

Epidemiology, Multidrug Resistance Patterns, and Artificial Intelligence-Driven Outcome Prediction in Vancomycin-Resistant and Vancomycin-Susceptible Enterococci: A 2020–2025 Longitudinal Cohort from Sohar Hospital, Oman

Mohan Bilikallahalli Sannathimmappa

drmohan123@gmail.com

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Mohammed Idris Qureshi

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Syeda Heyam

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Majid Al Lawati

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Tasnim Saif Alamri

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Qabas Hamood Al-harmali

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Vinod Nambiar

College of Medicine and Health Sciences, National University of Science and Technology, Sohar city, Oman

Salima Al-maqbali

Sohar Hospital, Sohar, Oman

Keywords: Vancomycin-resistant enterococci, Enterococcus faecium, multidrug resistance, antimicrobial resistance, bloodstream infection, in-hospital mortality, serum albumin, neutrophil-to-lymphocyte ratio, machine learning, Oman

Posted Date: August 10th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10589221/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Additional Declarations: No competing interests reported.

Abstract

Background. Vancomycin-resistant enterococci (VRE) are an escalating cause of healthcare-associated infection, yet regional data from the Arabian Peninsula and pragmatic outcome-prediction tools remain scarce. We characterized the epidemiology, resistance patterns and predictors of mortality of enterococcal isolates over six years at a tertiary hospital in Oman.

Methods. We analyzed 1,626 non-duplicate *Enterococcus* isolates (1,018 patients, 2020–2025). Resistance was interpreted as susceptible/intermediate/resistant; VRE was defined by vancomycin resistance or laboratory VRE flag; multidrug resistance (MDR) followed standard criteria. A chart-reviewed VRE cohort (n = 213) provided comorbidity, biomarker and outcome data for univariable and multivariable logistic regression and cross-validated machine-learning models.

Results. VRE accounted for 24.3% of isolates and rose from 1.8% (2020) to 47.4% (2025) (trend $p < 0.001$). *E. faecium* carried 73.4% of resistance. Linezolid (0.9%) and tigecycline (1.9%) retained activity. In-hospital mortality in the VRE cohort was 31.9%; low serum albumin was the only independent predictor (adjusted OR 0.86 per g/L, $p = 0.004$).

Conclusions. VRE has risen sharply in this setting, concentrated in *E. faecium*, with preserved last-line susceptibility. Routine admission biomarkers, especially albumin, and machine-learning models offer accessible mortality risk-stratification.

1. INTRODUCTION

Enterococci have evolved from commensal gut organisms into leading causes of healthcare-associated infection, owing to intrinsic resistance to many antimicrobials and a remarkable capacity to acquire and disseminate resistance determinants [1]. Antimicrobial resistance (AMR) is now among the foremost global health threats, responsible for an estimated 1.27 million deaths attributable to bacterial resistance in 2019 [2], and vancomycin-resistant *Enterococcus faecium* is designated a high-priority pathogen for which new therapeutic options are urgently required [3]. Together with methicillin-resistant *Staphylococcus aureus*, VRE remains a defining nosocomial multidrug-resistant organism whose control challenges even well-resourced health systems [4].

The pathogenesis of invasive VRE infection typically begins with dense intestinal colonisation, which precedes bloodstream invasion in vulnerable hosts [5], and hospital transmission is now well documented through genomic surveillance of hyperendemic hospital-adapted lineages [6]. Clinically, vancomycin resistance is associated with worse outcomes: meta-analysis demonstrates higher mortality in VRE than in vancomycin-susceptible enterococcal (VSE) bacteraemia [7], and contemporary cohorts confirm that vancomycin resistance independently predicts death in *E. faecium* bloodstream infection [8]. Population-based surveillance from multiple regions documents a steadily rising incidence of enterococcal bacteraemia and resistance [9], frequently paralleling glycopeptide and oxazolidinone consumption [10].

Despite this global picture, high-quality longitudinal data from the Arabian Peninsula are limited. National surveillance from the United Arab Emirates has begun to define VRE epidemiology in the Gulf [11], complemented by genomic characterisation from Saudi Arabia [12] and bibliometric mapping of priority pathogens in Bahrain [13]; broader data from the Middle East and North Africa emphasize a heavy and heterogeneous multidrug-resistant burden [14]. Robust six-year, single-centre data from Oman spanning both VRE and VSE are, to our knowledge, lacking.

Beyond epidemiology, there is growing interest in accessible tools to predict outcomes in resistant infection. Routinely available inflammatory biomarkers such as the neutrophil-to-lymphocyte ratio (NLR) reflect the balance between innate activation and adaptive immunosuppression and carry prognostic value across infective and inflammatory states [15]. In parallel, machine-learning models built on structured electronic data are increasingly applied to predict multidrug-resistant infection and its outcomes [16]. Integrating conventional epidemiology, resistance surveillance and data-driven prognostication in a single cohort may therefore yield clinically actionable insight. We accordingly analyzed a 2020–2025 cohort of vancomycin-resistant and -susceptible enterococci from Sohar Hospital, Oman, to (i) describe species distribution and resistance patterns, (ii) quantify temporal trends, and (iii) identify clinical and biomarker predictors of in-hospital mortality using classical and machine-learning approaches.

2. METHODS

2.1. Study design and setting

We conducted a retrospective longitudinal cohort study of all *Enterococcus* isolates recovered from clinical and screening specimens at Sohar Hospital, a tertiary referral centre in the North Al Batinah Governorate of Oman, between January 2020 and 2025. Records comprised patient demographics, admitting location, specimen type and date, organism identification, antimicrobial susceptibility results, and, where available, admission and discharge details.

2.2. Microbiological definitions

Organism identification and antimicrobial susceptibility testing were performed by the hospital microbiology laboratory, with results interpreted categorically as susceptible (S), intermediate (I) or resistant (R) according to contemporaneous reference breakpoints [17]. VRE was defined by a resistant vancomycin result or a laboratory multidrug-resistant-organism flag of “VRE”; VSE was defined by a susceptible vancomycin result without such a flag. Multidrug resistance was defined, consistent with international consensus criteria, as non-susceptibility to at least one agent in three or more antimicrobial categories among those tested [18]. Isolates with fewer than three tested agents were not classified for MDR.

2.3. Data cleaning and analytical cohorts

Duplicate source datasets were reconciled to a single master file. Age recorded in mixed units was standardised to years; free-text categorical fields were harmonised; and rectal screening specimens were distinguished from clinical wound specimens using the test description. Two analytical units were derived: an isolate-level dataset (all cultures) and a patient-level dataset (first isolate per patient). A separately chart-reviewed VRE cohort provided structured comorbidity, treatment-exposure, biomarker and outcome variables. In-hospital mortality was derived from documented discharge disposition.

