

ORIGINAL ARTICLE

**Bacterial Investigation of Dug well water samples in and around Kaliyal and Arumanai villages of Kanyakumari district in Tamil Nadu**

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ABSTRACT

The present research work has been undertaken in this context in dug wells of Kaliyal and Arumanai villages located between 8.3662°N and 77.2434°E in Vilavankodetaluk, Kanyakumary district, Tamilnadu. The dug wells were selected based on the physical environment such as human settlement, proximity to septic tank, leach pits, waste heap, drainage, river, irrigation area, dam, mountain range, soil type, agriculture etc. Bacteriological examination of water in twenty dug wells were analysed monthly for a period one year from April 2018 to March 2019. *Escherichia coli*, *Klebsella sp.*, *Streptococcus sp.*, *Serratia sp.*, *Legionella sp.*, and *Enterobactersp* were identified from the study areas.

**Keywords :** Dug wells, bacteria, Kaliyal, Arumanai, E.Coli

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**INTRODUCTION**

The microbes are ubiquitous in the environment. They have been found in a variety of environmental situations, such as water, vegetation, or water, and they influence many biochemical and geochemical processes. They have been recovered from aquatic environments receiving industrial wastewaters, plant products, fresh vegetables, food with a high content of sugars and acids, frozen orange juice concentrate, sugarcane wastes, living trees, and plants and plant byproducts. They are commonly associated with wood, sawdust, and waters receiving industrial effluents from pulp and paper mills and textile finishing plants. The microbiological quality of random well waters from different locations was analysed by Mwekaven *et al* [17]. Aekis and Indirani [1] observed the water tested was positive for *Streptococcus faecalis* and *Klebsiella* species, when the count of coliform bacteria exceeded the standard limits set for untreated water

Kayowa and Ayanfemi [12] reported seasonal changes in water quality of well water samples collected near pit latrines in Oko, Nigeria tested during rainy and non-rainy seasons exhibited higher contamination. Owoeye and Akinneye [23] investigated the total and faecal coliform contamination of domestic well water through infiltration from sewage pits during dry and wet seasons.

Islam *et al* [11] studied on the safe distance between pit latrines and tube wells at different hydrogeological conditions. The Indian Standards under IS [10] drinking water specifications prescribed that all samples taken from the dug wells, should be free from coliform organisms. Also the presence of coliform organisms are tested against the IS 1622 standards and the results are compared. The standards propose that *E.coli* or pathogenic bacteria should not be present in any water intended for drinking.

Rare reports have described disease resulting from infection with *Serratiasps.* an opportunistic pathogen was isolated from drinking water [29].

Mishra *et al* [16] examined the potability of 100 different water samples from different wards of Belagavi city by analyzing total and fecal coliforms using MPN method and Membrane Filter technique and found that only 12 samples had unsatisfactory quality for drinking purpose. Auta *et al* [3] assessed the bacteriological quality of well water in DogonDawa district, Nigeria and found that the bacterial count was very high exceeding the recommended level of zero coliform per ml.

Sivasankar *et al* [25] prepared a comprehensive status report on drinking water quality of Nagercoil municipal area by examining the water quality of 58 sources comprising 18 wells, 16 ponds and 24 treated water samples. Most of the samples were found contaminated and a certain degree of treatment needs to be given before using them for drinking purpose.

To study the seasonal and annual variations in total bacterial count and species identification *in the* dug well water samples in the study area,

## MATERIAL AND METHODS

### Study area

Kanyakumari District is the southernmost part of Tamil Nadu in the Indian sub-continent with an area of 1672 square kilometres. This tiny district lies between 77° 15' and 77° 36' of the eastern longitude and 8° 03' and 8° 35' of the northern Latitude.

