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Phenotypic and molecular diversity of urinary isolates of *Pseudomonas aeruginosa*

A Cottalorda, S Dahyot, J Lebeurre, A Soares, M Réveillon, F Croustillères,
E. Jumas-Bilak, M. Pestel-Caron

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Cottalorda A¹, Dahyot S^{1,2}, Lebeurre J¹, Soares A^{1,2}, Réveillon M², Croustillères F², Jumas-Bilak E³, Pestel-Caron M^{1,2}¹ Microbiological Laboratory GRAM EA2656, Rouen University, FRANCE; ² Bacteriological Laboratory, Rouen University Hospital, FRANCE; ³ Microbiological Laboratory UMR 5569 Hydrosciences, Montpellier University, FRANCE.

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.

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).

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 ceftazidime) and more than 30% (fluoroquinolones) (Fig.2). The resistance phenotypes were different between isolates collected from 10 of the 58 urine samples.

Fig. 1 Antibiotic susceptibility profile of the urinary isolates of *P. aeruginosa* (%)

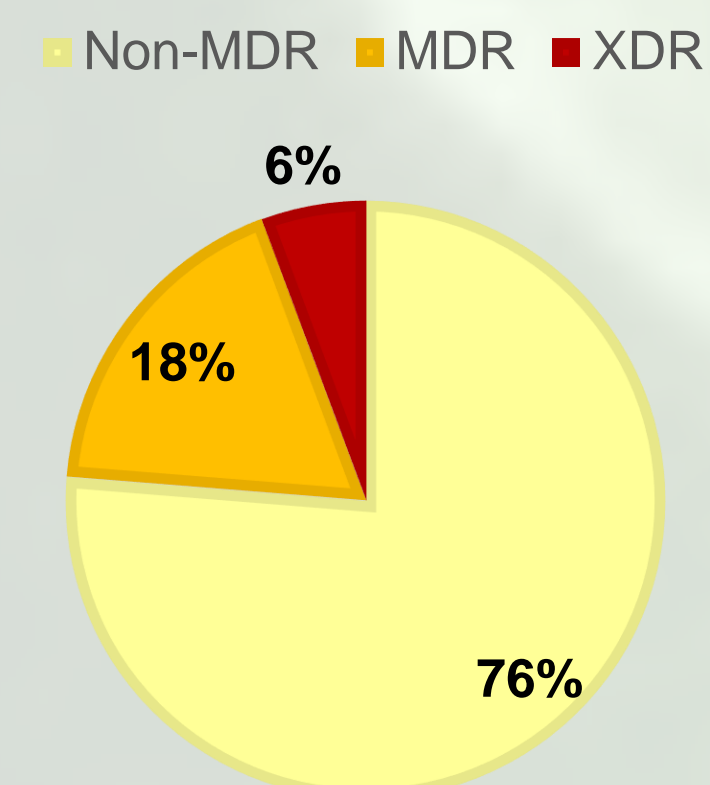
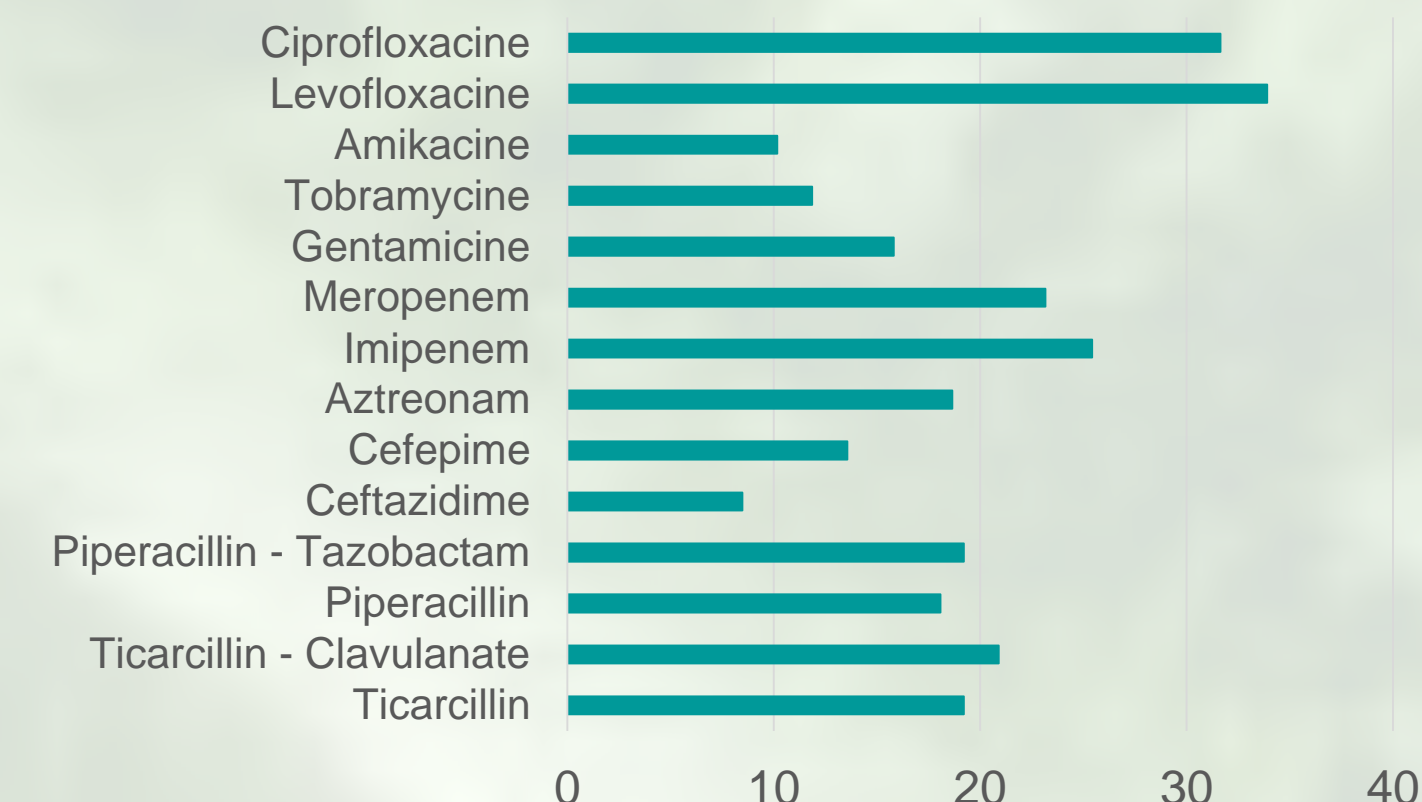


