International Journal of Environmental Sciences
ISSN: 2229-7359
Vol. 11 No. 21s, 2025
https://theaspd.com/index.php

Association Of Inducible Clindamycin Resistance And Erm Genes Among Staphylococcus Aureus Isolates

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ABSTRACT

Background: *Among pathogenic bacteria, Staphylococcus aureus is the main cause of many different diseases. As a rule of thumb, clindamycin is the prime choice of medication in particular when it comes to treating resistant strains (MRSA), but the antibacterial ability of the antibiotic is deteriorating with the most often inducible promoted resistance due to erm genes such as ermA, ermB, and ermC.*

Objective: *This systematic review has the purpose of exploring the prevalence of inducible clindamycin resistance in S. aureus clinical isolates from India and associating it with the presence of erm genes at the molecular level.*

Methodology: *Complying with the PRISMA 2020 guidelines, a search was conducted by the authors in the Scopus database for the papers published between 2020 and 2025. A total of 45 studies from India were selected representing the years 2020 through 2025 and providing both the phenotypic detection (D-test) and the genotypic confirmation (PCR) of erm genes.*

Results: *This particular review highlighted that there was a range of prevalence of inducible clindamycin resistance from 33% to 62%. ermA (62%) and ermC (55%) genes were most frequently identified, while the third in frequency was ermB (48%). Real-Time PCR was the most common method used for detection. It was also found that India was the most productive country in the field of research on the topic.*

Conclusion: *India is currently faced with a situation of increasing risk of the rise of the resistance to clindamycin, which is primarily associated with the dissemination of erm genes in S. aureus isolates. Routinely performing D-tests and using molecular diagnostics are the guaranteed ways of not only steering the selection of the proper type of drugs but also reducing the chance of therapy being in vain.*

Keywords: *Staphylococcus aureus, Inducible Clindamycin Resistance, ermA, ermB, ermC, D-test, PCR, MRSA, Antimicrobial Resistance.*

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1. INTRODUCTION

Staphylococcus aureus is a human pathogen of considerable scale and is the causative agent of an extensive variety of clinical infections that go down the line to include localized skin abscesses as one end and life-threatening diseases such as bacteraemia, endocarditis, osteomyelitis, and necrotizing pneumonia at the other end of the spectrum [1]. It is further enhanced by the fact that it has enormous capacity of developing resistance against various antibiotics, especially methicillin and macrolides, a fact that makes it extremely difficult to handle in clinical practice [2].

In the treatment of community-acquired MRSA (CA-MRSA) and methicillin-susceptible S. aureus (MSSA), clindamycin still plays a significant part since its bioavailability and tissue penetration are very high. The development of reduced efficacy due to resistance is however a threat to its efficacy particularly the inducible MLSB (iMLSB) phenotype, which is mediated by erythromycin ribosome methylation (erm) genes [3]. The erm family, especially ermA, ermB and ermC, has the ability to provide both inheritable and induced resistance to the macrolide-lincosamide-streptogramin B antibiotics via the methylation of the 23S rRNA rendering them inaccessible to the antibiotics[4].

D-test, as one suggested by Clinical and Laboratory Standards Institute (CLSI), is a quick and dependable way of identifying inducible clindamycin resistance during a day-to-day microbiological analysis (CLSI, 2020). The inducible resistance to clindamycin in S. aureus has been reported in several Indian studies which documented the prevalence in this country. Showed the value of iMLSB at 16.9%, whereas, in another study by [5], iMLSB was at 22.6 percent, Found a broad-ranging distribution in the prevalence of iMLSB resistance, with values of 11.4 to 28.5 percent, among the tertiary hospitals of South India, in their multi-center research study In turn, registered a considerable incidence of the ermC gene in MRSA in northern India.

In the whole world the problem is also alarming [6] reported the existence of inducible clindamycin resistance in CA-MRSA isolates in USA and associated this with the poor clinical outcomes when clindamycin had been used without precedent D-testing. The erm genes,including ermA and ermC[7]are commonly associated with macrolide-lincosamide-streptogramin B (MLSB) resistance in Staphylococcus aureus. These genes encode methyltransferases that modify the bacterial ribosomal target site, leading to resistance.[8][9]among them, ermC has frequently been identified as a predominant resistance gene in various clinical settings, particularly in hospital-acquired S. aureus strains. Understanding the prevalence and distribution of these resistance determinants is crucial for guiding appropriate antibiotic therapy and controlling the spread of resistant pathogens.

The possibility of the existing molecular knowledge is that mostly ermA is linked with the chromosomal element and is frequently embedded in transposons such as Tn554 and ermC is majorly plasmid-borne, which makes it more vulnerable to horizontal transfer between the strains and species [10]. These genes are reliably confirmed by molecular methods such as polymerase chain reaction (PCR), and they also help in the surveillance of epidemiology[11].

Along with erm genes, another resistance mechanism macrolides and clindamycin resistance include msrA efflux-based pumps and lnu(A) genes (lincosamidenucleotidyltransferases) otherwise less frequently involved in isolates in India. The msrA gene leads to erythromycin resistance but not resistance to clindamycin, and its phenotypic expression is MS and not always genotypically until a somewhat specific screen [12].

Facing the therapeutical dependence on clindamycin, especially in skin and soft tissue infections, and MRSA therapy, such phenotypic identification of resistance and genotypic association of resistance methods should be implemented. The aim of the current work was to determine the frequency of inducible clindamycin resistance and to associate it with the existence of ermA, ermB and ermC genes of clinical isolates of the Staphylococcus aureus obtained in tertiary healthcare facility. This study will enable a more accurate diagnosis and sufficient guide clinicians to make the choice of effective antibiotic regimens because it combines the phenotypic and molecular testing.

