

REVIEW ARTICLE

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Whole-Genome Sequencing vs. Conventional Molecular Methods in Hospital Bacterial Outbreak Investigations: A Rapid Review of Time to Resolution

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Abstract

Bacterial outbreaks have been a major threat throughout human history. Whole genome sequencing (WGS) is an emerging technology that reveals a wealth of information, and its use in epidemiologic surveillance has increased over the years. This rapid review aims to compare WGS with conventional molecular typing methods in hospital outbreak investigations, focusing on their impact on the duration of the outbreaks. This study performed a rapid systematic review from the PubMed database, following PRISMA guidelines. Searches were performed using combinations of Medical Subject Headings (MeSH) and free-text terms and were limited to studies published in English and involving human subjects from 2016-2026. The WGS usage (classified as intervention and non-intervention groups) and outbreak duration were analyzed with the Mann-Whitney U test and adjusted for covariates using linear regression. Duration of the outbreak was further categorized and analyzed with ordinal regression. The database search process yielded 358 articles, 34 of which consisted of 35 outbreak cases included in this study. The median outbreak duration was shorter in the intervention group (5 months; range 1-37) compared with the non-intervention group (14 months; range 2-82). In both adjusted and non-adjusted analyses, WGS-guided intervention was not significantly associated with shorter outbreak duration ($\beta = -0.170$; 95% CI -1.01 to 0.244; $P = 0.222$). While WGS enhances epidemiological resolution, current evidence remains insufficient to conclusively determine whether its implementation shortens hospital outbreak duration.

Keywords: Hospital-Outbreak, WGS, Outbreak-Duration, Conventional-Typing, Rapid Review

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Citation: Ong DT. Whole-Genome Sequencing vs. Conventional Molecular Methods in Hospital Bacterial Outbreak Investigations: A Rapid Review of Time to Resolution. Published online 12 October 2026. doi: 10.22207/JPAM.20.4.07

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INTRODUCTION

Bacterial outbreaks have been a major threat, taking many lives throughout human history.¹ Although vaccines and antibiotics have substantially limited the spread of infectious diseases and the risk of pandemics, the emergence of resistance, climate change, and increased human mobility and travel have enabled several infectious diseases to spread more widely.^{1,2} Novel infections will initially emerge as an illness or syndrome of unknown cause, and with limited diagnostic capabilities, many outbreaks may not have an identified cause.³ According to a study of 109 outbreaks of unknown cause identified during 2016-2019, a cause was later confirmed in only 18% of them.³ Misidentification will hinder the outbreak reporting process and affect the patient's individual care.^{3,4}

Whole-genome sequencing (WGS) has become an emerging technology that reveals a wealth of information, including gene number and density, repeat sequences, non-protein-coding ribonucleic acid (RNA) genes, and evolutionarily conserved sequences.⁵ WGS use in epidemiologic surveillance has increased over the years due to its ability to prospectively sequence potential pathogens and compare them across healthcare settings, enabling real-time action.⁶ Using conventional molecular methods, there is often a delay in the recognition of clusters or outbreaks, owing to the dependence on a clear epidemiologic link.⁶ This situation complicates control measures, as the issues leading to transmission may have been occurring unchecked for long periods of time.⁶ However, as some research indicates that WGS is beneficial in terms of outbreak identification, the impact of the employment of WGS in terms of ending the outbreak has not yet been explored.^{7,8} Therefore, this rapid review aims to compare WGS with conventional molecular typing methods in hospital outbreak investigations, focusing on their impact on time to outbreak resolution.

MATERIALS AND METHODS

This study is a single-author rapid systematic review, following Preferred Reporting Items for Systematic reviews and Meta-

Analyses (PRISMA) guidelines, to identify and analyze published studies of hospital outbreak investigations that used WGS or conventional molecular typing methods. The population was involved in bacterial outbreaks in hospital settings that used genomic typing methods to manage them. The PubMed database search was performed on February 9th, 2026, using combinations of Medical Subject Headings (MeSH) and free-text terms related to hospital outbreaks, whole-genome sequencing, and conventional molecular typing methods. Searches were limited to studies published in English that involved human subjects and were published from 2016-2026. The full search strategy is provided in Table 1.

