Titel: *Pseudomonas aeruginosa* virulence analyzed in a *Dictyostelium discoideum* model of infection

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Zusammenfassung: *Pseudomonas aeruginosa* is a major opportunistic human pathogen which produces a large variety of secreted and cell-associated virulence factors. Since *P. aeruginosa* infections are difficult to treat due to the emergence of highly antibiotic resistant strains, alternative drug targets including virulence factors are currently being under investigation. Recently, it has been shown that *P. aeruginosa* uses similar virulence factors when infecting mammalian systems or non-mammalian hosts like the social amoeba *Dictyostelium discoideum*, the nematode *Caenorhabditis elegans* or the fruit fly *Drosophila melanogaster* (1,2). In this study, we used a comprehensive *P. aeruginosa* PA14 transposon mutant library to screen for mutants with reduced virulence towards *D. discoideum*. A total of 198 *P. aeruginosa* PA14 transposon mutants were identified to have decreased virulence in this host model system. In addition to mutants with insertions in the type III secretion system (TTSS), we identified genes involved in type IV pili biosynthesis and function, PQS production, tryptophan synthesis, transport, central and amino acid metabolism and gene regulation including quorum sensing, global regulators and two-component regulatory systems. FACS analyses using a gfp-*exoT* reporter construct revealed reduced TTSS activity in several studied mutants including type IV pili, PQS biosynthesis and *cbrAB*, a two-component regulatory system involved in nitrogen and carbon metabolism. Microarray analyses were performed to gain a deeper insight into the interaction of *P. aeruginosa* with *D. discoideum*.