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Transcriptomic analysis of early and late clinical isolates *Pseudomonas aeruginosa* adaptation to the urinary tract

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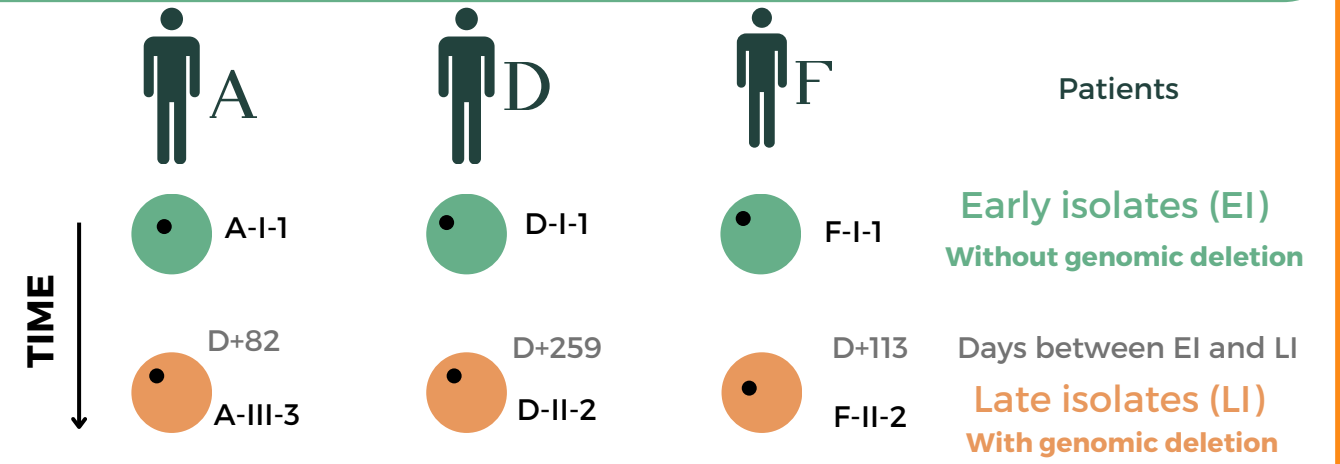
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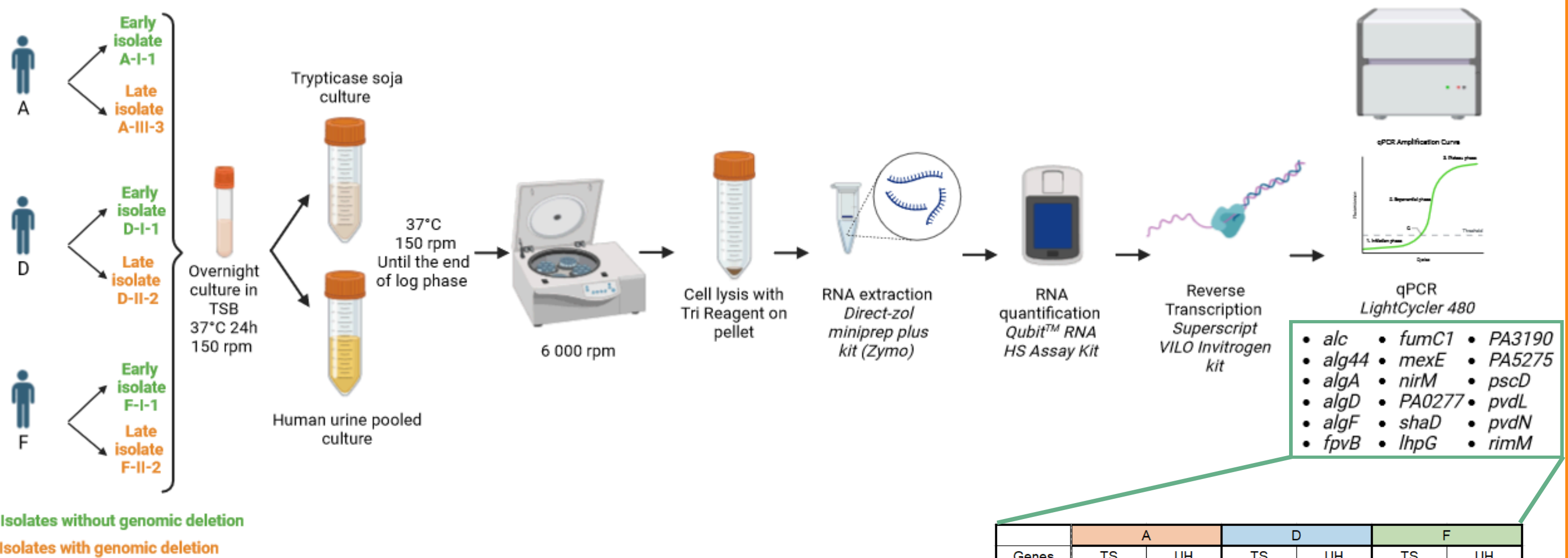
Background

Pseudomonas aeruginosa is a common opportunistic gram-negative pathogen responsible for health-care associated **urinary tract infections** that can lead to bacterial persistence. From isolate pairs collected longitudinally from 3 patients over time, a study is underway in the lab to characterize the adaptation mechanisms of *P. aeruginosa* to the urinary tract. Based on previously acquired **proteomic** data, the aim was here to validate the **differential transcription** of genes corresponding to the main proteins differentially expressed.



