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Letter to Editor

Changing Epidemiology of VAP Pathogens

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Ventilator-associated pneumonia (VAP) is a common healthcare-associated infection among patients in the intensive care units (ICUs) who have endotracheal intubation or a tracheostomy for mechanical ventilation. VAP is the most commonly acquired infection in ICUs worldwide, accounting for 25% of all types of ICU acquired infections and affecting an estimated 10 - 30% of ventilated patients. VAP can lead to 20% - 70% mortality in intubated patients with the rate depending on the location and the study population [1]. VAP increases the hospital stay by an average of 7 - 9 days per patient and incurs an additional cost of more than $40,000 per patient [2]. It also prolongs the required duration of mechanical ventilation and the ICU stay of the patient [3].

There is a pronounced association between the aetiology of VAP and economic development of the nation. For instance, in Europe and the USA, the most common organism associated with VAP is *Staphylococcus aureus* [4]. However, in Asia and Latin America, the Gram-negative organisms *Pseudomonas aeruginosa, Acinetobacter* spp. and *Klebsiella pneumoniae* predominate [5]. Though the geographical and temporal distribution of the infecting bacteria is variable, the causative agents of VAP are united in their ability to become resistant to a range of antimicrobials. This occurs due to the sustained use of the same antimicrobial(s) within the healthcare setting in which they circulate. With the rampant use of antimicrobials, the level of resistance amongst the nosocomial pathogens has been constantly increasing with no new antibiotics in the pipeline. Thus, we performed a retrospective study of the pathogens causing VAP in the ICUs of a 160 bedded level 1 trauma centre.

It was seen that during the study period (2012 - 2016), gram negative organisms were isolated more frequently than the gram positive organisms and among gram negative organisms, non-lactose fermenters were more frequent than enterobacteriaceae with *Acinetobacter* spp being most frequent. Unusual organisms i.e. *Burkholderia* spp, *Serratia* spp, *Stenotrophomonas* spp and *Sphingomonas* spp were also found to cause VAP in our patients and their rate of isolation was found to increase over the years. Isolation of atypical inherently colistin resistant pathogens from trauma patients (immunocompetent population) could be attributed to the change in the normal flora due to the widespread use of antibiotics. Distribution of all the pathogens and that of atypical pathogens over 5 years is given in figure 1A.

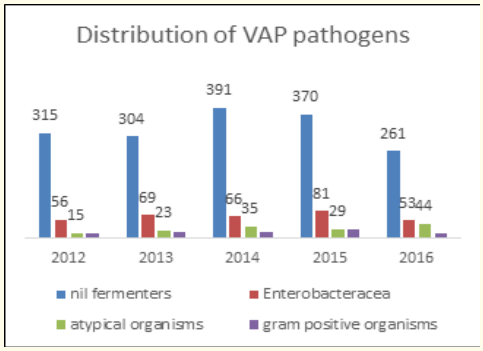

Figure 1A: *Distribution of VAP pathogens.*

Antibiotic resistance profile of the pathogens was also studied. The level of resistance of the organisms to third generation cephalosporins, imipenem and tigecycline was found to be nearly 90%, 75 - 80% and 20 - 25% respectively in all the years. However, the level of colistin resistance was seen to increase over the years being 4.8% in 2012 and 12.1% in 2016. The resistance profile of the isolates is shown in figure 1B.

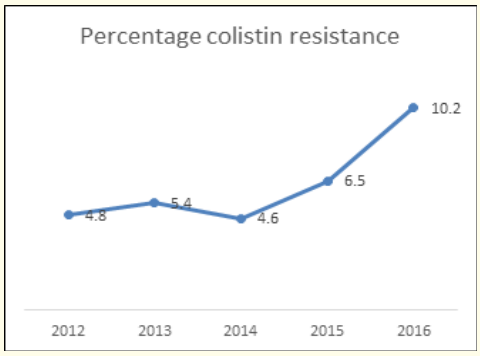

Figure 1B: *Percentage colistin resistance in VAP pathogens.*

The changing profile of our VAP pathogens from Enterobacteriaceae to atypical inherently colistin resistant organisms and the increasing level of colistin resistance in isolates is attributable to the injudicious excessive use of antibiotics in the hospitals and the Out Patient Departments. Thus to conclude, judicious use of antibiotics in the hospital setting is advocated to prevent the emergence of resistant pathogens.

Conflict of Interest

There is no conflict of interest between the authors.

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