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STUDIES ON THE LONGITUDINAL PROFILE OF THE BACTERIOLOGICAL QUALITY OF ABA RIVER, NIGERIA

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ABSTRACT

The longitudinal profile of the bacteriological quality of Aba River at six sampling stations (UP, UW, AB, CW, RL and DS) along the river course was studied. There was an upstream – downstream bacterial variations ($P < 0.05$) with UP showing initial lower counts (log_{10} 3.08 cfu $m1^{-1}$), while the maximum was observed at DS (log_{10} 5.60 cfu $m1^{-1}$). Three stations: UW, AB and DS showed increase in heterotrophic bacterial counts throughout the six months study period (Feb – July). Stations CW and RL showed decrease in bacterial counts after the third-month (April) of the investigation. Ten bacterial genera were isolated and the most prevalent in all the stations included *Staphylococcus* sp., *Pseudomonas* sp., *Escherichia coli* and *Micrococcus* sp. *Klebsiella* sp., *Streptococcus faecalis*, *Salmonella* sp., Shigella sp., *Bacillus* sp. and *Clostridium perfringens* were not detected in UP station. Of all the sampling stations, AB and DS showed the greatest variation of isolates followed by CW and RL. Station AB showed the highest coliform counts (1.26×10^3 MPN $100m1^{-1}$) while the lowest was observed at UP (24 to 70 MPN $100m1^{-1}$). The high bacterial and or coliform counts obtained along the course of the river depicts the public health risk associated with the domestic use of the river water and the need to plan an adequate pollution control strategy for Aba River.

KEY WORDS: Longitudinal profile, Aba River, bacterial variation, bacteriological quality, pollution control strategy.

INTRODUCTION

Surface waters are usually exposed to microbial contaminations from run-off inputs, soils and any waste deliberately or inadvertently dumped into such waters (Peele *et al.* 1981). In Nigeria, increased industrial activities and urbanization have led to wide scale contamination of surface waters from industrial, agricultural and domestic sources (Ajayi and Osibanjo, 1981). For long Aba River has been subjected to dumping of untreated wastes from various sources such as carwashing centres, abattoirs and markets sited near the river course. Such wastes invariably introduce a variety of microorganisms in addition to the authochthonous microflora of the river. Furthermore, most of the communities living near the river course defaecate and or dump their domestic wastes into the river thereby creating pollution problems.

Studies on the extent of effluent impact on bacterial population of temperate waters have been attempted by some workers (Ferris *et al.*, 1980; Peele *et al.*, 1981). However, little work has been done on bacterial distribution and effects of effluent discharge on few Nigerian rivers (Ajayi and Osibanjo 1981, Benka-Coker and Ohimain, 1995; Tatah and Ikenebomeh, 1999), despite the increase in industrialization and urbanization in recent times. Due to the diffuse nature of the influx of wastes into the Aba River, the investigation of the longitudinal profile of the bacterial quality of the river has become desirable for pollution control strategy, hence, the study reported here.

MATERIALS AND METHODS

Selection of Study Area

The Aba River which flows north to south started from the uninhabited area of Umunweke village and flows downstream to Ngwa Road, Aba. Six sampling stations designated as Upstream (UP), Umuweke (UW), Abattoir (AB), Carwash (CW), River Layout (RL) and Downstream (DS) were randomly chosen along the course of Aba River. Except UP, all other stations reflected points where wastes from different human activities enter into the river.

Sample Collection

Triplicate water samples (500 m1 each) were collected (about 5cm below the water surface) twice a month from each station after on-site rinse of the stoppered flasks and transported in ice-

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packed cooler to the laboratory for bacteriological analysis.

Bacteriological Analysis

The bacterial counts of the water samples were determined using pour plate technique. The plating was carried out on Plate Count Agar (PCA) (Biotec Laboratory, UK) for each of the samples and incubating one set of plates aerobically and another set anaerobically (Gas-Pak Oxoid, UK) both at 35-37°c for 18-24 hours. Spore forming bacteria were isolated by inoculating pre-heated (80°C for 15 min) water samples onto PCA and incubating at 35 – 37°C for 18 – 24 hours. Developed colonies were counted and recorded as cfu $m1^{-1}$. The population of coliforms were determined by the Most Probable Number (MPN) technique (APHA, 1992) following subculturing of positive tubes onto MacConkey and Eosine Methylene Blue Agar (Biotec, UK) and incubating at 35°C for 48 hours for coliforms and at 44.5°C for *E. coli*. The coliform population was recorded based on the MPN Table (APHA, 1992).

