

Comparative Effectiveness of Single, Dual, and Multi-Antibiotic Therapies in Managing Carbapenem-Resistant *Enterobacterales*: A Systematic Review and Meta-Analysis on Survival Rates

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Abstract

Carbapenem-resistant *Enterobacterales* (CRE) represent a major global health issue, linked to elevated rates of morbidity and mortality stemming from restricted treatment alternatives. The Gram-negative bacteria, such as *Klebsiella pneumoniae* and *Escherichia coli*, are significant contributors to severe infections, including bacteremia, pneumonia, and urinary tract infections. Mechanisms of resistance such as the production of carbapenemases, the action of efflux pumps, and mutations in porins diminish the effectiveness of carbapenems, which are frequently the antibiotics of last resort. In light of this escalating concern, the absence of a universally recognized global guideline for the management of CRE results in diverse treatment strategies. This systematic review and meta-analysis aimed to evaluate the effectiveness of monotherapy, dual therapy, and multi-antibiotic regimens in the treatment of CRE infections. In accordance with established guidelines, data from 5 major databases were analyzed, and the quality of the studies was evaluated using the Newcastle-Ottawa Scale. The findings indicated that combination therapy led to a notable enhancement in survival rates when contrasted with monotherapy (OR = 0.69, 95 % CI 0.62 - 0.78, $p < 0.00001$). In contrast, no significant difference was found between dual therapy and multi-antibiotic regimens (OR = 1.17, 95 % CI 0.95 - 1.46, $p = 0.15$). The combination therapy exhibited synergistic effects, improving bacterial eradication while reducing the emergence of resistance. Dual therapy demonstrated superior outcomes when contrasted with multi-antibiotic regimens, presenting lower toxicity risks and enhanced patient adherence. Nonetheless, the absence of stratification considering resistance mechanisms, infection severity, and patient characteristics highlights the necessity for tailored treatment strategies. In conclusion, this study emphasizes the critical necessity for internationally standardized protocols for CRE management to guarantee uniform and effective treatment. Future investigations should concentrate on resistance profiling, assessing the safety and cost-effectiveness of dual and multi-antibiotic regimens, and customizing therapies to individual patient factors to enhance outcomes.

Keywords: Antibiotic, Combination therapy, *Enterobacterales*, Monotherapy, Survival rate

Introduction

Infections caused by *Enterobacterales* represent a significant global health issue, particularly due to the prevalence of carbapenem-resistant *Enterobacterales*. *Enterobacterales*, an ordo of gram-negative bacteria, is associated with several diseases in humans and animals, such as bacteremia, pulmonary infections, and urinary tract infections [1]. Carbapenem-resistant *Enterobacterales* (CRE) have emerged as a substantial public health

concern, causing significant morbidity and mortality in hospital settings [2,3]. A meta-analysis revealed a global prevalence of carbapenem-resistant *Enterobacterales* (CRE) at 43.06 %, with *Klebsiella pneumoniae*, *Escherichia coli*, and *Enterobacter cloacae* as the predominant species [4]. A further analysis revealed carbapenem resistance in 31.4 % of *Escherichia coli* and 25.8 % of *Klebsiella pneumoniae* isolates [5]. Infections caused by

Enterobacteriales are prevalent in children, with *Escherichia coli* representing 47.69 % of cases, followed by *Salmonella* at 24.62 % and *Klebsiella* at 15.38 % [6]. Urinary tract infections were the predominant symptoms in both adults and children [5,6].

Infections caused by carbapenem-resistant *Enterobacteriales* (CRE) are linked to markedly elevated death rates in contrast to infections from carbapenem-susceptible *Enterobacteriales* (CSE), attributable to restricted treatment alternatives [7-10]. CRE infections provide a 3.39-fold increased risk of total death compared to CSE infections [9]. Carbapenems are last-resort antibiotics extensively employed to address bacterial infections caused by extended-spectrum β -lactamase (ESBL)-producing *Enterobacteriales*. Consequently, if a bacterial strain exhibits resistance to this antibiotic, it will pose significant challenges [11]. *Klebsiella pneumoniae* and *Escherichia coli* are the principal etiological agents of CRE infections, employing resistance mechanisms including enzyme production, efflux pumps, and porin mutations [12,13]. Carbapenemases encompass KPC, MBLs, and OXA-48-like enzymes that disseminate rapidly via plasmids [13].

The fast worldwide proliferation of carbapenemase-producing *Enterobacteriales* needs immediate investigation to identify effective treatments [2,13]. Current therapy comprise polymyxins, tigecycline, fosfomicin, and aminoglycosides [8]. Combination treatment of 2 or more pharmacological agents has demonstrated enhanced efficacy relative to monotherapy [14]. For carbapenem-resistant Enterobacteriaceae (CRE) with carbapenem minimum inhibitory concentrations (MICs) ≤ 8 mg/L, the combination of carbapenems with colistin, high-dose tigecycline, or aminoglycosides may be efficacious [15]. Recently introduced antibiotics, including ceftazidime-avibactam, meropenem-vaborbactam, plazomicin, and eravacycline, provide supplementary alternatives for the treatment of CRE [7,8]. Additional interesting pharmaceuticals under research are imipenem-relebactam and cefiderocol [8]. Strategies to address CRE including repurposing existing antibiotics, combining antibiotic therapies, or are seen as viable approaches in [13]. Treatment techniques must be tailored according to resistance mechanisms, susceptibility profiles, illness severity, and patient characteristics [7,8].

To address the lack of a widely recognized world-wide protocol for the management of carbapenem-resistant *Enterobacteriales* (CRE) infections, considering their considerable global health impact and correlation with elevated morbidity and death rates. This study aims to assess the relative efficacy of monotherapy, dual therapy, and multiple antibiotic regimens as reported in observational studies, offering essential insights into treatment alternatives customized to CRE infection as a consideration in the clinical setting.

Materials and methods

Study methodology

This meta-analysis and systematic review were performed following the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. The protocol for this review has been registered in PROSPERO under ID Number CRD42024629626. The independent variable consisted of the type of antibiotic therapy (dual-antibiotic or multi-antibiotic therapy compared to single-antibiotic therapy), whereas the dependent variable was the survival rates of patients with CRE infections.

Eligibility criteria

The inclusion criteria were established utilizing the PICOS framework. The criteria for study inclusion are as follows: (1) the population comprises patients with Carbapenem-Resistant *Enterobacteriales* (CRE) infections; (2) the intervention entails dual-antibiotic therapy and multi-antibiotic therapy; (3) comparator groups consist of populations receiving single antibiotic therapy; (4) outcome measures focus on survival rates; (5) the study design is observational studies. The exclusion criteria are: (1) irrelevant outcomes; (2) insufficient data; and (3) irretrievable studies.

Data sources and search strategies

The literature search was conducted on December 14, 2024, utilizing the following databases: PubMed, Cochrane CENTRAL, ScienceDirect, Scopus, and EBSCOhost. Search keywords were developed in line with the MeSH (Medical Subject Headings) browser and integrated using Boolean operators. The keywords used included: ("*Enterobacteriales*" OR "*Enterobacteriaceae*" OR "*Escherichia coli*" OR "*Proteus mirabilis*" OR *Enterobacter* OR "*Serratia marcescens*" OR

“*Citrobacter*” OR “*Klebsiella*”) AND (“ESBL” OR “Beta lactamase” OR “ β -lactamase”) AND (“Monotherapy” OR “Mono” OR “Combination”) AND (“Antibiotic”) AND (“Cohort” OR “Case control” OR “Retrospective” OR “Observational”) AND (Survive OR Survival OR Died OR Mortality OR Death). The search details for each database can be seen in **Table S1**.

