markers but the correlation of genotypic results with phenotypic antimicrobial susceptibility needs to be considered when interpreting the results of molecular diagnostics (Banerjee & Patel, 2023).

2.5. Bloodstream Bacterial Infections and Healthcare Associated Bacterial Infections

Bloodstream and healthcare-associated bacterial infections are important clinical issues due to the high prevalence of potentially life-threatening infections and resistance to antibiotics. *Staphylococcus aureus, Klebsiella pneumoniae* and *Pseudomonas aeruginosa* are common organisms that can be a therapeutic challenge because of limited antibiotic options due to resistance (Baciu *et al*., 2024). An appropriate microbiological identification and susceptibility testing is necessary to optimize antimicrobial treatment and minimise inappropriate prescribing, particularly in a timely fashion. Diagnostic stewardship can enhance the clinical interpretation of microbiological test results and can aid in appropriate diagnostic testing and treatment decisions and, when implemented as part of an antimicrobial stewardship programme, can improve patient outcomes (Claeys & Johnson, 2023).

2.6. Skin and Soft Tissue Bacterial Infections

These are bacterial infections of the skin and soft tissues which generally involve the *staphylococcus aureus* and *Streptococcal* species and are characterized by cellulitis, abscesses, wound infections, and complicated tissue infections. The rising prevalence of antimicrobial resistance in clinically relevant staphylococcal strains raises the difficulty and complexity of choosing an antibiotic and can narrow the therapeutic window for these microorganisms (Baciu *et al*., 2024). Microbiological culture and antibiotic sensitivity testing are useful in certain complicated, recurrent and resistant infections. Conventional and emerging susceptibility testing strategies can be used to characterize bacterial resistance patterns and aid in selecting the right antimicrobial therapy when clinically indicated by the onset of laboratory investigation (Gajic *et al*., 2022) (Table 1) (Figure 1).

Table 1. Clinical Characteristics of Common Bacterial Infections

Infection type	Common bacterial pathogens	Main clinical concern	References (APA style)
Respiratory tract	*S. pneumoniae, H. influenzae*	Pneumonia and resistant infections	(Lin *et al*., 2023)
Urinary tract	*E. coli, K. pneumoniae*	Resistant uropathogens	(Baciu *et al*., 2024)
Gastrointestinal	*Salmonella, Shigella* spp.	Gastrointestinal disease and treatment resistance	(Baciu *et al*., 2024)
Bloodstream	*S. aureus, E. coli*	Sepsis and systemic infection	(Baciu *et al*., 2024)
Skin and soft tissue	*S. aureus*, *Streptococcus* spp.	Cellulitis and wound infections	(Gajic *et al*., 2022)

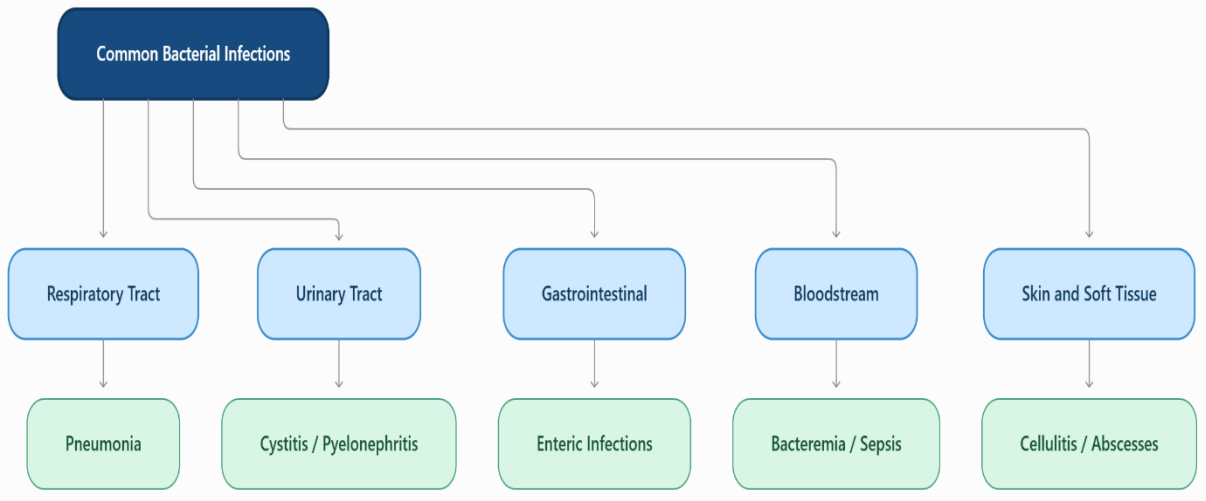

Figure 1. Classification and Clinical Distribution of Common Bacterial Infections

3. Diagnostic Strategies to Identify Bacterial Infections

3.1. The complete laboratory evaluation and the collection of specimens.

Correct diagnosis of bacterial infections starts with a thorough clinical evaluation and proper specimen collection, which affects the identification of the pathogen and the decision for antimicrobial therapy. Clinical evaluation takes into account the presenting symptoms, site of infection, underlying medical conditions, prior antibiotic use, and possible HA risk factors. Blood, urine, sputum, wound swabs, and other clinically relevant materials should be collected, as per established laboratory protocols and the suspected infection. When clinically possible, the correct time to collect the specimen, especially before using antimicrobials, can improve recovery of the pathogen and minimize false negative culture findings. There are many recommendations for surveillance, including standardized microbiological sampling and reliable identification procedures, which enable the collection of comparable antimicrobial resistance data in healthcare settings (WHO, 2023). There are also differences in resistance profiles depending on clinical characteristics and underlying patient-related factors, especially when patients present with urinary tract infections (UTI) (Shaker *et al*., 2024). Thus, clinical evaluation, coupled with specimen quality, timely arrival to the laboratory, and proper specimen processing, is essential to provide interpretable microbiologic results and facilitate correct diagnosis.

