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Vancomycin-resistant *Staphylococcus aureus* (VRSA): resistance mechanisms and therapeutic perspectives – a literature review

Staphylococcus aureus resistente à vancomicina (VRSA): mecanismos de resistência e perspectivas terapêuticas – uma revisão bibliográfica

Staphylococcus aureus resistente a la vancomicina (VRSA): mecanismos de resistencia y perspectivas terapéuticas – una revisión bibliográfica

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Scientific article submitted in partial fulfillment of the requirements for a bachelor's degree in Biomedical Science at the Centro Universitário Instituto de Ensino Superior de Brasília (IESB), under the supervision of Prof. Thais Santana de Oliveira, MSc. Brasília, DF, 2026.

Abstract:
INTRODUCTION: Vancomycin resistance in *Staphylococcus aureus* (VRSA) represents a challenge to public health and clinical microbiology due to the reduction in therapeutic options and the dissemination of genetic determinants of resistance. In this context, this study aimed to analyze the mechanisms involved in vancomycin resistance in *Staphylococcus aureus*, with an emphasis on the role of the *vanA* operon, as well as to discuss the main therapeutic perspectives described in the literature for addressing this issue. **METHODOLOGY:** This is an integrative literature review conducted between March and April 2026 using the PubMed Central and Google Scholar databases. The descriptors *Staphylococcus aureus*, Vancomycin, Resistance, Mechanisms, and Therapeutics were combined using the Boolean operator AND. After applying the inclusion and exclusion criteria, 13 articles were selected for analysis. **RESULTS:** The studies highlighted the importance of the *vanA* operon in vancomycin resistance, which is associated with alterations in bacterial cell wall precursors that reduce the antimicrobial agent's affinity for its target. Evidence of the horizontal dissemination of resistance genes and the presence of additional mechanisms associated with antimicrobial resistance was also identified. Among the therapeutic alternatives, linezolid stood out as an option for certain infections caused by resistant Gram-positive bacteria. Furthermore, natural compounds, such as *Nigella sativa* oil, and combinations with adjuvant substances showed promising experimental results, although limitations remain regarding the clinical validation of their efficacy. **FINAL CONSIDERATIONS:** Addressing VRSA requires microbiological surveillance, the rational use of antimicrobial agents, and the strengthening of infection prevention and control measures. Further studies are needed to expand therapeutic alternatives and validate the safety and efficacy of the compounds investigated.

Keywords:
Vancomycin-resistant *Staphylococcus aureus*; Bacterial resistance; *vanA* operon; Resistance mechanisms; Antimicrobial therapy.

Resumo:
INTRODUÇÃO: A resistência do *Staphylococcus aureus* à vancomicina (VRSA) representa um desafio para a saúde pública e para a microbiologia clínica, devido à redução das opções terapêuticas e à disseminação de determinantes genéticos de resistência. Nesse contexto, o estudo teve como objetivo analisar os mecanismos envolvidos na resistência do *Staphylococcus aureus* à vancomicina, com ênfase na atuação do operon *vanA*, bem como discutir as principais perspectivas terapêuticas descritas na literatura para o enfrentamento. **METODOLOGIA:**

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Trata-se de uma revisão integrativa da literatura, realizada entre março e abril de 2026, nas bases PubMed Central, e Google Acadêmico. Foram utilizados os descritores *Staphylococcus aureus*, Vancomycin, Resistance, Mechanisms e Therapeutics, combinados pelo operador booleano AND. Após a aplicação dos critérios de inclusão e exclusão, foram selecionados 13 artigos para análise. **RESULTADOS:** Os estudos evidenciaram a importância do operon *vanA* na resistência à vancomicina, relacionada à alteração dos precursores da parede celular bacteriana, que reduz a afinidade do antimicrobiano pelo seu alvo. Também foram identificadas evidências sobre a disseminação horizontal de genes de resistência e a presença de mecanismos adicionais associados à resistência antimicrobiana. Entre as alternativas terapêuticas, a linezolida destacou-se como opção para determinadas infecções causadas por bactérias Gram-positivas resistentes. Além disso, compostos naturais, como o óleo de *Nigella sativa*, e associações com substâncias adjuvantes apresentaram resultados experimentais promissores, embora ainda existam limitações quanto à comprovação de sua eficácia clínica. **CONSIDERAÇÕES FINAIS:** O enfrentamento do VRSA requer vigilância microbiológica, uso racional de antimicrobianos e fortalecimento das medidas de prevenção e controle de infecções. Novos estudos são necessários para ampliar as alternativas terapêuticas e validar a segurança e a eficácia dos compostos investigados.