Study selection results

Three independent reviewers (MFH, DEP and SAA) will apply the eligibility criteria and select studies for inclusion in the systematic review and meta-analysis. All studies from databases were collected in Rayyan.ai (Rayyan Systems Inc., Doha, Qatar). All collected articles were screened for year, title, and abstract by 3 independent reviewers after duplicates were removed. Each reviewer will independently screen the titles and abstracts of identified records and select potentially relevant studies. Full texts of these potentially relevant studies will then be retrieved and independently assessed for eligibility by both reviewers. The reviewers will be blinded to each other’s decisions during this process. Any disagreements between the reviewers during the study selection process will be resolved through discussion until consensus is reached. If consensus cannot be reached, a fourth reviewer (ES) will be consulted.

Data extraction

The data obtained from the chosen studies comprised the author’s name and publication year, sample size in the intervention group, sample size in the control group, age, treatment regimens, type of infection, type of bacteria, and duration of observation. Survival rate data were extracted for each study.

Study quality and risk of bias

The studies obtained were subsequently evaluated for quality and risk of bias. Fifty-one studies were evaluated utilizing the Newcastle-Ottawa Score (NOS). Bias assessment encompasses 3 primary domains: selection, comparability, and outcome in cohort studies, as well as exposure in case-controlled studies. Each domain comprises multiple criteria, with a maximum score of 9 points representing the highest quality. Selection, scoring up to 4 points, evaluates the representativeness of research groups and the participant selection method. This includes assessing the representativeness of cases

or exposed groups, the source of controls, and the validation of exposure through reliable data. Comparability, with a scoring range of up to 2 points, assesses the extent to which the study addresses confounding variables. Points are awarded for the consideration of relevant factors that may impact the study’s findings, facilitating a balanced comparison. The outcome or exposure, which can receive a maximum of 3 points, evaluates the quality of outcome assessment in cohort studies or exposure ascertainment in case-control studies. This includes considerations of follow-up adequacy, consistency in outcome measurement, and bias reduction. Research exhibiting elevated NOS scores, reaching a maximum of 9 points, is deemed to possess a reduced risk of bias and enhanced methodological quality.

Quantitative data synthesis (meta-analysis)

Statistical analysis was conducted using Review Manager 5.4.1. (Nordic Cochrane Center, The Cochrane Collaboration, Copenhagen, Denmark). We will use a random-effects meta-analysis to combine individual study data, given the likely clinical and methodological diversity among the included studies. This approach assumes that the true effect size varies from study to study and provides a more conservative estimate of the effect size and its confidence interval.

The type of data used is dichotomous and the outcomes will be synthesized using odds ratio (OR) with a 95 % Confidence Interval (CI). If heterogeneity is low, the meta-analysis forest plot will use a fixed effect model. The I^2 statistic will be calculated to evaluate the degree of heterogeneity, ranging from 0 to 100 %, indicating the extent of heterogeneity from none to high. Typically, an I^2 value greater than 50 % indicates moderate to high heterogeneity. Meta-regression towards age was conducted using Comprehensive meta-analysis v3.

Results and discussion

Study selection and quality assessment

After the search process in 5 databases, 1,023 articles were collected. A total of 267 duplicate articles, were removed. leaving 756 articles for manual selection based on title and abstract. A total of 532 articles were excluded because they met the exclusion criteria or did not meet the inclusion criteria by reading the title and abstract. This left 224 articles to be accessed but only 84

articles that can only read in full-text for the comprehensive assessment. A total of 28 articles had irrelevant outcome and insufficiency data in 5 articles. The final re-

sults were 51 studies, which were included in the quantitative synthesis. The flow of article searches and study selection can be seen in the PRISMA 2020 diagram in **Figure 1**.

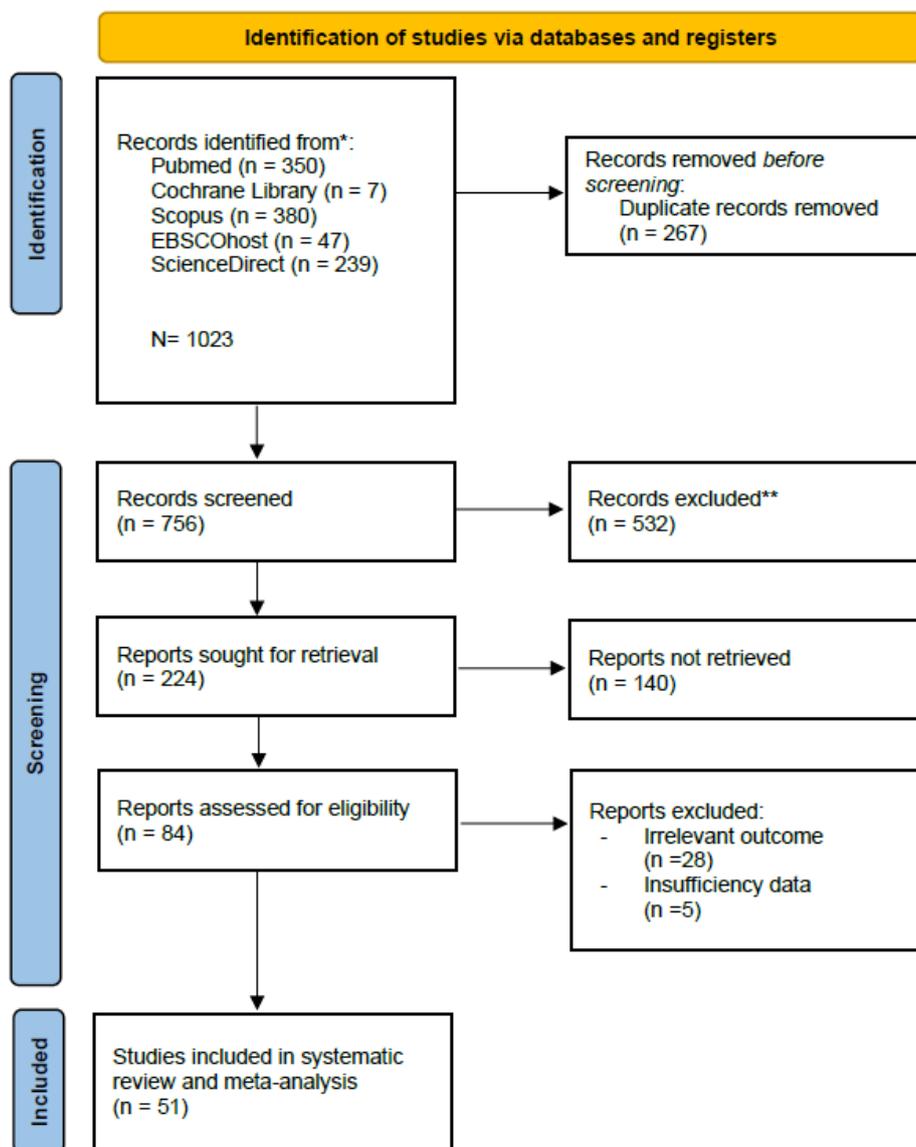


Figure 1 Prisma 2020 diagram.

According to **Figure 2**, the predominant overall score among studies is 8, with 9 being the second most prevalent score. A limited number of studies indicate scores of 6 and 7. Research with elevated scores (8 - 9) exhibits a decreased risk of bias, as it reflects more robust selection methodologies, enhanced comparability among groups, and more explicit result reporting. Research with lower scores (6 - 7) may exhibit an elevated risk of bias (moderate risk of bias), possibly because to

insufficient control of confounding factors or methodological deficiencies. The majority of research in this study exhibits low to moderate bias risk, suggesting that their results are generally trustworthy; nevertheless, certain studies may necessitate more careful interpretation. Thirty-seven inclusion studies demonstrated a low risk of bias, while the remaining studies exhibited a moderate risk of bias. This suggests that the evidence quality in this review is relatively high.

