Mexico, Guatemala, and Honduras in 2009–2010, our data suggest emergence of the previously rare G9P[4] group A rotavirus genotype in these countries. Whether the G9P[4] genotype becomes the common strain in Latin America or elsewhere remains to be determined.

Osbourne Quaye,1 Sharla McDonald, Mathew D. Esona, Freda C. Lyde, Slavica Mijatovic-Rustempasic, Sunando Roy, Dina J. Castro Banegas, Yolanda Mencos Quiñonez, Blanca L. Chinchilla, Fabián Gómez Santiago, Herlinda García Lozano, Gloria Rey-Benito, Lúcia H. de Oliveira, Jon R. Gentsch, and Michael D. Bowen

Author affiliations: Centers for Disease Control and Prevention, Atlanta, Georgia, USA (O. Quaye, S. McDonald, M.D. Esona, F.C. Lyde, S. Mijatovic-Rustempasic, S. Roy, J.R. Gentsch, M.D. Bowen); Nacional Colonia La Campaña, Tegucigalpa, Honduras (D. J. Castro Banegas); Ministerio de Salud Pública y Asistencia Social, Guatemala City, Guatemala (Y. Mencos Quiñonez, B.L. Chinchilla); Instituto de Diagnóstico y Referencia Epidemiológico, Mexico City, Mexico (F. Gómez Santiago, H. García Lozano); and Pan American Health Organization, Washington, DC, USA (G. Rey-Benito, L.H. de Oliveira)

DOI: http://dx.doi.org/10.3201/eid1908.130288

References

1. Bányaí K, Laszlo B, Duque J, Steele AD, Nelson EA, Gentsch JR, et al. Systematic review of regional and temporal trends in global rotavirus strain diversity in the pre rotavirus vaccine era: insights for understanding the impact of rotavirus vaccination programs. Vaccine. 2012;30(Suppl 1):A122–30. http://dx.doi.org/10.1016/j.vaccine.2011.09.111

2. Santos N, Volotao EM, Soares CC, Albuquerque MC, da Silva FM, de Carvalho TR, et al. Rotavirus strains bearing genotype G9 or P[9] recovered from Brazilian children with diarrhea from 1997 to 1999. J Clin Microbiol. 2001;39:1157–60. http://dx.doi.org/10.1128/JCM.39.3.1157-1160.2001

3. Linhares AC, Stupka JA, Ciapponi A, Bardach AE, Gljovskys D, Arij PK, et al. Burden and typing of rotavirus group A in Latin America and the Caribbean: systematic review and meta-analysis. Rev Med Virol. 2011;21:89–109. http://dx.doi.org/10.1002/rmv.682

4. Yen C, Figueroa JR, Uribe ES, Carmena-Hernandez LD, Tate JE, Parashar UD, et al. Monovalent rotavirus vaccine provides protection against an emerging fully heterotypic G9P[4] rotavirus strain in Mexico. J Infect Dis. 2011;204:783–6. http://dx.doi.org/10.1093/infdis/jir390

5. Hull JJ, Teel EN, Kerin TK, Freeman MM, Esona MD, Gentsch JR, et al. United States rotavirus strain surveillance from 2005 to 2008: genotype prevalence before and after vaccine introduction. Pediatr Infect Dis J. 2011;30(Suppl):S42–7. http://dx.doi.org/10.1097/INF.0b013e3181fed78

6. Cortes J, Arvelo W, Lopez B, Reyes L, Kerin T, Gautam R, et al. Rotavirus disease burden among children <5 years of age—Santa Rosa, Guatemala, 2007–2009. Trop Med Int Health. 2012;17:254–9. http://dx.doi.org/10.1111/j.1365-3156.2011.02911.x

7. Patel MM, de Oliveira LH, Bispo AM, Gentsch J, Parashar UD. Rotavirus P[4] G2 in a vaccinated population, Brazil. Emerg Infect Dis. 2008;14:863–5. http://dx.doi.org/10.3201/eid1405.071440

