

Authors

Zuraifah Asrah Mohamad¹, Nur Fatimah Sholehah Zakaria¹, Mohd Azerulazree Jamilan², Muhd Iqbal Hafiz Saad¹, Nur Hidayah Ahmad³, Norhafizan Daud⁴, Sophia Karen Bakon¹

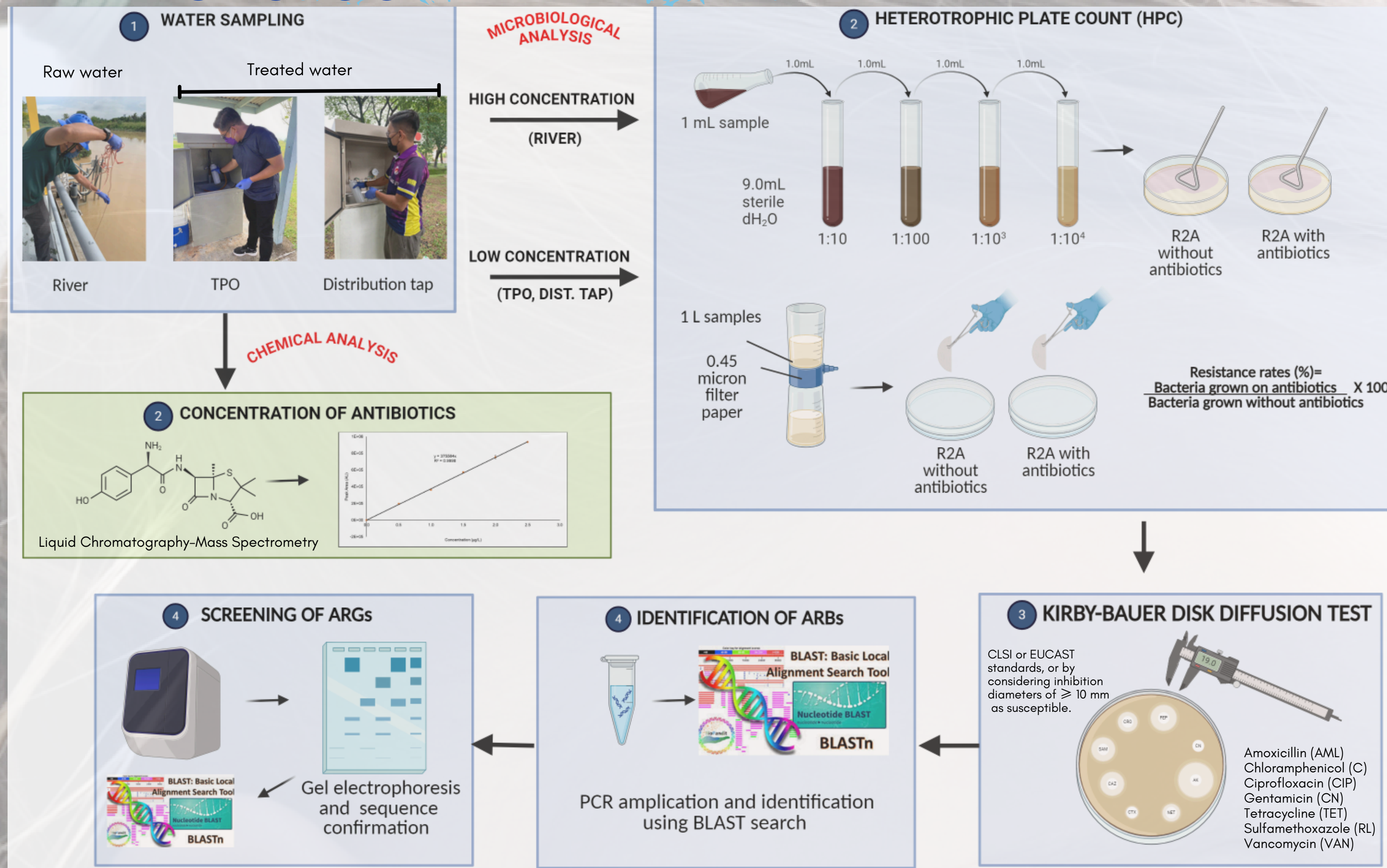
Affiliations

- 1 Health Risk Assessment Unit, Environmental Health Research Centre, Institute for Medical Research, National Institutes of Health, Shah Alam, Selangor, Malaysia
- 2 Nutrition Unit, Nutrition, Metabolic, and Cardiovascular Research Centre, Institute for Medical Research, National Institutes of Health, Shah Alam, Selangor, Malaysia
- 3 Selangor State Health Department, Selangor
- 4 Engineering Service Division, Ministry of Health Malaysia, Putrajaya

BACKGROUND

The water environment plays a prominent role in the spread of antimicrobial resistance (AMR). Water discharges from hospitals and animal farms have been identified as hotspots harbouring antibiotic resistant bacteria (ARB). However, due to inefficient removal or leachate, these ARB can be further transmitted via water bodies, including river used for drinking water and hygiene purposes as well as recreational activities, posing risks to the community. Despite surveillance efforts of AMR in Malaysia targeting clinical and agricultural settings, monitoring of drinking water system (DWS) has been neglected. AMR is not yet listed as a parameter of water quality