Abstract

**Background & Problem Statement:** Recent studies have shown that certain strains of M. tuberculosis are more virulent than others because these strains have been isolated from both immuno-competent and immuno-compromised individuals. A recent study done in Uganda showed that Uganda strains were the most prevalent. Genetic variations in these strains have been implicated as the cause of variations in their virulence abilities. However, no definitive case links or specific genomic characteristics regarding these strains have been detected which may have restricted efforts to reduce their transmission.

**Specific objectives:** To define putative genes associated with virulence of Uganda strains and to determine the association between virulence and specific genomic characteristics.

**Methodology:** The bacterial strains are archived isolates of five Uganda strains and three other East African strains. H37Rv and H37Ra are being used as positive and negative controls respectively. The DNA isolation is being done using a standard protocol. PCR is being used to amplify the DNA regions of interest. Definition of putative genes and other genomic characteristics will be done using DNA microarray analysis technique. Scanning of slides will be done in UK.

**Ongoing activities:** Extraction of DNA from the archived isolates and preparation of microarray analysis slides.

**Expected outcomes:** Genomic characteristics responsible for the high virulence of Uganda strains will be determined and the association between virulence and wide spread transmission established.