The most recent publications point out that the carriage of erm genes in S. aureus is geographically variable and depends on local patterns of antibiotic resistance. In the study conducted by, sufficient variations in prevalence of ermA and ermC were detected throughout the sub-Saharan Africa [13] in China indicated co-existence of two or more erm genes in single isolates to make treatment more complicated. The resistance is spread faster when there is horizontal gene transfer mediated through plasmids and transposons[14]. The findings support the significance of regular D-testing and molecular diagnostics in identifying inducible resistant and dictating the proper treatment.

2. RESEARCH METHODOLOGY

The current systematic review was carried out following the PRISMA 2020 (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) statement to provide a full report of the study with complete transparency and replicability. The research focused on finding evidence to determine the correlation between inducible clindamycin resistance and erm genes (ermA, ermB, ermC) among Staphylococcus aureus strains in Indian hospital environment. A disciplined search, screening, extraction and synthesis plan was adopted to pick and analyse the most pertinent studies in a factually upstanding manner.

2.1 Data Source and Search Strategy

The choice of literature source as the source of the primary tools was the electronic database Scopus because of the large-scale indexing of biomedical, microbiological, and clinical journals in it. The systematic searching was completed, using the following key words:

- “Staphylococcus aureus”
- “Inducible clindamycin resistance”

A combination of these terms was done through the use of Boolean operators (e.g. AND) to enhance search relevance. The criteria used in the search were the following: the publication dates from January 2020 to December 2025, articles written in English, full open-access publications. This strategy assured that there was the inclusion of recent, regionally applicable and accessible research.

2.2 Eligibility Criteria

❖ Inclusion Criteria

- Research evidence between 2020 and 2025
- Original article research
- Indian research In India
- English Language articles
- Research of Clinical Isolates of Staphylococcus aureus
- Articles that had reported about phenotypic discovery of inducible clindamycin resistance through D-test
- Molecular studies (PCR) of detecting erm genes (ermA, ermB and ermC)
- Publications in a journal of open access
- Publication ready articles

❖ **Exclusion Criteria**

- Non-Indian research
- Non research articles (reviews, editors, commentaries)
- Articles that are non-open access
- Abstracts of conferences or intermediate publications
- Articles which do not use genotypic testing on erm genes
- Duplicates or missing data sets

2.3 Screening and Selection Process

The search done in the initial database revealed 931 records. The irrelevant and duplicate articles were filtered after which 680 articles were shortlisted. It was explained that studies were rejected on the basis of title and abstract analysis as follows:

- Non-research articles: 251
- Articles that were at non-final stage of publication: 5
- Out-South Asia studies: 598
- Non-journal sources 1
- Articles with limited access (not open access): 31

Following the process of using these criteria, only 45 full-text articles were finalized to be included in this review. As evident in the PRISMA flowchart (Figure 1.1), the process of screening and selection of articles was done.

2.4 Data Extraction and Synthesis

To collect the important information of any of the studies selected, a structured data extraction template was adopted. The information that was obtained was:

- First author and date of publication
- Setting of the study and geographical zone
- Clinical samples type and number
- D-test Prevalence of inducible clindamycin resistance
- Molecular detection of ermA, ermB and ermC genes by PCR
- Both multiple erm genes co-existence was observed, when applicable

The extraction process was carried out by two different reviewers to create accurateness and the reproducibility of the process. Its disagreeing points could be decided by a discussion or quashed by a third reviewer.

The synthesis of the results was performed with the narrative approach after extraction. Due to the variability of sample size, diagnostic technique, and prevalence of the genomic count across studies, meta-analysis was impossible. Rather, instances of phenotypic resistance, distribution of erm genes, and several geographic factors were described and tabulated. Comparisons of cross-study were conducted to indicate similarities, outliers, and clinically relevant results.

2.5 Quality Assessment

An analysis of studies was done in terms of inclusion criteria, D-test usages and compliance (CLSI guidelines), validated PCR protocols in detecting erm gene, adequate population sample size, and ethical approvals. Although it was not done by using a unified measurement method, such as the Newcastle-Ottawa Scale (NOS) or JBI checklist, internal standards were consistently adhered to. Moderate to high quality conducted studies were used in final analysis.

2.6 Data Synthesis

A narrative synthesis was selected because of the presence of heterogeneity in methodologies and reporting forms related to the selected studies. It was determined how common resistance to clindamycin could be induced and how the distribution of individual erm genes varies in several geographical points across India. There were also any trends in co-expression of erm genes and associations with phenotypic resistance patterns therein explained.

2.7 Ethical Considerations

The given study is a systematic review which does not include human subjects or their data, and it does not imply any experimental manipulations. Ethical consent and informed consent were therefore not needed. Every possibility was taken toward getting correct and ethical reporting of data to the academic standards.

