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Global trends in norovirus genotype distribution among medically attended children with acute gastroenteritis, 2020–2025

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JLC and JV conceptualized this study. JLC performed data curation. KB, MEH, C-YP, J-HC, DC, LKM, WC, FJDM, MLM, LMH, SJ, CDA, KAG AI, EB, and BR performed laboratory analyses and results interpretation. JLC, LB and JV were responsible for development and design of methodology. JV, JB, TMF, CP, MDG, RS, JB, JH, PAW, GVT, JM, SN, LM, JID, TV, MKL, FGS, MS, CL, MR, YP, F-TW and XP provided oversight and supervision. JLC conducted data visualization and drafted the manuscript. All authors reviewed the manuscript and had the final responsibility for the decision to submit for publication.

Disclaimer

The findings and conclusions in this article are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention, the California Department of Public Health or the California Health and Human Services Agency.

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Declaration of Competing Interest

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Abstract

Background: Norovirus is a leading cause of acute gastroenteritis, with a broad diversity of genotypes infecting children. NoroSurv is an established global network for norovirus strain surveillance among medically attended children < 5 years of age.

Methods: Participating laboratories uploaded norovirus sequences from stool specimens collected from 2020 to 2025 to a web portal, which assigned norovirus genotypes and strain data. Norovirus seasons were defined as September 1 to August 31.

Results: Participants in 22 countries across 6 continental regions uploaded 4113 norovirus sequences, including 26 genotypes and 53 strains. GII.4 accounted for 53% (2167/4113), followed by GII.3 (12%), GII.17 (11%), GII.6 (7%), and GII.2 (5%). GII.4 Sydney was the most common variant (47%; 1912/4113), but new GII.4 variants/clusters emerged regionally, with GII.4 San Francisco, GII.4 Wichita and GII.4 Allegany more frequently detected than GII.4 Sydney in 2021–2022 in Africa, 2022–2023 in Central and South America and 2023–2024 in Central America. In 2023–2024, a dramatic rise in GII.17 detection was observed in most regions (32% of all 2024–2025 sequences). In North, Central and South America, Europe and Asia Pacific, GII.17 detection increased as GII.4 detection declined in 2024–2025. Other genotypes (GI.3, GII.1, GII.2, GII.3 and GII.6) had regional peaks, accounting for up to 37% of sequences during a specific season.

Conclusions: Our data may help guide norovirus vaccine development and provide a baseline of global norovirus strain distribution for evaluating the effectiveness of future vaccines in children. We continue to monitor the shifting distribution of norovirus genotypes through NoroSurv surveillance.

Keywords

norovirus; NoroSurv; acute gastroenteritis; genotype; children; global; viral gastroenteritis; GII.4; GII.17

1. Introduction

Among children under 5 years of age, acute gastroenteritis (AGE) is a major contributor to morbidity and mortality worldwide [1,2]. As a leading cause of medically attended pediatric AGE, norovirus results in > 30,000 global deaths annually [1,2]. The economic impact is also substantial, with estimated global costs reaching $2.7 billion USD for direct healthcare costs and $39.8 billion for societal costs among children under 5 years old [3]. Norovirus vaccines are currently in clinical development but their design is complicated by the virus's vast genetic diversity. Effective vaccines must not only protect against current circulating strains but also adapt to rapidly emerging new strains [4].

There are at least 34 norovirus genotypes known to infect humans of which the majority belong to genogroup I and II [5]. Genotypes are defined by the amino acid sequences of the major capsid protein VP1, the primary site recognized by neutralizing antibodies following infection or vaccination [6]. For three decades, GII.4 has been the dominant, with new variants periodically replacing older ones. While GII.4 Sydney has predominated since 2012 [7], several novel GII.4 variants have recently emerged [7]. Due to frequent

recombination, noroviruses are defined as specific strains (dual types) based on their genotype and polymerase type [5].

Developing pediatric norovirus vaccines is uniquely challenging because children encounter a wider variety of norovirus strains than adults [8]. Since 2018, the NoroSurv network has monitored these circulating and emerging strains in children under 5 with medically-attended AGE [9]. This report analyzes nearly five years of global NoroSurv data.

