

RESEARCH

Mycobacterium tuberculosis strains are evolving to have a greater propensity to spread and cause disease

Mycobacterium tuberculosis strains with the Beijing genotype are thought to have evolved unique properties, including increased virulence, ability to transmit more frequently, evade protection by BCG vaccination and acquire drug resistance more frequently. Comparison of the Beijing genotype population structure among strains collected in Cape Town with published literature found that the strains in Cape Town had their evolutionary origin in East-Asia and were probably introduced by sea trade in the 18th century. Phylogenetic analysis of the Cape Town Beijing strains demonstrated that they could be partitioned into 7 independently evolving sublineages. Strains from the most recently evolved sublineage were found to have a greater propensity to spread and cause disease. However, these strains were not successful in East-Asia suggesting host-pathogen compatibility. This may be explained by the host population genetics of the indigenous population in Cape Town which was unable to contain the spread of the sublineage 7 strains. Alternatively, the initial introduction of sublineage 7 strain into the Cape Town population precipitated an evolutionary event resulting in an increase in pathogenicity. The emergence of a sublineage of Beijing strains with increased pathogenicity may have important implications for the Tuberculosis Control Program. Early diagnosis and contact tracing will be essential to curb the spread of these strains. Furthermore, it will be important to ensure that future vaccines protect against these strains.

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