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REVIEW ARTICLE OPEN ACCESS

Enterococcus Species: A Systemic Review

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Abstract

Enterococci **are gram-positive facultative anaerobes, these are commensals in the intestinal system of numerous animals, including humans. They affect hospitalized patients and cause nosocomial infections, respiratory infections, endocarditis, wound infections, UTIs, and other *enterococcal* infections. This discovery can be explained by hemolysin, gelatinase, aggregation substances, hyaluronidase, capsular polysaccharides, and cell wall carbohydrate. Various *enterococcal spp*. include *Enterococcus avium* Vancomycin resistance was acquired by enterococci throughout the antibacterial spectrum, primary antibiotic used regimen based on dual β-lactams and aminoglycosides.**

Keywords: Dual β-lactam's Aminoglycosides Resistance, *Enterococci*, Urinary Tract Infections, Bacteremia, Endocarditis Antibiotic

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INTRODUCTION

Enterococci are Gram-positive catalase-negative, non-spore-forming, facultative anaerobic lactic acid bacteria and normal inhabitants of the gut flora of humans, many different mammals, birds, fish, reptiles, amphibians and insects, as well as nematodes.[1]

Enterococci, which are gram-positive facultative anaerobes, are present commensals in the digestive tracts of numerous animals, including humans.[2] They are also present in the soil, water, dairy foods, and even plant, primarily present on the mucosal surfaces of people and animals. Because these illnesses have the potential to spread human pathogens to hospitalized patients, they are referred to as nosocomial infections.[1] UTIs and wounds in bacteremia bacteremias are all examples of *enterococci* infections. They frequently come with endocarditis, pelvic infections, and intra-abdominal infections. Otitis, sinusitis, septic arthritis, endophthalmitis, and pathogens infections of the nose, throat, and brain can also happen.[3]

Many *Enterococcus* species [105–108 colony-forming units] coexist in the wild as nosocomial pathogens and have grown in recent decades. The natural bacterial ecology in both human and animal intestines is made up of gram-positive, facultative anaerobic cocci called *Enterococcus* species. A high death rate and protracted hospitalization are two effects of enterococcal bacteraemia.[1-3] The two most common *Enterococcal spp.* that cause bacteremia is *Enterococcus faecalis* and *Enterococcus faecium*.[4]

These two *enterococci* species most frequently isolated and linked to infections contracted in hospitals are *Enterococcus faecalis* and *Enterococcus faecium*. Sequencing has been done on the genomes of *E. faecalis* and *E. faecium*.[5] There is only one VRE strain, Faecalis strain V583, that exhibits the Van B trait A pathogenicity island, several recombinant and composition -displacement, integration plasmids sequences, phage sections, a significant amount of insertion sequences and about 25 percent of the genome are mobility or extracellularly acquired DNA (IS).[6] 134 potential surface-exposed proteins that may be connected to virulence or colonization were discovered by a comprehensive genome-wide investigation.[7]

Virulence factors

Numerous *enterococci* strains that were antibiotic-resistant were first identified in the 1970s, except those that cause endocarditis infections. Up until the discovery of numerous multidrug resistances in the 1970s, *enterococci* were thought to be innocuous bacteria, except those that may cause endocarditis. There has been an increase in enterococcal nosocomial pathogens among hospitalized patients during the past 20 years.[8] These specifically happened in intensive care settings, which are conducive hosts for bacterial colonization outside of the body. UTIs occasionally lead to GIT, which can result in abdominal injury. Numerous nosocomial illnesses resulting in the production of Intent carditis bacteremia have discovered enterococcal surface protein is one of many bacterial pathogens (Esp.) gelatinase, hemolysin, aggregation substance (AS).

