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Paper Poster Session

Surveillance and control of nosocomial pathogens and infection

A longlasting outbreak of MRSA in a Dutch nursing home

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Background: Due to the successful Search and Destroy(S&D) policy on methicillin-resistant *Staphylococcus aureus*(MRSA) the prevalence of MRSA in the Netherlands is still very low (0,11%, on admission to hospitals, Bode et al, 2011). Outbreaks occur sporadically in hospitals and most of them are relatively easy to control. However, outbreak control is much more difficult in nursing homes(NHs) due to prolonged length of stay and limitations with the implementation of isolation measures. This report describes a large, long lasting and difficult to control outbreak in a Dutch NH

Material/methods: Active microbiological screening was regularly performed in residents and health care workers(HCWs) of the NH. HCWs wore gown, gloves, surgical mask and cap when delivering care to the residents. MRSA-positive HCWs were suspended from work. MRSA-positive residents were placed in a cohort, in a separate location in the NH. Molecular typing was performed using multiple locus variable number of tandem repeat analysis(MLVA) and a subset of 24 isolates was subjected to whole genome mapping(WGM), a high-resolution typing technique based on the restriction map of the bacterial chromosome. HCWs and residents were treated for MRSA carriage, in accordance with the national guidelines.

Results: In September 2014, a resident developed a urinary tract infection, caused by a MRSA. Contact tracing revealed that 17/20 (85%) residents and 13/94 (14%)HCW's were MRSA positive. MLVA showed that there were two types, MT0237-MC0008 and MT0491-MC0022. WGM of 24 MT0237-MC0008 isolates originating from 12 patients showed indistinguishable maps for 22 of the isolates (>98% similarity), while the two remaining maps were highly related (>97% similarity). From September 2014 until April 2015, the colonised residents and HCWs were treated. All 13 HCWs were treated successfully, but 6/17 residents remained MRSA positive despite repeated treatments. In two residents, treatment was discontinued prematurely, due to side effects. No recolonisation or new acquisitions of residents or HCWs was seen after April 2015.

Conclusions: This study revealed an extensive outbreak in a Dutch NH caused by two MRSA strains. The extremely high rate of colonisation among residents was likely caused by a prolonged period of undetected presence in the NH. The restrictive use of microbiological diagnostics in NH has likely contributed to the late detection of this outbreak. The fact that six residents could not be decolonised poses a continuing threat for renewed spread in the NH. This outbreak shows that NH are a potential source of MRSA and that the restrictive use of diagnostics in NH should be reconsidered in the light of the ever increasing threat caused by antimicrobial resistance.