in the National Drinking Water Quality Standards (NDWQS, MOH, Malaysia). Thus far, the WHO has set standards for reducing fecal contamination in drinking water, by using *E. coli* and coliforms as key indicators. WHO tricycle protocol has also identified ESBL-*E. coli* as a common indicator, which may not be dominant in water bodies unpolluted with faecal contamination. Studies from other countries have evidenced the presence of ARB in drinking water supplies such as the UK, the US, and China. In Malaysia, evidence of AMR in drinking water system is still lacking, indicating an urgency for public health and its importance to direct the policy makers towards achieving Sustainable Development Goals (SDGs), particularly SDG 6: "Clean water & Sanitation", and SDG 3: "Good health and well-being". Therefore, this cross-sectional study aimed to address this gap by providing evidence on the prevalence of AMR in Malaysia's drinking water systems.

METHODOLOGY

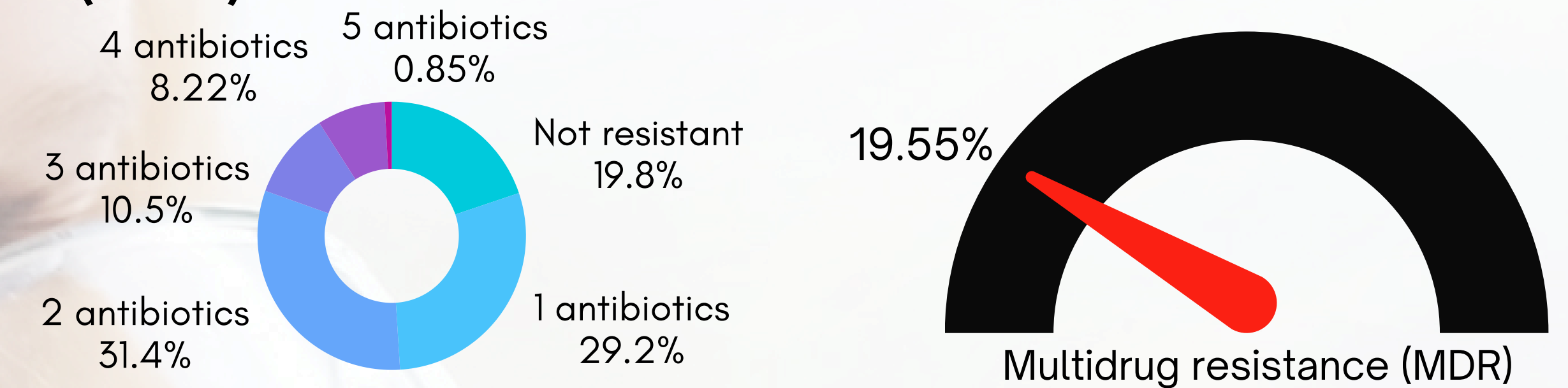


AIM AND OBJECTIVES

1. General aim:
 - To study the baseline level of antibiotic-resistant bacteria in the drinking water distribution systems of Malaysia
2. Specific objectives:
 - To determine the prevalence of antibiotic-resistant bacteria and its antibiotic-resistant genes
 - To quantify the level of antibiotics present in the drinking water systems