Because many studies did not explicitly report outbreak resolution time, we accepted studies with sufficient data to estimate the case-detection period. Outbreak durations were standardized to month ranges. The duration of outbreak certainty was further categorized into 3 levels: High (for papers that explicitly defined the outbreak duration), Medium (for papers that did not report the outbreak period but explicitly stated the date of last case detection), and Low (for papers that only reported the range of the last case detection). Outbreak settings were classified as single department if the article stated the outbreak was localized to a single ward or department; if the transmission involved more than 1 ward, the outbreak was classified as multiple departments. The outbreak setting and the number of cases were included as covariates in the adjusted analyses. Since not all outbreaks had non-patient tracing documented, non-patient involvement, such as environmental or healthcare workers, was included for descriptive purposes only.

If sufficient comparable data were available, a meta-analysis was planned. However, because no paper pooled from this search method compared WGS results with conventional typing in outbreak settings, and the articles provided only start and end dates without measures of variance, comparable effect sizes could not be derived. We divided the outbreaks into 3 categories for descriptive purposes: the intervention group, the investigation group, and the no-WGS group. The intervention group is for outbreaks where the WGS result affected infection control measures,

whether by being the only genomic typing used in the outbreak or by informing control measures with new information not obtained from other genomic typing methods. The investigation group is for outbreaks in which other molecular typing methods guided the detection and/or intervention, and WGS results served only as confirmatory or did not provide any new information that affected the intervention. The third group, a no-WGS group, is for outbreaks that used a conventional typing method but did not use WGS. Since neither the investigation group nor the no-WGS group used WGS in their infection control measures, their outbreak durations were grouped into a non-intervention group and compared with the intervention group in the analysis.

Numerical data on both outbreak duration and number of patients were assessed for normality using the Shapiro–Wilk test and were not normally distributed; therefore, results are presented as median (range). Outbreak duration and number of patients were log-transformed to reduce skewness before univariate and multivariable analyses. Outbreak duration was further categorized based on quartiles of observed values into: ≤ 3 months; 4–6 months; 7–12 months; and > 12 months. Both the log-scaled and categorized outbreak intervals were compared between the intervention and non-intervention groups. Since the duration and number of patients remain skewed after log transformation, a non-parametric analysis was used. The log data were

analyzed using the Mann-Whitney U test and adjusted for covariates using linear regression. Given the limited sample size of 35 outbreaks, the linear regression analysis was considered exploratory. Regression assumptions were assessed through visual inspection of residual diagnostic plots. Linearity and homoscedasticity were evaluated using residual-versus-fitted plots, while the distribution of residuals was assessed using normal quantile-quantile (Q-Q) plots. Independence of observations was assumed based on the study design, with each outbreak treated as a separate observational unit. The categorized outbreak comparison was done through ordinal regression. The proportional-odds assumption for the ordinal regression was assessed using parallel-lines tests. The results were synthesized narratively, with exploratory study-level regression analyses performed using Jamovi 2.6.44.

RESULTS

The database search yielded 358 articles (Figure 1). No duplicates were found, and 41 articles were removed before the screening stage because they were not in English or were not human studies. At the title and abstract screening stage, 217 articles were excluded as reviews, editorials, letters, consensus statements, or irrelevant studies, leaving 101 for further review. However, the full text of 23 articles could not be obtained, leaving 78 articles that could be fully

Table 1. Search strategy

Database	Search strategy	Date
PubMed	(("Disease Outbreaks"[MeSH] OR "Cross Infection"[MeSH] OR outbreak*[tiab] OR nosocomial[tiab] OR healthcare-associated[tiab]) AND ("Whole Genome Sequencing"[MeSH] OR "Genomics"[MeSH] OR "Molecular Epidemiology"[MeSH] OR WGS[tiab] OR "whole genome sequencing"[tiab]) AND ("Molecular Typing"[MeSH] OR "Electrophoresis, Gel, Pulsed-Field"[MeSH] OR "Multilocus Sequence Typing"[MeSH] OR PFGE[tiab] OR MLST[tiab] OR "conventional typing"[tiab]) AND ("Hospitals"[MeSH] OR "Infection Control"[MeSH] OR "outbreak investigation"[tiab]))	Feb. 9 th , 2026

Note. PFGE = Pulsed Field Gel Electrophoresis; MLST = in silico Multilocus Sequence Typing

assessed for eligibility. From this assessment process, 44 articles were excluded because 34 articles did not define the duration of the outbreak; four articles described outbreak occurrence, but the molecular typing methods were not used in the outbreak investigation; three were hospital research defining outbreaks in a community, and three articles were about outbreak detection; the outbreak management and resolution were not documented. Among the 34 articles, one paper described 2 distinct outbreaks occurring in the same hospital, so we counted them as separate outbreaks.⁹ In total, 34 articles, comprising 35 outbreaks, were included for analysis (Table 2).

