

BACKGROUND

- Enteroviruses (EV) = large genus including fifteen species: Enterovirus species A-L and Rhinovirus A-C
- Human enteroviruses infect millions of people worldwide every year: most often asymptomatic infections
- Also associated with a wide spectrum of both common and uncommon illnesses
- Since 2014, EVD68 is emerging worldwide – high attention of public health authorities because of its magnitude and clinical presentation

MATERIALS

- Epidemiological surveillance of Enteroviruses in Belgium: genotyping of enterovirus positive samples at NRC UZ/KU Leuven
- Respiratory samples: broad respiratory panel including entero/rhinovirus
- Molecular typing by RT-PCR using different primer sets
 - EV species A & B: sequencing part of VP1
 - EV species C & D: sequencing VP4/VP2, VP1 and non-coding region

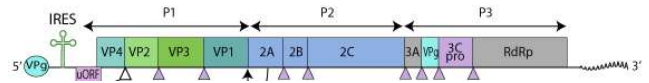


Figure 1: Linear ssRNA(+) genome of enterovirus (source: ViralZone)

RESULTS

- Overall number of samples for detection of Enterovirus:
 - Year **2020**: 4885 samples from 90 Belgian laboratories
 - EV-positive: 577 samples (11.8%) from 393 cases
 - 85.4% are respiratory samples
 - Year **2021**: 4511 samples from 47 Belgian laboratories
 - EV-positive: 560 samples (12.4%) from 413 cases
 - 83.8% are respiratory samples
 - Genotyping EV-positive cases (deduplication multiple samples per case):
 - Year 2020:**
 - Respiratory samples: 95.2% not typed
 - Cerebrospinal fluid (CSF, n=11): Coxsackievirus (CV) A10, EVA71 and Echoviruses (n=9): E3, 2 E6, E7, E9, E11, E13 and 2 E14
 - Faeces (n=5): Rhinovirus (RV) C, CVA4, CVA5, CVB and E3
 - Due to the SARS-CoV-2 pandemic, a lower number of CSF and faecal samples was referred to the NRC enteroviruses for this year
 - Year 2021:**
 - Respiratory samples: 88.7% were typed (n = 322)
 - RV (67.3%), EVB (19.7%), EVA (7.7%) and EVD68 (5.3%)
 - CSF (n=39): RVC, CVA, CVA7, CVA9, CVA10, CVB3, 2 CVB4, 5 CV5B and Echoviruses (n=26): 2 E5, E6, E9, 7 E18, 9 E21 and 6 E25
 - Faeces (n=11): CVA2, CVB4, CVB5, EVD68 and Echoviruses (n=7): E9, 3 E18, 2 E21 and E25

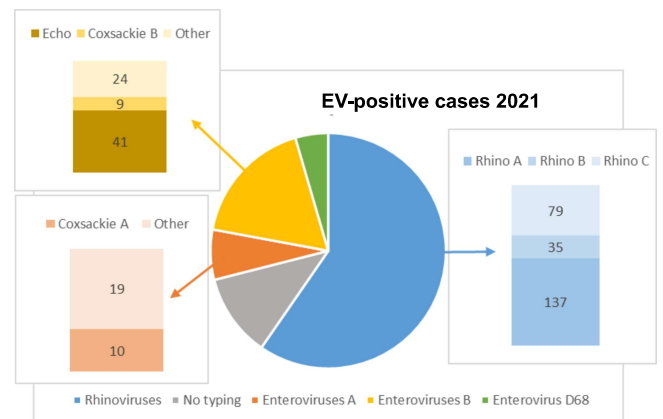


Figure 1: Genotyping of enterovirus-positive samples for the year 2021.

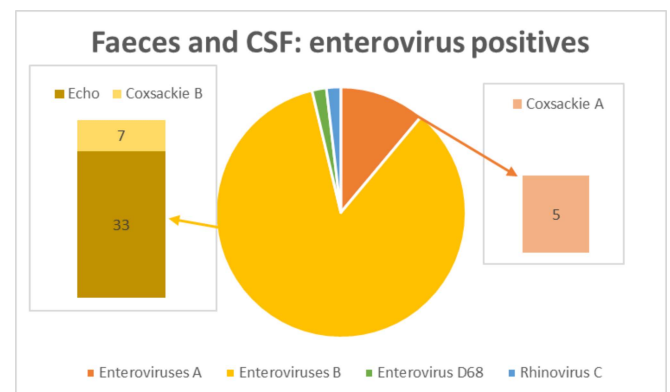


Figure 2: Molecular typing of faecal and CSF samples for 2021 stresses the wide circulation of enterovirus species B, more in detail Echoviruses.

CONCLUSION

Due to the lower number of CSF and faeces samples received at the NRC enteroviruses in the year 2020, as a consequence of the SARS-CoV-2 pandemic, molecular typing information was prioritized for the year 2021. Based on the set of respiratory samples that was typed for 2021, a prevalence of 5.3% was detected for EVD68. Focusing on the sample types CSF and faeces for the year 2021, Echoviruses 18 and 21 were most often identified, accounting for 38.2% of typed EV-positive cases.