Table. Positivity rates for companion animals owned by SARS-CoV-2–positive persons in study of human-to-animal transmission of SARS-CoV-2, South Korea, 2021*

Animal	Test results, no. (%)		χ^2 distribution	p value
	Positive	Negative		
Dogs, n = 271	65 (24.0)	206 (76.0)	5.100	0.024
Cats, n = 104	37 (35.6)	67 (64.4)		
Total, n = 375	102 (27.2)	273 (72.8)		

*Positivity rate for cats was significantly (p = 0.024) higher than that for dogs.

Our study was limited by having been conducted with animals consigned to the protection facilities of the Seoul City Government and those whose tests were requested by their owners because of the animals' clinical signs. Owner bias might have affected the population in this setting.

Our study could provide epidemiologically meaningful data for public health. As SARS-CoV-2 spreads as a pandemic, reverse zoonotic infections will continue, and viruses will mutate to adapt to the new host. For companion animals living near humans, continuous epidemiologic investigations and monitoring will be needed.

This research was supported by COVID-19 Animal Inspection Project of Seoul Metropolitan Government.

About the Author

Dr. Bae is a leader of the veterinary public health section of the Seoul Metropolitan government. Her research interests include the epidemiology of zoonoses, infectious disease prevention policies and administrative affairs such as quarantine.

References

1. Segalés J, Puig M, Rodon J, Avila-Nieto C, Carrillo J, Cantero G, et al. Detection of SARS-CoV-2 in a cat owned by a COVID-19–affected patient in Spain. Proc Natl Acad Sci U S A. 2020;117:24790–3. https://doi.org/10.1073/pnas.2010817117
2. Hamer SA, Pauvolid-Corrêa A, Zecca IB, Davila E, Auckland LD, Roundy CM, et al. SARS-CoV-2 infections and viral isolations among serially tested cats and dogs in households with infected owners in Texas, USA. Viruses. 2021;13:938. https://doi.org/10.3390/v13050938
3. Calvet GA, Pereira SA, Ogrzewalska M, Pauvolid-Corrêa A, Resende PC, Tassinari WS, et al. Investigation of SARS-CoV-2 infection in dogs and cats of humans diagnosed with COVID-19 in Rio de Janeiro, Brazil. PLoS One. 2021; 16:e0250853. https://doi.org/10.1371/journal.pone.0250853
4. Colitti B, Bertolotti L, Mannelli A, Ferrara G, Vercelli A, Grassi A, et al. Cross-sectional serosurvey of companion animals housed with SARS-CoV-2–infected owners, Italy. Emerg Infect Dis. 2021;27:1919–22. https://doi.org/10.3201/eid2707.203314
5. Bessière P, Vergne T, Battini M, Brun J, Averso J, Joly E, et al. SARS-CoV-2 infection in companion animals: prospective serological survey and risk factor analysis in France. Viruses. 2022;14:1178. https://doi.org/10.3390/v14061178
6. World Organisation for Animal Health. Consideration for sampling, testing, and reporting of SARS-CoV-2 in animals [cited 2023 Mar 9]. https://rr-asia.woah.org/wp-content/uploads/2020/05/sampling_testing_and_reporting_of_sars-cov-2_in_animals_7may_2020.pdf
7. Corman V, Bleicker T, Brünink S, Drosten C, Zambon M. Diagnostic detection of 2019-nCoV by real-time RT-PCR [cited 2023 Mar 9]. https://www.who.int/docs/default-source/coronaviruse/protocol-v2-1.pdf
8. Meisner J, Baszler TV, Kuehl KE, Ramirez V, Baines A, Frisbie LA, et al. Household transmission of SARS-CoV-2 from humans to pets, Washington and Idaho, USA. Emerg Infect Dis. 2022;28:2425–34.
9. Kannekens-Jager MM, de Rooij MMT, de Groot Y, Biesbroeck E, de Jong MK, Pijnacker T, et al. SARS-CoV-2 infection in dogs and cats is associated with contact to COVID-19–positive household members. Transbound Emerg Dis. 2022;69:4034–40. https://doi.org/10.1111/tbed.14713

