

Evaluation and characterization of viral respiratory tract infection etiologies in Turkey between March 2009 and September 2014

EV1107

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Objectives

Acute respiratory tract infections are one of the most significant sources of health burdens including increased morbidity and mortality rates among populations. These infections can be caused by various viral pathogens. However, there is limited information on the etiology and epidemiology of these in Turkey. In this study, we aimed to determine the viral respiratory tract infection etiologies in Turkey.

Methods

Between March 2009 (starting from influenza pandemic) and September 2014 viral respiratory etiologies causing acute respiratory tract infections were evaluated from both outpatients and inpatients who sought medical treatment in Acibadem Hospitals Group in Turkey. Sputum, bronchoalveolar lavage, nasopharyngeal, nasal and throat swab samples taken from 1256 acute respiratory tract infection patients were investigated for the presence of 12 respiratory viruses.

A multiplex polymerase chain reaction assay (RV12-ACE, Seegene, South Korea) for common respiratory viruses, including human adenovirus, human coronavirus 229E/NL63, human coronavirus OC43/HKU1, human metapneumovirus, human parainfluenza virus 1, human parainfluenza virus 2, human parainfluenza virus 3, human respiratory syncytial virus A, human respiratory syncytial virus B, human rhinovirus A/B, influenza A virus and influenza B virus, was used.

Table 1. Distribution of viral respiratory tract infection etiologies in Turkey between March 2009 and September 2014

Virus	Age				Patient characteristic				Total	
	Pediatric n	Pediatric %	Adult n	Adult %	Inpatient n	Inpatient %	Outpatient n	Outpatient %	n	%
Human rhinovirus A/B	110	78,0	31	22,0	93	66,0	48	34,0	141	21,2
Human respiratory syncytial virus A	83	72,2	32	27,8	95	82,6	20	17,4	115	17,3
Influenza A virus	62	68,1	29	31,9	52	57,1	39	42,9	91	13,7
Human adenovirus	61	92,4	5	7,6	39	59,1	27	40,9	66	10,0
Human respiratory syncytial virus B	43	82,7	9	17,3	38	73,1	14	26,9	52	7,8
Human coronavirus OC43/HKU1	35	83,3	7	16,6	32	76,2	10	23,8	42	6,3
Human metapneumovirus	24	75,0	8	25,0	19	59,4	13	40,6	32	4,8
Human parainfluenza virus 3	23	79,3	6	20,7	14	48,3	15	51,7	29	4,4
Influenza B virus	19	65,5	10	34,5	23	79,3	6	20,7	29	4,4
Human parainfluenza virus 2	22	78,6	6	21,4	15	53,6	13	46,4	28	4,2
Human coronavirus 229E/NL63	19	82,6	4	17,4	14	60,9	9	39,1	23	3,5
Human parainfluenza virus 1	11	68,8	5	31,2	12	75,0	4	25,0	16	2,4
Total	512	77,1	152	22,9	446	67,2	218	32,8	664	100,0

Results

During the study period among 1256 respiratory samples 602 (47.9%) were found positive for at least one respiratory tract virus. Samples with positive results were from male (n=341, 56.6%) and female (n=261, 43.4%) patients and ranged in age from 11 days to 87 years with a median age of 40.0 years and a mean age of 12.7 years (SD ± 18.9 years). Pediatric age group constituted 67.6% of the study population and 32.4% of the cases were among outpatient group. A single etiology was identified in 602 (47.9%) patients and co-infection with two or more viruses was observed in 62 (4.9%) patients. The most frequently detected virus was human rhinovirus A/B (n=141, 21.2%), followed by human respiratory syncytial virus A (n=115, 17.3%) and influenza A virus (n=91, 13.7%) (Table 1). The same order of viruses was also observed when etiologies in single infections were examined: human rhinovirus A/B (n=114, 18.9%), followed by human respiratory syncytial virus A (n=93, 15.5%) and influenza A virus (n=82, 13.6%). The most frequent combinations were human respiratory syncytial virus A plus human coronavirus OC43/HKU1 (six cases), followed by human respiratory syncytial virus A plus human rhinovirus A/B (five cases) and human coronavirus 229E/NL63 plus human rhinovirus A/B (4 cases).

Conclusion

Our findings showed that a wide range of respiratory viral pathogens are circulating in Turkey. The significant difference between the etiologies of inpatient/outpatient and pediatric/adult patient groups reveals the need for the detection of the etiologic agents in acute respiratory tract infections. These results may aid the clinicians in the development of safe and effective therapeutic approaches and prevent unnecessary usage of antimicrobials.