2. Methods

Stool specimens from children with AGE were obtained and processed at participating NoroSurv laboratories, hospitals, medical centers, or universities. Laboratories applied standardized protocols for detecting and genotyping/strain typing noroviruses by conventional RT-PCR and Sanger sequencing [9,10], whole genome sequencing [11], or nanopore sequencing. Norovirus sequences (raw DNA chromatogram or fasta files), patient demographic data (deidentified patient age and sex), and information on setting (e.g., hospital, outpatient clinic) and date of specimen collection, were uploaded to the NoroSurv web portal (https://www.norosurv.org). Norovirus sequences were automatically typed in NoroSurv using the most recent reference sequences and classification for genotypes (capsid only) and strains (dual-type, polymerase and capsid) [5,7]. The United Nations geoscheme was used to define geographic regions, collapsing European and African regions into single categories. All data analyses, descriptive statistics, statistical tests, and visualizations were performed in R (https://www.r-project.org).

3. Results

A total of 4113 norovirus sequences from sites in 22 countries on six continental regions with specimen collection dates between September 1, 2020 to August 31, 2025 (norovirus season in countries in the Northern Hemisphere) were included in the analysis after excluding data from children over 60 months (n = 233), asymptomatic status (n = 79), community setting without medical attendance (n = 109), unknown sample collection date (n = 2), incomplete or low-quality sequences that precluded strain typing (n = 132), or those meeting multiple exclusion criteria (n = 10). Sequence counts varied by geographic region (Table 1), with a median of 138 [interquartile range (IQR) 86 – 307] sequences per country and a median of 506 [IQR 251 – 545] regionally (Table 1). A median of 833 [IQR 537–1095] sequences were submitted each norovirus season (spanning September 1 to August 31 each year); 2020–2021 (n = 492), 2021–2022 (n = 833), 2022–2023 (n = 1095), 2023–2024 (n = 1156) and 2024–2025 (n = 537) (Fig. 1A).

Among all norovirus sequences, 26 genotypes (Table 2) and 53 strains (defined as polymerase-capsid dual-types) (Supplemental Table 1) were identified, with a median of 21 [IQR 18–23] genotypes and 35 [IQR 32–36] strains per norovirus season (Fig. 1A). Genotype and strain counts from each region differed across norovirus seasons (Kruskal-Wallis; p = 0.02 and p = 0.01) (Fig. 1A) but counts generally increased with sequence counts (Pearson correlation; 0.62 and 0.68) without clear points of saturation (Supplemental Figure 1; Supplemental Table 2). This trend was seen across all regions (Supplemental Table 2;

Supplemental Figures 2A–10A), but in Africa and Europe in the 2022–2023 season, the number of strains detected was high (18 in each country), despite low sequence counts (<100 sequences) and in the Oceania and West Pacific region, 4 strains were detected in the 2020–2021 season among the 132 sequences submitted.

During the 5 years of study, over half of all sequences 53% (2167/4113) typed as GII.4, followed by GII.3 (12%; n = 486), GII.17 (11%; n = 456), GII.6 (7%; n = 271), and GII.2 (5%; n = 211). Overall, GII.4 was represented in 47%-58% of sequences each norovirus season (Fig. 1B). Proportions of other genotypes fluctuated, with higher proportions of GII.3 and GII.2 in earlier seasons and higher proportions of GII.17 in the 2024–2025 season (Fig. 1B; Fig. 2A). Trends across norovirus seasons were regional (Supplemental Figures 2B–10B; Supplemental Figures 2C–10C); GII.4 viruses were detected in < 40% of sequences per norovirus season in some regions (Supplemental Figures 4B–10B) and in less than 20% of sequences in Europe and South Asia in 2020–2021 (Supplemental Figures 5B and 7B). Increases in the proportion of other genotypes often coincided with lower percentages of GII.4 (Fig. 1B; Fig. 2A).

