

Genetic analysis of virulence factors, biofilm formation ability, and clonal diversity in community-acquired methicillin-resistant *Staphylococcus aureus* strains isolated from patients in Tehran

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Abstract

Background: Community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) is responsible for a wide range of infections, from skin and soft tissue infections to severe systemic diseases. This study aimed to determine the prevalence and genetic profiles of virulence factors among CA-MRSA isolates in Tehran.

Materials and Methods: Between 2022 and 2024, a total of 279 suspected MRSA isolates were collected from the microbiology laboratory of a referral hospital in Tehran. Identification of isolates was performed using PCR with specific primers targeting the *nucA* and *mecA* genes, as well as the cefoxitin disk diffusion test. Virulence factors were detected by PCR using gene-specific primers. Biofilm formation ability was evaluated using Congo red agar and the microtiter plate assay. SCCmec typing, prophage typing, and *agr* typing were carried out using multiplex PCR, and clonal diversity was assessed by PhP typing.

Findings: In total, 47 isolates (17%) carrying SCCmec types IV and V and prophage type SGA were identified as CA-MRSA. These isolates exhibited two prophage patterns and three *agr* types. All isolates possessed the *sea*, *sek*, *seq*, *sak*, *hly*, and *pvl* genes. Moreover, 29 isolates were slime-positive or slime-variable, and overall, 76% of isolates were capable of biofilm formation. Based on PhP typing, 11 distinct patterns were identified, including seven unique and four shared types, with CT2 being the most prevalent (43%).

Conclusion: Limited clonal diversity among CA-MRSA isolates harboring multiple virulence factors indicates the spread of dominant, highly pathogenic clones between hospital and community environments. Continuous monitoring is essential to prevent their dissemination.

Keywords: Methicillin-resistant *Staphylococcus aureus*, Virulence factors, Biofilms, Molecular Epidemiology, Prophage Type, *agr* Type

Evaluation of the Short- and Long-Term Adverse Effects of COVID-19 Vaccines (Inactivated, Adenovirus, and Protein Subunit Vaccines) in the Iranian Population with Chronic Cardiopulmonary Diseases

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Abstract

Background: According to the widespread outbreak of the coronavirus (COVID-19) and global efforts to control it, vaccination has been used as the most effective preventive tool against infection and mortality caused by this disease. However, individuals with underlying health conditions such as diabetes, heart diseases, immune deficiencies, and chronic respiratory illnesses, due to their specific health status, may show different effectiveness and reactions to the vaccines. Since this group is more at risk of severe COVID-19 complications than others, having a precise understanding of the potential side effects of vaccines in these individuals is of particular importance.

The necessity of conducting precise and systematic studies on the side effects of vaccines in populations with underlying health conditions not only helps optimize vaccination strategies but also increases public trust, improves clinical decision-making, and enhances collective immunity. Identifying and accurately analyzing potential side effects can be crucial for developing appropriate care guidelines and selecting the safer type of vaccine for these high-risk groups.

Materials and Methods: In this study, individuals with chronic heart and/or pulmonary disease were followed up after obtaining written consent. For this purpose, a researcher made questionnaire including demographic information, disease status, vaccination history and type, and vaccine outcomes were recorded in the first 7 days and thereafter. After collecting the data, statistical analysis was performed for short-term events in two time periods: 7 days after vaccination and days 8 to 21.

This analysis was performed based on vaccine doses, study groups, and vaccine platforms. All late events up to two years after vaccination were also evaluated.

Results: The study results showed that the most common side effects in the short term up to 21 days after vaccination were related to reactogenicity outcomes such as fever, body aches, fatigue, and injection site pain. More serious side effects such as memory loss, impaired concentration, and decreased libido were also reported to a lesser extent and usually after the first week.

In the long-term period of up to two years after vaccination, more serious complications such as ischemia, Alzheimer's, urinary problems, and changes in blood factors were recorded, which were mainly seen in recipients of the Sinopharm vaccine and then in the AstraZeneca group. Although the PastoCovac vaccine had a higher rate of reporting in short-term complications, in long-term follow-up it was considered safer than the mobile vaccines and had fewer complications.

Conclusion: Although the occurrence of reported adverse events does not necessarily indicate a causal relationship with vaccines, and factors such as physical condition, underlying diseases, and lifestyle may also influence these outcomes, long-term monitoring of the safety of COVID-19 vaccines particularly among individuals with underlying medical conditions is essential for informed vaccine policy-making. Continuous surveillance of these populations can also help in selecting the optimal vaccine platform and improving immunization strategies.

Keywords: COVID-19; cardiovascular or pulmonary disease; vaccine platform; reactogenicity; adverse effects.