Identification of Isolates

Representative discrete colonies were purified by streaking on Nutrient agar and then subjected to Gram and spore, staining, motility tests, cultural and morphological characterization, biochemical tests (0xidase, catalase, MRVP, indole, citrate utilization, coagulase, hydrogen sulphide production and oxidative/fermentative utilization of glucose, sucrose, lactose, mannitol, arabinose) and identified based on earlier descriptions (Harrigan and McCance, 1976, Krieg and Holt, 1984, Sneath *et al.*, 1986).

Statistical Analysis

The statistical analysis of the data obtained was made using Analysis of Variance (ANOVA) and the significant difference of the means determined at P=0.05 (Snedecor and Cochran, 1980).

RESULTS

Table 1 indicates some variations in the mean bacterial counts, with the UP showing initial lower counts (log_{10} 3.08 $cfum1^{-1}$) and a maximum at DS

Table 1: Mean monthly bacterial counts (log_{10} cfu $m1^{-1}$) of different sampling stations of Aba River.

Duration of sampling (months)	Sampling stations					
	UP	UW	AB	CW	RL	DS
0	3.08	4.30	5.46	4.53	4.56	5.60
1	3.26	4.38	5.51	4.56	4.60	5.68
2	4.30	5.49	5.57	5.54	5.49	6.51
3	4.45	5.54	6.60	4.57	4.58	6.61
4	4.46	5.56	6.68	4.51	4.53	6.72
5	4.38	5.58	6.71	4.48	4.49	6.75

Each value represents the mean of 3 determinations of 2 independent experiments.

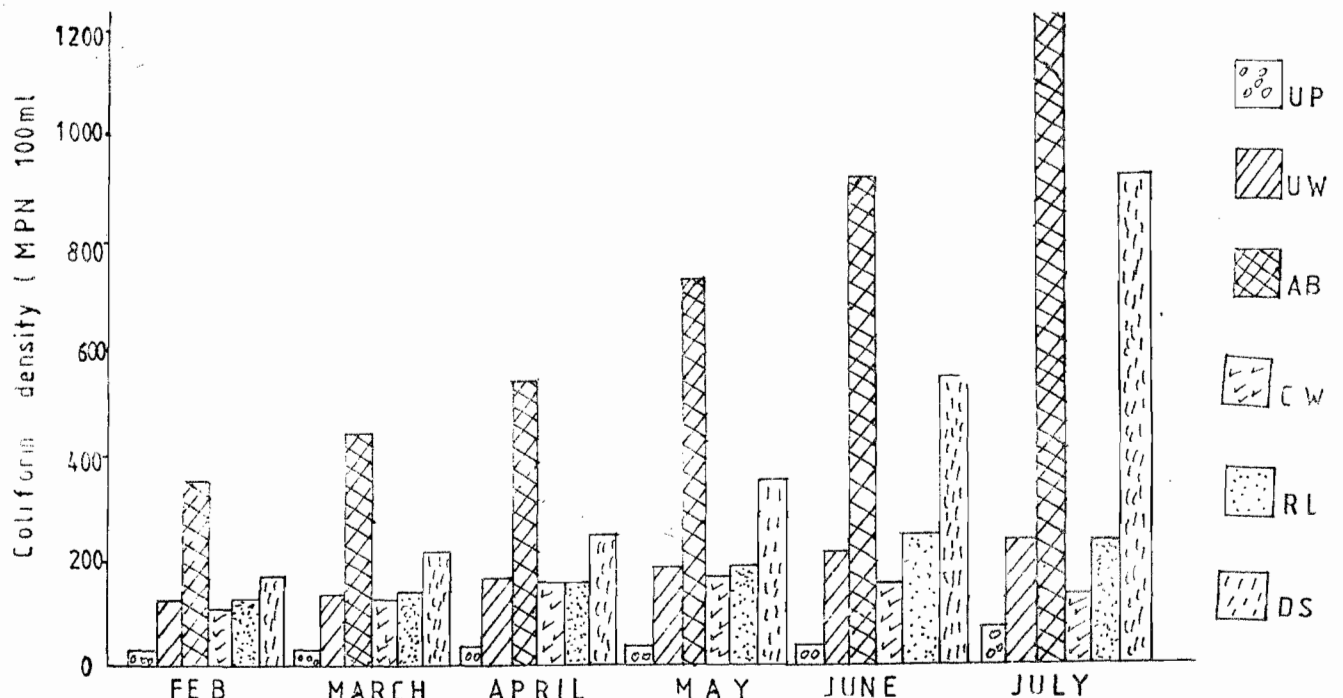

Fig. 1: Coliform density (MPN 100ml $^{-1}$) of different sampling stations.

