Common infectious and communicable diseases among a nomadic Fulani population in Kano, Nigeria


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Background: Infectious diseases are an important cause of morbidity and mortality in sub-Saharan Africa. Access to healthcare among nomads has been identified as a major deterrent against effective control, elimination and eradication of infectious diseases in Nigeria. We conducted a community survey among nomadic Fulanis in Kano state to determine the prevalence of common infectious diseases.

Methods & Materials: We interviewed consenting adults 15 years and above to obtain socio-demographic information, social habits and symptoms of common infectious diseases. Rapid Diagnostic Tests (RDT) and tuberculin sensitivity test (TST) were conducted to determine prevalence of malaria, tuberculosis and exposure to Mycobacterium. Focused group discussions were conducted with selected members of the community to determine their felt needs, knowledge, perceptions and awareness about preventive measures against common infectious diseases with emphasis on malaria, tuberculosis, sexually transmitted infections (STI), and human immunodeficiency virus infection (HIV).

Results: Of 229 respondent interviewed, 100 (43.7%) were females. A total of 153 (68.8%) respondents had fever within the previous 3 months. Cough and urethral discharge were documented among 29 (14.1%) and 31 (13.9%) respectively. Malaria RDT positivity was found among 24 (10.5%) subjects. Of the 167 respondents who consented and had TST read, 45 (26.9%) were positive. Sixty five (34.0%) respondents reported having sick animals; 51 (78.5%) of which had cough. Findings from FGDs conducted revealed that majority of the respondents consider malaria as a common cause of morbidity and mortality especially among paediatric age groups. They also consider tuberculosis as common with potential for animal to human transmission. However, they failed to link seeking treatment and care for their sick animals as a preventive measure against common human infectious diseases. Regarding appropriate preventive measures against malaria and other infectious diseases, the respondents failed to demonstrate adequate knowledge. Majority of the respondents identified as their priority needs portable water supply, access roads and health facility in order of priority.

Conclusion: Communicable diseases are common among nomadic Fulanis and their livestock. Lack of access to health care facilities for this vulnerable and neglected population could militate against effective control of infectious diseases. Diseases control programmes should evolve innovative ways of reaching nomads with their interventions.

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Molecular epidemiology of Vibrio cholerae O1 in Mozambique

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Background: Africa is increasingly affected by cholera, accounting in 2009 for 98% of the officially reported cases worldwide. In Mozambique cholera appeared in early 1970’s when the seventh pandemic entered Africa from the Indian Subcontinent. In the following decades, several epidemics were registered in the country, with the ‘97–’99 being the most extended. Since then, Mozambique is considered an endemic area for cholera, characterized by outbreaks occurring yearly with a seasonal pattern. Despite improving sanitary conditions, cholera continues to represent a major public health issue for the country: 12,819 cases were reported in 2012, with a 1.1% mortality rate. From an epidemiological standpoint, the cholera seventh pandemic is caused by V. cholerae O1 strains genetically related but differentiated by their content of mobile genetic elements (the mobilome), such as plasmids, Pathogenicity Islands and Integrative Conjugative Elements. At least five pandemic variants are thought to have originated in the Indian Subcontinent and spread worldwide at different times.

Methods & Materials: In this study we investigated the epidemiology of cholera in Mozambique through the molecular characterization of clinical V. cholerae O1 isolated during 1997–1999 and 2012–2013 epidemics. By detecting and characterizing seven genetic elements, we obtained the mobilome profile of each isolate and, by comparing it to known seventh pandemic reference strains, it was possible to discern among different V. cholerae O1 variants present in the country.

Results: According to our results, during 1997–99, the epidemic strains showed two genetic profiles, both related to the pandemic clone originated from India and reported in other African countries in those years. Differently, isolates from 2012–2013 outbreaks showed a genetic background related to the more recent pandemic clone, at first reported in India and currently the prevalent causative agent of cholera worldwide.

Conclusion: Therefore, our study highlighted the possibility that, despite cholera is endemic in Mozambique, the epidemiology of the disease in the past 20 years has been strongly influenced by the cholera seventh pandemic waves originated in the Indian