None of the included outbreak reports provided summary statistics such as means, medians, or measures of dispersion. Outbreak duration was calculated from reported start and end dates, and definitions varied across

studies. Because variance estimates were unavailable, quantitative meta-analysis was not feasible. Given that most included studies were descriptive outbreak investigations and retrospective case series, methodological quality was appraised using the Joanna Briggs Institute Critical Appraisal Checklist for Case Series. Several studies incompletely reported participant demographic characteristics, likely reflecting the genomic epidemiology focus of outbreak investigations rather than patient-centered clinical reporting. This limitation was considered less likely to substantially affect the review objective, which focused on the outbreak's molecular method implementation and outbreak duration.

Among the 35 included outbreak cases, 17 (48.6%) used WGS to guide the outbreak intervention strategy (Table 3). The certainty of outbreak duration estimates in both groups

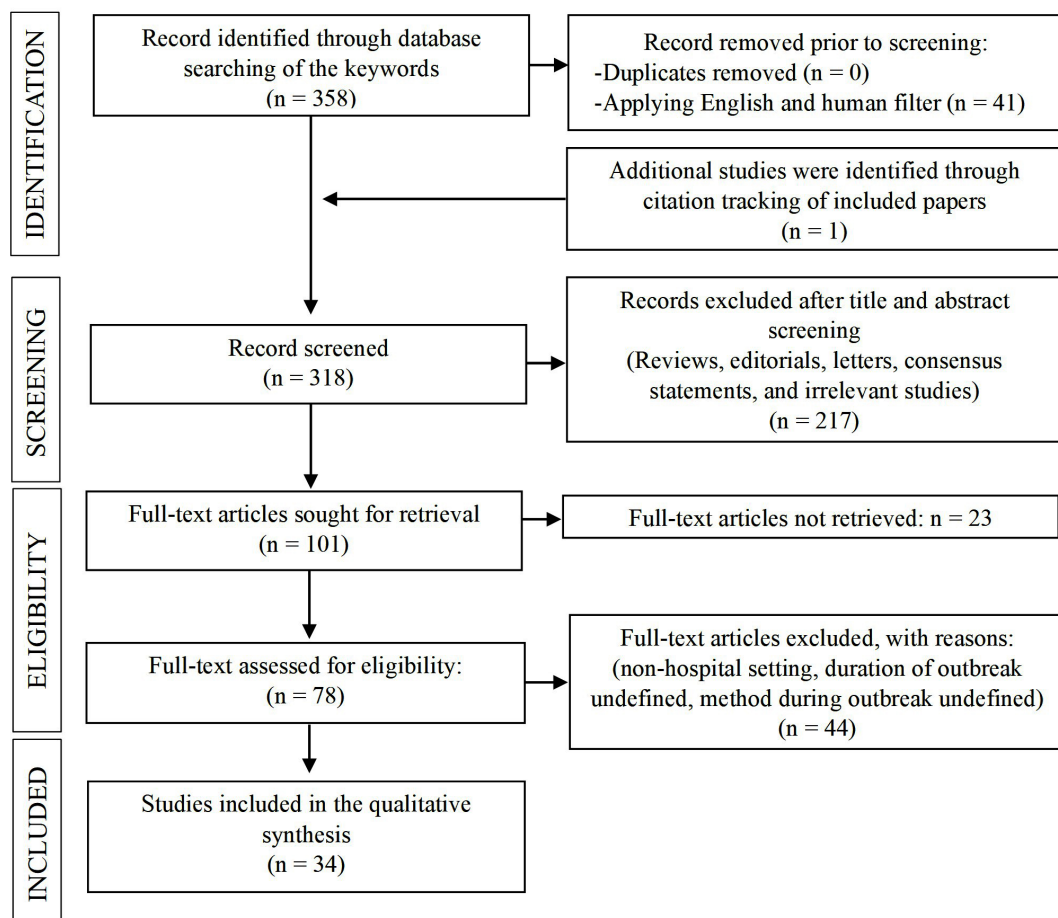


Figure 1. PRISMA flow diagram of included studies

Table 2. Literature review

Author (Year)	Country	Pathogen	Outbreak Setting	Use of WGS	Additional typing Method	No. of patients	Non-patient sources	Outbreak duration (months)	Duration category	Outbreak duration certainty
Qin et al. ¹⁰	China	<i>Clostridioides difficile</i>	Multiple departments	Intervention	MLST	15	E	2	≤3 months	High
Kossow et al. ¹¹	Germany	MRSA	Single department	Intervention	None	5	HCW	19	>12 months	Low
Pletz et al. ¹²	Germany	CPC	Multiple departments	Intervention	None	76	E	5	4-6 months	High
Wendel et al. ¹³	Germany	<i>Enterobacter hormaechei</i> ssp. <i>steigerwaltii</i>	Multiple departments	Investigation	PFGE, rep-PCR, MLST	23	E	82	>12 months	Low
Wisgrill et al. ¹⁴	Austria	<i>Klebsiella pneumoniae</i>	Single department	Intervention	None	14	None	4	4-6 months	Low
Chen et al. ¹⁵	China	CRKP	Single department	Intervention	None	8	None	7	7-12 months	High
Kerschner et al. ¹⁶	Austria	LREfm	Multiple departments	Intervention	None	27	Not performed	4	4-6 months	High
Liese et al. ¹⁷	Germany	VRE	Multiple departments	Intervention	None	561	Not performed	15	>12 months	High
Gideskog & Melhus ¹⁸	Sweden	MRSA	Single department	Investigation	spa typing	13	None	3	≤3 months	Medium
