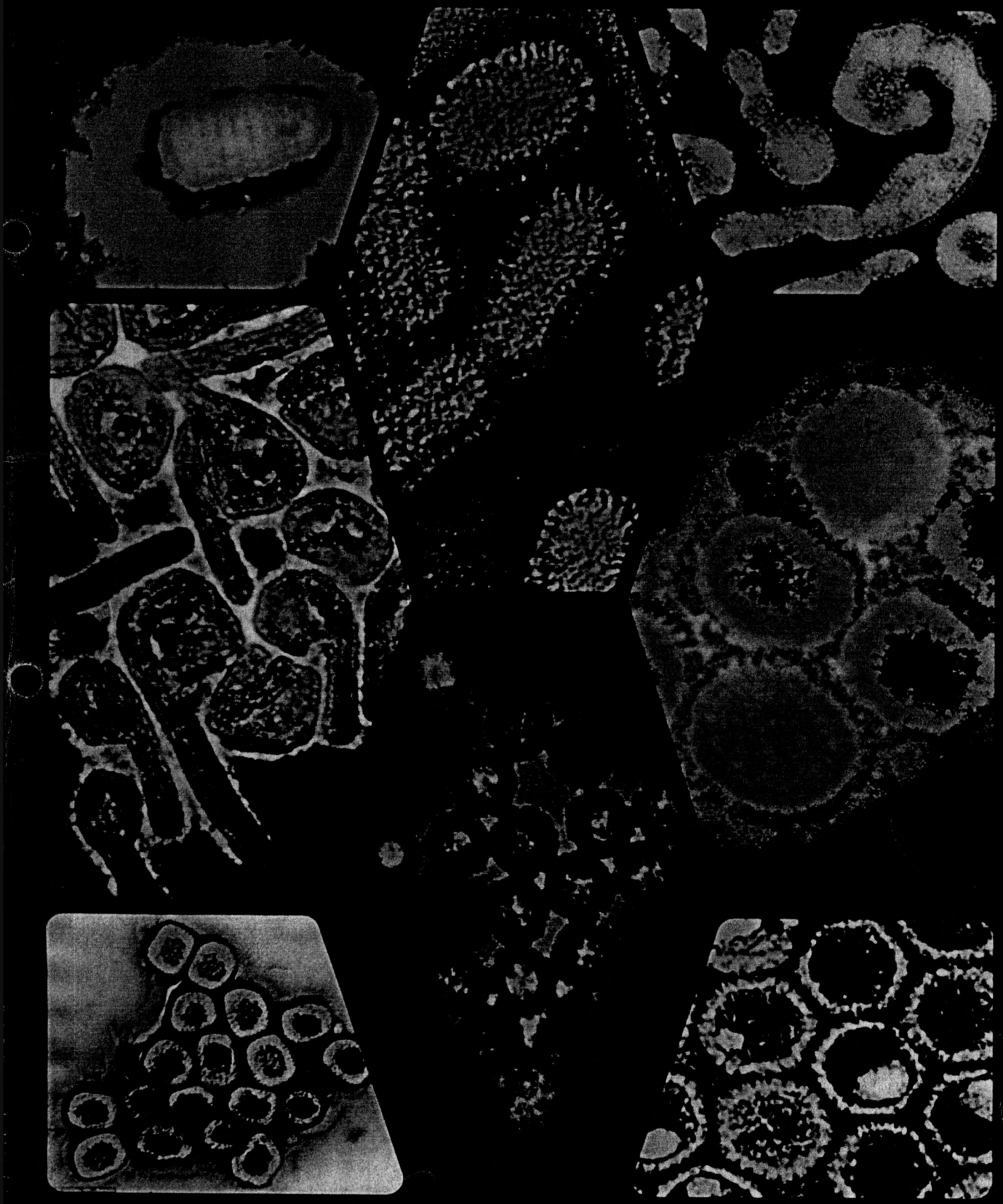




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Design, setting and methods

This descriptive cross-sectional study conducted at NHSL from 01.12.2014 to 31.03.2015 had all patients with deep-seated collections of pus undergoing drainage/aspiration, accounting to 185 samples. Following routine microbiological processing, further identification of isolates was done with RapID manual identification systems. Antibiotic susceptibilities were determined by CLSI disc diffusion method and MIC where applicable. A data extraction sheet was used to assess the associated factors and outcome.

Results

Aerobic bacterial growth was seen in 54.59% of samples. This resulted in 125 isolates. Poly-microbial growth was seen in 18.8% of the positives. The most frequent organism was *Escherichia coli* (14.4%). Most samples were cerebral. Most yield was from gastro-intestinal and intra-peritoneal samples (95.65%) followed by renal and peri-nephric collections (83.33%). 50% of *Staphylococcus aureus* were MRSA and 35.14% of relevant enterobacteriaceae were probable ESBL producers; acquisition was equally from community and hospital. Among all Gram negatives 6.9% and 2.3% were carbapenem resistant and multidrug-resistant respectively; all were hospital-acquired. Diabetes mellitus and alcoholism were significantly associated with positive growth. One patient succumbed to the pathogen.

Conclusions

In a 54.59% of aerobic bacterial growth were enterobacteriaceae, Highest yield was from gastro-intestinal and peri-nephric collections. MRSA, probable ESBL producing enterobacteriaceae and carbapenem and multidrug resistant Gram negatives were detected with notable hospital acquisition.

PP 17

Clinical audit on external ventricular drain management at the National Hospital of Sri Lanka

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Introduction

Cerebrospinal fluid diversion through an external ventricular drain (EVD) is an important procedure for patients with elevated intracranial pressure.

