Predicting Vaccine Safety Profiles Using Immunoinformatics: From Adverse Event Surveillance to Personalized Safety and Immunogenicity

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Abstract

Introduction: Vaccine safety is a fundamental pillar of successful vaccination programs, and the timely detection, accurate assessment, and effective management of adverse events following immunization (AEFIs) are of critical importance. As the volume and complexity of data generated from safety-reporting systems, health records, and immunological studies continue to increase, artificial intelligence (AI) has the potential to transform conventional approaches to vaccine safety surveillance. This perspective review aims to explore the emerging applications of AI in the detection, prediction, and management of vaccine-related adverse events, with particular emphasis on their relationship with immune responses.
Methods: In this perspective review, relevant studies investigating the use of machine learning, deep learning, natural language processing, and large language models in vaccine safety surveillance, adverse-event detection, safety signal identification, reactogenicity prediction, and causality assessment were reviewed and critically interpreted from immunological and vaccinological perspectives.
Results: Current evidence indicates that AI can extract adverse-event information from narrative reports and electronic health records, identify potential safety signals, and predict the severity of certain post-vaccination reactions. Moreover, integrating immunological data with machine-learning algorithms has enabled the identification of molecular and cytokine patterns associated with vaccine reactogenicity. These findings raise the possibility of using baseline immune phenotypes to predict individual responses to vaccination.
Conclusion: The future of vaccine safety may evolve from reactive pharmacovigilance toward predictive immunosafety, in which clinical, immunological, molecular, and digital data are integrated to enable early adverse-event detection and individualized risk profiling. However, external validation, prospective studies, mitigation of algorithmic bias, and expert oversight will be essential for translating these technologies from research settings into clinical and regulatory practice.
Keywords: Artificial intelligence; Vaccine safety; Adverse events following immunization; Immunology; Pharmacovigilance.

Pneumococcal Serotype Replacement Following Universal PCV Vaccination: Surveillance Requirements for Iran's National Immunization Program

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Abstract

Background: Pneumococcal conjugate vaccines (PCVs) target specific serotypes of *Streptococcus pneumoniae*. Reductions in nasopharyngeal colonization and disease caused by vaccine serotypes may be accompanied by a relative or absolute increase in non-vaccine serotypes, a phenomenon referred to as serotype replacement. Since PCV was introduced into Iran's national immunization program in 2024 (1403 in the Iranian calendar), reviewing the evidence on epidemiological changes in serotypes, and clarifying the requirements for monitoring them, is of particular importance for evaluating the effectiveness of the vaccination program. This study aimed to review the global evidence on serotype replacement following the implementation of universal vaccination programs and to define surveillance priorities in Iran.

Results: International evidence indicates that the universal use of PCVs has substantially reduced pneumococcal disease caused by vaccine serotypes. However, the extent and consequences of serotype replacement have varied across countries. In some settings, an increase in disease caused by non-vaccine serotypes has partially offset the reduction achieved through vaccination, although the magnitude and clinical significance of this trend have not been uniform. Available data from Iran mainly relate to the pre-universal-vaccination period and can provide a baseline for assessing future changes in serotype distribution.

Conclusion: Evaluating the effectiveness and long-term outcomes of the pneumococcal vaccination program in Iran requires establishing and strengthening continuous serotype surveillance among invasive pneumococcal disease cases and nasopharyngeal carriage. Accurate recording of vaccination status, the use of high-resolution molecular methods, including whole-genome sequencing, and concurrent monitoring of antibiotic resistance patterns can provide the evidence needed to assess the program's impact and to inform decisions on the composition of future vaccines.

