Comparison of Community-Associated and Healthcare-Associated Methicillin-Resistant Staphylococcus aureus (MRSA) in Canada: CANWARD 2007-2010

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ABSTRACT

Background: This study assessed the demographics, antimicrobial susceptibility and molecular epidemiology of MRSA among patients with healthcare-associated and community-associated MRSA bacteremia through the CANWARD network.

Methods: MRSA isolates were collected from 28 participating laboratories in Canada. Information on patient demographics, clinical characteristics and antimicrobial susceptibilities were collected from the CANWARD database.

Results: One thousand one hundred and fourteen isolates of MRSA were collected between January 2007 and December 2010, inclusive, as part of the ongoing CANWARD study. There were 775 isolates of healthcare-associated MRSA and 328 isolates of community-associated MRSA. The prevalence of CA-MRSA was 69.5% of MRSA isolates, which was significantly higher than that of HA-MRSA (30.5%). Intriguingly, the majority of CA-MRSA (59.7%) were hVISA, while only 40.3% of HA-MRSA were hVISA. The majority of CA-MRSA isolates were more susceptible to linezolid and vancomycin than HA-MRSA. The susceptible phenotype was determined by population analysis profile (PAP) and clonal typing.

Conclusions: The majority of CA-MRSA isolates were hVISA, while only 40.3% of HA-MRSA were hVISA. Future studies are needed to further understand the pathogenesis of CA-MRSA and HA-MRSA CA-MRSA genotype continued to vary within the community and to replace healthcare-associated (HA-MRSA) in the hospital setting. Most CA-MRSA isolates differ from their healthcare-associated counterparts in their microbiological, epidemiological and molecular characteristics.

MATERIALS & METHODS

RESULTS

CONCLUSIONS

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