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Investigation of Clusters of MRSA Cases in a Hospital in Western Kenya

Authors : Lillian Musila, Valerie Oundo, Daniel Erwin, Willie Sang

Abstract : Staphylococcus aureus infections are a major cause of nosocomial infections in Kenya. Methicillin resistant S. aureus (MRSA) infections are a significant burden to public health and are associated with considerable morbidity and mortality. At a hospital in Western Kenya two clusters of MRSA cases emerged within short periods of time. In this study we explored whether these clusters represented a nosocomial outbreak by characterizing the isolates using phenotypic and molecular assays and examining epidemiological data to identify possible transmission patterns. Specimens from the site of infection of the subjects were collected, cultured and S. aureus isolates identified phenotypically and confirmed by APIStaph™. MRSA were identified by cefoxitin disk screening per CLSI guidelines. MRSA were further characterized based on their antibiotic susceptibility patterns and spa gene typing. Characteristics of cases with MRSA isolates were compared with those with MSSA isolated around the same time period. Two cases of MRSA infection were identified in the two week period between 21 April and 4 May 2015. A further 2 MRSA isolates were identified on the same day on 7 September 2015. The antibiotic resistance patterns of the two MRSA isolates in the 1st cluster of cases were different suggesting that these were distinct isolates. One isolate had spa type t2029 and the other had a novel spa type. The 2 isolates were obtained from urine and an open skin wound. In the 2nd cluster of MRSA isolates, the antibiotic susceptibility patterns were similar but isolates had different spa types: one was t037 and the other a novel spa type different from the novel MRSA spa type in the first cluster. Both cases in the second cluster were admitted into the hospital but one infection was community- and the other hospital-acquired. Only one of the four MRSA cases was classified as an HAI from an infection acquired post-operatively. When compared to other S. aureus strains isolated within the same time period from the same hospital only one spa type t2029 was found in both MRSA and non-MRSA strains. None of the cases infected with MRSA in the two clusters shared any common epidemiological characteristic such as age, sex or known risk factors for MRSA such as prolonged hospitalization or institutionalization. These data suggest that the observed MRSA clusters were multi strain clusters and not an outbreak of a single strain. There was no clear relationship between the isolates by spa type suggesting that no transmission was occurring within the hospital between these cluster cases but rather that the majority of the MRSA strains were circulating in the community. There was high diversity of spa types among the MRSA strains with none of the isolates sharing spa types. Identification of disease clusters in space and time is critical for immediate infection control action and patient management. Spa gene typing is a rapid way of confirming or ruling out MRSA outbreaks so that costly interventions are applied only when necessary.

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