Biotyping of multidrug-resistant Klebsiella pneumoniae clinical isolates from France and Algeria using MALDI-TOF MS.

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BACKGROUND: Klebsiella pneumoniae is one of the most important pathogens responsible for nosocomial outbreaks worldwide. Epidemiological analyses are useful in determining the extent of an outbreak and in elucidating the sources and the spread of infections. The aim of this study was to investigate the epidemiological spread of K. pneumoniae strains using a MALDI-TOF MS approach.

METHODS: Five hundred and thirty-five strains of K. pneumoniae were collected between January 2008 and March 2011 from hospitals in France and Algeria and were identified using MALDI-TOF. Antibiotic resistance patterns were investigated. Clinical and epidemiological data were recorded in an Excel file, including clustering obtained from the MSP dendrogram, and were analyzed using PASW Statistics software.

RESULTS: Antibiotic susceptibility and phenotypic tests of the 535 isolates showed the presence of six resistance profiles distributed unequally between the two countries. The MSP dendrogram revealed five distinct clusters according to an arbitrary cut-off at the distance level of 500. Data mining analysis of the five clusters showed that K. pneumoniae strains isolated in Algerian hospitals were significantly associated with respiratory infections and the ESBL phenotype, whereas those from French hospitals were significantly associated with urinary tract infections and the wild-type phenotype.

CONCLUSIONS: MALDI-TOF was found to be a promising tool to identify and differentiate between K. pneumoniae strains according to their phenotypic properties and their epidemiological distribution. This is the first time that MALDI-TOF has been used as a rapid tool for typing K. pneumoniae clinical isolates.

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