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REVIEW

Prevalence of human respiratory syncytial virus circulating in Iran

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Summary Respiratory syncytial virus (RSV) is a leading cause of acute respiratory infection during early childhood and is associated with a great burden on patients, parents, and society. While no treatment is yet available, results from recent phase 2 clinical trials of cell-entry inhibitors and RSV vaccines are promising. To prepare for introduction of these novel therapeutics, good understanding of its molecular epidemiology and continuous RSV surveillance data are necessary. This paper provides an overview of RSV prevalence and genotype distribution in Iran from 1996 to 2013. This meta-analysis includes 21 published studies. In total, 775 (18.7%) of 4140 respiratory specimens were positive for RSV infection. The male-female ratio of RSV-positive patients was 1.5:1. Significant peaks of RSV infection were detected during the cold season (November—March). RSV infection was mainly observed in patients <2 years of age. Phylogenetic studies showed that genotypes GA1, GA2, GA5, and BA co-circulated in Iran in 2007—2013. This review highlights the necessity of

Abbreviations: RSV, respiratory syncytial virus; Flu, influenza; PIV, parainfluenza; AdV, adenovirus; hBoV, human bocavirus; hMPV, human metapneumovirus.

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introducing standard molecular surveillance programs to inform the epidemiological, clinical, and pathological characteristics of various RSV genotypes. Improved understanding of the molecular epidemiology will be useful for development of novel RSV therapeutics.

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Introduction

Viral respiratory infections pose considerable health difficulties for people of various ages worldwide [1]. Respiratory syncytial virus (RSV) infection is a leading cause of hospitalization in infants less than 1 year old and an important cause of clinical referral among children less than 5 years of age in developed countries [2,3]; it is also considered a significant pathogen in adults [1]. The major viral respiratory pathogens include RSV, influenza (Flu) types A and B, parainfluenza (PIV) types 1—4, adenovirus (AdV), rhinovirus, enterovirus, human bocavirus (hBoV) and human metapneumovirus (hMPV), all of which present with similar clinical features in infected patients [4]. RSV is a pneumovirus belonging to the *Paramyxoviridae* family. This negative-sense single-stranded RNA virus is characterized by large syncytia in single-layer cells [5]. Epidemiological studies have reported that RSV has a seasonal distribution pattern, with peak prevalence between early November and late January in most communities [5]. RSV can be involved in upper and lower respiratory tract infections and progress to bronchiolitis and pneumonia in infants. Recent studies describe the increased risk of wheezing and asthma after RSV bronchiolitis [6].

Increased risk of severe RSV infection has been reported among premature infants; those with bronchopulmonary dysplasia, airway congenital abnormalities, cystic fibrosis, atopy, and Down syndrome; and preterm children with chronic lung disease [1,7]. Considering the critical role of the immune system, particularly neutrophils, in RSV infection, research has focused on its immunopathogenesis in order to characterize the molecular mechanisms of virus replication to design more efficient drugs and vaccines [8—10].

Both classical and molecular diagnosis methods are currently used for RSV detection; however, molecular assays, especially reverse transcription PCR (RT-PCR), offer increased sensitivity, specificity, and rapidity [5]. The RSV genome encodes 11 proteins, including two nonstructural proteins. The nucleotide sequence of the variable regions within the G glycoprotein are mainly used to determine RSV genotype and for epidemiological purposes [11]. Based on its reaction with monoclonal antibodies against glycoprotein G and fusion protein F, RSV has two main genetic subtypes,