

Outbreak Reports

Group C Rotavirus Gastroenteritis Outbreak in a Primary School — Luzhou City, Sichuan Province, China, October 2025

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Summary

What is already known about this topic?

Group C rotavirus (RVC) infections occur globally, but are still considered a relatively rare cause of acute gastroenteritis compared to group A rotaviruses. Prior to this outbreak, RVC had not been reported in southwestern China, and routine surveillance predominantly focused on group A rotaviruses. Most characterized Chinese RVC strains belong to the M3 genotype.

What is added by this report?

This investigation documented the first laboratory-confirmed RVC outbreak in southwestern China, which affected 32 students across multiple grades. Spatiotemporal analysis linked the transmission cluster to shared school facilities, specifically classrooms adjacent to male restrooms on floors 2 to 5. Whole-genome sequencing revealed that all five sequenced strains shared an identical genotype (G4-P[2]-I2-R2-C2-M2-A2-N2-T2-E2-H2) with 0–1 single-nucleotide polymorphism differences, confirming a single-source transmission chain. Phylogenetic analysis revealed that the Luzhou strains belonged to the M2 genotype and clustered with recent strains from the Yunnan Province, Russia, and European countries, challenging the previous understanding that Chinese RVC strains predominantly belong to the M3 genotype.

What are the implications for public health practice?

Public health laboratories should enhance surveillance of non-group A rotaviruses in gastroenteritis outbreaks with negative group A results, particularly in school settings. Standardized control measures effective for norovirus outbreaks, including proper vomitus management, dedicated toilet facilities, and strict hand hygiene enforcement, successfully contained this RVC outbreak within one incubation period, and should be adopted for RVC outbreaks despite the absence of pathogen-specific guidelines.

ABSTRACT

Introduction: In October 2025, an acute gastroenteritis outbreak occurred at a primary school in Luzhou City, Sichuan Province, China. An investigation identified the etiological agent and guided control measures.

Methods: Stool specimens were tested using a commercial multiplex gastrointestinal pathogen polymerase chain reaction assay targeting 8 viruses, 17 bacteria, and 3 parasites. Nanopore metagenomic and whole-genome enrichment sequencing generated complete genomes for phylogenetic and recombination analyses.

Results: Thirty-two patients were identified, with an overall attack rate of 1.65% (32/1,943). The outbreak peaked on October 15–16, 2025, with the highest attack rate in class 5.7 (23.08%). Infection control measures contained the outbreak within 15 days. Group C rotavirus (RVC) was identified as the etiological agent. All five sequenced strains shared the genotype G4-P[2]-I2-R2-C2-M2-A2-N2-T2-E2-H2, with differences of 0–1 single-nucleotide polymorphisms. All strains belonged to the M2 genotype and shared a close relationship with the strains from Yunnan Province of China (2025), Russia (2017), and Italy (2012). Also, clustering was observed in classrooms adjacent to shared male restrooms on floors 2–5, suggesting facility-mediated transmission.

Conclusion: This study confirms the first RVC outbreak in southwestern China. The identification of the M2 genotype expands the molecular epidemiology of RVC in China and highlights the need for enhanced surveillance.

Rotaviruses, classified into ten groups (A–J), are important enteric pathogens found in humans and animals (*1*). While group A rotavirus (RVA) accounts for the majority of rotavirus-associated gastroenteritis

cases globally, group C rotavirus (RVC) is a relatively rare but noteworthy cause of acute gastroenteritis outbreaks, particularly in children over five years of age and adults (2). Unlike RVA, for which effective vaccines are available, no licensed vaccines exist for RVC, creating a notable prevention gap. Human RVC strains are highly conserved and predominantly belong to G4-P[2]-I2-R2-C2-Mx-A2-N2-T2-E2-H2, with the VP3 gene exhibiting two major genotypes, M2 (represented by the UK Bristol strain, 1988) and M3 (represented by the Chinese Wu82 strain, 2001)(3–4). Human RVC strains outside East Asia primarily belong to the M2 genotype, whereas East Asian strains predominantly belong to the M3 genotype (5). Although RVC was first detected in China in 1986 (6), surveillance remains limited. Previous studies have detected RVC in several regions, with the most well-characterized strains belonging to the M3 genotype (7–9). No RVC outbreaks have been reported in southwestern China.

