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BACTERIOLOGICAL QUALITY OF WELL WATER USED FOR DOMESTIC PURPOSES IN OWO METROPOLIS, ONDO STATE, NIGERIA

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Abstract

Water from locally dug wells represent the major source of water supply for domestic purposes in most rural and sub-urban communities in Nigeria. Well water is prone to contamination from human and animal activities and from the environment with microorganisms that may include pathogens associated with water-borne illnesses or possess the potential to initiate diseases of opportunities. This study aimed to determine the bacteriological class of well water available for domestic use in Owo Metropolis, Ondo State, Nigeria. Well water samples collected, analyzed by the double-strength and single-strength McConkey broth for the most probable number, MPN of coliform bacteria, and their varieties from subcultures. Antimicrobial susceptibility tests and extended-spectrum beta-lactamase, ESBL were also determined. The MPN in all the samples were several folds higher (15-1800+ MPN/100 mL) than recommended upper limits. Klebsiella species was the most dominant microorganism 46(50%) of 92 isolates. Other isolates included Enterobacter species (25%), Pseudomonas aeruginosa (12.0%), Proteus mirabilis (8.7%) and Serratiamarcescens (4.4%) was the least recovered microorganism. Production of ESBL was highest amongst Klebsiella species (19.7%), Enterobacter species (16.0%), Proteus mirabilis (12.5%)and Pseudomonas aeruginosa (9.1%) and Serratiamarcescens tested negative. The sampled wells were profoundly polluted with microorganisms that carry resistance enzymes incriminated in most nosocomial infections thus, demanding concrete intervention strategiesto circumventmajor water-borne disease outbreaks.

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Introduction:-

Water supply has been a major determinant in location of human settlements for generations and there is always poor accessibility in most low-income countries [1,2]. The quality of water supply is dependent on the source and has critical influence on the health of the community [3]. The natural and traditional supply of water comes from

rivers, springs or underground water sourced through dug wells [4]. Hand dug well water represents a key water supply source for drinking and domestic use in poor-resource economies particularly in the rural and sub-rural settings [5]. Shallow wells are expected to be 15 m deep and deep wells 50 m at the minimum [6]. The geological constitution of the rock from which the well is dug (or karst) and sediment (or aquifer) in the water are keydeterminants of the water purity[7]. The physical, chemical and microbiological physiognomies of water reflect the properties of its potability [8]. Pollution of water is the consequence of anthropogenic and geogenic activities [9,10]. The pollution of ground water come with grave imports for drinking and domestic purposes [11]. Understandably, underground water, does not favor the growth of bacteria due to deficiency in sufficient nutrients to support multiplication and initiation of illnesses 12,13]. Pollution of water with pathogenic microorganisms is the main recurrent hazard of well water. The consistent presence of opportunistic pathogens in water and the detection of indicator microorganisms such as Ecsherichia coli and or Enterococcus faecal ispointedly indicate fecal pollution [1]. Coliform bacteria other than Escherichia coli are more abundant in the gut and survive longer in water thus making their presence in water a valuable indicator of fecal contamination [1,15-18].The quality of dug well water for drinking and domestic use requires assessment to ensure compliance with drinking water quality index, DWQI [19].Several diseases, especially those capable of originating diarrheal diseases are associated with unsanitary water sources [20,21].The study aimed to determine the bacteriological quality of well water used for drinking and domestic purposes in Owo Metropolis, Ondo State, Nigeria.

Materials and Methods:-

Study design:

Cross-sectional study of the bacteriological quality of well water used for domestic purposes in Owo Metropolis, Ondo State, Nigeria.

Collection of samples:

The tap source for each covered well water was washed wearing sterile gloves, allowed to flow for 30 sec and with sterile 250 mL bottle, approximately 200 mL of water was collected and kept in cold chamber for transportation to the laboratory for examination within 2 h.

Examination of samples:

Physical visual assessment of samples for turbidity was determined and measurement of pH with a meter (Ohaus® ST20) and values noted.

Bottles of 5 x 10 mL double-strength McConkey, MCC broth (Oxoid CM 0005) containing Durham tubes inoculated with 10 mL of water aseptically after discarding a third of the sample, single-strength MCC broth of 5 x 5 mL with 1.0 mL, and 5 x 5 mL with 0.1 mL respectively. Control tests involved a set of broth in each category inoculated with sterile water. Thereafter, the trapped gas in each tube was expelled priorincubation at 37^{o}C for 24 h. All negative bottles re-incubated for further examination at 48 h. The production of acid and gas indicated a presumptive positive test. The most probable number, MPN of coliform bacteria present in each sample was obtained using the McCrady's Probability Table for poor water source. Subsequently, sub-cultured onto MCC agar (CM 0007) and Salmonella-Shigella agar, SSA, (Oxoid CM 0099) incubated at 37^{o}C for 24 h. Each growth was picked up for characterization tests and identified by the scheme outlined by Cowan [22]. The double-disc synergy test, (amoxicillin-clavulante 30 µg plus ceftazidime30 µg combination) was applied for the detection of extended-spectrum beta-lactamase, ESBL. Susceptibility of isolates to antimicrobial agents was determined by the Kirby-Bauer disc diffusion technique with tetracycline (TE 10 µg),ampicillin (PN 10 µg), amoxicillin (A 10 µg), amoxicillin-clavulanate (AMC 30 µg), gentamycin (CN 10 µg), ciprofloxacin (CIP 10 µg), levofloxacin (LVX 10 µg), ceftazidime (CAZ 10 µg), cefotaxime (CTX 10 µg) and azithromycin (AZM 10 µg).The application of the Clinical Laboratory Standards Institute [23]guidelines assisted in the determination of isolates susceptibility.

