Differentiation and characterization of Trichophyton verrucosum field isolates in comparison to vaccine strains

Theresa Bartosch¹, Tilo Heydel¹, Silke Uhrlaß², Pietro Nenoff², Hendrik Müller³, Christoph Georg Baums¹, Wieland Schrödl¹ ¹ Institute for Bacteriology and Mycology, Centre for Infectious Diseases, Faculty of Veterinary Medicine, University Leipzig, Leipzig, Germany ² Laboratory for Medical Microbiology, Mölbis, Germany

³ Clinic for Ruminants and Swine, Faculty of Veterinary Medicine, University Leipzig, Leipzig, Germany

Introduction

Bovine trichophytosis is mainly caused by the zoophilic dermatophyte Trichophyton (T.) verrucosum and is a very wide spread infectious disease in cattle throughout the world. This keratinolytic fungus invades tissue like the skin, hair, nails and affects especially the main host cattle, but also humans and less common other animals. In cattle the disease is associated with skin lesions, impairment of juvenile development and reduction in milk production leading to substantial economic losses. Additionally it causes highly inflammatory cutaneous infections in humans often resulting in dermal scars. The correct identification of the isolates is crucial to detect the epidemiological origin and to initiate appropriate preventative measures.

UNIVERSITÄT LEIPZIG





Aim

T. verrucosum strains isolated from cattle and humans as well as vaccine strains were differentiated and characterized by matrix-assisted laser desorption/ ionisation time-of-flight mass spectrometry (MALDI-TOF MS) to better understand the epidemiology and to search for distinct features of the vaccine strains.

Material and methods

In this study, forty-one field isolates from twelve different cattle farms, two live vaccine strains and ten isolates from humans were identified as T. *verrucosum* by MALDI-TOF MS and sequencing of PCR amplification products. The mass-spectra of these strains were analyzed to evaluate different peaks in the spectra (A) for the differentiation of the *T. verrucosum* field strains. Furthermore, a dendrogramm of keratinophilic fungi (B) was generated to identify clusters of T. verrucosum and similarities to other dermatophytes.







Results (A)



Mass spectrometric profiles of *T. verrucosum* strains and *A. benhamiae isolates*. The spectra of the *T. verrucosum* isolates were very similar. For comparison distinct spectra of A. benhamiae, a closely related dermatophyte, are depicted. In this picture the characteristic peak group of *T. verrucosum* is marked which was missing in the spectra of other dermatophytes. This peak group appears in most of the field strains from cattle and humans, but not in the spectra of the vaccine strains.

Isolates of *T. verrucosum* were clearly distinguishable from other dermatophytes and keratinophilic fungi. The dermatophyte A. benhamiae was arranged closest to T. verrucosum suggesting a high similarity between the two species. Two clusters (blue and red) of *T. verrucosum* isolates were formed. Most field isolates of this study belonged to the cluster depicted in red.

Summary

MALDI-TOF MS differentiation of T. verrucosum from other dermatophytes was in accordance with the results obtained by PCR sequencing (results not shown). The spectra of *T. verrucosum* were most similar to the spectra of *Arthroderma benhamiae*, an emerging zoophilic dermatophyte. Major differences between the spectra of field strains, human isolates and the live vaccine strains were not recorded. Two distinct clusters of *T. verrucosum* isolates were found by MALDI TOF MS analysis. A characteristic peak group of many *T. verrucosum* field isolates was detected which is missing in the spectra of other dermatophytes and the vaccine strains. In conclusion, mass spectrometry allows advanced differentiation of dermatophytes including the important zoonotic agents T. verrucosum and A. benhamiae.