GII.4 Sydney was the predominant variant, detected in 47% (n = 1912/4113) of all norovirus sequences (42%-49% per season) and 88% of all GII.4 sequences (84%-91% per season). The recently reported GII.4 San Francisco and GII.4 Wichita variants and the GII.4 Allegany cluster circulated throughout the study seasons. GII.4 Wichita and GII.4 San Francisco peaked in frequency of detection in early 2023 (together accounting for 16% of all norovirus sequences and 25% of GII.4 sequences during the first trimester of 2023 (Fig. 2B). Additionally, GII.4 San Francisco (Fig. 2B) accounted for 4% of norovirus sequences and 8% of the GII.4 sequences during the 2023–2024 season and increased to 7% of norovirus sequences and 14% of the GII.4 sequences during the 2024–2025 season. Viruses from the GII.4 Allegany cluster were only found in Africa, peaking in late 2021 (Supplemental Figure 6D). Detection of these GII.4 variants, at times, equaled or exceeded GII.4 Sydney, particularly in Central America (GII.4 Wichita and GII.4 San Francisco), South America (GII.4 San Francisco), and Africa (GII.4 Allegany and GII.4 San Francisco) (Supplemental Figures 3D–4D and 6D). However, none of these variants were detected in Southeast Asia, East Asia and the Oceania and West Pacific regions, where only GII.4 Sydney was found (Supplemental Figures 8D–10D). Globally, neither an eastern-western region nor northern-southern hemisphere migration was found for the new GII.4 variants/cluster or for GII.4 Sydney (Supplemental Figures 2C–10C; 2D–10D).

In early 2024, GII.17[P17] strains dramatically increased and by mid-to-late year, its detection was similar to or exceeded that of GII.4 (Fig. 2C). Before the 2023–2024 season, ≤ 5% of sequence were GII.17, rising to 17% in the 2023–2024 season and to 32% in the 2024–2025 season (Fig. 1B). Most regions found sharp increases in GII.17 detection, particularly in the Americas, Europe, and East Asia and to a lesser degree in Southeast Asia (Supplemental Figures 2B–5B, 8B–9B, 2E–5E and 8E–9E). In other regions, GII.17 also appeared to increase in detection frequency (Supplemental Figures 6B–7B, 10B, 6E–7E and 10E), but fewer 2024–2025 season sequences were submitted from Africa (n = 6), South Asia (n = 18) and the Oceania and West Pacific region (n = 14).

As the global distribution of non-GII.4 genotypes fluctuated across seasons (Fig. 1B, Fig. 2A), regional distributions were also seen, particularly for GI.3, GII.1, GII.2, GII.3, GII.6 and GII.17 viruses. Detection of GII.3 increased in early 2021 in Europe and late 2021 in North America (Supplemental Figure 11 A). Subsequently, in 2022, GII.3 detection increased in South Asia, Southeast Asia and the Oceania and West Pacific regions (Supplemental Figure 11 A), and another peak of GII.3 in late 2023 to early 2024 occurred in Europe (Supplemental Figure 11 A). Trends indicative of eastern-western region or northern-southern hemisphere migration of GII.3 was not seen on the global scale, as GII.3 distribution was dispersed across seasons in other regions (Supplemental Figure 11 A). Similarly, peaks of GII.2 were seen in late 2020 in the Oceania and West Pacific region, in early 2021 in East Asia and again in both regions in early 2022, but GII.2 was dispersed across seasons in other regions (Supplemental Figure 11B). Peaks of GII.6 detection occurred in Africa (2021), South America (2022), the Oceania and West Pacific region (2022), East Asia (2022) and Central America (2024) (Supplemental Figure 11C). Detection of GI.3 increased in South Asia in 2021 (Supplemental Figure 7B) and GII.1 peaked in Africa during 2023 (Supplemental Figure 6B).

The distribution of norovirus sequences by child age category was 9% (n = 386) for 0–5 months, 23% (n = 947) for 6–11 months, 40% (n = 1639) for 12–23 months, and 28% (n = 1141) for 24–60 months of age. This pattern was similar for GII.4 (Fig. 3A), with 7% (n = 156) of sequences in the 0–5 month, 25% (n = 530) in the 6–11 month, 44% (n = 948) in the 12–23 month and 25% (n = 533) in the 24–60 month categories. GII.4 distribution remained consistent despite variation in sequence counts by norovirus season (Fig. 3B). Uniquely, proportions of GII.3 sequences were similar across age categories (21% (n = 102), 24% (n = 116), 30% (n = 145) and 25% (n = 123) for the 0–5 m, 6–11 m, 12–23 m and 24–60 m categories, respectively) (Fig. 3A) and despite differences in sequence counts per norovirus season, the pattern was consistent in all seasons except 2022–2023 (Fig. 3B). Distributions of GII.17 and GII.6 sequences across age categories increased from the 0–5 month (both 6%, n = 29 and n = 15, respectively) to 12–23 month [34% (n = 105) and 38% (n = 102)] categories and leveling thereafter, with 38% n = 173 and 35% (n = 96) of sequences in the 24–60 month category, respectively (Fig. 3A). The age distribution pattern for GII.2 showed 10% (n = 22) in the 0–5 month, 15% (n = 32) in the 6–11 month, 43% (n = 91) in the 12–23 month and 31% (n = 66) in the 24–60 month categories. All other genotypes (collectively) showed a similar age distribution to GII.4 viruses (Fig. 3A).