iii. Determination of ARB using Antibiotic Susceptibility Test

- A total of 353 isolates were examined from river intake (90.08%), TPO (7.37%) and tap (1.98%)
- Of these 66.29% were resistant to AML2, CIP5 (5.10%), VA30 (49.58%), CN10 (8.78%), C30 (10.20%), RL25 (19.83%), and TE30 (7.93%)
- Three isolates were resistant to five antibiotics, namely 2 isolates of *Klebsiella pneumoniae*, and 1 isolate of *Enterobacter cloacae* found in raw water
- Resistant ESKAPE (highly virulent and antibiotic resistant bacterial pathogens) bacteria such as *K. pneumoniae* (6.60%), *Acinetobacter baumannii* (1.26%), *Pseudomonas aeruginosa* (0.31%), and *Enterobacter sp.* (4.40%), were found in the river intake, with other bacteria such as *Staphylococcus sp.* (1.70%), and *Escherichia coli* (1.13%)



RESULTS AND DISCUSSION

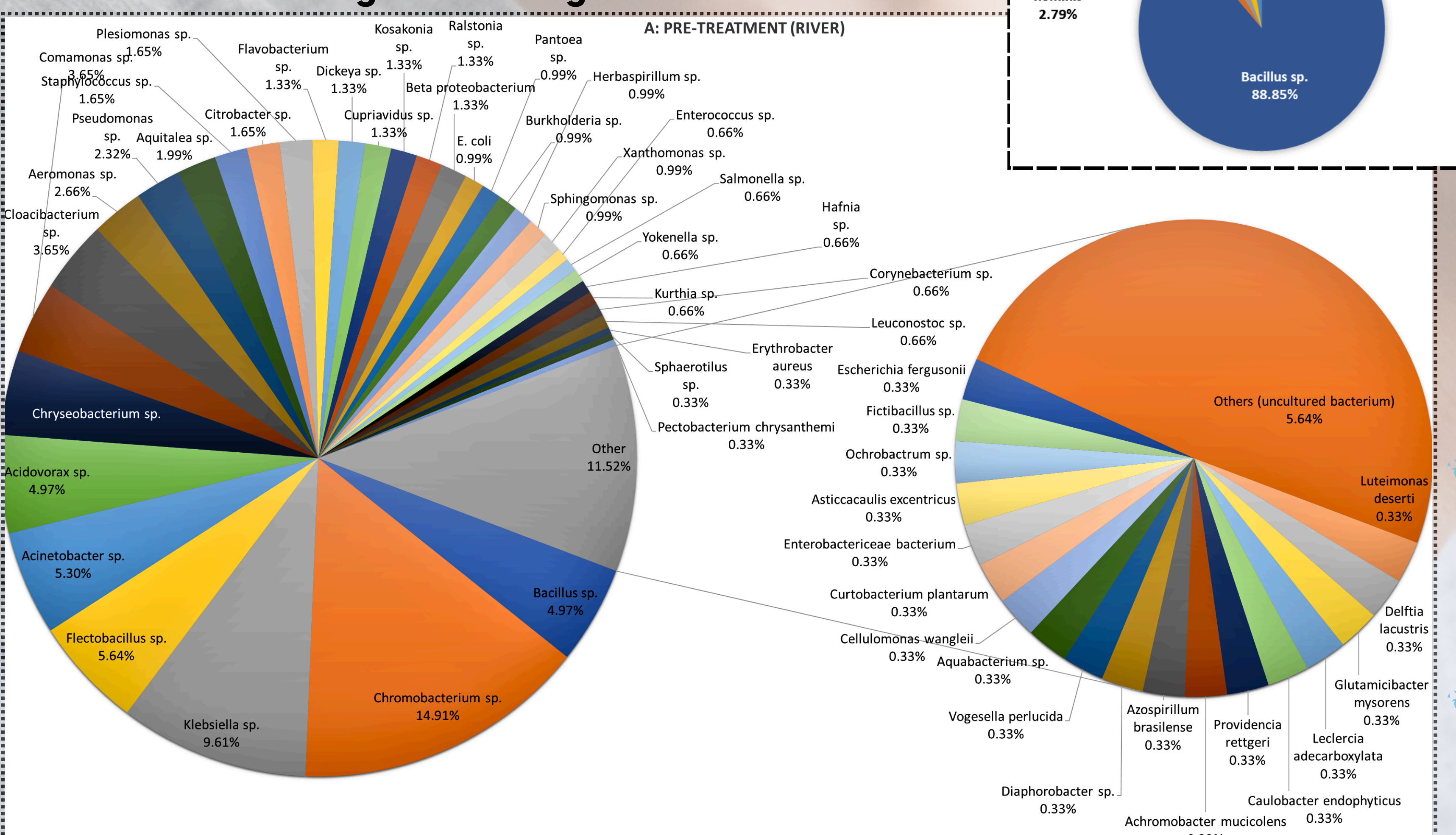
i. In situ Measurements of Raw and Treated Water

