

# *Pseudomonas aeruginosa* PcrV and Psl Antigens are Conserved in Diverse Hospital Isolates Collected from an International Surveillance Study

David E. Tabor<sup>1</sup>, Li Yu<sup>2</sup>, Andrew C. Nyborg<sup>1</sup>, Bob McLaughlin<sup>3</sup>, Hoyin Mok<sup>1</sup>, Vaheh Oganessian<sup>4</sup>, Hasan Jafri<sup>5</sup>, Michael McCarthy<sup>6</sup>, C. Ken Stover<sup>7</sup>, Mark T. Esser<sup>6</sup>, Antonio DiGiandomenico<sup>7</sup>

Session: Microbial Pathogenesis  
Session Date: Saturday, October 29, 2016  
Session Time: 12:30 PM - 2:00 PM

<sup>1</sup>Translational Sciences, Infectious Disease-Vaccines, <sup>2</sup>Non-Clinical Biostatistics, <sup>3</sup>Infection IMed, <sup>4</sup>Antibody Discovery and Protein Engineering, <sup>5</sup>Clinical Development-Infectious Diseases-Vaccines, <sup>6</sup>IMED-Infectious Diseases-Vaccines, <sup>7</sup>Infectious Diseases-Vaccine Research

tabord@medimmune.com 2211

## Background

Ventilator-associated pneumonia due to *Pseudomonas aeruginosa* (PA) is associated with high rates of mortality, morbidity, increased intensive care unit length of stay and substantial economic burden. MEDI3902 is a bivalent, bispecific human IgG1k mAb that selectively binds to both the type 3 secretion (T3S) injectisome protein PcrV and Psl exopolysaccharide on the surface of PA and is being developed for the prevention of nosocomial pneumonia caused by PA. MEDI3902 binding to PcrV prevents T3S injectisome-mediated host cell cytotoxicity, while binding to Psl mediates opsonophagocytic killing of PA by host phagocytic cells and may also inhibit attachment of the bacterium to host epithelial cells

## Methods

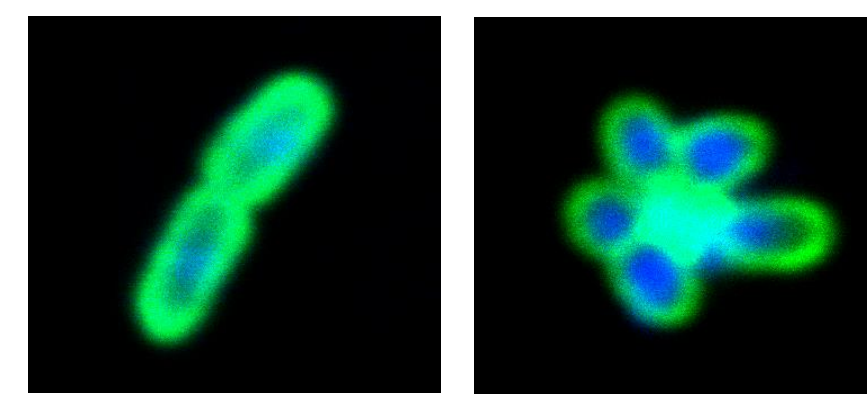
To better understand the prevalence of the *pcrV* gene and *psl* operon (expression of Psl is mediated via a 20 KB operon) in *P. aeruginosa* clinical isolates, we performed whole genome sequencing on 913 isolates collected from diverse patient populations and geographical locations in 43 countries from 2004-2014. Whole genome sequence data was analyzed for the presence of the *pcrV* gene and *psl* operon (*pslA* to *pslO*). The predicted amino acid sequence changes in the PcrV protein were compared to PA reference strain PAO1. Psl expression from select isolates lacking one or more genes from the *psl* operon was evaluated by an anti-Psl ELISA assay.

