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**Title:** Reporting a truncated IS6110 dimer [(IS6110)2] in the genome of some Beijing isolates of Mycobacterium tuberculosis

**Authors:** M. Zare Bidaki*, K. Forbes

**Abstract:**
Background and objectives:
The insertion sequence IS6110 has been supposed to be an important agent of genomic variation in Mycobacterium tuberculosis as its transposition events may disrupt open reading frames. Therefore, our knowledge of variations in IS6110 structure and the way it transpose may help us having a better understanding of IS6110 effects of M. tuberculosis genome. IS dimers are defined as two IS6110 copies separated by less than three base pairs and arranged in a head-to-tail order.

Method:
The genome of Mycobacterium 69 isolate was analyzed by IS6110 insertion site mapping. The mapping of IS6110 insertion sites was based on PCR amplification of the IS6110 flanking sequences.

Results:
Among 69 isolates from families Beijing, EAI, X, CAS, S, T, LAM and Haarlem, only three quarters (5 isolates) of Beijing family members showed a truncated IS dimer. The dimer was a pair of IS6110 insertions separated with no nucleotide (Accession No. AM690455). The head-to-tail arranged element had a 139 bp deletion at the inner tail of one of the IS6110 copies with the other IS copy intact. Due to the lack of intervening sequence and the lack of sequence from the outer ends of the elements, as the dimer was PCR-amplified using two internal IS6110 primers, the genomic location of this IS dimer could not be determined. It might be located in the iplB locus, as this was the only IS6110 hot-spot not fully mapped in this study (due to the difficulty of designing primers specific for this locus). Although there are a number of reports describing IS dimers for other insertion elements, intact IS6110 dimers seem to be rare, as they have not been reported previously.

Conclusion:
Although there are a number of reports describing IS dimers for other insertion elements, intact IS6110 dimers seem to be rare, as they have not been reported previously. Our report shows an IS6110 dimer in the genome of a group of Beijing family isolates. This finding can be used as a new genetic marker to classify Beijing family of Mycobacterium tuberculosis species in two subclasses.

**Key words:** Mycobacterium tuberculosis, IS6110 dimer

**Presentation:** Poster