Hemolysin

It is a cytolytic protein that can cause lysis in both people and horses and red blood cells from rabbits. *Enterococci* strains that cause hemolysis have been demonstrated to be hazardous to animals and humans. Increased infection severity hemolysis occurrence can be recognized by exposing oneself to newly manufactured *enterococci*. Horse blood should be infused into the Beef Heart Infusion Agar along with Ove. Plates were kept at 37°C in a carbon dioxide chamber for 24 hours of incubation; distinct hemolysis zones around colonies on horse blood agar it is regarded as positive.7 Cytolysin or hemolysis-dependent regulation of expression a novel quorum sensor-based two-component regulatory system.[9]

Gelatinase

A protease produced by *enterococci* that may hydrolyze peptides such as collagen, gelatine, casein, and hemoglobin. *E. faecalis* strains that produce gelatinase have been connected to the virulence of endocarditis in animal models. By inoculating freshly made gelatine plates with enterococci on peptone yeast extract agar, incubation at 37°C Overnight, and then chilling

to room temperature for two hours, it is possible to measure the generation of gelatinase in a laboratory setting positive for the synthesis of gelatinase.[10]

Aggregation Substances

It is an *E. faecalis* pheromone-induced surface protein that promotes the development of mating aggregation during bacterial conjugation.9 Aggregation Substance (AS) effectively enhances the transfer of plasmids between enterococcal donors and recipients. Through a variety of methods, aggregation material may be involved in the development of enterococcal infection.[10] In experiments using PCR amplification it was proven that there are no asa-type genes (encoding for the aggregation ingredient). Additionally, asa1- and asa373-specific gene probes.[11]

Hyaluronidase

When K-hyaluronate was provided in a suitable agar medium, it was shown that SF68 did not produce hyaluronidase because it was not broken down. Further evidence of the gene's absence was provided by PCR and a bioinformatics search inside the SF68 genomic sequence.[12]

MSCRAMM ace

The structural and functional similarities between staphylococcal Cna adhesion and the collagen-binding adhesin generated by *enterococci*, or "ace," are striking.[12] (MSCRAMM, or microbial surface component recognizing adhesive matrix molecule). Its occurrence in pathogenic and commensal *E. faecalis* isolates.[13]

Cell wall and capsular polysaccharide

Clinical isolates of *E. faecalis* have been reported to express an operon that codes for the production of a specific type of capsular polysaccharide.[14] A 14-second experiment utilizing a mouse infection model that showed the protective efficiency of antibodies produced against this refined carbohydrate component suggested the notion that these antibodies may help prevent enterococcal infections.[15] it was discovered that pure cellular glycogen components contained residues of glycol phosphatase, fructose, or lactate.

Emergence and Dissemination Trends of Vancomycin-Resistant *Enterococci* (VRE) Strains

Vancomycin-resistant *enterococci* (VRE) have spread with unanticipated rapidity and today are steadily increasing worldwide. However, European countries and the United States (US) have experienced differences in VRE emergence and epidemiology.[16] In the 1990s, the rapid emergence of VRE observed in the US was preceded by the emergence of ampicillin-resistant *E. faecium* in the early 1980s. At the same time, in Europe, the first VRE clinical isolates were only detected in 1986.[17] Although the proliferation of VRE strains currently posing a major threat to human infection management, vancomycin is still a commonly used antibiotic to treat infections brought on by multi-resistant *enterococci.*[18]

Control of vancomycin Resistant *Enterococci*

Controlling VRE dissemination in pediatric patients requires prompt detection of VRE by microbiology laboratories, education of staff and families about VRE, use of infection control measures to prevent person-to-person VRE transmission, and prudent vancomycin use.[19]

The Public Health Impact of VRE

Historically, *E. faecalis* was responsible for the majority of all enterococcal infections (80-90%); however, in recent years, the proportion of *E. faecium* infections has surpassed that of *E. faecalis*.[20]

Other Species of *Enterococci*

E. avium

Gram-positive, catalase-negative streptococcus known as *E. avium* is frequently isolated from birds. Previously, group Q streptococcus 16 was the name for *E. avium* even though these bacteria were known to cause bacteriemia and thus had the potential to cause other chronic infections, there aren't many reports about its involvement in human illnesses.[21] Only two cases of bacterial meningoencephalitis caused by *E. avium* have been reported, both of which had a successful result but did not involve persistent otitis media.[22] This condition appears to entail a different pathogenetic mechanism than brain abscesses. Ovoid cells elongated along the chain, usually in pairs or short chains. Non-motile:

On blood or nutrient agar, surface colonies are circular, smooth, and complete. Nonpigmented: On blood agar, the majority of strains produce an alpha-reaction.[9]

E. durians

The gastrointestinal tract's natural flora includes *E. durians*. Few case reports have been documented since Sherman and Wing discovered this rare *Enterococcus* species in human pathology in 1935. This is because there are few described pathogenic factors and low virulence of *E. durians,* like other species of the *enterococcus* genus, has positive results for the group D antigen in the Lancefield classification system.[16] It is stationary and does not require mannitol as a source of energy, in contrast to *E. avium, E. raffinoses,* and other *enterococcus* species.

Amino acids and B vitamins are required for growth in synthetic media, which is nutritionally demanding. It thrives on 0.1% methylene blue milk. Growth was not observed in media containing 0.04% tellurite and 0.01% tetrazolium. H2S is not formed.[17] Figure denotes the study selection Flow chart reporting screening of the database for eligibility criteria.[18]

E. raffinoses

Enterococcus raffinose, the most mysterious of the three species discussed in this research, was just recently separated. It is negative for tellurite and arginine but positive for mannitol, sorbose, arabinose, raffinose, and pyruvate.[23] Biological Profile 2022, 11, 598, and this biochemical profile Due to 13 of the 17 species' immobility, identification is exceedingly challenging in labs lacking an automatic detection tool The potential for *E. raffinoses* to possess the vanA gene, which confers resistance to glycopeptides, has been questioned. Recent research has shown that vanA outbreaks are indeed occurring in a variety of locations, making this OE extremely hazardous to the medical community and even to the general public health.[24]

Enterococcus gallinarum

Coccoid cells, mostly in pairs or short chains. Nonmotile. Colonies on blood agar or nutrient agar are circular, smooth, and entire. Beta-hemolytic on horse blood agar.[10] Nonpigmented: Most strains do not survive 30 minutes of heating at 60°C, but do survive 15 minutes of heating at

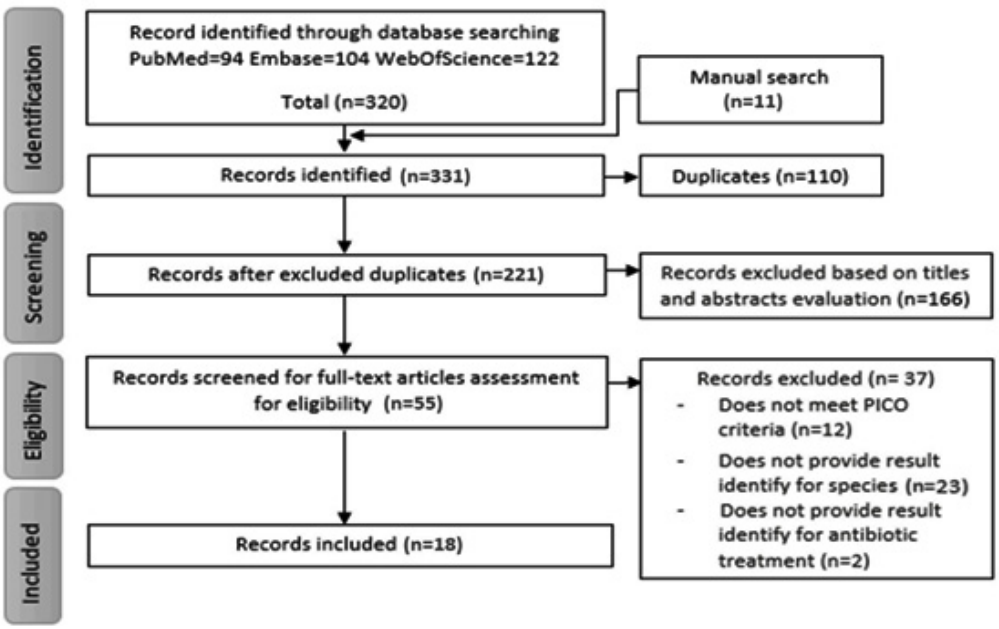

Figure. Study selection flowchart[18]