2.4. Statistical analysis

Continuous variables are summarized as median (interquartile range, IQR) and compared with the Mann–Whitney U test; categorical variables as counts (percentages) and compared with the χ^2 or Fisher exact test, with odds ratios (ORs) estimated using the Haldane–Anscombe correction where cells were sparse. Temporal trends were assessed with the Cochran–Armitage test. Predictors of in-hospital mortality were examined by univariable and multivariable logistic regression; a parsimonious multivariable model (age, NLR, albumin) was fitted on complete cases. Predictive performance was assessed by the area under the receiver-operating-characteristic curve (AUC), including 5-fold cross-validated logistic-regression and random-forest models. Analyses used Python (pandas, SciPy, statsmodels, scikit-learn); two-sided $p < 0.05$ was considered significant.

3. RESULTS

3.1. Study population and microbiological overview

After cleaning and de-duplication, 1,626 non-duplicate *Enterococcus* isolates from 1,018 unique patients were analysed. The median age was 54.5 years (IQR 33.0–74.0), with near-even sex distribution (495 [48.7%] male). Urine (43.3%), blood (26.9%) and wound/soft-tissue specimens (17.5%) predominated, with rectal screening swabs contributing 9.6% (Table 1). Overall, 395 isolates (24.3%) from 193 patients were VRE and 916 were VSE. VRE patients were significantly older (median 66.0 vs 52.0 years; $p < 0.001$), more often male (56.8% vs 47.7%; $p = 0.033$), and predominantly inpatients (82.8% vs 38.5%; $p < 0.001$), and were over-represented among rectal screening specimens (Table 1).

Table 1

Baseline characteristics of the study cohort, overall and by vancomycin phenotype. Median (IQR) or n (%); Mann–Whitney U and χ^2 /Fisher exact tests. Patients with indeterminate vancomycin status excluded from comparison.

Characteristic	Overall (n = 1018)	VRE (n = 193)	VSE (n = 642)	p-value
N (patients)	1018	193	642	
Age, years – median (IQR)	54.5 (33.0–74.0)	66.0 (45.0–78.0)	52.0 (31.2–72.0)	< 0.001
Sex: Male, n (%)	495 (48.7)	109 (56.8)	306 (47.7)	0.033
Sex: Female, n (%)	522 (51.3)	83 (43.2)	336 (52.3)	0.033
Specimen: Blood, n (%)	274 (26.9)	29 (15.0)	187 (29.1)	< 0.001
Specimen: Urine, n (%)	441 (43.3)	48 (24.9)	310 (48.3)	< 0.001
Specimen: Rectal/screening, n (%)	98 (9.6)	96 (49.7)	0 (0.0)	< 0.001
Specimen: Wound/soft tissue, n (%)	178 (17.5)	18 (9.3)	124 (19.3)	0.002
Specimen: Catheter, n (%)	10 (1.0)	0 (0.0)	9 (1.4)	0.128
Setting: IPD, n (%)	332 (51.0)	149 (82.8)	140 (38.5)	< 0.001
Setting: OPD, n (%)	121 (18.6)	8 (4.4)	79 (21.7)	< 0.001
Setting: Emergency, n (%)	104 (16.0)	12 (6.7)	83 (22.8)	< 0.001
Setting: Referral, n (%)	85 (13.1)	5 (2.8)	62 (17.0)	< 0.001
Acquisition: Hospital, n (%)	156 (86.7)	116 (84.7)	27 (96.4)	0.129
Antimicrobials resistant, n – median (IQR)	1.0 (0.0–3.0)	0.0 (0.0–4.0)	1.0 (0.0–3.0)	0.022
Multidrug-resistant, n (%)	321 (35.0)	80 (75.5)	216 (33.6)	< 0.001

IPD, inpatient department; OPD, outpatient department; MDR, multidrug-resistant. Percentages use non-missing denominators.

3.2. Species distribution and species-specific resistance

E. faecalis predominated (49.5%), followed by unspeciatiated enterococci (27.1%) and *E. faecium* (18.9%). Vancomycin resistance was strongly species-dependent: only 1.8% of *E. faecalis* were VRE, whereas

73.4% of *E. faecium* were vancomycin-resistant; *E. gallinarum* (81.2%) and *E. casseliflavus* (80.0%) showed expected intrinsic resistance (Table 2). *E. faecium* was also markedly over-represented among rectal screening isolates (45.8%).

Table 2

Distribution of *Enterococcus* species and species-specific vancomycin resistance and specimen source (patient-level).

Species	Patients (n)	% of cohort	VRE (n)	VRE (%)	Blood (%)	Urine (%)	Rectal (%)
<i>E. faecalis</i>	504	49.5	9	1.8	22.8	51.0	0.6
<i>Enterococcus</i> spp. (unspeciated)	276	27.1	13	4.7	40.2	40.9	2.5
<i>E. faecium</i>	192	18.9	141	73.4	20.3	26.6	45.8
<i>E. gallinarum</i>	32	3.1	26	81.2	15.6	53.1	0.0
<i>E. raffinosus</i>	5	0.5	0	0.0	40.0	0.0	0.0
<i>E. casseliflavus</i>	5	0.5	4	80.0	40.0	60.0	0.0
<i>E. avium</i>	4	0.4	0	0.0	0.0	0.0	0.0

3.3. Antimicrobial resistance profile

Resistance was highest to cephalosporins and macrolide/lincosamide agents, which lack reliable enterococcal activity and serve chiefly as intrinsic-resistance controls (Table 3). Among clinically relevant agents, ciprofloxacin resistance was 67.6% and high-level gentamicin resistance 37.2%, while the last-line agents linezolid (0.9%) and tigecycline (1.9%) retained near-complete activity (Table 3). Overall, 499 of 1,303 evaluable isolates (38.3%) were multidrug-resistant. The comparative antibiogram showed VRE to be far more co-resistant than VSE across nearly all agents (Table 4, Fig. 2): ampicillin (77.6% vs 22.0%; OR 12.1), high-level gentamicin (69.0% vs 24.5%; OR 6.7), high-level streptomycin (OR 49.0) and penicillin G (OR 19.3), all $p < 0.001$. Although absolute linezolid resistance was low, it was concentrated among VRE (3.9% vs 0.1%; OR 20.3).

Table 3
Antimicrobial susceptibility profile of all Enterococcus isolates, ranked by resistance.

