

Background

Rotavirus group A (RVA) was the most common cause of infectious gastroenteritis among young children before introduction of rotavirus vaccine in the United States in 2006. Following widespread vaccination, U.S. hospital acquired (HA) rotavirus cases are rare. We describe a cluster of rotavirus infections in a pediatric hospital with a genotype uncommon among U.S. children.

Methods

- Patient cases of HA gastrointestinal (GI) illness were detected through hospital-wide microbiology surveillance, performed by Infection Prevention and Control (IPC) practitioners.
- Cluster procedures were implemented on a unit when 3 or more cases were identified by symptoms within 48 hours.
- The hospital established a partnership with Centers for Disease Control and Prevention (CDC) laboratories to obtain sequencing results in addition to instituting local control measures.
- RVA strains were genotyped by using the genotype specific qRT-PCR assays for VP7 and VP4 genes.
- Next Generation Sequencing (NGS) was performed for RVA strain characterization on Illumina MiSeq.
- Genotypes for all 10 RVA were determined using NCBI's BLASTN program.

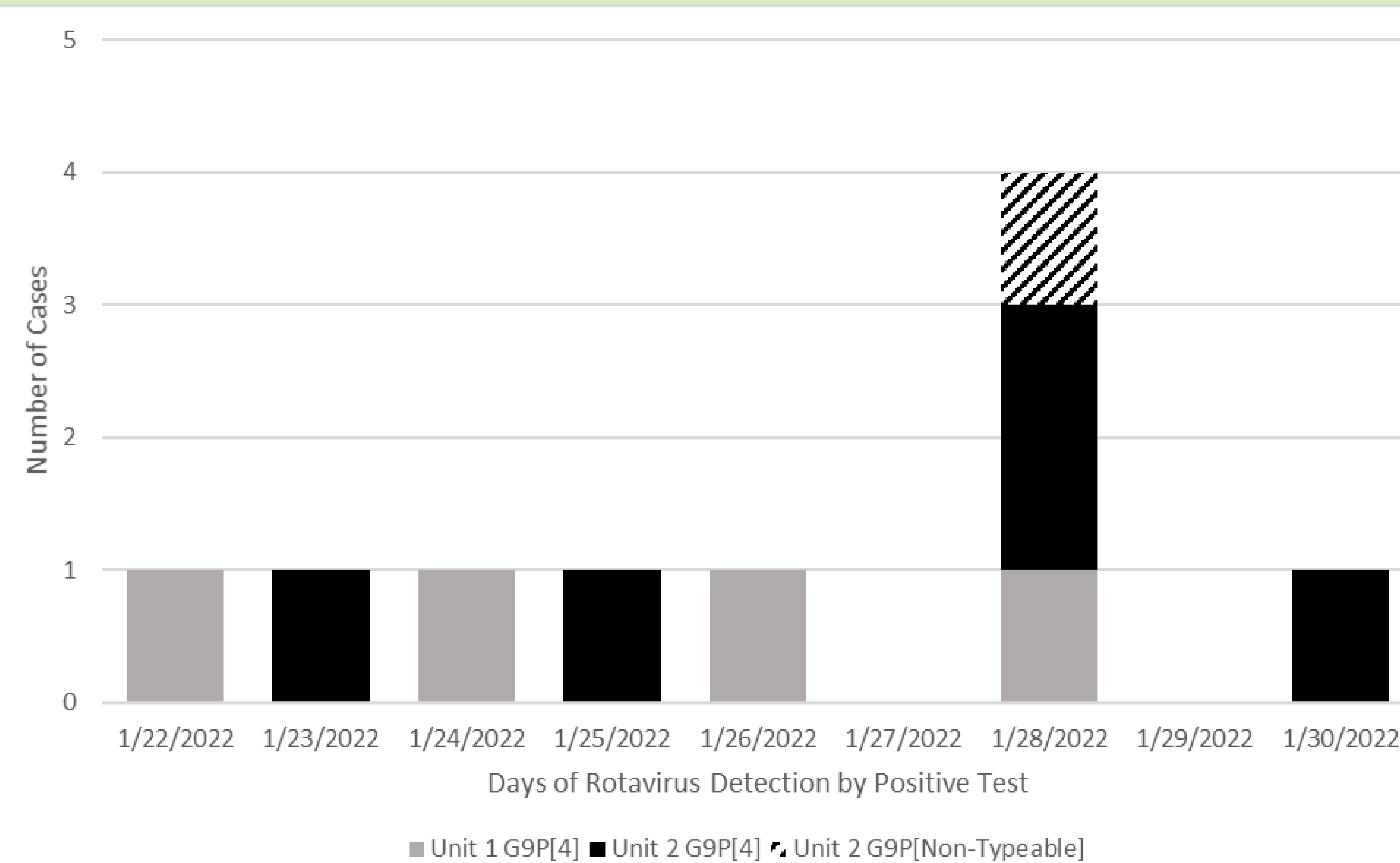


Figure 1. Epicurve of the Rotavirus Cluster. Date of rotavirus detection is shown by date of positive test.

Characteristic	N (%) or Median (Range)
Age (years) at time of positive result	1.8 (0.7 – 10)
Gender	
Male	6 (60%)
Female	4 (40%)
Ventilated	
Yes	8 (80%)
No	2 (20%)
Vaccinated for rotavirus	
Yes	5 (50%)
No	5 (50%)

Table 1. Demographic and Clinical Characteristics of 10 Patients with Rotavirus Infection

Results

Epidemiologic surveillance identified a rotavirus cluster of 10 patients aged 10 months to 10 years old on two adjacent units.

- Symptoms included emesis and diarrhea.
- Among the patients infected, 50% were vaccinated for rotavirus; none of these samples could be attributed to vaccine related shedding. [Table 1.]
- All patients had epidemiologic links by contiguous bed spaces or shared care teams.
- Sequencing was conclusive for 9 of the 10 stool samples to be a G9P[4] genotype, which is rarely detected amongst U.S. children. [Figure 1.]
- Local control measures of increased education and cleaning, isolation of positive patients in single rooms, use of soap and water on room exit, and furlough of symptomatic healthcare worker halted ongoing transmission within the hospital.

Conclusions

- Routine surveillance of HA GI illness led to identification of a cluster of infection.
- RVA strain genotyping and characterization identified unusual rotavirus genotype G9P[4] as the cause.
- Partnership between IPC practitioners and laboratorians with CDC demonstrated the need to enhance existing infection prevention measures to halt ongoing transmission and identified a rare rotavirus strain as the likely cause of the cluster.