UNEXPECTED DIVERSITY OF ROTAVIRUS GENOTYPES IN PEDIATRIC POPULATION

D.M. Koukou[1], P. Chatzichristou[1], E. Tatsi[1], T. Liakopoulou[2], G. Chronopoulou[3], A. Michos[1], V. Syriopoulou[1]

1. First Department of Pediatrics, National and Kapodistrian University of Athens, "Aghia Sophia" Children's Hospital, Division of Pediatric Infectious Diseases;

2. Pediatric Department, Iaso Children's, Athens; 3. Microbiology Department, EuroClinic Children's, Athens

Introduction

- Rotavirus gastroenteritis (RVG) is the leading cause of viral diarrhea in children.
- Although Rotavirus (RV) genotypes differ geographically and temporally, five are the predominant genotypes circulating worldwide.
- Aim of our study was to monitor possible changes in distribution of RV genotypes circulating in Greek pediatric population during the post vaccine era.

Methods

- Demographic data and fecal samples were collected from children ≤15 years old with symptoms of acute gastroenteritis who visited emergency units of 6 Pediatric Hospitals in Greece between 09/2016-08/2019.
- Samples were tested for RV Group A antigen with rapid immunochromatographic assay.
- Positive samples were further G and P typed through RT-PCR, multi-nested PCR and Sanger sequencing of *VP7* and *VP4* genes.

References

1. Hungerford D. et al. Euro Surveill. 2019;24(6)
2. Troeger C. et al. JAMA Pediatr. 2018; 172:958

Results

- **660** children participated in the study.
- **Males** outnumbered females (59%).
- **Mean age** was 31±29 months.
- **Age distribution**: 50,3% of children were ≤2 years old.
- **Geographical distribution**: 84,5% of children lived in urban cities.
- **Monthly distribution:** In periods 2016-2017 and 2017-2018 RVG peak was during winter and spring (December – May). In the last period there was no RVG peak **(Fig1).**

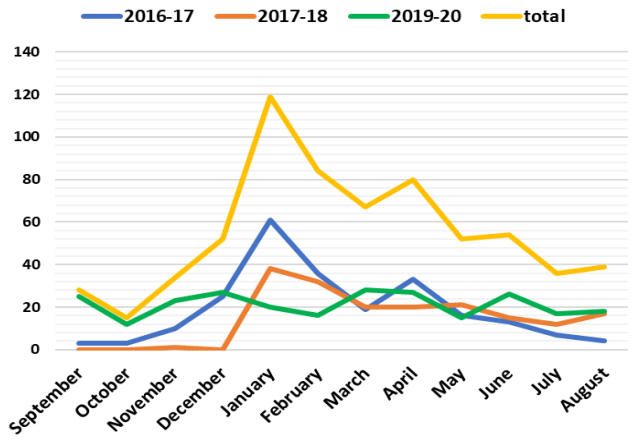

Fig 1. Monthly distribution of RV genotypes in Greek children per year 2016-2019 (N=660).

- **Genotyping distribution**: G4P[8] (41%), G1P[8] (22%), G2P[4] (14%), G9P[8] (8%), G9P[4] (5,5%), G12P[8] (2%) and G3P[8] (1,8%). Unusual and mixed genotypes were identified in 3,2% and 2,5% of the samples respectively **(Fig.2).**
- During seasons 2016-2017 and 2017-2018
  - G4P[8] was the predominant genotype in 67% and 51% of the samples **(Fig.3).**
  - G9P[4] was not detected at all
- In season 2018-2019 the most common genotypes were G9P[8] and G9P[4] (33% in total) followed by G2P[4] (27%). Significant detection of unusual genotypes (8%) was also mentioned **(Fig.3).**

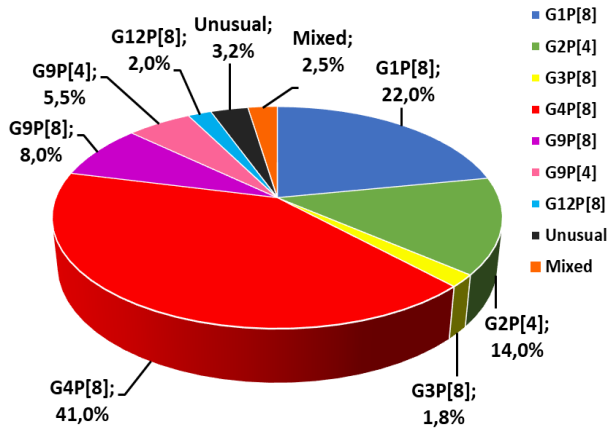

Fig 2. Distribution of RV Genotypes in Greek children during 2016-2019 (N=660).

Conclusions

- This study indicates diversity of the predominant RV genotypes in Greek children during 2016-2019.
- The emergence of G9 and G2 as the most common genotypes as well as the detection of uncommon ones during the last period highlight the importance of continuous surveillance of Rotavirus genotyping during the post vaccination period.

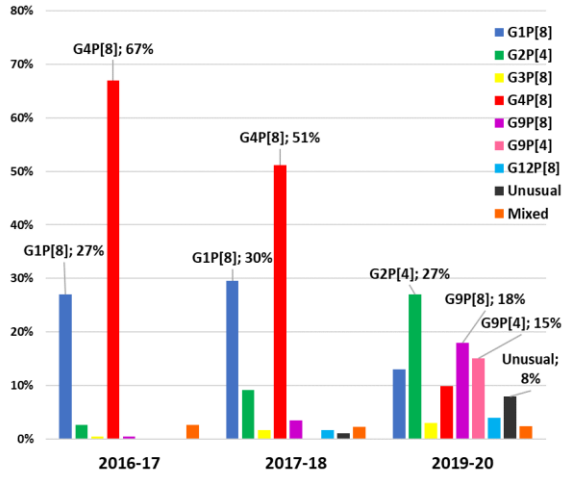

Fig 3. Annual distribution of RV genotypes in Greek children during 2016-2019 (N=660).