DRIP – Drug Resistance In Pneumonia: Derivation and Prospective multi-center Validation of a Scoring Model to predict Drug-Resistant Pathogens


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Background

Pneumonia is a leading cause of morbidity and mortality. Drug-resistant pathogens are a growing concern. Accurate prediction of resistant pathogens is critical in guiding treatment of patients with nosocomial pneumonia who, by definition, are at high risk due to underlying impaired host defenses, chronic disease, and utilization of potentially resistive antibiotics. This prospective multi-center cohort study aimed to develop and validate a novel cumulative probabilistic model to predict drug-resistant pathogens.

Methods

A derivation cohort of 200 culture-proven antibiotic resistant pneumonia cases was identified from 1000 patients consented, admitted with pneumonia to 7 ICUs. The GRIP software was used to identify patients with a > 50% risk of DRIP, who were included in the derivation group. The model was externally validated in a prospective multi-center cohort of 7 ICUs. Data were collected prospectively using a structured data collection tool. The model was internally validated by evaluating the performance of the model on a bootstrap sample of the derivation cohort. The model was externally validated using a second prospective multi-center cohort.

Results

In the derivation group, DRIP was superior to HCAP (AUROC 0.77 vs 0.64, P<0.001), and all other predictive models (PPV 76% vs 59%, NPV 89% vs 76%, accuracy 72%), and all other predictive models for CAP diagnosis, and all other predictive models for CAP diagnosis.

Conclusions

A novel cumulative, probabilistic model for predicting DRIP score is a novel, cumulative, probabilistic model for predicting antibiotic resistant pneumonia in patients admitted to ICUs.

Updated Abstract

Background

The DRIP score is a novel cumulative, probabilistic model for predicting antibiotic resistant pneumonia (DRIP) in ICUs. DRIP was derived using a comprehensive set of risk factors for antibiotic-resistant pneumonia from 8 ICUs in the United States. The model was externally validated in a multi-center prospective cohort of 7 ICUs. The model is simple, easy to use, and easily integrated into electronic medical records.

Methods

A derivation cohort of 200 antibiotic-resistant pneumonia cases was identified from 1000 patients consented, admitted to ICUs in 20 ICUs. The DRIP software was used to identify patients with a > 50% risk of DRIP, who were included in the derivation group. The model was externally validated in a prospective multi-center cohort of 7 ICUs. Data were collected prospectively using a structured data collection tool. The model was internally validated by evaluating the performance of the model on a bootstrap sample of the derivation cohort. The model was externally validated using a second prospective multi-center cohort.

Results

In the derivation group, DRIP was superior to HCAP (AUROC 0.77 vs 0.64, P<0.001), and all other predictive models (PPV 76% vs 59%, NPV 89% vs 76%, accuracy 72%), and all other predictive models for CAP diagnosis.

Conclusions

A novel cumulative, probabilistic model for predicting antibiotic-resistant pneumonia (DRIP) is a novel, cumulative, probabilistic model for predicting antibiotic-resistant pneumonia in patients admitted to ICUs.