4. Discussion

Children under 5 experience the highest burden of medically attended and severe norovirus AGE [12–16], making them an important group for vaccine interventions. Our analysis of 4113 sequences across nine global regions showed significant diversity, identifying 26 genotypes and 53 strains, underscoring the challenge of ensuring broad immune protection in this age group [8]. Consistent with our previous report [9], GII.4, GII.3, GII.17, GII.6 and GII.2 were the top 5 genotypes detected, together accounting for 87% of norovirus sequences from 2020 to 2025, with GII.4 comprising > 50%.

Variants within the GII.4 genotype frequently circulate at low levels before emerging globally [17,18]. GII.4 Sydney has been the predominant variant globally since 2012 [7], which was reflected in our data. We also observed three new GII.4 variants/cluster (GII.4 San Francisco, GII.4 Wichita, and GII.4 Allegany), reported recently as having antigenic distinction in the immunologically important P2 (protruding) domain of the major viral capsid protein (VP1) [7,19]. As the primary site for neutralizing antibody recognition and binding to genetic susceptibility factors (histo-blood group antigens), variation in this region is believed to be a key driver of immune evasion and expanding susceptibility [20]. In our data, these variants replaced GII.4 Sydney as the predominant variant at times in Central and South America and Africa. However, as of August 2025, none of these variants/clusters have yet become the predominant GII.4 strain globally.

Over the last two norovirus seasons (2023–2024 and 2024–2025), we saw a shift in the predominance of GII.4 as the frequency of GII.17 [P17] detection increased. Prior to the 2023–2024 season, GII.17 viruses were detected in ≤ 5% of sequences but increased to 32% during the 2024–2025 season. In some regions, GII.17 detection exceeded that of GII.4, as was reported in several European countries and the United States in 2023–2024 [21–23]. A similar pattern occurred a decade ago, when a GII.17[P17] strain (Kawasaki 308) emerged during the 2014–2015 season, increased in frequency of detection globally, and became the predominant norovirus genotype in China and Japan [24, 25]. However, the current GII.17[P17] strain is genetically similar to a strain first detected in a large outbreak in Romania in 2021 [26]. Viruses in this cluster (cluster C) are genetically more similar to GII.17[P17] viruses that primarily circulated prior to emergence of the GII.17[P17] (Kawasaki 308) strain (cluster D), including amino acid substitutions in the antigenic region of VP1 [21,22,27]. Furthermore, the GII.P17 polymerase of the current GII.17 cluster is genetically distinct from cluster C and D GII.17 viruses [21,22], with the potential to enhance replication rate and fidelity. Increased detection frequency of this new GII.17 cluster has also been reported in Argentina [27].

Beyond GII.4, GI.3, GII.1, GII.2, GII.3 and GII.6 circulated among the top 10 global strains, with regional peaks exceeding 20% of seasonal sequences. Notably, GII.3 activity has surged across all NoroSurv regions, driven by intergenic recombination and new polymerase types [28]. A recent example includes the 2021–2023 GII3[P12] outbreaks among Chinese children < 5 years old, which featured specific amino acid changes in the polymerase and other non-structural proteins [29]. While no global genotype shift was observed, NoroSurv reported GII.3 detections across South and Southeast Asia, Oceania and West Pacific in 2022. Conversely, GII.2 prevalence remained stable, contrasting with the 2016–2017 GII.P16 polymerase emergence that drove a sharp spike in Europe and Asia [30,31]. High genetic diversity with GII.4 predominance and periodic increases in other norovirus genotypes has been reported elsewhere in NoroSurv countries [27,31–45] and is supported by NoroSurv data. Generally, fewer norovirus infections occur during the first 6 months of life or are asymptomatic [46] due to protective factors associated with maternal antibody transfer and breastfeeding. Unlike GII.4, GII.17, GII.6 and other norovirus genotypes, medically attended infections by GII.3 and GII.2 may occur at earlier ages than other norovirus genotypes with similar distributions across age categories of 0–5 months, 6–11 months during the first year of life. There are several study limitations.