Palavras-chave:
Staphylococcus aureus resistente à vancomicina; Resistência bacteriana; Operon *vanA*; Mecanismos de resistência; Terapêutica antimicrobiana.

Resumen:
INTRODUCCIÓN: La resistencia de *Staphylococcus aureus* a la vancomicina (VRSA) supone un desafío para la salud pública y la microbiología clínica debido a la reducción de las opciones terapéuticas y la diseminación de determinantes genéticos de resistencia. Este estudio tuvo como objetivo analizar los mecanismos implicados en la resistencia de *Staphylococcus aureus* a la vancomicina, con énfasis en la función del operón *vanA*, y examinar las principales perspectivas terapéuticas descritas en la literatura. **METODOLOGÍA:** Se realizó una revisión integradora de la literatura entre marzo y abril de 2026 en PubMed Central y Google Académico. Se emplearon los descriptores *Staphylococcus aureus*, Vancomycin, Resistance, Mechanisms y Therapeutics, combinados mediante el operador booleano AND. Tras aplicar los criterios de inclusión y exclusión, se seleccionaron 13 artículos para el análisis. **RESULTADOS:** Los estudios destacaron la importancia del operón *vanA* en la resistencia a la vancomicina, asociada a la modificación de los precursores de la pared celular bacteriana, que reduce la afinidad del antimicrobiano por su diana. También se identificaron evidencias de la diseminación horizontal de genes de resistencia y de mecanismos adicionales asociados a la resistencia antimicrobiana. Entre las alternativas terapéuticas, el linezolid destacó como opción para determinadas infecciones causadas por bacterias grampositivas resistentes. Los compuestos naturales, como el aceite de *Nigella sativa*, y sus combinaciones con sustancias adyuvantes mostraron resultados experimentales prometedores, aunque su eficacia clínica aún no se ha establecido plenamente. **CONSIDERACIONES FINALES:** Abordar el VRSA requiere vigilancia microbiológica, uso racional de los antimicrobianos y fortalecimiento de las medidas de prevención y control de infecciones. Se necesitan nuevos estudios para ampliar las opciones terapéuticas y validar la seguridad y eficacia de los compuestos investigados.

Palabras clave:
Staphylococcus aureus resistente a la vancomicina; resistencia bacteriana; operón *vanA*; mecanismos de resistencia; terapéutica antimicrobiana.

Descriptors: *Staphylococcus aureus*; Vancomycin; Resistance; Mechanisms; Therapeutics.

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1. Introduction

Bacterial resistance to antimicrobial agents is one of the main challenges facing global public health. Inappropriate and indiscriminate use of these drugs favors the selection of resistant microorganisms and reduces the effectiveness of available treatments. Frequent exposure to antibiotics exerts selective pressure on bacterial populations, favoring the survival and multiplication of better-adapted strains. This contributes to higher morbidity and mortality, increased healthcare costs, and greater difficulty controlling bacterial infections, underscoring the need for surveillance strategies and new therapeutic alternatives (Li et al., 2022; Caetano; Silva, 2025).

One microorganism of clinical importance in this context is *Staphylococcus aureus*, a Gram-positive bacterium commonly found in the human microbiota, particularly on the skin and mucous membranes. It also has considerable pathogenic potential and can cause conditions ranging from skin infections to severe illnesses such as pneumonia, sepsis, osteomyelitis, and infective endocarditis. Its adaptability, virulence factors, and capacity to acquire antimicrobial resistance genes contribute to its importance in hospital-acquired infections and make certain strains harder to treat (Touaitia et al., 2025; Vivekanandan et al., 2025).