INVESTIGATION AND RESULTS

Epidemiological Investigation

On October 15, 2025, the Luzhou CDC was notified of an acute gastroenteritis outbreak that affected students from several classes in a primary school. The school has 1,831 students across 36 classes and 112 staff members, totaling a school-wide population of 1,943 individuals (Supplementary

Table S1, available at <https://weekly.chinacdc.cn/>). A laboratory-confirmed case was defined as an RVC polymerase chain reaction (PCR)-positive result in a student or staff member, and a clinically diagnosed case was defined as acute onset of vomiting and/or diarrhea with epidemiological linkage to a confirmed case.

A total of 32 cases (six laboratory-confirmed and twenty-six clinically diagnosed) were identified between October 13 and 21, 2025, yielding an overall attack rate of 1.65% (32/1,943) across the entire institutional population. The index case was an 11-year-old male student in class 5.7 who developed symptoms on October 13. Notably, his 5-year-old sister experienced abdominal pain and vomiting on October 9, suggesting possible household transmission before the school outbreak. The outbreak showed two distinct peaks on October 15 and 16 (Figure 1). Cases were distributed across 14 classes in 5 grades, with class 5.7 having the highest attack rate (23.08%, 12/52) (Supplementary Table S1). Among the patients, 56.25% were male, with a median age of 10 years. The clinical manifestations included vomiting (65.62%), diarrhea (46.87%), and abdominal pain (37.50%). The symptom duration was 1–3 days, with complete resolution after symptomatic treatment.

Environmental and Laboratory Investigation

The school cafeteria operated under standard food safety protocols, and no common food exposures were

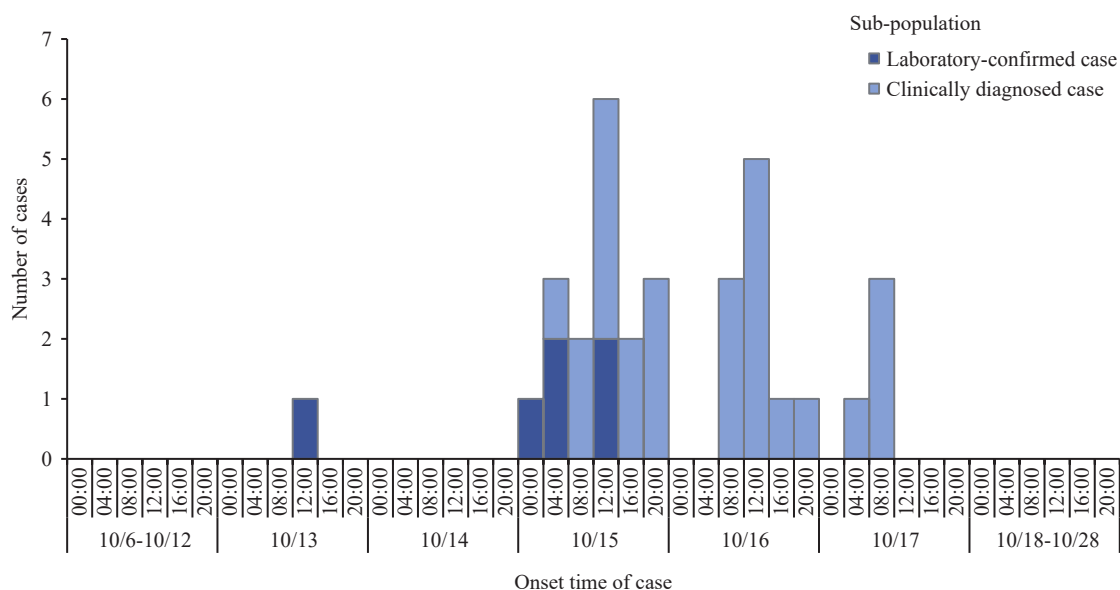


FIGURE 1. Epidemic curve of the group C rotavirus gastroenteritis outbreak, Luzhou City, Sichuan Province, China, October 2025.

