Poster P0273

Enhancing Pathogen Detection in Viral Respiratory Tract Infections Among Individuals Aged Over 55 Years Through Expanded PCR Panel Testing

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Introduction

Respiratory Tract Infections (RTI) pose a significant public health concern globally, especially among vulnerable populations including the elderly. The diverse etiology of RTIs involves a multitude of viral and bacterial pathogens causing similar clinical manifestations ranging from mild symptoms to life threatening conditions such as pneumonia. Coinfections with multiple pathogens in individuals with RTIs or pneumonia are not uncommon and contribute to the development of more complicated illnesses. Reliable testing methods are crucial for identifying the cause of infection. Expanded PCR panels can enable rapid identification of pathogens and coinfections within 24 hours. The goal of this study was to identify bacterial and viral coinfecting organisms in RTIs among patient samples positive for three common viral respiratory pathogens.

Methods

Nasopharyngeal swabs were obtained from a cohort of 30,083 individuals aged >55 years who presented with symptoms of RTI between January 2022 and October 2023 (Figure 1). All specimens were tested on Respira-ID™, an expanded PCR platform that employs TaqMan® OpenArray® plates (36 viral and bacterial targets) on the Applied Biosystems™ QuantStudio™ 12K Flex Real-time PCR system. Initial analysis involved categorizing results based on the detection of three primary viral organisms: SARS-CoV-2, Influenza A/B, and Respiratory Syncytial Virus (RSV). Further analyses were conducted to identify potential coinfections.

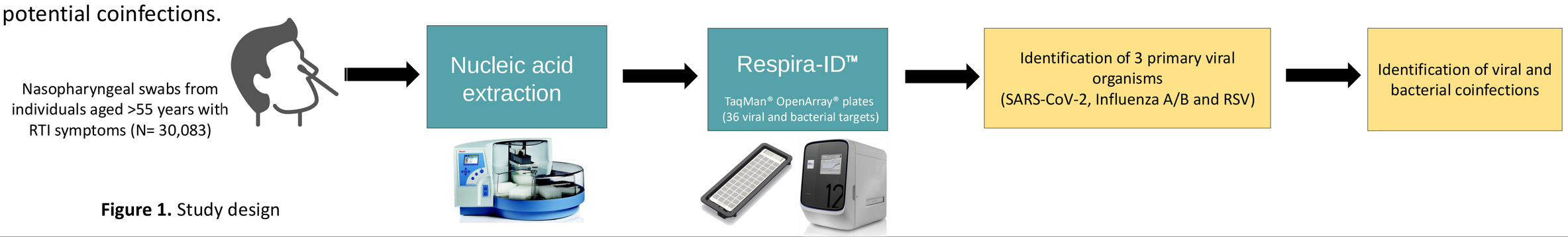

Figure 1. Study design

Results

A total of 6,303 samples were positive for SARS-CoV-2 (N=4,806), Influenza A/B (N=855) or RSV (N=642) (Table 1). Within this subset of positive samples, a high incidence of coinfections was observed, with 40.1% (N=2,528) testing positive for at least one coinfecting organism (Table 1). Among the identified coinfections, bacterial-viral were the most prevalent (76.8%, N=1942) while viral-viral accounted for only 23.2% (N=586) (Figure 2). *Staphylococcus aureus* was the most common coinfecting bacteria, representing 42.7%, followed by *Haemophilus influenzae* (18.3%), *Klebsiella pneumoniae* (15.2%) and *Streptococcus pneumoniae* (11.2%). Viral coinfections included Human Rhinovirus (15.2%), Epstein-Barr virus (11.4%), and human herpesvirus 6 (4.9%) (Table 2).

Table 1: Demographics of the population that tested positive for one of the three primary viral organisms

Characteristic		Sample Total	Co-Infection Negative	Co-Infection Positive
Total, n		6,303	3,775, (59.9)	2,528, (40.1)
Age, Mean, (SD)		72.3, (11.2)	72.3, (11.1)	72.2, (11.4)
Gender, N, (%)	Female	3,652, (57.9)	2,232, (59.1)	1,420, (56.2)
	Male	2,119, (33.6)	1,221, (32.3)	898, (35.5)
	Unknown	532, (8.4)	322, (8.5)	210, (8.3)
Race, N, (%)	Black / African American	289, (4.7)	160, (4.3)	129, (5.2)
	Other/Unknown	3,993, (64.3)	2,425, (65.0)	1,568, (63.2)
	White	1,927, (31.0)	1,143, (30.7)	784, (31.6)
Ethnicity, N, (%)	Hispanic	99, (1.6)	59, (1.6)	40, (1.6)
	Not Hispanic	989, (15.7)	568, (15.0)	421, (16.7)
	Unknown	5,215, (82.7)	3,148, (83.4)	2,067, (81.8)
RSV, N, (%)	Negative	5,661, (89.8)	3,401, (90.1)	2,260, (89.4)
	Positive	642, (10.2)	374, (9.9)	268, (10.6)
SARS-CoV-2, N, (%)	Negative	1,497, (23.8)	883, (23.4)	614, (24.3)
	Positive	4,806, (76.2)	2,892, (76.6)	1,914, (75.7)
Influenza A/B, N, (%)	Negative	5,448, (86.4)	3,266, (86.5)	2,182, (86.3)
	Positive	855, (13.6)	509, (13.5)	346, (13.7)

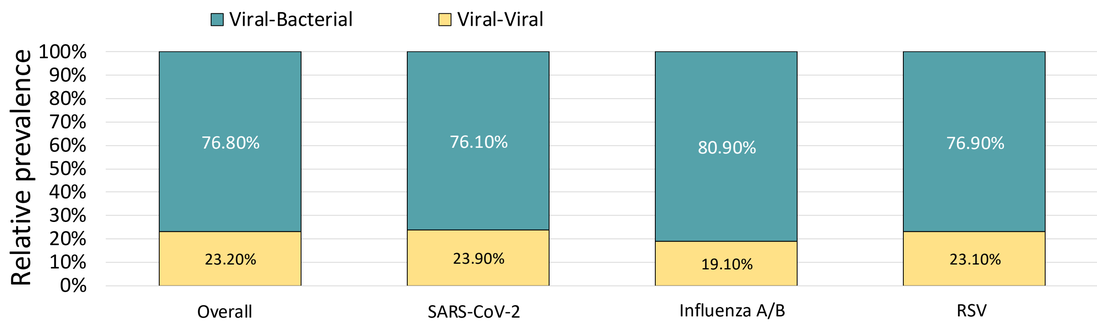

Figure 2: Relative prevalence of co-infecting types of pathogens among samples positive for SARS-CoV-2, Influenza A/B or RSV.

Table 2: Prevalence of co-infecting organisms in samples positive for SARS-CoV-2, Influenza A/B or RSV

Most frequent co-infections, N, (%)	
Staphylococcus aureus	1,080, (42.7)
Haemophilus influenzae	462, (18.3)
Klebsiella pneumoniae	385, (15.2)
Human Rhinovirus*	383, (15.2)
Epstein-Barr virus (EBV) (HHV4)	288, (11.4)
Streptococcus pneumoniae	284, (11.2)
Human herpesvirus 6 (HHV6)	125, (4.9)
Adenovirus*	46, (1.8)
Parainfluenza virus*	43, (1.7)
Human metapneumovirus	22, (0.9)

* Multiple test target names were pooled as aggregate results

Conclusion

Expanded syndromic panel PCR tests can provide valuable insight for treating RTIs, especially in the elderly, by identifying causative agents and addressing potential coinfections that can contribute to the progression of severe or fatal illnesses