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Novel Norovirus GII.4 Variant, Shanghai, China, 2012

To the Editor: Norovirus (NoV) has been identified as one of the major causal agents of nonbacterial, acute gastroenteritis in humans (7). The genetic diversity among NoVs is great, and human strains have been classified into 3 genogroups (GI, GII, and GIV). Despite this diversity, in recent years only a few strains, primarily those of genogroup II, genotype 4 (GII.4), have been responsible for most cases and outbreaks worldwide (1,2).

The pattern of epochal evolution of NoV is ongoing, and novel GII.4 variants emerge, which replace previously dominant strains and cause new pandemics. Surveillance systems worldwide showed an increase in NoV activity in late 2012 (3). Molecular data shared through NoroNet (http://www.rivm.nl/en/Topics/Topics/N/NoroNet) suggest that this increase is related to the emergence of a new GII.4 variant, termed Sydney_2012 (3). We found that this novel GII.4 variant also emerged in Shanghai, China, and caused increased levels of NoV activity during October–December 2012.

During July 2011–December 2012, fecal specimens from 748 outpatients (>16 years of age) with acute gastroenteritis who visited 1 of the 2 sentinel hospitals in Shanghai were collected and stored at Shanghai Public Health Clinical Center at −70°C. Molecular detection of GI and GII NoV was performed by using conventional reverse transcription PCR as described (4). Full-length viral protein 1 and 639 bp of the 3′ RNA-dependent RNA polymerase gene of 4 randomly selected GII-positive strains were amplified (5–7). NoV genotypes were classified on the basis of a 280-bp region for GI and a 305-bp region for GII by using the Automated Genotyping Tool (www.rivm.nl/mpf/norovirus/typingtool).

A total of 77 patients showed positive results for GII NoV. An increase in GII NoV activity was observed during October–December in 2012; the detection rate was 46.08% (47 cases in 102 outpatients). The prevalence of GII NoV during the same period in 2011 was low; the detection rate was 6.90% (8 cases in 116 outpatients). Genotyping analysis of the strains detected in these 3 months in 2012 (39 strains were sequenced) showed that except for 1 GII.6 strain and 3 GII.4 2006b strains, the other 35 strains sequenced all belong to the new established cluster of GII.4, termed Sydney_2012. Retrospective analysis indicated that the novel GII.4 variant had already been detected in 2 outpatients during September 2011 in Shanghai.

Phylogenetic analysis of full-length capsid nucleotide sequences for 4 strains randomly selected from the new cluster indicated a novel GII.4 pattern, and new strains clustering separately from previously identified GII.4 pandemic strains (Figure). On the basis of BLAST (http://blast.ncbi.nlm.nih.gov/BLAST.cgi) searches, the most closely related NoVs (98%–100% nucleotide identity) were 4 GII.4 viruses recently detected in Australia and Hong Kong. The new GII.4 strains detected in Shanghai also clustered with these strains, a finding that was supported by bootstrap values >70% (Figure). The 3′ end of RNA-dependent RNA polymerase gene sequences also confirmed that the new GII.4 strains were recombinants, with a GI.e polymerase and GII.4 capsid (3).

Despite improved control measures to combat NOV, this highly infectious agent continues to cause a large number of epidemics of gastroenteritis globally (approximately every 2 years), and most epidemics have been associated with emergence of a novel GII.4 cluster (9). The new cluster reported in the present study was first detected in Australia in March, 2012, followed by detection in France, New Zealand, Japan, the United Kingdom, the United States, and Hong Kong, where increased levels of NoV activity in late 2012 compared with previous seasons were also observed (3). This novel GII.4 strain has also emerged in Shanghai, China, and caused increased levels of sporadic cases during October–December 2012. This new variant has common ancestors, dominant NoV GII.4 variants Osaka_2007 and New
Orleans_2009, but is phylogenetically distinct from them. Amino acid changes are present in major epitopes located in the P2 domain, a finding that is consistent with observations from previous epidemics (3).

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References


with G3CREC derived from poultry sources were associated with 21 additional deaths. G3CREC-related illness also resulted in 908 hospital bed-days needed to treat persons with these antimicrobial drug resistant bloodstream infections. If these values were extrapolated to all of Europe (i.e., if 56% of G3CREC were derived from poultry), 1,518 additional deaths and an associated increase of 67,236 days of hospital admissions would be counted as a result of cephalosporin and other antimicrobial drug use in poultry.

To more accurately estimate the associated increased deaths among persons resulting from third-generation cephalosporin use in poultry, detailed data from more countries is essential. Needed data include records of antimicrobial drug use and resistant bacterial strains found in food animals and domestic and imported foods. However, we already know that G3CREC is rapidly rising in many countries, and in Europe, the infection rate is likely to have tripled from 2007 to 2012 (2). Globally, billions of chickens receive third-generation cephalosporins in ovo or as day-old chicks to treat E. coli infection, a practice that has resulted in large reservoirs of resistant bacteria. In Canada, this practice has been associated with substantial increases in resistance to third-generation cephalosporins in Salmonella enterica serovar Heidelberg isolates detected in humans. (7). The United States Food and Drug Administration recently prohibited the off-label use of cephalosporins, including prophylactic uses, in major food animal species, including poultry (8).

The number of avoidable deaths and the costs of health care potentially caused by third-generation cephalosporin use in food animals is staggering. Considering those factors, the ongoing use of these antimicrobial drugs in mass therapy and prophylaxis should be urgently examined and stopped, particularly in poultry, not only in Europe, but worldwide.

Human Deaths and Third-Generation Cephalosporin use in Poultry, Europe

To the Editor: Globally, antimicrobial drug resistance is rapidly rising, with resultant increased illness and death. Of particular concern is Escherichia coli, the most common bacterium to cause invasive disease in humans (1). In Europe, increasing proportions of bloodstream infections caused by E. coli are resistant to third-generation cephalosporins (1,2).

Resistant E. coli can be transmitted to humans from animals. A large proportion of resistant isolates causing human infections are derived from food animals (3–6). However, lack of data has made it difficult to quantify the proportion of antimicrobial drug resistant E. coli infecting persons through food sources and the resultant effects on human health. Recent data from the Netherlands now make such estimates possible (2,6). The additional illness and death among humans resulting from bloodstream infections caused by third-generation cephalosporin-resist-ant E. coli (G3CREC) has been calculated for Europe (2). In the Netherlands, there were 205 G3CREC cases during 2007 (4%) of all E. coli bloodstream infections (2). Another study in the Netherlands revealed that 56% of the resistance genes in G3CREC in humans were identical to genes derived from E. coli isolated from retail chicken samples (6). Using the findings of Overdevest et al. (6) and de Kraker et al. (2), we calculated that, in the Netherlands, infections in humans

References


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