The present research has been made to investigate the bacteria influencing the quality of 20 dug well water samples in and around Kaliyal and Arumanai Villages of Kanyakumari district by randomly selecting twenty sampling sites Kadayal (W1), Kaliyal (W2), Karode (W3), Arukani (W4), Pechiparai (W5), Chittar (W6), Arumanai (W7), Pokinkalai (W8), Ganapathikal (W9), Ambadi (W10), Thiruparapu (W11), Muzhucode (W12), Maruthamparai (W13), Thiruvarampu (W14), Marapady (W15), Kattavilai (W16), Manjalumoodu (W17), Malaicode (W18), Melpalai (W19) and Anducode (W20).

### Collection of dug well sample

The study was conducted for a period of one years from April 2018 to March 2019. Water samples were collected in clean two litre water plastic cans. The samples were analysed for presence of bacterial count.

The analysis of bacterial count in water samples of Kaliyal and Arumanai villages of KK district included Total Viable bacterial Count (TBC) which gives a quantitative estimate of the concentration of bacteria in a sample. The count represents the number of colony forming units (CFU) per ml of the sample. The bacteria were isolated and identified.

### Result

The data obtained from analysis of water samples from different wells in and around Kaliyal and Arumanai villages of KK district were measured and analysed.

In the bacterial identification analysis during the period 2018-19, it was found that *Escherichia sp.* was found in samples from all the wells while *Klebsiella sp.* was identified in wells such as W2, W4, W7, W11, W13, W16, W18 and W20. Furthermore, *Streptococcus sp.* was identified in wells such as W1, W5, W7, W10, W12, W14, W18, W19 and W20. Above and beyond, *Serratia sp.* was found in wells such as W2, W5, W6, W9, W12, W15, W17 and W19. Similarly, *Legionella sp.* was documented in wells such as W1, W3, W4, W5, W8, W10, W11, W16, W18 and W20. Moreover, *Enterobacter sp.* was found in wells such as W1, W2, W4, W6, W8, W11, W12, W13, W16, W18 and W17 (Table 1).

**Table 1: Identification of bacteria in the well water samples during 2018- 2019**

Wells	Bacteria					
	<i>Escherichia sp.</i>	<i>Klebsiella sp.</i>	<i>Streptococcus sp.</i>	<i>Serratia sp.</i>	<i>Legionella sp.</i>	<i>Enterobacter sp.</i>
W1	+	-	+	-	+	+
W2	+	+	-	+	-	+
W3	+	-	-	-	+	-
W4	+	+	-	-	+	+
W5	+	-	+	+	+	-
W6	+	-	-	+	-	+
W7	+	+	+	-	-	-
W8	+	-	-	-	+	+
W9	+	-	-	+	-	-

W10	+	-	+	-	+	-
W11	+	+	-	-	+	+
W12	+	-	+	+	-	+
W13	+	+	-	-	-	+
W14	+	-	+	-	-	-
W15	+	-	-	+	-	-
W16	+	+	-	-	+	+
W17	+	-	-	+	-	-
W18	+	+	+	-	+	+
W19	+	-	+	+	+	-
W20	+	+	+	-	-	+