Address for correspondence: Woonsung Na, College of Veterinary Medicine, Chonnam National University, Gwangju 61186, South Korea; email: wsungna@jnu.ac.kr; and Daesub Song, College of Veterinary Medicine, Seoul National University, Seoul 08826, South Korea; email: sds@snu.ac.kr

Norovirus GII.3[P25] in Patients and Produce, Chanthaburi Province, Thailand, 2022

Watchaporn Chuchaona, Sarawut Khongwichit, Woraya Luang-on, Sompong Vongpunsawad, Yong Poovorawan

Author affiliations: Chulalongkorn University, Bangkok, Thailand (W. Chuchaona, S. Khongwichit, S. Vongpunsawad, Y. Poovorawan); Ministry of Public Health, Nonthaburi, Thailand (W. Luang-on)

DOI: https://doi.org/10.3201/eid2905.221291

An increase in acute gastroenteritis occurred in Chanthaburi Province, Thailand, during December 2021–January 2022. Of the norovirus genotypes we identified in hospitalized patients and produce from local markets, genotype GII.3[P25] accounted for one third. We found no traceable link between patients and produce but found evidence of potential viral intake.

Noroviruses are the leading cause of sporadic and outbreak-associated, acute, nonbacterial gastroenteritis (*1*). They are genetically diverse and are classified into 10 genogroups (GI–GX) representing >40 genotypes, although most human noroviruses are GI and GII (*2*). Emergence of recombinant strains that have different combinations of the RNA-dependent RNA polymerase (RdRp) and viral protein 1 (VP1) genes can cause upsurge of new infections (*3*). In 2020, during the early months of the COVID-19 pandemic, public health measures resulted in the drastic reduction of norovirus outbreaks (*4*). We report a resurgence of norovirus in Chanthaburi Province, Thailand

During December 2021–January 2022, local health authorities in Chanthaburi Province contacted the university for assistance in investigating an increase of vomiting and diarrhea requiring hospitalization among healthy adults. Because preliminary findings by local officials over several weeks had not identified an obvious single-infection source, we suspected norovirus because of rapid widespread community infection. Subsequently, we obtained fecal samples from 34 patients for testing with the approval from the Institutional Review Board of Chulalongkorn University (approval no. 549/62).

Because many patients reported dining out at eateries serving uncooked vegetables, health officials suspected produce as a potential source of infection. Therefore, 24 samples of fresh produce (e.g., salad greens, basil, parsley, napa cabbage, and tomato) from open-air markets near the infection cluster were sent from local health officials for testing to determine a potential norovirus source.

We crushed vegetables in 1 mL nuclease-free water before RNA extraction. We used a bag of ice cubes, which we melted and concentrated from 1 L to 1 mL by using an Amicon Centrifugation Filtration Device (Merck Millipore, https://www.emdmillipore.com) before testing.

After we performed automated viral RNA extraction by using a magLEAD 12 gC Instrument (Precision System Science, https://www.pss.co.jp), we tested for noroviruses by using a real-time reverse transcription PCR (RT-PCR) (*5*). We dual-typed norovirus-positive samples for the RdRp and VP1 genes by using a conventional RT-PCR (*6*). We genotyped Sanger-sequenced nucleotide sequences by using the Norovirus Genotyping Tool (http://www.rivm.nl/mpf/norovirus/typingtool) and deposited them in GenBank (accession nos. OP210707–54, OP210788–834, OP218773–7, and OP218813–7). We performed phylogenetic analysis by using the maximum-likelihood method and 1,000 bootstrap replicates implemented in MEGA 11 (http://www.megasoftware.net).