Antimicrobial	N tested	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Cefuroxime	95	5 (5.3)	0 (0.0)	90 (94.7)
Ceftriaxone	163	12 (7.4)	0 (0.0)	151 (92.6)
Cefotaxime	219	18 (8.2)	0 (0.0)	201 (91.8)
Clindamycin	181	19 (10.5)	0 (0.0)	162 (89.5)
Erythromycin	238	30 (12.6)	4 (1.7)	204 (85.7)
Tetracycline	51	15 (29.4)	0 (0.0)	36 (70.6)
Ciprofloxacin	1198	355 (29.6)	33 (2.8)	810 (67.6)
Co-trimoxazole	56	23 (41.1)	0 (0.0)	33 (58.9)
Penicillin G	377	197 (52.3)	0 (0.0)	180 (47.7)
Gentamicin (high-level)	312	196 (62.8)	0 (0.0)	116 (37.2)
Nitrofurantoin	42	26 (61.9)	3 (7.1)	13 (31.0)
Streptomycin (high-level)	65	45 (69.2)	0 (0.0)	20 (30.8)
Ampicillin	1299	924 (71.1)	0 (0.0)	375 (28.9)
Amoxicillin-clavulanate	867	674 (77.7)	0 (0.0)	193 (22.3)
Teicoplanin	186	148 (79.6)	1 (0.5)	37 (19.9)
Vancomycin	1113	916 (82.3)	1 (0.1)	196 (17.6)
Tigecycline	108	106 (98.1)	0 (0.0)	2 (1.9)
Linezolid	934	926 (99.1)	0 (0.0)	8 (0.9)

Table 4

Comparative antimicrobial resistance in VRE versus VSE isolates. %R among tested; ORs (95% CI, Haldane–Anscombe); χ^2 /Fisher exact p. Glycopeptide comparisons are partly definitional.

Antimicrobial	VRE %R (n/N)	VSE %R (n/N)	Odds ratio (95% CI)	p-value
Ampicillin	152/196 (77.6)	199/904 (22.0)	12.12 (8.38–17.53)	< 0.001
Amoxicillin-clavulanate	51/69 (73.9)	128/619 (20.7)	10.65 (6.05–18.75)	< 0.001
Cefotaxime	9/9 (100.0)	188/199 (94.5)	1.16 (0.06–21.18)	1.0
Cefuroxime	3/3 (100.0)	84/88 (95.5)	0.37 (0.02–8.37)	1.0
Ciprofloxacin	152/177 (85.9)	529/838 (63.1)	3.5 (2.25–5.44)	< 0.001
Clindamycin	8/8 (100.0)	142/156 (91.0)	1.73 (0.09–31.53)	1.0
Co-trimoxazole	9/10 (90.0)	20/38 (52.6)	5.72 (0.91–35.74)	0.065
Ceftriaxone	8/8 (100.0)	141/149 (94.6)	1.02 (0.05–19.22)	1.0
Erythromycin	18/21 (85.7)	175/198 (88.4)	0.71 (0.21–2.4)	0.722
Gentamicin (high-level)	60/87 (69.0)	53/216 (24.5)	6.72 (3.89–11.61)	< 0.001
Linezolid	7/180 (3.9)	1/704 (0.1)	20.27 (3.48–117.95)	< 0.001
Nitrofurantoin	7/14 (50.0)	4/23 (17.4)	4.33 (1.03–18.3)	0.063
Penicillin G	26/27 (96.3)	151/316 (47.8)	19.3 (3.67–101.47)	< 0.001
Streptomycin (high-level)	15/17 (88.2)	5/48 (10.4)	49.04 (9.87–243.73)	< 0.001
Teicoplanin	37/46 (80.4)	0/139 (0.0)	> 100 (wide CI)	< 0.001
Tetracycline	19/26 (73.1)	17/23 (73.9)	0.97 (0.28–3.31)	1.0
Tigecycline	2/61 (3.3)	0/46 (0.0)	3.91 (0.18–83.39)	0.505
Vancomycin	196/196 (100.0)	0/916 (0.0)	Definitional	—

3.4. Temporal trends, 2020–2025

The VRE proportion rose steeply and monotonically, from 1.8% in 2020 to 47.4% in 2025 (Cochran–Armitage $Z = 16.6$, $p < 0.001$; Table 5, Fig. 1), with a parallel rise in vancomycin resistance on testing (2.2% to 27.7%). Multidrug resistance remained high (28–51%) but declined modestly ($Z = -5.19$, $p < 0.001$) as screening-derived isolates grew in later years; linezolid resistance appeared sporadically from 2022 (Table 5).

Table 5

Annual trends in vancomycin resistance, multidrug resistance and linezolid resistance, 2020–2025.

Year	Isolates (n)	VRE n (%)	Vancomycin-R n/N (%)	MDR n (%)	Linezolid-R n/N (%)
2020	222	4 (1.8)	4/186 (2.2)	93 (43.9)	0/128 (0.0)
2021	123	0 (0.0)	0/106 (0.0)	58 (50.0)	0/77 (0.0)
2022	219	15 (6.8)	15/142 (10.6)	86 (42.6)	0/145 (0.0)
2023	228	35 (15.4)	32/146 (21.9)	98 (50.8)	3/154 (1.9)
2024	331	109 (32.9)	57/207 (27.5)	68 (28.3)	2/189 (1.1)
2025	489	232 (47.4)	88/318 (27.7)	92 (28.1)	3/232 (1.3)

3.5. Clinical characteristics and predictors of in-hospital mortality

In the chart-reviewed VRE cohort (n = 213), in-hospital mortality among 185 patients with a documented outcome was 31.9%. On univariable logistic regression, increasing age, higher absolute neutrophil count, higher NLR, higher C-reactive protein and higher lactate were associated with death, while higher platelet count and serum albumin were protective (Table 6, Fig. 3). In a parsimonious multivariable model, low serum albumin remained the only independent predictor (adjusted OR 0.86 per g/L, 95% CI 0.77–0.95, p = 0.004). Cross-validated machine-learning models predicted mortality with a mean AUC of 0.66 (logistic regression) and 0.63 (random forest); the multivariable logistic model reached an apparent AUC of 0.809 (Fig. 4), with age, platelets, ANC, NLR and albumin the most informative features.

Table 6

Univariable and multivariable predictors of in-hospital mortality among VRE patients (logistic regression). *Multivariable model: age, NLR, albumin; $n = 82$, 24 events; apparent AUC = 0.809. Cross-validated AUC: logistic 0.663 ± 0.033 , random forest 0.631 ± 0.125 .

Predictor	N	Unadjusted OR (95% CI)	p-value	Adjusted OR (95% CI)*	p (adj)
Age (per year)	185	1.02 (1.01–1.04)	0.004	1.01 (0.98–1.04)	0.531
WBC (per $10^9/L$)	129	1.0 (0.99–1.0)	0.652	—	—
ANC (per $10^9/L$)	129	1.1 (1.04–1.17)	0.002	—	—
NLR (per unit)	129	1.26 (1.09–1.46)	0.002	1.1 (0.87–1.39)	0.424
Platelets (per $10^9/L$)	128	1.0 (0.99–1.0)	0.018	—	—
CRP (per mg/L)	101	1.01 (1.0–1.01)	0.024	—	—
Albumin (per g/L)	85	0.83 (0.75–0.92)	< 0.001	0.86 (0.77–0.95)	0.004
Lactate (per mmol/L)	63	1.57 (1.1–2.25)	0.012	—	—
Male sex	185	1.31 (0.69–2.49)	0.403	—	—
Diabetes	98	1.07 (0.34–3.44)	0.904	—	—
Cardiovascular disease	100	0.81 (0.18–3.6)	0.778	—	—
Chronic kidney disease	79	0.49 (0.14–1.69)	0.258	—	—
Immunocompromised	83	Not estimable (separation)	—	—	—
Haemodialysis	55	1.88 (0.51–6.9)	0.344	—	—
Prior vancomycin	71	1.97 (0.6–6.43)	0.26	—	—

4. DISCUSSION

In this six-year cohort of more than 1,600 enterococcal isolates from a tertiary Omani hospital, we observed a striking escalation in vancomycin resistance, a strong concentration of resistance within *E. faecium*, preserved susceptibility to last-line agents, and a set of accessible admission biomarkers—chiefly serum albumin—that discriminated survivors from non-survivors. These findings extend the limited Arabian Peninsula literature and align with global trajectories while highlighting locally actionable priorities.