identified. However, the investigation revealed that the vomitus from four students in class 5.7 was inadequately managed (swept and bagged directly without immediate crowd evacuation or air disinfection), which likely contributed to secondary transmission. Furthermore, random interviews revealed that some students lacked proper hand-hygiene practices. Mapping of the cases revealed a striking spatial clustering pattern: the affected classrooms were predominantly positioned on floors 2–5 and were physically adjacent to the shared male restrooms, aligning with potential aerosol or contact transmission routes secondary to initial vomitus accidents.

On October 15, initial testing for norovirus in ten anal swabs and four environmental swabs was negative. The following day, a commercial multiplex gastrointestinal pathogen real-time PCR assay (Beijing Zhuo Cheng Hui Sheng Biotechnology Co., Ltd., Beijing, China) was used in accordance with the Technical Scheme for National Sentinel Surveillance of Diarrheal Syndromes to screen for 28 targets: 8 viruses (norovirus GI/GII, rotavirus A/B/C, sapovirus, enteric adenovirus, astrovirus), 17 bacteria, and 3 parasites. The assay was applied to four newly collected typical samples and four previously collected samples, and group C rotavirus (RVC) was detected in six samples on October 17. To further characterize the virus, metagenomic sequencing was performed on a QPursue-6K nanopore platform (QitanTech, Beijing,

China), followed by whole-genome enrichment sequencing using a probe capture-based kit (Macro & Microtest, Jiangsu, China) and sequencing on a KM MiniSeqDx-CN platform (KingCreate, Guangzhou, China). Five complete RVC genomes (SC01–SC05) were assembled.

Genomic Characterization and Phylogenetic Analysis

SC01–SC05 shared the G4-P[2]-I2-R2-C2-M2-A2-N2-T2-E2-H2 genotype (Table 1). Single nucleotide polymorphism (SNP) analysis revealed 0–1 SNP differences among the five isolates, confirming that they originated from a single clonal source. Phylogenetic analysis of all 11 gene segments demonstrated that SC01–SC05 clustered together with high bootstrap support (>80%) (Figure 2). Furthermore, they clustered with strains from the Yunnan Province (2025), Russia (2017), Italy (2012), and Belgium (2025) for each segment. The consistent clustering pattern across all segments, coupled with the absence of recombination events ($P>0.05$), indicated that these viruses shared a common evolutionary origin and had not undergone recent reassortment.

Analysis of the VP3 (M) gene confirmed that the strains belonged to the M2 genotype, in contrast to the M3 genotype, which was predominant among previously characterized Chinese RVC strains. The VP7 and VP4 outer capsid proteins play important

TABLE 1. Nucleotide sequence identity between Luzhou outbreak strain SC01 and close strain(s) in each gene segment.

