



Title	Genetic characterization of <i>Mycobacterium orygis</i> isolates from animals of South Asia [an abstract of dissertation and a summary of dissertation review]
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学位論文内容の要旨
Abstract of the dissertation

博士の専攻分野の名称：博士（獣医学）

氏名：ジーワン タパ
Name Jeewan Thapa

学位論文題名
The title of the doctoral dissertation

Genetic characterization of *Mycobacterium orygis* isolates from animals of South Asia

(南アジアの動物から分離された *Mycobacterium orygis* の遺伝的特徴)

Mycobacterium orygis is a new member of *M. tuberculosis* complex (MTBC) and has been reported to cause tuberculosis (TB) in different animals and humans. This bacterium was initially isolated from antelopes (oryx and waterbuck) in early 1990s and reported as *M. bovis* with unusual genetic features. Later, its name was proposed to be *M. orygis* to convey the fact of its first characterization from oryx or considered as an antelope clade to convey the group of animals from which it was most frequently isolated. Subsequently, this bacterium has been isolated from different animals and humans challenging its previous concepts of host range. Most of the reported isolates have geographical links to South Asian subcontinent.

In my PhD study, I have analyzed 3 *M. orygis* isolates from different wild animals in Nepal and 20 *M. orygis* isolates from dairy cattle and captured monkeys in Bangladesh. All these isolates have been genetically characterized by standard tuberculosis (TB) genotyping tools like spoligotyping, multi locus variable number of tandem repeat (MLVA) analysis, region of difference (RD) analysis and multi locus sequence typing (MLST). And

I have compared genetic features of the isolates with others in previous reports to understand their genetic characteristics and distribution. This thesis consists of 2 chapters where I describe my TB suspected sample collection strategies, microbiological processing of samples and genotyping of TB isolates.

In chapter I, I have described the molecular characterization of *M. orygis* isolates from wild animals of Nepal. I have identified that *M. orygis* associated TB was the cause of death of a spotted deer, a blue bull and a free-ranging rhinoceros. Although all the 3 *M. orygis* isolates had identical spoligotype pattern of SIT 587, I found from additional MLVA analysis that spotted deer and blue bull isolates were identical whereas the rhinoceros isolate was a different type. I have hypothesized that different strains of *M. orygis* isolates may be circulating in CNP and this situation could be a threat to many endangered animals like rhinoceros, tiger and elephants in the park.

In chapter II, I also identified *M. orygis* associated TB was the cause of deaths in 18 dairy cattle and 2 captured rhesus monkeys. As was in the case of chapter I, all the 20 *M. orygis* isolates had identical spoligotyping pattern SIT 587 but had 3 different MLVA patterns. The diversity observed among isolates may suggest the bacteria have been established in that area for a long period.

Overall, I found that there were 5 MLVA strain types of *M. orygis* circulating in different animals in Nepal and Bangladesh. This finding along with other reports of different strain type of *M. orygis* from animals and people of South Asia indicate wide genetic diversity or potentially endemic distribution of *M. orygis* in South Asia region.