P0007
Paper Poster Session
Viral molecular epidemiology (other than Hepatitis/HIV)

A review of polio virus surveillance, Austria 2013- 2015

Birgit Prochazka*[1], Ernst Amtmann[1], Annette Jung[1], Radica Paunovic[1], Bettina Stegbauer[1], Anna Stöger[1], Alexander Indra[1], Peter Hufnagl[1]

[1]*Österreichische Agentur Für Gesundheit und Ernährungssicherheit GmbH, Institut Für Medizinische Mikrobiologie und Hygiene Wien/Zentrum Für Anthropogene Infektionen, Vienna, Austria*

Background: Due to the wild-type Poliovirus Type 1-outbreak in the Syrian Arab Republic in 2013 Austrian health authorities demanded mandatory screening of all refugees within first days of their arrival in Austria. Between November 2013 and July 2015 1.319 stool samples were submitted to the National Reference Laboratory for Poliovirus, Vienna. All specimens were screened for Enterovirus (EV) using RT-PCR, further investigations of the EV positive specimens were performed and cell culture isolates were molecular typed by sequencing of a fragment of the genomic region encoding VP1.

Material/methods: The stool specimens were screened directly for Enteroviruses using real time RT-PCR (AnDiaTec®). Positive specimens were pre-treated and tested on L20B and RD-Atlanta cell lines (according to WHO Polio guidelines). Viral RNA Extraction was performed with QIAmp Viral RNA Mini kit (Qiagen) and molecular analyses of the VP1-region-sequencing (Nix et al.) were done with ABI Prism 3130 (Applied Biosystems), Data were interpreted using CLC Workbench 7.

Results: Between November 2013 and July 2015 1.319 stool samples were submitted to the National Reference Laboratory for Poliovirus, Vienna. Out of these 286 Enterovirus-PCR positive specimens (21,7 %) were detected : 19 samples (6,6 %) were positive for Sabin-like Poliovirus (SL-PV Type 1, 2 and 3) and 137 samples gave a Nonpolio-Enterovirus (NPEV) positive result in the cell culture (47,9 %). Further investigations of the NPEV isolates using Sequencing technique showed different NPEV serotypes: We were able to identify 7 different serotypes of the Enterovirus group C (except Polioviruses). Furthermore we identified 10 different serotypes of the Enterovirus group A and 16 different serotypes were allocated to Enterovirus group B.

Conclusions: The main task of the introduced Refugee Polio Surveillance System in Austria was to find all potential existing wild-type Polioviruses within 3 days after the arrival. An interesting side effect of these investigations was to get an insight into the circulating NPEV population of the regions, where Polioviruses are still persistent.

In contrast to the official WHO Polio guidelines using only time and cost intensive cell culture technique for Poliovirus detection our “streamlined” method using RT-PCR as a screening method before culturing PCR-positive samples showed to be highly effective.

Our analysis showed a lot of different NPEV serotypes, which have been rarely or not detected in Austria before. The impact of these “new” NPEV serotypes within the endogenic NPEV population remains to be seen, but will be assessed due to the ongoing AFP and Enterovirus Surveillance in Austria.