Gene	Segment	Genotype	Closely related strains	Host	Country	Year	Accession No.	Identity (%)
VP7	1	G4	RVC/Hu-wt/RUS/Novosibirsk/NS17-A1035/2017	Human	Russia: Novosibirsk	2017	MN206053.1	98.78
VP4	2	P[2]	RVC/Human-wt/CHN/YN03/2025/G4P[2]*	Human	China: Yunnan	2025	PX123514.1	99.64
VP6	3	I2	RVC/Hu-wt/RUS/Novosibirsk/NS17-A1035/2017	Human	Russia: Novosibirsk	2017	MN206055.1	99.18
VP1	4	R2	RVC/Human-wt/CHN/YN02/2025/G4P[2]*	Human	China: Yunnan	2025	PX123506.1	99.66
VP2	5	C2	RVC/Human-wt/CHN/YN03/2025/G4P[2]*	Human	China: Yunnan	2025	PX123508.1	99.74
VP3	6	M2	RVC/Human-wt/CHN/YN03/2025/G4P[2]*	Human	China: Yunnan	2025	PX123511.1	99.86
NSP1	7	A2	RVC/Hu-wt/RUS/Novosibirsk/NS17-A1035/2017	Human	Russia: Novosibirsk	2017	MN206059.1	98.58
NSP2	8	N2	RVC/Human-wt/ITA/PR713/2012/G4P[2]	Human	Italy	2012	KT206200.1	99.04
NSP3	9	T2	RVC/Human-wt/ITA/PR713/2012/G4P[2]	Human	Italy	2012	KT206201.1	98.44
NSP4	10	E2	RVC/Hu-wt/RUS/Novosibirsk/NS17-A1035/2017	Human	Russia: Novosibirsk	2017	MN206062.1	98.21
NSP5	11	H2	RVC/Hu-wt/RUS/Novosibirsk/NS17-A1035/2017	Human	Russia: Novosibirsk	2017	MN206063.1	99.16

