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Epidemiological investigation of an acute gastroenteritis outbreak associated with norovirus GII.17[P17] in a cross-border travel group - Shanghai Port, China, 2024

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Abstract

Background Norovirus is a leading cause of acute gastroenteritis and spreads efficiently in closed, mobile cohorts such as organized travel groups. This case is notable for the real-time detection and genomic confirmation of a cross-border outbreak at a port of entry, including near-identical Norovirus GII.17[P17] genomes and documented asymptomatic carriage, illustrating the practical value of integrated metagenomic surveillance in border health operations.

Case presentation On July 21, 2024, 26 travelers arrived at Shanghai Port after a 12-day group tour in Europe. Clinical interviews identified 15 individuals (57.7%) with diarrhea, nausea, dizziness, and abdominal pain; no hospitalizations occurred. On-site anal swab testing was negative for SARS-CoV-2, influenza A and B, Vibrio cholerae, and Escherichia coli. RT-qPCR detected Norovirus GII in 10 samples (38.5%), including two asymptomatic individuals. Metagenomic sequencing generated near-complete genomes for all RT-qPCR–positive samples, which were 99.9–100% identical and classified as Norovirus GII.17[P17], confirming a cross-border outbreak within the travel cohort. Prompt public health response measures were initiated by Shanghai Customs and CDC authorities.

Conclusions This case demonstrates the feasibility and impact of rapid, genomically informed surveillance at the border for detecting and characterizing travel-associated enteric virus outbreaks. The findings underscore the need for robust port-of-entry monitoring, rapid diagnostics, and integrated genomic analysis to mitigate transmission in group travel settings.

Keywords Norovirus, Cross-border outbreak, Acute gastroenteritis, Metagenomic sequencing, Border surveillance

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Background

Norovirus (NoV) stands as a preeminent etiological agent of acute gastroenteritis (AGE) on a global scale, imposing substantial burdens on public health systems and incurring considerable socioeconomic costs across diverse populations [1, 2]. Characterized by its high infectivity, with as few as 10 viral particles sufficient to initiate infection, and its environmental persistence, NoV exhibits a remarkable capacity for rapid transmission through multiple routes, including person-to-person contact, consumption of contaminated food or water, and exposure to aerosolized viral particles generated during vomiting or diarrhea episodes [3].

In an era marked by unprecedented globalization, the cross-border transmission of NoV has emerged as an escalating public health concern, exacerbating the challenges of outbreak control and mitigation [4]. The increasing frequency of international travel has created intricate pathways for viral dissemination across geographical boundaries [5]. Notable outbreaks linked to travel-related clusters aboard international flights or cruise liners, underscore the transboundary nature of NoV threats [6]. These cross-border transmission events not only strain the capacity of individual nations' healthcare infrastructures but also necessitate coordinated international responses, which are often hindered by disparities in surveillance systems, diagnostic capabilities, and public health policies among countries.

Norovirus genotype dynamics further complicate outbreak prevention and control. While genotype GII.4 has dominated global norovirus epidemiology for decades, other genotypes have periodically emerged and caused large-scale outbreaks [7]. Notably, norovirus GII.17 caused major epidemics in parts of Asia during 2014–2016 but subsequently declined in prevalence. Recent genomic surveillance has revealed a renewed global expansion of GII.17[P17] since the early 2020s, with increasing detection across multiple regions [8]. The re-emergence of GII.17 underscores the dynamic nature of norovirus evolution and highlights the need for continuous genomic monitoring, particularly in settings that facilitate international spread [8, 9].

This report documents an AGE outbreak caused by Norovirus GII.17[P17] among a cross-border travel group arriving at Shanghai Port on July 21, 2024. The investigation aimed to address two key questions: (i) whether integrated RT-qPCR screening and metagenomic sequencing at a port of entry can enable real-time detection and confirmation of a cross-border norovirus outbreak, and (ii) whether surveillance of cross-border transmission events can effectively monitor circulating norovirus genotypes and track the global spread of emerging variants. By answering these questions, we sought to evaluate the operational feasibility and public health value of genomics-integrated border surveillance for infectious disease control and genomic epidemiology.

