

Molecular epidemiology of rotavirus in children under-5 in Lubumbashi, Democratic Republic of Congo

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Introduction

Rotavirus is responsible for 20-70% of hospitalizations and nearly 600,000-2 million deaths per year in developing countries. Several genotypes are in circulation and are different from one geographical area to another thus compromising the possibility of having an effective vaccine everywhere. Thus, the characterization of circulating genotypes is necessary for the development of an effective vaccine against the identified rotavirus genotypes.

Material and methods

This study was conducted between 2009 and 2015, in the Democratic Republic of Congo, at the Sendwe General Hospital of Lubumbashi. It concerns children admitted for diarrhea, whose stool sample was taken. These samples were tested by PCR. We then determined the molecular characteristics of rotavirus strains.

Results

A total of 483 children were included in the study. Among the 483 stool samples examined, 219 (45.3%) were rotavirus-positive. The median age of positive children was 7 months (Q1: 4.5 - Q3: 9.0). The proportion of females was 52.5% (115/219). Among the 219 samples, 70 or 32% underwent genotyping. The most common genotypes were G1P [8] (18.6%, 13/70) and G2P [6] (18.6%, 13/70) followed by G1P [6] (8.6%) And G3P [6] (8.6%, 6/70).

Conclusion

The results of this study could be used to assess the impact of rotavirus vaccination in Lubumbashi.