Assessment of pollution caused by tannery-waste and its impact on aquatic bacterial community in Hajaribag, Dhaka

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The leather industries of Hajaribag area, Dhaka city, produce hundreds of metric tons of inorganic and organic wastes which pollute the adjacent water bodies including the river Buriganga. In the present study, a total of 18 water samples from 6 different points along the effluent distribution route were examined. Along with the dissolved oxygen concentration (DO), acidity (pH), conductivity, and concentration of total dissolved solute (TDS), concentration of the samples were measured followed by the enumeration of total heterotrophic bacteria. Pure cultures of bacterial isolates were obtained after a brief enrichment and the isolates were biochemically identified up to genus level. The physicochemical test readings showed significant fluctuations in different points indicating radically different heterogeneous conditions throughout the distribution system. The total count varied from $1.2 \times 10^7$ to $6.3 \times 10^9$ cfu/ml. Different bacterial genera including Alcaligenes spp., Bacillus spp., Corynebacterium spp., Escherichia spp., Micrococcus spp., Pseudomonas spp., Shigella spp., Staphylococcus spp. and Streptococcus spp. were isolated from the collected samples. The bacterial community was found to be diversified where the concentration of tannery waste was less; thereby it was assumed that the tannery waste might affect the aquatic bacterial community both quantitatively and qualitatively.

Key words: Tannery waste; pollution; bacterial community

Today natural ecosystems have very little to do with the newer kinds of pollution as its self-purification systems are put to test by ever increasing human population and also by industrialization. Tanning industries are one of the major manufacturing processes which are responsible for tremendous pollution of water resources (1-3). In these industries, animal hides are transformed into leather through many complex stages, consuming high quantities of water and using large amounts of chemicals such as lime, sodium sulfide, ammonium sulfate, sodium chloride, bactericides, vegetable tannins, and chrome salts (4). Tannery wastewaters are mainly characterized by high salinity, high organic loading, and specific pollutants such as sulfide and chromium (5, 6).

The initial processing of raw hides release organic waste, and sulfide contents in the environment. The tanning process uses very high concentration of inorganic salts of chloride, ammonia, chromium, and sulfate, which may responsible to cause pollution (7). Presence of organic matter in the environment showing Chemical Oxygen Demand (COD) or Biological Oxygen Demand (BOD), is a matter of concern in governing the after-effect of these pollutants. Their disposal to water bodies might cause depletion of oxygen leading to harmful effects on living entities (8, 9). On the other hand, inorganic pollutants of chromium-rich tannery wastes to disposal sites cause significant changes to the physicochemical properties of that environment (10-12).

Substantial number of reports showed the effect of tannery wastes on water bodies. It is likely that changes in the physicochemical properties of water might directly or indirectly influence microbial populations and their activities. Such influences can be measured through monitoring the qualitative and quantitative changes in physicochemical properties of different locations and respective microbial community structure.

Moreover, information on the effect of contaminants on water microbial community is considered critical to the development of any sustainable bioremediation strategies for cleanup of tannery waste contaminated sites. For this reason, we investigated the impact of tannery-wastes on the physicochemical properties of the nearby water bodies at the Hajaribag site, and the associated effect on changing the population structure and microbial load of the water.

MATERIALS AND METHODS

Sample site and sampling. Six different locations (Table 1) from nearby locality of Hazaribagh tannery industries (Fig. 1) of Dhaka city and the flow path of the disposed effluent were selected for the collection of samples and 3 samples were
TABLE 1. Description of sampling sites.

<table>
<thead>
<tr>
<th>Serial no.</th>
<th>Sampling site</th>
<th>Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Tannery floor</td>
<td>TF</td>
</tr>
<tr>
<td>2</td>
<td>Retention tank for mixing salt with raw hide</td>
<td>RT</td>
</tr>
<tr>
<td>3</td>
<td>Tannery-exit for effluent</td>
<td>EP</td>
</tr>
<tr>
<td>4</td>
<td>Between tannery-exit and sluice slum</td>
<td>ES</td>
</tr>
<tr>
<td>5</td>
<td>Water logged sites in the sluice slums</td>
<td>SS</td>
</tr>
<tr>
<td>6</td>
<td>Burigonga River</td>
<td>RV</td>
</tr>
</tbody>
</table>

collected from each location. A total of 250 ml of water sample was collected aseptically from each point in sterile plastic bottle.

**Measurement of physicochemical parameters.** The physicochemical parameters were examined in the laboratory just after the samples had become available. Probe based detection of pH, dissolve oxygen (DO), conductivity and total dissolve solid (TDS) were performed.

