

Infection Dynamics of *Enterococcus faecium*: Understanding Pathogenicity, Resistance, and Clinical Implication

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Structured Abstract

Background: *Enterococcus faecium* is an opportunistic pathogen frequently implicated in healthcare-associated infections. Its ability to form biofilms, survive harsh conditions, and develop resistance to multiple antibiotics makes it a critical concern in hospital settings. This review aims to explore the infection dynamics of *E. faecium*, highlighting its virulence factors, antibiotic resistance mechanisms, and clinical consequences.

Methods: This review was conducted through a systematic search of peer-reviewed literature published between 2019 and 2024 from databases such as Scopus, ScienceDirect, PubMed, and SpringerLink. Articles were selected based on their relevance to the pathogenicity, resistance genes, infection outcomes, and transmission patterns of *E. faecium*.

Results: The review identifies multiple virulence factors, including *esp*, *agg*, *ace*, *gelE*, and *cyl*, which facilitate adhesion, colonisation, and tissue damage. Biofilm formation enhances resistance and immune evasion. *E. faecium* exhibits resistance to vancomycin, ampicillin, aminoglycosides, and occasionally to last-line drugs like daptomycin and linezolid, with genes such as *vanA*, *vanB*, and *pbp5* playing key roles. These genes are often located on mobile genetic elements, accelerating their spread. Clinical strains often carry a higher load of virulence and resistance genes compared to environmental strains. The organism's persistence in the gut and on hospital surfaces contributes to its successful transmission, particularly among immunocompromised individuals. The review also highlights increasing detection of multidrug-resistant (MDR) and even pan-drug-resistant (PDR) strains in both clinical and non-clinical environments.

Conclusion: *E. faecium* poses a growing threat due to its multidrug resistance, adaptability, and virulence. Its infection dynamics complicate treatment and increase morbidity in healthcare settings. There is an urgent need for improved diagnostics, antimicrobial stewardship, and development of novel therapeutic options. Adoption of a One Health approach that integrates clinical, environmental, and agricultural data is crucial to reduce transmission, especially in high-risk areas. Future research must focus on resistance gene tracking, therapeutic efficacy, and preventive measures to reduce its burden.

Keywords: *Enterococcus faecium*, Antibiotic Resistance, Virulence, Nosocomial Infection, Vancomycin-Resistant

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