Molecular epidemiology of norovirus in symptomatic and asymptomatic population in Burkina Faso

P. Huynen (1, 2), A. Mauroy (3, 4), C. Martin (2), L. Savadogo (3), M. Kinda (3), E. Thiry (4), P. De Mol (1), P. Melin (1)

(1) University Hospital of Liège, Belgium, (2) Pasteur Institute of Bangui, Central African Republic, (3) Superior Institute of Health Sciences of Bobo Dioulasso, Burkina Faso, (4) Faculty of Veterinary Medicine, University of Liège, Belgium

$The two authors contributed equally to this work$

BACKGROUND

Noroviruses (NoV), belonging to the family Caliciviridae, are now recognized as the leading cause of gastrointestinal outbreaks worldwide, and represent an important cause of sporadic gastroenteritis in both children and adults.

Many studies describe NoV epidemiology. However, few data are available about the NoV strains circulating in most of African countries, in particular in Burkina Faso. The population of Burkina Faso is characterized by the young age of its inhabitants, and most are living in rural environment.

OBJECTIVES

The purpose of this epidemiological study was to determine the prevalence of NoV infection in the area of Bobo Dioulasso (Southern part of Burkina Faso) by molecular diagnosis methods in patients presenting or not gastroenteritis symptoms, to quantify the excreted viral load, and to genotypes the circulating strains.

MATERIAL AND METHODS

Patients with and without gastro-intestinal disorders were selected in several Health Care Centres of Bobo Dioulasso (Fig.2) and during a campaign against malnutrition (Fig.3). Clinical and epidemiological data, as well as stool samples (n=453), were collected during 8 weeks through March to April 2011.

Viral genomic RNA was automatically extracted with a Maxwell® (Promega) instrument. Molecular detection of genogroups (GI), II and IV NoV in stool samples was performed by a home-made real-time RT-PCR (1), targeting the ORF1-ORF2 polymerase junction region. For each positive sample, viral load was estimated using standard curves (successive dilutions of recombinant GI and GI plasmids). Molecular characterization was performed on 27 detected strains, using both polymorphisms and capsid regions.

RESULTS

Clinical and epidemiological data

| Table I: Epidemiological data for asymptomatic (AP) and symptomatic patients (SP) |
| Age Group | SP | AP |
|<1 year | 33 | 5 |
| 1-2 years | 14 | 4 |
| 3-5 years | 27 | 5 |
| 6-10 years | 34 | 6 |
| 11-19 years | 26 | 9 |

Most of the selected patients in both symptomatic (SP) and asymptomatic patients (AP) were younger than 10 years, representing 91.9 and 93.3% respectively (Table I).

Molecular detection of NoV and genogrouping

NoV were detected in 21.6% of the 453 collected stool samples, with a distribution of 21.0% and 23.1% in the samples from the 319 symptomatic and the 134 asymptomatic patients respectively.

Genogroup distribution was 34.3% for GI, 50.7% for GII and 15% for both GI and GII among SP’s samples, and was 48.4% for GI, 45.2% for GII and 6.4% for both GI and GII among AP’s samples (Table II).

CONCLUSION

Even if a true pathogenic role of NoV could not be shown from the study design, it allowed to precise the molecular epidemiology of NoV strains prevalent in a representative country of the East African region. It also showed that asymptomatic patients could play an important role as a NoV "reservoir". Despite the fact that GI strains, and more precisely those belonging to GII4 genotype, are nowadays highly reported worldwide, the surprising proportion of NoV GI detected in this study suggests that GI and GII strains should be excreted in equal proportion in the environment. The origin of this epidemiologic difference, even if partially explained by the difference in immunity and genetic sensitivity of the population, is still to be solved.

ACKNOWLEDGMENTS

CECDOIL (University of Liège, Belgium). A. Saghro Foundation (University of Liège, Belgium). Dr Omsani (Head of Laboratory of Di, Bobo Dioulasso, Burkina Faso). Raphaël Boreux (Laboratory of Medical Microbiology, University Hospital of Liège, Belgium)

Bibliography

*Journal of Clinical Epidemiology, 2011, 64, 719-728.

*Clinicochimica Acta, 1999, 288, 185-190*

*Clinical Microbiology and Infection, 2003, 9, 1129-1133*

P190

P. Huynen

P.Huynen@chuulg.be