+ Presence - Absence

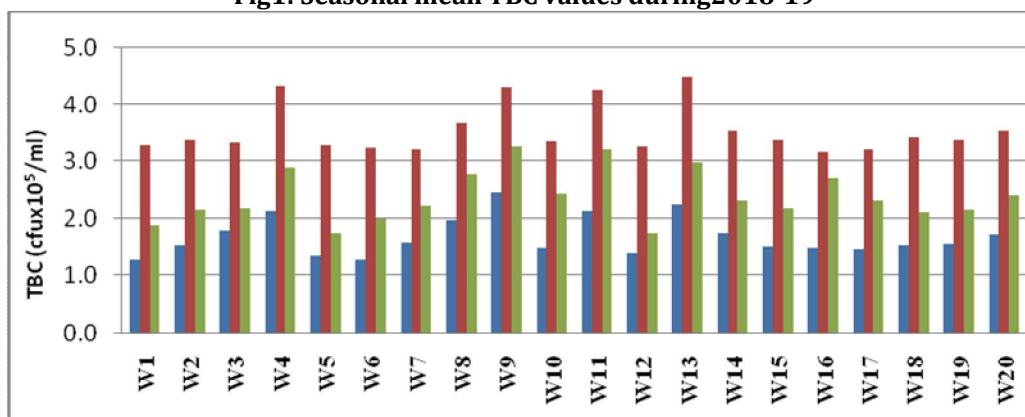
The annual mean values of TBC broadly fluctuated from  $2.32 \pm 1.01 \times 10^5$  cfu/ml at W1 to  $4.05 \pm 0.81 \times 10^5$  cfu/ml at W7 during 2017-18 and  $2.13 \pm 0.89 \times 10^5$  cfu/ml at W5 to  $3.35 \pm 0.79 \times 10^5$  cfu/ml at W9 during 2018-19 (Table 2).

It varied from  $1.28 \pm 0.23 \times 10^5$  cfu/ml at W6 to  $2.47 \pm 0.15 \times 10^5$  cfu/ml at W9 in premonsoon,  $3.09 \pm 0.34 \times 10^5$  cfu/ml at W7 and W17 to  $4.49 \pm 0.86 \times 10^5$  cfu/ml at W13 during monsoon and  $1.75 \pm 0.20 \times 10^5$  cfu/ml at W5 to  $3.28 \pm 0.21 \times 10^5$  cfu/ml at W9 during post monsoon during 2018-19. (Table 2 & Fig 1)

**Table 2: Seasonal and Annual mean values of TBC in dug well water**

Well no.	Mean +S.D 2018-19			
	PRM	MON	POM	Annual mean
W1	1.28+0.34	3.29+0.17	1.89+0.40	2.15+0.92
W2	1.53+0.35	3.38+0.14	2.16+0.33	2.35+0.84
W3	1.79+0.51	3.34+0.22	2.17+0.37	2.43+0.77
W4	2.13+0.09	4.33+0.85	2.90+0.27	3.12+1.06
W5	1.35+0.20	3.29+0.14	1.75+0.20	2.13+0.89
W6	1.28+0.23	3.26+0.13	2.00+0.54	2.18+0.91
W7	1.57+0.30	3.21+0.26	2.21+0.40	2.33+0.76
W8	1.98+0.31	3.68+0.20	2.78+0.52	2.81+0.80
W9	2.47+0.15	4.30+0.11	3.28+0.21	3.35+0.79
W10	1.49+0.17	3.37+0.13	2.44+0.20	2.43+0.82
W11	2.13+0.10	4.26+0.21	3.20+0.39	3.20+0.94
W12	1.39+0.18	3.28+0.12	1.76+0.19	2.14+0.87
W13	2.23+0.15	4.49+0.86	2.99+0.35	3.24+1.10
W14	1.76+0.42	3.55+0.05	2.30+0.16	2.54+0.82
W15	1.50+0.31	3.38+0.15	2.18+0.36	2.35+0.85
W16	1.49+0.15	3.17+0.16	2.71+0.44	2.45+0.79
W17	1.47+0.15	3.21+0.26	2.31+0.23	2.33+0.77
W18	1.52+0.40	3.42+0.12	2.11+0.42	2.35+0.89
W19	1.55+0.29	3.38+0.14	2.15+0.34	2.36+0.83
W20	1.72+0.32	3.55+0.05	2.41+0.15	2.56+0.81