Sharma et al. ¹⁹	UK	GAS	Single department	Intervention	emm typing	3	HCW	8	7-12 months	Medium
Warnke et al. ²⁰	Germany	<i>Moraxella catarrhalis</i>	Single department	Investigation	Rep PCR	9	None	2	≤3 months	High
Kampmeier et al. ²¹	Germany	VRE	Single department	Intervention	None	5	E	1	≤3 months	Medium
Hansen et al. ²²	Denmark	VRE	Multiple departments	Intervention	None	38	Not performed	16	>12 months	Low
Konstantinovskii et al. ²³	Netherlands	BORSA	Single department	Investigation	AFLP, MLVA, MLST	8	None	36	>12 months	Low

Table 2. Cont...

Author (Year)	Country	Pathogen	Outbreak Setting	Use of WGS	Additional typing Method	No. of patients	Non-patient sources	Outbreak duration (months)	Duration category	Outbreak duration certainty
Nguyen et al. ⁹	Vietnam	CRKP	Single department ^a	Intervention	None	3	E	3	≤3 months	High
Nguyen et al. ⁹	Vietnam	CRKP	Single department ^b	Intervention	None	5	E	3	≤3 months	High
Yashar et al. ²⁴	Slovakia	VRE	Multiple departments	Intervention	None	17	E	3	≤3 months	Low
Cabal et al. ²⁵	Austria	<i>Pseudomonas aeruginosa</i> CRKP	Multiple departments	Intervention	None	47	E	37	>12 months	High
Chen et al. ²⁶	China	CRKP	Single department	Intervention	None	6	E	2	≤3 months	High
Rankin et al. ²⁷	Florida	Carbapenem-resistant Gram-negative bacteria	Single department	Investigation	PFGE	69	E	18	>12 months	High
Toorop et al. ²⁸	Netherlands	<i>Serratia marcescens</i>	Single department	Intervention	None	17	None	5	4-6 months	High
Debast et al. ²⁹	Netherlands	<i>Pseudomonas aeruginosa</i> CRKP	Single department	Intervention	None	10	E	5	4-6 months	Low
Fraser et al. ³⁰	UK	CRAB	Single department	Investigation	MLST	12	Not performed	11	7-12 months	High
Kon et al. ³¹	Israel	CRAB	Single department	Intervention	None	22	E	9	7-12 months	High
Corredor et al. ³²	Colombia	VRE	Multiple departments	No	MLVA	13	E	2	≤3 months	High
Tissot et al. ³³	Switzerland	<i>Pseudomonas aeruginosa</i>	Single department	No	PFGE, DLST	218	E	37	>12 months	Low
Abdelfattah et al. ³⁴	Saudi Arabia	<i>Burkholderia cepacia</i> CRKP	Single department	No	PFGE	14	E	6	4-6 months	High
Brkic et al. ³⁵	Croatia	CRKP	Multiple departments	No	PFGE, MLST	12	None	8	7-12 months	High
Us et al. ³⁶	Turkey	<i>Serratia marcescens</i>	Multiple departments	No	PFGE	10	E	12	7-12 months	High

Table 2. Cont...

