P2340 Uncovering transmission events of vancomycin-resistant Enterococcus faecium in a tertiary care hospital by combining WGS, epidemiological data and contact network-based analyses

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Background: Enterococci are considered as a common cause of nosocomial infections, where treatment is limited as most of the hospital-adapted lineages are intrinsically resistant to a vast number of antibiotics or rapidly acquire resistance to the first line therapeutic agent vancomycin. Thus, vancomycin-resistant E. faecium (VRE) represent an enormous burden for hospitals worldwide and eradication of resistant bacteria often requires thorough and comprehensive hygienic practices. In order to understand the emergence and to prevent further spread of multi-drug resistant pathogens, it is important to monitor the prevalence and transmission in clinical settings. One key is the reconstruction of putative transmission chains, the identification and characterization of potential gaps in hygienic management.

Materials/methods: As part of a one year routine screening program, 111 VRE were isolated from patients admitted to a tertiary care hospital. Whole genome sequencing (WGS) was used for high-resolution genotyping and to determine phylogenetic relations. Different bioinformatics analyses were performed and compared. The analyses revealed the presence of one particular clone on all clinical wards investigated and over the entire period of screening. Clinical data and epidemiological information was used to manually overlay sequencing data in order to disclose transmission events and strain dynamics over time.

Results: Different genotypes were identified and were assigned to distinct clusters in the phylogenetic tree. VRE phylogeny was overlaid by adding clinical and epidemiological information. One clone seemed to be present on all clinical wards investigated and over the entire period of screening. Based on patient data about hospital stay and movement, putative transmission events were deduced. The data served as a basis for patient-contact network analyses, in order to generate an automated modelling and time related visualization of transmission dynamics.

Conclusions: Investigation of population dynamics by WGS and utilizing different bioinformatics approaches yielded concordant results in high resolution. The combination of WGS data analysis and epidemiological information is applicable to monitor the emergence and spread of VRE in clinical settings in high resolution. As part of an integrative risk assessment, these computations could potentially identify facilities and factors mainly associated with VRE spread.