**Fig1: Seasonal mean TBC values during 2018-19**



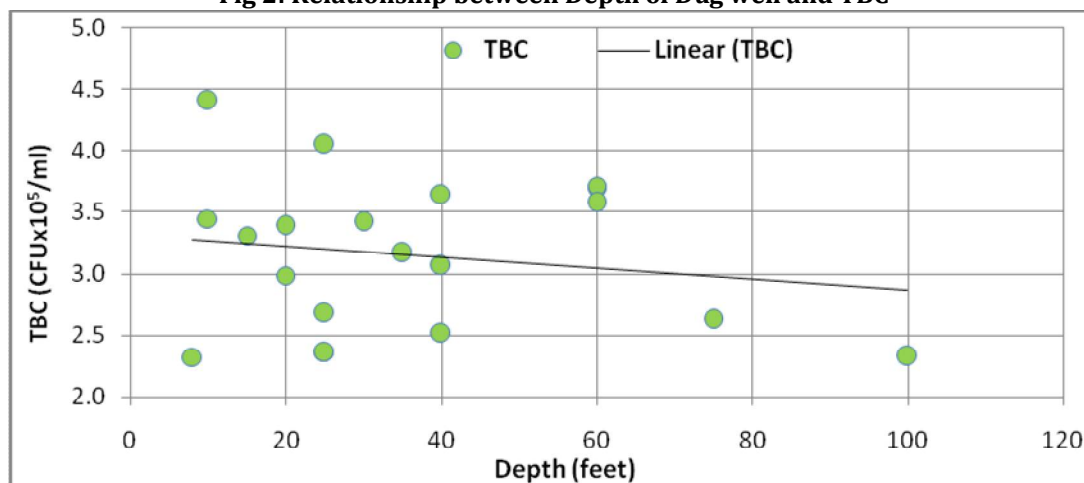
The analysis confirmed that the depth of well and Total Bacterial Viable count  $r = -0.42$ , ( $p < 0.05$ ) have a negative correlation which is considered to have a typical effect size. Likewise, presence of septic tank and Total Bacterial Viable count  $r = 0.78$ , ( $p < 0.05$ ) have a positive correlation which is considered to have a much larger than typical effect size. Likewise, the relationship between depth of dug wells and Total Bacterial Count in the well water collected during 2018-19 are analysed and detailed in (Table 3).

**Table 3: Correlation between physical environment of wells and TBC during 2018-19**

S. No.	Ecological Parameters	Depth of Well	Well Type	Presence of septic tank	Water logging	TBC
1	Depth of well	-	0.070	0.520	0.170	-0.440*
2	Well type	-	-	0.040	0.130	-0.420
3	Presence of septic tank	-	-	-	0.040	0.730*
4	Water logging	-	-	-	-	0.410
5	<b>TBC</b>	-	-	-	-	-

The analysis confirmed that the depth of well and total bacterial viable count  $r = -0.44$ , ( $p < 0.05$ ) have a negative correlation which is considered to have a typical effect size. Likewise, presence of septic tank and total bacterial viable count  $r = 0.73$ , ( $p < 0.05$ ) have a positive correlation which is considered to have a much larger than typical effect size. In order to understand the tendency of the relationship, the depth of dug well samples and the TBC are plotted along the axes and the trend line is generated. The analysis using scatter plot is depicted in (Fig.2).

**Fig 2: Relationship between Depth of Dug well and TBC**



## DISCUSSION

The microbial variables are caused by anthropogenic activities and greed of human kind. The delicate balance of the nature gets disturbed when the forced interventions are brought in to increase gluttony. During 2018-19 the minimum count was at Arumanai (W7) and Manjalumoodu (W17) and the maximum count at Maruthamparai. High contamination in monsoon season might be due to infiltration of leachates from sources such as solid waste dumps, leach pits and sewage drains. Such microbial contamination in ground water from drain leachate during monsoon was reported from Delhi by Kumar *et al* [14]. Similar results were observed by Vijaya and Raj [32].

Since some strains of *E. coli* cause diarrhea, while others cause urinary tract infections, respiratory illness and pneumonia, and other illnesses, the presence of *E.coli* in all samples during the present study is a matter of great concern. It was also reported by Susiladevi *et al* [27] from ground waters of Cuddalore in Tamilnadu.