60°C.[8] At room temperature, it grows slowly on thallous acetate-tetrazolium agar, producing deep pink colonies.[10] L-arginine produces ammonia. Gelatin has not been liquefied. There is no H2S produced.[25]

Review

Holzapfel *et al*. in studied He conducted assays to determine the presence of virulence factors such as hemolysin, gelatinase, hyaluronidase, endocarditis antigen, and aggregation material Because no adhesion was seen to any of the surfaces investigated, these results supported the notion that SF68 has a very limited ability to adhere to intestinal epithelial cells. The effectiveness and safety of pharmaceutical probiotics were evaluated using *Enterococcus faecium* SF68 as a model.[26]

In 2020, Laura Herrera-Hidalgo and others, among the study types utilized in the 18 publications that were selected were randomized clinical trials (n = 1), non-randomized clinical trials (n = 1), prospective cohort studies (n = 2), retrospective cohort study (n = 9), series study (n = 5). Only 10 of them looked at several potential treatments. Outpatient (n = 4), inpatient (n = 9), and mixed (n = 5) clinical settings were used for the investigation, nine studies included continuation therapy as a therapeutic indication. Except for three research that solely addressed left-sided IE, the bulk of investigations included both left- and right-sided endocarditis. There were significant differences in the follow-up time after the antimicrobial therapy ended, ranging from no follow-up[20,27]

Similarly, in 2020 according to Sayed Hossein Mousavi *et al*., who studied the PCR results, 59 (53.2%) and 25 (22.5%) of the 111 clinical isolates were *E. faecalis* and *E. faecium,* respectively. A total of 60.3%, 56.7%, and 51.35 percent of the isolates were (HLG) & (HLS), respectively. Thirteen (48.14%), 18 (72%), and 36 (61.01%) of the HLGR isolates were non-fecal non-faecium species, *E. faecalis* respectively. Among the HLSR isolates, *E. faecalis, E. faecium,* and non-fecal non-faecium species were represented by 33 (55.93%), 16 (64%), and 14 (51.85%), respectively. Every HLGR isolate had the aac (6') Ie-aph (2'') Ia gene. 17.1% of *Enterococcus* species have high levels of ampicillin resistance overall. Ampicillin resistance rates for *E. faecalis, E. faecium*, and non-fecal non-faecium spp. 11 (40.74%), 7 (28%), and 1 (1.69%), respectively, antibiotics called aminoglycosides.[28]

Alexander *et al*. in worked on *Enterococcus raffinoses*, *Enterococcus durians*, and Isolates of *Enterococcus avium* that were collected from the Romanian tertiary-care hospital. A (retrospective) study found that he performed antibiotic sensitivity by Vitek 2 compact and obtained 658 isolates of *enterococcus* involved in humans. Of these, 319 isolates, or 48%, were excluded because they were not identified using an automated vitek system.[29] From the remaining isolates, *E. faecalis* made up 126 (37.16%), *E. faecium* 155 (45.72%), and other *enterococci* made up 58 (17.10%). The strains were selectively isolated from hospital wastewater and then identified using matrix-assisted laser desorption and ionization time-of-flight mass spectrometry. Antibiotic susceptibility testing was performed using the disc diffusion method.[30]

CONCLUSION

Hence our study highlights the significance of virulence factors that are responsible for the pathogenicity of *enterococci* species, as this led to increasing multidrug resistance accounting for more hospital-acquired infections. Since some drugs are intrinsically resistant to *Enterococci* and mobile genetic elements are used to spread resistance to other bacteria. So, detection is based on conventional gram staining and culture methods, in addition to molecular methods such as MALDI-TOF, NAAT, and PCR. In comparison to older procedures, modern ones are believed to be more dependable and sensitive; therefore, this article examines how to diagnose and treat enterococcal infections.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

AUTHORS' CONTRIBUTION

Both authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

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None.

DATA AVAILABILITY

All datasets generated or analyzed during this study are included in the manuscript.

ETHICS STATEMENT

Not applicable.

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