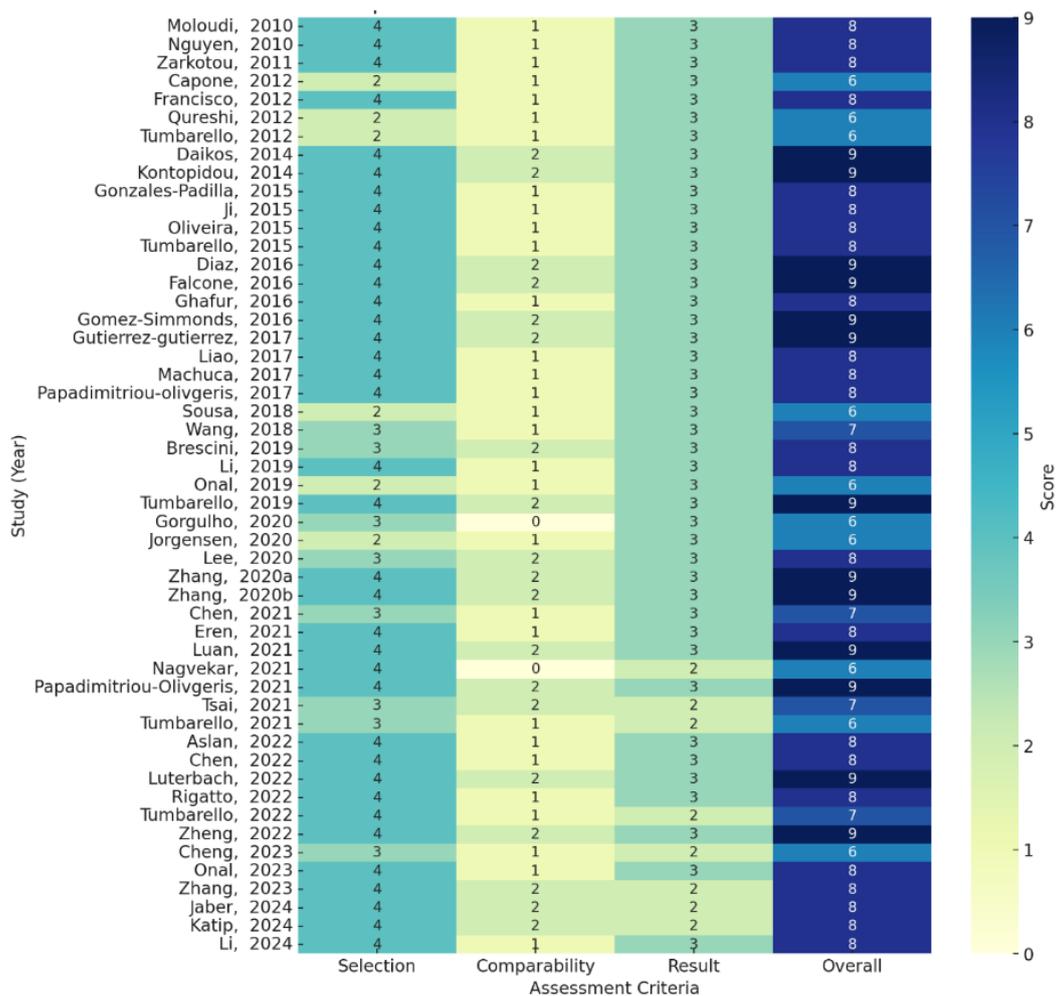


Figure 2 NOS score of risk assessment.

Studies characteristics

A total of 6,545 participants, aged 18 to 76 years, were included from the 51 articles, encompassing patients with CRE infections. The interventions employed consist of single antibiotic therapy, dual-antibiotic therapy, and multi-antibiotic therapy, with observation periods spanning 14 to 30 days. Detailed tables of study characteristics can be seen in **Table S2**. Research indicates that elderly patients in intensive care units exhibit a diminished immune response, with Gram-negative bacteria identified as the primary agents of bloodstream infections in this population, characterized by elevated antibiotic resistance levels [67]. This statement parallels the findings of the study, which involved predominantly middle-aged to elderly patients (45 - 74 years old) suffering from bloodstream infections. Long-term care facilities frequently act as reservoirs for bacteria that exhibit resistance to multiple drugs, thereby increasing patients' susceptibility to

bacterial infections, including carbapenem-resistant *Klebsiella pneumoniae* [68]. This finding aligns with the study, which indicated that most patients were ICU patients infected with *Klebsiella pneumoniae*.

Meta-analysis and meta-regression on patients age

Comparison of monotherapy and combination therapy antibiotic treatments indicates that 3combination therapy is superior regarding the survival rate of patients infected with CRE (**Figure 3**). The meta-analysis results indicate that combination therapy significantly enhances the survival rate (OR = 0.69, 95 % CI (0.62, 0.78), $p < 0.00001$, $I^2 = 49 \%$) in comparison to antibiotic monotherapy. The results are corroborated by a low level of heterogeneity ($I^2 = 49 \%$), suggesting that the variations among studies are minimal, thereby affirming the reliability and consistency of the meta-analysis finding [69].

In accordance with the results of our meta-analysis, several studies also indicate that combination therapy offers superior treatment benefits compared to monotherapy, as it enhances efficacy and decreases the risk of resistance, resulting in improved mortality outcomes [70,71]. Combination antibiotic therapy provides synergistic effects through the use of multiple drugs with diverse mechanisms of action, enhancing efficacy against resistant bacteria and decreasing the probability of resistance emergence [70,72]. Combination therapy, which employs 2 or more antibiotics targeting distinct mechanisms within bacterial cells, can achieve a synergistic effect, leading to a more comprehensive therapeutic outcome [73,74]. The combined effects lead to bacteria experiencing effective mutations against all agents simultaneously, a mechanism that is infrequently observed in antibiotic monotherapy [70]. Combination therapy enhances the effectiveness of drugs, leading to improved therapeutic success and higher patient recovery rates, which in turn reduces mortality rates [75]. The findings align with Schmid *et al.* [71], which indicated that combination therapy reduced mortality in infections caused by resistant gram-negative bacteria, especially in bloodstream infections and those involving carbapenemase-producing *Enterobacteriales*.

This study identifies CTN+TGC (Colistin + Tigecycline) as the most prevalent drug combination, with TGC + CBM (Tigecycline + Carbapenem) following closely behind. Numerous studies demonstrate the efficacy of these drug combinations. Zhou *et al.* [76] demonstrated that the combination of CTN and TGC produced significant effects compared to monotherapy with either drug, effectively reducing the density of carbapenem and colistin-resistant *E. coli* within 48 h. Cai *et al.* [77] reported that the combination

of CTN and TGC led to a greater reduction in bacterial density and significantly decreased the area under the bactericidal curve compared to colistin alone. The combination of TGC and CBM has been shown to produce superior effects compared to monotherapy. Fergadaki *et al.* [78] demonstrated that the combination of tigecycline and meropenem displayed superior bactericidal activity relative to monotherapy, particularly against carbapenemase-producing *Klebsiella pneumoniae* isolates. This combination effectively reduced bacterial load in tissues and enhanced survival rates in experimental infection models. Combination therapy utilizing carbapenems and tigecycline demonstrates greater efficacy than monotherapy in decreasing mortality rates among patients with pneumonia infections [72].

This study identifies colistin and tigecycline as the most prevalent monotherapy regimens. In contrast to the outcomes of combination therapy, monotherapy is frequently linked to reduced clinical and microbiological success rates when compared to combination therapy [79]. Wang *et al.* [80] demonstrated that monotherapy with Tigecycline resulted in a mortality rate 2.73 times greater than that of tigecycline-based combination therapy for bloodstream infections. A study by Cheng *et al.* [81] indicated that monotherapy with colistin was associated with a 1.03 times higher mortality risk ratio compared to combination therapy with colistin in infections caused by carbapenem-resistant gram-negative bacteria. Monotherapy is frequently inadequate for treating infections caused by multidrug-resistant (MDR), extensively drug-resistant (XDR), or pan-drug-resistant (PDR) bacteria, as it lacks the necessary broad spectrum to address these infections [72,79].

