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Epidemiology and phylogenic analysis of Human Bocavirus isolated in children with Acute Respiratory Infection in Cameroun, 2011-2014.

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Introduction

Human Bocavirus (HBoV) was identified for the first time in 2005.[1] Based on phylogenetic analysis of HBoV genomic sequences, it was assigned into *Parvoviridae* family, *Parvovirinae* subfamily, and Bocavirus gender. Currently four different species (HBoV-1 to 4) are described.[2] The literature review indicates that this virus is a common cause of respiratory infections and gastroenteritis in children. So far, several published studies on HBoV were performed in developed countries.[3] However, epidemiology and genetic characterization of this virus remains unknown in Central Africa, particularly in Cameroon. In this study, we evaluated the frequency, seasonality and molecular characteristics of HBoV strains in Cameroonian children with acute respiratory infections.

Methods

A set of 810 nasopharyngeal swabs were obtained from children aged less than 15 years between September 2011 and July 2014. These samples were screened by real time PCR/RT-PCR for the detection of common respiratory viruses including HBoV. The sequences of the VP1/2 gene were amplified and sequenced for HBoV positive samples. For statistical analysis, quantitative variables were presented as median and interquartile range. Categorical variables were expressed as numbers, proportions and analyzed using logistic regression with a significance level of 5%.

Results

HBoV genome was detected in 80/810 (9.9%) samples. Among these positive, 57 (71.2%) were positive for other respiratory viruses. Individuals at high risk of infection were between 6 months and 2 years (61.3%) followed by those aged less than six months (12.5%),] 2-5] years (20%), and] 5 -15] years (6.3%) (Table 1). A seasonal pattern was observed for detection of HBoV from September to April. Phylogenetic analysis of partial sequences of VP1/2 showed a low level of nucleotide variation and HBoV-1 circulation. The sequences showed similarity in amino acid and nucleotide ranging from 97.62% to 100% both between them and with the Swedish prototype sequences, ST1 and ST2. Three clades were obtained, two with prototype strains ST1 and ST2, and a third group consisting only of Cameroon strains (Figure 1).

Table 1: General data of the study participants.

Characteristics		Total	Human Bocavirus			
		No (810)	Negative 730 (90.1)	Positive 80 (9.9)	Monoinfection 23 (28.8)	Coinfection 57 (71.2)
Age						
	]0-6] Months	103 (12.7)	93 (12.7)	10 (12.5)	4 (17.4)	6 (10.5)
	]6-24] Months	407 (50.2)	358 (49)	49 (61.3)	15 (65.2)	34 (59.6)
	]2-5] Years	200 (24.7)	184 (25.2)	16 (20)	2 (8.7)	14 (24.6)
	]5-15] Years	94 (11.6)	89 (12.2)	5 (6.3)	2 (8.7)	3 (5.3)
	NA	6 (0.7)	6 (0.8)	0 (0)	0 (0)	0 (0)
Gender						
	Male	430 (53.1)	390 (53.4)	40 (50)	13 (56.5)	27 (47.4)
	Female	379 (46.8)	339 (46.4)	40 (50)	10 (43.5)	30 (52.6)
	NA	1 (0.1)	1 (0.1)	0 (0)	0 (0)	0 (0)
Patient						
	Inpatients	445 (54.9)	400 (54.8)	45 (56.3)	16 (69.6)	29 (50.9)
	Outpatients	365 (45.1)	330 (45.2)	35 (43.8)	7 (30.4)	28 (49.1)

NA: Not Available. Data are number (%= n/Column total).

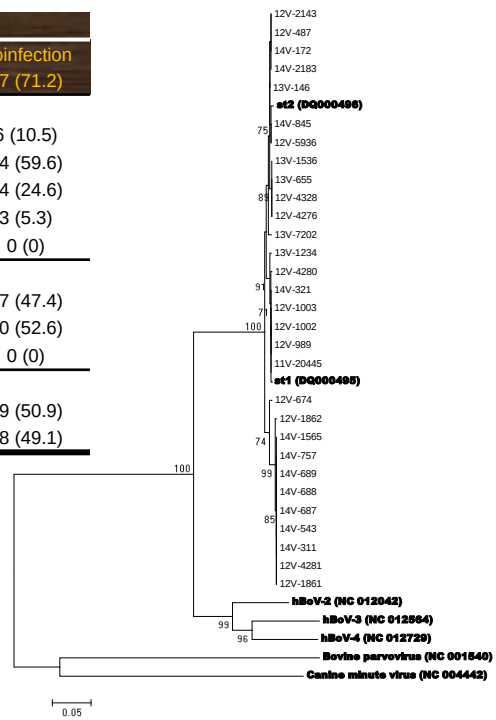

Figure 1: Phylogenetic tree of 29 Human Bocavirus strains from Cameroon, partial VP1/2 gene (717 bp). Phylogenetic tree was generated with the neighbor-joining method using MEGA 6 software. Prototypes strains in bold and other strains are from this study.

Conclusion and perspectives

✓HBoV-1 is present alone or in co-detection with other viruses in acute respiratory infections among children in Yaounde, Cameroon.
✓The detection of HBoV occurred from September to April.
✓These results can help improve the strategies for monitoring and control of respiratory infections in Cameroon.

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