

## Pediatrics Infectious Diseases 2018: Microbiological and molecular characterization of environmental *Mycobacterium* strains isolated from the Buruli ulcer endemic and non-endemic zones in Côte d'Ivoire

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Mycobacteria are germs that cause lung infections, skin or lymph. They are found in the environment like in the soil, water, aerosols, plants, aquatic animals. This Acid-Alcohol Bacillus Resistant (AFB) are not mandatory pathogens and for several years, the scientific community have not really shown interest in their study, but rather devoted to the study of TB epidemic. They were considered as saprophytic bacteria and their pathogenic potential are not recognized. However, some mycobacteria such as *Mycobacterium liflandii* and *Mycobacterium fortuitum* produce toxins causing skin infections. This is an extremely polymorphic bacterial genus that includes fast-growing species (less than 7 days), and slow growing species (7-60 days) and non-culturable outside animals species, *Mycobacterium leprae*, leprosy causing agent. Mycobacteria are divided into two major groups, they are complex tuberculosis and non-tuberculosis mycobacteria (NTM) also called environmental mycobacteria (mycobacteria of leprosy and atypical mycobacteria). Although, molecular biology has helped to discover the existence of diversity in environmental mycobacteria, culturing of species however, remains the most efficient means of knowing their physiology and their antibiotic sensitivity. The most important ones are *Mycobacterium avium*, *Mycobacterium intracellulare*, *Mycobacterium kansasii*, *Mycobacterium xenopi* and *Mycobacterium abscessus*. The complex *M. avium*, *M. kansasii*, *M. chelonae* and *M. xenopi* are responsible for the majority of infections in the developed countries, while *M. ulcerans* is responsible for ulcerative diseases in tropical and subtropical countries. The distribution of commonly isolated species is in constant change in most countries studied and new species emerge. They are part of the group of non-pigmented genes atypical mycobacteria such as *M. abscessus*, *M. chelonae*, *M. fortuitum* and *M. smegmatis*. Buruli ulcer, debilitating disease, is a serious public health problem. Almost all regions in Côte d'Ivoire are affected. The mode of transmission and environmental sources are unknown. To be able to understand the level of prevalence of skin infections in Côte d'Ivoire, it is important to identify species other than *M. ulcerans* that are involved. Given their large numbers, this study was undertaken with the aim to achieve the molecular characterization of potentially pathogenic environmental mycobacteria strains others than *M. ulcerans* from different aquatic environments in Côte d'Ivoire.

*Mycobacterium ulcerans* (MU), the causative agent of Buruli Ulcer (BU), skin disease, is considered to be an environmental pathogen. The pathogenic virulence of *Mycobacterium ulcerans*

is being linked to the expression of toxin called mycolactone. Genetic analyses have shown the high diversity with Variable Number Tandem Repeats (VNTR) and Mycobacterial Interspersed Repetitive Units (MIRU) in *M. ulcerans* and in Mycolactone Producing *Mycobacteria* (MPMs). The purpose of this study is the molecular characterization of potentially pathogenic environmental mycobacteria strain, apart from the *M. ulcerans*, from aquatic environments in Côte d'Ivoire. A total of 473 samples were collected comprising of 251 water and 222 sediment based on sampling sites. The sediments were the most contaminated by mycobacteria with 60% as against 43.3% in water samples from the hyperendemic areas. In hypoendemic areas, water was the most contaminated with 53.57% against 43.24% in sediment. Microscopy by Ziehl-Neelsen-staining and PCR diagnostics using IS2404 and ketoreductase (KR) were performed on strains. 20% fast growing isolated mycobacteria species including *Mycobacterium mucogenicum*, *Mycobacterium peregrinum* and *Mycobacterium sp.* was found carrying the IS2404 gene previously found in *Mycobacterium ulcerans*. 9.23% of strains carry the ketoreductase genes, one of the synthesis of mycolactone enzymes. In terms of genetic analysis using the MIRU/VNTR, the MIRU1 was the most amplified sequence and LOCUS 6 less amplified; no known profile have been identified in this study. This study is the first step taken in order to understand different skin infections encountered in Côte d'Ivoire.

The results of this study highlight the potential risk of contamination in humans especially people in permanent contact with the environment. These species discovered, would be responsible for ulcerations in Côte d'Ivoire, which could explain the very high level of endemicity. It is therefore important to identify the sequences of these species in order to set up appropriate diagnostic methods. This study is just the first step, we want to understand the different skin infections encountered in Côte d'Ivoire. This will help to better diagnose patients suffering from skin infections other than Buruli ulcer and to consider strategies and means of protection of the population against all mycobacterioses by breaking the epidemiological chain. In perspective, it would be good to continue studying the rapidly growing mycobacteria to determine their involvement in cutaneous ulcerations. The sequencing of the genes Kr and IS2404 isolated in the strains of this study for their eventual relationship with *M. ulcerans* could help for a better comprehension of the affection.