

## ABSTRACT

Understanding the molecular mechanism of PZA resistance is facilitated by these data points. In our isolates, an adenine to mannose point mutation in the -11 upstream region was the most frequent type of *pncA* mutation. It is important to carefully interpret the results of any PCR analysis for epidemiologic purposes.

## INTRODUCTION

A review of *pncA* mutations in clinical *Mycobacterium tuberculosis* isolates from Korea.

The *pncA* mutation in clinical *Mycobacterium tuberculosis* isolates from Korea is a rare one, and it is thought that this mutation may be responsible for the development of clinical disease in patients with this strain. Although there are several cases of *pncA* mutation in clinical *Mycobacterium tuberculosis* isolates from Korea, it is unclear whether this mutation is causative of the clinical disease in these patients.

In the present study, the *pncA* mutation in the clinical strain of *Mycobacterium tuberculosis* isolates from Korea was isolated using the polymerase chain reaction (PCR) method. The *pncA* mutation was isolated from a patient with *pncA* mutation in the clinical strain. The first-line drug for tuberculosis treatment, pyrazinamide (PZA), kills semidormant mycobacteria only at low pH; susceptibility testing in vitro sometimes fails due to poor growth at the low level of pH, and thus PZase (Prozal Alcohol) has been used since 1979 to identify susceptible strains of *M. tuberculosis* using the pZakamidase test because it converts the prodrug from the weakly navor molecular compound orthologue into

## CONCLUSION

These information help us understand the molecular basis of PZA resistance and add to the existing data on worldwide *pncA* mutations, which also showed that adenine to guanine point mutation (APM) mutation in the -11 upstream region are the most common type of phenylalanine-carnabine (pNcAA) mutants. Due to very different RFLP patterns in each strain, the results of all ppm PCR for epidemiologic purposes should be interpreted carefully.. The same strains may have them with the same mutation from those mutation