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Title: LSC 2013 abstract - Isolation and characterization of a novel pseudomonas species from an individual with chronic respiratory disease

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Body: Pseudomonads have strikingly limited nutritional requirements, are found in showerheads and cigarette smoke and display remarkable metabolic adaptability. *P. aeruginosa* is the most common pseudomonad isolated from human lungs; however, in diseased lungs other species can sometimes be isolated. We are studying one such isolate, whose 16S gene homology originally identified as *P. synxantha*. However, additional genetic analysis using *pfif* locus PCR indicates that the isolate is *P. fluorescens*. Growth curve, metabolic profile and phenotypic analysis shows the isolate differs from other *Pseudomonas* strains. In particular, growth at 37°C suggests the isolate is neither *P. synxantha* nor *P. fluorescens*, both which can't grow above 27°C. While the isolate was cleared from conventional C57BL/6 mice lungs, it persisted at low levels in the lungs of germ-free mice, while *P. aeruginosa* was cleared. Preliminary mouse studies reveals the isolate reaches higher CFUs in inflamed lungs, while becoming difficult to isolate by standard culture methods. We have begun full genome sequencing of the isolate on the PacBio and Illumina next-generation sequencing platforms. Initial assembly against all known published pseudomonad genome sequences showed that no sequenced pseudomonad has high enough genetic similarity to serve as a template, requiring de novo sequence assembly. Additional Illumina data will complete the genome and generate a taxonomic assignment. The pathogenic potential of this organism is intriguing since it appears to be suited for growth in diseased respiratory tracts of mice and humans.