Structural and functional exploration on Pdta, a 430kDa protein of Pseudomonas aeruginosa

Résumé

Pseudomonas aeruginosa (Pa) has several secretion systems that allow the exportation of proteins with diverse properties, including the two-partner secretion system (TPS). Pa has at least five TPSs: LepA (protease), CdiA (contact-dependent growth inhibition), CdrA (adhesin), Exolysin ExlA (pore-forming toxin) and PdtA, a filamentous hemagglutinin (FHA)-like adhesin(1). PdtA belongs to the HMW family of adhesins (2), such as HMW1 from Haemophilus influenzae, known for its immunogenic properties.

The pdtA gene is conserved among different strains of Pa and anti-PdtA antibodies have been detected in patients infected with Pa 3. Faure et al (2) showed that PdtA forms a TPS with PdtB, and that its production is activated upon depletion of organic phosphate in the medium. However, its exact role, structure and involvement in virulence (2,3) remain unknown.

We examined PdtA synthesis with specific polyclonal antibodies in a cohort of clinical strains. While reference strains (PAO1, PA7 and PA14) do not synthesize the protein, PdtA is detected in several clinical strains, independently of their origin or phylogenic affiliation. We imaged by confocal microscopy PdtA on the surface of three clinical strains. This result suggests that there are about five PdtA structures on the surface of bacteria.

We showed that PdtA has a role in bacterial auto-aggregation by comparing a wild-type clinical strain and the mutant strains, $\Delta pdtB$ and $\Delta pdtA$. We also examined by ELISA several sera from patients with cystic fibrosis who contracted Pa infection and found that the majority of sera contained anti-PdtA antibodies.

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Mots-Clés: interaction hôte pathogène, virulence