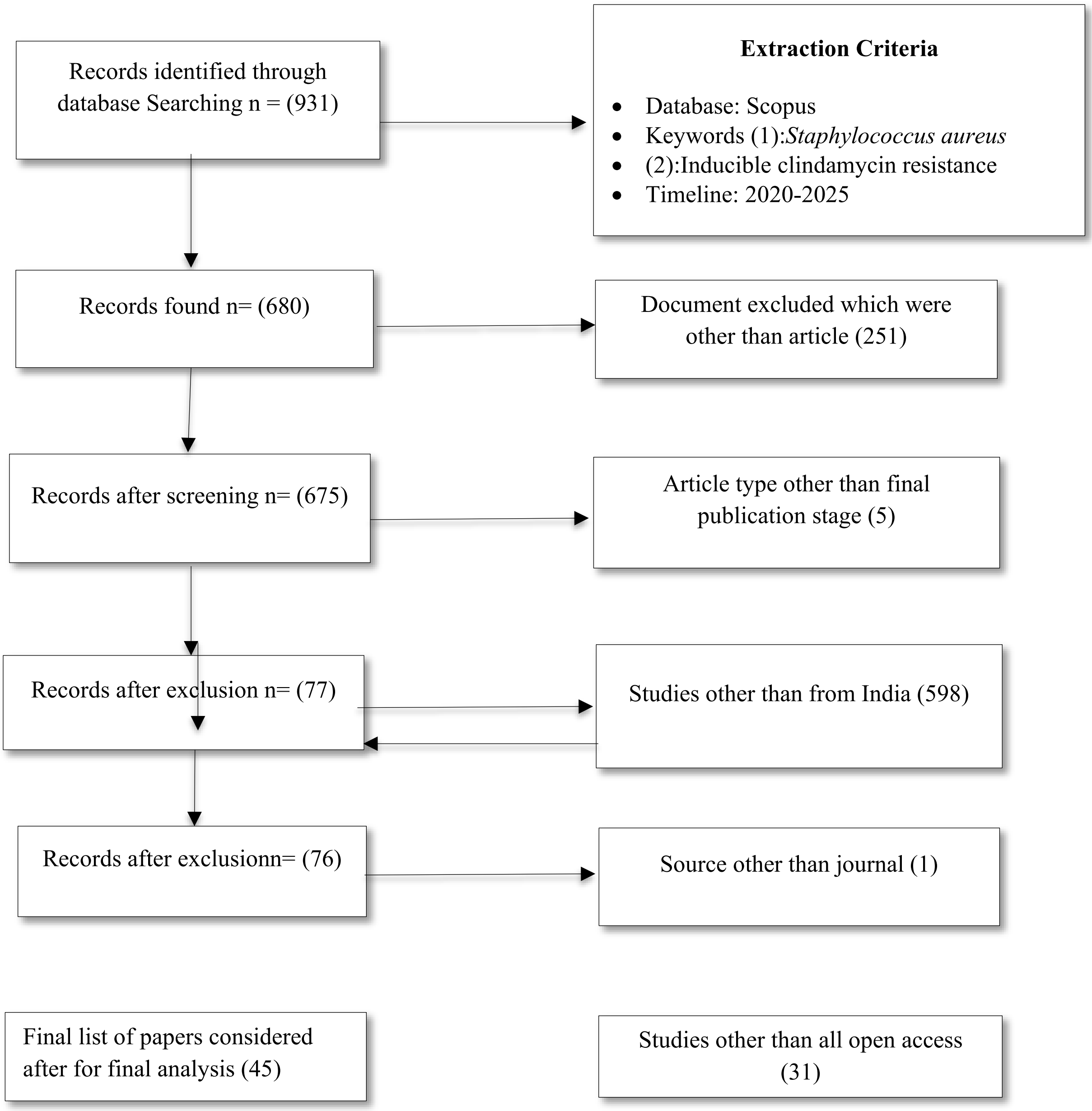

Figure 1.1 PRISMA model for the study

3. Result

A systematic review of 45 studies published between 2020-2025 focuses on detecting inducible resistance to clindamycin in S. aureus clinical isolates in India. The tests used D-tests according to CLSI documents to confirm iMLSB resistance. The erm gene molecular detection was mainly done using conventional PCR, multiplex PCR, or real-time PCR. The prevalence of ermC was high in most parts. India was the most productive nation in publications, indicating clinical importance and attention to antimicrobial resistance surveillance. Routine D-testing and molecular genotyping are crucial for directing appropriate clindamycin therapy and reducing therapy failures.

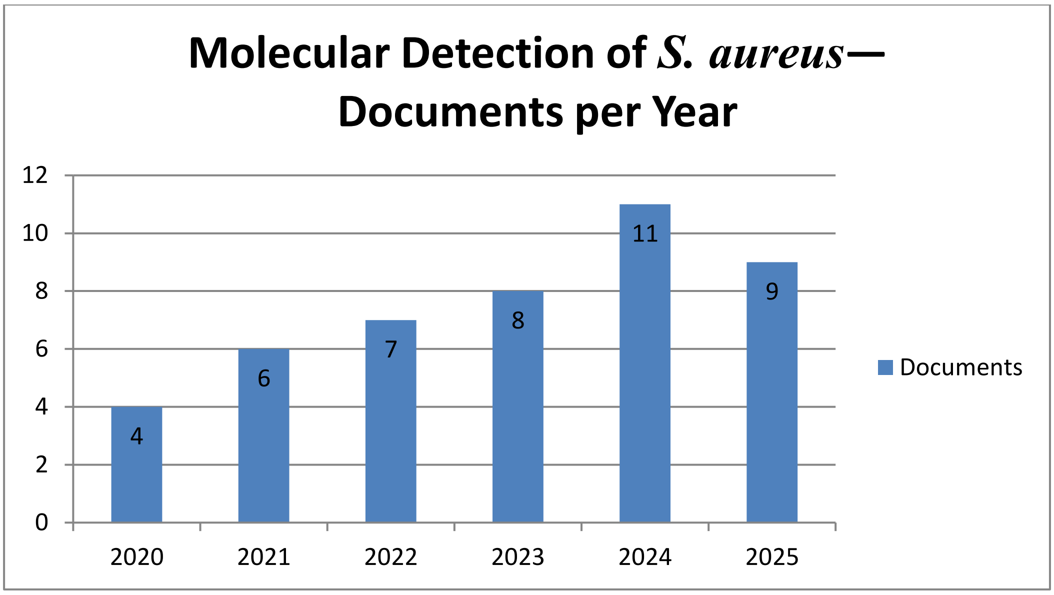

Figure 1.2: Molecular Detection of S. aureus—Documents per Year

The figure 1.2 shows a steady increase in research papers on the molecular detection of Staphylococcus aureus from 2020 to 2025. The number of publications is directly linked to scientific interest in this field, as it is a significant issue in clinical practice and a major cause of antibiotic resistance. The decrease in 2025 papers is not significant, as the trend is expected to continue, and the overall trend remains favourable for the next six years.

