



RESEARCH PAPER

Multidrug resistant gram-negative bacteria in Tasmania: An audit based pilot study

Thomas G. Heazlewood, Kathryn Ogden, Damhnat McCann*

University of Tasmania, Launceston, Tasmania, Australia

Received 30 January 2016; received in revised form 22 March 2016; accepted 22 March 2016
Available online 10 May 2016

KEYWORDS

Multidrug resistant;
Gram negative;
Antibiotics;
Audit;
Urinary tract
infection;
Nosocomial

Abstract *Objectives:* Multidrug resistant gram-negative (MRGN) bacteria are increasing in prevalence globally. Accurate prevalence data contributes to limiting the proliferation of these organisms. The aim of this research was to identify the prevalence of MRGN bacteria within an Australian health district and to establish the risk factors associated with their acquisition through the development and piloting of a novel audit tool.

Methods: An audit based pilot study was conducted using a specifically developed tool that collected pathology and patient data on all patients with new MRGN bacteria notifications during 2013 in one Australian health district.

Results: There were 68 new MRGN bacteria notifications in the health district in 2013; 42 of these had sufficient data for auditing. The majority of bacteria identified were *Escherichia coli* ($n = 43$, 63.2%) and the majority of specimens were urine ($n = 47$, 69.1%). Urine specimens were more prevalent in females compared to males (72% vs 28%, χ^2 13.98, $p < 0.001$). Sixty-five percent of patients were aged 65 and over ($n = 44$), and 25% were aged 85 and over ($n = 17$). More than half of the patients with full data available ($n = 22$) were administered antibiotics during admission, predominantly broad-spectrum varieties.

Conclusions: This pilot study identified several areas of concern, including poor documentation practices, and management of patients with dementia, particularly those with urinary catheters. Discrepancies between antibiotic prescribing practices and Therapeutic Guidelines were identified and an audit of antibiotic prescribing and reasons for deviation could improve practice and reduce the burden of multidrug resistance. Enhanced screening of MRGN bacteria should be considered to provide data for management and tracking of resistance, and could be enhanced through use of the audit tool.

© 2016 Australasian College for Infection Prevention and Control. Published by Elsevier B.V. All rights reserved.

* Corresponding author. School of Health Sciences, Newnham Campus, University of Tasmania, Locked Bag 1322, Launceston TAS 7250 Australia. Tel.: +61 3 6324 3812; fax: +3 6324 3952.

E-mail address: Damhnat.McCann@utas.edu.au (D. McCann).

Highlights

- Majority of MRGN bacteria at the study hospital were *Escherichia coli* found in urine specimens.
- Older patients and females constituted the majority of patients with MRGN bacteria.
- Local prevalence data contributes to managing the spread of MRGN bacteria.

Introduction

The increasing prevalence of multidrug resistant gram-negative (MRGN) bacteria portends a world where drug resistant bacteria are so pervasive, infections may be as difficult to treat as they were in the pre-antibiotic era [1]. The naturally occurring resistance conferred to gram-negative bacteria through their cell structure has compounded their ability to disseminate antibiotic resistance through horizontal gene transfer to other strains and species [2]. Transcontinental spread of genetic resistance has already occurred, resulting in a global dissemination of pandrug resistant gram-negative bacteria [2].

There is currently no single method for the classification of antibiotic resistance. The classification system developed by the European Centre for Disease Control and the Centre for Disease Control differentiates bacteria into: multidrug resistant MDR – resistant to at least one agent in three or more antimicrobial classes; extensively drug resistant XDR – resistant to at least one agent in all but two or fewer antimicrobial classes; and pandrug resistant PDR – resistant to all agents in all antimicrobial classes [3].

The spread of MRGN bacteria has resulted in increased patient complications, burgeoning costs for consumers and healthcare systems, and higher rates of mortality [4]. As greater numbers and varieties of antibiotics are required to treat infections, more time, effort and expense is required. Accurate and contemporaneous data for communities and hospitals is required to assist in developing effective public health and epidemiological systems to prevent and manage outbreaks of MRGN bacteria [5].

Despite the increased prevalence of MRGN bacteria, limited information exists regarding the prevalence of MRGN in Australia. No audit tool was identified that could collect data on the prevalence and risk factors associated with MRGN bacteria broadly. The aim of this study therefore was to develop, validate and pilot an audit tool to identify new notifications of MRGN bacteria in one Australian health service district.

Methods

This was a retrospective audit based pilot study conducted in a regional public hospital servicing a wider health service district in Tasmania, Australia.

Sample

Patients eligible for inclusion in the audit were identified through the hospital Infection Prevention and Control Unit

as having a new notification of MRGN bacteria between January 2013 and December 2013. The most recent admission prior to the MRGN bacteria being identified was audited, limited to admissions within two months prior to specimen collection.

Data collection

Audit tool

An audit tool was developed incorporating the collection of data on risk factors for MRGN bacteria as reported in studies identified in a structured literature review (Table 1). Given the extensive number of potential risk factors that were identified using a significance level of <0.05 , only those with a significance level of <0.001 were included in the audit tool (Table 1). Where applicable, further factors identified as significant through multivariate analysis or those identified as particularly important by the researchers were also selected. The majority of studies investigated only a single species of bacteria (Table 1), thus risk factors with a p-value of <0.05 but which were identified in multiple species were also included. In addition to the risk factors, demographic information for age, sex, hospital unit, length of stay, place of residence to and following admission and specimen collection date was included in the audit tool.

Establishing validity of the audit tool

A formal review process was undertaken to establish content validity. Six healthcare professionals working in infectious diseases were asked to comment on a draft version of the tool, specifically on whether any relevant risk factors were absent, if any included risk factors were unnecessary or required modification, and on the formatting and layout of the tool. Four responses were received. Changes as a result of the feedback included changing the route of antibiotic administration from a check box to a free entry to accommodate the range of possible administration methods. History of ICU admission was changed from yes/no to include the number of days spent in the ICU.

A pre-pilot study was conducted using 10% of the total patients available for auditing. Minor changes to improve the useability of the tool were made including changing intravenous catheters from an actual number to three categories (<3 devices, 3–5, >5) due to discrepancies in documentation. There were differences noted between the antibiotics prescribed in the emergency department compared to the inpatient units so information related to the location of antibiotic prescription was included (inpatient unit, emergency department, community). Data

Download English Version:

<https://daneshyari.com/en/article/2684267>

Download Persian Version:

<https://daneshyari.com/article/2684267>

[Daneshyari.com](https://daneshyari.com)