Participation in NoroSurv is voluntary, without centralized funding across sites. Stool specimen collection and testing is by convenience, leading to an uneven distribution in the number of sequences submitted each year and by each country. Sites join NoroSurv on a rolling basis and as such, country-specific data are not available for all study years. As sites continue submitting sequences from previous seasons, reported genotype distributions may change. When sample sizes are small, proportional data can be heavily influenced by fluctuating sample sizes. As such, regional and temporal data should be interpreted with caution when sample sizes are small, particularly for underrepresented regions such as Africa, Central America, East Asia and South Asia. In addition, study data are from children clinically presenting with AGE without distinction of medical setting or severity indicator, and therefore we are unable to monitor the distribution of norovirus genotypes causing mild infections or assess severity of disease.

Children < 5 years bear the highest burden of norovirus AGE morbidity and mortality [12–16] and are an important group to consider for vaccination. We found high genotype diversity among young children, with GII.4, GII.3, GII.17, GII.6 and GII.2 genotypes most common. Regional shifts in GII.4 distribution were observed, with recently emerging GII.4 variants and GII.17 viruses, at times, surpassing GII.4 Sydney in predominance. These findings highlight the need for vaccines that elicit cross-protective immunity against both emerging strains and evolving GII.4 variants. Continued monitoring among cases in young children allows early detection of changes in genotype distribution and emergence of new strains. This information can be used to inform efforts to develop and adapt future pediatric norovirus vaccines, and to document baseline genotype diversity, which can aid in the evaluation of vaccine efficacy in children.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Appendix A.: Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jcv.2026.105949.

Abbreviations:

AGE	acute gastroenteritis
RT-PCR	reverse transcription polymerase chain reaction
DNA	Deoxyribonucleic acid
IQR	Interquartile range

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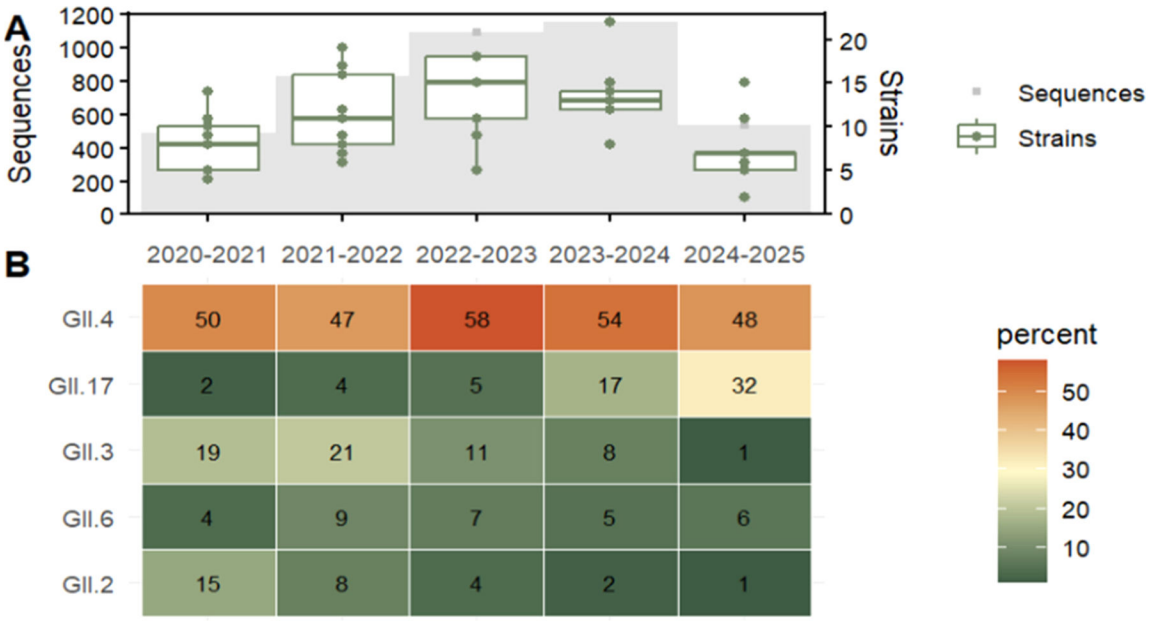

Fig. 1.

