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ORIGINAL ARTICLE

Epidemiology of Respiratory Pathogens Detected Using a Multiplex Polymerase Chain Reaction Panel at a University Hospital in Korea from 2019 through 2022

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SUMMARY

Background: **Respiratory infections are a significant global public health concern, influenced by diverse pathogens with seasonal and regional variations. This study aimed to investigate the patterns of respiratory pathogen infections in Daegu, Korea, providing foundational data for infection prevention and management strategies.**
Methods: **A retrospective analysis was conducted using a rapid multiplex polymerase chain reaction (PCR) respiratory pathogen panel. The study involved patients presenting with respiratory symptoms at a university hospital in Daegu between 2019 and 2022. A total of 8,396 specimens were collected from patients aged 0 – 105 years, and their data were analyzed to determine infection patterns.**
Results: **Out of the 8,396 specimens collected, 2,620 (31.2%) tested positive for respiratory pathogens. Human rhinovirus/enterovirus was the most commonly detected pathogen, present in 1,297 cases (49.5% of positive samples). Coinfections accounted for 20.3% of positive cases. Seasonal analysis indicated higher detection rates during winter months. The study also identified age- and gender-specific variations in pathogen prevalence.**
Conclusions: **The findings highlight the predominant respiratory pathogens in Daegu, with significant seasonal, age, and gender-related trends. These data are essential for informing the local public on health strategies and preventive measures for respiratory infections in the region.**
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Supplementary Data

Table S1. Distribution of coinfections with respiratory pathogens.

<table>
<tr><th>Coinfection</th><th colspan="10">Respiratory pathogen positivity n (%)</th></tr>
<tr><td rowspan="22">Double infection</td><td>AdV</td><td>CoV-HKU1</td><td>3 (0.7)</td><td></td><td colspan="2">FluB</td><td>1 (0.2)</td><td></td><td>BP</td><td>1 (0.2)</td></tr>
<tr><td></td><td>CoV-NL63</td><td>2 (0.4)</td><td></td><td colspan="2">PIV4</td><td>1 (0.2)</td><td></td><td>MP</td><td>1 (0.2)</td></tr>
<tr><td></td><td>CoV-OC43</td><td>4 (0.9)</td><td></td><td colspan="2">RSV</td><td>1 (0.2)</td><td>HRV/EV</td><td>FluA</td><td>18 (4.0)</td></tr>
<tr><td></td><td>hMPV</td><td>3 (0.7)</td><td>CoV-NL63</td><td colspan="2">hMPV</td><td>1 (0.2)</td><td></td><td>FluB</td><td>4 (0.9)</td></tr>
<tr><td></td><td>HRV/EV</td><td>137 (30.6)</td><td></td><td colspan="2">HRV/EV</td><td>11 (2.5)</td><td></td><td>PIV1</td><td>8 (1.8)</td></tr>
<tr><td></td><td>FluA</td><td>6 (1.3)</td><td></td><td colspan="2">FluA</td><td>6 (1.3)</td><td></td><td>PIV2</td><td>8 (1.8)</td></tr>
<tr><td></td><td>PIV1</td><td>3 (0.7)</td><td></td><td colspan="2">RSV</td><td>4 (0.9)</td><td></td><td>PIV3</td><td>39 (8.7)</td></tr>
<tr><td></td><td>PIV2</td><td>2 (0.4)</td><td>CoV-OC43</td><td colspan="2">hMPV</td><td>1 (0.2)</td><td></td><td>PIV4</td><td>7 (1.6)</td></tr>
<tr><td></td><td>PIV3</td><td>13 (2.9)</td><td></td><td colspan="2">HRV/EV</td><td>6 (1.3)</td><td></td><td>RSV</td><td>30 (6.7)</td></tr>
<tr><td></td><td>PIV4</td><td>2 (0.4)</td><td></td><td colspan="2">FluA</td><td>3 (0.7)</td><td></td><td>BP</td><td>4 (0.9)</td></tr>
<tr><td></td><td>RSV</td><td>13 (2.9)</td><td></td><td colspan="2">FluB</td><td>1 (0.2)</td><td></td><td>CP</td><td>2 (0.4)</td></tr>
<tr><td></td><td>CP</td><td>1 (0.2)</td><td></td><td colspan="2">PIV1</td><td>1 (0.2)</td><td></td><td>MP</td><td>18 (4.0)</td></tr>
<tr><td></td><td>MP</td><td>7 (1.6)</td><td></td><td colspan="2">PIV2</td><td>1 (0.2)</td><td>FluA</td><td>PIV2</td><td>1 (0.2)</td></tr>
<tr><td>CoV-229E</td><td>hMPV</td><td>2 (0.4)</td><td></td><td colspan="2">PIV3</td><td>1 (0.2)</td><td></td><td>PIV3</td><td>3 (0.7)</td></tr>
<tr><td></td><td>HRV/EV</td><td>2 (0.4)</td><td></td><td colspan="2">PIV4</td><td>1 (0.2)</td><td></td><td>PIV4</td><td>1 (0.2)</td></tr>
<tr><td></td><td>FluA</td><td>6 (1.3)</td><td></td><td colspan="2">RSV</td><td>5 (1.1)</td><td></td><td>RSV</td><td>7 (1.6)</td></tr>
<tr><td></td><td>FluB</td><td>1 (0.2)</td><td></td><td colspan="2">MP</td><td>1 (0.2)</td><td></td><td>MP</td><td>1 (0.2)</td></tr>
<tr><td></td><td>PIV3</td><td>1 (0.2)</td><td>hMPV</td><td colspan="2">HRV/EV</td><td>19 (4.2)</td><td>FluB</td><td>CP</td><td>1 (0.2)</td></tr>
<tr><td></td><td>RSV</td><td>4 (0.9)</td><td></td><td colspan="2">FluB</td><td>1 (0.2)</td><td>PIV3</td><td>PIV4</td><td>1 (0.2)</td></tr>
<tr><td>CoV-HKU1</td><td>CoV-OC43</td><td>1 (0.2)</td><td></td><td colspan="2">PIV2</td><td>1 (0.2)</td><td></td><td>RSV</td><td>3 (0.7)</td></tr>
<tr><td></td><td>HRV/EV</td><td>5 (1.1)</td><td></td><td colspan="2">PIV3</td><td>1 (0.2)</td><td>RSV</td><td>MP</td><td>1 (0.2)</td></tr>
<tr><td></td><td>FluA</td><td>2 (0.4)</td><td></td><td colspan="2">RSV</td><td>1 (0.2)</td><td></td><td>Total</td><td>448 (100)</td></tr>
<tr><td rowspan="4">Triple infection</td><td>AdV</td><td>CoV-229E</td><td>HRV/EV</td><td>1 (1.3)</td><td></td><td></td><td></td><td>RSV</td><td>1 (1.3)</td><td></td></tr>
<tr><td></td><td>CoV-HKU1</td><td>HRV/EV</td><td>1 (1.3)</td><td></td><td></td><td>PIV1</td><td>PIV4</td><td>1 (1.3)</td><td></td></tr>
<tr><td></td><td></td><td>FluB</td><td>1 (1.3)</td><td></td><td></td><td>PIV2</td><td>PIV3</td><td>1 (1.3)</td><td></td></tr>
<tr><td></td><td>CoV-NL63</td><td>CoV-OC43</td><td>1 (1.3)</td><td></td><td></td><td></td><td>PIV4</td><td>1 (1.3)</td><td></td></tr>
</table>