3.2. Diagnostic techniques used in the field of microbiology.

Traditional microbiological methods are critical for the diagnosis of bacterial infections as they facilitate the isolation of pathogens, pathogen characterization and determination of antimicrobial resistance. Gram staining gives a preliminary characterisation of the bacteria's morphology and cell-wall properties and culture-based methods enable the recovery of the organism and identification using biochemical or automated identification systems. Standardized antimicrobial susceptibility testing is especially critical in determining if bacteria are susceptible or resistant and to inform treatment recommendations. Phenotypic investigations can also be used to evaluate bacterial traits that are linked with persistence of the infection, such as biofilm formation and the link with antimicrobial resistance (Basnet *et al*., 2023). Standard diagnostic tests give clinically relevant information, but often need long incubation periods and other confirmatory tests. Therefore, consistent identification and susceptibility reporting of bacteria is crucial to ensure diagnostic consistency and better quality of surveillance among participating health care institutions (World Health Organization, 2023). Although new technologies, traditional microbiology is still a vital tool for the identification of pathogens and assessment of antimicrobial responses that are not always fully apparent from genetic data.

3.3. Molecular and Rapid Diagnostic Methods;

Molecular and rapid diagnostic technologies have broadened the possibilities to identify bacteria at an earlier stage and to recognise the presence of antimicrobial resistance determinants (Taha *et al*., 2024). Selected bacteria pathogens or resistance-associated genes can be identified by polymerase chain reaction, multiplex nucleic acid amplification assays and/or targeted molecular platforms without the need for long culture protocols. These methods are especially important if the typical microbiological results take time to arrive or if cultures are less sensitive because of previous antimicrobial use. Artificial Intelligence (AI) enabled diagnostic systems present another opportunity for analysis of complex microbiological patterns and to aid resistance decision-making (Rabaan *et al*., 2022). However, molecular detection of the organism is not always a valid method for confirming organism viability or distinguishing active infection from colonization, especially if bacteria can still be detected genetically after treatment. Rapid diagnostic results will need to be interpreted in the context of the patient's clinical history, quality of the specimen, and microbiological evidence. Local resistance rates and antibiotic prescribing influence the clinical utility of the findings of the diagnostic tests, and the recommendations for treatment (Torumkuney *et al*., 2022). Thus, molecular technologies have been optimally leveraged into the appropriate diagnostic workflow supporting timely, clinically relevant treatment decisions.

3.4. Genomic diagnostics and whole genome sequencing.

Whole genome sequencing gives a whole genome picture of the genetic composition of bacteria, and has potential for studying the relationship between bacteria, the development of resistance genes and the transmission of bacteria (Avershina *et al*., 2023). Confers ability to assess more than one genetic region at a time; provides detailed characterization of bacterial isolates, and identification of known resistance mechanisms, unlike targeted molecular tests. This information

could support epidemiological investigations and assist with separating among similar organisms in suspected healthcare-associated outbreaks. Standardized antimicrobial resistance surveillance systems highlight the need for uniform microbiological data gathering and interpretation and offer a baseline for incorporating extra-genomic data for resistance monitoring systems (World Health Organization, 2023). Genomic methods have particular relevance for the case of the spread of resistant organisms within institutions or across geographical regions. In the context of armed conflict, population displacement and disruptions to health care services and antibiotics availability may present further obstacles to understanding the spread of resistant pathogens (Granata *et al*., 2024). But routine clinical use is still limited by the cost of sequencing, the lack of bioinformatics infrastructure, lack of analytical standardization and incomplete genotype–phenotype relationships.

3.5. The detection of Antimicrobial Resistance

Rapid and precise identification of antimicrobial resistance is critical to the selection of appropriate antibiotics, the identification of multidrug-resistant organisms and to infection prevention measures. Unlike phenotypic susceptibility testing which uses standardized laboratory testing to assess the response to antimicrobial agents, molecular methods detect specific genes or mutations that confer resistance. These two methods provide complementary information, but the genetic markers for resistance do not always reflect the resistance phenotype. Other bacterial features, such as biofilm formation, could also affect antimicrobial tolerance and make it difficult to interpret traditional susceptibility results. The relevance and relevance of clinical bacterial isolates were demonstrated when comparative evaluation of phenotypic biofilm detection techniques were performed (Basnet *et al*., 2023). Antibiotic resistance is also dependent on the local epidemiological picture as the susceptibility of different species of bacteria, infection sites and health care environments may vary. It is important to note that there have been regional studies of UTI resistance trends and patient characteristics that are associated with resistance levels that could help guide treatment decisions (Shaker *et al*., 2024). Combined with clinical data, susceptibility results can therefore aid in the optimal use of antimicrobials and responsible prescribing.

3.6. Diagnostic Limitations and Clinical Challenges

Even though great advances have been made in clinical microbiology, there are still technological, operational and clinical limitations that affect bacterial infection diagnosis. The conventional culture-based approach may only allow confirmation after a delay and molecular-based processes require significant equipment costs, specialist staff and difficulties in the interpretation of positive results. Poor specimen quality, prior antibiotic use and poor separation of colonization from infection can also have a negative impact on diagnostic reliability. Artificial Intelligence (AI) has been shown to have potential for antimicrobial resistance prediction, but has not yet been used in practice in clinical settings due to the need for relevant training datasets, external validation, interpretability, and the ability to be integrated into existing laboratory workflows (Rabaan *et al*., 2022). Other medical systems also vary in terms of the accessibility of the diagnosis; laboratory capacity, the availability of antimicrobials and the recommendations for their use are not the same in all systems. Regional assessments highlight the need to integrate the susceptibility evidence with the local treatment recommendations and health services (Torumkuney *et al*., 2022). In a conflict context, these challenges could be exacerbated by infected individuals unable to access health services, as well as limited laboratory capacity, which affects infection diagnosis and resistance monitoring (Granata *et al*., 2024). Therefore, coordinated investment in laboratory capacity, standardization of procedures, antimicrobial stewardship, and the development of validated technological innovations, are necessary to improve diagnostic reliability (Table 2) (Figure 2).