The rise in VRE from under 2% to nearly half of isolates parallels rising enterococcal resistance reported in long-term surveillance elsewhere and the well-described relationship between glycopeptide and oxazolidinone pressure and resistance. Part of this apparent rise reflects intensified active rectal

screening in later years—an interpretive caveat well recognised in outbreak and surveillance studies [19] and in neonatal and other high-risk unit experiences [20]. The over-representation of *E. faecium* among screening isolates and its dominance of resistance are consistent with the hospital-adapted, clonally expanding nature of this species documented by comparative genomics [21] and by analyses linking its accessory genome to resistance and virulence [22]. By contrast, the largely susceptible *E. faecalis* population, in which resistance clusters in high-level aminoglycoside phenotypes associated with prolonged ward stay [23], behaved as expected.

Reassuringly, linezolid and tigecycline retained near-complete activity, supporting their role as reserve agents; nonetheless, the concentration of the few linezolid-resistant isolates within the VRE group is an early-warning signal, given emerging reports of treatment failure and the importance of appropriate, often combination, therapy in *E. faecium* bloodstream infection [24], including recognised daptomycin failure without beta-lactam companionship [25]. Established risk factors for VRE—advanced age, inpatient and intensive-care exposure, comorbidity and prior antimicrobials—were mirrored in our cohort and echo contemporary risk-scoring efforts [26].

Our observation that vancomycin resistance and *E. faecium* associate with worse outcomes accords with a substantial body of evidence: enterococcal bloodstream-infection cohorts from India [27], paediatric comparisons of VRE and VSE [28], and burn-unit series [29] all report higher mortality and multidrug resistance in resistant infection, while uropathogenic enterococcal disease contributes substantially to the overall burden [30]. The 31.9% in-hospital mortality in our VRE cohort sits within this range and reinforces the clinical seriousness of these organisms.

A central and clinically translatable finding was the independent prognostic value of serum albumin. Hypoalbuminaemia integrates nutritional depletion, capillary leak and the acute-phase response, and the C-reactive-protein/albumin ratio and albumin concentration are established mortality predictors in severe sepsis [31]; although albumin supplementation trials have not consistently improved survival [32], and large fluid trials show no clear benefit over crystalloid [33], the biomarker retains strong prognostic, if not therapeutic, importance. Consistent with the wider literature, higher NLR distinguished non-survivors [34]; NLR predicts mortality both in general populations [35] and in acute infective illness [36]. Elevated lactate—an anchor of sepsis risk-stratification [37]—and inflammatory markers such as procalcitonin [38] further reflect illness severity in bloodstream infection in the critically ill [39], a population in which enterococcal bacteraemia, including in febrile neutropenia, carries substantial risk [40].

Our machine-learning models achieved moderate cross-validated discrimination (AUC ~ 0.66), comparable with pragmatic models for multidrug-resistant infection prediction and with severity scores applied to resistant non-bacteraemic infection [41]. While the apparent AUC of the compact regression model was higher, the cross-validated estimate is the more honest reflection of generalisability given the modest event count; these models are therefore hypothesis-generating and require external validation. Their value lies in demonstrating that routinely collected admission variables—age and a handful of inexpensive laboratory results—can meaningfully stratify risk without specialised genomic or proteomic

inputs. Operationally, our findings reinforce the need for robust antimicrobial stewardship [42] and for judicious use of surveillance cultures to guide empirical therapy in high-risk patients [43], within a One Health context in which resistant enterococci circulate beyond the hospital, including in the food chain [44].

LIMITATIONS

This single-centre, retrospective study is subject to incomplete documentation, particularly for outpatient and screening records; the cohort was enriched for VRE through active surveillance, so annual VRE proportions reflect both true change and evolving sampling and should not be read as crude population prevalence. Vancomycin resistance was defined phenotypically, without vanA/vanB genotyping. Biomarker completeness varied, limiting multivariable modelling to complete cases, and procalcitonin and erythrocyte-sedimentation-rate data were too sparse to analyse. Finally, outcome data were confined to in-hospital disposition.

CONCLUSION

Over 2020–2025, vancomycin resistance among enterococci at this Omani tertiary centre rose sharply and became concentrated in *E. faecium*, while linezolid and tigecycline retained near-complete activity. Nearly one-third of patients with VRE infection died in hospital, and readily available admission biomarkers—most notably serum albumin, together with the neutrophil-to-lymphocyte ratio, lactate and platelet count—discriminated survivors from non-survivors and drove interpretable machine-learning risk models. These data argue for strengthened surveillance, targeted stewardship and prospective, externally validated prediction tools built on routinely collected clinical variables.

Declarations

Ethics approval and consent to participate.

This study was conducted in accordance with the Declaration of Helsinki and approved by the institutional research and ethics committee of Sohar Hospital, Ministry of Health, Oman [approval number to be inserted]. Because the study was a retrospective analysis of anonymised, routinely collected laboratory and clinical data, the requirement for individual informed consent was waived by the committee.

Consent for publication.

Not applicable; the manuscript contains no individually identifiable data.

Competing interests.

The authors declare that they have no competing interests.

Funding.

This research received no specific grant from any funding agency in the public, commercial or not-for-profit sectors.

Author Contribution

Mohan B. Sannathimmappa: Conceptualization, Methodology, Software, Formal analysis, Data curation, Writing – original draft, Writing – review & editing, Supervision, Project administration. Mohammed Idris Qureshi: Investigation, Data curation, Writing – Original Draft. Syeda Heyam: Investigation, Data curation, and Validation. Majid Al Lawati: Investigation, Data curation, Validation. Tasnim Saif Alamri: Investigation, Data curation. Qabas Hamood Al-harmali: Investigation, Data curation. Vinod Nambiar: Methodology, Validation, Writing – review & editing, Supervision. Salima Al-maqbali: Resources, Data curation, Validation, Writing – review & editing. All authors read, critically revised, and approved the final version of the manuscript and agree to be accountable for all aspects of the work.

Acknowledgement

The authors sincerely thank the staff of the Department of Microbiology, Sohar Hospital, for their assistance with isolate identification, susceptibility testing, and data retrieval. The authors also gratefully acknowledge Mr. Jaya Prakash, IT Manager, Sohar Hospital, for his invaluable support with data extraction and compilation. No person who contributed to the study meets the criteria for authorship beyond those listed.