Author (Year)	Country	Pathogen	Outbreak Setting	Use of WGS	Additional typing Method	No. of patients	Non-patient sources	Outbreak duration (months)	Duration category	Outbreak duration certainty
Bogaty et al. ³⁷	Canada	CRAB	Multiple departments	No	PFGE	28	Not performed	23	>12 months	High
Eldirdiri et al. ³⁸	UK	<i>Staphylococcus aureus</i>	Single department	No	PFGE, spa typing	8	E	5	4-6 months	Low
Pirs et al. ³⁹	Slovenia	CRKP	Multiple departments	No	PFGE, MLST	40	Not performed	17	>12 months	High
Caliskan et al. ⁴⁰	Turkey	<i>Stenotrophomonas maltophilia</i>	Single department	No	PFGE	23	E	17	>12 months	High
Cruz-Cordova et al. ⁴¹	Mexico	<i>Stenotrophomonas maltophilia</i>	Single department	No	PFGE, MLST	10	E	3	≤3 months	Medium
Protonotariou et al. ⁴²	Greek	<i>Proteus mirabilis</i>	Multiple departments	No	PFGE	14	None	8	7-12 months	High

Note: ^aOutbreak in Adult Intensive Care Unit; ^bOutbreak in Viet-Anh Ward; MRSA = Methicillin Resistant *Staphylococcus aureus*; BORSA = Borderline oxacillin-resistant *Staphylococcus aureus*; CPC = Carbapenemase-Expressing *Citrobacter freundii*; CRKP = Carbapenem-resistant *Klebsiella pneumoniae*; CRAB = Carbapenem-resistant *Acinetobacter baumannii*; GAS = Group A Streptococci; LREfm = Linezolid resistant *Enterococcus faecium*; VRE = Vancomycin Resistant Enterococci; ICU = Intensive Care Unit; NICU = Neonatal Intensive Care Unit; ER = Emergency Room; WGS = Whole Genome Sequencing; PFGE = Pulsed Field Gel Electrophoresis; MLST = Multilocus Sequence Typing; MLVA = Multiple-Locus Variable-number tandem repeat Analysis; Rep-PCR = Repetitive element sequence-based Polymerase Chain Reaction; E = Environmental source; HCW = Healthcare Workers source

was comparable, with high certainty (outbreak duration defined in the paper) reported in 58.8% of cases for the intervention group and 66.7% for the non-intervention group. The median outbreak duration was shorter in the intervention group (5 months; range 1-37) compared with the non-intervention group (14 months; range 2-82). Long-lasting outbreaks (>12 months) occurred less often in the intervention group (23.5% vs. 38.9%), whereas outbreaks lasting 4-6 months were more frequent in the intervention group (29.4% vs. 11.1%).

The median number of patients affected was similar between groups (14; range 3-561 and 13.5; range 8-218). Most outbreaks in this study occurred within single departments in

both groups. The majority of outbreaks in the intervention (82.4%) and non-intervention groups (83.3%) performed non-patient screening to identify the outbreak's source and mode of transmission. Environmental sources were identified in approximately half of the outbreaks (52.9% vs. 55.6%), while healthcare-worker involvement was reported only in intervention outbreaks (11.1%). Some outbreaks failed to identify environmental cases despite efforts, occurring in 17.6% and 27.8% of intervention and non-intervention outbreaks, respectively. The outbreak characteristics included in this study are shown in Table 4.

In unadjusted analysis (Table 5), log-transformed outbreak duration did not differ significantly between groups (Mann–Whitney U = 117; P = 0.233). In linear regression adjusting for outbreak setting and the number of patients (Table 6), WGS-guided intervention was not significantly associated with outbreak duration (β = -0.170; 95% Confidence Interval (CI): -1.01 to 0.244; P = 0.222). A higher number of patients was independently associated with longer outbreak duration (β = 0.419; 95% CI: 0.100 - 0.800; P = 0.014). Outbreak

Table 3. Whole Genome Sequencing Application During Outbreaks

WGS Usage	Counts	% of Total
Intervention	17	48.6%
Investigation	7	20.0%
No	11	31.4%