Table 2. Comparison of Diagnostic Approaches for Bacterial Infections

Diagnostic approach	Primary application	Main limitation	References (APA style)
Gram staining	Preliminary bacterial classification	Limited species identification	(World Health Organization, 2023)
Bacterial culture	Isolation of viable pathogens	Delayed results	(World Health Organization, 2023)
Susceptibility testing	Antibiotic susceptibility determination	Requires standardized interpretation	(World Health Organization, 2023)
Molecular diagnostics	Detection of selected genetic targets	Incomplete resistance coverage	(Rabaan *et al*., 2022)
Genomic sequencing	Genomic characterization and surveillance	Cost and bioinformatics requirements	(Granata *et al*., 2024)

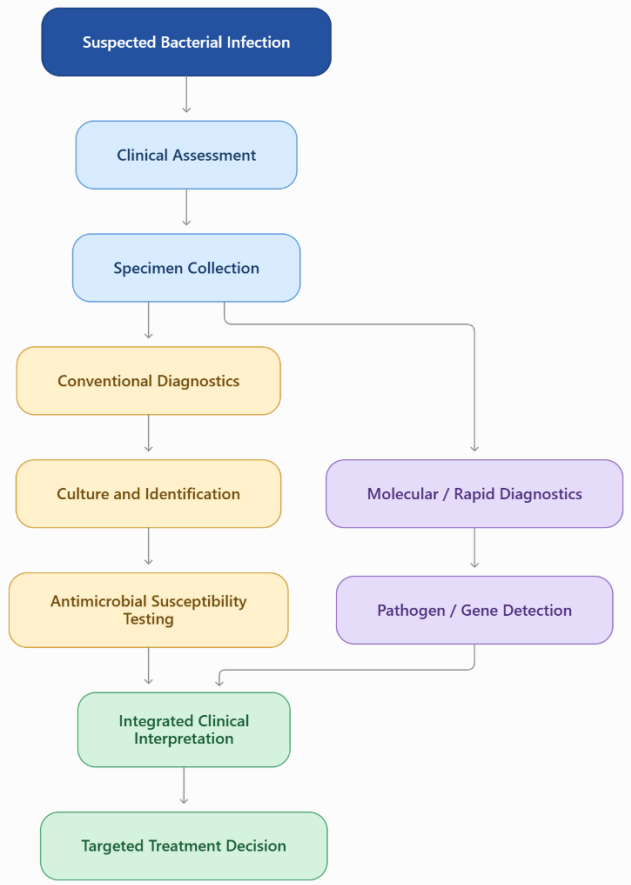

Figure 2. Integrated Diagnostic Workflow for Bacterial Infections

4. Antimicrobial Treatment of Common Bacterial Infections

When choosing an appropriate antibiotic for treatment, the drug must be chosen based on the probable cause of infection, its severity, anatomical location, and the patient's history. Drug spectrum and pharmacokinetic and pharmacodynamic properties, optimal dosage and duration are all taken into account when considering appropriate treatment. Avoid unnecessary broad-spectrum antibiotic exposures to limit the selection of resistance and complications of treatment. The main pillars of antimicrobial stewardship revolve around evidence-based antibiotic prescribing and ongoing re-evaluation of antibiotic therapy, while AI has been the subject of increasing research as a clinical decision support tool to optimize antibiotic use (Cesaro *et al*., 2025). Empirical antimicrobial therapy is commenced before definitive microbiological identification is made, if it is felt the clinical situation requires action to be taken and to be expedient. The choice of antibiotic should be based on the likely source of the infection, the severity of the disease, prior exposure to antimicrobials and local antimicrobial resistance. Refining treatment based on pathogen identification and susceptibility testing can be done by targeting the appropriate antibiotic or by de-escalating to a narrower range of antibiotics. Phenotypic and genotypic susceptibility testing could reduce the time from the first dose of antibiotic to the initiation of antibiotic therapy to microbiologically informed therapy, optimizing antibiotic selection and minimizing unnecessary broad-spectrum exposure (Hattab *et al.*, 2024). The site of action of the major classes of antibiotics are different bacterial targets such as cell-wall synthesis, protein synthesis, nucleic acid replication, and essential metabolic pathways. Medications that inhibit the synthesis of the cell wall of bacteria include the beta-lactams, while those that affect protein synthesis include macrolides, tetracyclines, and aminoglycosides. Fluoroquinolones interfere with the ability of the bacteria to reproduce their DNA, and trimethoprim-sulfamethoxazole slows down folate metabolism. Pathogen susceptibility and lack of clinically significant resistance mechanisms are important factors in the effectiveness of these agents. Single-cell approaches to diagnostics could prove useful for evaluating how well bacteria respond to antimicrobial therapy and inform personalized treatment decisions (Li *et al*., 2023). The choice of antibiotic varies in its use for respiratory and urinary infections, gastrointestinal infections, bloodstream infections and skin infections due to the different types of organisms, the severity of the illness, and variation in antibiotic resistance patterns. Short course, narrow-spectrum treatment may be appropriate for uncomplicated infections, while severe invasive infections may require intravenous treatment and a reassessment. An example of such challenges are urinary tract infections (UTIs): With rising resistance of uropathogens, empirical antibiotic selection is growing more difficult, and there is a decrease in commonly used therapeutic regimens (Von Vietinghoff *et al*., 2024). The use of uniform antimicrobial regimens should not be the sole basis for treatment decisions as classification of the infection and patient characteristics, culture results and current guidelines should be used (Table 3). Antimicrobial Susceptibility Testing (AST) is used to help determine antibiotic resistance, providing information about how bacteria will react to individual antibiotic agents. Phenotypic methods set the pattern of susceptibility, but genotypic methods reveal specific genetic factors that are associated with resistance. The use of rapid testing technologies could enhance the timeliness of treatment changes, especially in settings where initial treatment