Data Availability

The cleaned, de-identified datasets, codebook, and analytical outputs generated and analyzed during the current study are not publicly available in order to protect patient confidentiality but are available from the corresponding author on reasonable request and subject to institutional approval.

References

1. 1. Arias CA, Murray BE. The rise of the Enterococcus: beyond vancomycin resistance. *Nat Rev Microbiol.* 2012;10(4):266 – 78.
2. 2. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet.* 2022;399(10325):629 – 55.
3. 3. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, et al. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. *Lancet Infect Dis.* 2018;18(3):318 – 27.

4. 4. Lucian-Daniel P, Andreea-Eliza Z, Nicoleta-Maricica M, Cosmin-Răducu R, Elena-Roxana MV, Alice-Crina C, et al. Methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant enterococci (VRE) in nosocomial infections: a systematic review of resistance, pathogenesis, and clinical management. *Microorganisms*. 2026;14(2):428.
5. 5. Taur Y, Xavier JB, Lipuma L, Ubeda C, Goldberg J, Gobourne A, et al. Intestinal domination and the risk of bacteremia in patients undergoing allogeneic hematopoietic stem cell transplantation. *Clin Infect Dis*. 2012;55(7):905 – 14.
6. 6. Gouliouris T, Coll F, Ludden C, Blane B, Raven KE, Naydenova P, et al. Quantifying acquisition and transmission of *Enterococcus faecium* using genomic surveillance. *Nat Microbiol*. 2021;6(1):103 – 11.
7. 7. Prematunge C, MacDougall C, Johnstone J, Adomako K, Lam F, Robertson J, et al. VRE and VSE bacteremia outcomes in the era of effective VRE therapy: a systematic review and meta-analysis. *Infect Control Hosp Epidemiol*. 2016;37(1):26–35.
8. 8. Graziani L, Giani T, Farese A, Di Lauria N, Mantengoli E, Riccobono E, et al. Vancomycin resistance predicts increased mortality in patients with *Enterococcus faecium* bloodstream infections: a six-year experience at a large tertiary care Italian hospital. *J Antimicrob Chemother*. 2026;81(4):dkag069.
9. 9. Alhothali MT, Seemann T, Andersson P, Sherry N, Silver JD, Howden OC, et al. Rising burden of enterococcal bacteremia in Victoria, Australia: population-based incidence and antimicrobial resistance trends from three decades of surveillance. *Antimicrob Agents Chemother*. 2026;70(3):e0152625.
10. 10. Li Z, Wang T, Liu B, Fan C, Lin M, Zou Y, et al. Trends in vancomycin-resistant *Enterococcus faecium* and methicillin-resistant *Staphylococcus aureus* and their association with vancomycin/linezolid consumption in a tertiary hospital in China. *BMC Infect Dis*. 2026;26(1):638.
11. 11. Thomsen J, Abdulrazzak NM, AlRand H, Menezes GA, Moubareck CA, Everett DB, et al. Epidemiology of vancomycin-resistant enterococci in the United Arab Emirates: a retrospective analysis of 12 years of national AMR surveillance data. *Front Public Health*. 2023;11:1275778.
12. 12. Almasaud LD, Alkhulaifi MM, Ghazawi A, Strepis N, Manzoor A, Senok A, et al. High-resolution genomic and molecular characterization of vancomycin-resistant enterococci from hospitalized patients in a tertiary care center in Riyadh, Saudi Arabia. *Sci Rep*. 2025;15(1):39764.
13. 13. Asokan GV, Ramadhan T, Ahmed E, Sanad H. WHO global priority pathogens list: a bibliometric analysis of Medline-PubMed for knowledge mobilization to infection prevention and control practices in Bahrain. *Oman Med J*. 2019;34(3):184 – 93.
14. 14. El Harrak K, Al Faqir I, El Ghorba EM, Amrani Souhli R, Chahid N, Arbai M, et al. Epidemiological burden of multidrug-resistant bacteria and carbapenemases in Northern Morocco: a one-year observational study. *BMC Infect Dis*. 2026;26(1):805.
15. 15. Buonacera A, Stancanelli B, Colaci M, Malatino L. Neutrophil to lymphocyte ratio: an emerging marker of the relationships between the immune system and diseases. *Int J Mol Sci*.

16. Wang H, Yang C, Zhao M, Ren F, Wang X, Yan H, et al. Comparison and validation of multiple machine learning algorithms for predicting MDRO infection in catheter-related bloodstream patients: a multicenter cohort study. *Microbiol Spectr*. 2026;14(3):e0371325.
17. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 34th ed. CLSI supplement M100. Wayne (PA): CLSI; 2024.
18. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect*. 2012;18(3):268 – 81.
19. Shimizu H, Kawada T, Osumi T, Sakai M, Yoshimoto N, Sato A, et al. Dynamic screening strategies for the control of a prolonged vancomycin-resistant enterococci outbreak: a decade-long study in a Japanese tertiary hospital. *Epidemiol Infect*. 2026;154:e50.
20. Menzato F, Bianconi I, Loss R, Aschbacher R, Pagani E, Staffler A. Vancomycin-resistant *Enterococcus faecium* in a neonatal intensive care unit in Northern Italy: lessons from an outbreak and perspectives for infection control. *Infect Prev Pract*. 2026;8(3):100549.
21. Sittiyuno C, Yingkajorn M, Chusri S, Surachat K, Chukamnerd A, Sianglum A, et al. Comparative genomics of hospital-associated vancomycin-resistant *Enterococcus faecium* from regional tertiary hospitals in Thailand. *PeerJ*. 2026;14:e21354.
22. Sonbol S, Samad LA, Al-Marzooq F, Ziko L. The interplay of specialized metabolites, antibiotic resistance, and virulence in *Enterococcus faecium*: in silico analysis of bacterial genomes. *BMC Genomics*. 2026;27(1):505.
23. Sannikova L, Misiewska-Kaczur A, Dyaczyński M, Socha B, Gogichev G, Basiak M. Correlation between surgical ward stay and high gentamicin resistance of *Enterococcus faecalis*: a retrospective study. *Antibiotics (Basel)*. 2026;15(4):394.
24. Hsu CC, Jung CJ, Yang JL, Lin CY, Huang SH, Wang JT, et al. Clinical outcomes and molecular epidemiology of vancomycin-resistant *Enterococcus faecium* bloodstream infection: the importance of appropriate therapy and ST17 predominance. *J Infect Public Health*. 2026;19(7):103274.
25. Luque Paz D, Tattevin P. Daptomycin failure in the treatment of *Enterococcus faecium* bacteremia: microbiological insights and the importance of dual therapy including beta-lactam. *Crit Care*. 2026;30(1):188.
26. Wehage P, Fuge J, Hilberink L, Vonberg RP, Kinast L, Simon S, et al. Clinical characteristics, risk factors, and outcome of enterococcal bacteraemia: assessment of the DENOVA score in a diverse patient cohort. *Infection*. 2026. Epub ahead of print. doi:10.1007/s15010-026-02856-1.
27. Prasada S, Shenoy MS, Dhanashree B, Shenoy MS, Madi DR, Bhat KG. Antibiotic resistance, risk factors, and clinical outcome of enterococcal bloodstream infection in tertiary care hospitals in coastal Karnataka, India. *Indian J Public Health*. 2026. Epub ahead of print. doi:10.4103/ijph.ijph_432_25.