Objective

To establish demography, microbiology, current practices, outcomes and infection rates of EVD at the National Hospital of Sri Lanka (NHSL).

Design, setting and methods

A prospective clinical audit in neurotrauma units at NHSL was conducted for a period of 6 weeks. Patients of all ages who had undergone EVD during that period were enrolled using theater lists. Data was collected with data extraction form. They were followed up for 90 days from insertion, to assess the need of VP shunt. EVD related infection rate was calculated as primary outcome. GCS at day 30, mortality, need for permanent CSF diversion were taken as secondary outcomes. Qualitative and quantitative data analysis was done with SPSS system.

Results

Seventy one patients underwent EVD insertions. Majority of them (53) presented following trauma and forty seven of them were male. Fifty five insertions were done as emergency procedure. Twenty five patients developed EVD related infections (25/71, 35.21%). Coagulase negative *Staphylococci* and *Acinetobacter* spp. were the most common organisms isolated from CSF and the rest were coliforms, *Enterococcus* spp and *Pseudomonas* spp and most showed multidrug resistance phenotype.

There was no significant difference among gender, ethnicity, presentation (trauma/non trauma) and age between EVD infected and non-infected groups. The guidelines for prophylaxis and treatment of EVD related infections were followed. Low GCS level (<8) on day 30 (p<0.01) and mortality (p<0.001) were significant among those who developed EVD infections. Multiple EVD insertion (p<0.001) and the need for permanent VP shunt (p<0.005) were prominent among them. Prolonged duration of EVD (p<0.001), peri operative CSF sampling (p<0.005) and CSF leak (p<0.04), concurrent other body site infections (p<0.001) and prior CNS infection (p<0.001) were the other factors that increased the risk of EVD related infections.

Conclusions

EV related infection rates are high at NHSL. This study highlights the need for restriction of frequent manipulation of EVD, proper treatment, early removal and good infection control practices.

PP 18

Microbiological quality in ground water of the Kelani river basin, Sri Lanka

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Introduction

Global estimates suggest that nearly 1.5 billion people lack safe drinking water and that at least 5 million deaths

year can be attributed to waterborne diseases. Bacterial diseases are frequently linked to consumption of drinking water contaminated with *Shigella* spp., *Salmonella* spp., and *Campylobacter* spp. Kelani river basin is the third largest watershed and fourth longest of the country and provides 80% drinking water for Colombo area. Majority of the people who live in the river basin, use ground water for drinking and their daily needs.

Objective

The present study was carried out to assess the microbiological quality including presence of *Salmonella* spp., *Shigella* spp. and *Campylobacter* spp. of ground water from Kelani river basin.

Design, setting and methods

Water from seventy two ground water sampling locations in the river basin was tested for total coliform, fecal coliform, *Salmonella*, *Shigella*, and *Campylobacter*.

Samples were collected and transported according to the PHI manual, Ministry of Health, Sri Lanka (2010). Samples were analyzed following Health Protection Agency, National Standard Method for detection of *Salmonella* spp., *Shigella* spp. and *Campylobacter* spp. Sri Lanka Standard Institute test methods were used for the detection of fecal coliform and total coliform in groundwater.

Results

Twenty six percent of (70) ground water samples in the Kelani river basin were contaminated with total coliform and 17% (12) of samples were contaminated with *Salmonella* spp. Three percent of samples were contaminated with *Campylobacter* spp.

Conclusions

The results showed that ground water of the river basin is not suitable for direct consumption as drinking water and therefore it is important to educate the public of the need to use boiled cooled water for drinking.

PP 19

Retrospective analysis of laboratory data of foodborne outbreaks

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Introduction

Outbreaks due to consumption of contaminated food can adversely affect the health of the population in a country.

This study was carried out to analyze data on food borne outbreaks, reported to Medical Research Institute to understand the present situation of food borne outbreaks in Sri Lanka based on the laboratory evidence.

Objectives

1. To analyze the laboratory data related to food borne outbreaks.
2. To identify the food borne bacterial pathogens from the samples sent from the food borne outbreaks.
3. To identify the gaps related to the food samples sent from food borne outbreaks.
4. To determine the hygienic quality of the food.

Design, setting and methods

Retrospective analysis was carried out by collecting data from request forms and laboratory work sheets for the samples received from food borne outbreaks during 2012-2015. Per each outbreak a data extraction sheet was completed to record necessary data. Summary information was recorded and analyzed using Microsoft Excel 2013.

Gaps were identified in the process of submitting samples e.g. lack of implicated food samples, samples not submitted within the time and etc. when analysing the collected data. Using laboratory result sheets microbiology quality of food were analysed comparing to the standard levels.

Results

Total 46 outbreaks were reported during April 2012 – December 2015. 14 outbreaks were reported in 2012, 12 in 2013, 11 in 2014 and 9 in 2015. Highest number of outbreaks have been reported from Colombo district (12), followed by Gampaha (8) and Batticaloa (5) respectively. Out of 46 outbreaks nearly one third were reported from schools. There were 6 outbreaks associated with industrial zones and 4 in military establishments.

According to the data out of 46 outbreaks, 61 samples from 146 food samples received were unsatisfactory including 13 having potentially hazardous pathogens. *Salmonella* was isolated from 3 outbreaks, unsatisfactory levels of *Bacillus cereus* were isolated from 5 outbreaks and *Staphylococcus aureus* was isolated from 2 outbreaks.

Conclusions

Highest number of outbreaks were reported from schools. Bacterial pathogens identified during this period from implicated food were *Salmonella* sp. *Staphylococcus aureus* and *Bacillus cereus*.