The presence of *Escherichia sp.* is related to population density is the best biological indicator of drinking water quality for public health protection. Tya *et al* [31] reported that the presence of *Escherichia sp.* in dug well samples is due to proximity of the wells to stagnant wastewater, which may contain these harmful organisms. Odeyemi *et al* [18] conveyed similar conclusion where well water samples appeared to be clear and colourless but heavily contaminated with enteric pathogens. The survival and transport of *Escherichia sp.* dependent on rainfall after cattle slurry application were studied on drained plots [19].

The identification of *Escherichia sp.* in dug well water samples of all sites during the present study can be due to the rainfall and leaching of the bacteria to the ground water sources. The contamination of surface water, containing animal feces, leached into the unconfined aquifer can also be another reason for the identification of *Escherichia sp.* in dug well water samples as reported by Olsen *et al* [20].

The Count of *Klebsiella sp.* found in a few dug well water samples were in concurrence with other studies of well water investigations [22]. *Klebsiella sp.* were identified from drinking water samples collected from some rural habitations of northern Rajasthan, India [28]. Bacteriological analyses carried out by Antony and Renuga [2] on Ananthanar channel water of Kanyakumari district also reported the presence of *Klebsiella sp.* in the water samples.

Further, the *Streptococcus sp.* is identified in various water samples from wells present in pasture land. In an earlier study by Doran and Linn [7] and opined that fecal coliforms to fecal streptococci ratio in pasture runoff. Pinto *et al* [24] assessed the hygienic quality of environmental samples from a variety of drinking water sources and isolated 198 strains of *Streptococci sp.* Dalu *et al* [5] found *Streptococci sp.* in water sources with rivers, lake and wells showed the greatest diversity.

Dug well water samples in and around Kaliyal and Arumanai Villages of KK district indicate the presence of *Serratia sp.* in a few locations. Taylor *et al* [30] reported horizontal transportation of *Serratia sp.* to the ground water source and can be a reason for dug well water contamination.

*Legionella sp.* is found everywhere in the environment. It is a natural inhabitant of water and is found at the air-water interface in surface water (rivers, lakes and streams) and in aerated biofilms. *Legionella sp.* was identified in a few dug well water samples and similar findings were reported in the water systems of a tertiary healthcare center [7].

*Enterobacter sp.* were reported from more than half of the sample wells. Similar findings were reported by OmariandYeboah-Manu [22] in ground water investigations. Krishnan *et al* [13] isolated *Enterobacter sp.* from the water samples which provided examples of non-fecal coliforms. World Health Organization [33] recommended that wells should be located at least 30m away from latrines and 17m from septic tanks. Mahath and Kani [15] based on the samples from protected and unprotected wells and samples from wells near latrine (<30 m) in Meenambalam, Kollam District, Kerala reported that most of the water samples are contaminated. The correlation between temperature and depth profiles indicated ambient temperature variation on all the profiles, with a lag time of two to five months as reported by Calvache *et al* [4]. Similarly, negative relationship between depth and total coliform [6]. The well type was also found strongly associated with *E. coli* concentration as reported by Eisenhauer *et al* [9].

## CONCLUSION

High contamination in monsoon might be due to infiltration of leachates from sources such as solid waste dumps, leach pits and sewage drains. Majority of the dug well water samples studied in Kaliyal and Arumanai Villages of KK district enumerated *Escherichia sp.*, *Klebsella sp.*, *Streptococcus sp.*, *Serratia sp.*, *Legionella sp.* and *Enterobacter sp.* *E.coli sp.* was predominant in all well waters throughout the study period. The presence of different type of bacteria observed in well water indicates contamination due to ecological and anthropogenic activities. It leads to the transmission of diseases by water borne pathogens. The continuous monitoring should be maintained in order to promote and maintain a safe working

environment and ensure detection when abnormalities that could endanger both human and environment.

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