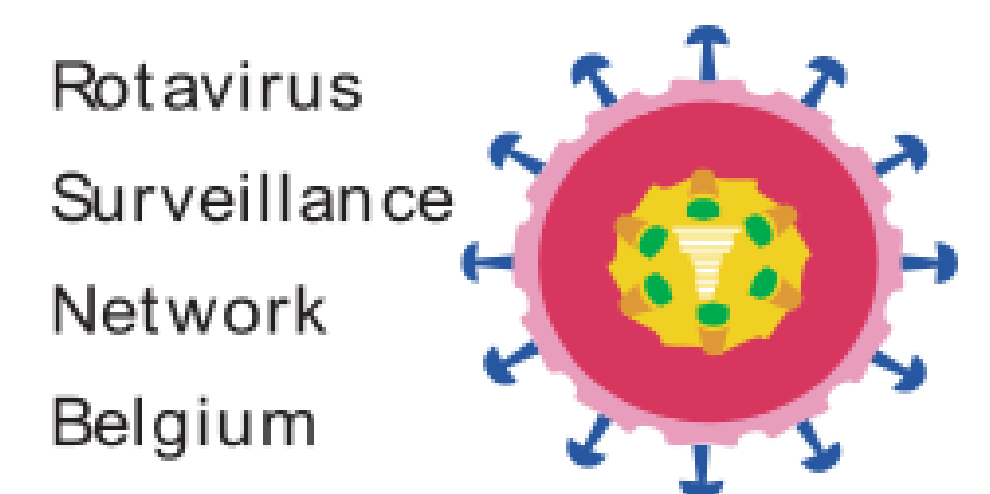


## BACKGROUND

- 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 vaccine escape mutants or animal-like genotypes into the human population

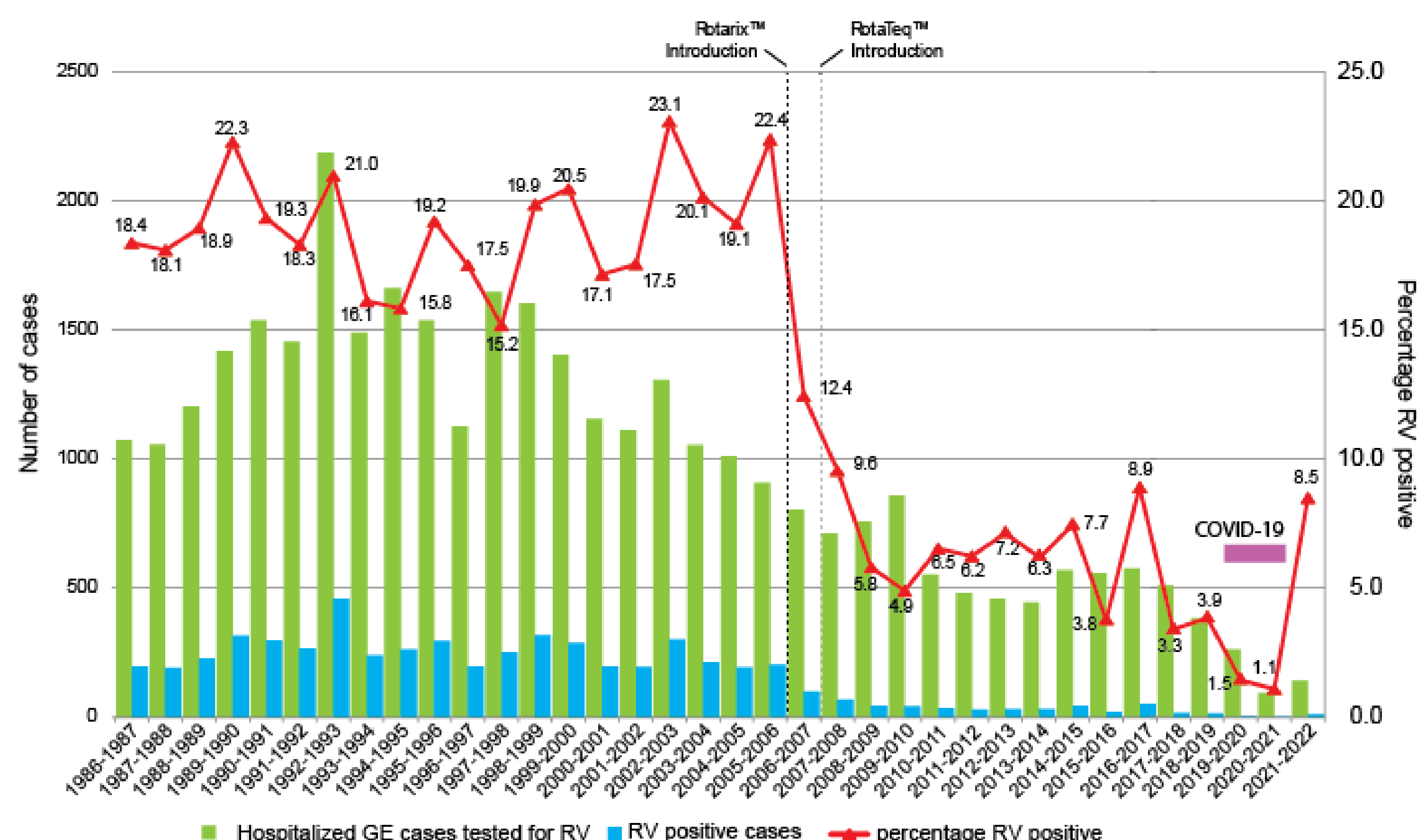
## MATERIALS

- 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 the fifteenth season 2021-2022: highest number of samples ever received at NRC for Rotaviruses, strong contrast compared to the previous two seasons that were impacted by the SARS-CoV-2 pandemic

