

中文題目：以總體基因體分析輔助診斷退伍軍人病合併感染新型冠狀肺炎之個案

英文題目：Metagenomic analysis of Legionnaires' Disease in COVID-19: a case report

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## Introduction:

Since the COVID-19 outbreak in 2019, various co-infections have been reported in COVID-19 patients. These patients are found to have higher rates of receiving invasive mechanical ventilation, prolonged hospital admissions, and higher mortality. Bacterial co-pathogens reported by studies include *Mycoplasma pneumoniae*, *Legionella pneumophila*, *Streptococcus pneumoniae*, and *Chlamydia pneumoniae*.

Legionnaires' disease, one of the co-infections with COVID-19, is caused by the gram-negative bacteria *Legionella pneumophila*. It is a common form of severe pneumonia and shares many similarities with COVID-19. Therefore, information on respiratory disease related to other species and serogroups of legionella is limited. In addition to this limitation, similarities in the clinical presentation of COVID-19 and Legionnaires' make an accurate and timely diagnosis of Legionnaires' disease challenging.

## Case Presentation:

A 58-year-old man with a history of hypertension developed fever, cough, and muscle aches five days after diagnosed to have mild COVID-19. CXR consisted of right lower lobe pneumonia. The real-time RT-PCR assay didn't detect SARS-CoV-2. Empiric piperacillin/tazobactam was started for four days without improvement. To investigate the etiology of his pneumonia, bronchoalveolar lavage was performed. Usual routine work-up, the specimen was also submitted for metagenomic analysis, and *L. pneumophila* was identified. Levofloxacin was started with rapidly resolved symptoms/signs. A real-time RT-PCR assay of the bronchoalveolar lavage fluid also confirmed the presence of *L. pneumophila*.

## Discussion:

It is estimated that the co-infection of influenza and bacteria is around 11% to 35%. The most common bacterial pathogen was *Streptococcus pneumoniae*, which accounted for 35%, and the second most common bacteria was *Staphylococcus aureus*, which accounted for 28%. When seeing COVID-19, bacteria co-infection with SARS-CoV-2 virus was less frequent, estimated at only about 1.2-3.5%. Bacteria secondary infection is slightly higher than co-infection, accounting for about 14.3%. Although the co-infection rate was relatively low, about two-thirds of patients received antibiotic treatment.

Not only bacterial co-infection with SARS-CoV-2 but several pathogens co-infection had also been reported. Patients diagnosed with tuberculosis are at increased risk of COVID-19 and tend to have worsened prognoses. Some invasive fungal infections were also documented, and it was underestimated. The risk

factors of fungal co-infection among COVID-19 patients were older age, diabetes, immunosuppression, racial or ethnic minority status, and smoking. Other fungal markers may be helpful for early detection of fatal invasive fungal infection.

We report a case of a 58-year-old man with co-infection with Legionnaires' disease and COVID-19 infection. So, we researched whether there are some case series or case reports. Most patients are reported in Europe. Most cases have existed comorbidities which diabetes mellitus and hypertension are most mentioned. For diagnostics, urine antigen are most used. Regarding clinical characteristics, the mortality rate is about one of third which is higher than in previous studies. It may be contributed to limited data.

### **Conclusion:**

The incidence of co-infection with Legionnaires' disease in patients with COVID-19 infection is estimated at about 0% to 1.5% from different studies. Due to limited sensitivity in the current diagnostic tool, alternative diagnostic measures are warranted, such as metagenomic sequencing. Current study demonstrated that metagenomic is a promising approach that facilitated the diagnosis of Legionnaires' disease.