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## Norovirus Variant GII.4/Sydney/2012, Bangladesh

**To the Editor:** Noroviruses (NoVs) are the most common cause of foodborne and waterborne outbreaks of gastroenteritis in persons from all age groups in industrialized and developing countries (*1*). Although NoV outbreaks occur throughout the year, activity increases in the winter months, especially in the countries with a temperate climate. As expected, during the last few months of 2012, outbreaks of NoV gastroenteritis markedly increased in Europe and the United States (*2*–*4*). These increases corresponded with the emergence of a variant of genotype GII.4, Sydney/2012, which was first reported from Australia in March 2012 and, subsequently, in the United States, Belgium, Denmark, Scotland, and Japan (*2*,*5*–*7*).

We identified the NoV GII.4 variant Sydney/2012 through hospital surveillance on diarrhea etiology in Bangladesh in December 2011 and then throughout 2012. These strains came from 3 hospitals in Dhaka, Matlab, and Mirzapur, where ≈150,000 patients with diarrhea are treated annually. We randomly selected 795 fecal specimens from patients of all ages who sought treatment for diarrhea in these hospitals during 2010–2012 and detected NoV RNA in 90 (33.6%), 72 (27.9%), and 92 (34.2%) samples in 2010, 2011, and 2012, respectively, by performing real-time PCR (*8*). For characterization, we amplified and sequenced 108 samples on the basis of the capsid genes (*9*).

Ages of diarrhea patients with NoV infection ranged from 1 month to 91 years (median 15 months; mean 11.9 years). Most (66%) NoV-positive patients were <5 years of age. Infection rates were lowest in patients <3 months (2.1%) and 5–18 years (2.5%) of age. A high number of NoV infections were recorded in adults (28.8% in patients ≥18 years of age). NoVs were detected throughout the year, and no clear seasonal peaks were observed.

Overall, GII was the most predominant genogroup (66.1%), followed by GI (18.1%) and GIV (3.9%). Mixed infections were detected in 11.8% of samples. We observed a high diversity in the GII genogroup and identified at least 11 different genotypes within the group, in which GII.4 constituted 30.1% of all GII strains. Until December 2011, the GII.4 variant NewOrleans/2009 was the most predominant strain (Figure). However, the new GII.4 variant, Sydney/2012, replaced the old variant and appeared as the dominant strain in 2012. We constructed a phylogenetic tree on the basis of 1,026 bases around the junction region of *pol* and *cap* genes, and it revealed that the newly identified variant has evolved from previous NoV GII.4 variants Apeldoorn/2007 and NewOrleans/2009 (data not shown).

NoVs, old and new, remain a substantial threat to human health, with a new variant emerging every 2–3 years. The Sydney/2012 strain appears to have replaced the previously predominant strain, but its clinical effects and epidemiology are largely unknown and warrant further investigation.

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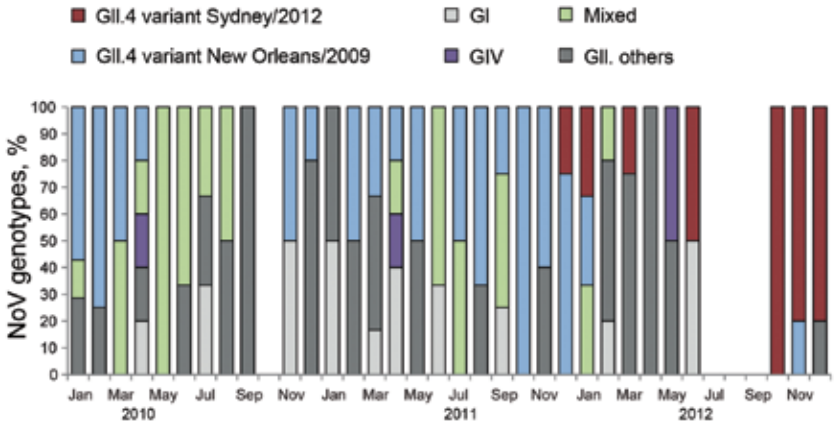


Figure. Distribution of 108 norovirus (NoV) genotypes in Bangladesh, 2010–2012. Bar chart shows the percentage of NoV genotypes. Mixed genotypes comprise NoV GI and GII. GI comprises GI.1, GI.3, GI.4, GI.5, and GI.9. GII.others comprises GII.2, GII.3, GII.4, GII.6, GII.10, GII.13, GII.16, GII.17, and GII.21.

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# Norovirus GII.4/Sydney/2012 in Italy, Winter 2012–2013

**To the Editor:** Noroviruses (NoVs) are the major cause of acute gastroenteritis in children and adults; they are responsible for sporadic cases and outbreaks of gastroenteritis in various epidemiologic settings. NoVs can be classified genetically into at least 5 genogroups, GI to GV (*1*). Although >30 genotypes within genogroups GI, GII, and GIV can infect humans (*2*), a single genotype, GII.4, has been associated with most NoV-related outbreaks and sporadic cases of gastroenteritis worldwide (*3*).

GII.4 NoV strains continuously undergo genetic/antigenic diversification and periodically generate novel strains through accumulation of punctate mutations or recombination. New GII.4 variants emerge every 2–3 years (*4*). Increased incidence of NoV-related illness and/or outbreaks in various countries in late 2012 has been related to the emergence of a novel GII.4 variant, Sydney 2012. This variant was first identified in March 2012 in Australia (*5*).

The Italian Study Group for Enteric Viruses (ISGEV; http://isgev.net) monitors the epidemiology of enteric viruses in children through hospital-based surveillance (*6*–*8*). NoVs are monitored and characterized by multitarget analysis in the diagnostic regions A (open reading frame 1, polymerase) and C (open reading frame 2, capsid) of the NoV genome (*9*) and interrogation of the Norovirus Typing Tool database (www.rivm.nl/mpf/norovirus/typingtool). During November 2011–March 2012, the prevalence of sporadic NoV infections detected (in samples from newborns, infants, and children up to 5 years of age) by real-time reverse transcription PCR was 22.2% (121/545). A subset (≈50%) of the NoV-positive samples representative of the whole winter period was selected for sequence analysis, and 48 were successfully characterized in region A and region C.

Among these 48 NoV strains, 20 (41.7%) were characterized as the variant GII.4 New Orleans 2009, a smaller number, 6 (12.5%), displayed a New Orleans 2009 polymerase (pol) but 2 distinct GII.4 capsid sequences, which were not typeable in the Norovirus Typing Tool database, and only 2 (4.2%) GII.4 strains of the variant Den Haag 2006b were detected. Moreover, 4 sporadic cases in November 2011 and January 2012 and a small outbreak in February 2012 were related to a GII.Pe_GII.4 recombinant strain. After the set of sequences of GII.4 variants from the Norovirus Typing Tool database was updated (access to the updated database: April 11, 2013), 5 (10.4%) GII.Pe_GII.4 recombinant strains were characterized as variant Sydney 2012.

From April through October 2012, a total of 56 (7.6%) NoV-positive samples were detected from 737 analyzed samples, of which 34 (60.7%) NoV-positive samples could be sequenced. Of