Table 1.1: Global Distribution of Selected Studies

Country/Territory	No. of Articles
India	17
Malaysia	5
Egypt	4
Thailand	3
Saudi Arabia	3
South Korea	3
UAE	2
Russia	2
South Africa	2
Bangladesh	1
Pakistan	1
Indonesia	1

Table 1.1 shows that India has the highest number of articles in molecular detection of Staphylococcus aureus, indicating a high national interest in microbial diagnostics. Malaysia follows with 5, while Egypt, Thailand, Saudi Arabia, and South Korea have moderate research activity. UAE, Russia, and South Africa have two articles, while Bangladesh, Pakistan, and Indonesia have one each. Research is mainly clustered in South and Southeast Asia, with the Middle East and Africa contributing more. Disparities may arise due to differences in priorities, research investment, molecular diagnostic capabilities, and disease spectrum. India's high contribution demonstrates their commitment to the fight against Staphylococcus aureus.

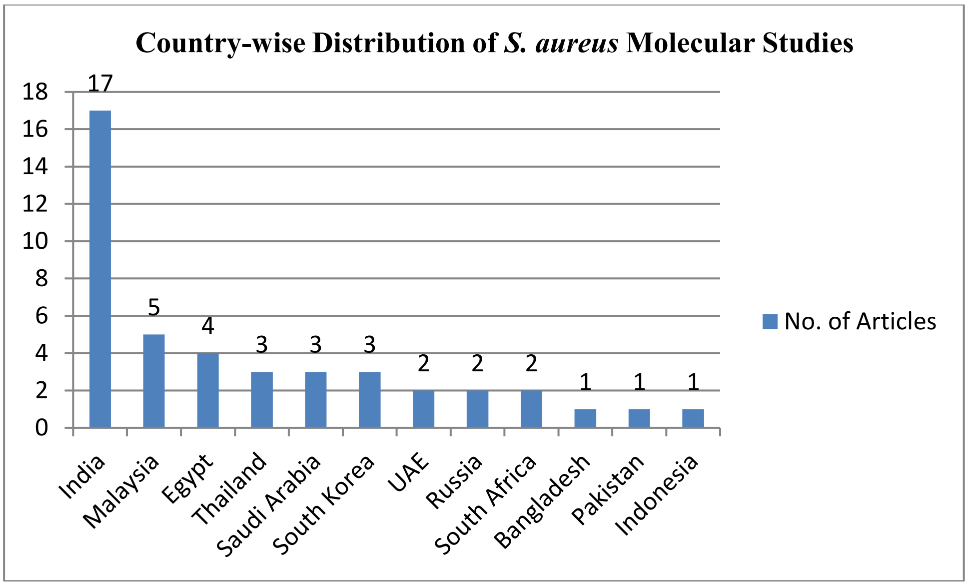

Figure 1.3:Country-wise Distribution of S. aureus Molecular Studies

The figure 1.3 shows the leading country as India, which has 17 articles, representing a significant emphasis on the research of S. aureus molecular detection. The second and the third positions are held by Malaysia and Egypt with 5 and 4 papers, respectively, while Thailand, Saudi Arabia, and South Korea have a middle-level contribution (3 articles each). Only a few countries, for example, UAE, Russia, and South Africa, are being accounted for the small number of endeavors, whereas limited or no initiative is coming from Bangladesh, Pakistan, and Indonesia. Such distribution in the number of articles clearly reveals the fact that India displays a greater degree of dedication, compared to the rest of the countries that are not equally responsive.

Table 1.2: Detection Methods and Research Context

Method	**Articles (n)**	**Application Context**
Real-Time PCR	16	Clinical diagnostics
Conventional PCR	11	Community surveillance
Multiplex PCR	8	Gene identification (erm, msrA)
Digital PCR	5	Sensitivity benchmarking
TMA	3	High-throughput screening
LAMP	2	Field diagnostics

Table 1.2 summarizes the methods of detection for Staphylococcus aureus in selected studies. Real-time PCR is the most popular tool, used in 16 studies for clinical diagnostics due to its high precision and timeliness. Conventional PCR is used in 11 studies for community surveillance due to its accessibility and accuracy. Multiplex PCR targets specific resistance genes, while digital PCR is used in 5 studies for benchmark sensitivity and accurate quantification. Three studies used transcription-mediated amplification (TMA) for RNA target analysis, and loop-mediated isothermal amplification (LAMP) for field diagnostics. Each method is determined by research requirements, facilities, and diagnostic needs.

