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The contribution of comparative genomics to health geography research: a case study on the identification of M. ulcerans contamination sites in Benin

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Buruli ulcer or Mycobacterium ulcerans infection is a neglected tropical disease that causes necrotising skin lesions. The endemic areas most affected are located in West and Central Africa, where direct contact with stagnant open surface water has long been the only risk factor identified [1]. In these environments, aquatic bugs are strongly suspected of acting as hosts and vectors of the bacillus [2]. Despite a great deal of research [3], it is still impossible to identify the precise sites of contamination and the mechanisms of transmission for several reasons. Firstly, incubation times are long and variable. Secondly, PCR extraction of the bacteria from living organisms and plants taken from the environment is complicated. And thirdly, patients generally have no recollection of the place or circumstances in which they contracted the disease.

Faced with this relative impasse in research, it seems necessary to develop new approaches to improve prevention. With this in mind, a mixed research method has been developed as part of the COPTER-UB project (ANR funding) by health geographers from the ESO team at the University of Angers (France). These are geographical health surveys that combine a classic case-control study with a census of all water points likely to be contaminated and with microbiological sampling in the environment. Mapping of land use and the presence of water completes this work (using remote sensing).

The study area is the endemic focus of the Ouémé-Plateau region in south-east Benin, and the areas considered potentially at risk are not limited to water supply points alone, but also include flooded crossings, ditches and ponds used in farming activities, as well as other, sometimes seasonal, water points (e.g. fishing ponds). This work made it possible to reduce the potential number of contaminated sites as it became clear that no patients or control-individuals frequented them. Nevertheless, the etiology of the disease remained too uncertain.

Genomic analysis is a new approach. A study of M. ulcerans strains among patients at the Buruli ulcer treatment centre in Pobè has identified 8 distinct genotypes whose geographical distribution is not random. This study, carried out by the ATOMycA team at INCIT, highlighted an area of interest, in the south of the Ouémé region, where there is a spatial clustering of two specific genotypes. In this communication, we will present this new approach, which crosses the data obtained by comparative genomics with that collected in geographical health surveys. We will show the advantages of using this mixed research method to highlight common areas of infection and gain a better understanding of the ecological reservoir(s) of M. ulcerans. In conclusion, we will discuss how ongoing progress in genetic technologies can help to modify our practice of health geography, particularly on smaller scales, by including here the spatial distribution of micro-organisms capable of partitioning M. ulcerans in places with strong local roots.

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