

# Emerging superbugs: What clinical microbiologists need to know?

Lisa Aliberti\*

College of Agricultural and Life Sciences, University of Wisconsin-Madison, United States

**Correspondence to:** Lisa Aliberti, Department of Nutrition and Food Science, University of Maryland, Maryland, United States. E-mail: [lisaas190@gmail.com](mailto:lisaas190@gmail.com)

**Received:** 03-Sep-2025, *Manuscript No. AABID-25-171189*; **Editor assigned:** 05-Sep-2025, *Pre QC No. AABID-25-171189 (PQ)*; **Reviewed:** 11-Sep-2025, *QC No. AABID-25-171189*; **Revised:** 25-Sep-2025, *Manuscript No. AABID-25-171189 (R)*; **Published:** 28-Sep-2025, *DOI: 10.35841/aabid-9.3.210*

## Introduction

Antimicrobial resistance (AMR) has escalated into a global health crisis, threatening the effectiveness of modern medicine. Among the most alarming developments is the rise of “superbugs”—microorganisms that have acquired resistance to multiple antimicrobial agents, rendering standard treatments ineffective. For clinical microbiologists, understanding these pathogens is essential for timely diagnosis, containment, and therapeutic guidance. Superbugs are strains of bacteria, fungi, viruses, or parasites that have developed resistance to several classes of antimicrobial drugs. This resistance can arise through genetic mutations, horizontal gene transfer, or selective pressure from overuse and misuse of antibiotics in healthcare, agriculture, and community settings [1].

Timely and accurate identification of superbugs is critical to prevent outbreaks, guide therapy, and protect vulnerable populations. Traditional culture-based methods, while reliable, are often slow. Advances in molecular diagnostics have revolutionized the detection of resistance genes and mechanisms. Detect specific resistance genes (e.g., *mecA* for MRSA, *blaKPC* for CRE). Offers comprehensive insights into resistance profiles and transmission dynamics. Rapid microbial identification, though limited in resistance detection [2].

Common mechanisms include: e.g., beta-lactamases that break down penicillins and cephalosporins. Expel antibiotics from the cell. Alteration of drug-binding sites. Protects bacteria from immune responses and antibiotics. Clinical microbiologists must stay updated on emerging resistance genes like *mcr-1* (colistin resistance) and

NDM-1 (New Delhi metallo-beta-lactamase), which have global implications [3].

Healthcare settings are hotspots for superbug transmission due to high antibiotic usage and vulnerable patients. Common culprits include: Causes bloodstream infections, pneumonia, and surgical site infections. Often found in urinary tract and bloodstream infections. Associated with high mortality rates and limited treatment options. Routine screening, environmental monitoring, and strict infection control protocols are essential to contain these pathogens. Superbugs are not confined to hospitals—they are spreading globally through travel, food, water, and community transmission. Antimicrobial resistance (AMR) has escalated into a global health crisis, threatening the effectiveness of modern medicine. International surveillance programs like: These initiatives rely on data from clinical microbiology labs to track resistance trends and inform public health responses [4].

Clinical microbiologists play a vital role in antimicrobial stewardship programs (ASPs), which aim to optimize antibiotic use. Their contributions include:

Clinical microbiologists must embrace innovation while advocating for equitable access to diagnostics and therapeutics. Timely and accurate identification of superbugs is critical to prevent outbreaks, guide therapy, and protect vulnerable populations. As superbugs evolve, so must the microbiology workforce. Training programs should include: Molecular biology and genomics, Bioinformatics and data analysis, Infection control principles Communication skills for interdisciplinary collaboration [5].

## Conclusion

Enables detection of unculturable organisms and resistance genes directly from clinical samples. These tools allow for faster diagnosis and more targeted treatment, reducing empirical antibiotic use. Timely and accurate identification of superbugs is critical to prevent outbreaks, guide therapy, and protect vulnerable populations. Understanding how superbugs evade antibiotics is crucial for diagnostics and treatment.

## References

1. Deressa A, Ali A, Beyene M, et al. The status of rabies in Ethiopia: A retrospective record review. *Ethiop J Health Dev.* 2010;24(2):127-32.
2. Yimer E, Mesfin A, Beyene M, et al. Study on knowledge, attitude and dog ownership patterns related to rabies prevention and control in Addis Ababa, Ethiopia. *Ethiop Vet J.* 2012;16(2):27-39.
3. Eshetu Y, Bethlehem N, Girma T, et al. Situation of rabies in Ethiopia: A retrospective study 1990-2000. *Ethiop J Health Dev.* 2002;16:1-6.
4. Ajoke ME, Ikhide OE. Rabies—its previous and current trend as an endemic disease of humans and mammals in Nigeria. *J Exp Biol Agr Sci.* 2014;2:144.
5. Evans JS, Horton DL, Easton AJ, et al. Rabies virus vaccines, is there a need for a pan-lyssavirus vaccine. *Vaccine.* 2012;30:7447-54.