


Prevalence and genetic characterisation of respiratory syncytial viruses circulating in Bulgaria during the 2014/15 and 2015/16 winter seasons

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Abstract

The respiratory syncytial virus (RSV) is a leading cause of acute respiratory illnesses (ARI) in infants and young children. The objectives of this study were to investigate the RSV circulation among children aged <5 years in Bulgaria, to identify the RSV-A and RSV-B genotypes and to perform an amino acid sequence analysis of second hypervariable region (HVR2) of the G gene. During the 2014/15 and 2015/16 winter seasons, nasopharyngeal specimens of 610 children aged <5 years with ARI were tested using Real Time RT-PCR for influenza viruses, RSV, metapneumovirus, parainfluenza viruses, rhinoviruses and adenoviruses. Viral respiratory pathogens were detected in 429 (70%) out of 610 patients examined and RSV was the most frequently identified virus (26%) followed by influenza A(H1N1)pdm09 virus (14%) ($p < .05$). RSV was the most prevalent pathogen in patients with bronchiolitis (48%) and pneumonia (38%). In the 2014/15 season, RSV-A dominated slightly (53%), while in the next season RSV-B viruses prevailed more strongly (66%). The phylogenetic analysis based on the G gene indicated that all 21 studied RSV-A strains belonged to the ON1 genotype; the vast majority (96%) of the RSV-B strains were classified into BA9 genotype and only one - into BA10 genotype. All Bulgarian RSV-A and RSV-B sequences contained a 72-nt and a 60-nt duplication in the HVR2, respectively. The study showed the leading role of this pathogen as a causative agent of serious respiratory illnesses in early childhood, year-on-year fluctuations in RSV incidence, a shift from RSV-A to RSV-B subgroup dominance and relatively low genetic divergence in the circulating strains.

[Korsun, N. et al.](#) (2017) Prevalence and genetic characterisation of respiratory syncytial viruses circulating in Bulgaria during the 2014/15 and 2015/16 winter seasons. *Pathogens and Global Health*. **111** (7).