Norovirus is a major cause of nonbacterial acute gastroenteritis; sporadic cases and outbreaks occur among children and adults (1). Most strains infecting humans belong to genogroups I and II (GI and GII), of which GII.4 has been most predominant (2). Reemergence of norovirus infection is attributed to new variants resulting from frequent recombination between the end of open reading frame (ORF) 1, encoding the RNA-dependent RNA polymerase (RdRp), and ORF2, encoding the major capsid protein (VP1) of the norovirus genome. Lack of a robust cell culture system for human norovirus infection in humans and lack of long-lasting neutralizing antibodies in previously infected persons present challenges for vaccine development.

In recent years, a relative increase in global prevalence of norovirus has been attributed to GII.P16-GII.4 Sydney (3–5). As in temperate regions, norovirus infection in Thailand occurs as sporadic cases and outbreaks year-round. After the recent increase of GII.P16-GII.2 in Thailand in late 2016 (6), we sought to identify the most frequently identified genotypes.

During June 2017–December 2018, we tested 2,704 fecal samples from patients at Chulalongkorn University Hospital (King Chulalongkorn Memorial Hospital and Bangpakok 9 International Hospital; n = 2,385 patients), Khon Kaen (n = 70), Phitsanulok (n = 199), and Saraburi (n = 50), Thailand. Mean patient age ± SD was 27.9 ± 25.1 years (range 3 months–88 years). A minority of strains (42/296) were genotype GI (GI.3 15/42, GI.5 14/42, GI.1 6/42, GI.7 6/42, GI.4 1/42) (Appendix Figure 1, https://www.cdc.gov/EID/article/25/8/19-0365-App1.pdf). Most positive samples (266/296) were GI strains, of which 12 were co-infected with GI/GII. The 3 most common RdRp genotypes were GII.Pe (40.6%, 108/266), GII.P16 (28.6%, 76/266), and GII.P17 (16.2%, 43/266) (Figure, panel A). Among samples for which VP1 genotyping was successful, most were GII.4 Sydney (56.8%, 151/266), followed by GII.17 (16.2%, 43/266), GII.6 (5.3%, 14/266), GII.13 (4.9%, 13/266), GII.2 (4.1%, 11/266), and others (7.5%, 20/266) (Figure, panel B). The most prevalent strains were recombinant GII.Pe-GII.4 Sydney (39.9%, 106/266), GII.P16-GII.4 Sydney (17%, 45/266), and GII.P17-GII.17 (15%, 39/266). Although RdRp genotype GII.Pe is usually associated with VP1 genotype GII.4 Sydney, we identified 1 strain each of GII.Pe-GII.3 and GII.Pe-GII.13.

In this study, norovirus infections were frequently detected in children ≤5 years of age (60.1%, 178/296, mean age ± SD 2.2 ± 1.3 years). Using cycle threshold (Ct) as a surrogate for viral load, we age stratified norovirus-positive patients (GII.Pe-GII.4 Sydney) into 3 age groups, <2, 2–5, and >5 years (Appendix Figure 2). Mean viral load was higher among children ≤5 years of age (Ct = 19.0) than among those >5 years of age (Ct = 25.1) (p < 0.01).

In Thailand, the most frequently identified norovirus genotype throughout 2018 was GII.Pe-GII.4 Sydney. In the United States, GII.Pe-GII.4 Sydney first emerged in 2012 and was prevalent until mid-2015 (3,8); however, it represented minor variants elsewhere and has not been previously associated with increased norovirus activity in Thailand (9). Although GII.P16-GII.4 Sydney subsequently emerged in many industrialized countries, both GII.Pe-GII.4 Sydney and GII.P16-GII.4 Sydney circulated concurrently in Thailand after the upsurge of GII.17 in 2015–2016 and GII.P16-GII.4 Sydney.
GII.2 in 2016–2017 in Thailand (6). Three years later, GII.17 continued to be detected sporadically, albeit at low levels. Therefore, norovirus circulation in Thailand at times differed from the global trend, which cannot be explained by factors such as geographic location and warm climate alone.

The significance of GI/GII co-infection in some samples is unclear but is probably not the result of laboratory contamination because as many as 7 combinations were identified (4 samples of GI.5/GII.17; 2 each of GI.3/GII.P16-GII.4 Sydney and GI.5/GII.P8-
GII.6, GII.3/GII.17, GI.7/GII.17, and GI.7/GII.P7-GII.6). We did not perform dual typing on GI strains because they were less predominant than GII strains. However, future analysis of their recombination patterns will be useful for better characterizing these rare but potentially significant genotypes. This study was somewhat limited by lack of detailed clinical information accompanying the submitted samples and absence of surveillance from southern Thailand (≈14% of the country’s population). Molecular epidemiology and continued surveillance of norovirus strain diversity will increase awareness among clinicians and help epidemiologists determine global transmission patterns.

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RESEARCH LETTERS

Sneathia amnii and Maternal Chorioamnionitis and Stillbirth, Mozambique

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