Summary of the Thesis

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„Taxonomy, epidemiology, genotyping and immunopathology of clinical *Staphylococcus*-isolates“

Staphylococci, including *S. aureus*, generally are opportunistic pathogens or commensals on host skin. They are human pathogens, responsible for causing infections ranging from relatively mild involvement of the skin and soft tissue to life-threatening sepsis, necrotizing pneumonia and toxic shock syndrome. The emergence of *S. aureus* strains resistant to methicillin (MRSA) has become a major concern, especially in the hospital environment, and a precise knowledge of this strains is important. Also, the accurate species identification of *S. aureus* as well as that of the other staphylococcal species in microbial communities is highly desirable to permit a more precise determination of the host-pathogen relationships. Colonization and infection with staphylococci is also a serious issue in skin disorders especially atopic dermatitis (AD). Therefore the innate immune defence of the skin by producing cytokines, cationic antimicrobial peptides, e.g. β-defensins (hBD) and the cathelicidin LL-37, was also observed.

A brief summary of the major findings are present below:

I. Methicillin-sensitive (MSSA) and Methicillin-resistant (MRSA) *S. aureus* strains are heterogen, concerning their antibiotic resistance patterns, toxin profiles and clonal relationships, at the university hospital Magdeburg. Interestingly, MSSA strains positive for Toxic-Shock-Toxin-1 were predominantly isolated from departments at high risk for MRSA. From this results we conclude that the pool of circulating MSSA strains is an important parameter with regard to the epidemiology of hospital- and community-acquired MRSA clones and their potential virulence.

II. Partial sequences of the glyceraldehyde-3-phosphate dehydrogenase-encoding (*gap*) gene of validly described *Staphylococcus* species were sequenced. By using the respective sequence information a terminal-restriction fragment length polymorphism (T-RFLP) analysis was established. Applying T-RFLP with double-fluorescently labelled fragments of the *gap*-gene and three independent restriction digests, we were able to identify Staphylococci rapid and accurate.

III. Comparative studies using various methods for identification of clinical *Staphylococcus* species revealed, that when unambiguous identification of distinct *Staphylococcus* species is necessary, molecular identification, e.g., gap-based T-RFLP analysis, is still superior to phenotypic automated identification systems.

IV. Staphylococci from AD patients showed various pathogenicity profiles and triggered the production of cytokines and antimicrobial peptides. Therefore our results mark them as potential pathogens in skin infections, especially atopic dermatitis.