For decades, vancomycin has been one of the main treatments for severe infections caused by multidrug-resistant Gram-positive bacteria, particularly methicillin-resistant *S. aureus* (MRSA). It inhibits bacterial cell wall synthesis by interfering with proper peptidoglycan formation. Reduced susceptibility and the emergence of vancomycin-resistant *S. aureus* (VRSA), however, present a significant clinical and epidemiological problem because they compromise the effectiveness of this antimicrobial and may limit the options available for treating infections (Amer et al., 2025; Wu et al., 2021).

One mechanism involved in VRSA resistance is acquisition of the *vanA* operon, originally identified in *Enterococcus* species. Horizontal gene transfer, chiefly through bacterial conjugation, allows genetic elements containing resistance genes to move between bacterial species. Once acquired by *S. aureus*, *vanA* is associated with the production of proteins that modify vancomycin's target. In this process, the D-Ala-D-Ala terminus of peptidoglycan precursors is replaced by D-Ala-D-Lac, substantially reducing vancomycin's affinity for its target and impairing its ability to inhibit bacterial cell wall synthesis (Tao et al., 2023; Tabashsum et al., 2024).

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These resistance mechanisms present a challenge to antimicrobial therapy because they may lead to treatment failure, longer hospital stays, and higher morbidity and mortality. In response, several alternatives are being investigated and used against infections caused by resistant strains, including combinations of vancomycin with other antimicrobials. Combination therapies, antimicrobial peptides, bacteriophages, and substances that interfere with resistance mechanisms are also being studied as ways to improve treatment efficacy and address the spread of resistant strains (Davis et al., 2024; Taha et al., 2023).

This study aimed to analyze the mechanisms involved in vancomycin resistance in *Staphylococcus aureus*, with an emphasis on the role of the *vanA* operon, and to discuss the main therapeutic approaches to VRSA described in the literature.

2. Methodology

This descriptive integrative review used a structured search of PubMed Central and Google Scholar conducted between March and April 2026, with no language restrictions. Articles published in the preceding five years (2021–2026) were selected using the following terms obtained from Health Sciences Descriptors (DeCS): "*Staphylococcus aureus*," "Vancomycin," "Resistance," "Mechanisms," "Therapeutics," and "VRSA," combined with the Boolean operator AND.

Eligible articles were full-text scientific publications freely available in full, published in the preceding five years and directly related to the topic. Original studies, literature reviews, and systematic reviews were included if they addressed molecular mechanisms of vancomycin resistance in *Staphylococcus aureus*, the presence and role of the *vanA* operon, therapeutic alternatives for VRSA strains, or the clinical effects of antimicrobial resistance.

Exclusion criteria covered duplicates across databases, incomplete studies, standalone abstracts, publications unrelated to the topic or outside the defined period, material lacking adequate scientific rigor, and studies conducted exclusively in animal models.

3. Results

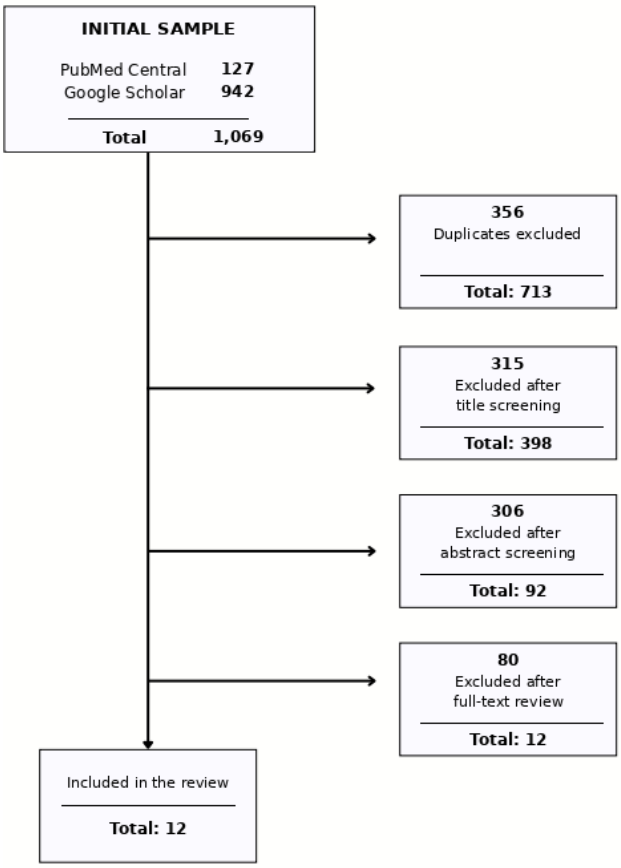
The structured search of PubMed Central and Google Scholar initially identified 1,069 studies, 127 from PubMed Central and 942 from Google Scholar. Removing 356 duplicates left 713 studies for the next stage. Title screening excluded 315 studies that were unrelated to the topic or failed to meet the selection criteria, leaving 398 articles.

