Exploring the use of molecular epidemiology to track bovine tuberculosis in Nigeria: An overview from 2002 to 2004


Tuberculosis remains a major public health problem in Nigeria. While human to human transmission of *Mycobacterium tuberculosis* is clearly of major importance in driving the tuberculosis epidemic in Nigeria, the impact of *Mycobacterium bovis* transmission from infected cattle is largely unknown. Molecular epidemiology of *M. bovis* in Nigeria will increase our understanding of this endemic disease and provide tools to assess cattle-to-human transmission. Between 2002 and 2004, molecular techniques including spoligotyping, variable number of tandem repeats (VNTR) typing and deletion typing were used to track and analyze a sample of strains of the *M. tuberculosis* complex circulating in the cattle population in Ibadan, Southwestern Nigeria. In all, 180 isolates were typed with a view to elucidating epidemiological information on circulating strains, occurrence of trans border transmission and molecular diversity of the *M. bovis* strains. Results obtained showed that 99% (178/180) of the isolates were *M. bovis*, while the remaining were *M. tuberculosis* and *M. africanum*. In all, strains of *M. bovis* had 34 different spoligotypes: strains with spoligotype pattern SB0944 (as designated by www.mbovis.org) were the most common (46% of strains). This molecular type is also common in countries neighbouring Nigeria. Strains with this spoligotype pattern could be further divided into 40 different VNTR types. This analysis shows the value of simple molecular epidemiological techniques applied to strains of *M. bovis* and suggests that further epidemiological studies will shed more light on the transmission dynamics of bovine tuberculosis locally and across neighbouring African countries.