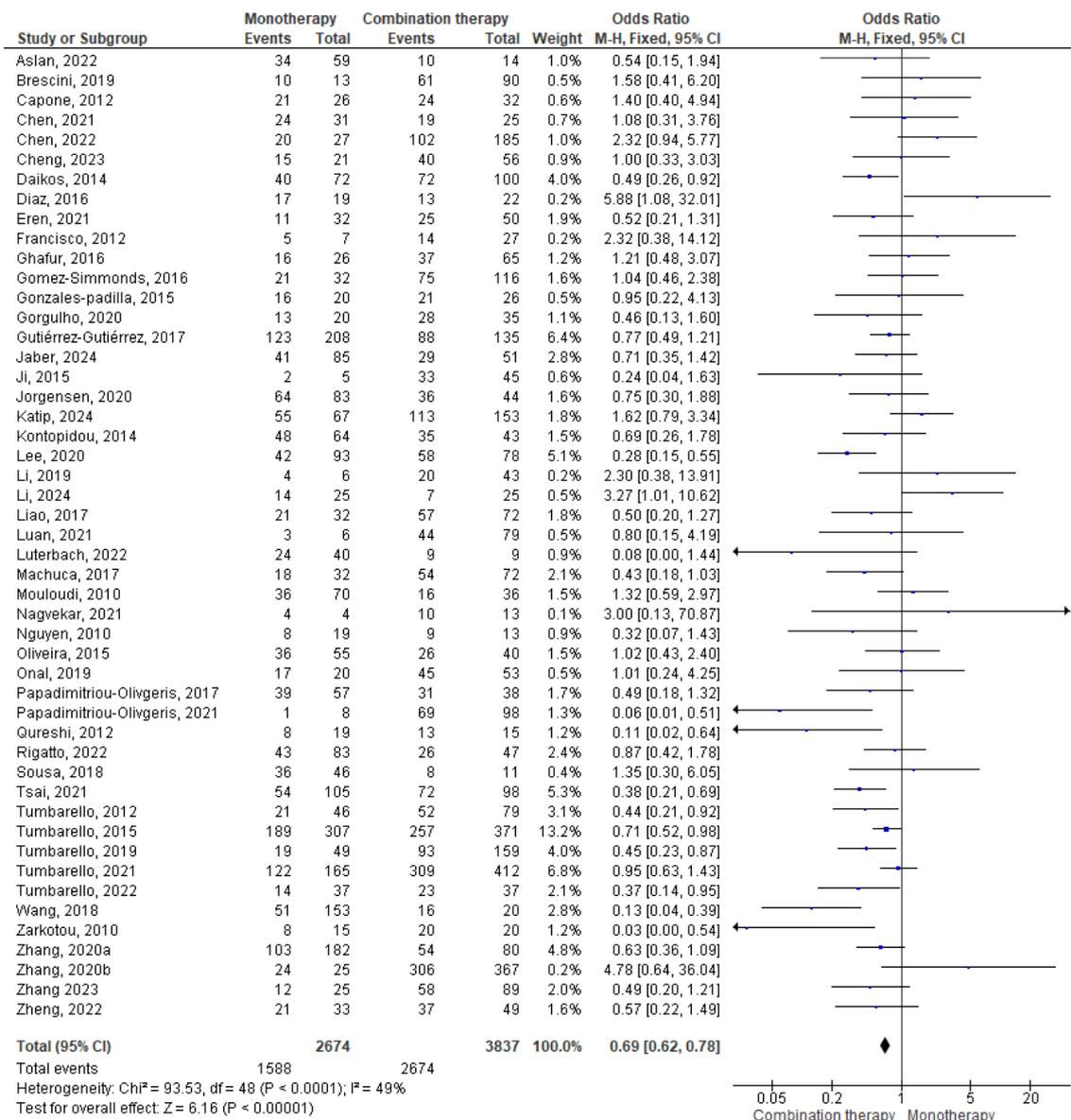


Figure 3 Forest plot of survival rate monotherapy vs combination therapy.

The meta-analysis assessment on survival rates between dual antibiotic combination therapy and multiple combination therapy (more than 2 antibiotic regimens) revealed no significant difference (**Figure 4**). Nonetheless, the meta-analysis indicated a positive trend in survival rates for the double combination group relative to

the double combination group (OR = 1.17, 95 % CI (0.95, 1.46), $p = 0.15$, $I^2 = 44\%$). The result exhibited a low degree of heterogeneity ($I^2 = 44\%$), signifying a high level of confidence in the findings [69].

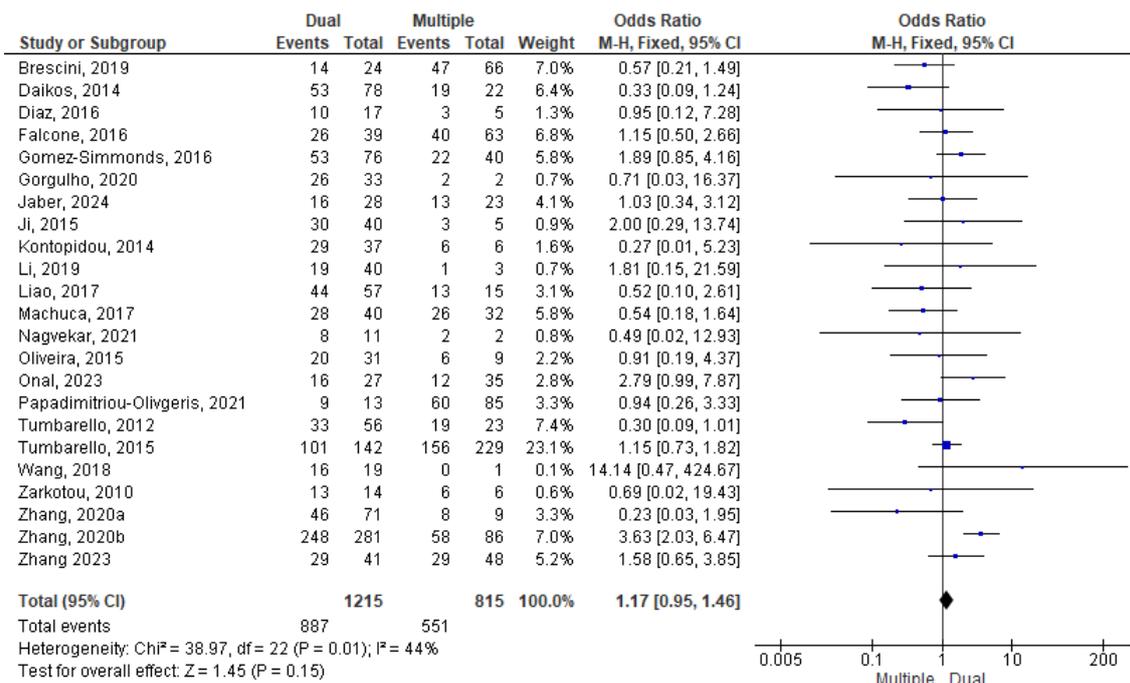


Figure 4 Forest plot of survival rate dual combination therapy vs multiple combination therapy.

To detect potential publication bias and Outcome Variability, a funnel plot analysis was performed. The first funnel plot in **Figure 5(A)** compares the survival rates of monotherapy versus combination therapy, while the second funnel plot in **Figure 5(B)** compares dual combination therapy versus multiple combination therapy. In both plots, the symmetry around the vertical line at OR = 1 suggests no significant publication bias. The concentration of data points at the top of the plots indicates larger sample sizes and more precise estimates.

Most data points cluster around the OR = 1 line, indicating no strong evidence favoring 1 therapy over the other in terms of survival rates. Both plots also have a few outliers, which may represent studies with extreme results or potential biases. Overall, the interpretation of both funnel plots is similar, with no significant publication bias and no strong preference for either therapy in terms of survival rates. The main distinction is the specific therapies being compared in each plot.