28. 28. Yakin H, Acikalin B, Demir OO, Aykac K, Hazirolan G, Cengiz AB, et al. Comparison of vancomycin sensitive and resistant enterococcal infection in children. *BMC Pediatr*. 2026;26(1):468.
29. 29. Fredj H, Cheikhrouhou M, Aloui A, Alouini A, Thabet L, Messadi AA, et al. Bacteraemias due to enterococci in burns: incidence and factors associated to mortality. *Ann Burns Fire Disasters*. 2026;39(2):123 – 32.
30. 30. Korochikar SP, Mane PM, Patil SR, Shelke YP, Patil SN, Korochikar PV. Antimicrobial resistance and clinical outcomes of uropathogenic enterococcal infections in hospitalised patients. *Cureus*. 2026;18(5):e108614.
31. 31. Kim MH, Ahn JY, Song JE, Choi H, Ann HW, Kim JK, et al. The C-reactive protein/albumin ratio as an independent predictor of mortality in patients with severe sepsis or septic shock treated with early goal-directed therapy. *PLoS One*. 2015;10(7):e0132109.
32. 32. Patel A, Laffan MA, Waheed U, Brett SJ. Randomised trials of human albumin for adults with sepsis: systematic review and meta-analysis with trial sequential analysis of all-cause mortality. *BMJ*. 2014;349:g4561.
33. 33. Finfer S, McEvoy S, Bellomo R, McArthur C, Myburgh J, Norton R; SAFE Study Investigators. Impact of albumin compared to saline on organ function and mortality of patients with severe sepsis. *Intensive Care Med*. 2011;37(1):86–96.
34. 34. Islam MM, Satıcı MO, Eroglu SE. Unraveling the clinical significance and prognostic value of the neutrophil-to-lymphocyte ratio, platelet-to-lymphocyte ratio, systemic immune-inflammation index, systemic inflammation response index, and delta neutrophil index: an extensive literature review. *Turk J Emerg Med*. 2024;24(1):8–19.
35. 35. Song M, Graubard BI, Rabkin CS, Engels EA. Neutrophil-to-lymphocyte ratio and mortality in the United States general population. *Sci Rep*. 2021;11(1):464.
36. 36. Simadibrata DM, Calvin J, Wijaya AD, Ibrahim NAA. Neutrophil-to-lymphocyte ratio on admission to predict the severity and mortality of COVID-19 patients: a meta-analysis. *Am J Emerg Med*. 2021;42:60 – 9.
37. 37. Evans L, Rhodes A, Alhazzani W, Antonelli M, Coopersmith CM, French C, et al. Surviving Sepsis Campaign: international guidelines for management of sepsis and septic shock 2021. *Intensive Care Med*. 2021;47(11):1181 – 247.
38. 38. Masson S, Caironi P, Spanuth E, Thomae R, Panigada M, Sangiorgi G, et al. Presepsin (soluble CD14 subtype) and procalcitonin levels for mortality prediction in sepsis: data from the Albumin Italian Outcome Sepsis trial. *Crit Care*. 2014;18(1):R6.
39. 39. Timsit JF, Ruppé E, Barbier F, Tabah A, Bassetti M. Bloodstream infections in critically ill patients: an expert statement. *Intensive Care Med*. 2020;46(2):266 – 84.
40. 40. Tarhan MS, Özdemir YE, Çamber L, Hindilerden F, Gültürk E, Gedik H, et al. Evaluation of bloodstream infections in febrile neutropenic patients with hematological malignancy: a retrospective cohort study. *BMC Infect Dis*. 2026;26(1):1152.

41. 41. Jaber F, Rawas SE, Faraj S, Zoghby LA, Khalil JB, Abdulhalim R, et al. Value of the Pitt bacteremia score in predicting the outcome of non-bacteremic patients with infections caused by multidrug-resistant organisms. *Int J Infect Dis.* 2026. Epub ahead of print. doi:10.1016/j.ijid.2026.108960.

42. 42. Tebano G, Convertino C, Raumer L, Sgarzani R, Melandri D, Cristini F. Challenges in antimicrobial treatment and antimicrobial stewardship in hospital-acquired infections in adult burn patients. *Eur Burn J.* 2026;7(2):35.

43. 43. Závora J, Adámková V, Studená A, Kroneislová G. The role of routine surveillance cultures in optimising sepsis management in high-risk patient groups. *Pathogens.* 2026;15(1):82.

44. 44. Sallam SA, Abd-Elghany SM, Sallam KI. Extensively drug-resistant and heat-resistant *Enterococcus faecalis* and *Enterococcus faecium* in ready-to-eat meat products. *NPJ Sci Food.* 2026;10(1):117.

