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Cytotoxicity is correlated with Type III Secretion System expression and inflammasome activation but not with motility in clinical isolates of *Pseudomonas aeruginosa* from acute infections

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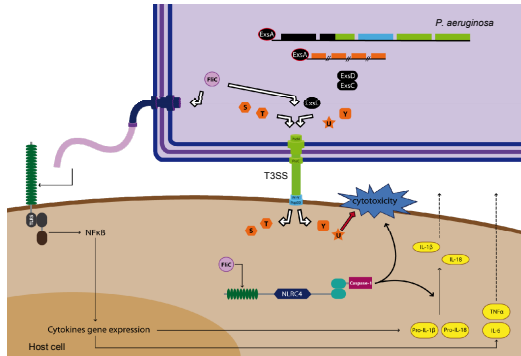
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INTRODUCTION

Expression of Type III secretion system (T3SS) in *P.aeruginosa* (*P.a*) is associated with poor clinical outcome and high morbidity in acute infections. T3SS allows bacteria to inject exotoxins (e.g. ExoU or ExoS) into the host cell cytoplasm, causing cytotoxicity and preventing P.a. internalization [1]. T3SS can also deliver flagellin or T3SS rod proteins into the mammalian cytosol, inducing caspase-1 proteolysis via NLR4 inflammasome activation. Active caspase-1 causes not only cytotoxicity but also the secretion of the IL-1 β and IL-18 inflammatory cytokines [2], thereby impairing P.a. clearance [3,4]. Flagellum-mediated motility has also been recently suggested to modulate inflammasome response [5].



Schema: Type III secretion system

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OBJECTIVES

Using strains differing in their expression of T3SS (both laboratory engineered mutants and clinical isolates):

- to compare bacterial motility
- to evaluate their capacity to induce inflammasome activation and cytotoxicity in THP-1 monocytes
- to examine how these parameters are correlated.

MATERIALS & METHODS

Strains: CHA (clinical isolate expressing T3SS) and derivatives thereof (CHA\ASTY [no toxin production]; CHA\ExsA [deletion of T3SS regulon] and CHA\popBD [deletion of genes encoding translocation apparatus]); PA103 (cytotoxic strain expressing ExoU); PAO1 (reference strain); 13 clinical strains isolated from patients suffering from acute infections

Cells: THP-1 monocytes

Cell viability: release of the cytosolic enzyme lactate dehydrogenase (LDH) in the culture medium after 5 h of incubation P.a strains (10⁶ bact./cell)

Inflammasome activation: IL-1 β secretion (ELISA)

Motility: swimming in 0.3% agar

T3SS transcription: Real-time PCR of genes encoding toxins or translocon

Statistical analysis: correlation coefficients determined using JMP version 10.0.2.

REFERENCES

- [1] Hauser AR *et al* Nat Rev Microbiol 2009;7:654-65
- [2] Miao EA and Warren SE, Journal of Clinical Immunology 2010; 30(4): 502-506
- [3] Cohen TS and Prince AS, Journal of Clinical Investigation 2013; 23(4):1630-7
- [4] Faure *et al.*, Am J Respir Crit Care Med. 2014;189(7):799-811
- [5] Patankar YR *et al.*, Infect Immun 2013;81:2043-52
- [6] Franck *et al.*, J Infect Dis. 2002;186(1):64-73