(log_{10} 5.60 cfu $m1^{-1}$). Three stations: UW, AB and DS showed increase in bacterial population throughout the period of study. However, there existed significant differences between sampling stations and between months of sampling (Table 1). The coliform density of each station depicted in Fig 1 showed that AB had the highest coliform counts (3.50×10^2 to 1.26×10^3 MPN 100 $m1^{-1}$) followed by DS (1.70×10^2 to 9.20×10^2 MPN 100 $m1^{-1}$). The lowest (24 to 70 MPN 100 $m1^{-1}$) was observed in UP. The distribution of bacterial isolates is shown in Table 2. The most prevalent bacteria included *Staphylococcus, Pseudomonas, Escherichia* coli and *Micrococcus. Klebsiella* sp., *Streptococcus faecalis*, *Salmonella* sp., *Shigella* sp., *Clostridium perfringens* and *Bacillus* sp were not detected in UP. Of all the stations, DS and AB showed the greatest variation of isolates followed by CW and RL (Table 2).

DISCUSSION

The microbial population of aquatic environment may vary both in number and type with the source and component of the water playing critical roles (Rheinheimer, 1991). The results (Table 1) indicate some variations in the bacterial population of the stations and during months of sampling. These variations suggest the impact of human activities and natural changes. For example, the bacterial population increase in AB may be attributed to wastes from the slaughterhouse (Benka – Coker and Ojior, 1995) and run-off input during the rains. Furthermore, the proximity of the cattle - grazing area to the station may partly explain the increase in bacterial population and this corroborates the findings of Harwood *et al.* (1999) and Paul *et al.* (1995). Similarly, the maximum bacterial population increase observed in DS (Table 1) may be attributable to greater human activities with concomitant increase in organic matter input emanating from the untreated wastes from nearby Ngwa Road Market, Aba. The significantly lower bacterial count (P=0.05) in UP when compared to other stations (Table 1) may be due to no human activities (uninhabited area) and fast-flowing nature of the river at the station. This assertion agrees with the earlier report of Anson and Ware (1974). On the other hand, the decrease in bacterial counts in stations CW and RL after the third month of sampling could be as a result of dilution resulting from high rainfall in May – July (Table 1). However, the increase in coliform counts in RL (Fig.1) during the period may be attributable to indiscriminate defaecation habit of the nearby inhabitant without toilet facilities. Furthermore, the observed low coliform counts in UP (Fig. 1) may be attributed to self-purification process of the river as well as lower faecal contamination at the station.

The relatively high coliform counts at AB station (Fig.1) may not be unconnected with the high rate of cattle defaecation habit near the station as earlier indicated by Paul *et al.* (1995). In addition, the defaecation habit of teenage hawkers around DS may have also contributed to the high coliform counts in that station. Okoronkwo and Odeyemi (1985) had similar observation at sewage

Table 2: Occurrence and Spatial distribution of bacterial isolates in Aba River

	Sampling stations					
Bacterial isolates	**UP**	**UW**	**AB**	**CW**	**RL**	**DS**
Klebisella sp	-	+	+	+	+	+
Staphylococcus sp	+	+	+	+	+	+
Pseudomonas sp	+	+	+	+	+	+
Streptococcus faecalis	-	+	+	+	-	+
Salmonella sp	-	-	+	+	+	+
Shigella sp	-	+	+	+	+	+
Escherichia coli	+	+	+	+	+	+
Micrococcus sp	+	+	+	+	+	+
Clostridium perfringens	-	-	+	-	+	+
Bacillus sp	-	-	+	+	+	+

+ = isolated,

- = not isolated.

discharge points of receiving streams. The presence of *E. coli, Streptococcus faecalis* and *Klebsiella* sp. in the present study (Table 2) gives credence to these findings. In addition, the presence of *C. perfringens* in AB, RL and DS stations further confirms the human faeccal contamination of these stations since *C. perfringens* have been shown to be better indicator of human faecal contamination in tropical surface waters (Fujioka *et al.* 1985). The presence of *Salmonella* and *Shigella* spp. at AB, CW, RL and DS (Table 2) and the coliform counts of all the stations not falling within internationally recommended standard (Anon, 1971) is of public health concern and therefore waters from Aba river need to be pre-treated before consumption.

The study has indicated some outstanding variations in bacterial loads at different sampling stations and in different months which reflected the diverse kinds of wastes that enter Aba River. With the high bacterial loads likely to create pollutional stress, the results could be useful for the Federal Environmental Protection Agency (FEPA) in designing appropriate pollution control strategy for the river.

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