- Water quality parameters met the acceptable limits set by the NDWQS, MOH Malaysia
- Chlorine levels in the DWTPs remained consistent within acceptable limits, as detected in both treated water from the treatment plant outlet (TPO) and the distribution tap



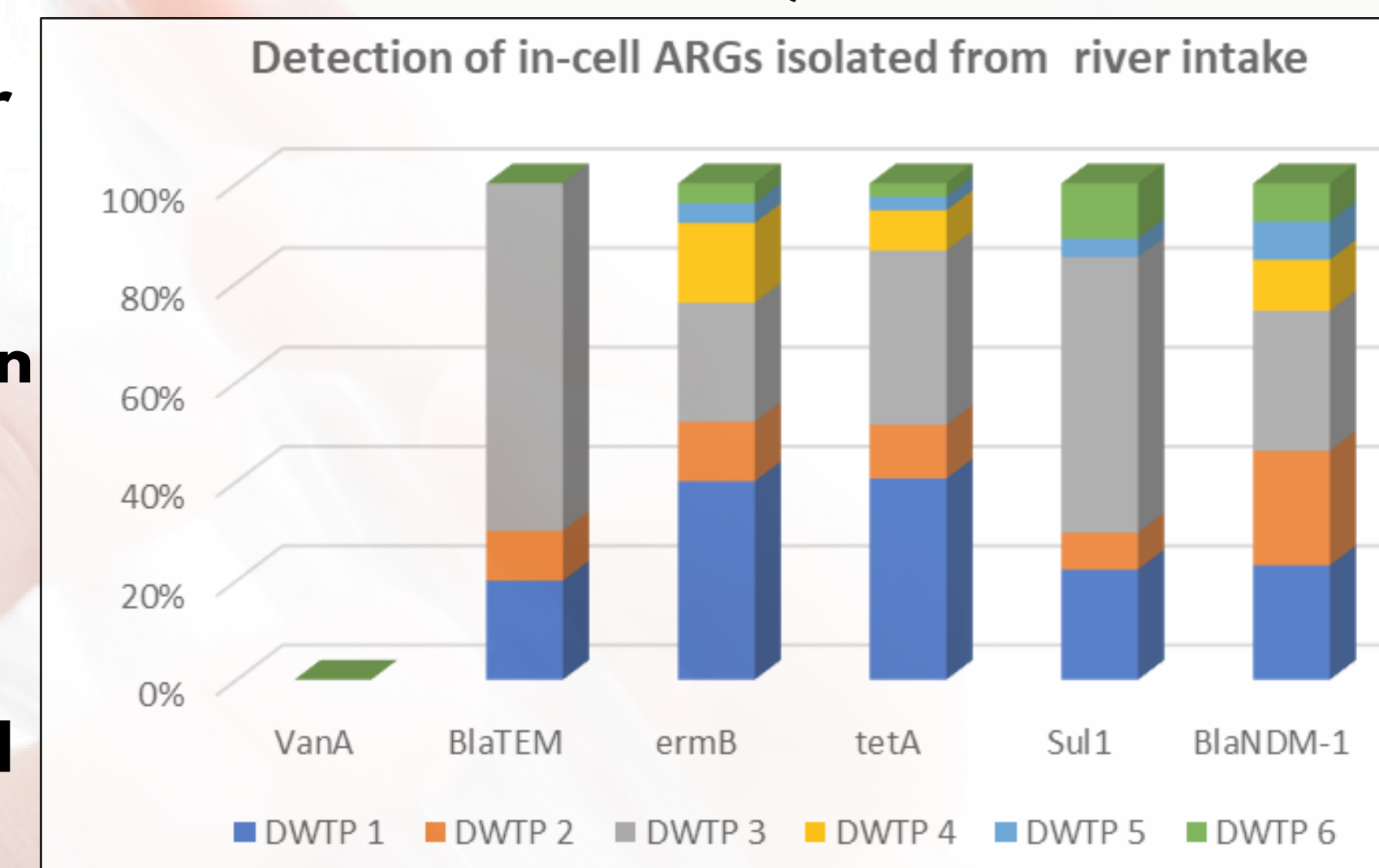
ii. Distribution of Heterotrophic Bacteria (HPC) in Raw and Treated Water