A total of 32/34 patients (age range 1–82 years, mean age ±SD 31.4 ±19.7 years) were positive for norovirus; they had GI only (2/32), GII only (23/32), and GI and GII (7/32) infections. We ascertained nucleotide sequences for all 30 GII-positive samples (Table).

Analysis of the RdRp gene identified GII.P25 (10/30), GII.P7 (8/30), GII.P17 (6/30), and 2 each of GII.P12, GII.P21, and GII.P31 (Appendix Figure, https://wwwnc.cdc.gov/EID/article/29/5/22-1291-App1.pdf). Analysis of the VP1 gene identified GII.3 (15/30), GII.6 (4/30), GII.21 (4/30), GII.17 (2/30), GII.4 Sydney (2/30), GII.4 Hong Kong (2/30), and GII.7 (1/30). Defined genotypes were GII.6[P7] (3/30); 2 each of GII.3[P7], GII.3[P12], GII.17[P17], GII.21[P17], and GII.21[P21]; and 1 each of GII.3[P17], GII.3[P31], GII.4 Sydney[P7], GII.4 Sydney[P25], GII.4 Hong Kong [P7], GII.4 Hong Kong [P31], GII.6[P17], and GII.7[P7]. We also observed the relatively rare GII.3[P25] genotype (9/30) (*7*).

Table. Detection of GII noroviruses in patients and produce samples, Chanthaburi Province, Thailand, 2022*

	RdRp gene					
VP1	P7	P12	P17	P21	P25	P31
GII.3	2/4	2/ND	1/1	ND	9/1	1/ND
GII.4 Hong Kong	1/ND	ND	ND/1	ND	ND	1/2
GII.4 Sydney	1/ND	ND	ND	ND	1/ND	ND
GII.6	3/5	ND	1/1	ND	ND/1	ND
GII.7	1/ND	ND	ND	ND	ND	ND
GII.17	ND	ND	2/1	ND	ND	ND
GII.21	ND/1	ND	2/ND	2/ND	ND	ND

*Values indicate patient samples/produce samples positive for norovirus (e.g., the GII.3[P7] combination was detected in 2 patient and 4 produce samples). Several VP1 and RdRp combinations are detected in patient and produce samples. Produce samples were obtained from open-air markets near the infection cluster and sent by local health officials for testing to determine a potential norovirus source. ND, not detected; P, polymerase; RdRp, RNA-dependent RNA polymerase; VP, viral protein.