decisions have significant implications such as in severe infections (Hattab *et al*., 2024). Combining laboratory data with clinical evaluation may help guide antibiotic therapy, de-escalate or avoid unnecessary antibiotics. The interpretation must also take into account the penetration of the drug into the infection site and pharmacologic factors in the individual patient. Failure of antimicrobial therapy can be caused by resisting organisms, delayed use of proper antibiotic, inadequate exposure to antibiotic, lack of antibiotic source control, and/or patient-related complications. Areas of particular difficulty may be in the hospital setting, where fewer treatment options may exacerbate clinical outcomes and healthcare burden in patients with multidrug-resistant infections (Peñalva *et al.,* 2025). Other challenges are diagnostic uncertainty, inappropriate prescribing and delayed susceptibility reporting. Artificial intelligence (AI) enabled stewardship systems are being explored to enhance antimicrobial decision-making, but considerations such as clinical validation, data quality, and implementation hurdles are significant (Ghafur *et al*., 2026).

Table 3. Antimicrobial Treatment Considerations for Common Bacterial Infections

Infection category	Treatment consideration	Resistance-related challenge	References (APA style)
Respiratory infections	Pathogen-directed antibiotics when indicated	Resistant respiratory organisms	(Hattab *et al*., 2024)
Urinary tract infections	Infection-specific, susceptibility-guided therapy	Resistant uropathogens	(Von Vietinghoff et al., 2024)
Bloodstream infections	Prompt appropriate therapy and source control	Delayed effective treatment	(Peñalva *et al*., 2025)
Skin and soft tissue infections	Drainage when indicated and appropriate antibiotics	Methicillin-resistant pathogens	(Hattab *et al*., 2024)
Multidrug-resistant infections	Mechanism-informed treatment selection	Limited therapeutic alternatives	(Peñalva *et al*., 2025)

5. Antimicrobial Resistance in Bacterial Pathogens

Antimicrobial resistance (AMR) is a significant challenge in the field of clinical microbiology today, and it undermines the success of current antibiotic treatment, makes infectious disease management more difficult and adds to the burden of infectious disease in the healthcare sector. Epidemiological patterns of antimicrobial resistance are different between geographical regions, bacterial species, infection site and healthcare settings, and these variations are due, at least in part, to differences in the consumption of antibiotics, the capacity for laboratory surveillance, infection prevention practices, and socioeconomic conditions. Resistant bacterial infections are becoming more common, especially in settings with limited resources, where the availability of diagnostic services is limited and susceptibility testing is not always performed. Therefore, enhanced laboratory surveillance, diagnostic standardization, and quality management are needed to generate quality resistance data and to facilitate coordinated public health responses (Musa., 2023). Bacterial resistance occurs at several molecular levels: the production of enzymes that inactivate antibiotics, changes in target sites for the antibiotic, decrease in entry into the cell, active efflux of antibiotics and acquisition of resistance-associated genetic elements. Multidrug resistance can spread within bacterial populations by means of horizontal gene transfer (HGT) via plasmids, transposons and other mobile genetic elements. These mechanisms have been studied in detail with the development of genomic technologies, which have allowed for the complete sequencing of resistance genes, genetic relationships and transmission between clinically relevant isolates of bacteria (Bianconi *et al*., 2023). Resistant pathogens, such as multidrug-resistant (MDR) pathogens including methicillin-resistant *Staphylococcus aureus*, extended-spectrum beta-lactamase-producing *Escherichia coli*, carbapenem-resistant *Klebsiella pneumoniae* and resistant *Pseudomonas aeruginosa*, create significant therapeutic challenges as a result of their resistance patterns. These challenges are of clinical significance, as illustrated by UTIs, where the distribution and susceptibility of the bacteria contributes to the choice of empirical treatment, especially in children. Studies on children with UTI have shown the significance of identification of common pathogenic bacteria present in the urine, assessing the antibiotic resistance, and studying related factors to aid in the best antibiotic choice (Mekonnen *et al*., 2023). Gastrointestinal infections, especially those due to Salmonella spp., also raise concerns about antimicrobial resistance, as this may make it more difficult to manage invasive disease and make preventive measures more critical. Resistant Salmonella strains have led to renewed interest in vaccination, surveillance and other non-antibiotic prevention strategies to decrease Salmonella infection burden and reduce dependence on antibiotics (Nazir *et al*., 2025). Various interrelated factors play a role in the emergence and spread of antimicrobial resistance such as inappropriate antibiotic prescribing, unnecessary empirical treatment, incomplete infection control practices, underuse of diagnostics, and frequent exposure to broad-spectrum antimicrobial agents. These issues are further exacerbated by the presence of healthcare-associated infections (HAI) in inpatients, where they may be exposed to prolonged antimicrobial use, invasive procedures and higher exposure to resistant strains of bacteria. The secondary bacterial respiratory infections in patients with coronavirus disease 2019 (COVID-19) illustrate the complexity of COVID-19 in terms of bacterial complications during viral illness and discuss the distinction between the true bacterial infection and those where antimicrobial treatment may be of limited benefit (Mumcuoğlu *et al*., 2022). The presence of diagnostic uncertainty may lead to inappropriate antibiotic prescribing, especially when the antibiotic is started without adequate microbiological data. Diagnostic stewardship then helps antimicrobial stewardship efforts by enhancing the selection of appropriate tests, the quality of samples, the interpretation of tests, and the communication of clinically-relevant results. Greater coordination between diagnostic and prescribing can help ensure timely initiation, adjustment and discontinuation of antibiotic therapy as well as limit unnecessary use of antimicrobials (Ku *et al*., 2023). The clinical ramifications of

