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研究課題名(和文) Pathogenomics and eco-epidemiology of *Mycobacterium orygis*, an emerging zoonotic tuberculosis organism研究課題名(英文) Pathogenomics and eco-epidemiology of *Mycobacterium orygis*, an emerging zoonotic tuberculosis organism

研究代表者

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交付決定額(研究期間全体)：(直接経費) 3,600,000円

研究成果の概要(和文)：我々が行った *Mycobacterium orygis* の比較全ゲノム解析により、この菌が南アジアの風土病起因菌として分布しており、南アジア近隣地域では *Mycobacterium orygis* 関連結核の脅威があることが明らかになった。ネパールのサイから分離された *Mycobacterium orygis* のゲノム解析により、*Mycobacterium orygis* に特有の変異があることが判明した。そこで、簡易診断法として RD301 領域をターゲットとした *Mycobacterium orygis* 特異的 PCR 法を開発した。更にはネパールにおける人獣共通感染症結核の生態疫学を理解するために調査を実施した。

研究成果の学術的意義や社会的意義

The research identified that the *Mycobacterium orygis* is an important causative agent of zoonotic tuberculosis (TB) in south Asia region, and there is a threat from *Mycobacterium orygis*-associated TB in south Asia and beyond.

研究成果の概要(英文)：Our comparative whole genome analysis of *Mycobacterium orygis* revealed that it is endemically distributed in South Asia, and there is a threat from *Mycobacterium orygis*-associated tuberculosis in South Asia and beyond. We did genome analysis of *Mycobacterium orygis* that was isolated from rhinoceros in Nepal, and the genome analysis showed that it had *Mycobacterium orygis* specific mutation in anti-SigK factor, which is responsible for higher production of mpt70 and mpt83. We found that *Mycobacterium orygis* isolates have specific polymorphisms in gyrB, mmpL6, PPE55, Rv2042c, TbD1. We developed a PCR diagnostic method targeting RD301 region that can specifically detect *Mycobacterium orygis* by differentiating it from other members of *Mycobacterium tuberculosis* complex. We performed molecular epidemiological surveillance to understand tuberculosis eco-epidemiology across the human/livestock/wildlife interface in Nepal.

研究分野：Veterinary Medicine

キーワード：Tuberculosis *Mycobacterium orygis* Pathogenomics Molecular epidemiology Nepal

1 . 研究開始当初の背景

Mycobacterium orygis, initially referred to as oryx bacillus or the antelope clade of *M. tuberculosis complex* (MTBC), was recognized as a sub-species of *M. tuberculosis complex* that can cause tuberculosis (TB) in animals and humans in 2012. Among the few known isolates at that time, most of them had an epidemiological link to South Asia and South-East Asia. From our previous studies, we discovered that *M. orygis* was the cause of death of an endangered rhinoceros in Chitwan National Park (CNP). We also found that different strains of *M. orygis* were circulating in CNP, and speculated that an unknown maintenance host of *M. orygis* exists in wildlife or livestock in and around CNP. Similarly, from our work in Bangladesh, we found that diverse genetic variants of *M. orygis* were circulating in livestock and captured monkeys. Thus, based on our studies and available information regarding *M. orygis*, we have hypothesized that *M. orygis* is endemically distributed in South Asia. Our hypothesis on the epidemiological link of *M. orygis* to South Asia has now been supported by many recent studies as they reported several cases of *M. orygis* in people and animal of South Asian countries and in people of South Asian origin in the USA, UK, and Europe.

TB is caused by different members of MTBC, for example, human TB is mostly caused by *M. tuberculosis* and the common cause of animal TB is *M. bovis*. Although these MTBCs bacteria are genetically 99.9% similar, they have specific host pathogenicity. Even within *M. tuberculosis*, different strains have strong geographic links for disease and drug resistance. *M. orygis* is considered animals adapted MTBCs but still has caused many cases of human TB with South Asian epidemiological links. The reasons for this unique phenomenon are unclear. In this perspective, whole genomic analysis, and eco-epidemiological studies on *M. orygis* will provide a unique opportunity to further understand how *M. orygis* has evolved and caused TB.

2 . 研究の目的

The main purpose of this study is to better understand the pathogenomics and eco-epidemiology of *M. orygis* as a model to understand its geographic distribution and its unique genetic features. We also aim to understand molecular epidemiology of *M. orygis* and zoonotic tuberculosis across the human/wildlife/livestock interface in Nepal to understand its zoonosis.

3 . 研究の方法

We performed the next generation sequencing of *M. orygis* isolate using Illumina MiSeq technology. Library preparation was performed using Nextera XT DNA library Preparation kit. Publicly available *M. orygis* and representative sequences of other members of MTBCs from SRA database were downloaded and analyzed using different bioinformatics softwares. Phylogeographic analysis was performed using the single nucleotide polymorphisms among genomes to understand the molecular epidemiology of *M. orygis*. We performed molecular epidemiological surveillance across the human/wildlife/livestock interface in Nepal. The obtained *M. tuberculosis complex* strains were analyzed by PCR, loop-mediated isothermal amplification (LAMP), and genotyping methods.

