

pncA mutations in clinical Mycobacterium tuberculosis isolates from Korea

ABSTRACT

These data help in the understanding of the molecular basis of PZA resistance. An adenine to guanine point mutation in the -11 upstream region was the most common type of pncA mutation in our isolates. The results of pncA mutation analyses should be carefully interpreted for epidemiologic purposes.

INTRODUCTION

Background Pyrazinamide (PZA) is among the first-line drugs used to treat tuberculosis. In vitro, it kills semidormant mycobacteria only at low pH. In vitro susceptibility testing sometimes fails because of the poor growth of mycobacteria at low pH. Therefore, the pyrazinamidase (PZase) test, which was originally used for the differentiation of Mycobacterium tuberculosis from weakly niacin-positive strains of M. bovis, has been used to identify susceptible strains of M. tuberculosis, because PZase converts the prodrug PZA to pyrazinoic acid, the active form of the drug. The pncA gene encodes PZase, and mutations in pncA are associated with resistance to PZA or loss of PZase activity. The purpose of this study was to compare PZase activity with the genotype to better understand the molecular basis of PZA resistance and to expand the profile of pncA mutations worldwide.

CONCLUSION

These data provide a better understanding of the molecular basis of PZA resistance and expand the data on pncA mutations worldwide. Furthermore, it was demonstrated that adenine to guanine point mutations in the -11 upstream region are the most common type of pncA mutations. Because of the different RFLP patterns in the strains having the same mutations, the results of pncA mutations should be carefully interpreted for epidemiologic purposes.