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# Preliminary characterization of adaptation mechanisms of sequential urinary isolates of *Pseudomonas aeruginosa*

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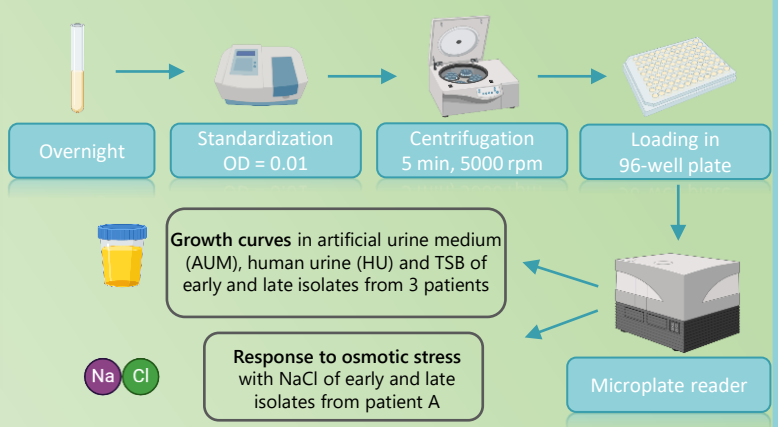
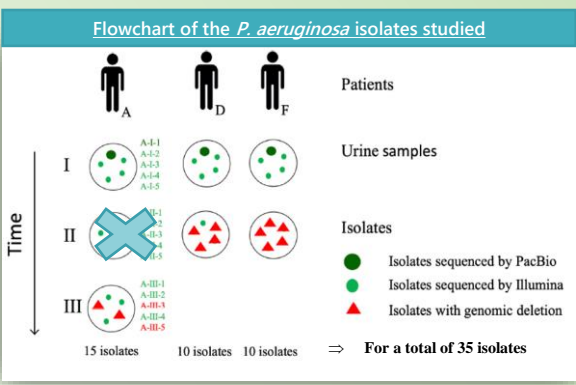
## Introduction

*Pseudomonas aeruginosa* is a Gram-negative opportunistic pathogen responsible for difficult-to-treat healthcare associated urinary tract infections (UTI), leading to relapses (chronic infections). While the adaptation mechanisms of *P. aeruginosa* in the respiratory tract are well studied, its adaptation and survival mechanisms in the urinary tract are very poorly understood.

The aim of this study was to better understand the mechanisms associated with *P. aeruginosa* recurrent UTI using a collection of sequential clinical urinary isolates for which genomic deletions have been previously described over time (isolates from 82 to 259 days apart) in 3 patients.

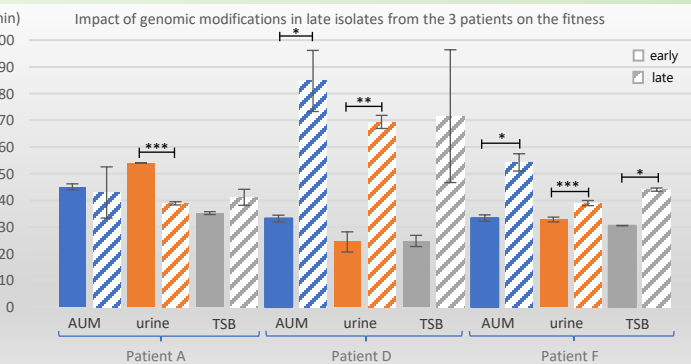
## Methods

### Phenotypic characterization of early (non-deleted) versus late isolates (deleted)



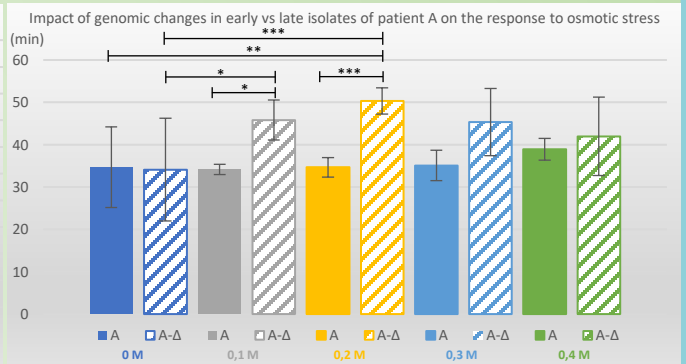
Early isolates → samples I (non-deleted)  
 Late isolates → samples II and III (deleted)

## Results



**Figure 1:** Generation time (G) (min) in TS, AUM and HU of early isolates and late isolates. The results are expressed as mean value +/- standard deviation (SD) of three independent experiments performed in triplicates. Significance was identified as P < 0,05 (\*), P < 0,01 (\*\*), P < 0,001 (\*\*\*)

Late isolates from patient D and F have a slower fitness than early ones in the 3 media.  
 However for patient A, impact on fitness of late isolates in HU only.



**Figure 2:** Generation time (G) (min) in TS of early isolates (A) and late isolates (B) in presence of osmotic stress compared to the G without NaCl. The results are expressed as mean value +/- standard deviation (SD) of three independent experiments performed in triplicates. Significance was identified as P < 0,05 (\*).

Late isolates from patient A respond differently to osmotic stress (longer generation time) from early ones.

## Conclusion

These preliminary results show that the genomic deletions observed in sequential isolates associated with urinary persistence may impact the growth and stress response of *P. aeruginosa*. This needs further studies by transcriptomic and metabolomics approaches to identify the regulatory and metabolic pathways underlying the evolutionary adaptation of this species to the urinary tract.