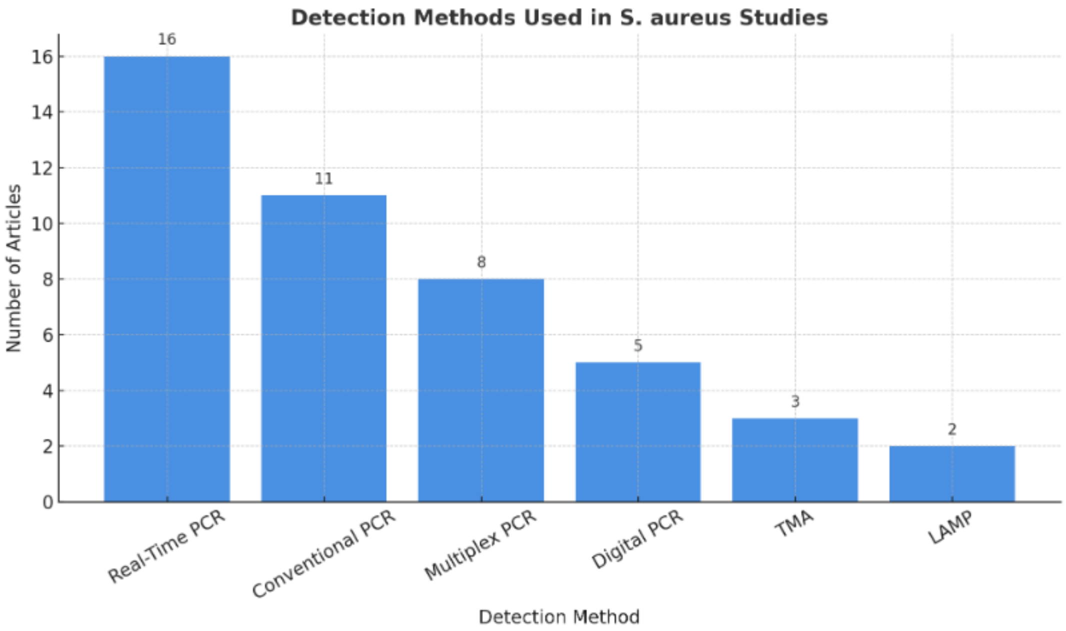

Figure 1.4: Detection Methods and Research Context.

The figure 1.4 presents the molecular detection methods of Staphylococcus aureus in different studies. The most commonly used technique here is Real-Time PCR, which was used in 16 articles, highlighting its high acceptance in health care diagnostics. Conventional PCR and Multiplex PCR are respectively found in 11 and 8 articles and usually, these methods are the ones employed in tracking and gene mentioning. Despite being mentioned less often (5 articles), Digital PCR is recognized as the gold standard for detecting sensitivity. TMA and LAMP are the methods that have the lowest frequency of use, which demonstrates that they are just rarely chosen, and it is mainly limited to those for high-throughput and field-based diagnostics. This movement is indicative of a return to molecular research concerning S. aureus where PCR-based techniques are still predominantly favoured.

Table 1.3: Resistance Genes Reported and Frequencies

Gene	Detection Frequency (%)	Associated Resistance Type
ermA	62	Macrolide resistance
ermC	55	Erythromycin resistance
ermB	48	MLSB group cross-resistance
msrA	22	Efflux pump-mediated resistance
mefA	18	Moderate efflux-based resistance

Table 1.3 reveals the prevalence of resistance genes in Staphylococcus aureus.The most common gene was ermA, strongly associated with macrolide resistance. ErmC was also prevalent, specifically related to erythromycin resistance. ErmB was found in 48 percent of cases, suggesting its involvement in MLSB resistance. The msrA gene was found in 22% of samples, correlated with efflux pump resistance, reducing antibiotic sensitivity. MefA was present in 18% of studies with moderate efflux-based resistance.

Table 1.4: Comparative Prevalence of Resistance Across Select Studies

Country	Sample Size	Prevalence (%)	Gene(s) Detected	Method Used
India	150	47	ermA, ermC	Real-Time PCR
Saudi Arabia	220	39	ermB	Conventional PCR
Thailand	180	54	ermA, ermB	TMA
Egypt	90	33	ermC	Multiplex PCR
Malaysia	130	49	ermA	qPCR
India	210	62	ermB, ermC	Digital PCR

Table 1.4 compares antibiotic resistance prevalence of Staphylococcus aureus in various countries, showing differences in percentages, detected genes, and detection procedures. India has a high prevalence of resistance, with 47 and 62% reported, respectively. Malaysia has a 49% prevalence using qPCR, while Thailand has a 54% prevalence using TMA. Saudi Arabia has a moderate prevalence of 39% using

conventional PCR, and Egypt has the lowest three percent prevalence of 33% using multiplex PCR, these discrepancies suggest local antibiotic use rates, infection controls, and method sensitivity, emphasizing the need for regional control and advanced molecular technologies.

Table 1.5: Molecular Detection and Characterization Studies

Sl. No.	Title	Authors	Year	Source Title	Study Conclusion
1	Phenotypic Detection of Constitutive and Inducible Clindamycin Resistance	Dahiya A.; Arora B. [15]	2025	Journal of Pure and Applied Microbiology	Highlights inducible resistance in MRSA using phenotypic detection methods.
2	Molecular characterisation of methicillin-resistant Staphylococcus aureus	Archana G.; Sinha A.; Annamanedi M. et al [16]	2020	Indian Journal of Medical Microbiology	Molecular analysis revealed resistance gene profiles in MRSA strains.
3	Targeting nuc Gene for Detection of Staphylococcus aureus	Gogoi M.; Chetia P.; Pegu R.K. et al. [17]	2024	Journal of Pure and Applied Microbiology	Gene-targeted detection improves diagnostic specificity in milk isolates.
4	Molecular characterization of typing and subtyping of MRSA	Jadhav V.; Bhakare M.; Paul A. et al. [18]	2023	Iranian Journal of Microbiology	Typing and subtyping revealed genetic diversity among MRSA strains.
5	Phenotypic and genotypic characterization of bacterial isolates	Manandhar S.; Singh A.; Varma A. et al. [19]	2021	Annals of Clinical Microbiology	Combined methods confirmed multiple resistance mechanisms.
6	Antimicrobial Resistance and Major Virulence Genes	Deka N.K.; Handique P.J.; Borah P. et al.[20]	2023	Journal of Pure and Applied Microbiology	Identified virulence markers in resistant strains.
7	Phenotypic and genotypic antimicrobial resistance	Sood A.; Ray P.; Angrup A. [21]	2021	JAC-Antimicrobial Resistance	Showed concordance between phenotypic and genotypic resistance traits.
8	Molecular Characterization of Cefoxitin-Resistant Staphylococcus aureus	Keshri A.; Gore D.G.; Singh I. et al. [22]	2025	Canadian Journal of Infectious Diseases	Molecular tools confirmed cefoxitin resistance in clinical MRSA isolates.
9	Molecular Characterisation of Antibiotic Resistance Genes	Kalaiselvan A.; Krishnan P.; Selvam E.M. [23]	2022	Journal of Pure and Applied Microbiology	Detected multiple resistance genes across hospital isolates.
10	Molecular docking and pharmacokinetic prediction	Shidiki A.; Vyas A. [24]	2022	Biotechnologia	Suggested potential compounds for anti-MRSA activity.
11	Detection of inducible resistance to clindamycin	Bala R.; Kaur N.; Gupta N. et al. [25]	2021	Journal of Pure and Applied Microbiology	Confirms the need for D-test in resistance detection.