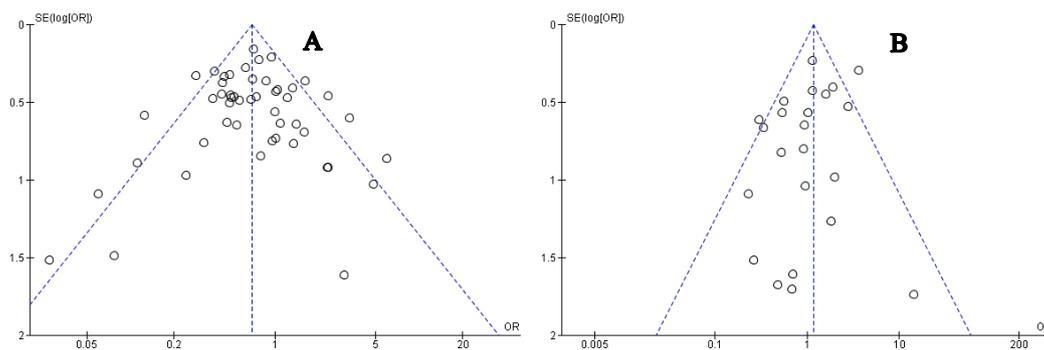


Figure 5 (A) Funnel plot of survival rate monotherapy vs combination therapy; (B) Funnel plot of survival rate dual combination therapy vs multiple combination therapy.

Dual therapy antibiotics are believed to enhance survival rates more effectively than multiple combinations, as fewer and simpler regimens can mitigate the

risk of drug toxicity [82]. This may happen because the medicine combination enhances the synergistic benefits of the healing mechanisms while simultaneously posing

the danger of synergistic drug toxicity. Research indicates that the cumulative toxicity of many antibiotics may exceed the toxicity of each antibiotic administered individually [82]. The toxicity of antibiotic combinations varies based on the specific antibiotic, dosage, and usage conditions. [83]. This results in considerable variability in effects among people; hence, whereas dual combination antibiotics demonstrate a higher survival rate, the difference relative to multiple combination treatment is not substantial.

One of the factors that can potentially affect the success of therapy is the age of the patient. Studies examining the correlation between age and infection survival rates in hospitalized patients yield inconsistent findings. Therefore, a meta-regression on age was conducted to determine how significant an effect age has on the outcome of mono vs combination therapy. The

results of the meta-regression analysis (**Figure 6**) showed that age had no significant influence on the effectiveness of combination therapy versus monotherapy in patients infected with *Enterobacterales*. The regression coefficient for age was -0.0191 with a p -value of 0.0826 , which showed a negative trend meaning as age increases, the survival rate decreases but was not statistically significant. Simultaneous tests showed that all coefficients, including age, were not significantly different from zero ($p = 0.0826$). Although there was variability between studies ($I^2 = 45.92\%$), the model explained only a small amount of variability ($R^2 = 0.07$), indicating that other factors may play a greater role in influencing the effectiveness of therapy. The regression graph also shows that the relationship between age and log odds ratio tends to be weak and inconsistent.

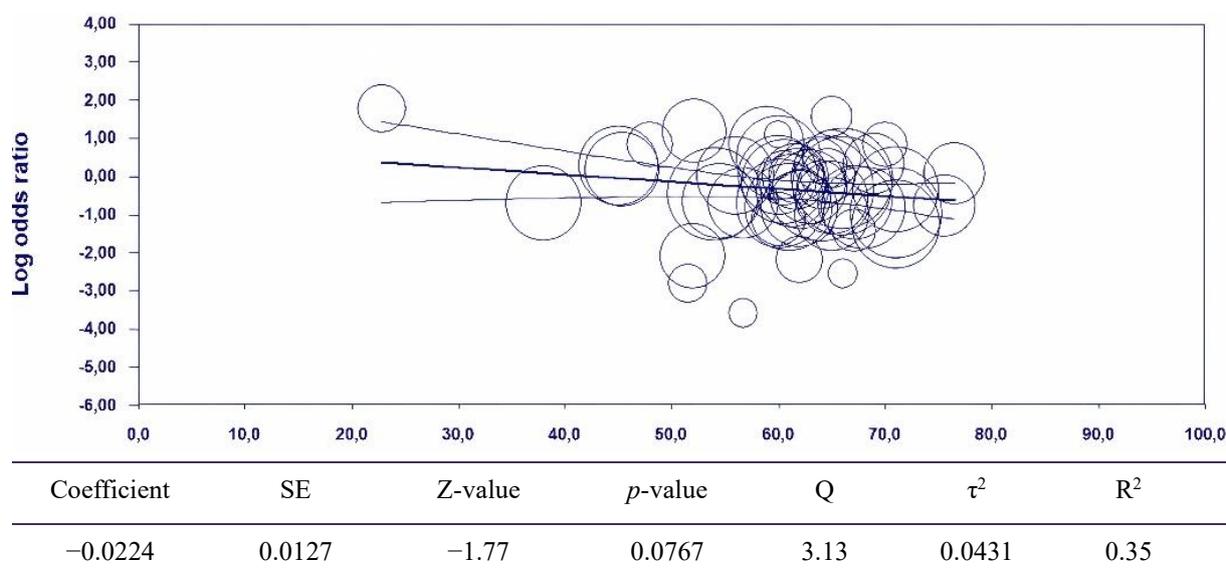


Figure 6 Meta-regression analysis of the log odds ratio in relation to age.

The dose and ratio of antibiotic combinations significantly determine whether their harmful effects are synergistic or antagonistic [84], therefore the management of drug dosage and adherence to combination antibiotic regimens are critical for controlling drug effects in patients. Administering multiple antibiotic combination therapy (more than 2 antibiotic regimens) is more complex than dual combination therapy, resulting in a higher risk of non-adherence among patients. This elevates the risk of toxicity within the multiple combination group [85],

making dual combination therapy safer. In addition, the use of 2 antibiotics is expected to be more cost-effective compared to the use of more than 2 drugs, as it reduces the risk of resistance and increases treatment effectiveness, which can reduce the need for additional care or further treatment [86,87].

Overall, the use of dual combination antibiotics shows the best effect in increasing patient survival rates. However, this study did not compare the effects of antibiotics based on the classification of severity levels and

comorbidities, raising concerns about potentially inaccurate comparisons that may not align with the conditions of each patient. This is due to inconsistencies in reporting patient severity at hospital presentation among the inclusion studies. In addition, this study also does not compare the safety rate of both combination types, so further research is needed for a more detailed investigation.

Conclusions

The use of combination antibiotics markedly enhances the survival rate when compared to monotherapy antibiotics. Nonetheless, the use of a dual antibiotic combination yields a superior survival rate in comparison to multiple antibiotics, albeit not to a significant extent. Further studies are recommended to explore the safety and cost-effectiveness of both combination types. Furthermore, it is advisable for subsequent studies to present more comprehensive findings that include classifications of patient severity and comorbidities. Furthermore, conducting a network meta-analysis is essential to provide more precise recommendations regarding which combination therapies exhibit greater potential.

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Supplementary Materials

Table S1 Search strategies.

