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Abstract (poster session)

**Phylogenetic analysis of an echovirus 30 outbreak in Austria, 2008**

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**Objectives:** Tasks of the National Reference Centre for Poliovirus (NRCP) in Vienna is the nationwide AFP (acute flaccid paralysis) surveillance among children aged less than 15 years and the laboratory based surveillance of enterovirus (EV) infections in Austria. In 2008 there was an Echovirus 30 (E30) outbreak in children (mean age 8 years) with symptoms of aseptic meningitis. The aim of our investigation was to compare virus isolates gained from outbreak cases by phylogenetic analyses with other E30 strains found in Austria in the years 2000, 2001, 2002 and 2010. **Methods:** 731 stool specimens from 9 cases and case related contact persons were screened for EV by use of real time RT-PCR Kit (AnDiaTec®). The 68 specimens tested PCR positive for EV and further 66 specimens (all specimens revealed an unreliable PCR result and arbitrarily selected specimens tested negative for EV) were additionally examined in cell-culture (in accordance with WHO manual). EV isolates were thereafter identified by molecular analysis of the VP1 genome region. For further genotyping a 3D-polymerase-(3DPol) gene fragment as described by Leitch et al. as a second target region was used. Viral RNA was extracted with QIAmp Viral RNA Mini kit (Qiagen). Sequencing analyses were done with ABI Prism 3130 (Applied Biosystems), Data were interpreted by using CLC workbench 5. **Results:** 51 EV isolates (50 recovered from the EV-PCR positive specimens and one from a specimen with inhibited EV-PCR) were related to the E30-outbreak. Out of these isolates, 44 were identified by VP1 sequencing as E30 (86.3%), 3 as E25 (5,9%), 3 as Coxsackie A4 (5,9%) and one isolate as Non Polio EV(1,9%). The phylogenetic analyses of the E30 case isolates revealed a higher sequence similarity in the 3DPol region to an E30 outbreak strain isolated in Finland in 2007 (FJ538707.1) than to 6 E30 isolates found in 2000 (n=2), 2001 (n=1), 2002 (n=1) and 2010 (n=2) in Austria. **Conclusion:** Our investigation in connection with the E30 Outbreak in 2008 showed that the 3DPol-region of the genome of EV strains circulating in Austria remained highly conserved. Further investigations may be helpful to get more information about virulence and relationship between the virus strains of outbreaks and epidemiologically unrelated strains. The planned whole genome sequencing may give us more insights.