

Project 7 (P7): Lectins and hydrolytic enzymes as virulence factors of *Pseudomonas aeruginosa*

Principal Investigators: Univ.-Prof. Dr. rer. nat. Karl-Erich Jaeger, Dr. rer. nat. Filip Kovacic

Institut für Molekulare Enzymtechnologie
Heinrich-Heine-Universität Düsseldorf
Forschungszentrum Jülich
Stettericher Forst, Geb. 15.8
52426 Jülich

Telefon: +49 2461-61-3716

Telefax: +49 2461-61-2490

E-Mail: karl-erich.jaeger@fz-juelich.de; f.kovacic@fz-juelich.de

Homepage: www.iet.uni-duesseldorf.de/en.html

Pseudomonas aeruginosa is a Gram-negative opportunistic pathogen infecting immunocompromised humans with high mortality rates. Acute infections are associated with the production of many virulence factors including exotoxins, proteases and phospholipases whereas chronic infections are associated with the formation of biofilms resulting in high resistance against antibiotics. We aim at understanding the role of phospholipases and lectins for bacterial pathogenicity as well as identifying novel targets for treatment of *P. aeruginosa* infections. Hydrolytic enzymes including lipases and phospholipases are known to contribute to damage of host cell membranes and modulation of lipid signaling in eukaryotic cells. Recently, fatty acid derivatives called diffusible signal factors (DSF) were related to virulence and biofilm formation of several bacterial pathogens, however, DSF biosynthesis and signaling pathways are largely unknown. We have already identified PlbF, a novel virulence factor of *P. aeruginosa* with phospholipase A activity which releases medium chain fatty acids from membrane phospholipids *in vitro* and *in vivo*. The lectins LecA and LecB contribute to bacterial pathogenicity by mediating bacterial attachment to human tissue during the initial biofilm formation through binding to oligosaccharides of human and mammalian glycoproteins. Hence, these proteins are potential targets to prevent *Pseudomonas* infections.

In this project, we will clone *P. aeruginosa* genes of unknown function in a high-throughput approach trying to identify, purify and characterize additional and so far unknown hydrolytic enzymes and carbohydrate-binding proteins. Furthermore, we will investigate the role of selected candidate proteins for pathogenicity of *P. aeruginosa*.