Keywords: Streptococcus pneumoniae; serotype replacement; pneumococcal conjugate vaccine; surveillance; Iran

Cybersecurity in Healthcare and the Care of Patients with Infectious Diseases: Implications for Patient Safety and Public Health

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Abstract

With the increasing use of digital technologies in healthcare, laboratory and imaging systems, communication platforms, and electronic prescribing have become important components of healthcare delivery. Cyberattacks, particularly ransomware attacks, are not merely technological incidents or events limited to breaches of information confidentiality; they can also jeopardize continuity of care and patient safety by disrupting access to diagnostic results, prescribing processes, and information exchange. Unauthorized disclosure of clinical and microbiological data may additionally expose information about antimicrobial resistance patterns and the epidemiological distribution of communicable diseases across different geographical areas. The nature and extent of these consequences depend on the degree of digitalization within a healthcare system. In Iran, although inpatient medical records are predominantly paper-based, electronic prescribing in outpatient care and the use of digital laboratory, imaging, and communication systems create continuing dependencies on digital infrastructure. This narrative review examines published evidence on the effects of cyberattacks on access to clinical information, continuity of diagnostic and therapeutic services, and public health. With a focus on infectious diseases specialists, it also considers the potential consequences of disrupted access to culture and antimicrobial susceptibility results, antimicrobial stewardship processes, infection surveillance, and disease reporting. Available evidence, derived mainly from observational studies and case reports in countries with digital infrastructures that differ from Iran’s, indicates disruptions to healthcare delivery, delays in diagnostic and therapeutic processes, and the transfer of some patient-care burden to neighboring facilities. However, extrapolation of these findings to Iran requires consideration of differences in healthcare infrastructure and medical record systems. Preparedness tailored to each facility’s infrastructure including alternative pathways for documenting and transmitting information, continuity of care for critically ill patients, protection of data confidentiality and integrity, and data recovery and reconciliation after service disruption should be integrated into patient safety and healthcare continuity plans alongside preventive cybersecurity measures.

Keywords: Cyberattacks; Cybersecurity; ransomware; patient safety; infectious diseases; antimicrobial resistance; public health; Electronic Prescribing

Ethylenic and Acetylenic Motifs in Antimicrobial Drug Discovery: Structure–Activity Relationships, Mechanisms of Action, and Potential Applications Against Bacterial and Fungal Pathogens

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Carbon–carbon double (C=C) and triple (C≡C) bonds represent important structural features of numerous natural products and synthetic bioactive molecules with potential antimicrobial properties. These unsaturated structural motifs are found in diverse chemical classes, including cinnamic acids and their derivatives, chalcones, phenylpropanoids, unsaturated fatty acids, natural polyacetylenes, and synthetic compounds containing enyne and diyne functionalities. Accumulating evidence suggests that the antimicrobial activity of these compounds is not exclusively determined by the presence of ethylenic or acetylenic bonds. Instead, their biological properties are influenced by several structural and physicochemical factors, including molecular geometry, conjugation, carbon-chain length, lipophilicity, electronic distribution, and the nature and position of neighboring functional groups.In ethylenic compounds, substituents such as hydroxyl, methoxy, carbonyl, carboxyl, ester, amide, halogen, and nitro groups can substantially modify antibacterial and antifungal activity by influencing molecular reactivity, hydrogen-bonding interactions, membrane affinity, and other physicochemical characteristics. Similarly, acetylenic compounds, particularly naturally occurring polyacetylenes and related synthetic derivatives, constitute an important group of bioactive molecules with reported antibacterial, antifungal, and, in some cases, antibiofilm properties. Their biological activities may be modulated by the presence of hydroxyl, carbonyl, ether, alcohol, and other functional groups, as well as by variations in chain length, unsaturation pattern, and stereochemical configuration. However, the potential cytotoxicity and limited selectivity of certain compounds remain important considerations in their further development. This review provides a comparative analysis of ethylenic and acetylenic compounds, focusing on their antibacterial and antifungal properties *and* the contribution of neighboring functional groups to their structure–activity relationships. The proposed and experimentally investigated mechanisms of antimicrobial action, including interactions with microbial membranes, interference with cellular targets, and inhibition of biofilm formation, are discussed in relation to the available evidence.

Keywords: Ethylenic bonds; Acetylenic bonds Antibacterial activity; Antifungal activity; Structure–activity relationships; Functional groups