Database	Keywords	Total articles
PubMed	#1 Enterobacteriaceae[Mesh Terms]	350
	#2 ("Enterobacteriaceae" OR "Escherichia coli" OR "Proteus mirabilis" OR Enterobacter OR "Serratia" OR "Citrobacter" OR "Klebsiella" OR "Salmonella" OR "Shigella")	
	#3 #1 OR #2	
	#4 β -lactamase[Mesh Terms]	
	#5 (" β -lactamase" OR "ESBL" OR "beta lactamase")	
	#6 #4 OR #5	
	#7 Antibiotic[Mesh Terms]	
	#8 (Antibiotic OR Antimicrobial OR Antibacteria)	
	#9 #7 OR #8	
	#10 (Combination OR Combined OR mono)	
	#11 (Survive OR Survival OR Died OR mortality OR death)	
	#12 #3 AND #6 AND #9 AND #10 AND #11	
Cochrane Library	#1 Enterobacteriaceae[Mesh Terms]	7
	#2 ("Enterobacteriaceae" OR "Escherichia coli" OR "Proteus mirabilis" OR Enterobacter OR "Serratia" OR "Citrobacter" OR "Klebsiella" OR "Salmonella" OR "Shigella")	
	#3 #1 OR #2	
	#4 β -lactamase[Mesh Terms]	
	#5 (" β -lactamase" OR "ESBL" OR "beta lactamase")	
	#6 #4 OR #5	
	#7 Antibiotic[Mesh Terms]	
	#8 (Antibiotic OR Antimicrobial OR Antibacteria)	
	#9 #7 OR #8	
	#10 (Combination OR Combined OR mono)	
	#11 (Survive OR Survival OR Died OR mortality OR death)	
	#12 #3 AND #6 AND #9 AND #10 AND #11	
	#13 (Cohort OR Case control OR Retrospective OR Observational)	
	#14 #12 AND #13	
SCOPUS	("Enterobacteriaceae" OR "Escherichia" OR "Proteus" OR Enterobacter OR "Serratia" OR "Citrobacter" OR "Klebsiella" OR "Salmonella" OR "Shigella") AND (" β -lactamase" OR "ESBL" OR "beta lactamase") AND ("Monotherapy" OR "Mono" OR "Combination") AND ("Antibiotic") AND ("Cohort" OR "Case control" OR "Retrospective" OR "Observational") AND (Survive OR Survival OR Died OR mortality OR death)	380
EBSCOhost	("Enterobacteriaceae" OR "Escherichia" OR "Proteus" OR Enterobacter OR "Serratia" OR "Citrobacter" OR "Klebsiella" OR "Salmonella" OR "Shigella") AND (" β -lactamase" OR "ESBL" OR "beta lactamase") AND ("Monotherapy" OR "Mono" OR "Combination") AND ("Antibiotic") AND ("Cohort" OR "Case control" OR "Retrospective" OR "Observational") AND (Survive OR Survival OR Died OR mortality OR death)	47
ScienceDirect	("Enterobacteriaceae") AND (" β -lactamase") AND ("Monotherapy" OR "Combination") AND ("Antibiotic") AND ("Observational") AND (Survival OR mortality)	239

Table S2 Extraction table.