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Abstract screening then excluded 306 studies, mainly because they did not directly address the molecular mechanisms of vancomycin resistance in *Staphylococcus aureus* or therapeutic approaches to VRSA, leaving 92 articles. Full-text review subsequently excluded 80 articles that failed to meet the inclusion criteria, resulting in 12 articles in the final corpus of this integrative review (Figure 1).

Figure 1 – Article selection flowchart



Source: Prepared by the author.

The 12 articles included in this review were examined for molecular mechanisms of vancomycin resistance in *Staphylococcus aureus* (VRSA), with an emphasis on the presence of *vanA* and *vanB* genes, horizontal transfer of resistance genes, and the occurrence of resistant strains in clinical samples. Therapeutic approaches to these infections were also investigated, including alternative antimicrobial agents, antimicrobial peptides, plant-derived compounds, and combinations of substances with potential antibacterial activity.

The main approaches identified in the studies were characterization of resistance mechanisms, investigation of the spread of resistant strains, and evaluation of new treatment options. Table 1 presents the article titles, authors, publication years, objectives, and results.

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Table 1 – Characteristics of the selected scientific articles by title, authors, publication year, objective, and results

Title	Year	Authors	Objective	Results
Prevalence and management of vancomycin non-susceptible *Staphylococcus aureus*: A narrative review	2026	Aroonlug Lulitanond; Aroonwadee Chanawong; Chikara Kaito	Present current data on the prevalence, resistance mechanisms, detection, and treatment of vancomycin-nonsusceptible *S. aureus*.	Vancomycin resistance varies by region, complicates treatment, and calls for therapeutic alternatives and improved detection of resistant strains.
Effect of Organic Acids and Probiotics on Methicillin and Vancomycin-Resistant *Staphylococcus aureus* Isolated from Patients in the Dhi Qar Governorate: Effect of Organic Acids and Probiotics on Methicillin and Vancomycin-Resistant *Staphylococcus aureus*	2026	Riyadh M. J. Alzamili; Hiyam A. Altaii	Determine the effectiveness of selected organic acids and probiotics in eliminating clinical isolates of methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant *Staphylococcus aureus* (VRSA).	Organic acids showed substantially greater antibacterial efficacy than probiotic therapy.
Antibacterial activity of camel milk and whey in combination with some antibiotics against vancomycin resistant *Staphylococcus aureus*	2025	Abdallah et al.	Examine the antibacterial activity of camel milk and whey combined with antibiotics against VRSA.	Camel milk is considered a promising natural product that plays a role in increasing bacterial susceptibility to some antibiotics.
Unveiling the spectrum of vancomycin resistance in *Staphylococcus aureus* from Hospital-acquired urinary tract infections (HA-UTI) in cardiac patients	2025	Asghar et al.	Investigate vancomycin resistance genes in VRSA isolates and their relationship to virulence, efflux pumps, and antimicrobial susceptibility.	*VanA*-mediated resistance in VRSA was associated with efflux pump activity and virulence gene expression. Genomic and transcriptomic studies are essential to develop effective therapies and improve infection control.
In silico evaluation of chrysin: pharmacokinetics, toxicity, and potential as an adjuvant in combating vancomycin-resistant *Staphylococcus aureus*	2024	Harika Mudumbai; Lakshmi Velaga; Sri Ramya Balijepalli	Evaluate the pharmacokinetics, toxicity, and efficacy of chrysin against MRSA and VRSA infections.	High gastrointestinal absorption, moderate blood –brain barrier permeability, and a low potential for cytochrome P450 inhibition suggested a minimal risk of drug interactions.