Case presentation

Demographic details and travel history

On July 21, 2024, public health authorities were alerted to a cluster of acute gastroenteritis (AGE) among travelers arriving at Shanghai Pudong Airport. The cohort consisted of 26 individuals who had recently completed a 12-day tour through Turkey, Serbia, Montenegro, Bosnia and Herzegovina, and Albania. The group had a median age of 44 years (range: 9–74 years) and comprised 19 females (73.1%) and 7 males (26.9%). Epidemiological data were collected via structured in accordance with the Epidemiological Investigation Form for Port-Related Infectious Diseases, which has been provided as Supplementary Material.

Symptoms and signs

Based on the presence of symptoms consistent with AGE - including diarrhea, nausea, vomiting, and abdominal pain – 15 travelers (57.7%) were classified as suspected cases, while the remaining 11 (42.3%) were identified as close contacts (Table 1). The clinical presentation among symptomatic individuals included diarrhea, nausea, dizziness, abdominal pain, and vomiting. The illness duration was short, ranging from 1 to 2 days (median: 2 days). One individual presented with an elevated body temperature (> 37.3 °C). No cases required hospitalization, and no fatalities were reported.

Intervention, diagnostic findings, and outcomes

Following the alert, a public health investigation was initiated. Anal swab samples were collected from all 26 travelers after obtaining informed consent. On-site rapid testing was performed, which excluded SARS-CoV-2, Influenza A and B viruses, *Vibrio cholerae*, and pathogenic *Escherichia coli*.

Samples were subsequently transferred under cold chain conditions to the Shanghai International Travel Healthcare Center for comprehensive molecular diagnosis. Nucleic acid extraction and quantitative PCR (qPCR) testing for a panel of gastroenteritis pathogens were conducted according to established border screening protocols [4]. Laboratory analysis confirmed Norovirus GII infection in 10 of the 26 samples (38.5%) by RT-qPCR, with a mean Ct value of 27.0 (range: 19.1 to 34.7). Of these confirmed cases, 20% (2/10) were asymptomatic. All samples tested negative for other common bacterial and viral enteric pathogens, including *Salmonella spp.*, *Shigella spp.*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Escherichia coli* O157:H7, and Rotavirus A.

To genetically characterize the outbreak strain, metagenomic next-generation sequencing (NGS) was performed

Table 1 Detailed summary of the epidemiological characteristics of the norovirus outbreak that occurred among 26 travelers at Shanghai Port on July 21, 2024

Characteristic	Value
Onset of illness	2024/7/21
Total no. travelers	26
Total no. ill	15(57.7%)
Total no. close contacts	11(42.3%)
Hospitalized	0
Died	0
Duration of illness, d	2
Laboratory analysis	26
qPCR confirmed	10(38.5%)
NGS confirmed	10(38.5%)
Sex	
Male	7(26.9%)
Female	19(73.1%)
Unknown	0
Age range, y(median)	9–74(44)
Age group, y	
< 1	0(0)
1–4	0(0)
5–9	1(3.8%)
10–19	3(11.5%)
20–49	11(42.3%)
50–74	9(34.6%)
≥75	0(0)
Unknown	0(0)
Case-patients with known illness duration	14
Duration range, d	1–2
Duration median, d	2
Symptom	
Diarrhea	3(11.5%)
Nausea	8(30.8%)
Dizziness	3(11.5%)
Abdominal pain	2(7.7%)
Vomiting	8(30.8%)
Temperature exceeding 37.3 °C	1(3.8%)

on all RT-qPCR-positive samples [10, 11]. This analysis yielded near-complete Norovirus genomes (7,329-7,575 nucleotides) from all 10 samples. The sequences were highly conserved, showing 99.9–100% identity to each other, and were genotyped as Norovirus GII.17[P17] using the CaliciNet typing tool [12]. Phylogenetic analysis of the whole genome sequences placed the outbreak strain in a tight cluster with a recent GII.17[P17] strain from the USA, sharing 99.51% nucleotide identity (Fig. 1) [13, 14].

