

P0755 **Gut microbiome dynamics during an outbreak of shiga-toxin producing *Escherichia coli***

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Background: Shiga-toxin producing *Escherichia coli* (STEC) can cause devastating outbreaks of infections, especially among susceptible individuals. The gut microbiome is increasingly being implicated in the pathogenesis of infections but its role during STEC infection is yet undetermined. We therefore studied the microbiome of stool samples obtained during an investigation of an STEC outbreak in a nursery (O26:H11 *stx2a+* strain).

Materials/methods: The outbreak involved three cases of the haemolytic-uremic syndrome (HUS), five cases of STEC diarrhoea and five asymptomatic carriers. Stool samples were available for seven patients (two HUS, one diarrhoeae, 4 carriers) for a total of 45 samples, obtained during initial diagnosis and sequential follow-up, until stools became PCR-negative for STEC. The samples were subject to DNA extraction and 16S amplicon sequencing on an Illumina Miseq. Bioinformatics analysis was carried out using the QIIME 1.9.1 pipeline including OTU picking and assignment, determination of abundancies and analysis of alpha and beta diversity. Statistical analysis employed the ANOVA, Welch's t-test and G-test with Storey FDR correction.

Results: The abundance of different taxonomic groups is shown in the Figure. For each patient, samples are ordered chronologically and broken lines denote first negative sample. *Enterobacteriaceae* are shown in dark brown. While each patient demonstrated a different microbiome composition, significant changes in abundance were noted in six cases for whom follow-up samples were available. A statistically significant change in abundance of *Enterobacteriaceae* over time was noted ($p < 1e-15$, this trend was evident to all but one individual). When comparing all positive to all negative samples (for all patients), significantly greater abundance of *Desulfovibrionaceae* ($p = 0.045$) and *Verrucomicrobiaceae* ($p = 0.025$) were observed in the negative samples. Principal component analysis and hierarchical clustering did not detect consistent patterns that were associated with clinical STEC infection as opposing to asymptomatic carriage.

Conclusions: During STEC infection, the abundance of *Enterobacteriaceae* was demonstrated by microbiome analysis in most cases and thus dynamics of abundance might correlate with cease of shedding. No consistent microbiome profile was shown for STEC infection in this group but the greater abundance of certain taxa in negative samples may suggest a role in the recovery from infection.