drug-resistant bacterial infections is significant, as inadequate initial treatment can result in prolonged illness, chronic infection, higher hospitalization rate, further diagnostic testing, and higher healthcare costs. With severe infections, resistant organisms might necessitate the use of other antimicrobials that are more toxic, more expensive, or not as widely available. In situations where the pathogen is not identified promptly or there are underlying diseases, immune-suppression, or significant bacterial resistance, difficulty in treatment also increases (Alara & Alara, 2024). Moreover, it is not always possible to reliably predict resistance from clinical presentation, and microbiological confirmation and susceptibility analysis is necessary for making proper treatment decisions. The application of advanced genomic strategies could be beneficial for resistance characterization and epidemiological investigation, but it is limited by infrastructure requirements, the complexity of the analyses and the fact that there is not yet a clear connection between resistance phenotypes and the resistance markers expressed by the pathogen (Bianconi *et al*., 2023). Reliable laboratory diagnostics, antimicrobial stewardship, infection prevention and locally relevant resistance surveillance need to be integrated to meet these challenges. Resistance information may not be comparable between healthcare institutions, especially if there are differences in the microbiological testing capacity, due to differences in laboratory resources and quality control systems. Investment in lab infrastructure, human capacity building, standardized reporting and regional surveillance networks is therefore key to enhance resistance detection and facilitate evidence-based interventions (Musa *et al*., 2023). In conclusion, coordinated clinical and public health approaches are essential for the effective management of ARBIs, linking pathogen identification, susceptibility testing, antibiotic targeting and use of appropriate antibiotics, and preventive interventions (Table 4). Enhancing the relationship between diagnostic stewardship and antimicrobial stewardship provides opportunities to decrease over-treatment, aid in timely therapeutic adjustments, and maintain the clinical effectiveness of available antimicrobials (Ku *et al*., 2023) (Figure 3).

Table 4. Major Mechanisms and Clinical Implications of Antimicrobial Resistance

Resistance mechanism or concern	Clinical implication	References (APA style)
Antibiotic-inactivating enzymes	Reduced antibiotic effectiveness	(Bianconi *et al*., 2023)
Target-site modification	Reduced drug binding	(Bianconi *et al*., 2023)
Efflux and permeability changes	Reduced intracellular drug concentration	(Bianconi *et al*., 2023)
Resistance among uropathogens	Complicated empirical treatment selection	(Mekonnen *et al*., 2023)
Resistant Salmonella	Increased treatment and prevention challenges	(Nazir *et al*., 2025)
Inadequate surveillance	Delayed detection of resistance trends	(Musa *et al*., 2023)

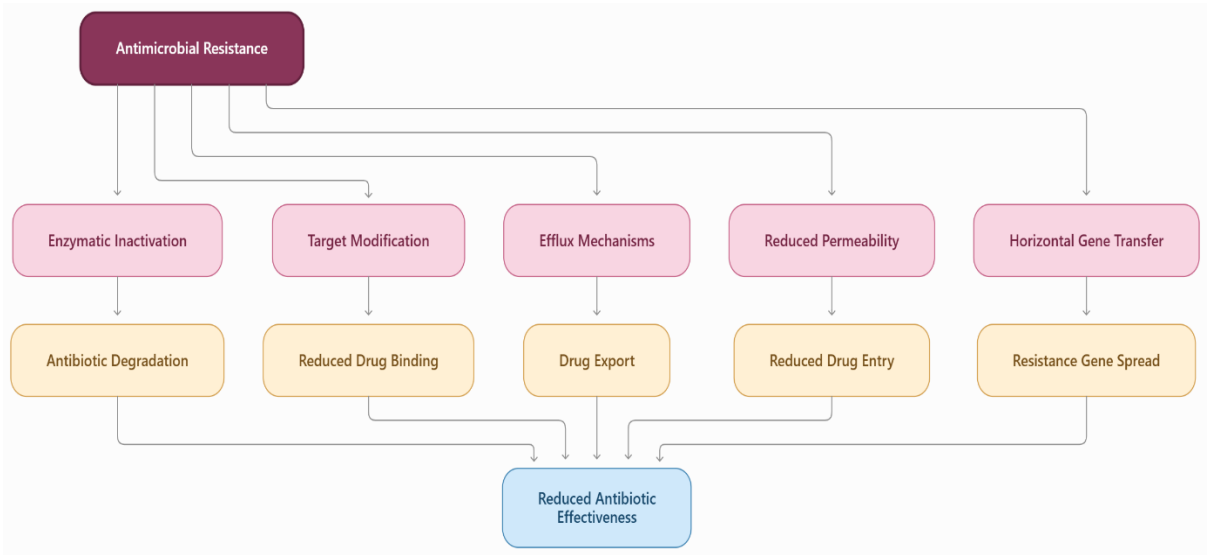

Figure 3. Molecular Mechanisms of Antimicrobial Resistance

6. Emerging Advances in Bacterial Diagnosis and Treatment

6.1. Artificial Intelligence in Clinical Microbiology

AI is proving to be a valuable resource for improving the capability of identifying bacteria, forecasting antimicrobial resistance and informing clinical decisions. The patterns identified in the microbiological data, the susceptibility data, and the patient-related data can be analysed using machine learning algorithms to identify patterns that are associated with resistant infections (Kim *et al*., 2022). The ability to integrate with automation diagnostic platforms could enhance lab efficiency, and allow more timely recognition of clinically important pathogens. Development of detection technologies for bacteria has also led to opportunities for computational analysis and enhanced interpretation of diagnostic signals (Yamin *et al*., 2023). The quality of data, representativeness of the population and external data validation, however, affect algorithm performance. Practical use of predictive tests will depend on their predictive ability, they must be easily interpreted, and they must be easily adaptable to other microbiological methods.