Table 4. Outbreaks Characteristics

	Intervention (n = 17)	Non-intervention (n = 18)
Outbreak duration (months)		
Median (range)	5 (1-37)	14 (2-82)
Duration category		
>12 months	4 (23.5)	7 (38.9)
7-12 months	3 (17.6)	4 (22.2)
4-6 months	5 (29.4)	2 (11.1)
≤3months	5 (29.4)	5 (27.8)
Outbreak duration certainty		
High (%)	10 (58.8)	12 (66.7)
Medium (%)	3 (17.6)	2 (11.1)
Low (%)	4 (23.5)	4 (22.2)
Number of patients		
Median (range)	14 (3-561)	13.5 (8-218)
Outbreak settings		
Single departments (%)	11 (64.7)	10 (55.6)
Multiple departments (%)	6 (35.3)	8 (44.4)
Non-patient sources		
Environment (%)	9 (52.9)	10 (55.6)
Healthcare Workers (%)	2 (11.8)	0
None	3 (17.6)	5 (27.8)
Not performed (%)	3 (17.6)	3 (16.7)

setting (single vs. multiple departments) was not significantly associated with duration ($\beta = -3.3\text{e-}4$, 95% CI -0.706 to 0.704; $P = 0.998$). Visual inspection of the residual diagnostic plots showed no substantial evidence of non-linearity or heteroscedasticity (Figure 2). The normal Q-Q plot indicated that residuals were approximately normally distributed, with minor deviations at the distribution tails (Figure 3). The model explained approximately 25% of the variance in log-transformed outbreak duration ($R^2 = 0.255$).

In ordinal regression (Table 7) of outbreak duration categories, WGS-guided intervention was not significantly associated with shorter outbreak duration either (Odds Ratio (OR) = 0.565, 95% CI 0.147-2.11; $P = 0.396$). Larger outbreaks, as measured by the log-transformed number of patients, were associated with longer duration categories (OR = 21.19; 95% CI 2.9-307.68; $P = 0.01$). Outbreak setting (single vs. multiple departments) was not significantly associated with duration category (OR = 1.254; 95% CI 0.288-5.88; $P = 0.766$). The proportional-odds assumption was

assessed using parallel-lines tests. The assumption was met for WGS usage and outbreak setting but was violated for log-transformed patient number ($\chi^2 = 8.491$, degree of freedom (d_f) = 2, $P = 0.014$). Therefore, the ordinal regression results should be interpreted cautiously. The model showed modest fit (McFadden $R^2 = 0.131$). Model comparison metrics were Deviance = 83 and Akaike information criterion (AIC) = 95.

DISCUSSION

In this systematic review of 35 hospital outbreaks reported across 34 studies, outbreaks in which whole-genome sequencing (WGS) guided intervention strategies showed a shorter median duration compared with outbreaks managed using conventional molecular methods (5 vs. 14 months). Long-lasting outbreaks (>12 months) were less frequent in the WGS-guided group, while outbreaks lasting 4-6 months were more common. However, this apparent difference did not reach statistical significance in either unadjusted or adjusted analyses. In multivariable linear regression, WGS-guided intervention was not independently associated with shorter log-transformed outbreak duration. Similarly, ordinal regression analysis showed no significant association between WGS use and outbreak duration category. In contrast, the number of patients involved in an outbreak was independently

Table 5. The Mann-Whitney U test of Outbreak Duration

	Statistic	P
Mann-Whitney U	117	0.233

Note. All numerical variables are log-transformed

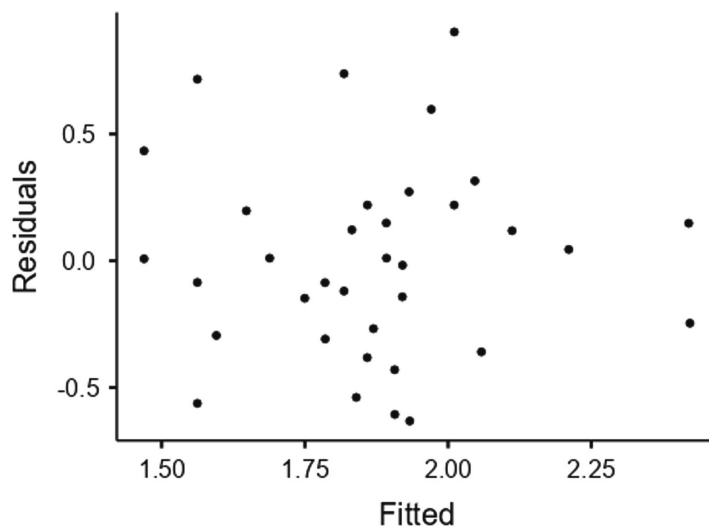


Figure 2. Residuals versus fitted values for the linear regression model

Table 6. Linear Regression of Outbreak Duration

Predictor	Estimate	Standard Error	t	p	95% CI
Intercept ^a	1.021	0.415	2.458	0.02	
WGS Usage:					
Intervention - none	-0.170	0.137	-1.245	0.222	-1.01 to 0.244
The number of patients	0.419	0.160	2.620	0.014	0.100 to 0.800
Setting:					
Single department - Multiple departments	-3.3e-4	0.154	-0.002	0.998	-0.706 to 0.704
R = 0.504; R ² = 0.255					