The role of artificial intelligence and large language models in infectious disease consultation: opportunities, challenges, and future prospects

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Abstract

Background: Artificial Intelligence (AI) has recently emerged as one of the most transformative technologies in healthcare. Advances in large language models and machine learning-based systems have enabled the application of AI in patient education, answering medical questions, supporting clinical decision-making, and managing infectious diseases. Due to their widespread prevalence, the need for rapid diagnosis, and the importance of epidemic control, infectious diseases are among the fields that can significantly benefit from AI applications. The aim of this article was to review the role of artificial intelligence and large language models in infectious disease consultation and to analyze the applications, advantages, limitations, and challenges of this technology in patient communication and healthcare support systems.

Methods: This study was conducted as a narrative review. Relevant articles were retrieved from major scientific databases including PubMed, Scopus, and Google Scholar using keywords such as “Artificial Intelligence,” “ChatGPT,” “Infectious Diseases,” “Clinical Microbiology,” and “Medical Consultation.” Recent studies on the application of AI in infectious diseases, medical consultation, and patient education were evaluated.

Results: The reviewed studies demonstrated that AI can play an effective role in answering patients' questions, health education, preliminary symptom screening, epidemic prediction, epidemiological data analysis, and assisting in the diagnosis of infectious diseases. Models such as ChatGPT are capable of providing rapid and understandable information and may improve patients' access to health-related information. However, several limitations remain, including the potential generation of inaccurate information, errors in therapeutic decision-making, lack of transparency in scientific sources, ethical concerns, and issues related to data privacy and confidentiality.

Conclusion: Artificial intelligence has considerable potential to enhance infectious disease consultation and patient education, while also providing new opportunities in medical question answering, epidemiological data analysis, and support for therapeutic decision-making. Nevertheless, limitations such as the possibility of scientific inaccuracies, hallucinations, algorithmic bias, lack of clinical examination capability, ethical concerns, and issues related to data confidentiality prevent AI from being considered a complete replacement for physicians. Therefore, under current conditions, the most appropriate approach is to use AI as a supportive tool alongside physicians and infectious disease specialists rather than as a substitute for them.

Keywords: Artificial Intelligence, Infectious Diseases, ChatGPT, Large Language Models, Medical Consultation, Patient Education

The Role of Artificial Intelligence in the Diagnostic and Therapeutic Approach to Tuberculosis: From Clinical Suspicion to Treatment Decision-Making

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Abstract

Background: Tuberculosis (TB) remains one of the most important infectious diseases worldwide. Despite considerable advances in diagnosis and treatment, diagnostic delays, difficulties in diagnosing certain high-risk populations, drug resistance, and limited access to diagnostic facilities remain major challenges to TB control. In recent years, artificial intelligence (AI), particularly machine learning and deep learning, has emerged as a promising tool for improving various stages of TB management. This article aims to review the role of AI across an integrated diagnostic and therapeutic pathway for TB, from modifying the probability of clinical suspicion and screening to diagnosis, assessment of drug resistance, treatment decision-making, and monitoring of treatment response.

Methods: This narrative review examines the applications of AI across different stages of the clinical approach to TB. Current evidence regarding the use of AI algorithms for chest radiography analysis, TB screening and triage, interpretation of clinical, laboratory, and molecular data, prediction of drug resistance, assessment of treatment response, and prediction of clinical outcomes was reviewed.

Results: Available evidence indicates that AI can be applied across multiple stages of the diagnostic and therapeutic pathway for TB. At the screening stage, Computer-Aided Detection (CAD) systems can automatically analyze chest radiographs to identify individuals with findings suggestive of TB and prioritize them for further diagnostic testing; the WHO has endorsed the use of certain CAD systems for TB screening and triage in individuals aged 15 years and older. Machine-learning and deep-learning algorithms have also been investigated for integrating clinical symptoms and findings, epidemiological information, laboratory results, and imaging data to estimate the probability of TB and support diagnostic decision-making. In the field of molecular diagnosis and drug resistance, AI-based models are being developed to identify resistance patterns and predict the likelihood of resistance to anti-TB drugs. In addition, AI applications have been explored for predicting treatment response, identifying patients at risk of adverse outcomes, predicting treatment failure and disease relapse, and supporting treatment monitoring.

Conclusion: Overall, current evidence suggests that the most clinically mature applications of AI are in chest radiograph analysis and support for TB screening and triage, whereas applications in drug-resistance prediction, treatment selection and monitoring, and prediction of clinical outcomes remain largely under development and require further validation.

AI has the potential to extend beyond a single diagnostic tool and serve as a complementary technology across the clinical pathway of TB, from strengthening initial clinical suspicion and screening to treatment decision-making and patient monitoring. However, safe and effective integration of AI into clinical practice requires external validation across diverse populations and settings, attention to interpretability, and preservation of clinical judgment in final decision-making.

Keywords: Tuberculosis; Artificial Intelligence; Machine Learning; Deep Learning; Computer-Aided Detection; Chest Radiography; Drug Resistance; Clinical Decision-Making