

ABSTRACT

Background information: The post-2015 Sustainable Development Goals for sanitation call for universal access to adequate and equitable sanitation and an end to open defaecation by 2030. In Isiolo County, a semi-arid region lying in the northern part of Kenya, poor sanitation and water shortage remain a major problem facing the rural communities.

Objective: The overall aim of the study was to assess the relationship between sanitation practices and the bacteriological quality of drinking water sources. The study also assessed the risk factors contributing to open defaecation in the rural environments of the study area.

Methods: A cross-sectional study of 150 households was conducted to assess the faecal disposal practices in open defaecation free (ODF) and open defaecation not free (ODNF) areas. Sanitary surveys and bacteriological analyses were conducted for selected community water sources to identify faecal pollution sources, contamination pathways, and contributory factors. Analysis of data was performed using SPSS (descriptive and inferential statistics at $\alpha = .05$ level of significance).

Results: Open defaecation habit was reported in 51% of the study households in ODNF villages and in 17% households in ODF villages. Higher mean colony counts were recorded for water samples from ODNF areas 2.0, 7.8, 5.3, and 7.0 ($\times 10^3$) colony-forming units (CFUs)/100 mL compared with those of ODF 1.8, 6.4, 3.5, and 6.1 ($\times 10^3$) areas for *Escherichia coli*, faecal streptococci, *Salmonella typhi*, and total coliform, respectively. Correlation tests revealed a significant relationship between sanitary surveys and contamination of water sources ($P = .002$).

Conclusions: The water sources exhibited high levels of contamination with microbial pathogens attributed to poor sanitation. Practising safe faecal disposal in particular is recommended as this will considerably reverse the situation and thus lead to improved human health.

Keywords: Bacteriological water quality; open defaecation; water-related diseases.