^aRepresent Reference level; All numerical variables are log transformed**Table 7.** Ordinal Regression of Duration Category

Predictor	Estimate	Standard Error	Z	p	Odds ratio	95% CI
WGS Usage:						
Intervention - none	-0.57	0.672	-0.848	0.396	0.565	0.147 to 2.11
Number of patients	3.054	1.180	2.588	0.010	21.19	2.9 to 307.68
Setting:						
Single department - Multiple departments	0.226	0.762	0.297	0.766	1.254	0.288 to 5.88
Deviance = 83.0; Akaike information criterion (AIC) = 95.0; R ² mcf = 0.131						

Note. All numerical variables are log-transformed

associated with longer outbreak duration in the linear regression analysis. A significant association was also observed in the ordinal regression analysis, although the proportional-odds assumption was violated for this predictor, and the ordinal regression results should therefore be interpreted cautiously. Overall, these findings suggest that outbreak size may be an important factor associated with outbreak duration.

The consistent direction of effect favoring WGS suggests a possible modest benefit, but several factors likely limited statistical significance. First, only 17 outbreaks used WGS to guide intervention, resulting in limited statistical power and wide confidence intervals. A prolonged low-frequency outbreak was included, which contributed to the skewness of the outbreak-duration data in this study due to its inherently long duration.¹³ Second, the implementation of WGS varied substantially across studies. In some outbreaks, WGS directly informed infection-control actions, whereas in others it was used primarily to

confirm transmission links after conventional-typing guided measures were already in place. There were some situations where conventional typing was unable to distinguish the transmission pattern, but with the more detailed information provided by WGS, the clusters of the outbreak were able to be differentiated from the concurrent isolates, and the transmission was able to be determined.^{10,19} Third, more complex or prolonged outbreaks may have been more likely to adopt WGS, which could attenuate observable benefit. Finally, delays in sequencing turnaround time in some settings may have limited real-time impact on outbreak control. Other reviews stated that a delay in the use of WGS reduces the benefits, as early detection of outbreaks enables the timely implementation of interventions to interrupt transmission. In order for this benefit to be realized maximally, WGS needs to be employed early in the analytical pipeline.⁷

In some settings, WGS results may not have been available in real time, limiting their

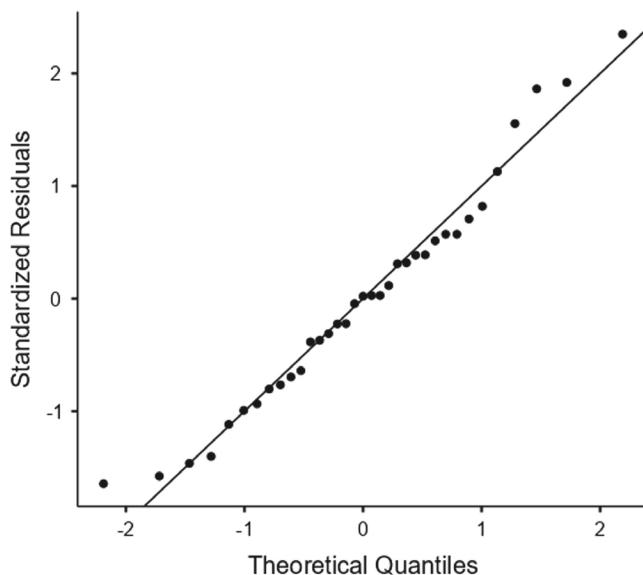


Figure 3. Normal Q-Q plot of standardized residuals for the linear regression model

immediate impact on outbreak control. Thus, while WGS may enhance understanding of transmission pathways, this review suggests that its effect on time to outbreak resolution is not consistently demonstrable across published hospital outbreaks. Previous reports have emphasized the superior discriminatory power of WGS compared with conventional typing methods such as MLST.^{10,19} WGS improves understanding of transmission pathways and identification of hidden links, but most studies focus on epidemiologic clarification rather than operational outcomes.