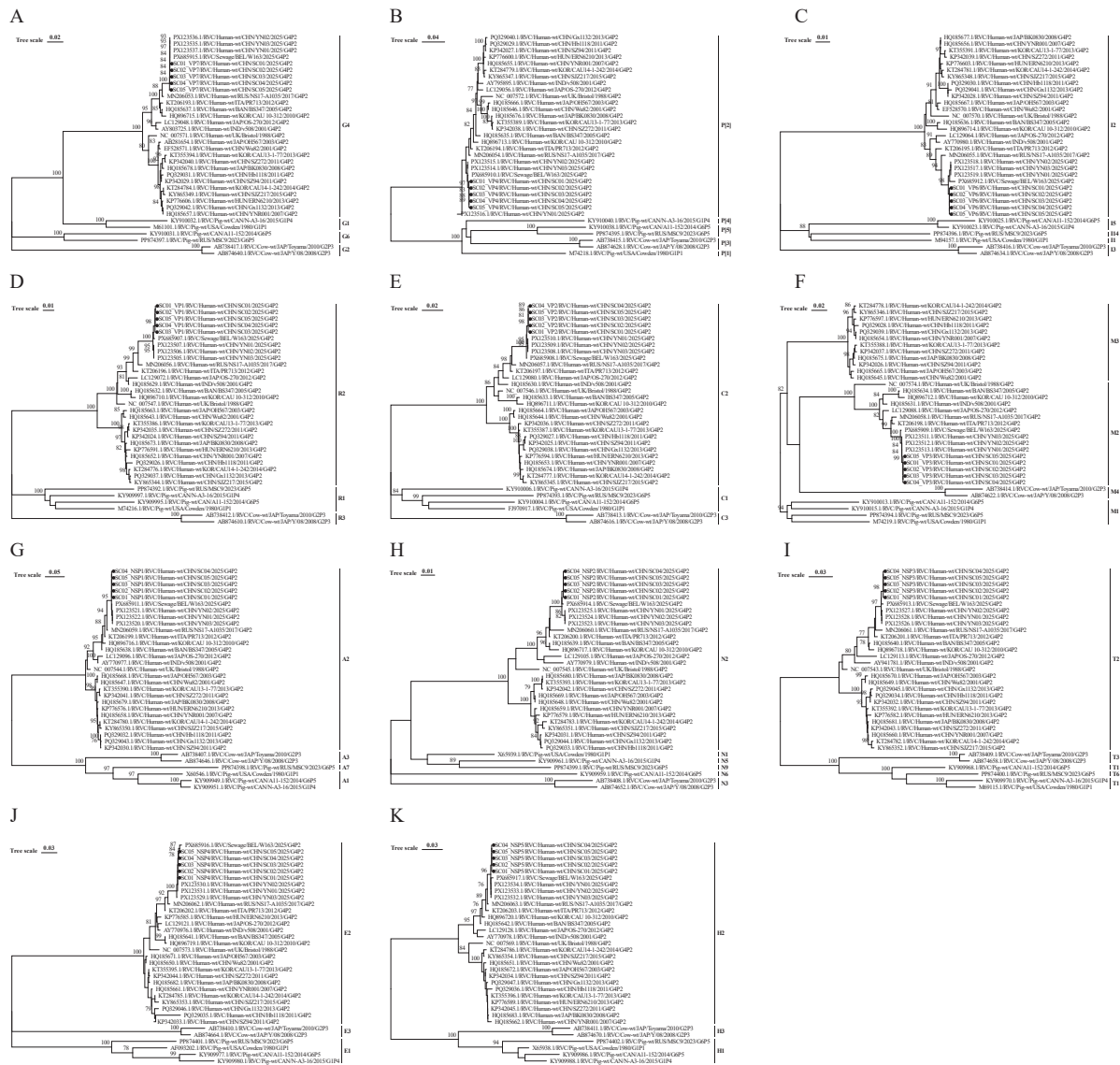


FIGURE 2. Phylogenetic analysis of the 11 gene segments of the Luzhou group C rotavirus strains. (A)The VP7 phylogenetic analysis. (B)The VP4 phylogenetic analysis. (C)The VP6 phylogenetic analysis. (D)The VP1 phylogenetic analysis. (E)The VP2 phylogenetic analysis. (F)The VP3 phylogenetic analysis. (G)The NSP1 phylogenetic analysis. (H)The NSP2 phylogenetic analysis. (I)The NSP3 phylogenetic analysis. (J)The NSP4 phylogenetic analysis. (K)The NSP5 phylogenetic analysis.

Abbreviation: VP=viral protein; NSP=non-structural protein

roles in viral entry and immune evasion. The CHN/SC01/2025 strain shared 100% identity with contemporary 2025 strains from Yunnan and Belgium but showed a distinct evolutionary shift from historical lineages. Key substitutions included A33T and T282N in VP7 and a 33-amino-acid deviation in VP4 (Supplementary Figure S1, available at <https://weekly.chinacdc.cn/>). These variations in the VP8* and VP5* subunits suggest significant antigenic drift, potentially allowing the evasion of pre-existing immunity.

PUBLIC HEALTH RESPONSE

Upon confirming the outbreak, the Luzhou CDC implemented comprehensive control measures. The epidemic curve exhibited a rapid decline. All confirmed and clinically diagnosed cases were placed under home isolation for at least seven days after symptom resolution. Enhanced morning and afternoon health screenings were implemented schoolwide. Environmental disinfection protocols were strengthened by the daily disinfection of classrooms

and restrooms using disinfectants containing 1,000 mg/L chlorine. Vomitus management was reinforced through staff training: upon vomiting occurrence, immediate evacuation of the area and proper disinfection using 10,000 mg/L chlorine-containing absorbent materials, followed by ultra-low-volume aerosol air disinfection. Following joint multi-department evaluations on October 16, class 5.3 and class 5.7 (each exceeding 10 active/suspected cases) were suspended for three days (October 17–19). On their return on October 20, continuous segregation measures (such as dedicated toilet facilities and staggered school schedules) were implemented to prevent cross-contamination. Health education was provided to students, parents, and staff with an emphasis on hand hygiene and early symptom reporting. Following these interventions, no new cases were reported after October 21, and the outbreak was declared closed on October 28, after seven consecutive days without new cases.