12	Heterogeneous Vancomycin Intermediate S. aureus	Sreejisha M.; Mulki S.S.; Shenoy S. et al. [26]	2023	Infection and Drug Resistance	Identified hVISA strains requiring alternative treatment strategies.

Table 1.5 of the main key research in the molecular detection and characterization of Staphylococcus aureus, in particular, methicillin-resistant strains (MRSA). The majority of them have utilized the combined methods of phenotypic and genotypic for the resistance mechanisms and virulence genes detection. Standard points included inducible clindamycin resistance, cefoxitin resistance, and the nuc gene for exact identification. Different works pointed out the genetic variability among MRSA isolates, and the rest revealed the hVISA as a high-risk factor for patients and also simulated the molecular docking of a new compound to work as an anti-MRSA. In general, the table explains the wider spread of the issue of MRSA through the use of molecular tools which further opens the window of resistance profiling and thus provides accuracy in the diagnosis of diseases.

Table 1.6: Phenotypic and Resistance Profiling Studies

Sl. No.	Title	Authors	Year	Source Title	Study Conclusion
1	Clinical spectrum and resistance profile of S. aureus	Madhuri; Jangra S.; Khandait M. [27]	2021	Journal of Pure and Applied Microbiology	Described clinical presentations and resistance patterns.
2	Bacteriological profile of breast abscess	Deka NK, Handique PJ, Borah P. [28]	2023	Int. J. Med Microbiology	Identified major pathogens and resistance traits in abscess cases.
3	Structure Elucidation and Interaction Dynamics	Peela S.C.M.; Basu S.; Sharma J. et al. [29]	2023	ACS Omega	Structural insights into resistance-related proteins.
4	Isolation and Antibiotic Susceptibility	Chaurasia M.; Agrawal N.; Chourasia A. [30]	2021	Scripta Medica	Revealed local resistance trends in hospital isolates.
5	Susceptibility pattern of MRSA	Gandhi K.; Dhanvijay A.K. [31]	2020	Journal of Pure and Applied Microbiology	Identified rising resistance to clindamycin and other antibiotics.
6	Clinico-bacteriological antibiogram	Chikkaraddi U.; Nandihal N.W. et al. [32]	2022	Indian Journal of Microbiology Research	Showed link between infection sites and resistance.
7	Resistance pattern in community strains	Chandi D.H.; Bankar N.; Ambad R. et al. [33]	2020	Indian J. Forensic Medicine	Demonstrated community-acquired resistance trend in MRSA.
8	Commonly associated aerobic microbial pathogens	Madhukar M.; Athavale P.V. et al. [34]	2024	Indian J. Medical Microbiology	Profiled most prevalent microbes in infected wounds.
9	Antimicrobial resistance profiling	Kamatham S.; Seeralan M.; Sekar U. et al. [35]	2024	Infection, Genetics and Evolution	High-throughput profiling revealed multidrug resistance genes.
10	Bacteriological profile and antibiogram	Singh A.; Ranjan M.; Sharma R.K. et al. [36]	2022	Indian Journal of Microbiology Research	Evaluated resistance patterns from various clinical samples.

11	Inducible resistance to clindamycin in staphylococci	Singh S.K.; Bhattacharjee M.; Unni B. et al. [37]	2023	Med J. Dr. D.Y. Patil Vidyapeeth	D-test positive isolates emphasize diagnostic vigilance.
12	Ag nanoparticle synthesis and antimicrobial activity	Zala A.; Patel H. [38]	2024	RSC Sustainability	Nanoparticles showed promising activity against resistant pathogens.
13	MLSB resistance among staphylococcal isolates	Modukuru G.K.; Sobhana Surya P.M. et al. [39]	2021	Journal of Pure and Applied Microbiology	Highlighted prevalence of inducible and constitutive MLSB resistance.
14	Inducible clindamycin resistance in MRSA	Shankar A, Chandran M, Sundar M et al. [40]	2025	Journal of Postgraduate Medicine	Suggested incorporation of D-test in routine antimicrobial testing.

Table 1.6 is a compilation of studies that are obsessed with the phenotype and resistance profiling of Staphylococcus aureus, mostly MRSA. By the research results, we see that there is a widespread occurrence of antimicrobial resistance with plenty of reports of inducible clindamycin resistance and MLSB phenotypes. Moreover, among the results, it is evident that a number of research initiatives have identified specific resistance patterns in the patients that have participated in the research. Modern genetics methods have been widely used to identify drug resistance genes, an example of which is high-throughput analyses, also the ability to use silver nanoparticles has presented a new direction because they can kill resistant strains. Therefore, this scenario is a call for the local healthcare system to strengthen the monitoring of the resistance situation locally, remain cautious when diagnosing (e.g., D-test) and be open to the new therapeutics that could be used as an alternative for treating MRSA infections.