4 . 研究成果

1. Comparative whole genome analysis of *Mycobacterium orygis*

Single nucleotide polymorphism (SNP) based phylogenetic analysis of *M. orygis* isolates confirmed that the *M. orygis* strains are epidemiologically related to South Asia (Figure 1). A pair-wise SNP distance matrix analysis showed that there was 0 - 460 SNP difference among the globally available *M. orygis* isolates. When this SNP difference is compared with *M. tuberculosis*, it is very less, suggesting that the strain diversity is significantly lower. This phenomenon further confirms that the geographic focus area of *M. orygis* is narrow, perhaps specific to South Asia. We found that there were 0 – 6 SNP difference among some isolates in different clusters in animals in India, suggesting a close transmission *M. orygis* in those animals (Figure 1). All the *M. orygis* isolates that were isolated outside of South Asia had at least greater than 100 SNP difference. This finding suggests that *M. orygis* in those countries were uniquely imported, and no transmission of *M. orygis* had happened in those countries. The closest relative of *M. orygis* strain from Nepal was the strain that was isolated from a human in New York in USA, and there was a difference of 197 SNPs between these isolates. Our study concludes that *M. orygis* is endemic in South Asia and is an important causative agent of zoonotic tuberculosis in the region. Taken together, there is a threat of *M. orygis*-associated tuberculosis in South Asia and beyond.



Figure 1. Whole genome-based phylogeny of *Mycobacterium orygis* and others strains of *Mycobacterium tuberculosis* complex.

2. Genomic signatures specific in *Mycobacterium orygis*

We did genome analysis of *M. orygis* that was isolated from rhinoceros in Nepal, and the genome analysis showed that it had *M. orygis* specific mutation (G698C) in anti-SigK factor (Rv044c), which is responsible for higher production of mpt70 and mpt83. We confirmed that *M. orygis* isolates had specific polymorphisms in *gyrB*, *mmpL6*, TBD1, *PPE55*, and Rv2042c (Table 1).

Table 1. *Mycobacterium orygis* specific SNPs

	<i>gyrB</i>				<i>mmpL6</i>	TbD1	<i>PPE55</i>		Rv2042c
	756	1113	1410	1450	551	171	2162	2163	38
<i>M. tuberculosis</i>	G	G	C	G	C	C	T	C	T
<i>M. bovis</i>	A	G	T	T	G	C	T	C	T
<i>M. bovis</i> BCG	A	G	T	T	G	C	T	C	T
<i>M. orygis</i>	G	A	C	T	G	G	G	T	G

3. Development of *Mycobacterium orygis* specific rapid molecular diagnostic method

We targeted several *M. orygis* specific genetic regions such as RD12, RD301, and RD315 for developing rapid detection methods employing PCR and loop-mediated isothermal amplification method. Finally, we developed a PCR detection method targeting RD301 region that can specifically detect *M. orygis* by differentiating it from other members of MTBCs (Figure 2).

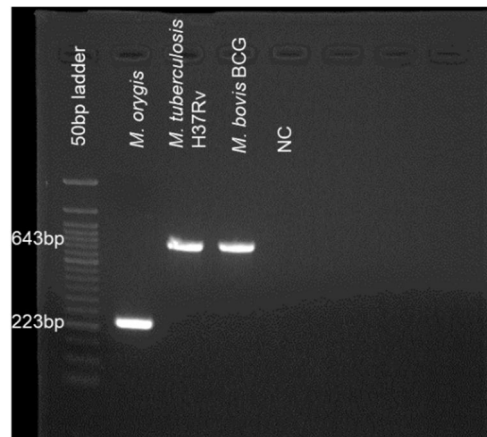


Figure 2. Development of RD301 based *M. orygis* specific PCR detection method.

4. Surveillance of zoonotic tuberculosis in Nepal

We performed surveillance of tuberculosis across the human/wildlife interface in Nepal. We developed a fecal mycobacterial assay that can be used to detect *M. tuberculosis* complex in wild animals by using PCR and LAMP methods. We were successful in detecting *M. tuberculosis* in elephants; however, we did not detect new strains of *M. orygis* during this study period. We will use the knowledge and skill developed during this study to continue our surveillance work on zoonotic tuberculosis in across the human/livestock/wildlife interface in Nepal and other countries.

5. 主な発表論文等

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〔図書〕 計0件

〔産業財産権〕

〔その他〕

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6. 研究組織

	氏名 (ローマ字氏名) (研究者番号)	所属研究機関・部局・職 (機関番号)	備考
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7. 科研費を使用して開催した国際研究集会

〔国際研究集会〕 計0件

8. 本研究に関連して実施した国際共同研究の実施状況

共同研究相手国	相手方研究機関
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