

# Estimates for the mutation rates of spoligotypes and VNTR loci of tuberculosis

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Knowledge about the rate at which molecular fingerprints change, or the mutation rate, is helpful in assessing the utility of molecular markers in genotyping. Estimates for the mutation rate of spoligotypes and variable numbers of tandem repeat (VNTR) loci for *Mycobacterium tuberculosis* have been recently reported. These estimates are either based on a large collection of isolates with known epidemiological links, or a data set from a single region on which approximate Bayesian computation is applied. In this paper, we propose a different method of estimation for the mutation rates of spoligotypes and VNTRs using published data sets from different epidemiological studies. The key parameter involved in our method is  $\theta = 2N\mu$ , a quantity for genetic diversity that involves the mutation rate. Our findings show much higher estimates than those previously reported. We discuss the implications of these results in studies of the evolution and molecular epidemiology of tuberculosis.

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