RESULTS

	strains	T3SS mRNA expression *				swimming (area [cm ²])	activation (IL-1 β secretion (pg/mL))	cytotoxicity (LDH release [%])
		exoS	exoU	popB/popD	pcrV			
reference strains	T3SS+ ExoU+	PA103	-	-	+	1.0 ± 0.1	78.1 ± 19.3	88.1 ± 18.7
	T3SS+ ExoU-	CHA\ASTY	-	-	+	18.0 ± 3.3	460.5 ± 43.3	54.7 ± 4.3
		CHA	-	-	+	23.3 ± 4.5	311.6 ± 34.8	50.0 ± 2.8
		PAO1	+	-	+	32.3 ± 8.9	255.0 ± 55.9	45.2 ± 5.1
	T3SS- ExoU-	CHA\ExsA	-	-	-	18.0 ± 2.2	61.4 ± 28.4	15.8 ± 4.6
clinical isolates	T3SS+ ExoU+	CHA\popBD	+	-	+	20.3 ± 3.1	50.4 ± 8.4	8.5 ± 9.6
		NSIH 4603	-	-	-	0.4 ± 0.1	81.9 ± 27.1	89.9 ± 27.7
	T3SS+ ExoU-	2554i6	-	-	+	2.2 ± 1.0	158.2 ± 5.4	81.2 ± 10.2
		9101/2*	-	-	+	2.5 ± 0.4	172.9 ± 1.8	83.2 ± 8.6
		141*	-	-	+	4.2 ± 2.1	171.9 ± 3.1	95.5 ± 1.8
	T3SS- ExoU-	142*	-	-	+	6.0 ± 2.5	184.4 ± 5.9	94.0 ± 5.3
		120*	-	-	+	2.2 ± 0.3	682.2 ± 68.0	62.8 ± 11.3
		9101/1*	-	-	+	2.5 ± 0.6	354.3 ± 15.3	42.5 ± 13.8
		150*	-	-	+	5.5 ± 0.1	286.7 ± 18.0	33.0 ± 9.8
		316*	-	-	+	12.6 ± 2.5	409.6 ± 82.0	42.7 ± 5.3
T3SS- ExoU+	316*	-	-	+	17.5 ± 6.2	355.4 ± 31.8	32.4 ± 7.4	
	328*	-	-	+	56.6 ± 6.3	299.2 ± 13.8	34.6 ± 2.4	
	NSIH 4603	-	-	+	54.3 ± 4.1	230.9 ± 22.7	32.4 ± 2.2	
T3SS- ExoU-	9101/3*	-	-	-	0.3 ± 0.1	43.3 ± 1.9	0.7 ± 2.8	

* (+): expression detected by RT-PCR; (-): no expression detected

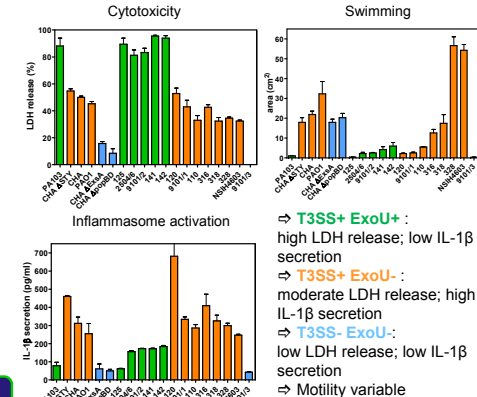
Origin of the strains: * lower respiratory tract; † blood; ‡ wound; § abdominal collection; ¶ urines; †† eyes; ††† upper respiratory tract

Main observations & Conclusions

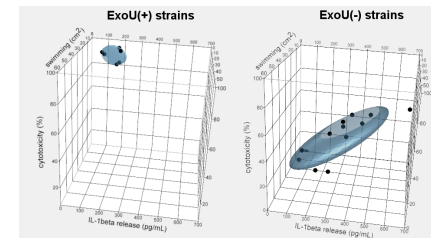
- **T3SS+ ExoU+ strains:** high cytotoxicity, causing cell death without inflammasome activation
- **T3SS+ ExoU- strains** (expressing ExoS or no toxins): moderate cytotoxicity, related to inflammasome activation, which induces IL-1 β secretion.
- **Motility:** low predictive value.

⇒ Studying these parameters in clinical strains may help predicting toxin expression. They may also be used for evaluating anti-virulence therapeutic strategies that target T3SS and impair toxin translocation [6] or prevent inflammasome activation (ICAAC 2013; B1055).

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⇒ **T3SS+ ExoU+ :**
high LDH release; low IL-1 β secretion
⇒ **T3SS+ ExoU- :**
moderate LDH release; high IL-1 β secretion
⇒ **T3SS- ExoU- :**
low LDH release; low IL-1 β secretion
⇒ Motility variable



parameter	correlation coefficient	
	ExoU(+) strains	ExoU(-) strains
IL-1 β release vs cytotoxicity	0.3	0.8
IL-1 β release vs swimming	0.8	-0.1
cytotoxicity vs swimming	0.7	0.1

Correlation between swimming capacity, induction of IL-1 β secretion (inflammasome activation) and reduction of LDH release (cytotoxicity) for the 19 strains shown in the Table. Normal control algalate and correlation coefficients were calculated using JMP version 10.0.2.