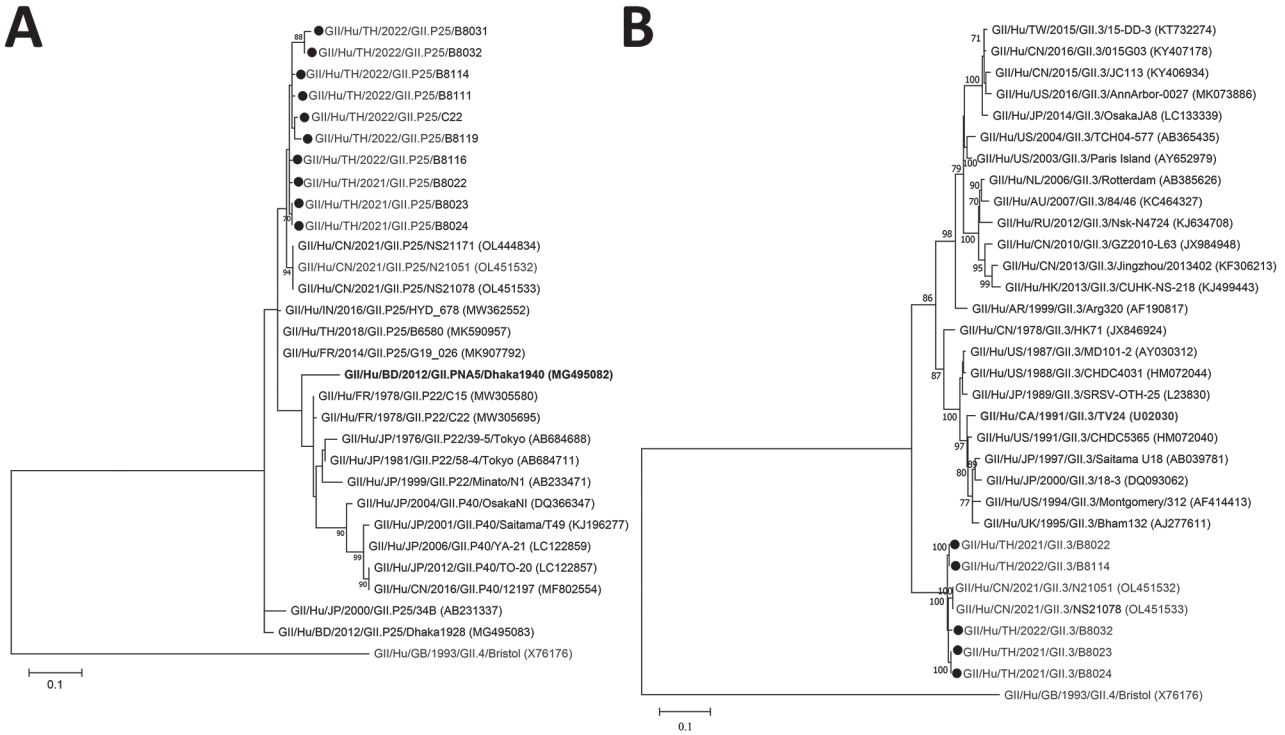


Figure. Phylogenetic analysis of norovirus strains, Chanthaburi Province, Thailand, 2022. A) Partial sequence of the RNA-dependent RNA polymerase gene (187 bp). B) Complete sequence of the capsid gene (1,644 bp). Strains identified in this study (black circles) were compared with the reference (bold) and global strains. GenBank accession numbers for strains are indicated in parentheses. Trees were generated by using the maximum-likelihood method with 1,000 bootstrap replicates implemented in MEGA 11 (https://www.megasoftware.net). Bootstrap values ≥70 are indicated at the nodes. Only strains of sufficient nucleotide sequence length needed for analysis are included. Scale bars indicate nucleotide substitutions per site.

Testing for a possible source showed that 8/24 produce samples and ice were norovirus-positive; GII.3[P25] was identified in a tomato (Appendix Table). Partial RdRp genes and entire VP1 genes showed closest phylogeny with unpublished GenBank sequences OL451532 and OL451533, which were deposited by health authorities in China during November 2021. GII.3[P25] from Thailand and China clustered away from global strains (Figure).

Although only 5 GII.3[P25] strains from Thailand yielded full-length VP1 sequences, deduced amino acid residues in the P2 domain (residues 385–420) were possible for all 10 strains. Alignments showed residue changes D388N, Q391M, N404T, E405D, S412I, N415R, and F420V compared with the prototypic GII.3/TV24 (GenBank accession no. U02030) and more recent GII.3 VP1 strains.

Many different norovirus genotypes found in samples from patients during this investigation did not implicate an overwhelmingly predominant strain responsible for the infection cluster. However, emergence of GII.3[P25] in Thailand identified in patients and produce (sample C22) indicated a potential source of infection. The diversity of norovirus strains in produce sampled warrants increased awareness of food safety in preventing norovirus infection. In addition, we identified GII.4 Hong Kong [P31] and 2 novel variants, GII.4 Hong Kong [P7] (patient B8045) and GII.4 Hong Kong [P17] (sample C30), which were reported recently (*8*,*9*), and GII.21[P17], previously reported in South Korea (*10*).

Combined investigation of illness in patients and of potential sources of infection is often challenging. A limitation of our study was low viral loads (cycle threshold ≥30) for many of the samples, which hindered confirmation of minor recombinants found. Our study was also limited by the lack of a definitive traceable link between patients and produce but does provide evidence of potential ingestion of the virus. Although contaminated fruits and vegetables can serve as a source of outbreaks in countries in temperate zones, this study paralleled similar transmission, but in a tropical country. Continuous molecular and epidemiologic surveillance of emerging norovirus variants is needed to detect future outbreaks.