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
1	Mouloudi <i>et al.</i> [16]	59	45 [15-78]	Mono: CTN Dual: CTN+GTC	Bloodstream	<i>Klebsiella pneumoniae</i>	N/A
2	Nguyen <i>et al.</i> [37]	48	60 [37-86]	Mono: PMB, TGC Dual: PMB+TGC	Bloodstream	<i>Klebsiella pneumoniae</i>	30 days
3	Zarkotou <i>et al.</i> [17]	53	56.7 (20.9)	Mono: CTN, TGC, GTC, CBM Dual: TGC+CTN, TGC+GTC, TGC+CBM, TGC+AMC Multiple: TGC+CTN+CBM, TGC+CTN+GTC, TGC+CBM+GTC	Bloodstream	<i>Klebsiella pneumoniae</i>	14 days
4	Capone <i>et al.</i> [38]	91	69 [50-77]	Mono: GTC, CTN Dual: CTN+TGC, CTN+FMC, CTN+GTC, TGC+FMC	Lung, Bloodstream, Urinary tract, Skin and soft tissue, intra-abdominal	<i>Klebsiella pneumoniae</i>	N/A
5	Francisco <i>et al.</i> [18]	40	70 [38-92]	Mono: CTN, TGC, AMC, CBM Combination: Not elaborated	Urinary tract, intra-abdominal, bloodstream, others	<i>Klebsiella pneumoniae</i> , <i>Escherichia coli</i>	30 days
6	Qureshi <i>et al.</i> [39]	41	62 [25-90]	Mono: TGC, CBM, GTC, BL/BLI, CLX Dual: TGC+CBM, TGC+AGS, CBM+FQL, AZT+FQL, CFM+GTC, CLX+CBM, CLX+TGC, CLX+FQL	Bloodstream	<i>Klebsiella pneumoniae</i>	28 days
7	Tumbarello <i>et al.</i> [19]	125	68 [55 -76]	Mono: TGC, CTN, GTC Dual: TGC+CTN, TGC+GTC Others Multiple: TGC+CTN+MRM, Others	Bloodstream	<i>Klebsiella pneumoniae</i>	30 days
8	Daikos <i>et al.</i> [40]	205	60.2 (18.9)	Mono: TGC, CTN, AGS, CBM, Others Dual: CBM+TGC, CBM+AGS, CBM+CTN, TGC+AGS, TGC+CTN, AGS+CTN Multiple: CBM+TGC+AGS/CTN, TGC+AGS+CTN.	Bloodstream	<i>Klebsiella pneumoniae</i>	28 days
9	Kontopidou <i>et al.</i> [20]	127	61.3 [17-86]	Mono: CTN, AGS, TGC, QNL Dual: TGC+AGS, CTN+AGS, CTN+TGC Multiple: CTN+TGC+AGS, CTN+TGC+CBM	Lung, bloodstream, urinary tract, skin and soft tissue, intra-abdominal	<i>Klebsiella pneumoniae</i>	14 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
10	Gonzalez-Padilla <i>et al.</i> [41]	50	60.5 [19-86]	Mono: TGC, GTC, MRM Dual: TGC+GTC, MRM+FMC, TGC+CTN Multiple: MRM+CTN+FMC	Lung, urinary tract, intra-abdominal, skin and soft tissue, bloodstream, nervous system, luka operasi, endocardium	<i>Klebsiella pneumoniae</i>	30 days
11	Ji <i>et al.</i> [21]	51	67.1 (16.1)	Mono: TGC Dual: TGC+FMC, TGC+CFM, TGC+MRM, CFM+ BL/BLI Multiple: CFM+BL/BLI+ FMC, TGC+AMC+LVX	Lung, intra-abdominal, bloodstream, urinary tract, others	<i>Klebsiella pneumoniae</i>	28 days
12	Oliveira <i>et al.</i> [42]	118	56 [1-87]	Mono: CBM, PMN, AGS, TGC Dual: PMN+CBM, AGS+CBM. AGS+TGC, TGC+CBM, PMN+AGS Multiple: PMN+AGS+CBM, TGC+CBM+PMN, AGS+PMN+TGC, AGS+CBM+TGC	Bloodstream, lungs, urinary tract, surgical site infection, Intra-abdominal	<i>Klebsiella pneumoniae</i>	30 days
13	Tumbarello <i>et al.</i> [22]	661	64 [51-75]	Mono: TGC, CTN, GTC Dual: Not elaborated Multiple: Not elaborated	Bloodstream, lung, intra-abdominal, urinary tract, others	<i>Klebsiella pneumoniae</i>	14 days
14	Díaz <i>et al.</i> [43]	89	22.8 [0-156]	Mono: CTN, AGS, CPF Dual: MRM+CTN, MRM+CPF, CTN+AGS, CTN+TGC, CTN+CPF, CFM+AZT, CFM+AGS, CPF+AGS, TGC+AGS Multiple: CTN+AGS+TGC, CTN+CPF+AGS	Urinary tract, Intra-abdominal, lung, skin and soft tissue, bloodstream, others	<i>Klebsiella pneumoniae</i>	N/A
15	Falcone <i>et al.</i> [23]	111	59 (15.2)	Dual: MRM+CTN, CTN+TGC, TGC+GTC, MRM+TGC Multiple: CTN+TGC+MRM, TGC+MRM+FMC, CTN+TGC+IMP, CTN+TGC+RIF, CRM+ETP+CTN, CTN+TGC+MRM+GTC	Bloodstream, lung, urinary tract, intra-abdominal, others	<i>Klebsiella pneumoniae</i>	30 days
16	Ghafur <i>et al.</i> [44]	91	45.4 (16.3)	Mono: CTN Dual:	Bloodstream	<i>Klebsiella pneumoniae</i> ,	28 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
				CTN+TGC CTN+MRM		<i>Acinetobacter baumannii</i> , <i>Escheria coli</i> , <i>Pseudomonas</i>	
17	Gomez-Simmonds <i>et al.</i> [24]	36	60 [47-74]	Mono: PMB, TGC, AGS Dual: PMB+BL, TGC+BL, BL+AGS, Other+BL TGC+AGS, PMB+TGC, PMB+AGS Multiple: PMB+AGS+BL, PMB+TGC+BL, TGC+AGS+BL, PMB+TGC+AGS+BL, PMB+TGC+AGS	Lung, intra-abdominal, mukosa, soft tissue, urinary tract, mix	<i>Klebsiella pneumoniae</i>	30 days
18	Gutiérrez-Gutiérrez <i>et al.</i> [45]	437	66 [55.5-76]	Mono: CTN, CBM, BL, TGC, AGS, Others Combination: TGC/CTN/AGS/CBM/ FMC/Others based therapy	Bloodstream, lung, intra-abdominal, skin, others	<i>Klebsiella pneumoniae</i>	30 days
19	Liao <i>et al.</i> [25]	107	67.2 (15.7)	Mono: BL/BLI, AGS, CEF, QNL, CBM, TGC, MNC Dual: FMC+MRM, TGC+MRM, TGC+MNC, MNC+CBM, MNC+BL/BLI, GTC+MRM, AMC+MRM, AMC+CFM, AMC+BL/BLI, CFM+BL/BLI, CFM+STX, CFM+AZT, BL/BLI+QNL, CBM+QNL, BL/BLI+CBM Multiple: FMC+MRM+TTC, TGC+MRM+AMC, TGC+MNC+MRM	Bloodstream, lung, urinary tract, intra-abdominal	<i>Klebsiella pneumoniae</i>	45 days
20	Machuca <i>et al.</i> [46]	72	62 [74.25-47]	Mono: TGC, GTC, FMC Dual: TGC+GTC, TGC+FMC, GTC+FMC, Multiple: TGC+FMC+GTC	Bloodstream, urinary tract, lung	<i>Klebsiella pneumoniae</i>	30 days
21	Papadimitriou-Olivgeris <i>et al.</i> [26]	95	56.7 (18.0)	Not elaborated	Bloodstream, abdominal, skin and soft tissue, lungs, urinary tract	<i>Klebsiella pneumoniae</i>	30 days
22	Sousa <i>et al.</i> [47]	57	64 [26-86]	Mono: CAZ/AVI Multiple: CTN+TGC+ AMC+IMP	Intra-abdominal, lungs, urinary tract	<i>Klebsiella pneumoniae.</i>	30 days
23	Wang <i>et al.</i> [48]	98	52.0 [34.3-73]	Mono: TGC, CBM, AGS, QNL, STX Dual: TGC+AGS, TGC+CBM, TGC+PMB, TGC+STX, CBM+QNL, AGS+QNL,	Abdominal, skin and soft tissue, lungs, catheter	<i>Klebsiella pneumoniae</i> , <i>Escherichia coli</i> , <i>Enterobacter spp.</i> ,	14 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
				AGS+CEF, BLI+CEF, BLI+AZT, BLI+MNC, BLI+QNL Multiple: AGS+CAZ/AVI+CEF	related, urinary tract	<i>Citrobacter freundii</i> , and <i>Serratia marcescens</i> .	
24	Brescini <i>et al.</i> [49]	112	65 [54-75]	Mono: TGC, CTN, GTC Multiple: <i>Not elaborated</i>	Lung, intra-abdominal, urinary tract, wounds, others	<i>Klebsiella pneumoniae</i>	30 days
25	Li <i>et al.</i> [27]	98	47.93 (27.5)	Mono: CTN, CFM, MXF, LTX Dual: CBM+AMC, CBM+TGC, TGC+AMC, TGC+QNL, AMC+QNL, TGC+CTN, AMC+Other, QNL+Other, TGC+Other Multiple: CBM+TGC+QNL, CBM+TGC+AMC	Bloodstream	<i>Klebsiella pneumoniae</i> , <i>Klebsiella oxytoca</i> , <i>Enterobacter cloacae</i> , <i>Escheria coli</i> , <i>Citrobacter freundii</i>	30 days
26	Önal <i>et al.</i> [50]	100	61.69 (1.65)	Mono: CTN, TGC, CBM Dual: 2 CBM, CTN+CBM, CTN+TGC, TGC+GTC Multiple: contains CTN, CBM, TGC	Urinary tract	<i>Klebsiella pneumoniae</i>	30 days
27	Tumbarello <i>et al.</i> [28]	104	61 [27-79]	Mono: CTN, CAZ/AVI Dual: CTN+TGC, 2 CBM, FMC+TGC, CTN+MRM, GTC+TGC, CAZ/AVI+GTC, CAZ/AVI+CTN, CAZ/AVI+CBM, CAZ/AVI+TGC, CAZ/AVI+FMC, CAZ/AVI+AMC Multiple: CTN+TGC+MRM	Bloodstream, urinary tract, lungs, abdominal, others	<i>Klebsiella pneumoniae</i>	30 days
28	Gorgulho <i>et al.</i> [51]	54	75.6 [0-100]	Mono: MRM, CTN, CIPRO, CAZ/AVI, Others Dual: MRM+AMC, MRM+CTN, TGC+CTN, AMC+CTN, MRM+GTC, MRM+CAZ, CAZ+LZD, CTN+AMP, CTN+TGC, CTN+GTC, GTC+CFM Multiple: TGC+PPC/TZB+CLIN, AMC+CTN+CAZ/AVI,	Abdominal, heart disease, skin, others	<i>K. pneumoniae</i> , <i>Enterobacter cloacae</i> , <i>E. coli</i> , <i>Citrobacter freundii</i> ,	30 days
29	Jorgensen <i>et al.</i> [52]	109	63 [53-74]	Mono: CAZ/AVI, AMC, PMN, TGC Combination: CAZ/AVI combined with others	Lungs, intra-abdominal, urinary tract, skin and soft tissue, osteoarticular, others	<i>K. pneumoniae</i> , <i>Enterobacter spp</i> , <i>E. coli</i> , <i>K. oxytoca</i> , <i>Citrobacter spp</i> , <i>Serratia</i> , <i>Proteus mirabilis</i>	30 days
30	Lee <i>et al.</i> [53]	171	71 (60-82)	Mono: MRM, CTN, CFM Dual: CBM+CTN, CBM+AMC, MRM+CPF, CTN+CPF, CTN+AMC, CFM+AMC, PPC+AMC.	Lungs, intra-abdominal, urinary tract, skin and soft tissue	<i>Klebsiella pneumoniae</i>	30 days
31	Zhang <i>et al.</i> [29]	297	54 (16)	Mono: CBM, BL/BLI, CAZ, CFM, CMX Dual: TGC+CBM, TGC+PMB, TGC+BL/BLI, TGC+AGS, CBM+PMB, CBM+BL/BLI, CBM+CAZ, BL/BLI+AGS,	Bloodstream	<i>Klebsiella pneumoniae</i>	28 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
				CBM+AGS Multiple: TGC+CBM+BL/BLI, TGC+CBM+AGS, TGC+CBM+PMB			
32	Zhang <i>et al.</i> [54]	281	65 [46-75]	Mono: CBM Dual: CBM+TGC Multiple: CBM+TGC+others	Bloodstream	<i>Klebsiella pneumoniae</i>	28 days
33	Chen <i>et al.</i> [30]	56	76.5 [63.8-85]	Mono: TGC, CTN Dual: TGC+CTN Multiple: Others	Not elaborated	<i>Klebsiella pneumoniae</i>	14 days
34	Eren <i>et al.</i> [55]	82	54.5 [16-88]	Mono: TGC, CTN, BL/BLI Dual: TGC+CTN, CTN+CBM, CTN+CFM, CTN+ BL/BLI	Bloodstream, lung, urinary tract, others	<i>Klebsiella pneumoniae</i>	28 days
35	Luan <i>et al.</i> [31]	89	64.0 [48-77]	Mono: TGC Dual: TGC+FMC, CBM+CBM, QNL+BL/BLI, AMC+Other, CBM+AMC, QNL+CBM, CBM+BL/BLI, FMC+CBM, TGC+CBM, PMB+FMC, QNL+AMC Multiple: TGC+FMC+GTC	Bloodstream, lung, intra- abdomen, nervous system, urinary tract, skin and soft tissue, mix	<i>Klebsiella pneumoniae</i>	28 days
36	Nagvekar <i>et al.</i> [56]	57	60	Mono: CAZ/AVI Dual: CAZ/AVI+PMN, CAZ/AVI+TCN Multiple: CAZ/AVI+PMN+FMC	Intra-abdominal, lungs, urinary tract, bloodstream, others	<i>Klebsiella pneumoniae, E. coli</i>	30 days
37	Papadimitriou- Olivgeris <i>et al.</i> [57]	115	51.5 (18.6)	Mono: CBM, CTN, GTC Dual: CBM+AMG, CTN+TGC, CBM+TGC, CBM+TCN Multiple: CTN+TGC+AMC, CBM+TGC+AMC, CTN+TGC+CBM, CTN+CBM+AMC+ CTN+TGC+CAZ/AVI, CTN+TGC+FMC, CBM+CTN+TGC+AMC, CBM+CTN+TGC+AMC+Others,	Abdominal, lungs, urinary tract, meningitis, others	<i>Klebsiella pneumoniae</i>	N/A
38	Tsai <i>et al.</i> [58]	203	71 [60.8-78.3]	Mono: CTN, TGC, CBM Dual: CBM+CTN, CBM+TGC, CBM+AMC, CTN+TGC	Bloodstream, urinary tract, lung, intra-abdominal, skin and soft tissue	<i>Klebsiella pneumoniae</i>	30 days
39	Tumbarello <i>et al.</i> [59]	577	66 [56-76]	Mono: CAZ/AVI Dual: CAZ/AVI+FMC, CAZ/AVI+TGC, CAZ/AVI+GTC, CAZ/AVI+MRM, CAZ/AVI+CTN, CAZ/AVI+AMC, CAZ/AVI+Others Multiple: Not elaborated	Bloodstream, urinary tract, lung, intra-abdominal, others	<i>Klebsiella pneumoniae</i>	30 days
40	Aslan <i>et al.</i> [60]	124	62.1	Mono: CBM, CTN, CPF, Others	Bloodstream	<i>Klebsiella pneumoniae</i>	30 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
			(18.0)	Dual: MRM+CTN, CTN+TGC, MRM+AGS, Others			
41	Chen <i>et al.</i> [61]	212	58.9 (16.0)	Not elaborated	Bloodstream, lungs, intra- abdominal, urinary tract, skin, cerebrospinal fluid	<i>Klebsiella pneumoniae</i>	28 days
42	Luterbach <i>et al.</i> [62]	49	66 [51-75]	Mono: TGC CTN, CAZ/AVI Dual: CTN+CAZ/ AVI	Bloodstream	<i>Klebsiella pneumoniae</i>	30 days
43	Rigatto <i>et al.</i> [32]	279	60.5 (16.1)	Mono: PMB AMC, TGC, CBM Dual: CBM+PMB, CBM+ AMC, CBM+TGC Multiple: 2 CBM+PMB, 2 CBM+AMC, 2 CAR+TGC	Lungs, abdominal, urinary tract, skin and soft tissue, catheter, others	<i>Enterobacteriales (K. pneumoniae, E. coli, Enterobacter cloacae, Providencia stuartii, Serratia marcescens, Citrobacter freundii)</i>	30 days
44	Tumbarello <i>et al.</i> [63]	37	65 [31-71]	Mono: FMC, TGC, GTC, CTN, AMC Multiple: MRM/VRB+2 others	Lungs, intra- abdominal, urinary tract, skin and soft tissue, bloodstream	<i>Klebsiella pneumoniae</i>	N/A
45	Zheng <i>et al.</i> [33]	164	65	Mono: CAZ/AVI Dual: CAZ/AVI+CBM, CAZ/AVI+TGC, CAZ/AVI+AMC, CAZ/AVI+FMC	Bloodstream, urinary tract, lung, intra-abdominal, others	<i>Klebsiella pneumoniae</i>	30 days
46	Cheng <i>et al.</i> [64]	98	61.58 (19.07)	Mono: Not elaborated Dual: mono+TGC, mono+CBM	Lung, blood, others	<i>Klebsiella pneumoniae</i>	30 days
47	Önal <i>et al.</i> [34]	62	64.68 (3.15)	Dual: FMC+MRM, PMC+PMN, FMC+AGS, FMC+Others Multiple: FMC+MRM+PMN, FMC+MRM+AGS, FMC+PMN+AGS, Others	lung dan bloodstream	<i>Klebsiella pneumoniae</i>	30 days
48	Zhang <i>et al.</i> [65]	94	38 [25-49]	Mono: CAZ/AVI, PMB Dual: CAZ/AVI+ATM, CAZ/AVI+TGC, TGC+AGS, TGC+FMC, TGC+ATM, TGC+ CBM, AGS+ CBM, FQL+CBM, AGS+FQL Triple: CAZ/AVI+ATM+TGC, CAZ/AVI+ATM+AGS, CAZ/AVI+ATM+PMB, TGC+AGS+ CBM, TGC+AGS+FQL, PMB+TGC+AGS/FQL, PMB+TGC+CBM, PMB+TGC+ATM	Bloodstream	<i>Klebsiella pneumoniae, Escherichia coli, Enterobacter cloacae, Raultella planticola</i>	30 days
49	Jaber <i>et al.</i> [35]	114	71 [20.0-102.0]	Mono: CAZ/AVI, AGS, AZT, CTN, TGC, MRM Dual: Not elaborated Triple: Not elaborated	Bloodstream, lung, urinary tract, soft tissue	<i>Klebsiella pneumoniae</i>	30 days