Diversity of norovirus genotypes by norovirus season*. A) Total number of norovirus sequences and strains detected**; B) Heatmap of the frequency of detection for the top 5 norovirus genotypes (GII.4, GII.17, GII.3, GII.2, and GII.6) circulating globally. *A norovirus season spans September 1 to August 31 each year **Bar plot indicates total number of sequences from each season, green points indicate the number of strains detected in each region during each season, with the median and interquartile range shown on the boxplots.

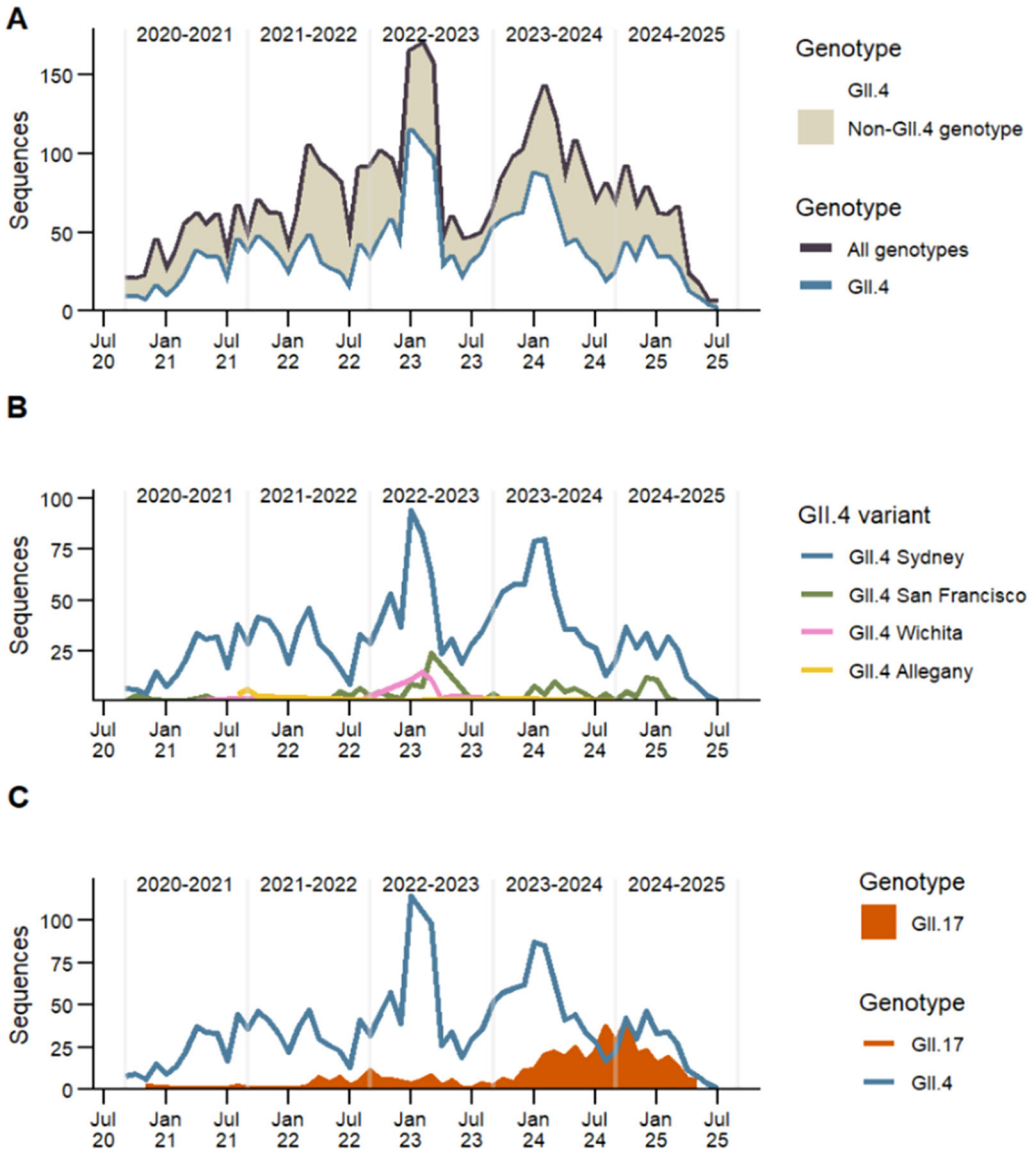

Fig. 2.