Acknowledgments

We thank staff members of the Chanthaburi Provincial Health Office and the Office of Disease Prevention and Control Region 6 Chonburi for supporting sample collection.

This study was supported by the Center of Excellence in Clinical Virology of Chulalongkorn University and Hospital. W.C. was supported by Chulalongkorn University's Second Century Fund (C2F).

About the Author

Dr. Chuchaona is a postdoctoral fellow at the Center of Excellence in Clinical Virology in the Faculty of Medicine at Chulalongkorn University, Bangkok, Thailand. Her primary research interests are molecular epidemiology and evolution of human noroviruses.

References

1. Ahmed SM, Hall AJ, Robinson AE, Verhoef L, Premkumar P, Parashar UD, et al. Global prevalence of norovirus in cases of gastroenteritis: a systematic review and meta-analysis. Lancet Infect Dis. 2014;14:725–30. https://doi.org/10.1016/S1473-3099(14)70767-4
2. Chhabra P, de Graaf M, Parra GI, Chan MC, Green K, Martella V, et al. Updated classification of norovirus genogroups and genotypes. J Gen Virol. 2019;100:1393–406. https://doi.org/10.1099/jgv.0.001318
3. Bull RA, White PA. Mechanisms of GII.4 norovirus evolution. Trends Microbiol. 2011;19:233–40. https://doi.org/10.1016/j.tim.2011.01.002
4. Kraay AN, Han P, Kambhampati AK, Wikswo ME, Mirza SA, Lopman BA. Impact of nonpharmaceutical interventions for severe acute respiratory syndrome coronavirus 2 on norovirus outbreaks: an analysis of outbreaks reported by 9 US States. J Infect Dis. 2021;224:9–13. https://doi.org/10.1093/infdis/jiab093
5. Debbink K, Costantini V, Swanstrom J, Agnihothram S, Vinjé J, Baric R, et al. Human norovirus detection and production, quantification, and storage of virus-like particles. Curr Protoc Microbiol Clin Virol. 2013;31:15K1.1–15K1.45. https://doi.org/10.1002/9780471729259.mc15k01s31
6. Chhabra P, Browne H, Huynh T, Diez-Valcarce M, Barclay L, Kosek MN, et al. Single-step RT-PCR assay for dual genotyping of GI and GII norovirus strains. J Clin Virol. 2021;134:104689. https://doi.org/10.1016/j.jcv.2020.104689
7. Kendra JA, Tohma K, Parra GI. Global and regional circulation trends of norovirus genotypes and recombinants, 1995–2019: a comprehensive review of sequences from public databases. Rev Med Virol. 2022;32:e2354. https://doi.org/10.1002/rmv.2354
8. Chan MC, Roy S, Bonifacio J, Zhang LY, Chhabra P, Chan JC, et al.; for NOROPATROL2. Detection of norovirus variant GII.4 Hong Kong in Asia and Europe, 2017–2019. Emerg Infect Dis. 2021;27:289–93. https://doi.org/10.3201/eid2701.203351
9. Mabasa VV, van Zyl WB, Ismail A, Allam M, Taylor MB, Mans J. Multiple novel human norovirus recombinants identified in wastewater in Pretoria, South Africa by next-generation sequencing. Viruses. 2022;14:2732. https://doi.org/10.3390/v14122732
10. Koo ES, Kim MS, Choi YS, Park KS, Jeong YS. Occurrence of novel GII.17 and GII.21 norovirus variants in the coastal environment of South Korea in 2015. PLoS One. 2017;12:e0172237. https://doi.org/10.1371/journal.pone.0172237