Results:-

Forty-seven representing 78.3% of 60 samples were turbid or had color and the pH of all samples ranged from 6.0-6.9. The least range of MPN in 100 mL sample was 15-100 in 22(36.7%) of60 well water samples (Table 1).The MPN range 101-200/100 mL occurred in 16(26.7%), 201-300 in 8(18.3%), 301-400, 7(11.7%) and the highest MPN/100 mL, ≥401 occurred in 4(6.4%) of the samples.

The distribution of microorganisms recovered from the well water samples is shown in Table 2, with Klebsiella species 46(50%) of 92 isolatesas the most frequent isolate made up of Klebsiellapneumoniae 31(33.7%) and Klebsiellaaerogenes 15(16.3%). Other microorganisms recovered were Enterobacter species 23(25.0%) consisting of Enterobacter cloacae 17(18.5%) and Enterobacteraerogenes 6(6.5%), Pseudomonas aeruginosa 11(12.0%), Proteus mirabilis 8(8.7%) and Serratiamarcescens 4(4.4%) was the least isolated microorganism.Extended-spectrum beta lactamase, ESBLs detection was highest within isolates of Klebsiella species 9(19.6%). The detection rate of ESBLs in isolates of Enterobacter species was 17.4%, Pseudomonas aeruginosa 9.1% and Proteus species 12.5%. Isolates ofSerratiamarcescens tested negative.

The susceptibility of isolates to antimicrobial agents (Table 3) shows the Klebsiella species and Enterobacter species were most susceptible to gentamycin, ciprofloxacin, levofloxacin, ceftazidime and cefotaxime at a range of 65.5-86.7%. The susceptibility of Pseudomonas aeruginosa was 36.4-54.5% for these same agents. Proteus mirabilis was most susceptible to cefotaxime (75%) and least to amoxicillin-clavulanate (12.5%). Serratiamarcescens was the only isolate that showed susceptibility to amoxicillin (25%) and susceptibility was highest with gentamycin (100%). No isolate showed susceptibility to either of tetracycline or ampicillin.

Table 1:- The most probable number (MPN) of coliform/100 mL of well water.

MPN Range	No. of Cases (%)
15-100	22(36.7)
101-200	16(26.7)
201-300	11(18.3)
301-400	7(11.7)
≥401	4(6.7)

Table 2:- Distribution of isolates and detection rate of ESBL within each genus.

Isolate	No. of Cases (%)	ESBL (%)
Klebsiellaspp	46(50.0)	9(19.6)
Enterobacterspp	23(25.0)	4(17.4)
Pseudomonas aeruginosa	11(12.0)	1(9.1)
Proteus mirabilis	8(8.7)	1(12.5)
Serratiamarcescens	4(4.4)	0(0.0)

Table 3:- Susceptibility of isolates to antimicrobial agents.

Isolate / Antimicrobial agent (%)	TE	PN	A	AMC	CN	CIP	LVX	CAZ	CTX	AZM
Klebsiellaspp	0.0	0,0	0.0	0.0	71.7	69.6	71.7	65.2	67.4	47.2
Enterobacterspp	0.0	0.0	0.0	0.0	4.3	73.3	86.9	65.2	73.9	43.5
Pseudomonasspp	0.0	0.0	0.0	0.0	54.5	45.4	54.5	36.4	54.5	18.2
Proteus mirabilis	0.0	0.0	0.0	12.5	75.0	50.0	50.0	65.5	75.0	75.0
Serratiamarcescens	0.0	0.0	25.0	50.0	100	75.0	75.0	50.0	50.0	25.0

