# **Tuberculosis SNP typing with Luminex® devices at the genomic era: advantages and limitations**

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Tuberculosis is caused by *Mycobacterium tuberculosis* bacillus. This bacterium is characterized by an impermeable cell-wall, a slow growth rate, the absence of horizontal gene transfer and the presence of repetitive elements in the genome. Treatment is long and requires multitherapy but resistance does not spread rapidly as it can only emerge by point mutation in the genomic DNA. Present concern is the contamination of patients by multi-drug and extreme-drug-resistant isolates that develop in countries with poor antibiotic supply and/or in patients with high drug-metabolization rate. Detection of drug resistance and exploration of strain diversity to identify expanding clones are standing priority goals of tuberculosis epidemiology.

Several techniques to explore strain diversity and resistance have been successfully set-up on Luminex® platforms. Recently, we developed for instance TB-EFI to detect resistance to second-line drugs, and TB-SNPID to detect simultaneously main resistance mutations and mutations characteristic of phylogenetic sublineages. Other well adopted methods are TB-SPOL that assesses strain diversity through the profile at the CRISPR locus of the bacterium, a technique referred to as spoligotyping, and TB-SPRINT that combines spoligotyping to the detection of drug resistance.

These methods have been used on a variety of samples and proved very sensitive on cultured samples, with 100% concordance with sequencing data. To improve throughput of data analysis, we developed different Excel® tools that will be presented. I will also present the type of studies which these methods have contributed to in the last 15 years.

Since 2011, the democratization of Whole genome sequence (WGS) data makes it possible to turn towards point mutations to follow tuberculosis diversification, relativeness between isolates, and to predict resistance. In this context, we will examine how Luminex®-based techniques can still contribute to the molecular epidemiology of tuberculosis. Among the advantages of Luminex® techniques, we will highlight turn-around time, throughput and cost. We will clarify the contexts and the conditions at which we think they may bring substantial input to global surveillance during the next decade.