## Results

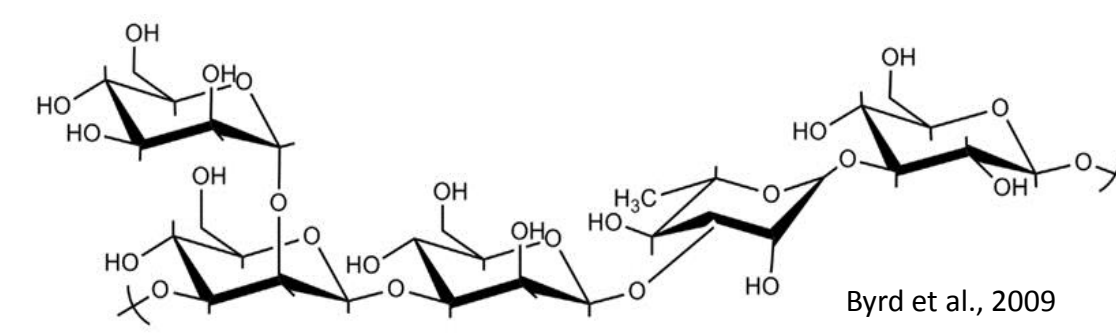
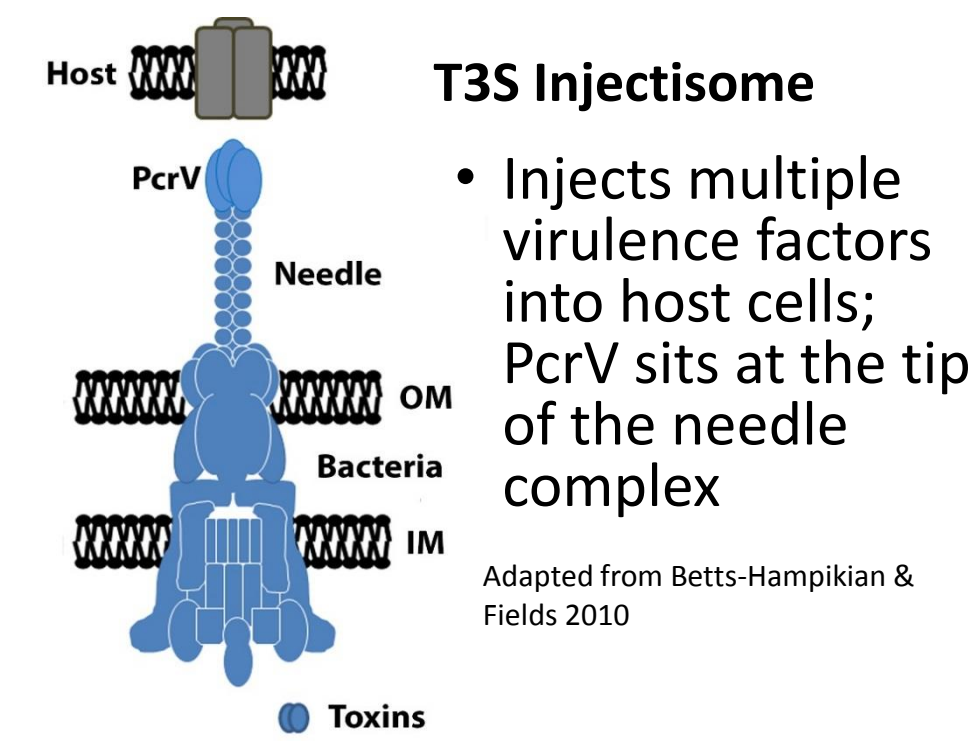
Analysis showed that the *pcrV* and *psl* genes were present in 99% and 96% of the isolates, respectively. PcrV amino acid sequence variation revealed 46 clusters/genotypes. A naturally occurring set of isolates that are null in one or more *psl* genes was uncovered. In addition, a set of PA7-like isolates with wide temporal and global distribution were identified.

