

O560

1-hour Oral Session

Harnessing whole-genome sequencing for diagnostics and typing

Whole genome sequencing (WGS) to investigate a series of *Corynebacterium diphtheriae* wound infections in East African refugees, May to August 2015 in Switzerland and Southern Germany

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Background: Rapid identification and typing of *Corynebacterium diphtheriae* is crucial during suspected outbreaks, as toxin-carrying strains are a threat for public health. Whole genome sequencing (WGS) may allow describing an outbreak at the highest molecular resolution. However, the impact of WGS in outbreak investigations with *C. diphtheriae* has not yet been studied.

Material/methods: We used conventional and selective cultures to investigate a case series of wound infections from refugees associated with *C. diphtheriae*. MALDI-TOF mass-spectrometry (Microflex, Bruker, Germany) determined the species identification and PCR was used to detect toxin production. Pulsed field gel electrophoresis and WGS was used for typing of the suspected outbreak strains, always running unrelated strains for control. WGS was performed on a MiSeq Illumina platform with >70x coverage, 2x250bp read length, and mapping against a reference genome. Data analysis was carried out using a local Galaxy instance, R and MEGA 6.0 and included quality trimming, mapping (Bowtie2.0) and variant calling (Varscan).

Results: We report 18 cases with *C. diphtheriae* wound infection in Eastern African refugees from Eritrea and Somalia. Patients presented to the emergency room shortly after arrival in refugee camps from April to August 2015. Toxin production was detected in 50% of *C. diphtheriae* isolates. In addition, we isolated methicillin-resistant *Staphylococcus aureus* (22%) and *Streptococcus pyogenes* (83%) as additional causing agents. WGS typing of the isolates showed the relatedness between the isolates using a minimal spanning tree (Figure 1). Whereas some isolates were related (see circles), some of the isolates were clearly independent suggesting no common shared transmission chain.

Conclusions: WGS may provide useful information for outbreak investigation, where epidemiological data is difficult or impossible to generate e.g. refugees. Our finding that some of the *C. diphtheriae* isolates were genetically related indicates transmission within defined populations. Whereas non-related isolates indicate several infection reservoirs exist on the origin and/or route of the refugees. Thus *C. diphtheriae* associated wound infections with toxin-positive strains may be observed more frequently in Europe due to the recent increase of refugees from Eastern Africa with similar travel routes to Europe under poor hygienic conditions. WGS offers the potential to describe potential outbreaks in a very high resolution and will be a helpful tool in epidemiology in the future.

Figure. Minimal spanning tree based on WGS data. Three clusters of *C. diphtheriae* isolates are shown. Cluster A includes only isolated from one country.

