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Epidemiological and clinical characterization of respiratory syncytial virus subtype -A and -B in infants with bronchiolitis

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Background: Human respiratory syncytial virus (RSV) is the major cause of bronchiolitis in infants. Different genotypes of RSV-A and -B co-circulate during successive epidemic seasons, with a (not regular) pattern of alternating prevalence. According to most studies, RSV-A causes a more severe bronchiolitis course; however, no significant differences were found in several reports. Inconsistency could be due to the different genotypes circulating in different epidemic seasons but there is still limited data on specific strains. A new RSV-A strain (ON1), characterized by an insertion of 24 aminoacids in the G glycoprotein, has been identified in 2010. All studies reported ON1 rapid spread and dominance during the subsequent seasons but are not concordant about its clinical severity. Since RSV subtype and genotype may influence clinical outcomes, we sought to study bronchiolitis caused by well characterized RSV strains, over eight epidemic seasons.

Material/methods: From December 2008 to March 2016, nasal washings from infants hospitalized for bronchiolitis were tested for 14 respiratory viruses and RSV-positive samples were sequenced. Patient and family data were obtained from medical files and from a structured questionnaire. A 0–8 severity score based on respiratory rate, arterial oxygen saturation in room air, retractions and oral feeding ability was determined on admission.

Results: Out of 274 bronchiolitis positive only to RSV, 202 were successfully sequenced; 155/202 (76.7%) samples were RSV-A, 47/202 (23.3%) were RSV-B. RSV-A dominated in six seasons and RSV-B in two (2010/11 and 2014/15). A phylogenetic analysis of the G gene revealed that in the first three epidemic seasons, of RSV-A only genotype NA1 was detected. In 2011/12 20% of RSV-A cases were ON1 whereas in the subsequent seasons 95-100% of RSV-A cases were ON1. All RSV-B belonged to genotype BA, bearing the 60-nt insertion. Overall, demographic and clinical data did not differ between RSV-A and –B cases. RSV-A cases were then divided in two groups (NA1 and ON1) and compared with RSV-B. No significant differences between the three groups were found in terms of demographic data (sex, age, weight, birth weight); a few difference were found analyzing familial risk factors. The more relevant finding was that, stratifying infants according to severity score values 0-4 or 5-8, a significantly higher number of NA1 than ON1 and RSV-B cases had a worse severity (values 5-8; p=0.001). Respiratory rates and oral feeding ability were significantly worse in NA1 than ON1 and RSV-B cases; other clinical parameters were comparable among the three groups.

Conclusions: Our results suggest that genotype NA1 was associated with greater severity of RSV bronchiolitis than were ON1 and subtype B strains. Improving RSV surveillance would allow a deeper understanding of the epidemiological and clinicopathological features of the different RSV genotypes.