**Inoculation of samples.** All samples (6×3=18) were divided into 2 sets of aliquots. One set was selected for the direct measurement of total heterotrophic plate count and the other set was subjected to enrichment. Both the enriched and non-enriched sets of samples were serially diluted up to 100 fold using physiological saline and all the dilutions were used for the assessment of bacterial composition in qualitative and quantitative manner, respectively. Enrichment of the samples was done with peptone water at room temperature in test tubes for 3 hours. Three milliliter from each water sample was mixed with previously prepared and autoclaved 3 ml 2X peptone water. This enrichment was done to revive the vitiated organisms. Nutrient agar (NA) and peptone agar (PA) were used for the enumeration and isolation of aerobic heterotrophic bacteria by using spread plate technique and incubated at 37 °C as described by Sharp and Lyles in 1969 (14).

**Identification of microorganisms.** Identification of bacterial isolates was carried out according to Bergey’s Manual (15, 16). For further confirmation, several biochemical tests were performed according to the Manual of Methods for General Bacteriology by American Society for Microbiology (17) to identify bacteria.

**RESULTS**

**Physicochemical parameters.** The trend of change in the physicochemical parameters (Fig. 2) which is depicted taking the average of the three samples collected for each of the parameters. DO was found in its highest level in the tannery floor to be 5.9 mg/L before declining drastically in mixing tank to 0.3 mg/L. It then increased again to 4.8 mg/L at exit point before fluctuating further a little in later sampling sites. TDS showed its peak value of 5.1 mg/L at mixing tank and continued to decrease gradually afterwards. pH was somewhat neutral in the beginning and was highly alkaline in the mixing tank. Then it reverted to slight acidity in the rest of the points. Conductivity was found in its highest degree (1966 μS/cm) in the mixing tank and then decreased dramatically to 3.1 μS/cm in the exit point. In between exit point and the sluice slum conductivity increased to 8.2 μS/cm before decreasing gradually in the sluice-slum and in Buriganga.

**Determination of Microbiological Quality.** It was obvious that the range of bacteria (Table 2)
DO = Dissolve oxygen; TDS = Total dissolve solid; Avg = Average; TF = Tannery floor; RT = Retention tank; EP = Exit point; ES = In between exit point and sluice slum; SS = Sluice slum; BR = Buriganga River

FIG. 2. Trend of changes in physicochemical properties along the sampling sites. TDS and conductivity shows somewhat similar pattern of fluctuation. pH is seen to be roughly uniform except sharp rise in the retention tank and abrupt fall in the exit point. Dissolved oxygen (DO) shows highest level of fluctuation depending on the type of samples.

TABLE 2. Bacterial spectrum at different sampling points that shows significant variation from site to site referring much to their adaptability to the prevailing conditions. Not all bacteria are found everywhere.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Burigonga River</th>
<th>Sluice slum</th>
<th>Between exit and sluice slum</th>
<th>Exit Point</th>
<th>Retention Tank</th>
<th>Tannery Floor</th>
</tr>
</thead>
<tbody>
<tr>
<td>Staphylococcus aureus</td>
<td>Micrococcus luteus</td>
<td>Pseudomonas aeruginosa</td>
<td>Shigella dysenteriae</td>
<td>Escherichia coli</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Streptococcus spp.</td>
<td>Staphylococcus spp.</td>
<td>Corynebacterium xerosis</td>
<td>Shigella spp.</td>
<td>Alcaligenes faecalis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bacillus spp.</td>
<td>Streptococcus lactic</td>
<td>Corynebacterium xerosis</td>
<td>Staphylococcus spp.</td>
<td>Streptococcus aureus</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Streptococcus lactis</td>
<td>Alcaligenes faecalis</td>
<td>Streptococcus lactic</td>
<td>Staphylococcus spp.</td>
<td>Staphylococcus aureus</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Micrococcus luteus</td>
<td>Corynebacterium spp.</td>
<td>Shigella dysenteriae</td>
<td>Shigella dysenteriae</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bacillus cereus</td>
<td>Pseudomonas spp.</td>
<td>Staphylococcus aureus</td>
<td>Pseudomonas aeruginosa</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pseudomonas spp.</td>
<td>Staphylococcus aureus</td>
<td></td>
<td>Shigella dysenteriae</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Escherichia coli</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

No. of variants (genus) | 8 | 10 | 6 | 3 | 7 | 11 |
Higher HPC as well as higher variation was observed (Fig. 3) where the parameters were found within the limit supportive to growth of organisms. On the other hand, where conditions were highly unfavorable, e.g. in retention tank, the count and the variation of organisms were strikingly less.

Same bacteria were not found everywhere. It depended on their source to be introduced in an environment as well as the relevant parameters for growth and survival in that environment (18). It was clear from the data of physicochemical parameters of different samples that not all situations throughout the flow path were suitable for growth or even survival for all type of bacteria. In the end, with the more clear insight of microbiological interactions with tannery-waste our research can be proved important for designing more efficient processing to make it environment-friendly and cost effective.

REFERENCES


FIG 3: Correlation of changes in HPC and number of variants along the sampling locations indicating association of higher count with greater diversity of bacteria. It is obvious that the tannery floor was the most favorable site for thriving microbes whereas retention tank was the least favorable site for microbial growth. Other sites were found to be moderately supporting growth with notable exception of logged water body of sluice slum where low HPC count was found.

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