Abstract
During a population-based study to genotype isolates of Mycobacterium tuberculosis from Buenos Aires Northern suburbs, we found isolates with molecular patterns related to those of the Beijing genotype. Five out of 590 (0.85%) patients had isolates with spoligopattern identical to that of the Beijing family. Since two of these isolates showed identical IS6110RFLP pattern, we found only four different patterns containing 11 to 19 bands. The isolates were obtained from young people (including a 7 years-old child) who were born in Argentina, and were living in a small area of our region. However, conventional contact tracing did not prove epidemiological linkage among them. These isolates were fully drug-susceptible to the first-line drugs. The comparison of the IS6110RFLP patterns from our isolates against a set of 19 reference Beijing patterns from the RIVM (The Netherlands) confirmed that the strains belonged to the Beijing lineage. These findings might be partially explained by the important migration phenomena occurred during the last decade. Further surveillance studies would help in the following of Beijing family strain dissemination in our community.

Keywords
Mycobacterium tuberculosis, Beijing, W-strain, spoligotyping, epidemiology