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Title	Year	Authors	Objective	Results
Phytocompounds from Saudi medicinal plant *Ziziphus nummularia* against vancomycin-resistant *Staphylococcus aureus* (VRSA) causing atopic dermatitis (AD)	2023	Muhammad Musthafa Poyil; Mohammed H. Karrar Alsharif	Explore the newly identified antibacterial properties of the Saudi plant *Ziziphus nummularia* for treating atopic dermatitis.	*Ziziphus nummularia* contained phytocompounds with anti-VRSA activity.
Luteolin and Vancomycin Synergistically Resisted Methicillin-Resistant *Staphylococcus aureus*	2022	Sun et al.	Investigate the *in vitro* antibacterial activity of luteolin combined with vancomycin against MRSA.	Luteolin showed *in vitro* activity against MRSA and, when combined with vancomycin, may enhance antibacterial activity, promote synergistic or additive effects, and reduce selection of resistant bacteria.
Nigella sativa oil extract: A natural novel specific conjugal transfer inhibitor of vancomycin resistance from *vanA/B*-resistant *Enterococcus faecium* to *Staphylococcus aureus*	2022	Ahmad et al.	Investigate the effect of *Nigella sativa* oil on conjugative transfer of vancomycin resistance genes from *Enterococcus faecium* to vancomycin-susceptible *S. aureus*.	Transfer of the Tn1546 transposon and its vancomycin resistance markers to VSSA was effectively inhibited in donor strains of VREtfm treated with a minimal subinhibitory concentration of *N. sativa* oil.
Detection of *vanA* and *vanB* genes among vancomycin resistant *Staphylococcus aureus* isolated from clinical samples in Baghdad hospitals	2022	Ansam Basil AbdulRazzaq; AbdulMuhsin Moslim Shami; Kais Kassim Ghaima	Identify vancomycin resistance genes (*vanA* and *vanB*) in clinical VRSA isolates from hospitalized patients in Baghdad, Iraq, using microbiological and molecular analyses.	All isolates showed vancomycin resistance associated with *vanA*, while *vanB* was present in 66.6% of cases.
Vancomycin resistance in *Enterococcus* and *Staphylococcus aureus*	2022	Gen Li; Mark J. Walker; David M. P. De Oliveira	Analyze the epidemiology and mechanisms of vancomycin resistance in *Enterococcus spp.* and *Staphylococcus aureus* and investigate therapeutic alternatives for infections caused by these resistant bacteria.	*Enterococcus spp.* and *Staphylococcus aureus* can cause severe infections and develop vancomycin resistance through genetic mechanisms and mutations. Despite the availability of therapeutic alternatives, new antibiotics and treatment strategies are needed to address growing bacterial resistance.
Antimicrobial peptides with antibacterial activity against vancomycin-resistant *Staphylococcus aureus* strains: classification, structures, and mechanisms of action	2021	Isabella Hernández-Aristizábal; Iván Darío Ocampo-Ibáñez	Review research on antimicrobial peptides (AMPs) active against vancomycin-resistant or vancomycin-intermediate *S. aureus* strains, covering their classification, origin, structural characteristics, and mechanisms of action.	Several antimicrobial peptides produced naturally by different animal and bacterial species showed *in vitro* and *in vivo* antibacterial activity against VRSA and VISA strains.

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Title	Year	Authors	Objective	Results
Safety and efficacy of linezolid treatment in comparison with vancomycin for methicillin-resistant *Staphylococcus aureus* nosocomial infection: A prospective study in Mysore City, South India	2021	MK Jayanthi; VK Jatin; Ramith Ramu	Evaluate clinical evidence for linezolid treatment in patients with MRSA infections in Mysore.	Linezolid offered the same benefit as vancomycin, with substantially fewer adverse effects.

Source: Prepared by the author.

