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Outbreak of G2P[4] rotavirus gastroenteritis in a retirement community, Brazil, 2015: An important public health risk?

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ABSTRACT

The present study described a group A rotavirus (RVA) outbreak in an age-care facility in Brazil, using epidemiologic and molecular diagnostic methods. A descriptive clinical, epidemiological and environmental investigation was conducted. Stool samples were collected and screened for RVA, Norovirus (NoV), Enteric Adenovirus 40/41 (AdV 40/41) and Astrovirus (AstV) using ELISA, RT-PCR, qRT-PCR, electron microscopy and sequencing methods. Outbreak occurred during 26th–29th October, 2015; 28 individuals affected (22 residents; 6 staff). The attack rate was 25.9% and 8.5% among residents (median-age: 85.5 years) and staff (median-age: 28 years), respectively. Female staff was identified as the index case. RVA G2P[4] genotype was detected in 87.5% (7/8). Genetic analysis demonstrated that the outbreak involved one single strain, suggesting a common-source infection. RVA should be considered during outbreaks investigations in residential facilities, and raise the question if the current licensed RVA vaccines for children could also be helpful for the elderly.

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Introduction

Rotaviruses are the major etiologic agents of acute viral gastroenteritis in humans, and is a global public health concern, accounting for over half a million deaths and two million hospitalizations each year.^{1,2} Rotaviruses are members of the *Reoviridae* family, and their genome is enclosed in a triple layered capsid

comprising 11 segments of double-stranded RNA (dsRNA) that encode six structural proteins (VP1-VP4, VP6, and VP7) and six nonstructural proteins (NSP1-NSP5/6).³ Rotavirus group A (RVA) is one of the nine groups (Rotavirus A to I), and the most common group responsible for endemic human disease.⁴ RVA are classified in a binary system based upon the main neutralization antigens, namely, the spike protein (VP4) and the major outer capsid glycoprotein (VP7). Currently, 32 G genotypes and 47 P genotypes have been described.⁵ Globally, the vast most human RVA have the genotype combination G1P[8], G2P[4], G3P[8], G4P[8] or G9P[8], and studies from all around the world have recently shown a high prevalence of G12P[8] strain,⁶ including Brazil.⁷

RVA is the most common cause of severe gastroenteritis in young children worldwide and associated with approximately 28% of diarrheal deaths.^{2,8} Nevertheless, RVA is also the leading cause of vaccine-preventable diarrhea among children under 5.⁸ Two safe and effective RVA vaccines (Rotarix™, GlaxoSmithKline Biologicals, Belgium and RotaTaq™, Merck Inc., USA) have been licensed in approximately 100 countries worldwide since 2006.⁹ In countries

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Competing interest: None declare.

Ethical approval: This study was carried out in accordance with the Declaration of Helsinki as revised in 2000, and approved by the Ethics Committee of the Adolfo Lutz Institute, São Paulo, Brazil. Study participants were not required to provide informed consent as this study was considered by the Ethics Committee to be part of routine surveillance activities.

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without RVA vaccination, virtually all children become infected during the first years of life, regardless of hygiene or sanitation conditions or whether they live in high-income or resource-poor settings.¹⁰ Rotarix™ vaccine was included into the Brazilian's National Immunization Program from March 2006, and a significant impact on the RVA disease burden in the country has been seen ever since.^{11–14}

Older children and adults are susceptible to reinfection with RVA, which can cause mild but rarely severe disease.^{15,16} In fact, among adults, it is difficult to provide a concise description of a typical clinical presentation of RVA infection, because the infection has been associated with a wide spectrum of disease severity and manifestations.¹⁷ In addition, RVA disease is less common in adults than in young children due to both: immunity from prior infections and RVA testing is usually not performed.¹⁸ Curiously, RVA infections in adults most frequently occur in communities that are otherwise sheltered from more routine exposure to rotavirus-infected children.¹⁷

Considering the elderly population in particular, outbreaks of RVA gastroenteritis in aged-care facilities have been reported globally.^{15,19–23} Outbreaks of RVA infection in long-term health-care facilities, particularly those with close living quarters; compromised host immunity and multiple comorbid disorders might help facilitate the spread of the infection, and can represent an important public health risk with occasional fatalities.^{15,19,20} Despite outbreaks of RVA gastroenteritis in retirement communities have been described worldwide, the frequency, periodicity and RVA types involved in such outbreaks have not been recorded in detail. Therefore, the global impact of the disease burden among inmate geriatric population is not entirely recognized. Focusing on the economic impact of an outbreak of RVA gastroenteritis in long-term facility for elderly patients, Piednoir et al.²⁴ showed a cost of €285,10 per case (comprising medical investigation, treatment costs, isolation, infection control staff and bed-day loss) in a general hospital in France. In Brazil, norovirus (NoV), has been more frequently reported as cause of diarrhea outbreaks among elderly in nursing homes,²⁵ and the frequency of RVA outbreaks among elderly in residential facilities is virtually unknown.