Recent evidence suggests that the role of WGS in hospital epidemiology is evolving from retrospective confirmation of suspected outbreaks toward prospective and near-real-time genomic surveillance.^{5,6} Real-time sequencing programs have demonstrated that systematic genomic surveillance can identify previously unrecognized transmission clusters and enable infection prevention teams to implement targeted interventions based on genomic and epidemiological data.^{43,44} In complex outbreaks, WGS may provide particular advantages by identifying transmission pathways that involve multiple bacterial species or mobile genetic elements, which may not be adequately resolved by conventional typing methods.⁴⁵ Nevertheless, improved genomic resolution does not necessarily

translate directly into shorter outbreak duration. A recent systematic review of WGS for nosocomial SARS-CoV-2 transmission similarly found that sequencing frequently clarified transmission events, but evidence that WGS altered the trajectory of active outbreaks or reduced nosocomial transmission remained limited.⁴⁶ The effectiveness of WGS therefore appears to depend not only on its discriminatory capacity, but also on turnaround time, integration with epidemiological information, and the ability of infection prevention teams to rapidly translate genomic findings into actionable interventions.^{43,44}

Several methodological considerations should be noted. As a rapid review conducted by a single author, there is a potential for selection and interpretation bias. Efforts were made to apply consistent and systematic criteria to minimize this risk, but the findings should be interpreted with caution. Definitions of outbreak start and end varied across studies, although the certainty of duration estimates was similar between groups. Residual confounding is likely, as pathogen type, infection-control resources, sequencing turnaround time, and healthcare infrastructure were not consistently reported. The varied operational definitions of an outbreak across studies may introduce systematic bias, as they depended on the outbreak guidelines the

respective authors employed.^{47,48} For instance, in the study by Sharma et al., an outbreak was defined as the occurrence of a single new fatal case of *Streptococcus pyogenes* infection rather than an excess of cases above baseline incidence.¹⁹ Such a sensitive definition is more likely to trigger earlier recognition and a broader investigation, including retrospective case finding, which can artificially lengthen the recorded outbreak period compared with studies using stricter epidemiologic thresholds. Conversely, definitions requiring multiple linked cases may delay detection and shorten the measured duration.¹³ This methodological heterogeneity complicates cross-study comparisons and may partly explain variability in outbreak duration independent of interventions such as WGS. Therefore, differences in outbreak definitions should be considered as a potential source of bias when interpreting pooled results or drawing conclusions about intervention effectiveness. The critical appraisal, study selection, and data extraction were performed by a single reviewer, which may have increased the risk of reviewer bias and data extraction errors. The small number of outbreaks included in this study also limits precision. In addition, published outbreaks may overrepresent complex or unusual events. The inability to perform a quantitative meta-analysis reflects the heterogeneity and reporting limitations of outbreak investigations. Differences in outbreak definitions, surveillance intensity, and WGS implementation may have influenced measured durations.

Despite these limitations, this review has strengths. It used systematic inclusion criteria, focused on a clinically meaningful outcome (time to outbreak resolution), and applied multiple analytical approaches with adjustment for outbreak size and setting. Transparency in reporting, including the use of skewed data through log transformation and non-parametric analysis, further supports the robustness of the findings. From a practical perspective, WGS should be considered a complementary tool rather than a standalone solution. Its effectiveness likely depends on rapid turnaround, integration with infection-control teams, and actionable interpretation. Outbreak size and operational factors may ultimately play larger roles in determining resolution time. Future research

should include larger datasets with standardized definitions of both outbreak definition and duration, reporting of sequencing turnaround time, pathogen-specific analyses to determine whether WGS shortens outbreaks in specific contexts, and the use of standardized outcome measures with dispersion measures to enable quantitative synthesis.

CONCLUSION

In this systematic review, WGS-guided outbreak management was associated with a shorter median outbreak duration (5 vs. 14 months), although this difference was not statistically significant after adjustment. The observed direction of effect suggests a potential benefit, but the small sample size, heterogeneity, and wide confidence intervals preclude definitive conclusions. Exploratory regression analysis suggested that larger outbreaks were associated with longer outbreak duration. While WGS enhances epidemiological resolution, current evidence remains insufficient to conclusively determine whether its implementation shortens hospital outbreak duration.

ACKNOWLEDGMENTS

None.

FUNDING

None.

DATA AVAILABILITY

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

ETHICS STATEMENT

Not applicable.

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