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The role of *Pseudomonas aeruginosa* ‚small colony variants' in the pathogenesis of chronic cystic fibrosis lung infection

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The opportunistic pathogen *Pseudomonas aeruginosa* is the key etiological agent of chronic lung infection in cystic fibrosis (CF) patients. Apart from the best studied mucoid *P. aeruginosa* phenotype and other colony morphotypes, it has been recognized for many years that dwarf colonies can be isolated from the chronically infected respiratory tract of CF patients. A study from our laboratory showed that dwarf or so called small colony variants (SCVs) of *P. aeruginosa* could be correlated with parameters revealing poor lung function and the use of inhalative antibiotics. However, their role in the pathogenesis of chronic CF lung infection remains to be determined. This project aims to elucidate the role of *P. aeruginosa* ‚small colony variants'(SCVs) in the pathogenesis of chronic *P. aeruginosa* lung infection by i.) identifying differences in gene expression between SCVs, corresponding clonal wild types and *in vitro* generated revertants using a comparative transcriptome and proteome analysis to get information on possible mechanisms of SCVs to adapt to nutrient deprivation or to escape host defense and ii.) by characterizing SCV-host interactions using *in vitro* cell culture models and iii.) by using *in vivo* infection models of the murine respiratory tract and of the nematode *Caenorhabditis elegans*.