The aim of the present study was to describe a RVA outbreak in a private residential care home for older people in São Paulo, Brazil, using epidemiologic and molecular diagnostic methods. As far as we're aware there have been no reports of RVA outbreaks in elderly care home in the country.

Material and methods

Clinical and epidemiological investigation

On 28th October 2015, the Public Health Department (Coordenação de Vigilância em Saúde da Secretaria Municipal de Saúde de São Paulo – COVISA and Coordenadoria de Controle de Doenças – CCD) in São Paulo County, São Paulo State, Brazil was notified about an outbreak of gastroenteritis in a private nursing home for the elderly located in the south zone of the city of São Paulo. The nursing home is subdivided into small buildings. All buildings are at ground level, divided into rooms and interconnected. The rooms for residents are either equipped with one, two or three beds, as well as dorms. The nursing home also has separate rooms for bed-bound residents. In addition, there are one kitchen, a dining hall, a living room, and a garden. The elderly care home comprised 85 residents cared for by 71 staff members. Mobile residents can go about freely in and around the nursing home. Most residents are visited regularly by family members.

Viral gastroenteritis infection was suspected based on the symptoms, especially on symptoms onset time. A probable case

was defined as any resident or employee of the nursing home with two or more episodes of vomiting and/or diarrhea, with or without other symptoms (i.e. elevated body temperature or malaise) and with or without laboratory confirmation, between 26th and 29th October. A confirmed case was considered as a case with clinical symptoms and laboratory confirmation. During the outbreak period, measures to prevent the spread of the disease were taken. In addition to epidemiological outbreak investigation, stool samples for diagnosis were collected.

A list of affected residents and staff members was compiled, containing information on the date of onset, symptoms and duration of symptoms. Information on a range of potential exposures were collected when possible, including places recently visited such as physicians and families with small children. Comorbidities (i.e. diabetes mellitus, cardiovascular disease, Alzheimer disease) and possible gastrointestinal symptoms in their family members were also assessed.

Environmental investigation

Many residents suffer from dementia. It was therefore deemed unreasonable to undertake a study of possible exposures including food consumed during few days prior to the outbreak. A concurrent investigation was carried out by the department of sanitary health of São Paulo County. The environmental health investigation included inspection of the institution's sanitary conditions. The audit of infection control practices included observing of environmental cleanliness, hand-washing facilities, safe handling and disposal of waste, disinfection standards, and the state of hygiene in the food preparation areas.

Because of the highly likely person-to-person transmission, no food samples were taken to test during this outbreak. Moreover, one of the ill patients was a resident who feeds exclusively by industrialized parental diet. Hence, public health authorities (COVISA/CCD) could presume that this was not a foodborne gastroenteritis outbreak.

Laboratory investigation

The collected stool samples were sent to the Enteric Disease Laboratory of Adolfo Lutz Institute (IAL), a regional reference center for gastroenteritis surveillance and a member of the Acute Diarrheic Disease Monitoring Program (ADDMP).

The fecal samples were screened for the presence of RVA, NoV, enteric adenovirus 40/41 (AdV 40/41), and Astrovirus (AstV). RVA was searched for by commercial immunoenzymatic assay (RIDASCREEN® Rotavirus, R-Biopharm AG, Germany), polyacrylamide gel electrophoresis (SDS-PAGE),²⁶ and reverse transcription followed by nested PCR (RT-PCR) with type-specific primers following previously described protocols.^{27,28} NoV were screened with commercial immunoenzymatic assay (RIDASCREEN® Norovirus, R-Biopharm AG, Germany), RT-PCR and real-time PCR (qRT-PCR) according to the protocols described by Morillo et al.,²⁹ Kitajima et al.³⁰ and Morillo et al.³¹ The stools samples were tested for AdV 40/41 and AstV using PCR and RT-PCR, respectively, following protocols and primers previously stated.^{32–34} In order to complete the viral diagnosis, all fecal samples were also subjected to negative staining techniques³⁵ or transmission electron microscopy (TEM) analysis.

Molecular investigation

The positive RVA samples were selected for sequencing in order to achieve the molecular identification of the isolated strains and, eventually, to link the cases through molecular epidemiology. PCR amplicons were sequenced using the BigDye Terminator v3.1 Cycle

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