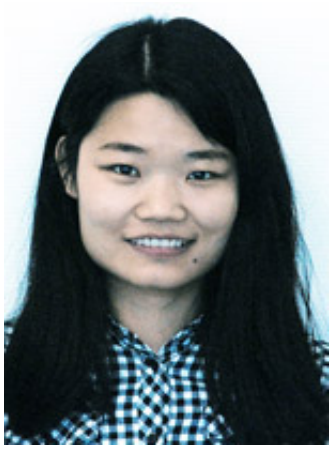

Shanshan Du

Immune evasion of *Streptococcus pneumoniae* in patients with kidney disease

The Department of Infection Biology at the Leibniz Institute for Natural Product Research and Infection Biology is interested to understand the immune evasions strategies of human pathogenic microbes, in particular how microbial pathogens control the innate immune system and how they modulate inflammation. Such evasion strategies are characterized by multiplicity and redundancy. In this project, we want to understand the immune evasion strategies of *Streptococcus pneumoniae*, a human respiratory pathogen that causes invasive and mucosal diseases and is also associated with hemolytic uremic syndrome (HUS), a severe human kidney disease.

In order to define the immune evasion strategies of this pathogenic Gram positive bacterium in detail, we characterize the pneumococcal moonlighting proteins PspC (pneumococcal surface protein C) and Tuf (translation elongation factor Tu). We are interested in identifying the repertoire of host proteins that are bound by the two pneumococcal proteins, in identifying new ligands and in defining how host regulators attached to the bacterial surface assist the bacterium in immune evasion. By characterizing clinical pneumococcal isolates derived from infant HUS patients we aim to define how the microbial pathogens contribute to disease pathogenesis and to endothelial damage in the microvasculature. We postulate that these clinical isolates express unique PspC and Tuf variants and therefore plan to clone the corresponding proteins and analyze how such new variants control virulence and bacterial immune evasion and how they

lead to disease pathology and ultimately to kidney damage.

Publications

Du S, Vilhena C, King S, Sahagún-Ruiz A, Hammerschmidt S, Skerka C, Zipfel PF (2021) Molecular analyses identifies new domains and structural differences among Streptococcus pneumoniae immune evasion proteins PspC and Hic. *Sci Rep* 11(1), 1701. Details PubMed

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