6.2. Rapid Molecular and Point-of-Care Diagnostics

Conventional bacterial culture and antimicrobial susceptibility testing has been complemented by significant advances in molecular and point-of-care diagnostics, that have created opportunities to minimize delays. Targeted pathogen detection

and, in some cases, identification of genetic markers associated with resistance, is possible using the techniques of polymerase chain reaction, isothermal amplification, biosensors and microfluidic platforms. New diagnostic technologies aim to improve analytical sensitivity, portability and speed, and to minimize complex laboratory requirements (Yamin *et al*., 2023). But the diagnostic sensitivity varies between different specimen properties, different targets to be detected and technical limitations. The clinical presentation and evidence of phenotypic susceptibility should be taken into account with rapid molecular findings. Appropriate reporting of accelerated diagnostic testing still needs to be done and standardised testing procedures are part of informing actions to take in relation to antimicrobial treatment (Wenzler *et al*., 2023).

6.3. Genomic Surveillance and Resistance Prediction

Genomic surveillance offers significant potential to study resistance mechanisms of bacteria, detect resistant strains in circulation, and to characterize possible transmission links. Whole genome sequencing (WGS) allows for a detailed evaluation of genetic markers associated with resistance, and can be used for molecular epidemiological studies. Evolution of Klebsiella resistance mechanisms further illustrate the clinical importance of linking molecular characterization with diagnostic interpretation and antimicrobial management (Li *et al*., 2025). Also, genomic data might contribute to the prediction of resistance by computational analysis of bacterial genome data (Jauneikaite *et al*., 2023). Resistance-associated genes, however, do not always confer phenotypic resistance, especially when gene expression and regulatory mechanisms affect the susceptibility of the antibiotic. Conventional laboratory testing is still required to support reliable clinical interpretation and effective resistance surveillance, even with the advent of genomics.

6.4. Combination Therapies & New Antibiotics

Multidrug resistant bacterial infections have become more common and have made antimicrobial agents and combination therapy more of a focus as of late. Selected resistant Gram-negative infections may have several therapeutic options with newer beta-lactam and beta-lactamase inhibitor combinations, depending on the pathogen and resistance mechanism. The guidelines for the management of carbapenem-resistant Gram-negative bacteria include microbiological identification, susceptibility testing, and the selection of the correct antibiotic for each patient (Pintado *et al*., 2023). Combination therapy is reserved for certain clinical situations and will depend on the severity of the infection, characteristics of the pathogen and the interaction of the drugs as well as on supporting clinical evidence. The use of routine combination treatment is not universally beneficial and may lead to a greater number of side-effects. Therefore, antimicrobial selection must be guided by those factors that have been demonstrated to be susceptible, exposure to the drug at the site of infection and recommended treatment guidelines.

6.5. Bacteriophage Therapy and Alternative Treatments

There has been a renewed interest in the use of bacteriophages as an alternative or complementary method for treating infections due to multidrug-resistant bacteria. Bacteriophages are virus-like particles that infect specific bacteria, and have the potential to target pathogens while not harming non-target bacteria. Other investigational strategies include anti virulent methods and antimicrobial peptides and biofilm disrupting methods. In the future, these technologies could be used alongside traditional antibiotics, especially in cases where there are no known antibiotics available. Phage-host specificity, however, bacterial resistance to phages, formulation issues, and the lack of clinical evidence confines the use to rare cases. New technologies for bacterial detection can aid in the characterization of the pathogen and the identification of therapies specifically designed to it. Clinically controlled studies are needed to determine comparative effectiveness, safety, and standard procedures.

6.6. The Management of Bacterial Infection using Precision Medicine

Precision medicine in the context of bacterial infections focuses on pathogen characteristics, antimicrobial susceptibility, severity of infection and patient-specific clinical factors to make treatment decisions that are tailored to individual patients. Advanced diagnosis technologies, which enable the combination of microbiological identification and resistance-associated molecular information, could help guide treatment selection. Special care should be taken in older people whose susceptibility to infections and treatment outcomes could be affected by other medical conditions, prior antibiotic use, physiological changes and risk factors associated with healthcare settings (Theodorakis *et al*., 2024). Individual treatment plans rely on accurate susceptibility interpretations and timely and correct antibiotic dosing (Wenzler *et al*., 2023). Clinician education, inter-professional collaboration and antimicrobial stewardship are also needed for implementation. Responsible antibiotic use and decision-making is achieved by increasing the understanding of antimicrobial resistance in the profession through structured education (World Health Organization, 2024). Together, these advances point to the promise of combining cutting-edge diagnostics, patient-specific data, and evidence-based prescriptions to enhance the care of bacterial infections (Figure 4).