To further contextualize the outbreak strain within the re-emerging GII.17 lineage, amino acid alignments were performed focusing on insertions and deletions within the VP1 P domain, using the strain AB983218 (Japan, 2014) as reference [8]. Comparative analysis included representative strains from cluster A-D, and cluster New (subcluster 2014–2016, 2021–2024, 2023–2024). The new GII.17 noroviruses showed the same indel patterns exhibited by cluster C (compared to A and B). Notably, the 396Q substitution within motif D was exclusively found in sequences from subcluster New 2023–2024 subcluster, distinguishing recent strains from earlier variants. The outbreak strain (SHHG2407215037/China/2024) exhibited an amino acid deletion pattern and residue composition consistent with the recently re-emerged GII.17 sub-cluster circulating during 2023–2024 (Fig. 2).

Public health response and outcome

Shanghai Customs promptly notified the Shanghai Municipal Health Commission and the Shanghai Municipal Center for Disease Control and Prevention (CDC). A joint risk assessment was conducted, and the event was officially determined to be a cross-border Norovirus outbreak. The CDC implemented subsequent monitoring and control measures. The outbreak was contained with no reported secondary spread beyond the initial travel group.

Discussion and conclusions

The re-emergence of the GII.17 strain, which has overtaken GII.4 as the dominant cause of norovirus outbreaks in 2024, has drawn significant public attention [8]. This study identified Norovirus GII.17[P17] as the causative agent of a cross-border Norovirus outbreak through entry health quarantine surveillance at Shanghai Port. Near-complete genomes obtained from all RT-qPCR–positive samples showed extremely high nucleotide identity (99.9–100%), indicating a single-source exposure within the travel cohort. Although environmental or food samples could not be collected, the convergence of timing, genomic homogeneity, and absence of onward transmission supports infection occurring during travel.

The outbreak strain displayed a deletion pattern and residue composition characteristic of the recently re-emerged GII.17 sub-cluster rather than earlier epidemic variants. In particular, conserved deletions and substitutions, previously implicated in antigenicity and host interaction, were shared with GII.17 strains reported in Europe during 2021–2024. The use of NGS enabled comprehensive genomic surveillance, providing critical insights into transmission dynamics and viral evolution. Such advanced diagnostic capabilities are vital for effective outbreak management and prevention.

This study has several limitations. The investigation involved a small, single travel cohort ($n = 26$), limiting statistical power and generalizability. Environmental or food sampling during the international tour was not feasible due to jurisdictional constraints, preventing identification of the exact transmission vehicle. In addition, metagenomic sequencing was performed only on

