Background

Human Rhinovirus (HRV) is a highly sensitive and specific method for pathogen detection. While direct methods enable rapid identification, they are limited to detecting the available virus or sampling variability. A novel approach to address these limitations is the utilization of human transcriptome analysis, which can provide a more comprehensive analysis of viral infections. The use of transcriptome analysis in clinical settings is growing and can be used to determine if a patient is at risk for viral respiratory illness. In this study, we evaluated the performance of a commercial human transcriptome analysis platform in identifying children with HRV infections.

Methods

A logistic regression model was developed to classify the cause of illness as viral or non-viral using multiplex polymerase chain reaction (PCR) and the BioFire FilmArray® Respiratory Panel (BioFire RP2). The performance of the model was evaluated by comparing it to the BioFire FilmArray® (BioFire) and the FilmArray® Respiratory Panel 2 (RP2). The model was trained on a dataset of 361 samples, and the performance was evaluated using receiver operating characteristic (ROC) curves and the F1 statistic.

Results

The BioFire FilmArray® Respiratory Panel 2 (RP2) detected 25 HRV infections, of which 24 were confirmed by the model. The sensitivity of the model was 77%, specificity was 79%, and the accuracy was 81%. The model also showed good performance for other respiratory viruses, with sensitivity ranging from 68% to 84% and specificity ranging from 77% to 84%.

Conclusions

The BioFire FilmArray® Respiratory Panel 2 (RP2) is a promising tool for the detection of HRV infections. The model developed in this study demonstrated good accuracy and sensitivity, and can be used to improve the diagnostic accuracy of HRV infections. Further studies are needed to evaluate the model in a larger cohort and to compare it with other commercial platforms.

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