To systematically prevent future occurrences, the local CDC prioritizes the building of laboratory capacity. RVC testing has now been officially integrated into the multi-pathogen screening algorithm for all acute gastroenteritis outbreaks that return negative results for group A rotaviruses and noroviruses, ensuring early detection and rapid deployment of high-concentration environmental disinfection protocols.

DISCUSSION

This investigation documents the first laboratory-confirmed RVC outbreak gastroenteritis in southwestern China, and provides critical genomic insights that expand our understanding of the molecular epidemiology of RVC. All sequenced strains shared an identical genotype belonged to the M2 genotype. This finding challenges the previously described geographic paradigm that identified a clear segregation of M2 and M3 genotypes (3). The identification of the M2-genotype of RVC in southwestern China has substantially expanded the known geographic distribution of this genotype within the country and globally.

Phylogenetic analysis revealed that the Luzhou strains formed monophyletic clusters with the strains from Yunnan, Russia, Italy, and Belgium across all 11 gene segments. This consistent clustering pattern, coupled with the absence of recombination events, provides compelling evidence of a shared evolutionary

history. In contrast to previous Chinese RVC genomic studies, which reported M3-genotype strains (7–9), the Luzhou outbreak represents the first detection of M2-genotype RVC in southwestern China, filling a critical gap in the national distribution map of this pathogen.

The outbreak primarily affected school-aged children and demonstrated clustering in school settings, consistent with that of previous RVC outbreaks (7). The 0–1 SNP differences among the five strains support a common-source outbreak with subsequent clonal spread. This study documents the first M2-genotype RVC in southwestern China, demonstrating that both major RVC genotypes circulate throughout the country and necessitate updated molecular surveillance strategies. Furthermore, the close phylogenetic relationships with strains from Yunnan, Russia, and Europe provide molecular evidence to support an active Eurasian transmission network. Finally, despite the absence of RVC-specific guidelines in China, the implementation of standardized enteric infection control protocols effectively contained an outbreak within one incubation period, providing field evidence supporting their effectiveness.

These findings highlight the need to include RVC testing in multi-pathogen panels for gastroenteritis outbreaks with negative RVA results, particularly in school settings; establish national RVC genomic surveillance to monitor genotype distribution; and develop China-specific RVC outbreak response guidelines.

This study has several limitations. First, human RVC infections have historically exhibited a highly sporadic pattern with rarely documented cluster outbreaks, resulting in limited baseline data on their etiological, epidemiological, and clinical characteristics. Consequently, reporting of the outbreak was delayed. Second, comprehensive epidemiological studies have not been conducted; specifically, efforts to trace the definitive source of infection and determine the duration of viral shedding are lacking. Third, the scope of data collection was not expanded, suggesting that the findings may have been constrained by the potential limitations of insufficient surveillance.

