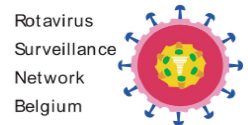


BACKGROUND

- Rotavirus incidence and genotype distribution in Belgium: monitored since the 1999-2000 rotavirus season at UZ Leuven
- Introduction of Rotarix® and RotaTeq® vaccines into the Belgian childhood vaccination program in 2006 and 2007: strong decrease of rotavirus incidence
- Remains key to evaluate the effects of vaccination on the rotavirus population and to monitor possible appearance of animal-like genotypes into the human population

MATERIALS

- Participation of large number of hospitals, private laboratories and paediatricians across Belgium
- Rotavirus genotype determination using RT-PCR (Zeller *et al.* Vaccine 2010): dual classification of G- and P-genotypes based on nucleotide sequence variation in the two outer capsid proteins VP7 and VP4
- Data for seasons 2019-2020 and 2020-2021: substantial lower number of samples received at NRC for Rotaviruses, most likely due to the SARS-CoV-2 pandemic



RESULTS

- Share of rotavirus positive samples that could be genotyped:
 - Season 2019-2020: 82.4% or 94 out of 114 samples received at the NRC
 - Season 2020-2021: 65.5% or 72 out of 110 samples received at the NRC
 - No bi-annual pattern (alternating strong and weak rotavirus seasons) observed as proposed for previous seasons and other countries
- Low positivity rate of rotavirus gastroenteritis at UZ Leuven, respectively 1.1% (2019-2020) and 1.5% (2020-2021) (Figure 1)
- Genotype distribution: in line with the two previous seasons (Figure 2)
 - For 2019-2020: multiple co-circulating strains without clear dominant genotype: G1P[8] (11.7%), G2P[4] (26.6%), G3P[8] (14.9%) and G9P[4] (27.7%)
 - For 2020-2021: circulation of a dominant genotype = G2P[4] (55.6%)
 - Very little evidence of circulation of live attenuated vaccine types in the human population

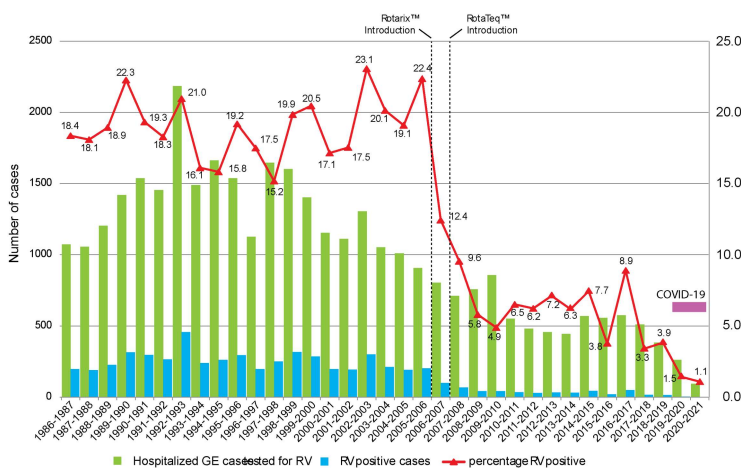


Figure 1: Number of hospitalized gastroenteritis cases (green), of which tested rotavirus positive (blue) per season at UZ Leuven from 1986-1987 until 2020-2021. The red line indicates the percentage of rotavirus positivity in a particular season, while the black dotted lines indicate the vaccine introductions in Belgium.

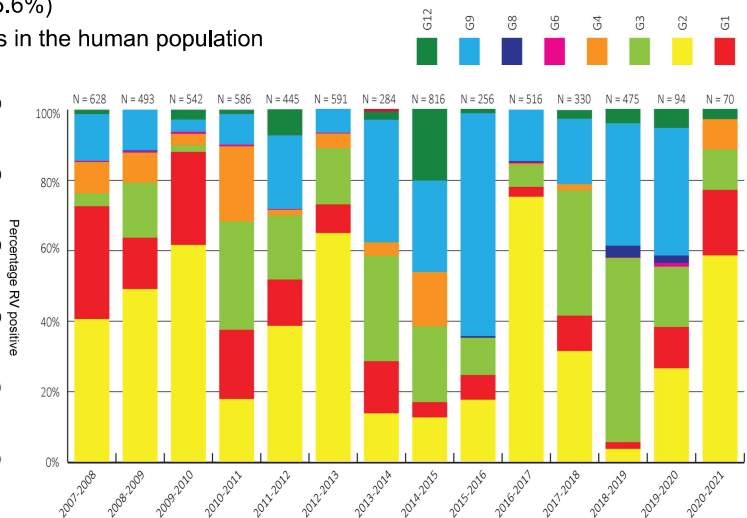


Figure 2: G-genotype distribution from positive rotavirus cases collected by the Rotavirus Surveillance Network Belgium from seasons 2007-2008 until 2020-2021.

CONCLUSION

For the last two years, a very low number of samples has been sent to the NRC. While it will be hard to predict the impact of the SARS-CoV-2 pandemic on future rotavirus seasons, it could be speculated that more severe seasons are to be expected due to a decreased viral circulation and an increasing number of susceptible infants. Following the lowest prevalence of G2 since the start of surveillance in Belgium for 2018-2019, in 2019-2020 this genotype was again detected in a quarter of cases, and this increasing tendency was continued in 2020-2021 with more than half of the cases being caused by G2 rotavirus strains. To retain a strong surveillance in a country with a high rotavirus vaccination coverage, we stress the importance of sending rotavirus positive samples to the national reference centre.