## Introduction

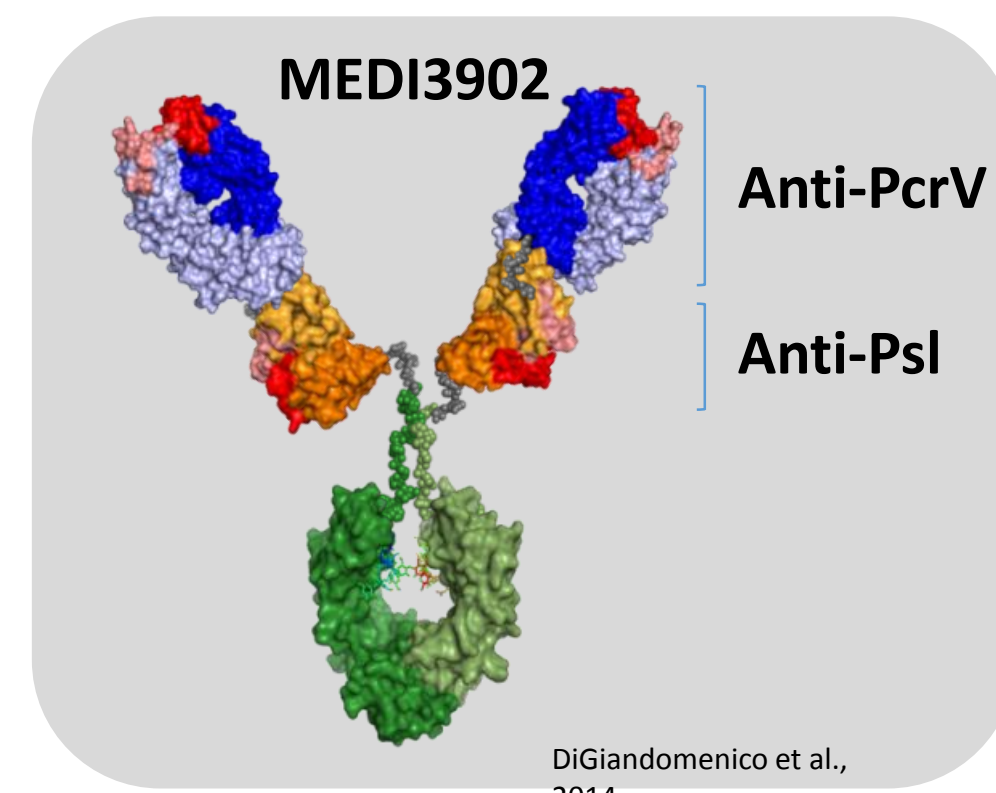
- We recently described mAbs targeting the *P. aeruginosa* T3SS protein PcrV (Warrener et al., 2014) and Psl EPS (DiGiandomenico et al., 2012), which are components of bispecific clinical candidate MEDI3902 (DiGiandomenico et al., 2014).
- Psl EPS is an abundant, serotype independent surface sugar polymer that is important in tissue colonization, biofilm formation (persistence) and immune evasion.
- PcrV forms the tip of the T3SS which can inject exotoxins into host target cells.



Confocal microscopy images of *P. aeruginosa* stained with an Alexa Fluor 488 labelled anti-Psl mAb