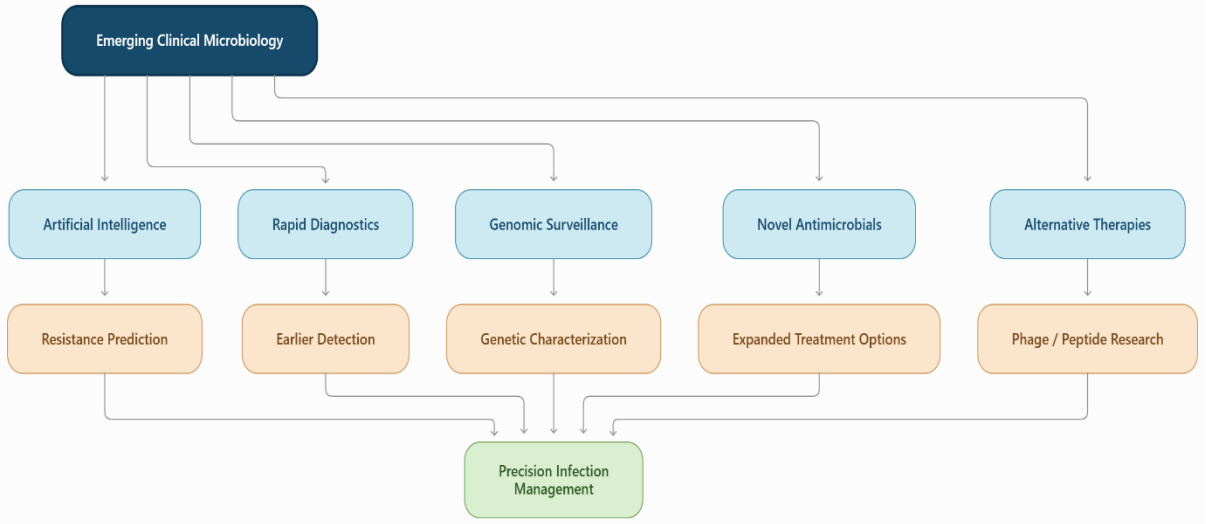

Figure 4. Emerging Technologies for Precision Management of Bacterial Infections

7. Antimicrobial Stewardship and Infection Prevention

Antimicrobial stewardship and infection prevention should be part of any multi-faceted approach to managing inappropriate antibiotic use and the prevention of HAI and the transmission of antimicrobial resistant bacterial pathogens. AMS programs promote evidence-based antibiotic choice or use, length of therapy, and ongoing review of antibiotic effectiveness. Multidisciplinary team formation, between a group of infectious disease specialists, clinical microbiologists, pharmacists, and infection control professionals is a common part of hospital-based stewardship interventions aimed at optimizing prescriptions and patient safety. Resistance containment is supported by structured interventions, such as prospective audit and feedback, antibiotic restriction policies and antibiotic treatment guidelines, which promote appropriate antimicrobial use (Giamarellou *et al*., 2023). When deciding on antibiotic use, clinical indications, likely pathogens, the severity of the infection, characteristics of the patient and local patterns of antimicrobial resistance and susceptibility should be considered. Treatment of nonbacterial infections, unnecessary broad-spectrum antibiotic treatment and prolonged courses of treatment can contribute to an upsurge in the selection pressure for the emergence of resistance. Adopting "indicated" antimicrobial treatment, rather than "empiric" treatment, will require accurate and timely identification of microbiological pathogens, and will decrease the number of unnecessary antibiotic exposures. In combination with antimicrobial stewardship practices, rapid blood culture identification technologies are useful tools for identification of bacterial pathogens and some antimicrobial resistance genes that could prove helpful to optimize antibiotic therapy sooner than later (Rhoads *et al*., 2023). In addition to infection prevention and control measures, interventions to prevent the spread of bacteria in the healthcare environment are also important. Important interventions include good hand hygiene, good environmental hygiene, and sterilisation of medical equipment, as well as evidence-based practice to prevent device-associated infection, which may include isolation. In particular, these measures are crucial in hospitals where there are numerous risk factors for the spread of resistant organisms, e.g. due to long hospital stays, repeated exposure to antimicrobials and invasive procedures (Ghafur *et al*., 2026). As well, the use of effective antibiotics, vaccines and diagnostic technologies is an important component of a comprehensive antimicrobial resistance prevention strategy, particularly in health care systems where there are substantial resource limitations (Laxminarayan *et al*., 2024). Monitoring of antimicrobial resistance allows the epidemiological data required to detect changes in bacterial susceptibility, the emergence of antimicrobial resistance patterns and to guide antimicrobial treatment recommendations at a local and national level. Standardized microbiological testing, harmonized reporting of data and standardized surveillance networks facilitate the identification of patterns of antimicrobial effectiveness and pathogen distribution in health care institutions. National antimicrobial resistance surveillance programs have proven to be effective when implemented early on, as they require active involvement of laboratories, organization of reporting and systematic monitoring of antimicrobial resistance (Thomsen *et al*., 2023). Further advances in next-generation sequencing and other genomic technologies could support surveillance efforts, allowing for the identification of resistance-associated genes, the identification of the relationships between the bacteria and assistance in investigations of potential transmission routes (Hilt & Ferrieri, 2022). AI also provides further opportunities to analyze big surveillance data, recognize emerging patterns of resistance and provide assistance in antimicrobial resistance management prediction models. The effectiveness and dependability of these use-cases rely on the representative datasets, validated algorithms, and seamless integration with existing healthcare systems (Branda & Scarpa, 2024). Amidst other settings, a One Health approach is required to address and act upon the interdependencies of human, animal, agriculture and environmental health and ecosystems in combating AMR. Use of antimicrobials in these sectors may result in selection of resistance, and there are interconnected pathways through the environment and organisms that may result in dissemination of resistant organisms and resistance genes. An integrated approach to antimicrobial resistance control will thus need coordinated interventions, including equitable access to diagnostics and vaccination, infection prevention, and antimicrobial use practices. Wider access to effective antibiotics, vaccines and diagnostic innovations need to be matched with policies to enable their responsible use and equitable access to different populations (Laxminarayan *et al*., 2024). Finally, successful antimicrobial stewardship and infection prevention will require an intertwining of clinical decision making, antimicrobial laboratory surveillance, antimicrobial

lab innovations, institutional accountability, and coordinated public health action to ensure antimicrobials remain effective and are not adversely affected by antimicrobial resistance from bacterial infections (Table 5) (Figure 5).