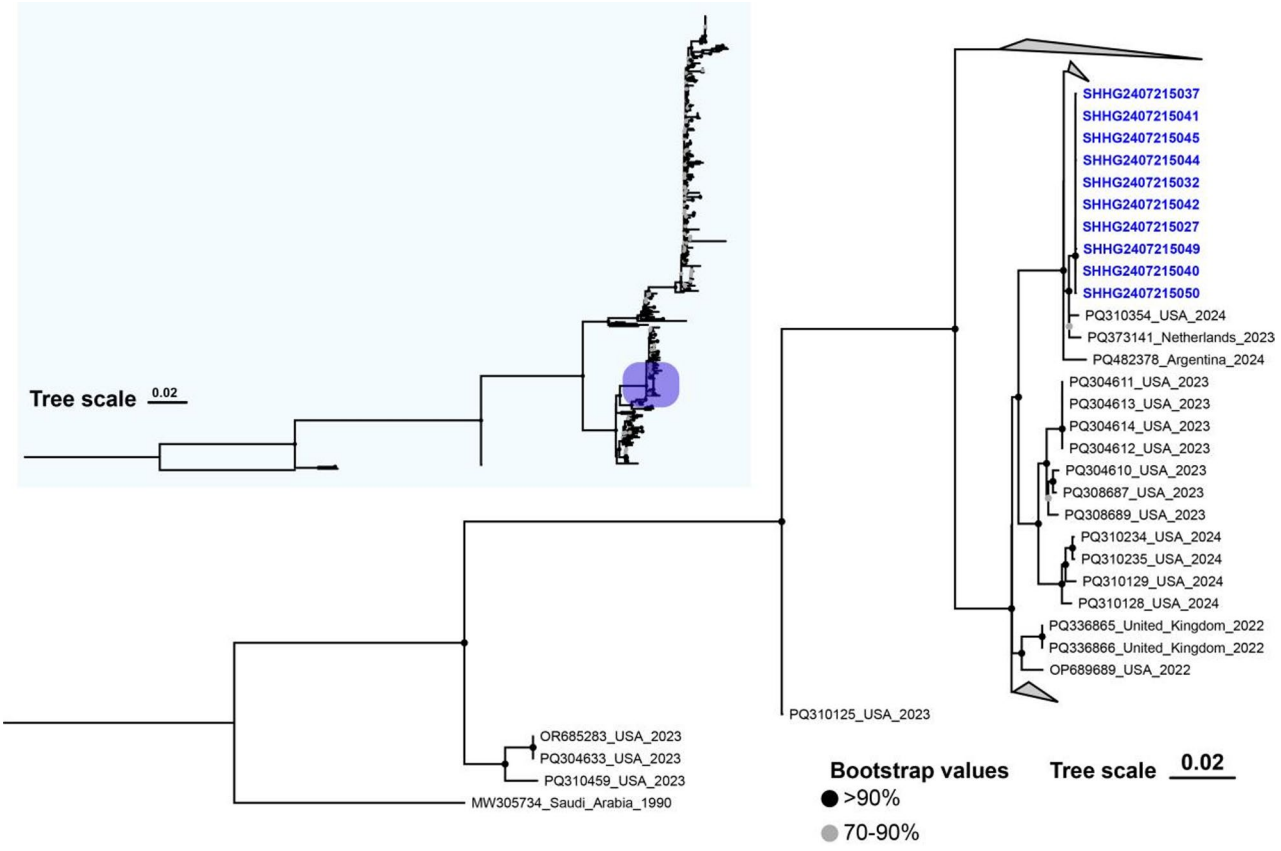

Fig. 1 Maximum-likelihood phylogenetic analysis of whole genome sequences of Norovirus GII.17[P17]. Reference strains are denoted by GenBank accession number and metadata collected by Norovirus Classification Working Group. Bootstrap support for 10,000 replicates is indicated on branches

