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Assessment of Bacteriological contamination of groundwater used for drinking in Zolozolo, Nkhorongo and Ndirande townships in Blantyre and Mzuzu cities

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Access to safe drinking water in some townships of Mzuzu and Blantyre Cities is a big problem. As a result, some residents drink water from unsafe sources. This study was conducted in Mzuzu and Blantyre to assess the bacteriological contamination of groundwater used for drinking. Water samples collected from unprotected shallow wells and boreholes in the study areas were analyzed for total coliforms and *Escherichia coli* (*E. coli*) using membrane filtration method. One way ANOVA was used to test for statistical differences in total coliforms and *E. coli*. Differences between means were determined using Tukey's studentized test. All water samples in the study areas contained total coliforms. In Ndirande, 100% of boreholes and 80% of shallow wells contained *E. coli* ranging from 3 counts to too numerous to count (>70). In contrast, only 36% of the water samples from 5 shallow wells in Zolozolo and Nkhorongo Townships, Mzuzu City contained *E. coli*. The distance from shallow wells and boreholes to the nearest pit latrines ranged from 5 to 30 m against the minimum accepted distance of 100 m by the Malawi Standards Board for sitting a borehole or shallow well. Presence of *E. coli* in water indicates fecal contamination from human beings or animals. This means that an unacceptable number of boreholes and shallow wells provide unsafe water especially in the City of Blantyre. Further studies are required to investigate disinfection of the drinking water from the borehole and shallow wells including the use of solar radiation.

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Biomedical applications of laser induced breakdown spectroscopy in bacterial identification

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Antibiotic resistant bacterial strains belonging to same species were identified and discriminated using laser induced breakdown spectroscopy (LIBS) and neural networks (NN) algorithm. The method has been applied to identify 40 bacterial strains i.e. *Escherichia coli* (Ec), *Pseudomonas aeruginosa* (Pa), *Klebsiella pneumoniae* (Kp), *Salmonella typhimurium* (St), *Salmonella pullorum* (Sp) and *Salmonella salamae* (Ss). The bacterial samples analyzed included strains isolated from clinical samples and constructed in laboratory. The strains differed from each other in mutations as a result of their resistance to one or more antibiotics. Kp, Ec and Pa strains showed multidrug antibiotic resistance and multiple genes mutations whereas St, Sp and Ss were resistant to kanamycin and differed in only one gene. LIBS are a non-microbiological technique which has been used in various studies to deal with rapid bacterial identification based on the elemental composition of bacterial cells. In a previous study by our group, LIBS/NN has shown to be a promising methodology to classify and predict bacterial samples at genus level. This work is an extension of the previous study in order to investigate the application of LIBS/NN to discriminate different antibiotic resistant strains of same bacterial species and address its use as a rapid potential diagnostic methodology. The objective was to determine if genetic variations between bacterial strains of the same bacterial species even when there is a difference in only one gene, generate sufficient or significant changes in their atomic composition which can be detected by LIBS/NN method in order to achieve their identification and discrimination. Single shot LIBS measurements combined with supervised neural network method were sufficient for a clear identification and classification of bacterial strains differing in multiple and even single mutation. The results demonstrate the potential of this method to be used for continuous monitoring of the bacterial infections and identify pathogenic bacteria at an early stage of infection which can be significant towards an early treatment of the infections.

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