- The level of HPC bacteria reduced significantly from pre- to post-treatment river (1.87×10^4) to 5.07×10^4 cfu/mL, as compared to the TPO (5.0×10^{-3} to 2.0×10^{-2} cfu/mL) and distribution tap (5.0×10^{-3} to 1.0×10^{-2} cfu/mL) ($p=0.000$)
- Distribution of bacteria in pre-treatment was more diverse compared to post-treatment
- ESKAPE bacteria eg. *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter sp.* were only found in pre-treated water
- Bacillus sp.* was predominantly found (88.9%) in treated water
- Resistance rates ranged from 1.8% to 129%



iv. Detection of ARGs

- ARGs were found in isolates from the river water (n=137) and TPO (n=6)
- 20 isolates carried 2 ARGs (5 isolates were pathogenic identified as *Klebsiella pneumoniae* and *Enterobacter hormaechei*)
- 5 isolates carried 3 ARGs (1 isolate was *Enterobacter cloacae*, a well-known nosocomial pathogen)
- tetA and BlaNDM-1 were the most prevalent found in river and TPO
- No vanA was detected
- The presence of ARGs is a concern as the ARB can transfer and spread their resistance genes inter- and intra- species



v. Detection of Antibiotics

- Antibiotics residues of chloramphenicol, ciprofloxacin and tetracycline were detected in 2 DWTPs at the river intake and 1 DWTP at the distribution point
- Chloramphenicol was found in DWTP 3 (distribution) (0.012 ± 0.003 µg/L) and DWTP 4 (river) (0.021 ± 0.018 µg/L), whereas ciprofloxacin was detected in DWTP 3 (distribution) and tetracycline was detected in DWTP3 (river)
- Farming and agriculture industries were located nearby the rivers area which explains the detection of chloramphenicol and tetracycline in the sampling point of DWTP3 river and DWTP4 river, respectively

CONCLUSION AND RECOMMENDATIONS

- Our findings revealed the occurrence of ARB and ARGs in both raw and treated water, but had significantly decreased after treatment. This indicates the importance of maintaining and improving an effective DWTP to reduce the risks of exposure to the healthy community.
- DWTP 3 was more contaminated than other DWTPs might be due to the anthropogenic activities nearby the raw water source.
- This data can guide policymakers to integrate AMR in the Malaysia's drinking water surveillance, to reduce or eliminate the contaminants from entering our drinking water system.

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