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# Acute Respiratory Tract Infection by Rhinovirus in Adults at Jaipur

**Dr. Niketa Gupta[1], Dr. Jitender Tiwari[2], Dr. Pratibha Sharma[3], Dr. Bharti Malhotra[4*]**
[1]Resident, Department of Microbiology, SMS medical college and attached group of Hospitals, Jaipur, India
[2]Research Scientist, Department of Microbiology, SMS medical college and attached group of Hospitals, Jaipur, India
[3]Research Scientist, Department of Microbiology, SMS medical college and attached group of Hospitals, Jaipur, India
[4]Senior Professor, Department of Microbiology, SMS medical college and attached group of Hospitals, Jaipur, India

**Original Research Article**

***Corresponding author**
*Dr. Bharti Malhotra*

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**Abstract:** Human Rhinoviruses (HRVs) are a group of positive-sense ssRNA viruses belonging to the genus Enterovirus in the family Picornaviridae. Adult disease with *Human Rhinovirus* (HRV) typically follows a mild course, but it is the most frequent viral infection associated with exacerbations of chronic obstructive pulmonary disease. The HRVs can increase the severity of disease of respiratory infection as pathogen or co pathogen mainly in case of bronchitis, bronchiolitis and pneumonia .The present study was conducted in SMS Medical College and attached hospitals, Jaipur, India, over a period of 1 month (January, 2016). Consecutive adults more than 15 years of age presenting with fever, cough, shortness of breath, sore throat and nasal catarrh. A total of 44 throat swab samples were collected from equal number of consecutive patients with acute respiratory illness. Viral nucleic acid was extracted from 200 µl sample using NucliSENS EasyMAG automated nucleic acid extractor as per manufacturer's instructions. RT-PCR assay was performed on ABI7500 Fast for the detection of HRV. Among the 44 cases included in the month of January, 2016, 2 cases were positive for Rhino virus (4.5%). This research article will provide the prevalence of HRV in adult population.
**Keywords:** Human Rhinovirus (HRV), Picornaviridae, Respiratory infection, RT-PCR.

## INTRODUCTION

*Human Rhinoviruses* (HRVs) are a group of positive-sense ssRNA viruses belonging to the genus *Enterovirus* in the family Picornaviridae. Currently divided into two species HRV A, HRV B and more than 100 serotypes have been found [1, 2].

Adult disease with human Rhinovirus (HRV) typically follows a mild course, but it is the most frequent viral infection associated with exacerbations of chronic obstructive pulmonary disease [3-6]. Immuno-compromised adults can have more severe disease, including lower respiratory infections [7-11] and higher mortality [12].

HRV causes symptoms as for other upper respiratory viruses [13,14] and patients can present with an influenza-like illness (ILI) or an afebrile upper respiratory illness. The HRVs can increase the severity of disease of respiratory infection as pathogen or co pathogen mainly in case of bronchitis, bronchiolitis and pneumonia [15].

One study reported that in developing countries, HRVs were associated with severe pneumonia both in paediatric and adult population and also in immuno suppressed subjects [16]. The association of HRVs in paediatric pneumonia has been studied previously but its association with viral pneumonia among adult population of north Indian region is still unknown. The aim of this study is to analyse the prevalence of HRV in adult patients having acute respiratory illness at Jaipur region.

## MATERIALS AND METHODS

The present study was conducted in SMS Medical College and attached hospitals, Jaipur, India, over a period of 1 month (January, 2016). Consecutive adults more than 15 years of age presenting with fever, cough, shortness of breath, sore throat and nasal catarrh, to the SMS and attached hospitals were included in the study. The subjects with chronic respiratory ailments, non-consenting caregivers, with history of hospitalisation in preceding 14 days, and children aged less than 15 years were excluded.

### Sample collection and transportation

A total of 44 throat swab samples were collected from equal number of consecutive patients with acute respiratory illness using a sterile nylon flocked swabs and placed in viral transport medium,

labelled and transported on ice at the earliest to the laboratory. Informed consent was obtained from the parents/guardians of the patients. The study protocol was approved by the institutional ethics committee.

**Nucleic acid extraction**

Viral nucleic acid was extracted from 200 µl sample using NucliSENS EasyMAG automated nucleic acid extractor (Biomeuriex, France) as per manufacturer's instructions. At the final step, the nucleic acid was eluted in a volume of 55 µl and processed immediately for PCR. Internal control was added to each sample during nucleic acid extraction to validate the process of extraction and PCR technique used in the study.

**Real-time reverse transcription polymerase chain reaction (RT-PCR)**

RT-PCR assay was performed on ABI 7500 Fast (Life Technologies, USA) using 1 µl AgPath-IDTM One-Step RT-PCR kit (Ambion, USA), 12.5 µl assay buffer and 1.5 µl primer probe mix for the detection of HRV. The real-time RT-PCR thermal profile was as follows: 50°C for 15 min, 95°C for 10 min, 40 cycles of 95°C for 8 sec, 60°C for 34 sec. The time taken for extraction, amplification and detection was three hours.

## RESULTS

Among the 44 cases included in the month of January, 2016, 2 cases were positive for Rhino virus (4.5%). Both the cases were female and their age was less than 30 yrs. In the positive cases one was treated in OPD and one was hospitalised with no mortality reported.

## DISCUSSION

Previous reports have suggested that HRVs are responsible for various acute respiratory illnesses (ARIs) including the common cold, bronchiolitis and pneumonia [17]. In addition, recent reports strongly suggest that HRVs may induce exacerbation of wheezing and/or asthma (virus-induced asthma) [18].

Thus, these viruses may be associated with ARIs and other severe respiratory illnesses, such as wheezy bronchiolitis and asthma [18]. Notably, HRV can be detected in most countries and may be associated with various ARIs including upper respiratory infection (URI), bronchiolitis, wheezy bronchiolitis and pneumonia [19, 20] although the epidemiology is not exactly known. In addition, the epidemiology of HRV-ABCs detected from patients with ARI is unclear in Asian areas. Large scale studies are required to study the trends of *Rhinovirus* infection in adults in our region.

## CONCLUSION

Substantial advances in the field of HRV research have occurred in the last decade, due primarily to improvements in molecular diagnostics. HRV is not just a cause of benign upper respiratory illness; rather, it is a significant lower respiratory tract pathogen in patients with chronic pulmonary disease, children, and immunocompromised hosts. Additionally, whole genome sequencing may provide insight into the observed differences in clinical symptoms and outcomes according to the HRV strain. There is also a need to identify other modifiable risk factors for the acquisition and severity of HRV infection. A better understanding of the mechanisms leading to manifestations of HRV infection and the role of the host immune response is needed to guide future efforts at HRV prevention and treatment.

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