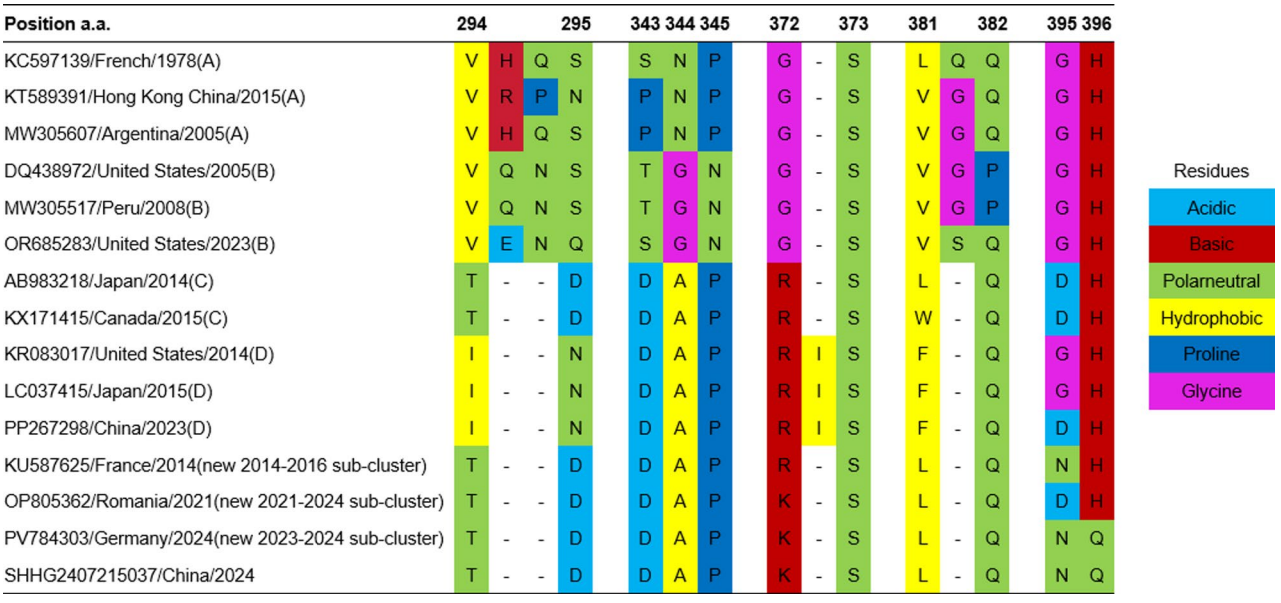

Fig. 2 Alignments of insertions and deletions of GII.17 noroviruses are rendered of the P domain (AB983218/Japan/2014). The alignments were colored by chemical properties of the amino acids

RT-qPCR-positive samples, and infections with very low viral loads may have been missed. Despite these limitations, the high genomic concordance across cases provides robust evidence supporting a cross-border outbreak and demonstrates the feasibility of real-time genomic surveillance at points of entry.

In conclusion, this investigation illustrates how entry health quarantine surveillance integrated with genomic sequencing can enable timely detection and confirmation of cross-border norovirus outbreaks. Such approaches strengthen the capacity of ports of entry to identify circulating variants and support evidence-based public health responses in the context of increasing international travel.

Abbreviations

AGE	Acute Gastroenteritis
CDC	Center for Disease Control and Prevention
Ct	Cycle Threshold
NGS	Next-Generation Sequencing
NoV	Norovirus
qPCR	quantitative Polymerase Chain Reaction
RT-qPCR	Reverse Transcription quantitative Polymerase Chain Reaction

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-026-12978-4.

Supplementary Material 1

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Author contributions

Danlei Liu and Shiwei Yu conceived the study. Xiangting Tian, Zhiyi Wang, Ye Lu and Yue Dai led the epidemiological investigation. Xinyi Ma, Mao Mao, Zaijiong Yi and Guannan Zhang performed the laboratory testing and molecular analysis. Liming Xue, Shenwei Li and Qiang Wang conducted the bioinformatics and phylogenetic analysis. Danlei Liu and Chunli Hu drafted the initial manuscript. Zilong Zhang and Zhengan Tian supervised the overall project and critically revised the manuscript. All authors read and approved the final manuscript.

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Data availability

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2025) in National Genomics Data Center (Nucleic Acids Res 2025), China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA034637) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa [15, 16].

Declarations

Ethics approval and consent to participate

This outbreak investigation was conducted as part of public health surveillance and response activities under the authority of the Shanghai Customs District and the Shanghai Municipal Health Commission. The need for individual ethics approval was waived by the Institutional Review Board of the Shanghai International Travel Healthcare Center. Verbal informed consent was obtained from all adult participants and from parents or legal guardians for minors prior to the collection of anal swab samples and epidemiological data. All procedures were performed in accordance with relevant guidelines and regulations.

Consent for publication

Not applicable. This manuscript does not contain any individual person's data in any form.

Competing interests

The authors declare no competing interests.

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