

Identification of a novel group B genotype of Human Respiratory Syncytial Virus during a three-year study period in Cameroonian children

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Background

Human Respiratory Syncytial Virus (HRSV) is the main cause of severe lower respiratory tract disease in infants and young children. Nair and his colleagues found during a meta-analysis an incidence of 33.8 (95% CI, 19.3 to 46.2) million cases of acute lower respiratory infections with 66-199 thousands of deaths associated to HRSV each year in children under 5 years. The incidence in developing countries was more than twice greater than that of developed countries. A total of 91% of hospitalizations and nearly all deaths (99%) were registered in developing countries where access to health care is limited.¹ An initial study in Cameroon showed that HRSV circulated in rainy season from October to December at 5.7% in outpatient with influenza-like illness visiting influenza surveillance centers in 2009.² We report identification of a new group B genotype of HRSV during the first study of the molecular characterization of HRSV in Cameroonian children for 3 consecutive epidemic seasons (September 2011-October 2014).

Materials and methods

This prospective observational study was conducted in the paediatric service of the "Centre Hospitalier d'Essos" in Yaounde, Cameroon. Viral RNA and DNA were extracted using QIAamp Viral RNA Mini kit and QIAamp DNA Mini kit (Qiagen, Hilden, Germany), respectively. These samples were screened by a commercially available Respiratory Multi Well System r-gene™ (bioMérieux, France) for the detection of common respiratory viruses including HRSV. For HRSV-positive samples, we performed semi-nested RT-PCR, sequencing, and molecular analysis of the second variable region of the G gene.

Results

Seventy-four HRSV-positive samples were included in the study. HRSV-A (9/74; 12.2%) and HRSV-B (8/74; 10.8%) were observed almost at the same frequency and 40.5% (30/74) of cases were HRSV-A/HRSV-B coinfection (Table 1). Phylogenetic analysis revealed that HRSV-A strains clustered in the NA-1 genotype while HRSV-B strains clustered in the BA-9 genotype. Two identical HRSV-B sequences on the HVR2 region of the G gene formed a branch supported by a 99% bootstrap. Thus, according to the criteria of a new genotype given by Venter et al.³ these samples could belong to a new genotype. According to the BA-13 genotype recently described by Gimferrer et al.,⁴ this new genotype was named BA-14. The new genotype had four specific mutations: P231S, K233T, P238R, and S309P. Temporal trends for BA-9 detections in Yaounde show that BA-9a and BA-9b were detected in the 2011/12 and 2012/13 epidemic season, respectively (Figure 1).

Table 1: Annual distribution of Human Respiratory Syncytial Viruses group A and B.

	2011/2012	2012/2013	2013/2014	Total
HRSV-A	3 (25)	1 (2.6)	5 (20.8)	9 (12.2)
HRSV-B	3 (25)	2 (5.3)	3 (12.5)	8 (10.8)
HRSV-A/HRSV-B	1 (8.3)	20 (52.6)	9 (37.5)	30 (40.5)
Undefined*	5 (41.7)	15 (39.5)	7 (29.2)	27 (36.5)
Total	12	38	24	74

*27 undefined are 17 Influenza positive samples not tested and 10 non amplified G gene.

Conclusion and perspectives

- ✓ The results obtained in the current study provides for the first time data on HRSV genotypes circulating in Cameroon and in the Central African sub region.
- ✓ This work also reports the detection of a new HRSV genotype, BA14, among Cameroonian children.
- ✓ This study highlights the importance to perform large-scale studies in limited-resource countries like Cameroon where the data are still very scarce.
- ✓ This work also highlights the need for constant monitoring of the emergence of new HRSV genotypes to support vaccine development.

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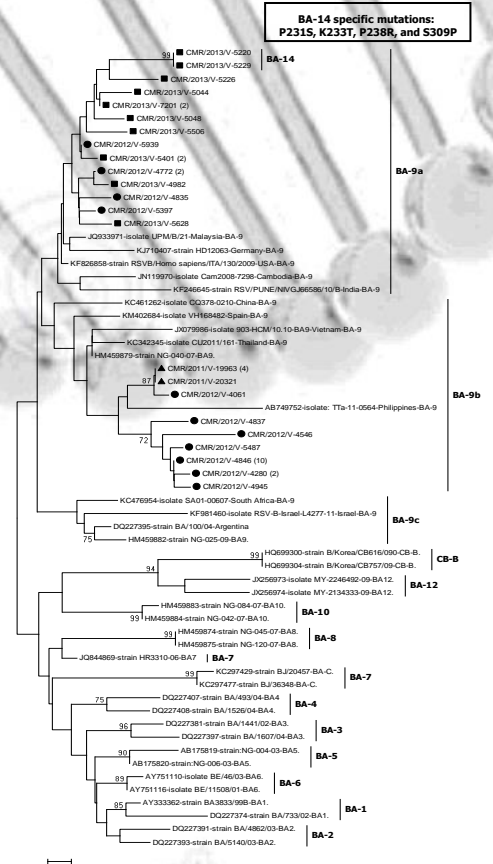


Figure 1: Phylogenetic trees of HRSV-B strains detected in Cameroon from 2011 to 2014. The unrooted trees were generated based on nucleotide sequences of the C-terminal HVR2 region of the G gene. Current study strains are identified from left to right by CMR (Cameroon), the year of detection and the laboratory number. The sequences of Cameroon are marked with (▲), (●) and (■) for the 2011, 2012 and 2013, respectively. The number of identical sequences is indicated in parenthesis following the name of the strain. The genotypes assigned to branches are in the right after the bars.