Figures

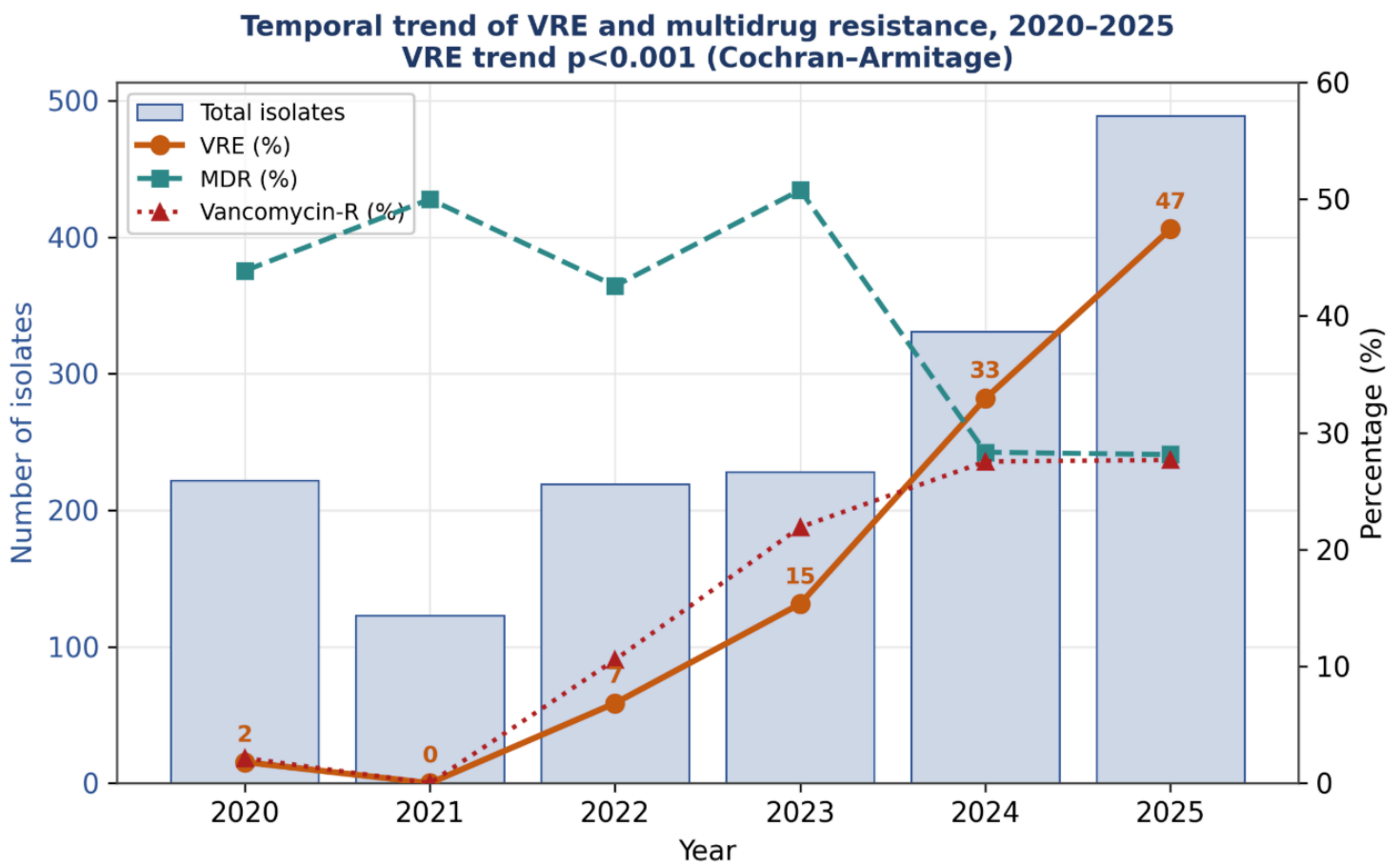


Figure 1

Longitudinal trend of total isolates (bars) and the proportion vancomycin-resistant, multidrug-resistant and vancomycin-resistant on testing (lines), 2020–2025.

Comparative resistance profile: VRE vs VSE

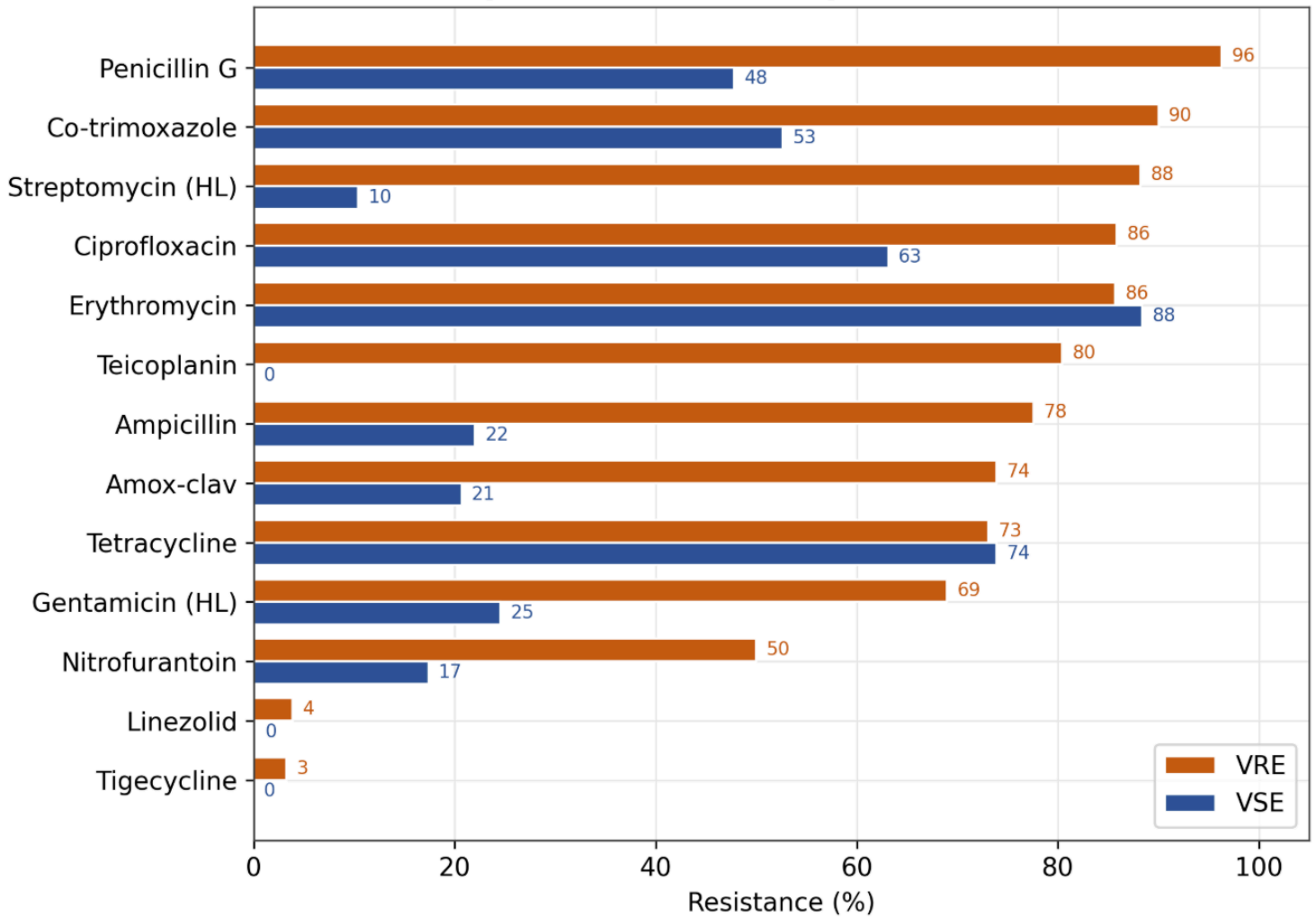


Figure 2

Comparative resistance profile of VRE versus VSE isolates across clinically relevant antimicrobials.

