

Infectious Diseases 2018: Study of potentially pathogenicity of environmental mycobacteria non-ulcerans isolated in Cote d'Ivoire

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Mycobacteria are germs that cause lung infections, skin or lymph (Griffith et al., 2007). They are found in the environment like in the soil, water, aerosols, plants, aquatic animals (Winthrop et al., 2002; Sniezek et al., 2003; Marsollier et al., 2002, 2004). 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 (Ziza and Desplaces, 2006). However, some mycobacteria such as *Mycobacterium liflandii* and *Mycobacterium fortuitum* produce toxins causing skin infections (Williamson et al., 2008; Kakou-Ngazona et al., 2015). 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 (Euzéby, 2010). 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) (Inderlied et al., 1993; Caruso et al., 2009; del Rio Camacho et al., 2010). Although, molecular biology has helped to discover the existence of diversity in environmental mycobacteria (Domenech et al., 1994; Menendez et al., 2002; Williamson et al., 2008; Kakou-Ngazona et al., 2015), culturing of species however, remains the most efficient means of knowing their physiology and their antibiotic sensitivity (Kubica et al., 1964; Trujillo et al., 2004). The most important ones are *Mycobacterium avium*, *Mycobacterium intracellulare*, *Mycobacterium kansasii*, *Mycobacterium xenopi* and *Mycobacterium abscessus* (Falkinham, 1996; Dailloux et al., 2010). The complex *M. avium*, *M. kansasii*, *M. chelonae* and *M. xenopi* are responsible for the majority of infections in the developed countries (Horsburgh, 1996), while *M. ulcerans* is responsible for ulcerative diseases in tropical and subtropical countries (Pedley et al., 2004). The distribution of commonly isolated species is in constant change in most countries studied and new species emerge (Martin-Casabona et al., 2004). They are part of the group of non-pigmented genes atypical mycobacteria such as *M. abscessus*, *M. chelonae*, *M. fortuitum* and *M. smegmatis* (Brown and Wallace, 1992). 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.

Present Study: The natural environment is considered a potential source of Non-Tuberculous Mycobacteria (NTM). They are responsible for lung and skin infections. In Cote d'Ivoire, the only recognized etiological agent responsible for ulcerations is *M. ulcerans*. It is a real public health problem with about 2000 cases reported annually according to the WHO. This ulcerative disease is caused by *Mycobacterium ulcerans*, from the environment. It would act in humans under the influence of a toxin, mycolactone. However some environmental mycobacteria could be involved in its occurrence. The lack of knowledge about the mode of transmission, the ecological niches constitute a real obstacle to the diagnosis and the establishment of an effective treatment. There is very little information on the presence of environmental mycobacteria in Cote d'Ivoire.

Place & Duration of the Study: The analysis of the samples took place in the laboratories of Institute Pasteur of Côte d'Ivoire in Abidjan City between June 2014 and December 2015. Sampling was done in some sites of Buruli Ulcer of Côte d'Ivoire. **Materials:** Sites (Sokrogbo, Bodo (Tiassalé), Adiopodoumé, Adzopé, Ioka (Bouaké), Agboville, Aghien) were studied. The biological material consisted of water and sediment samples. **Methods:** The techniques of classical bacteriology and biochemistry were used for culture and identification of species, PCR diagnostics using IS2404 and KR were performed on strains, MIRU/VNTR were used for the genetic analyzes. **Results:** A total of 473 samples were obtained in this study. A total of 7 fast-growing species were identified. They are: *M. peregrinum*, *M. immunogenicum*, *M. chelonae*, *M. mucogenicum*, *M. abscessus*, *M. smegmatis*, *Mycobacterium sp.* 20% of the species of rapidly growing mycobacteria isolated were carrying the gene IS2404 found in *M. ulcerans*. 9.23% of the strains harbor the Ketoreductase (Kr) gene, one of mycolactone synthesis enzymes. At the level of genetic analyzes using MIRU/ VNTR, MIRU 1 was the most amplified sequence and the least amplified LOCUS 6, no known profile was identified in this study. **Conclusion:** This study allowed the presence of potentially pathogenic rapidly growing mycobacterial species possessing virulence genes previously attributed to *M. ulcerans*, responsible for Buruli Ulcer. It also confirms the role of water and sediments as a risk factor for the population vulnerable to mycobacterial diseases. This study would be the first step to understand the origin of the different cutaneous infections encountered in Ivory Coast.