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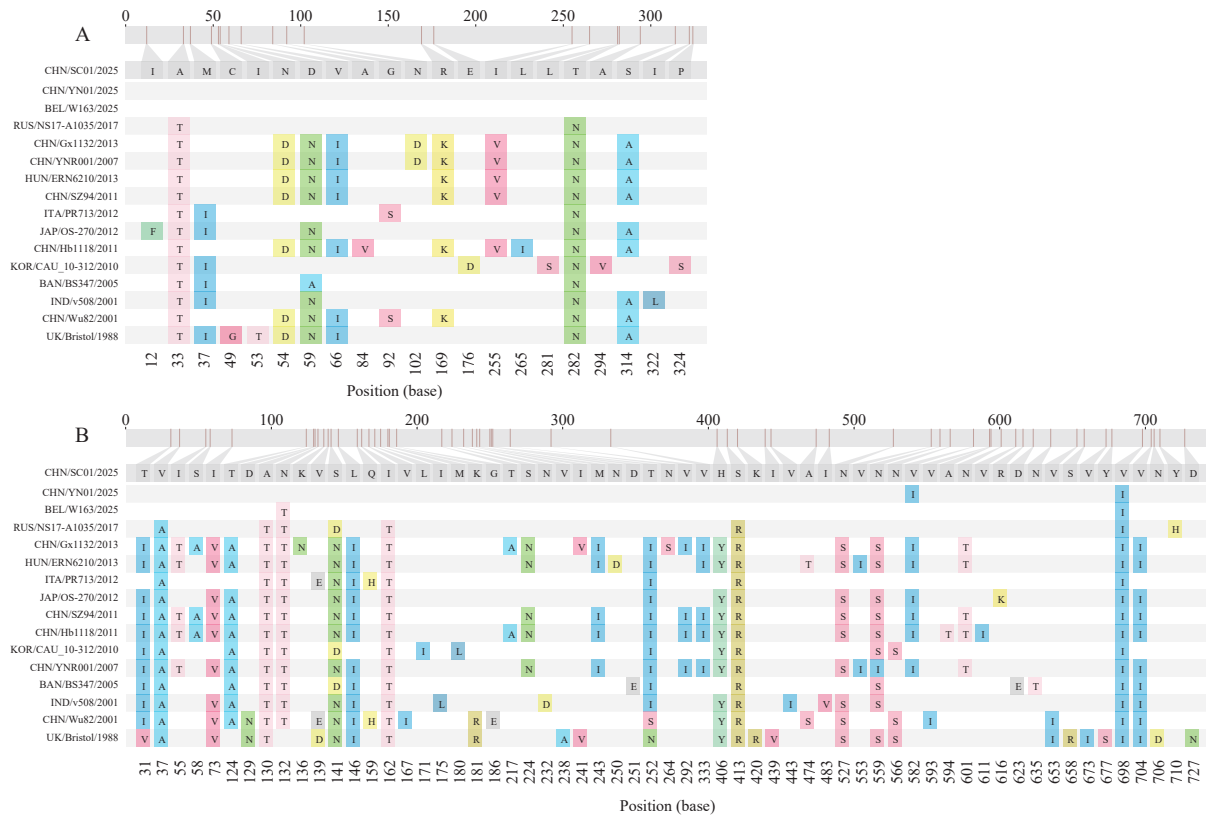
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SUPPLEMENTARY MATERIALS

SUPPLEMENTARY TABLE S1. Distribution of cases and attack rates by class during the group C rotavirus outbreak, Luzhou City, Sichuan Province, China, October 2025.

Population Group / Class	Number of Individuals	Laboratory-Confirmed Cases	Clinically Diagnosed Cases	Attack Rate (%)
Grade 2, Class 5	49	0	1	2.04
Grade 3, Class 1	49	0	2	4.08
Grade 3, Class 2	52	0	1	1.92
Grade 3, Class 4	51	0	2	3.92
Grade 3, Class 5	52	0	1	1.92
Grade 4, Class 5	55	0	1	1.82
Grade 4, Class 6	53	0	1	1.89
Grade 5, Class 2	47	0	2	4.26
Grade 5, Class 3	52	0	1	1.92
Grade 5, Class 5	51	0	3	5.88
Grade 5, Class 7	52	6	6	23.08
Grade 6, Class 2	52	0	2	3.85
Grade 6, Class 3	54	0	1	1.85
Grade 6, Class 5	51	0	2	3.92
Unaffected Classes (<i>n</i> =22)*	1,111	0	0	0
Teachers and staff	94	0	0	0
Cafeteria staff	18	0	0	0
Total (School-wide population)	1,943	6	26	1.65

* Includes 1,111 students from the remaining 22 unaffected classes



SUPPLEMENTARY FIGURE S1. Comparison of amino acid variations in the VP7 and VP4 proteins of the 2025 Luzhou RVC outbreak strain against historical reference strains. (A)The VP7 amino acid variations. (B)The VP4 amino acid variations.

Abbreviation: VP=viral protein.