8. Rahman M, Yang XL, Sun H, Mahzehin K, Verstappen NW, Novo L, et al. Emerging G9 rotavirus strains in the northwest of China. Virus Res. 2008;137:157–62. http://dx.doi.org/10.1016/j.virusres.2008.07.004

9. Rahman M, Matthijssens J, Yang X, Debeke T, Arij I, Taniguchi K, et al. Evolutionary history and global spread of the emerging G12 human rotaviruses. J Virol. 2007;81:2382–90. http://dx.doi.org/10.1128/JVI.01622-06

10. Sharma S, Paul VK, Bhan MK, Ray P. Genomic characterization of nontypeable rotaviruses and detection of a rare G8 strain in Delhi, India. J Clin Microbiol. 2009;47:3998–4005. http://dx.doi.org/10.1128/JCM.00809-09

Address for correspondence: Michael D. Bowen, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Mailstop G04, Atlanta, GA 30333, USA; email: mkb6@cdc.gov

Recently Identified Novel Human Astroviruses in Children with Diarrhea, China

To the Editor: Human astroviruses (HAstVs), first identified in 1975, are now considered an important cause of viral gastroenteritis, predominantly infecting children ≤2 years of age (1,2). HAstVs are classified into 8 serotypes. A unique astrovirus, MLB1 (AstV-MLB1), recently was discovered in a fecal sample from a child with diarrhea in Australia (3); subsequently, at least 6 novel astroviruses have been discovered from fecal samples, including AstV-MLB2, AstV-MLB3, HMO AstV-A/VA2, HMO AstV-C/VA1, HMO AstV-B/VA3, and AstV-VA4 (4–7). The prevalence of novel astroviruses in China remains unclear.

Fecal specimens were collected during July 2010–June 2011 from 723 children <5 years of age who had acute gastroenteritis. Samples were from all of 295 eligible children brought for care to First Hospital of Lanzhou University (Lanzhou, China) and every fifth eligible child (n = 428) brought for care on 2 days of the week (Tuesday and Thursday) at Nanjing Children’s Hospital (Nanjing, China). The children’s parents provided informed consent. The ethics committees of both hospitals approved the study.

Nucleic acids were extracted from specimens by using the Viral Nucleic Acid Extraction Kit II (Geneaid, Taoyuan, Taiwan). Adenovirus and caliciviruses were detected by PCR and reverse transcription PCR, respectively (8). Rotavirus was detected from fecal samples by ELISA (Oxoid, Cambridge, UK). Primers Mon269/Mon270 detected a region of the capsid gene (449 bp) from classic HAstV-1–8 by reverse transcription PCR (8). Additional astrovirus types were detected by using primers SF0073/SF0076, amplifying a
409-bp fragment of the astrovirus gene open reading frame 1b (5). All amplification products were sequenced and analyzed by using the software package DNAStar (DNAStr, Madison, WI, USA). Phylogenetic trees were constructed by using the neighbor-joining method and the software program MEGA4 (www.megasoftware.net). Statistical analyses were performed by using SPSS, version 17.0 (SPSS Inc., Chicago, IL, USA).

A total of 320 (44.3%) samples were positive for rotavirus and 102 (14.1%), 27 (3.7%), and 32 (4.4%) for calcicviruses, adenoviruses, and astroviruses, respectively. A total of 17 positive samples were detected with Mon269/Mon270, and an additional 15 samples were found with primers SF0073/SF0076. Phylogenetic analysis revealed that 21 of the 32 astrovirus-positive isolates were classic HAstV, dominated by HAstV-1 (12 samples); 7 samples were AstV-MLB1 (GenBank accession nos. JQ673575–JQ673581), and 4 were AstV-MLB2 or HMOAstV-A (2 isolates each) (GenBank accession nos. JQ673582–JQ673585). Primers SF0073/SF0076 detected 4 classic astroviruses that were not detected by Mon269/Mon270. We found no statistically significant differences in mean age (p = 0.209, Student t test), rate of fever and vomiting (p = 0.712 and p = 0.472, respectively, Fisher exact test), or mean duration and frequency of diarrhea (p = 0.231 and p = 0.177, respectively, Student t test) were observed between the classic and novel astrovirus groups.

