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Study of potentially pathogenicity of environmental mycobacteria non-ulcerans isolated in Cote d'Ivoire

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Introduction: 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, loka (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.

Biography

Sabine N'dri Vakou holds a PhD in Bioscience and is a graduate the Microbiology Laboratory in the Environment and Health Department. She has contributed to numerous studies on bacteria responsible for skin ulcers, particularly mycobacteria. She has chosen to focus on non-ulcer mycobacteria which could have a role in maintaining the endemicity of Buruli ulcer in Côte d'Ivoire.

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