

Genomic Evolution Of The Mdr Serotype O12 *Pseudomonas Aeruginosa* Clone - DTU Orbit (08/11/2017)

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Introduction: Since the 1980's the serotype O12 of *Pseudomonas aeruginosa* has emerged as the predominant serotype in clinical settings and in epidemic outbreaks. These serotype O12 isolates exhibit high levels of resistance to various classes of antibiotics. **Methods:** In this study, we explore how the *P. aeruginosa* LPS biosynthesis gene clusters evolve in the population by investigating the phylogenetic relationship among 83 *P. aeruginosa* strains and their serotype. In the process we develop a program for in silico serotyping of *P. aeruginosa* isolates, the *P. aeruginosa* serotyper (PAst). **Results:** While most serotypes were closely linked to the core genome phylogeny we observed horizontal exchange of LPS genes among distinct *P. aeruginosa* strains. Specifically, we identified a 'serotype island' containing the *P. aeruginosa* O12 LPS gene cluster and an antibiotic resistance determinant (*gyrAC*²⁴⁸¹) that has been transferred among *P. aeruginosa* strains. Acquisition and recombination of the 'serotype island' resulted in expression of the O12 serotype in the recipient strains. **Conclusions:** This observation demonstrate a strong selective advantage for this type of genomic recombination, and suggest that serotype switching in combination with an antibiotic resistance determinant contributed to the dissemination of the O12 serotype in the clinic. This selective advantage coincides with the introduction of fluoroquinolones in the clinic. With the PAst program isolates can be serotyped using WGS data, and dangerous clones like O12 can be identified quickly.

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