Address for correspondence: Yong Poovorawan, Center of Excellence in Clinical Virology, Faculty of Medicine, Chulalongkorn University, 1873 Rama 4 Rd, Pathumwan, Bangkok 10330, Thailand; email: yong.p@chula.ac.th

COVID-19 Vaccine Uptake by Infection Status in New South Wales, Australia

Heather F. Gidding, Sandrine Stepien, Jiahui Qian, Kristine K. Macartney, Bette Liu

Author affiliations: University of Sydney Northern Clinical School, St. Leonards, New South Wales, Australia (H.F. Gidding); National Centre for Immunisation Research and Surveillance, Westmead, New South Wales, Australia (H.F. Gidding, S. Stepien, J. Qian, K.K. Macartney, B. Liu); University of New South Wales School of Population Health, Kensington, New South Wales, Australia (H.F. Gidding, J. Qian, B. Liu); University of Sydney Faculty of Medicine and Health, Camperdown, New South Wales, Australia (H.F. Gidding, K.K. Macartney)

DOI: https://doi.org/10.3201/eid2905.230047

Using linked public health data from Australia to measure uptake of COVID-19 vaccination by infection status, we found coverage considerably lower among infected than uninfected persons for all ages. Increasing uptake of scheduled doses, including among previously infected persons after the recommended postinfection delay, is needed to reduce COVID-19 illness rates.

Although coverage with 2 doses of COVID-19 vaccine rapidly reached >95% in adults in Australia by late 2021 (*1*), by December 4, 2022, uptake had slowed and plateaued at much lower levels for 2 doses among children 5–15 years of age (52.1%) and for boost-

Article DOI: https://doi.org/10.3201/eid2905.2211291

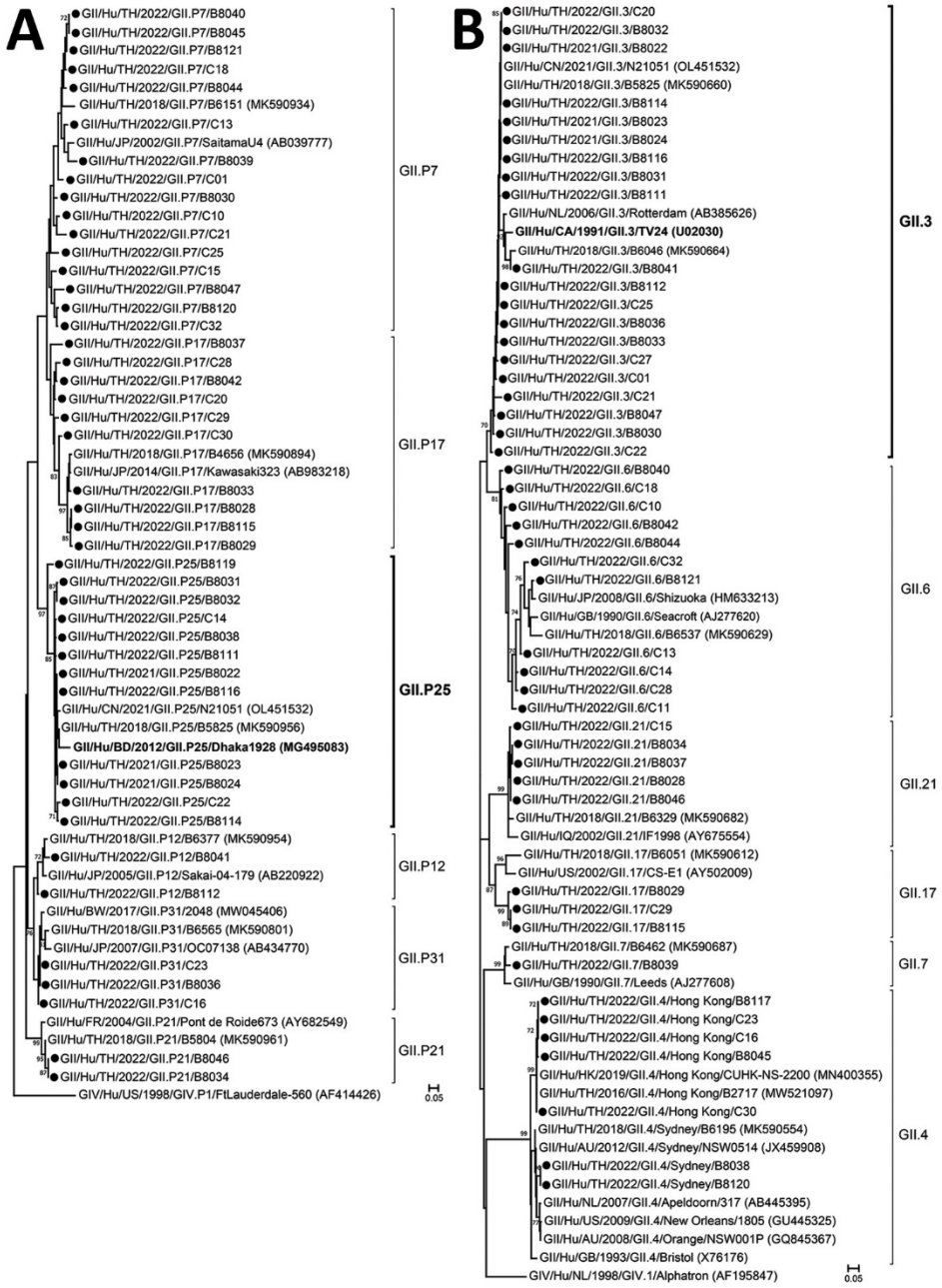
EID cannot ensure accessibility for Supplemental Materials supplied by authors. Readers who have difficulty accessing supplementary content should contact the authors for assistance.

