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Detection of a novel Tropheryma species in a kidney transplant recipient with nodular pulmonary infiltrates

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Background: A kidney transplant recipient suffering of recurrent pleuritis underwent an open lung biopsy of the left lower lobe showing multiple nodular infiltrates. Gram staining for bacteria and acid fast staining for mycobacteria of the paraffine inbedded (FFPE) lungbiopsy were negative. The Grocott and PAS staining demonstrated multiple oval shaped structures within the cytoplasm of the histiocytes. These findings were suggestive for either a mycotic infection or Whipple's disease.

Material/methods: FFPE extraction was performed using the FFPE extraction kit (Qiagen). *T. whipplei* was searched for using a real time PCR targeting the non-coding repeat specific for *T. whipplei* (Fenollar et al, 2004). Subsequently, identification of the bacteria in the extract was done using 16S rRNA and 23s rRNA sequencing and Blast analysis (ncbi). ITS2 sequence analysis was used for fungal DNA identification.

Results: The FFPE extract was negative for fungi. The real time PCR targeting the non-coding repeat of *T. whipplei* was also negative suggesting that the patient was not suffering from Whipple's disease. 16S rRNA sequence and blast analysis of a 1375 bp fragment gave *T. whipplei* as the best match with 22 mismatches resulting in only 98% agreement. However, all *T. whipplei* 16S rRNA sequences in Genbank show only minimal variance (99%-100% agreement with maximal 2 mismatches). To further identify the bacterial DNA, sequence analysis of the 23S rRNA gene was performed. *T. whipplei* gave again the best match but only with 95% agreement. The patient received antimicrobial treatment targeting *T. whipllei* with good clinical outcome.

Conclusions: Pulmonary involvement by Whipple's disease is a very rare complication. In the described patient, lung tissue was positive for Grocott and PAS staining. *T. whipplei* specific real time PCR was negative but 16S and 23S rRNA sequencing gave *T. whipplei* as the best hit albeit with limited agreement. These findings might suggest that a novel *Tropheryma* species that lacks the non-coding repeat, most frequently used for molecular detection of Whipple's disease, might be the cause of the pulmonary disease. Whole genome sequencing is needed to further characterise the bacterial genome.