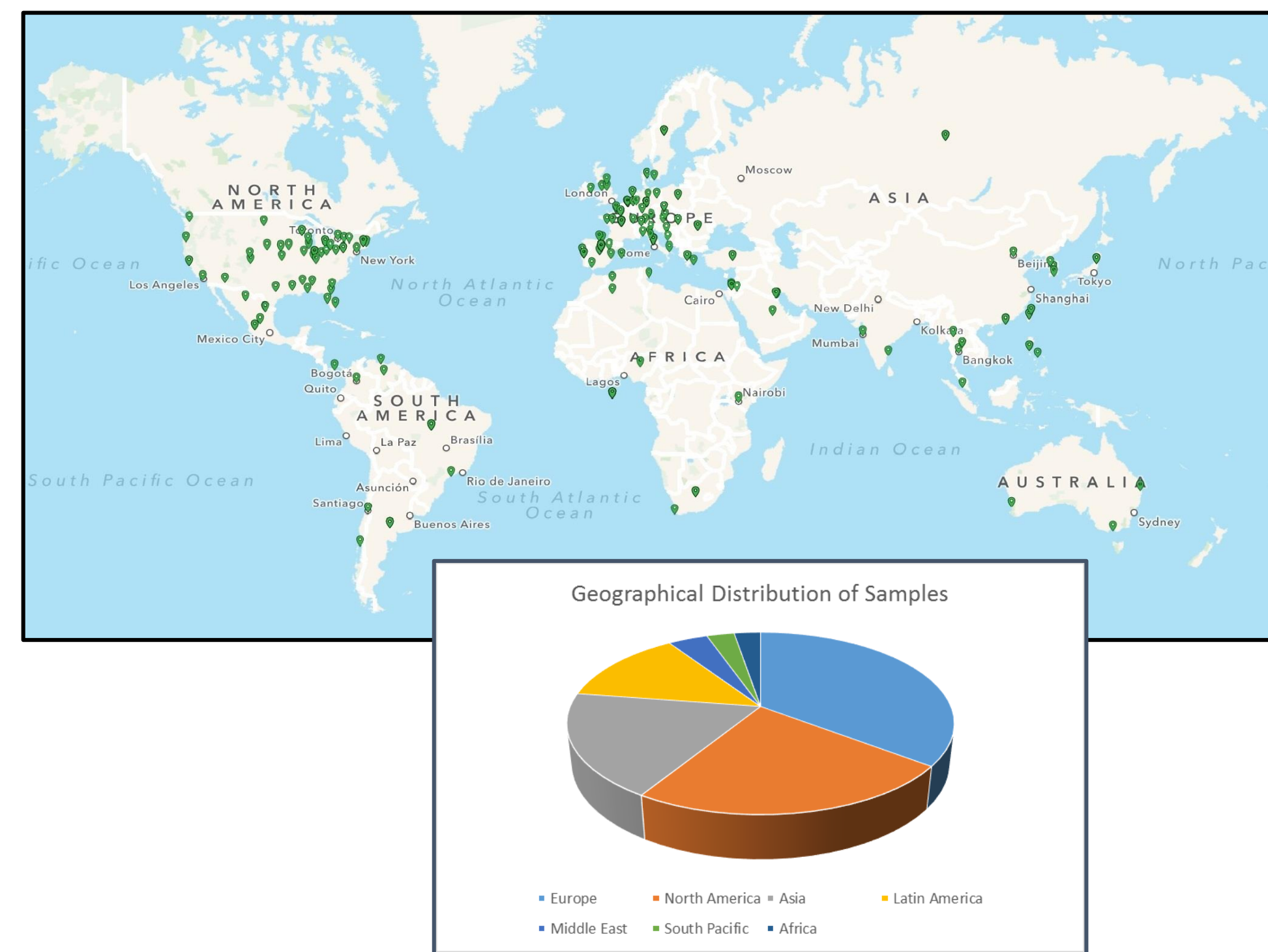


Psl EPS individual subunit



**Figure 1:** *P. aeruginosa* Psl exopolysaccharide and the T3SS injectisome

- MEDI3902 prevents *P. aeruginosa* cytotoxicity (anti-PcrV) and promotes Psl mediated opsonophagocytic killing activity (anti-Psl)



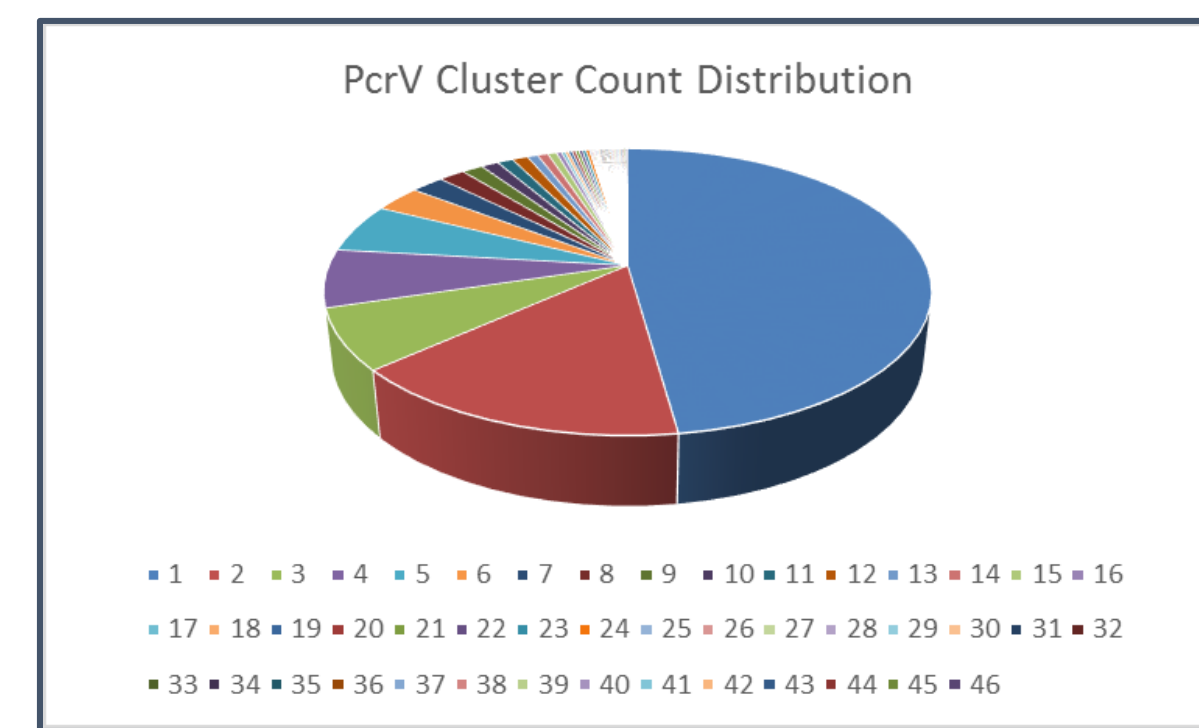
**Figure 2:** Map of *P. aeruginosa* isolates collection sites and plot of geographical distribution.