Study flowchart of the *P.aeruginosa* isolates

Materials and Methods



Results

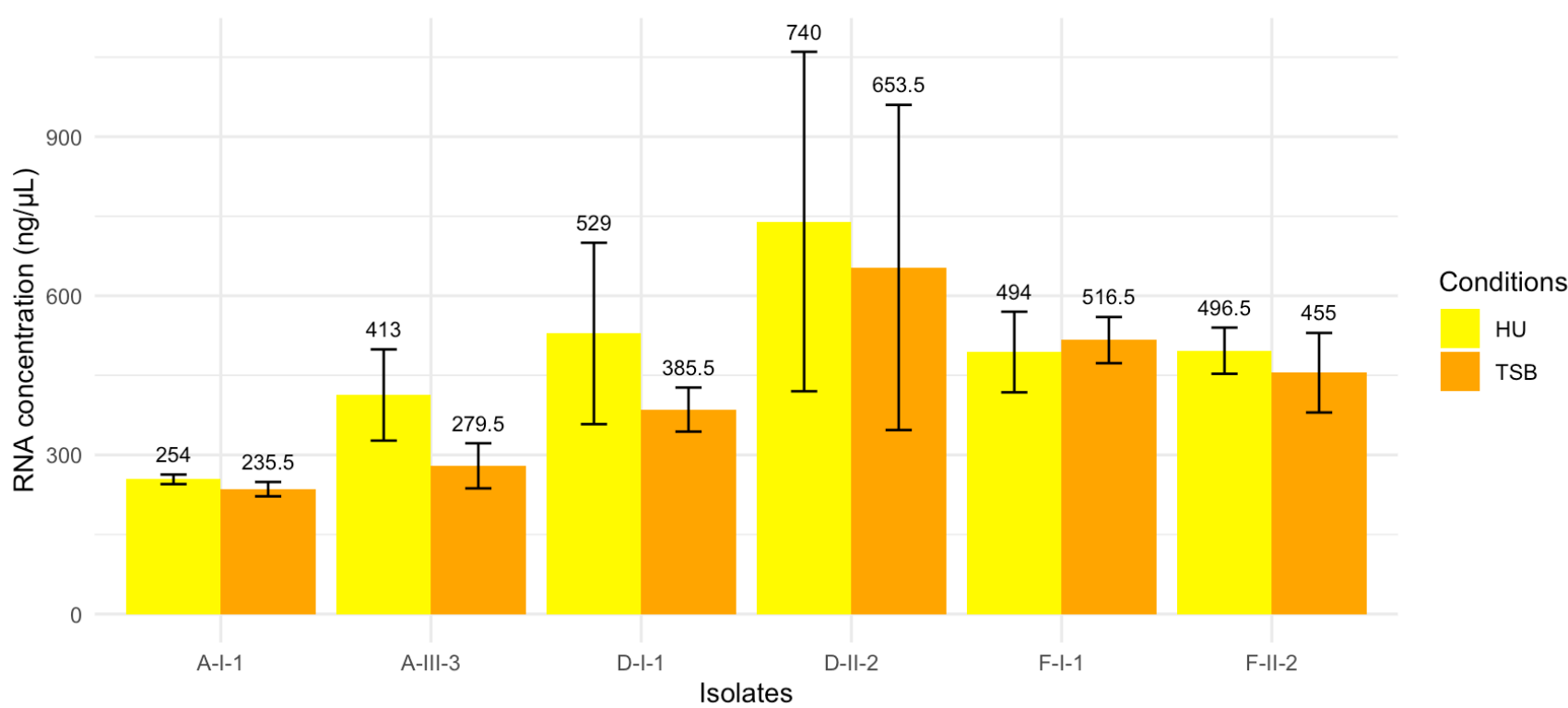


Figure 1 : Quantity of extracted RNA in each sample

From bacterial pellets, RNA extraction was performed for the 6 strains in the 2 conditions (HU and TSB) and in duplicate. Qubit dosage revealed a RNA concentration ranging from 235,5 ng/μL to 740 ng/μL.

Genes	A		D		F	
	TS	UH	TS	UH	TS	UH
alc		-				
alg44			-		-	
algA	-			-		-
algD					-	-
algF	-					
fpvB		+				+
fumC1						+
mexE				+		
nirM			+			
PA0277	+				+	
shaD			-	-		
lhpG	+					
PA3190				+		
PA5275			+			
pscD					+	
pvdL	+					
pvdN		+				+
rimM		-				

- : down-abundant protein = lower protein abundance in the early isolate than in the late isolate

+ : up-abundant protein = higher protein abundance in the early isolate than in the late isolate

List of selected genes coding up-abundant or down-abundant proteins

Among the proteins selected are virulence factors and proteins coding the following genes: *pvdN* (pyoverdine synthesis), *algD* (alginate synthesis, biofilm formation and mucoid profile) and *fpvB* (pyoverdine ferric receptor)

Conclusion

This transcriptomic analysis is the first step towards a better understanding of the regulatory mechanisms inherent to *P. aeruginosa* adaptation to the urinary tract