Phenotypic and molecular diversity of urinary isolates of Pseudomonas aeruginosa
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Background
Pseudomonas aeruginosa (PA) is an opportunistic pathogen causing frequent healthcare associated Urinary Tract Infection (UTI). Due to a range of mechanisms for adaptation and antibiotic resistance, PA infections are difficult to treat and often associated with increased morbidity or mortality. Many studies explored the diversity of cystic fibrosis strains but little is known about the diversity of urinary strains. Thus, the aim of our study was to describe phenotypic and molecular diversity:
- (i) of isolates causing Asymptomatic Bacteriuria (AB) or UTI and;
- (ii) between isolates from a same sample.

Results
177 isolates were phenotypically and genetically characterized.

Phenotypic diversity
78% of our isolates were Non-MultiDrug Resistant (MDR) (isolates resistant to less than 3 antibiotic families), 16% were MDR (isolates resistant to at least 3 antibiotic families) and 6% were Extensively Drug Resistant (XDR) (isolates resistant to at least 6 antibiotic families) (Fig. 1). The rate of antibiotic resistance varied between 8% (for cefazidime) and more than 30% (fluoroquinolones) (Fig. 2). The resistance phenotypes were different between isolates collected from 10 of the 58 urine samples.

Molecular diversity
MLST identified 34 Sequence Types (STs) for the 58 urine samples. Eight STs were identified for at least 2 patients. As previously described [1], ST76 was associated with antibiotic resistance (MDR or XDR profiles) (Fig. 3) and known as high-risk clones like ST232 and ST372. STs of isolates from a given urine sample were different for only 3 patients. Of note, no ST was specifically associated with UTI (Fig. 4).

Materials and methods
We studied 2 to 5 isolates of PA from 58 urine samples (38 AB and 20 UTI) sent to the Rouen University Hospital from June through November 2016. More than one urine sample were analyzed for 5 of the 51 patients included.
Antibiotic susceptibility was studied by disk diffusion method, according to the 2017 French recommendations. Genetic diversity was assessed by MultiLocus Sequence Typing (MLST). Typing data were uploaded into BioNumerics software 7.6 to generate Minimum Spanning Trees (MST).

Conclusion
This study showed an important genotypic diversity of PA urinary isolates. There was no epidemic clone. The MLST analysis of 2 of 5 isolates per urine sample showed that AB or UTI were rarely polyclonal (5%). In contrast, a phenotypic diversity (antibiotic susceptibility) was more frequently observed (17%). These results should be confirmed by the study of more isolates per urine sample and more patients.

References

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