4. Discussion

Analysis of the selected articles identified several aspects of vancomycin resistance in *Staphylococcus aureus* (VRSA), including the underlying molecular mechanisms, the spread of resistance genes, the occurrence of resistant strains in clinical samples, and the therapeutic approaches investigated in the literature. The studies highlight the importance of understanding genetic mechanisms, particularly those associated with *vanA* and *vanB*, and of seeking alternatives to address these infections.

Vancomycin is a glycopeptide antibiotic used primarily to treat severe infections caused by Gram-positive bacteria, including methicillin-resistant *Staphylococcus aureus* (MRSA). It inhibits bacterial cell wall synthesis by binding with high affinity to the terminal D-Ala-D-Ala dipeptide of peptidoglycan precursors. The emergence of vancomycin-resistant strains presents a therapeutic challenge because it compromises this antimicrobial's effectiveness (Sun et al., 2022).

Li, Walker, and Oliveira (2022) note that vancomycin resistance may be related to the acquisition of genetic determinants and to changes in bacterial mechanisms involved in the drug's action. The development of vancomycin resistance is directly linked to acquisition of resistance genes, particularly the *vanA* operon (AbdulRazzaq, Shami, and Ghaima, 2022). According to Lulitanond, Chanawong, and Kaito (2026), *S. aureus* can acquire *vanA* by horizontal transfer, often from *Enterococcus* species carrying the Tn1546 transposon. This operon modifies bacterial cell wall synthesis by replacing the D-Ala-D-Ala terminus with D-Ala-D-Lac. The change substantially reduces vancomycin's affinity for its site of action, conferring high-level resistance (Li, Walker, and Oliveira, 2022).

The importance of this mechanism was observed by AbdulRazzaq, Shami, and Ghaima (2022), who analyzed clinical isolates from hospitals and found that 100% of vancomycin-

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resistant strains carried *vanA*, whereas *vanB* was detected in 66.6% of cases. The authors showed that *vanA* was the principal determinant of established resistance and that *vanB* alone was insufficient to produce the same profile.

Asghar et al. (2025) investigated isolates from healthcare-associated urinary tract infections and linked vancomycin resistance to resistance genes, efflux pumps, and virulence factors. The review by Lulitanond, Chanawong, and Kaito (2026) also underscores the importance of epidemiological surveillance, accurate detection of resistant strains, and the search for therapeutic alternatives. Together, the studies highlight the importance of *vanA* in vancomycin resistance and the need to monitor its spread, especially in hospitals, where additional resistance and virulence mechanisms can complicate treatment.

Reduced vancomycin effectiveness has required new approaches to the clinical management of VRSA infections and the use of alternative antibiotics. The review by Lulitanond, Chanawong, and Kaito (2026) emphasizes that once reduced vancomycin susceptibility is confirmed, treatment should promptly switch to other antimicrobial agents. It identifies linezolid as a viable treatment option with good activity against resistant strains.

Jayanthi, Jatin, and Ramu (2021) demonstrated the clinical efficacy of this approach in a prospective study comparing the safety and effectiveness of linezolid and vancomycin in treating hospital-acquired infections caused by multidrug-resistant *S. aureus*. The authors found that linezolid administered orally or intravenously achieved a 100% clinical cure rate, equivalent to the efficacy expected with vancomycin, with a significantly lower incidence of severe adverse events such as thrombophlebitis and diarrhea. This evidence establishes linezolid as both a rescue antibiotic and a safer, clinically equivalent alternative in current treatment protocols.

Linezolid is an oxazolidinone antibiotic that inhibits bacterial protein synthesis, whereas vancomycin interferes with cell wall formation (Li, Walker, and Oliveira, 2022). According to Jayanthi, Jatin, and Ramu (2021), linezolid halts bacterial growth by impairing protein production and, consequently, cellular functions. It therefore offers a therapeutic alternative for certain infections caused by resistant Gram-positive bacteria, depending on the organism's susceptibility profile.

In addition to antimicrobials already used in clinical practice, the selected studies investigated substances that may interfere with the spread of resistance genes. Ahmad et al. (2022), for example, evaluated the effect of *Nigella sativa* oil on the conjugative transfer of vancomycin resistance determinants from *Enterococcus faecium* to *S. aureus*. *Nigella sativa* oil

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is an accessible natural product rich in unsaturated fatty acids and contains bioactive compounds whose antimicrobial properties have been investigated (Ahmad et al., 2022). The results indicated that transfer of the Tn1546 transposon associated with resistance genes was inhibited after donor bacteria were treated with subinhibitory concentrations of the oil.