Discussion:-

The study revealed that 78.3% of well water samples were turbid, cloudy or colored as opposed toa clear and colorless appearance of potable water amongst other physical attributes recommended by the World Health[24]. Water turbidity is an indication that the water contains dissolved substances and particulate matter as a sign of microbiological pollution and poor quality[25]. The pH of the samples ranged from 6.5-6.9, all within recommended limits of 6.5-8.5[24,26-28]. However, acidic drinking water can result in metallic taste due to dissolved chemicals and modulate microbiome constitution and alterations in function [29,30]. The least MPN or coliform organisms in the well water samples was 15/100 mL, this is much higher than the maximum for non-chlorinated water, thus inferring poor quality or pollution. These observations are consistent with reports from other studies[31,32]. Quite unpredictably, the isolated microorganisms did not include Escherichia coli, the classical marker of water pollution;

nevertheless, the very high number of coliform bacteria (MPN) recorded in each of the water samples make them of equal relevance.Klebsiella species was the most prevalent microorganism recovered,representing 50% of all isolates. This observation simulates reports from earlier studies[33,34], and involving markedly higher proportion ofKlebsiellapneumoniae (33.7%) than other Klebsiellaspecies (16.3%), indicating that Klebsiellapnuemoniaewas the most dominant species in these water sources [35].Klebsiella species natural habitat includes fresh water sources, vegetation, and the gut of humans and animals, this interestingly, enhances the capacity of the microorganism tocontaminate water easily in poor sanitary settings. This microorganism is associated with complicated urinary tract infections, UTIs and sepsis chiefly in individuals with pre-existing health challenges, posing major fears due to accumulative number of hyper-virulentand carbapenem-resistant phenotypes being reported globally[36,38]. Enterobacter species (25.0%) was the next common isolate - a fecal microorganism previously used in combination with Escherichia coli as marker organisms for fecal pollution of water, this denotes pollution of the water as other studies have indicated [27,39]. Pseudomonas aeruginosa occurred at a rate of 12.0%. The recovery of the microorganism from domestic water source points to a source ofperil, mimicking reports from earlier studies [40,41], Water source burdened with Pseudomonas aeruginosa is consequentially an indication of water insecurity. This in part due to the microorganism's intrinsic resistance to many antimicrobial agents and a major initiator of nosocomial infections in clinical sceneries[42-45]. The isolation of Proteus mirabilis (8.7%) from the water samples infers that the microorganism as a regular contaminant in bodies of fresh water and signifies organic matter pollution of the wells [46-48]. The association of Proteus species with domestic water source inevitably portendsdanger for public health. The microorganism is one of the commonest in catheter-associated urinary tract infections, cUTIsowing to the pathogenicity potential via the production of urease that breaks down urea in urine releasing ammonia leading to alkalizationand precipitation of nephrolithiasis (or kidney stones) [49].Serratiamarcescens (4.4%) was the least frequent isolate. The habitat of this microorganism includesfresh water bodies, soil, insects and vegetation, and a regular environmental pollutant of fresh water, thus showing its presence in water as an index of poor water quality. Many Serratiamarcescens isolates are multidrug resistant, MDR and linked to infections of opportunities, and as a consequence represents a dangerous water source or channel of health hazard [50,51]. This microorganism typically causes infections in persons with depressed immunity and in individuals with other clinical conditions [52]. In spite of higher susceptibility rates of the isolates to ciprofloxacin, levofloxacin, ceftazidime, cefotaxime and gentamycin (45.4-100%). All isolates showed resistance to tetracycline and ampicillin, this is in consonance with prior observations on susceptibility of the isolates to first-line antimicrobial agents [53]. The production of extended-spectrum beta-lactamase, ESBL was highest amongst Klebsiella species (19.7%) and Serratiamarcescens isolates tested negative. Klebsiella species, Enterobacter species and Pseudomonas aeruginosaclassified into theESKAPE group of bacteria and included in the World Health Organization priority list of microorganisms resistant to a wide range of antimicrobial agents requiring extra precautionary measures in their infections [54]. This in addition, creates direpredicaments in making treatment decisions, hampering the ability to provide effective clinical care [35,52,55-58], and also the leading bacteria involved in hospital-acquired infections, HAIs [59]. The presence of ESKAPE and MDR bacteria in water negates the requirement for freedom of domestic water source from harmful microorganisms as a basic prerequisite for healthy living [60]. This study infers that the isolated microorganisms were regularly present in the environment of the wells as underground water does not support multiplication of bacteria [13]. Antimicrobial resistance, AMR has been a key challenge for humans, animals and the environmentin the last half century requiring concerted control efforts and adoption of novel strategies towards the attainment of one health goal [61,62]. Insufficiency or failure to provide potable water in this community is the main driver for well water for home use [63] and unfortunately, these wells are dug by artesians who possessed no professional competence, further exacerbating the risk of pollution [64]. The responsibility for the safety and or purity of private well water lies with the individual owner unlike public water systems with testing schedules and set standards [65].

Conclusion:-

The study highlights insecure water source exemplified by poor physical and bacteriological properties of well water used for domestic purposes in Owo metropolis laden with ESKAPE member bacteria amongst others including MDR strains that can be contributory to the growing burden of disease and mortality rates in infections related to these microorganisms internationally. The provision of potable water as a right of all citizens in any nation requires the action of appropriate government agency in providing potable water in Owo and education on domestic wells specifications, safety testing and maintenance where potable or pipe-bornechlorinated water is impracticable.

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