

Identification of Pathogenic Bacteria (*Escherichia coli*) in Drinking Water Sources and Detection of their Antibiotic Resistant Genes in Gampaha District, Sri Lanka

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Abstract

Water plays a critical role on Earth, and its significance is particularly evident in relation to human beings. The present study aimed to identification of *Escherichia coli* and detection of their antibiotic resistant genes in drinking water sources of five different regions Gampaha district, Sri Lanka. Five resources of randomly collect drinking water samples (n = 50) from every 10 samples from five different regions were used for analysis. The pathogenic microorganisms were isolated via membrane filtration technique (0.45 μ m) and identified via conventional standard biochemical keys including Indole, Citrate, MRVP, TSI, Motility and Chromogenic culture and Gram stain. The DNA extraction was performed via column-based method. The disk diffusion method was performed to access the antibiotic sensitivity of the isolated *Escherichia coli* following CLSI guidelines via Ampicillin, Gentamicin and Tetracycline antibiotics (10 mg). From total sample 18% were positive with *Escherichia coli* in unprotected well, protected well and tap line samples. All nine samples exhibit resistance to Ampicillin (< 13 mm), sensitive to the Gentamicin (> 15 mm) and resistant to Tetracycline (< 11 mm). Molecular determination, 2% agarose gel image, confirmed the presence of *E. coli* DNA as evidenced by the presence 400 base pairs (bp) band size and UidA gene found in one sample confirmed the presence of different strains of isolated *E. coli*. The specific antibiotic resistant genes were analyzed and all three samples were negative for the *tet (a)*, *tet (C)*, *tet (m)* and bla_{TEM} antibiotic resistant genes which confirms that isolated *E. coli* were not resistant for the Tetracycline and Ampicillin due to mentioned genes.

Keywords: *Pathogenic microorganism, Bacterial contamination, Antibiotic resistance*