Table 5. Antimicrobial Stewardship and Infection Prevention Strategies

Strategy	Primary objective	Expected contribution	References (APA style)
Antimicrobial stewardship	Optimize antibiotic prescribing	Reduced inappropriate antibiotic use	(Giamarellou *et al.*, 2023)
Rapid diagnostic testing	Earlier pathogen identification	Improved treatment targeting	(Rhoads et al., 2023)
Infection prevention	Limit bacterial transmission	Reduced healthcare-associated infections	(Giamarellou *et al.*, 2023)
AMR surveillance	Monitor resistance patterns	Better public health planning	(Thomsen *et al.*, 2023)
Genomic monitoring	Characterize resistance and transmission	Improved outbreak investigation	(Hilt & Ferrieri, 2022)
One Health coordination	Address resistance across sectors	Integrated resistance prevention	(Laxminarayan *z*, 2024)

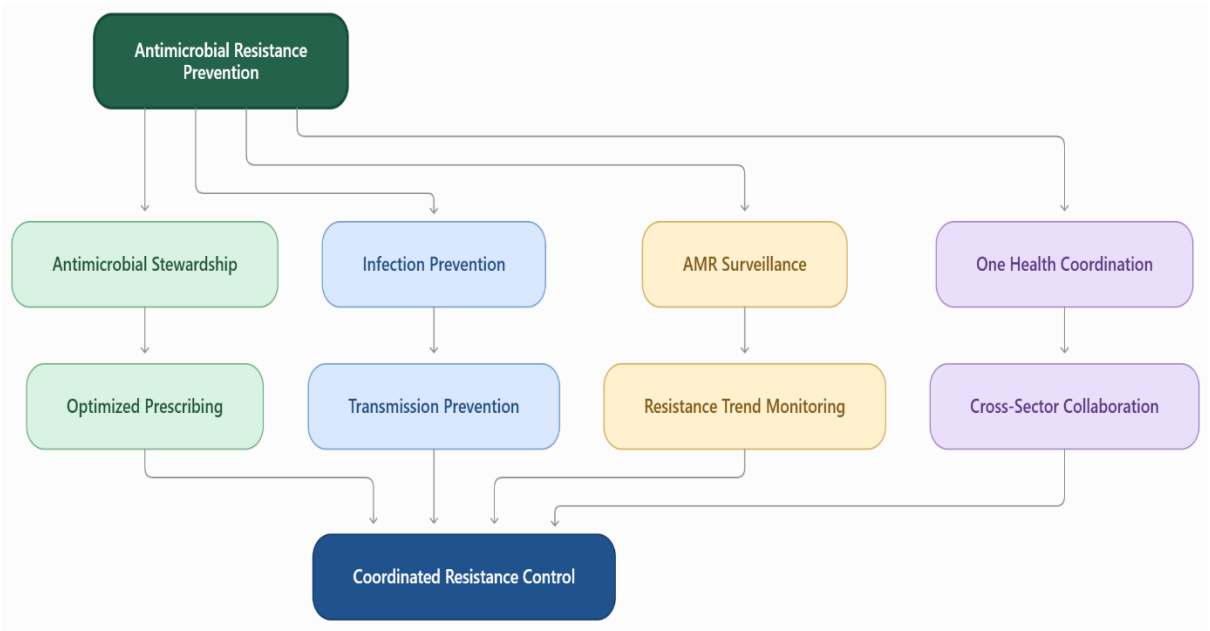

Figure 5. Integrated Antimicrobial Stewardship and Infection Prevention Framework

8. Future Directions and Research Perspectives

The need of the future is for new clinical microbiology methods to be rapid, accurate, and available for early identification of the pathogen and the detection of antimicrobial resistance. Molecular diagnostics, point of care testing and automated microbiological platforms can help to decrease diagnostic delay and facilitate prompt antibiotic selection. AI and machine learning provide further potential to analyze intricate microbiological information, forecast patterns of resistance, and make informed clinical decisions. Their use, however, demands good clinical evidence, algorithm standardization, and representative datasets to guarantee performance in various healthcare settings. Whole genome sequencing (WGS) and genomic surveillance will help enhance the description of resistance determinants, the means by which bacteria can be transmitted, and new multidrug-resistant variants. Novel antimicrobial agents, combination regimens, bacteriophage use, and antimicrobial peptides should also be investigated in future studies, for the treatment of infection with resistant pathogens. Another aspect is the personalized antimicrobial treatment that involves the incorporation of pathogen-specific susceptibility data, patient-specific information, severity of the infection and pharmacological parameters into individual therapeutic decisions. In addition, antimicrobial resistance surveillance systems at the international level need to be enhanced through laboratory network and standardisation of reporting and information sharing. One Health programs can help facilitate multi-sectoral resistance prevention. However, there are still significant hurdles to be overcome, such as costs of diagnosis, technological infrastructure, staffing capacity and access to sophisticated treatments. Multi-center clinical validation, comparative effectiveness research, cost effectiveness and implementation research should all be prioritized for future investigations to explore the utility of these emerging technologies in practice. Building partnerships between clinical microbiologists, infectious disease physicians, researchers and public health officials will be critical to realizing the use of scientific advances to ensure long-term, sustainable clinical use and better prevention and control of resistant bacterial infections.

9. Conclusion

In the context of rising antimicrobial resistance, clinical microbiology is a crucial component in the diagnosis, treatment and prevention of common bacterial infections. Proper identification of pathogens, sample collection and microbial susceptibility testing are still essential in clinical management. Although conventional microbiological methods remain the backbone of diagnostics, molecular, genomic technologies and rapid diagnostic platforms are expanding areas of opportunity for pathogen detection and speeding up treatment decisions. The selection of therapy is complicated by antimicrobial resistance, which involves various molecular mechanisms and is growing in its prevalence, due to the presence of multidrug-resistant bacterial pathogens. Good management depends on combining microbiological data with clinical evidence of antibiotic prescribing, tailoring therapy to the individual patient and on the area of antimicrobial stewardship. Efforts to prevent infection, standardised resistance monitoring and coordinated public health interventions are also crucial for reducing the spread of bacteria and maintaining the efficacy of antimicrobials. New advances in AI, precision medicine, novel antimicrobials, and alternative treatment approaches could further bolster the battery of weapons at the disposal for managing bacterial infections. But their effectiveness will rely on clinical validation, available diagnostic infrastructure, and equitable access to health care resources. Research, laboratory facilities, professional training, and cross fertilization of disciplines continue to be essential to solve current challenges in diagnosis and therapy. In conclusion, the implementation of technological innovation along with a responsible use of antimicrobial agents and a comprehensive infection prevention strategy represents a strategy of sustainability to achieve the best clinical results and the control of the spread of antimicrobial resistance.

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