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Paper Poster Session

Influenza - clinical epidemiology

Emergence of the novel ON1 genotype of respiratory syncytial virus A in France in between 2010 and 2014 : relations with clinical features

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Background : Respiratory syncytial virus (RSV) is a well-recognised cause of respiratory tract infections in young children. The two groups, A and B, are related to antigenic variations in the G glycoprotein. Many of them have been reported, mostly in its extracellular domain and it has been shown that G protein can sustain large genetic variations without loss of functionality. Based on G gene variations, a total of 11 genotypes of RSV A and 23 genotypes of RSV B have been described. During the 2010-2011 winter season, a novel genotype of RSV A with a 72 nucleotides duplication in the G gene has been detected in Ontario. This genogroup ON1 has been subsequently ~~detected~~ reported in several countries. Our objective was to ~~assess~~ detect the level of circulation of this new RSV variant in France throughout several years.

Materials/Methods : Between 2010 and 2014, 28200 samples were routinely screened for RSV by PCR using Respiratory MWS RSV/hMPV r-gene® (bioMérieux), 3050 were tested positive (11%). A selection of 123 samples was conducted with positive samples detected during the 3 most important RSV peak weeks of each winter season. RSV typing was conducted by sequencing a 500 bp G gene fragment.

Results : Group A was predominant during the first two seasons, representing 70 and 79% of all RSV samples. The first ON1 variant was detected during the 2010-2011 season. The detection of ON1 variant was increasing each year, reaching 55% of all RSV positive samples in 2013-2014. The proportion of RSV B ~~was~~ was inconstant from year to year, in between 14 and 48%. ON1 variants were detected in less than one year old patients in 79% of the cases, and 4 cases were in more than 65 year old patients (14%). Only one of these patients was hospitalised in a paediatric intensive care unit. This new RSV genotype does not seem to be related to an increase in disease severity.

Conclusion : As for influenza, RSV is characterized by a constant evolution of circulating genotypes. As previously reported in different countries including European ones, RSV-A/ON1 variants was first detected in our study in February 2011 and became the major RSV-A circulating genotype from the 2012-2013 winter season. Implementation of RSV multiple genotypes co-circulation surveillance network is relevant as RSV vaccine will soon become available.