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Streptomyces mutabilis ISOLATION FROM A DROMEDARY LUNG AND ITS HISTOPATHOLOGICAL LESIONS

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ABSTRACT

An abattoir-harvested lung specimen of a 4-year-old dromedary was cultured. The obtained microorganism was assessed for its phenotypic and biochemical characteristics. The isolate was Gram-positive, rod-shaped, and non-acid fast. On sheep blood agar it displayed white and haemolytic colonies. It was catalase and CAMP positive, fermented glucose and xylose, hydrolysed urea and reduced nitrate. Genome DNA was isolated and purified, and 16S rRNA was amplified by PCR. The amplified isolate was sequenced and using the BLAST search tool from NCBI, the microorganism was recognised as *Streptomyces mutabilis* strain 13676F.

Key words: Camel lung, histopathology, *Streptomyces mutabilis*

Streptomyces species are abundant Gram positive microorganisms, which are predominantly found in soil and are capable of producing biologically active secondary metabolites, particularly antibiotics (Loria *et al,* 1997). *Streptomyces mutabilis* is one of several *Streptomyces* bacteria (Pridham *et al,* 1958), which has been reported to have antibacterial and antifungal activities (El-Shanshoury *et al,* 1996, Sanasam and Ningthoujam, 2010).

This report describes the first isolation and pathological lesions of *Streptomyces mutabilis* strain 13676F in a dromedary camel lung.

Materials and Methods

A lung specimen, harvested from a slaughtered dromedary was cultivated in enrichment medium, buffered peptone water broth, and incubated at 37°C for 24 hours. The enriched culture was then subcultured onto 2 sheep blood agar plates, one for aerobic and another for anaerobic culture, and Mac Conkey agar and incubated at 37°C for 48 hours. The bacteria were Gram stained and stained using modified Ziehl-Neelsen technique. Production of catalase was tested with 15% H_2O_2. *Staphylococcus aureus* was used as an indicator strain for the CAMP test. The enzyme tests (Merck, Germany) including hydrolysis of urea and esculin, fermentation of arabinose, glucose, mannitol, maltose, raffinose, sucrose, trehalose and xylose, reduction of nitrate, MR, and VP were performed in triplicate.

Isolation and purification of genome DNA was performed using high pure PCR template preparation kit (Roche Applied Science, Germany) and agarose gel DNA extraction kit (Roche Applied Science, Germany), respectively. The 16S rRNA gene was amplified by PCR using a pair of universal primers (Qiagen, Germany), 27F (59-AGAGTTTGATCC/ATGGCTCAG- 39) and 1541R (59-AAGGAGGTGATCCAGCC-39), corresponding to base positions 8–27 and 1541–1525 of the 16S rRNA gene of *E. coli* (Winker and Woese, 1991), respectively. The amplified isolate was then sequenced (MWG Biotech, Germany). The 16S rRNA gene sequence of strain 13676F has been deposited in GenBank under accession number JF950560.

Tissue specimens harvested from infected lung were fixed in 10% buffered formalin, embedded in paraffin, sectioned and stained with hematoxylin-eosin following standard procedures (Luna, 1968).

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Table 1. Phenotypic and biochemical characteristics of *Streptomyces mutabilis* strain 13676F, with accession number JF950560 in Gen Bank, isolated from camel lung.

Catalase production	Nitrate reduction	CAMP test	MR	VP	Hydrolysis of:		Fermentation of:							
					Urea	Esculin	Arabinose	Glucose	Monnitol	Maltose	Raffinose	Sucrose	Trehalose	Xylose
+	+	+	-	-	+	-	-	+	-	-	-	-	-	+

Results and Discussion

The isolate was Gram-positive, rod-shaped, and non-acid fast. The strain grew well on sheep blood agar under aerobic, but not in anaerobic condition, on which the colonies were convex, embedded, white and haemolytic. It was catalase and CAMP positive, and MR and VP negative. It formed acid from glucose and xylose, but not from arabinose, mannitol, maltose, raffinose, sucrose, and trehalose, hydrolysed urea but not esculin, and also reduced nitrate (Table 1).

Using the BLAST search tool from NCBI (http://www.ncbi.nlm.nih.gov/BLAST/), the isolate was recognised *Streptomyces mutabilis* strain 13676F, and as aforementioned has been deposited in GenBank under accession number JF950560.

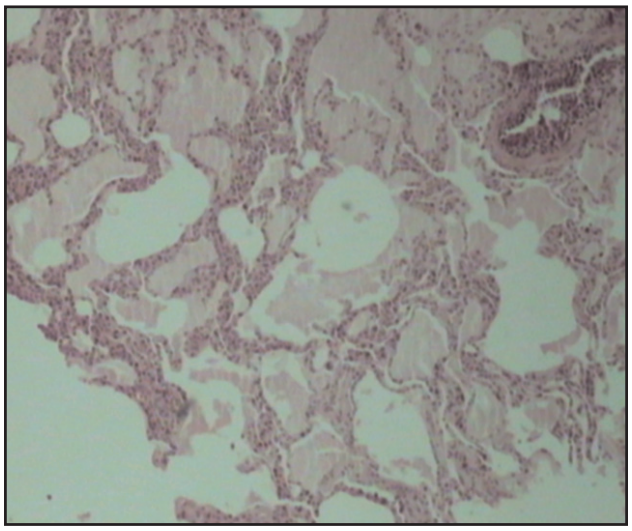

Fig 1. Accumulation of fluid in the alveolar spaces, air ducts, and air sacs, and infiltration of mononuclear inflammatory cells into the alveoli and their walls.

Histopathological examination revealed that there was abnormal accumulation of fluid in the alveolar spaces, air ducts and air sacs. Mononuclear inflammatory cells infiltrated into alveoli and their walls. Histopathological findings were indicative of acute serosal pneumonia. There was no evidence of a purulent infection (Fig 1). Among the big *Streptomyces* genus, only a small number of *Streptomyces* species have been reported to be animal pathogens (Loria *et al*, 1997).

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