

# IS6110, an IS-like element of *Mycobacterium tuberculosis* complex

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Mobile genetic elements are useful genetic tools. They have been found in most organisms which have been examined (for recent reviews see 1). *IS900* was isolated from *M. paratuberculosis* (2) and *IS6100* from a *M. fortuitum* strain (our unpublished results). IS elements have been used as taxonomic markers useful for diagnostic purposes, (2, 3). From a *M. tuberculosis* cosmid library constructed in pHc79 (4), an IS-like element, *IS6110*, was identified as a repeated sequence, by screening the library with labelled *M. tuberculosis* total DNA. This sequence (1361 nt) possesses characteristics of IS elements, i.e., inverted (28bp with 3 mismatched bp) and direct (3bp) repeats of the target sequence at its extremities. A search in the EMBL data bank has revealed homologies with *IS3411*, an insertion element from *E. coli* (5). Cross-hybridization was observed between *IS6110* and a repeated sequence previously isolated from *M. tuberculosis* (6). *IS6110* has been found in *M. tuberculosis* and *M. bovis* but not in any of the other mycobacteria tested (our unpublished data). Therefore, *IS6110* will be used as probe for the identification of the *M. tuberculosis* complex.

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### DR INV. REP.

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CGATGAACCG CCCCGGCATG TCCGGAGACT CCAGTTCTTG GAAAGGATGG GGTCATGTCA GGTGGTTCAT
CGAGGAGGTA CCCGCCGGAG CTGCGTGAGC GGGCGGTGCG GATGGTCGCA GAGATCCGCG GTCAGCACGA
TTCGGAGTGG GCAGCGATCA GTGAGGTGCG CCGTCTACTT GGTGTTGGCT GCGCGGAGAC GGTGCGTAAG
TGGGTGCGCC AGGCGCAGGT CGATGCCGGC GCACGGCCCC GGACCACGAC CGAAGAATCC GCTGAGCTGA
AGCGCTTAGC GGCGGGACAA CGCCGAATTG CGAAGGGCGA ACGCGATTTT AAAGACCCGCG TCGGCTTTCT
TCGCGGCCGA GCTCGACCGG CCAGCACGCT AATTAACGGT TCATCGCCGA TCATCAGGGC CACCGCGAGG
GCCCGATGG TTTGCGGTGG GGTGTGAGT CGATCTGCAC ACAGCTGACC GAGCTGGGTG TGCCGATCGC
CCCATCGACC TACTACGACC ACATCAACCG GGAGCCCAGC CGCCCGGAGC TGCGCGATGG CGAACTCAAG
GAGCACATCA GCCCGGTCCA CGCCGCCAAC TACGGTGTTT ACGGTGCCCG CAAAGTGTGG CTAACCCTGA
ACCGTGAGGG CATCGAGGTG GCCAGATGCA CCGTCAACCG GCTGATGACC AAACCTCGGCC TGTCGGGAC
CACCGCGGC AAAGCCCAGC GGACCACGAT CGCTGATCCG GCCACAGCCC GTCCCAGCCGA TCTCGTCCAG
CGCCGCTTCG GACCACCAGC ACCTAACCGG CTGTGGGTAG CAGACCTCAC CTATGTGTCG ACCTGGGCAG
GGTTCGCCTA CGTGGCCTTT GTCACCGACG CCTACGCTCG CAGGATCCTG GGCTGGCCGG TCGCTTCCAC
GATGGCCACC TCCATGGTCC TCGACGCGAT CGAGCAAGCC ATCTGGACCC GCCAACAAAGA AGGCGTACTC
GACCTGAAAG ACGTTATCCA CCATACGGAT AGGGGATCTC AGTACACATC GATCCGGTTC AGCGAGCGGC
TCGCCGAGGC AGGCATCAA CCGTCGGTCC GAGCGGTCCG AAGCTCCTAT GACAATGCAC TAGCCGAGAC
GATCAACGGC CTATACAAGA CCGAGCTGAT CAAACCCGGC AAGCCCTGGC GGTCCATCGA GGATGTGCGA
TTGGCCACCG CGCGCTGGGT CGACTGGTTC AACCATCGCC GCCTTACCA GTACTGCGGC GACGTCCCGC
CGTTCGAACT CGAGGCTGCC TACTACGCTC AACGCCAGAG ACCAGCCGCC GGCTGAGGTC TCAGATCAGA
GAGTCTCCGG ACTCACCGGG GCGGTTCACGA
INV. REP. DR

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Figure 1. Complete nucleotide sequence of *IS6110*. Direct (DR) and inverted (INV.REP.) repeats are shown by lines.