This approach is of scientific interest because it targets a process involved in the spread of resistance rather than merely inhibiting bacterial growth. The results indicate an experimental potential to reduce horizontal gene transfer, but do not establish that the compound prevents VRSA spread among patients or in hospitals. Its potential application depends on further investigations of safety, efficacy, and feasibility under clinical conditions (Ahmad et al., 2022).

Another approach under investigation combines natural compounds with conventional antimicrobial agents to enhance antibacterial activity. Sun et al. (2022) studied luteolin combined with vancomycin against methicillin-resistant *S. aureus* (MRSA) and reported findings on the combination's antibacterial activity. Mudumbai, Velaga, and Balijepalli (2024) likewise investigated chrysin as a possible adjuvant against vancomycin-resistant *S. aureus*, including computational analyses of molecular interactions, predicted pharmacokinetic properties, and toxicity. Such results help identify candidates for further study. Computational predictions alone cannot establish therapeutic efficacy or safety in humans.

Other studies examined the antibacterial potential of *Ziziphus nummularia* phytocompounds (Poyil and Alsharif, 2023), organic acids (Alzamili and Altaii, 2026), and camel milk combined with conventional antibiotics (Abdallah et al., 2025). Although these studies broaden the scope for investigating substances with antimicrobial activity, their results should be interpreted in light of the experimental models, concentrations tested, microorganisms assessed, and outcomes observed. Antibacterial activity under laboratory conditions alone does not establish that these substances can effectively treat VRSA infections. Similarly, a combined effect is insufficient to establish synergy without appropriate methods for assessing it.

Despite promising findings, the literature reviewed has limitations that must be considered when interpreting therapeutic prospects. Some studies use *in vitro* assays to evaluate antibacterial activity under controlled conditions. Others use *in silico* approaches to predict molecular interactions and pharmacokinetic properties. Although these methods are important for identifying therapeutic candidates, they do not fully reproduce the complexity of the human body.

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Further investigations of toxicity, bioavailability, efficacy, dosage, and potential drug interactions are therefore needed, along with *in vivo* studies and clinical trials where appropriate. In summary, linezolid and other antimicrobials with proven activity against the organism and for the clinical condition under consideration are options for clinical practice. Natural compounds and adjuvant strategies remain at various stages of investigation. Advancing these approaches depends on robust evidence that establishes their effectiveness and safety and clarifies their possible role in addressing infections caused by vancomycin-resistant *S. aureus*.

5. Final considerations

This review found that vancomycin resistance in *Staphylococcus aureus* (VRSA) poses a challenge to public health and clinical microbiology, chiefly because of the acquisition of genetic resistance determinants, particularly the *vanA* operon. This mechanism changes bacterial cell wall precursors, reducing vancomycin's affinity for its target and compromising its antimicrobial activity. The potential for horizontal transfer of resistance genes further underscores the importance of monitoring these strains, especially in hospitals.

Among therapeutic approaches, the studies reviewed highlighted linezolid as an alternative for certain infections caused by resistant Gram-positive bacteria. Its use should take into account the organism's susceptibility profile and the patient's clinical condition. Promising research was also identified on natural compounds that may interfere with resistance gene transfer and substances with the potential to enhance conventional antimicrobial activity. These approaches still have limitations because a substantial share of the evidence comes from *in vitro* experiments and *in silico* analyses. Further work is needed to determine their efficacy, safety, and clinical applicability.

Biomedical scientists contribute to addressing antimicrobial resistance by performing laboratory tests, identifying resistant microorganisms, investigating genetic determinants, and carrying out quality control procedures. Their work also supports epidemiological surveillance and provides reliable laboratory information to healthcare teams and infection control services.

Further studies of resistance mechanisms, the dynamics of horizontal dissemination of van genes, and the clinical validation of adjuvant compounds are important to advance therapeutic strategies and preserve the effectiveness of antimicrobials.

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