Table S1. Distribution of coinfections with respiratory pathogens (continued).

Coinfection	**Respiratory pathogen positivity n (%)**									
Triple infection			**HRV/EV**	**1 (1.3)**		**CoV-229E**	**HRV/EV**	**FluA**	**1 (1.3)**	
			FluA	**1 (1.3)**			**FluA**	**RSV**	**1 (1.3)**	
			MP	**1 (1.3)**		**CoV-HKU1**	**CoV-NL63**	**HRV/EV**	**1 (1.3)**	
		CoV-OC43	**HRV/EV**	**3 (3.9)**			**hMPV**	**PIV3**	**1 (1.3)**	
			FluA	**2 (2.6)**		**CoV-NL63**	**CoV-OC43**	**RSV**	**1 (1.3)**	
			RSV	**1 (1.3)**			**HRV/EV**	**FluA**	**1 (1.3)**	
		hMPV	**HRV/EV**	**3 (3.9)**				**PIV4**	**1 (1.3)**	
		HRV/EV	**FluA**	**2 (2.6)**				**RSV**	**1 (1.3)**	
			PIV1	**2 (2.6)**		**hMPV**	**HRV/EV**	**PIV3**	**3 (3.9)**	
			PIV2	**3 (3.9)**				**RSV**	**1 (1.3)**	
			PIV3	**15 (19.7)**		**HRV/EV**	**PIV1**	**RSV**	**1 (1.3)**	
			PIV4	**6 (7.9)**			**PIV3**	**PIV4**	**2 (2.6)**	
			RSV	**5 (6.6)**			**RSV**	**MP**	**2 (2.6)**	
			MP	**5 (6.6)**				**Total**	**76 (100)**	
		FluA	**PIV1**	**1 (1.3)**						
Quadruple infection	**AdV**	**CoV-229E**	**HRV/EV**	**RSV**	**1 (11.1)**	**CoV-229E**	**CoV-NL63**	**HRV/EV**	**MP**	**1 (11.1)**
		CoV-HKU1	**hMPV**	**HRV/EV**	**1 (11.1)**	**CoV-HKU1**	**HRV/EV**	**FluA**	**RSV**	**1 (11.1)**
		CoV-NL63	**HRV/EV**	**PIV4**	**1 (11.1)**	**CoV-OC43**	**HRV/EV**	**PIV3**	**RSV**	**1 (11.1)**
		HRV/EV	**FluB**	**PIV1**	**1 (11.1)**	**HRV/EV**	**PIV1**	**PIV3**	**RSV**	**1 (11.1)**
			PIV1	**PIV3**	**1 (11.1)**				**Total**	**9 (100)**

AdV - adenovirus, CoV-229E - coronavirus 229E, CoV-HKU1 - coronavirus HKU1, CoV-NL63 - coronavirus NL63, CoV-OC43 - coronavirus OC43, hMPV - human metapneumovirus, HRV/EV - human rhinovirus/enterovirus, FluA - influenza virus A, FluB - influenza virus B, PIV1 - parainfluenza virus 1, PIV2 - parainfluenza virus 2, PIV3 - parainfluenza virus 3, PIV4 - parainfluenza virus 4, RSV - respiratory syncytial virus, BP - *Bordetella pertussis*, CP - *Chlamydophila pneumoniae*, MP - *Mycoplasma pneumoniae.*