Admission biomarkers by in-hospital survival (VRE cohort)

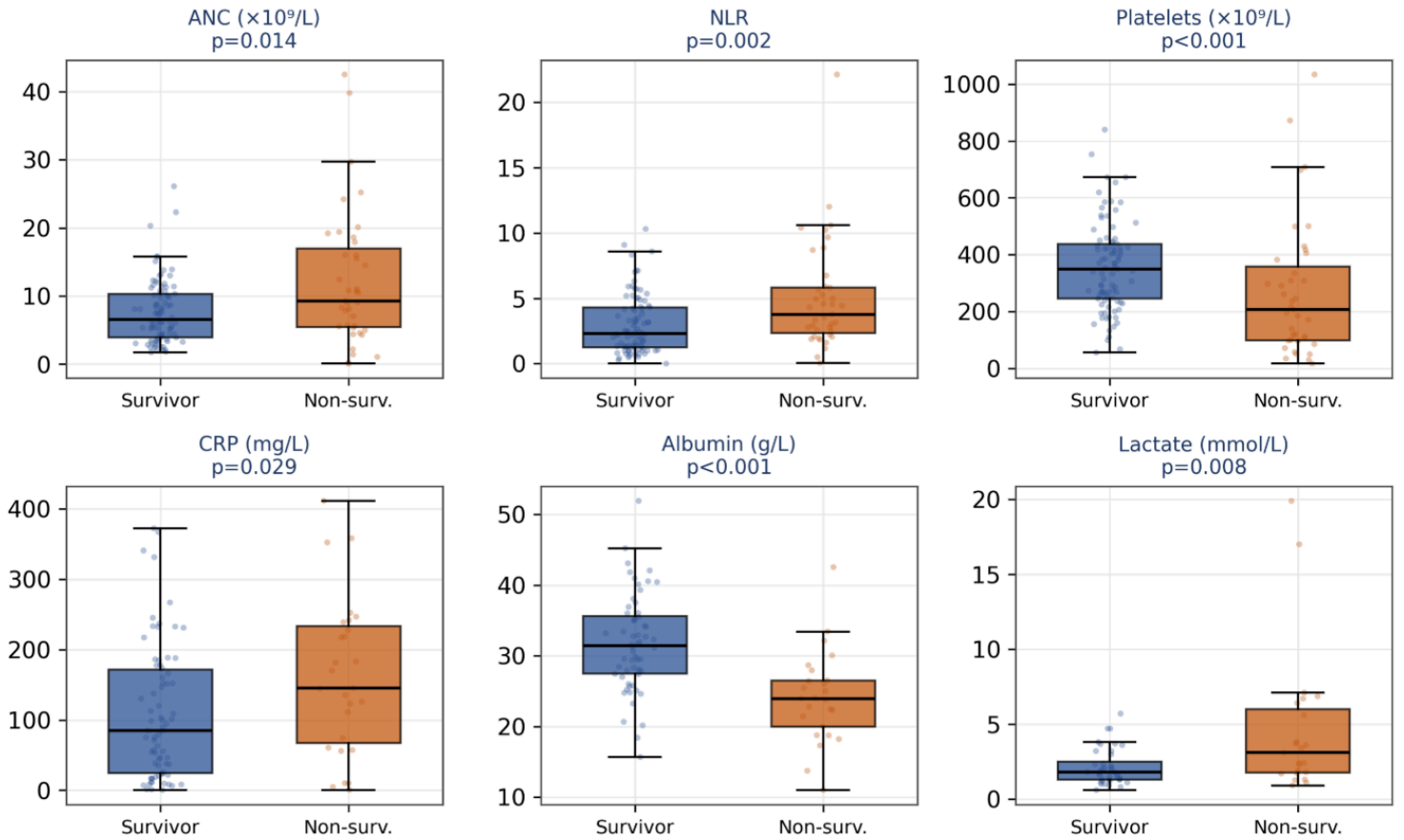


Figure 3

Distribution of admission biomarkers among survivors and non-survivors in the VRE cohort. Boxes, median and IQR; whiskers, $1.5 \times IQR$; points, individual patients; p , Mann–Whitney U .

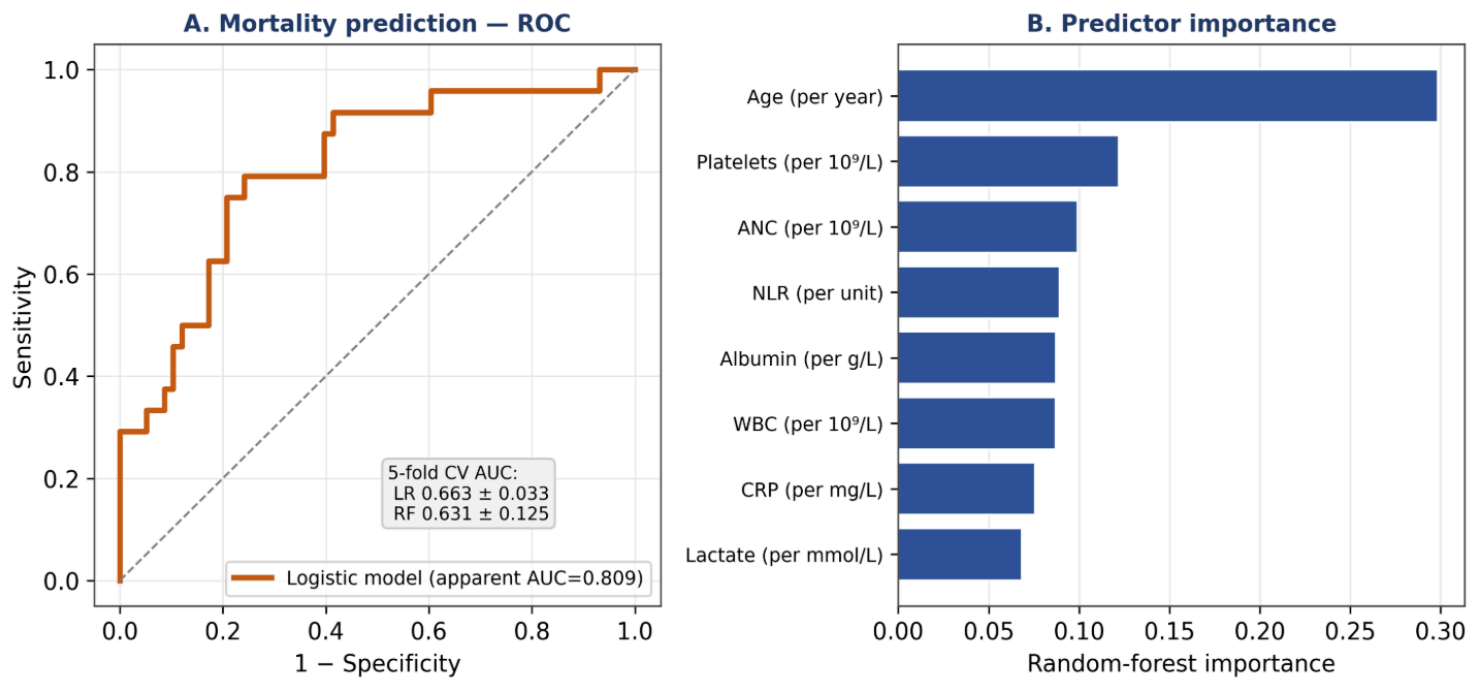


Figure 4

Prediction of in-hospital mortality. (A) ROC curve of the multivariable logistic model with cross-validated AUCs inset. (B) Random-forest predictor-importance ranking.