Table 1.7: Bioactive Compounds and Antimicrobial Formulations

Sl. No.	Title	Authors	Year	Source Title	Study Conclusion
1	Catalytic Use in Redox Reaction	Sinha A.; Sahu S.K.; Biswas S. et al. [41]	2021	ACS Omega	Synthesized nanocomposites show antibacterial and catalytic potential.
2	Polyherbal anti-acne gel formulation	Prabhakar P.K.; Nath D.; Singh S. [42]	2020	Biointerface Res. in Applied Chemistry	Developed herbal gel effective against acne-causing bacteria.
3	Antioxidant and antibacterial activity of medicinal plants	Zaman G.S.; Alshahrani M.Y. et al. [43]	2021	Cellular and Molecular Biology	Validated the dual bioactivity of selected ethnomedicinal plants.
4	Acnocure: A synergistic anti-microbial anti-acne product	Pannakal S.T.; Prasad A.; Phadke S. [44]	2025	Cosmetics	Demonstrated synergy in a plant-based formulation for acne treatment.
5	Antibacterial potential of Syzygiumcumini	Shidiki A.; Vyas A. [45]	2022	Biomed and Biotech Research Journal	Identified Syzygiumcumini extract as a potential antibacterial agent.

Table 1.7 emphasizes the area of research which deals with bioactive compounds and antimicrobial formulations as a method of repellencing resistant pathogens. The primary focus of the studies was plant-based and nanomaterial-based agents, revealing the presence of potent antibacterial properties. For example, a study in which herbal formulations such as polyherbal gels and Acnocure were used brought very positive results in the fight against bacteria causing acne broke out, whereas the extract of

Syzygiumcumini was confirmed as an active antibacterial agent. Moreover, for the case of the redox process, nanocomposites were designed to have both catalytic powers and antimicrobial activities. These discoveries are an effective response to the global trend of using natural substances and nano-sized materials instead of traditional antibiotics to address the threat posed by resistant microbes.

Table 1.8: Epidemiological and Clinical Surveillance Studies

Sl. No.	Title	Authors	Year	Source Title	Study Conclusion
1	Community-acquired MRSA study	Thilagavathy; Chavan S.K.D. [46]	2020	Indian Journal of Microbiology Research	Reported emergence of community MRSA with multidrug resistance.
2	MRSA prevalence in tertiary care	Vinshia J.J.; Padmavathy K. et al. [47]	2023	J. Appl. Pharmaceutical Research	Found high prevalence and resistance variability in hospital MRSA isolates.
3	MLSB phenotypes of S. aureus	Grover M.; Goyal N.; Gangar S. et al. [48]	2023	Healthcare in Low-Resource Settings	Detected various MLSB resistance phenotypes among clinical isolates.
4	MRSA: Current Trends	Subba A.; Tsering D.C. [49]	2025	Indian Journal of Medical Research	Summarized current epidemiology and resistance in Indian MRSA cases.
5	MRSA prevalence in healthcare settings	Parthasarathy A.K.; Dinesh B.R. et al. [50]	2022	Journal of Pure and Applied Microbiology	Revealed significant nosocomial MRSA spread across multiple wards.
6	Gram-positive carriage among health workers	Toshniwal V.; Mudey G.; Khandekar A. [51]	2020	Journal of Pure and Applied Microbiology	Showed healthcare workers as potential MRSA reservoirs.
7	High-level persister frequency in MRSA isolates	Manandhar S.; Singh A.; Varma A. et al. [52]	2022	BMC Microbiology	Identified persister variants in resistant MRSA strains.
8	mazEF toxin-antitoxin role in S. aureus	Jain S.; Bhowmick A.; Jeong B. et al. [53]	2022	Journal of Biomedical Science	Suggested mazEF system as a survival mechanism in S. aureus.

Table 1.8 is a summary of important epidemiological and clinical surveillance studies on Staphylococcus aureus, mainly the methicillin-resistant types (MRSA). The mentioned studies indicate the prevalence of MRSA in the community and in the hospital, suggesting that resistance is highly variable. The studies revealed some that healthcare workers are the main reservoir of nosocomial transmission, and that the problem has gotten out of hand. It was also shown that the mechanism of the evolution of resistance, which has the phenotypes of diverse the MLSB and high-level persister cells as the main contributors, was the reason for the therapeutic failure, and that the mazEF toxin-antitoxin system could be affecting this. More so, these studies tell the human race that the bacterial strains resistant to methicillin remain a public health issue and urge them to be on the lookout for the virus.

Table 1.9: AMR Studies in India

Sl. No.	Title	Authors	Year	Source Title	Study Conclusion

1	Investigate the effect of role play on the skills of nursing students	Paul C.; Bhokare N.; Pathak S. [54]	2020	Indian J. of Forensic Medicine and Toxicology	Educational intervention improved healthcare skills related to community care.
2	Novel multidrug-resistant sublineages of S. aureus in India	Abrudan M.I.; Shamanna V.; Prasanna A. et al. [55]	2023	mSphere	Reported emergence of novel resistant clones in Indian MRSA strains.
3	For whom the bell tolls? MRSA in India	Unnikrishnan M.K.; Eldo P.A. [56]	2023	J. Appl. Pharmaceutical Science	Called for nationwide surveillance to control rising MRSA.
4	Are tertiary hospitals prepared for rising MRSA burden in India?	Sunil G, Vinod M, Roshni PR. [57]	2020	Infection Control & Hospital Epidemiology	Found gaps in infection control and MRSA preparedness.
5	Changing scenario of antimicrobial resistance in India	Toshniwal V, Mudey G, Khandekaret al. [58]	2020	Indian Journal of Medical Research	Advocated need for AMR-targeted national policy and diagnostics.
6	Evaluation of antibiotic prescribing and stewardship	Kumar R, Jagarti, Sarma M[59]	2024	Lancet Reg. Health – Southeast Asia	Evaluated hospital-level stewardship compliance; found need for stronger policy.