Reference: NC\_002516.pcrV\_cds

Cluster Size Percentage S G 9 10 21 27 30 33 53 68 69 98 106 112 118 119 123 143 146 154 172 181 182 184 188 199 200 205 220 226 237 256 275 285

Cluster	Size	Percentage	S	G	9	10	21	27	30	33	53	68	69	98	106	112	118	119	123	143	146	154	172	181	182	184	188	199	200	205	220	226	237	256	275	285
1	1	1.0%	N	L	A	R	S	A	E	L	A	S	A	P	H	D	K	D	T	K	S	A	V	V	G	P	D	D	E	S	P	P	V	N	A	S

**Table 1:** The sequence of the *pcrV* gene was determined by whole genome sequencing. The consensus DNA sequences were translated to PcrV protein sequences, and amino acid variants were noted based on comparison to the published PAO1 sequence.



**Figure 3:** PcrV Cluster Count Distribution.

Sample	Region	Country	Year	ST	MIST Alleles					T3SS Genes			T2SS Genes																								
					pcrV	exoS	exoT	exoU	exoY	PA7_1410_gspI*	PA7_1412_ompP*	PA7_1419_CbpD*	PA7_1420_regulator*	PA7_1410_gspI*	PA7_1412_ompP*	PA7_1419_CbpD*	PA7_1420_regulator*	PA7_1410_gspI*	PA7_1412_ompP*	PA7_1419_CbpD*	PA7_1420_regulator*																
1	Asia	India	2008	2212*	87	70	79	80	53	487	129*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

**Figure 4:** PA7-like isolates lacking T3SS elements but contain a T2SS as described by Cadoret et al. Gene presence is indicated by gene name and absence is indicated by a '-' in the table.

USA-NEG  
USA-POS

**Table 2:** The presence of the *psl* operon was determined by analysis of whole genome sequencing data. Gene presence is indicated by gene name and absence is indicated by a '-' in the table. Psl expression was determined by western blot.

## Conclusions

- To our knowledge, this is the first international study to examine *pcrV* and *psl* gene conservation and diversity in hospital-associated isolates.
- Analysis showed that the *pcrV* and *psl* genes were present in 99% and 96% of the isolates, respectively.
- A naturally occurring set of isolates that are null in one or more *psl* genes was uncovered.
- 11 PA7-like isolates were identified with wide temporal and global distribution.
- PcrV and Psl are good targets for prophylactic mAb and vaccine development.

## References:

- Byrd et al., 2009 Mol. Microbiol. **73**:22
- DiGiandomenico et al., 2012 J. Exp. Med. **209**:1273
- Warrener et al., 2014 Antimicrob. Agents. Chemother. **58**:4384-91
- DiGiandomenico et al., 2014 Sci. Trans. Med. **262**:ra1155
- Roy et al. 2010 PLoS ONE **5**:1-10.
- Frédéric Cadoret et al. 2014 J. Bacteriol. **196**:2376-2386