Fig. 2 Antibiotic resistance (%) of the urinary isolates of *P. aeruginosa*



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], ST235, ST175, and ST111 were associated with antibiotic resistance (MDR or XDR profiles) (Fig. 3) and known as high-risk clones like ST253 and ST395. STs of isolates from a given urine sample were different for only 3 patients. Of note, no ST was specifically associated with AB or UTI (Fig. 4).

Fig.3 MST of the STs depending on the antibiotic susceptibility profile

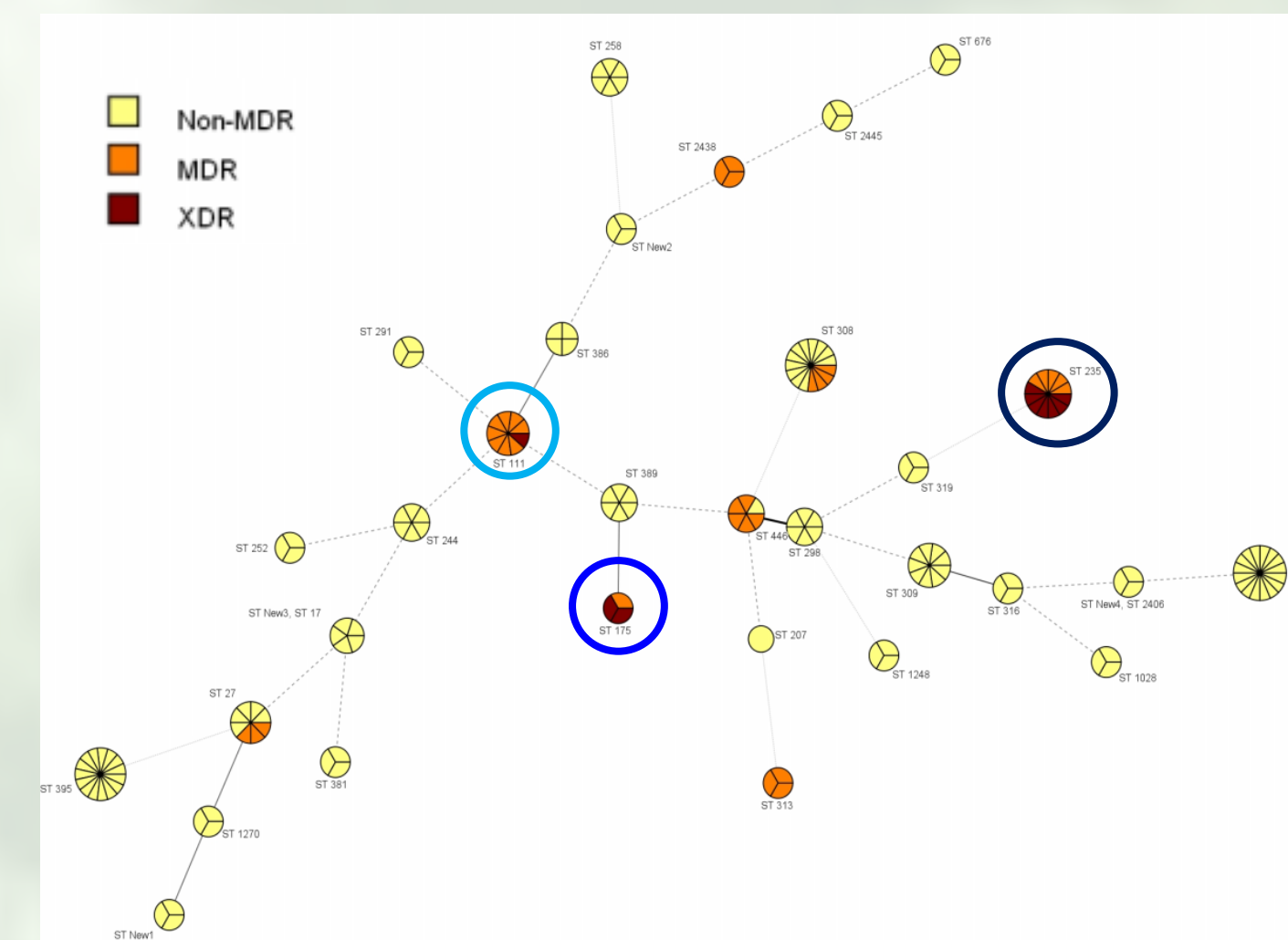
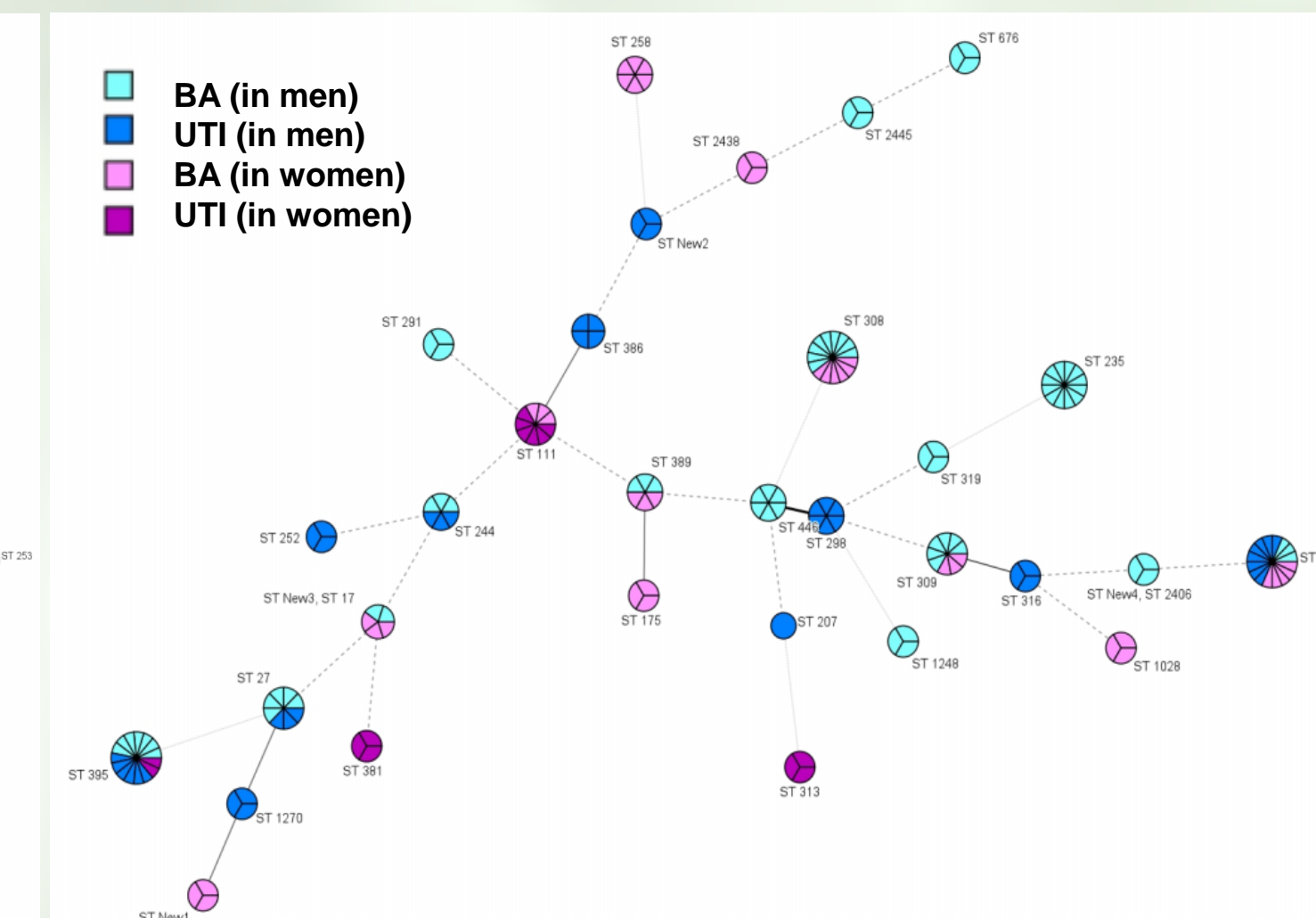


Fig.4 MST of the STs depending on the clinical data



Conclusion

This study showed an important genotypic diversity of PA urinary isolates. There was no epidemic clone. The MLST analysis of 2 to 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.