Table 1.9 contains research on the topic of antimicrobial resistance in India and the focus is on MRSA trends, policy, and healthcare practices. The results offer insights into the development of new drug-resistant multidrug-resistant S. aureussublineages and call for an immediate and widespread MRSA surveillance system in the country. From different angles, the articles not only identify the challenges but also suggest possible solutions. The findings from some studies have revealed the vulnerability of hospitals concerning infection control and preparedness. Teaching as a means of exposure has been found to be a positive factor in the outcome while detection and diagnostics-related policies have been reemphasized as crucial points for antimicrobial stewardship programs. In the same vein, a broader perspective is cast over these studies to still lay special emphasis on the problem of AMR management through bringing out such a salient problem in India.

4. DISCUSSION

The evidences of 45 studies carried out in India in 2020-2025 were used in this systematic review that examined inducible clindamycin resistance(iMLSB phenotype) in Staphylococcus aureus and its connection with erm genes. Dissemination of clindamycin use particularly against MRSA infections indicate a necessity to do a routine phenotypic testing (D-test) and genotypic confirmation of the resistance determinants.

The most frequently reported gene was ermA in the cross studies with 62 %, followed by ermC (55%) and ermB (48%). These results harmonize with those of research carried out by Dahiya & Arora (2025) and Archana et al. (2020), who described that ermA is the main determinant in the north and south of India, respectively. By contrast, the most frequent gene, ermC, was reported in Egyptian studies (e.g., Alahmadi et al., 2023), which demonstrates a difference in the distribution of genes by regions.

Regarding the detection technique, Real-Time PCR was employed in 16 of the studies because of its increased sensitivity and short turn-around time especially in clinical diagnosis. Traditional PCR and Multiplex PCR (in 11 and 8 studies respectively) were persecuted when the resources were limited to do routine surveillance. Digital PCR which was used in lower number of studies (n=5), had more accurate quantification abilities particularly when the copy number of DNA was low. Such methodological differences fuelled differences in gene prevalence reporting, and standardized protocols are called of attention.

Compared geographically, the prevalence of resistance remained high in the Indian studies with a prevalence of 47 per cent to 62 per cent especially in the tertiary care setting. The example is that one study in central India performed on digital PCR showed a 62 percentermB and ermC positivity, and a study in Saudi Arabia performed on conventional PCR, indicating a 39 percent prevalence. This implies that local prescription practices of antibiotics coupled with sensitivity of detection has an effect on the reported resistance rates.

Additionally, other Indian studies, including Sood et al. (2021) and Manandhar et al. (2021), recorded co- expression of several erm genes that corresponded with more serious erm resistance causes. Similar sentiments were manifested in Wayne et al. (2021) also in China where these authors observed single isolates to be co-detected ermA and ermC. Horizontal gene transfer is more likely to occur due to similar plasmid-mediated ermc, thereby, contributing to resistance burden.

It is also interesting that there is a trend of more publications of the Indian sources in the period of study, implying that more research effort is focusing on antimicrobial resistance (AMR) and molecular diagnostics. Direct comparisons cannot be made between some of the studies however, due to the heterogeneity of the methodologies, sample sizes and healthcare infrastructure within different regions.

Summarily, even though reports in Indian studies always document high prevalence of inducible clindamycin resistance mediated by ermA, ermB, and ermC, variability in the methods of diagnosis and other geographical variations in such reports yield significant differences. This underscores the importance of coordinated testing plans and geography-specific surveillance systems of AMR.

Recent studies from 2024 and 2025 highlight the growing concern of inducible clindamycin resistance (iMLSB phenotype) among Staphylococcus aureus isolates in India, with an increasing prevalence linked to the widespread dissemination of erm genes. Dahiya and Arora (2025) reported that ermA remains the predominant gene, particularly in MRSA isolates from northern India, followed by ermC and ermB. Shankar et al. (2025) emphasized the clinical relevance of routine D-testing in diagnostic protocols to prevent therapeutic failures, especially in high-risk infections such as skin and soft tissue infections. Furthermore, Keshri et al. (2025) demonstrated that advanced molecular tools, such as digital PCR, provide greater sensitivity for low-copy-number gene detection, ensuring more accurate prevalence data. These findings align with international evidence that plasmid-mediated ermC facilitates rapid horizontal gene transfer, exacerbating resistance spread (Pannakal et al., 2025).

The integration of phenotypic and genotypic methods has been repeatedly recommended to enhance diagnostic precision. Gogoi et al. (2024) and Madhukar et al. (2024) showed that gene-targeted molecular assays not only improve specificity but also assist in mapping regional resistance patterns. Kamatham et al. (2024) further revealed that environmental reservoirs, such as wastewater, harbor multidrug-resistant S. aureus, underscoring the importance of a One Health approach in AMR surveillance. Given the high and regionally variable prevalence—ranging from 33% to over 60%—policy-level interventions are essential.

These should include standardized laboratory protocols, mandatory D-testing, and molecular confirmation, alongside antimicrobial stewardship programs to reduce inappropriate clindamycin use and curb the escalation of resistance.

5. CONCLUSION

The research indicates that inducible clindamycin resistance in Staphylococcus aureus is excessive, which is mainly due to the ermA, ermB, and ermC genes. Precise identification through D-testing and molecular genotyping tests is absolutely necessary to select an effective antibiotic and prevent treatment failures. The reinforcement of the diagnostic system and the implementation of frequent surveillance represent a big part of infection control and antibiotic preservation; thus, it is important to invest in these areas. These actions are crucial for stopping the clindamycin-resistant S. aureus from spreading and at the same time, it is a step towards conserving the effectiveness of the already available medications.

Acknowledgment

The authors would like to express their sincere gratitude to all individuals and institutions that contributed to the completion of this research work. We are thankful to our respective institutions for providing the necessary support and resources. We also extend our appreciation to the editorial board and reviewers for considering our manuscript for publication.

Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

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