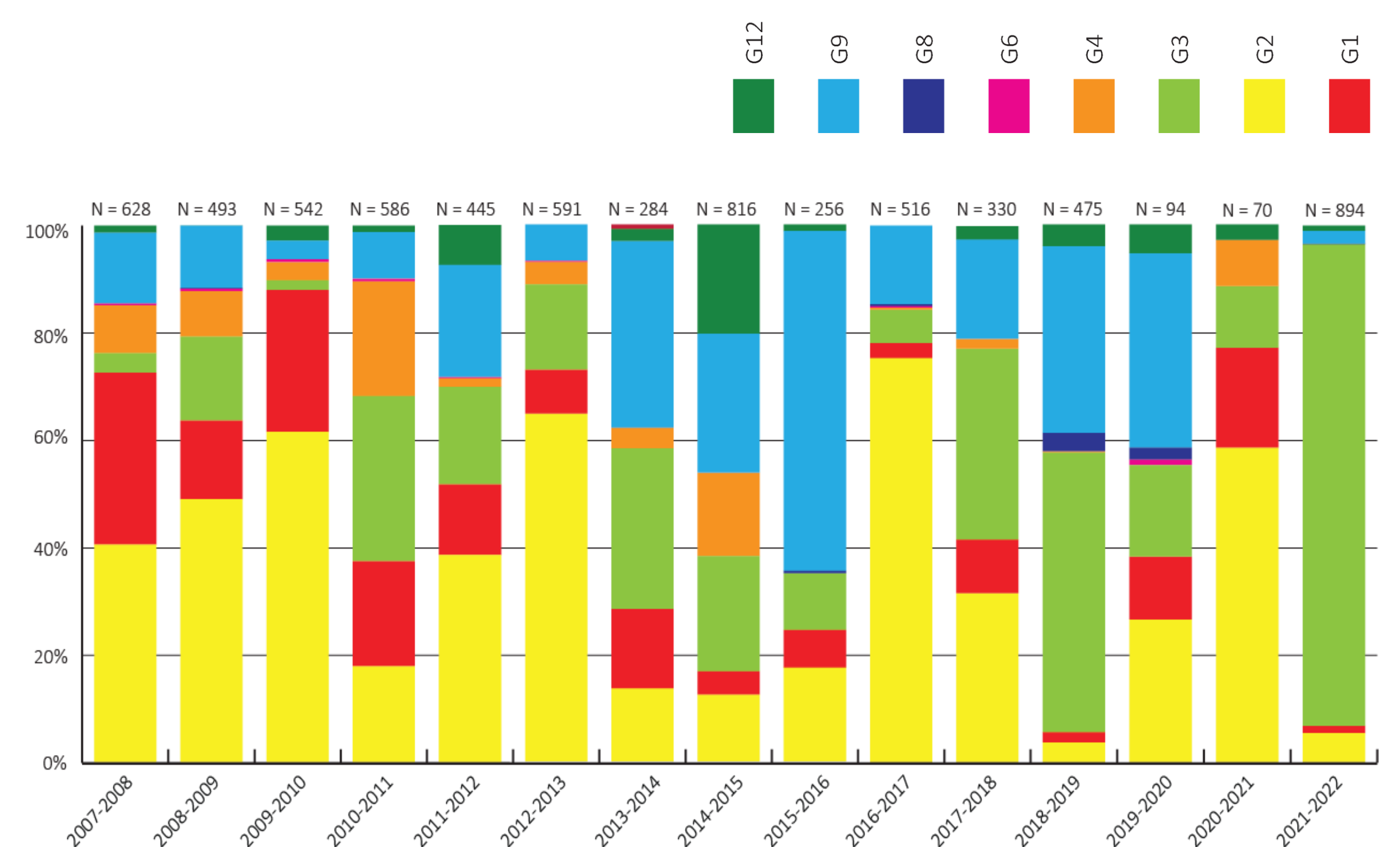


## RESULTS

- Compared to the seasons 2019-2020 and 2020-2021 for which both a low number of samples was received at the NRC (pre-COVID years): a record breaking number of 1045 samples was analysed for the season 2021-2022
  - Share of rotavirus positive samples that could be (partially) genotyped: 85.6% or 894 out of 1045 samples
  - Reflection of high number of cases in a strong rebound in the positivity rate of rotavirus gastroenteritis at UZ Leuven, from 1.1% and 1.5% for seasons 13 and 14, to 8.5% for the season 2021-2022 (Figure 1)
  - Peak of rotavirus cases observed in March 2022
- Genotype distribution (Figure 2)
  - For 2019-2020: no clear dominant genotype – for 2020-2021: circulation of a dominant genotype = G2P[4] (55.6%)
  - For 2021-2022: complete dominance of one genotype
    - G3P[8] (85.9%): genotype present in each of the 15 previous seasons, however this large dominance was never observed before
    - G2P[4] reduced to only 5.3%



**Figure 1:** Number of hospitalized gastroenteritis cases (green), of which tested rotavirus positive (blue) per season at UZ Leuven from 1986-1987 until 2021-2022. 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 2007 to 2022.

## CONCLUSION

For the last two years, a very low number of samples has been sent to the NRC. Our previous speculation that more severe rotavirus seasons are to be expected due to a decreased viral circulation and an increasing number of susceptible infants, as a consequence of the COVID-19 pandemic, has come true. The 2021-2022 rotavirus season represented the season in which the Rotavirus Surveillance Network Belgium received the highest number of samples in its 15 years of existence. Typing of more than 85% of the 1045 samples received, demonstrated the large dominance of one particular genotype, G3P[8]. While this genotype is detected for each of the previous 15 seasons, a dominance of >85% for any genotype has never been observed.