Norovirus GII.3[P25] in Patients and Produce, Chanthaburi Province, Thailand, 2022

Appendix.

Appendix Table. Ice and produce tested for norovirus

		Detectable	GII genotyping	
Sample code	Description	Ct value	RdRp	VP1
C01	Ice cubes	33.1	P7	GII.3
C10	Salad greens	32.9	P7	GII.6
C11	Salad greens	33.0	P7	GII.6
C12	Thai basil	–	–	–
C13	Cabbage	30.3	P7	GII.6
C14	Napa cabbage	32.7	P25	GII.6
C15	Salad greens	32.3	P7	GII.21
C16	Salad greens	33.0	P31	GII.4 Hong Kong
C17	Celery	–	–	–
C18	Water spinach	32.5	P7	GII.6
C19	Holy basil	–	–	–
C20	Thai basil	33.0	P17	GII.3
C21	Cucumber	32.5	P7	GII.3
C22	Tomato	30.7	P25	GII.3
C23	Daikon radish	31.2	P31	GII.4 Hong Kong
C24	Water spinach	–	–	–
C25	Salad greens	36.0	P7	GII.3
C26	Culantro	–	–	–
C27	Cilantro	35.4	P7	GII.3
C28	Napa cabbage	33.3	P17	GII.6
C29	Chinese broccoli	34.1	P17	GII.17
C30	Diplazium esculentum fern	34.9	P17	GII.4 Hong Kong
C31	Pak choi	–	–	–
C32	Culantro	36.5	P7	GII.6
C33	Water spinach	–	–	–



Appendix Figure. Phylogenetic analysis of norovirus strains from Chanthaburi Province, Thailand, 2022. A) Partial sequence of RdRp gene (187 bp). B) Partial sequence of VP1 gene (207 bp). Strains identified in this study (dotted) were compared with the reference (bolded) and global strains. Strain accession numbers are indicated in parentheses. Trees were generated by using the maximum-likelihood method with 1,000 bootstrap replicates implemented in MEGA11 (https://www.megasoftware.net). Bootstrap values ≥70 are indicated at the nodes. Scale bars indicate nucleotide substitutions per site.