P0305

Paper Poster Session II

Focus: Acinetobacter, Pseudomonas and other nonfermenters

Occurrence of 16S rRNA methylase armA in K. pneumoniae, P. aeruginosa, and A. baumannii isolates in a patient repatriated from China to France

F. Janvier¹, A. Mille², S. Pons¹, E. Meaudre-Desgouttes³, P. Brisou¹, P. Plésiat², K. Jeannot²

Objectives. Since its first description in *Klebsiella pneumoniae*, the 16S ribosomal RNA methylase (rRNA) ArmA has increasingly been reported in various *Enterobacteriaceae* and *Acinetobacter* species worldwide, but detected only in a few isolates of *P. aeruginosa* from Asia. This study describes the characterization of a multidrug resistant *P. aeruginosa* strain (PA1819) co-producing ArmA, the metallo-ß-lactamase IMP-45, and the fluoroquinolone resistance determinant QnrVC1. The strain was isolated in a patient co-infected with two other ArmA-producing bacteria, *K. pneumoniae* KP1875 and *A. baumannii* AB447.

Methods. The bacteria were isolated in both a rectal screening sample and a tracheal aspirate from a 75-year-old French man repatriated from China to France in November 2013, and admitted to one ICU of military hospital Sainte Anne, Toulon. Drug susceptibility testing, strain genotyping by MLVA, PCR and DNA sequencing experiments were performed according to standard protocols. Whole DNA sequences were obtained with a PGM Ion Torrent equipment (Life technologies).

Results. The three strains were highly resistant to all the aminoglycosides tested including arbekacin (MIC>256 mg/L). All of them contained 100% identical sequences of the *armA* gene. Whole DNA sequencing revealed the presence of Tn1548::armA on a plasmid of 500-kbp and 20.3-kbp in PA1819 and AB447, respectively. In the *P. aeruginosa* strain, the transposon is flanked by IS26 elements and located downstream of two class 1 integrons of 4- and 3.5-kbp, respectively. The 4-kbp integron which contains the *bla*_{IMP-45}, *aacA4*, *bla*_{OXA-1}, and *catB3* gene cassettes is identical to an element identified recently in a canine isolate from China. The second (3.5-kbp) transposon present in PA1819 (*aacA4*, *qnrVC1*, *arr-2*, and *dfrA22*) has never been reported before. Detailed analysis of the plasmid bearing *armA* in AB447 showed its close relatedness with pMDR-ZJ06, a plasmid found in another multidrug resistant *A. baumannii* strain from China (MRD-ZJ06). Different from pMDR-ZJ06, the AB447 plasmid harbors the integron-borne gene cassettes *aacA4*, *catB8*, and *aadA2*. Finally, the presence of gene *bla*-OXA-23 in the chromosome of strain AB447 accounts for the high level resistance of the strain to imipenem.

Conclusion. This study shows that *P. aeruginosa* is able to acquire 16S rRNA methylase genes confined so far in *Enterobacteriaceae* and *Acinetobacter* sp., and suggests that co-infections may promote the transfer of such resistance determinants. Emergence of 16S rRNA methylase-producing *P. aeruginosa* is now a matter of concern in Europe.

¹Laboratoire de Microbiologie-Hygiène- Hôpital d'instruction des Armées Sainte ANNE, Toulon, France

²Laboratoire de Bactériologie- CNR de la Résistance aux Antibiotiques, CHRU Jean Minjoz, Université de Franche-Comté, Besançon, France

³Service d'anesthésie-Réanimation-Soins continus- Hôpital des Armées Sainte-ANNE, Toulon, France