1. Introduction

Since tuberculosis had been described by Koch in 1882, mycobacteriosis was most often determined as the *M. tuberculosis*-associated disease including the other members of *M. tuberculosis* complex (*M. bovis, M. africanum, M. microti*). Based on causative agents, diseases caused by mycobacteria were devided in two groups: tuberculosis and mycobacterioses, which were caused by atypical mycobacteria including the most important atypical mycobacteria, *Mycobacterium avium-intracellulare* complex (MAIC).

MAIC refers to a heterogeneous collection of acid-fast, slowly growing organisms. These include strains of *Mycobacterium avium* ssp. *avium, M. intracellulare* and the newly reserved designation for human/porcine strains*, M. avium* ssp. *hominissuis* (Mijs et al., 2002). The causative agent of Johne's disease, *Mycobacterium avium* ssp. *paratuberculosis,* is not always considered as a member of MAIC, although it is very closely related to the members of this group. The MAIC organisms can be isolated from numerous environmental sources, such as water supplies, soil, dust, as well as a wide range of animal species (Pozniak et al., 1996).

MAIC organisms have long been recognized as pathogenic agents in birds but they did not play a major role in the aspect of public health. Since the emergence of AIDS in 1990s, MAIC became the most significant opportunistic pathogen for AIDS patients, which is estimated to occur in up to 60% (Pozniak et al., 1996). MAIC infection is responsible for disseminated diseases, pulmonary diseases and localized lymphadenitis in AIDS patients.

On the other hand, MAIC may cause pulmonary, soft tissue infections and cervical lymphadinitis in immunocompetent individuals (Horsburgh, 1997).

Since the epidemiology of MAIC infection is not completely understood, numerous of laboratory diagnostic methods have been applied to trace back the routes of infection with different degree of success. The DNA-based methods, which typically use agarose gel electrophoresis of restriction enzyme-digested DNA, are now widely used to determine the degree of diversity among the strains.

Pulsed-field gel electrophoresis (PFGE), in which the entire genome can be presented as the distinct DNA pattern (Maslow et al., 1993), was described as the powerful method in epidemiology for the determination of clonal relationship of numerous bacterial species including mycobacteria. The analysis of restriction fragment length polymorphism (RFLP) based on insertion sequence (IS) 1245 has also been proposed as a suitable technique to show similarity among mycobacterial isolates.

The aim of this study was to characterise the genetic diversity of MAIC isolates collected from 3 conventional pig farms located in three different regions of Germany (south-west, north-west and middle), one “ecological“ pig farm in middle region of Germany and also MAIC isolates from different wild animal isolates in Thuringia (middle), Germany.