



## Bacteriological Drinking Water Potability at Al-Madinah Al-Mounwwarah in Relation to Plasmid-Linked Multidrug-Resistance

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**Abstract:** The principle drinking water sources at the Kingdom of Saudi Arabia (KSA), including Al-Madinah Al-Mounwwarah are the desalinated and underground well water. The present study focused on evaluating this drinking water sources portability from the bacteriological point of view. Searching for any possible correlation between bacteria present in the studied drinking water and those which have been isolated from the final effluent waste water of hospitals, is a crucial target. Water samples were collected from underground well water, underground reservoirs and taps at the nearest neighbourhood to previously-studied five hospitals namely; King Fahd, Ohod, Al-Mouassat, Women and Maternity and Saudi-German. Water samples from two additional sites namely; Al-Eskan and Al-Bsateen, away from these hospitals were investigated as control remote areas. Drinking bottled water (6 trade marks) processed at Al-Madinah Al-Mounwwarah namely; Doraq, Nada, Quba, Sarat, Taibah and Watanya, were also studied. Qualitative and quantitative bacteriological full analyses for water samples collected from the 27 sites, including enumeration of total viable (TVB), total coliform (TC) and faecal coliform (FC) bacteria in addition to the identification of the purified isolates to the specific level using API 20E strips and its software program, have been accomplished. Antibiotic-resistance profiles, expressed in MIC  $\mu\text{g/ml}$ , of the most important Gram- ve rods against 9 antibiotics namely; bacitracin, chloramphenicol, erythromycin, impenim, penicillin G, rifampicin, streptomycin, tetracycline and vancomycin, were also drawn up. Screening for plasmids in the antibiotic-resistant isolates was fully studied. Results showed high and fluctuated TVB, TC and FC bacterial counts ranged between 100 : 1000, 90 : 800 and 1 : 3 cfu/100 ml, respectively, in the studied underground well water, indicating its unacceptable quality for drinking. Underground reservoirs and tap water samples were free from TC and FC, giving acceptable drinking water according to both the local and international standards, although having low to moderate TVB counts (1 : 15 cfu/ 100 ml). No direct correlation between the bacterial counts and the neighborhood hospitals, compared with counts detected in water samples from the two remote control areas. The study clearly-assured the bacteriologically-high grade quality of all the six investigated bottled water, showing no counts for TC and/or FC, so safe to drink. The low TVB counts (3 : 24 cfu/ 100 ml) seemed, numerically-potable according to standards, but health threatens are alarming because of the ability of some of these commensals to accept extrachromosomal elements changing their characteristics and impose pathogenic behaviours. Identification revealed that 74% were Gram -ve, 56% of it are rods, while 18% are cocci, only 26% were Gram +ve rods, 19% are spore-formers and 7% are non spore-formers, while no Gram +ve cocci were detected. Gram -ve rods belonged to 8 strains, 7 species and 7 genera namely; *Escherichia coli* 1, *Citrobacter frundii*, *Providencia stuartii*, *Proteus vulgaris*, *Cryseomonas leteula*, *Stenotrophomonas maltophili* (which have been heavily-isolated from almost all the studied bottled water but non of the other sources), *Aeromonas hydrophila* (group 1&2). The most distributed species were *Aeromonas hydrophila* (group 1), *Cryseomonas leteula* and *Stenotrophomonas maltophilia*. All of the 8 studied strains resist from 3 : 9 of the antibiotics at MIC(s) from 50 :100  $\mu\text{g/ml}$ . Molecular studies resulted in the detection of plasmids in 5 out of the 8 strains. Miniprep, alkaline lysis and 1% agarose gel protocols, along with electrophoresis against Hind III partially-digested Lambda phage, showed only one plasmid in each, all of the same size; 23130 bp. It is very important here to record that only 3 isolates namely; *Escherichia coli* 1, *Providencia stuartii* and *Stenotrophomonas maltophilia*, out of 5 isolates of these were identical; from the points of antibiotic-resistance profiles, MIC(s) and plasmid content, with 3 of those isolated from hospitals waste water in the previous study.

**Keywords:** Potability, Plasmid DNA, Antibiotic-resistant bacteria, Escaping of pathogenic bacteria from hospitals wastewater to drinking water.

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