Distribution of norovirus sequences detected from September 1, 2020 to August 31, 2025: A) Comparison of GII.4 and non-GII.4 genotypes detected by month; B) Comparison of the four GII.4 variants detected by month; C) Comparison of GII.4 and GII17 genotype detection over time.

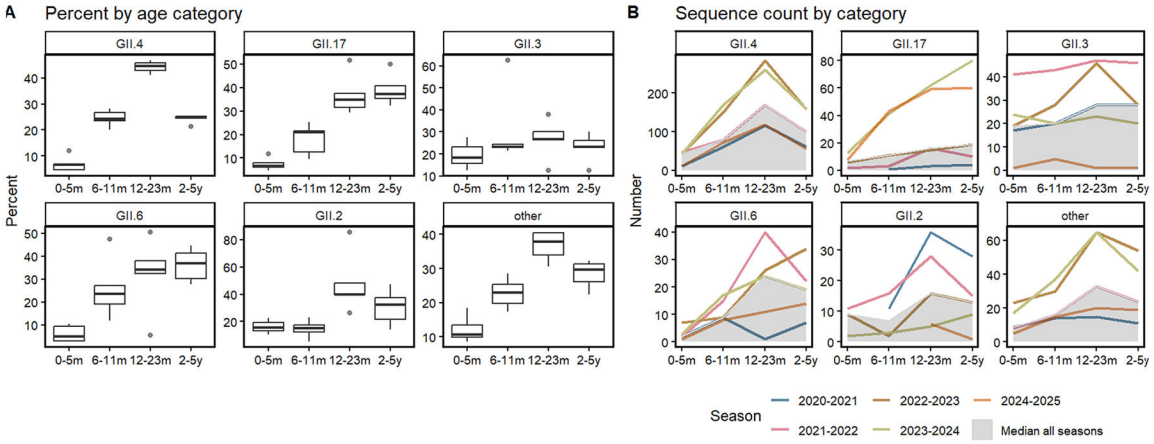

Fig. 3.

Distribution for norovirus sequences by child age category and genotype. A) Percent of sequences (boxplot shows median and IQR of the percent values across norovirus seasons); B) Sequence counts with values for each season shown with colored lines and the median sequence counts across all norovirus seasons shaded in grey.

Table 1

Number of sequences uploaded to NoroSurv by region and country, 2020–2025.

Region (sequence counts)	Country	Sequences (n)
North America (n = 945)	United States	643
	Canada	302
South America (n = 779)	Brazil	415
	Peru	308
	Argentina	53
	Chile	3
Southeast Asia (n = 545)	Philippines	328
	Vietnam	121
	Thailand	96
Europe (n = 507)	Germany	327
	Spain	180
Oceania and West Pacific (n = 506)	Australia	383
	New Zealand	123
Central America (n = 254)	Costa Rica	152
	Guatemala	85
	Mexico	17
East Asia (n = 251)	Taiwan	161
	Japan	90
South Asia (n = 173)	Bangladesh	162
	India	11
Africa (n = 153)	South Africa	112
	Zambia	41

Table 2

Genotype diversity of noroviruses as percentage of the total sequences (n = 4113) in NoroSurv, 2020–2025.

Genotype	Sequences (n)	Percent*
GII.4 Sydney	1912	46.5
GII.3	486	11.8
GII.17	456	11.1
GII.6	271	6.6
GII.2	211	5.1
GII.4 San Francisco	178	4.3
GII.7	114	2.8
GI.3	102	2.5
GII.4 Wichita	60	1.5
GI.5	42	1.0
GII.27	37	0.9
GII.12	28	0.7
GII.13	27	0.7
GI.7	23	0.6
GII.10	20	0.5
GI.2	18	0.4
GI.6	18	0.4
GII.14	17	0.4
GII.4 Allegany	17	0.4
GII.1	15	0.4
GI.1	12	0.3
GI.4	8	0.2
GII.21	8	0.2
GII.8	8	0.2
GII.9	8	0.2
GII.20	5	0.1
GIX.1	5	0.1
GII.5	4	0.1
GI.8	3	0.1

* Combined percentage for 4 GII.4 variants is 52.7%.