No.	Study	N	Age, Mean (SD)/Median [range/IQR]	Regimens	Type of infection	Type of bacteria	Observation length
50	Katip <i>et al.</i> [66]	220	[18-100]	Mono: CTN Dual: CTN+FMC	Bloodstream, urinary tract, Lung, others	<i>Klebsiella pneumoniae</i> , <i>Escherichia coli</i> , <i>Enterobacter cloacae</i>	30 days
51	Li <i>et al.</i> [36]	25	52.1 (15.7)	Mono: TGC, CTN, CAZ/AVI Dual: Not elaborated	Lung, abdominal, urinary tract, soft tissue	<i>Klebsiella pneumoniae</i>	30 days

Noted: n, total sample; CTN, Colistin; TGC, Tigecycline; PMB, Polymyxin B; GTC, Gentamicin; CBM, Carbapenem; AMC, Amikacin; FMC, Fosfomycin; BL/BLI, Beta-lactamase Inhibitor; AGS, Aminoglycoside; QNL, Quinolone; MRM, Meropenem; CFM, Cefepime; AZT, Aztreonam; FQL, Fluoroquinolone; CAZ/AVI, Ceftazidime/Avibactam; STX, Sulfamethoxazole; MXF, Moxifloxacin; LTX, Levofloxacin; PPC, Piperacillin; CLIN, Clindamycin; IMP, Imipenem; RIF, Rifampicin; ETP, Ertapenem; TTC, Tetracycline; ATM, Aztreonam; LVX, Levofloxacin; MNC, Minocycline; PMC, Polymyxin C; PMN, Polymyxin; CEF, Cephalosporin; SFM, Sulfonamide; CPF, Ciprofloxacin; RIF, RIF, Rifampicin; IMP, Imipenem; MXF, Moxifloxacin; TZB, Tazobactam; CLIN, Clindamycin; LZD, Linezolid; CMX, Cefminox; VRB, Vaborbactam; CLX, Colixin; N/A, not available.