Statistical analyses were performed by using SPSS, version 17.0 (SPSS Inc., Chicago, IL, USA).

Figure. Phylogenetic analyses of human astroviruses, China. Construction of phylogenetic trees was based on alignment of a region of the open reading frame 1b nucleic acid sequence (409 bp), generated by the neighbor-joining method with 1,000 bootstrap replicates. Each strain from this study is indicated by the patient number (10621012, 10621144, 10621141, 10621144, 10621237, 10621246, 10621264, 10621268, 10322603, 10322608, 10322651, 10322706) or GenBank accession number (JQ673575–JQ673585) as indicated. AstV, astrovirus; AstV-MLB, human astrovirus MLB; HAstV, human astrovirus; HMO-A, B, C, human-, mink-, and ovine-like astrovirus species A, B and C; AstV-VA, human astrovirus VA.
the strain CRJ41435, sharing 99% sequence identity. AstV-MLB1 and AstV-MLB2 are phylogenetically related to the rat astroviruses RS118 and RS126. The remaining novel astroviruses, 10322603 and 10621246, clustered closely with human, mink, and ovine astrovirus strain NI-295 (Figure).

This study documented that multiple novel astroviruses circulated simultaneously with common human astrovirus types in China. The detection rates of novel astroviruses, especially Ast-MLB1, were higher than in previous reports (3,4), although lower than in a study from Egypt (9). These results indicate that multiple novel astroviruses are spread worldwide. The differences in prevalence may have been caused by the geographic and/or study cohort differences. The phylogeny of astroviruses determined in our study basically agrees with previous analyses (5), supporting the idea that the novel astroviruses are related to other animal astroviruses. Additional studies using full-genome sequencing should be done to clarify the origin of the novel astroviruses.

One limitation of this study was that no asymptomatic control was included. A recent case–control study has suggested that AstV-MLB1 was not associated with diarrhea (70). However, other novel astroviruses were not assessed. Further study, especially with a large case–control cohort, should be initiated to determine the correlation of unique astroviruses with gastrointestinal and extraintestinal diseases.

Acknowledgments

We thank Wenjuan Gao and Xiaojun Zhou for collection of samples.

Yongxia Wang,1 Yuning Li,1 Yu Jin, Dan-di Li, Xiaole Li, and Zhao-jun Duan

Address for correspondence: Zhao-jun Duan, National Institute for Viral Disease Control and Prevention, China Center for Disease Control and Prevention, Beijing, China; email: zhaojund@126.com

Call to Action for Dengue Vaccine Failure

To the Editor: Dengue is one of the most widespread infectious diseases globally; transmission now occurs in 128 countries. Although dengue virus (DENV) control strategies have targeted vector control and disease surveillance, the development of an effective vaccine is the holy grail of prevention.

Dengue vaccine development has spanned many decades. A candidate vaccine (Sanofi Pasteur, Swiftwater, PA, USA) containing all 4 DENV serotypes is in advanced clinical testing. However, when given to school children in Thailand, this live-attenuated, tetravalent, dengue–yellow fever 17D chimeric virus vaccine showed major but incomplete efficacy against 3 of the 4 DENV serotypes (DENV 1 [61.2%], DENV-3 [81.3%], and DENV-4 [89.9%]) in the intention-to-treat group but no protection against DENV 2, the most pathogenic of the DENV serotypes (1).

Two observations from the efficacy trial in Thailand provide insights into protective immunity that could greatly improve second-generation vaccines. The first observation was that a single dose of 4 live-attenuated chimeric DENVs given subcutaneously at a single site failed to raise type-specific protective immunity against the 4 DENV serotypes, and 2) doses 2 and 3 of the Sanofi Pasteur vaccine given to children over a 1-year period failed to improve efficacy outcomes. These results were