

Health Risk Associated with Diverse Bacterial Species in a Salt Lick in Kapit, Malaysian Borneo**Farahfaiza C.^{1*}, Samuel L.², Mohd-Azlan J.², Scholastica R.²**

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Salt licks are naturally occurring areas in the forest with high concentrations of minerals which supply nutrients to animals and plants in their vicinity ^[1,2]. Microbes, on the other hand, are widespread in the environment, and their presence always has an influence on the habitat in which they thrive. This study was conducted to analyse the diversity of bacteria species in the water of a salt lick in the area of Kapit, Sarawak. The analysis was carried out to determine if there is the presence of the potentially pathogenic species and therefore determine the risk associated with the bacteria in the salt licks environments.

Different volumes of samples (2.0 mL and 4.0 mL) were used to determine the fecal coliform count (FCC) and total coliform count (TCC). Molecular identification was carried out using 16S RNA sequencing polymerase chain reaction (PCR). The PCR product of the bacterial genomic DNA of the water samples were examined using 1% (w/v) agarose gel electrophoresis and a single band was observed in all lanes after the agarose gel electrophoresis of the PCR product was done. The PCR products were sent for sequencing in Serdang, West Malaysia. The species were then identified by comparing their sequences with the sequences deposited in the GenBank, NCBI using basic local alignment search tools (BLAST).

Table 1 shows the fecal and total coliform count in the water from the salt lick. Both sample dilutions yielded colony counts in the required range. The average reading of both sample dilutions was calculated in which Station 2 had a larger number of FCC (312.5 count/mL) compared to Station 1 (215.5 count/mL). Subsequently, Station 2 also had a higher TCC reading of 8412.5 count/mL compared to Station 1 which had TCC reading of 8237.5 count/mL. This study has revealed the presence of *Escherichia coli*, *Aeromonas* sp., *Aeromonas hydrophila*, *Enterobacter cloacae*, *Enterobacter soli* and *Enterobacter lignolyticus* in the water samples from the salt lick (Table 2).

Table 1: Fecal and total coliform count for ST1 and ST2

Sample Filtered (mL)	FCC Reading (count/mL)		TCC Reading (count/mL)	
	ST1	ST2	ST1	ST2
2.0	150	300	10100	10200
4.0	275	325	6375	6625
Average	212.5	312.5	8237.5	8412.5

Isolates Code	Accession Number	Identified Species	Percentage of similarities
UK2	CP053080. 1	<i>Escherichia coli</i>	100%
UK3	MN208081. 1	<i>Escherichia coli</i>	100%
UK5	CP038515. 1	<i>Aeromonas</i> sp.	100%
UK6	CP053859. 1	<i>Aeromonas hydrophila</i>	99.79%
UK7	KT260587. 1	<i>Enterobacter cloacae</i>	99.79%
UK8	MW947078. 1	<i>Enterobacter soli</i>	100%
UK10	CP012871. 1	<i>Enterobacter lignolyticus</i>	99.79%
UK12	CP012871. 1	<i>Enterobacter lignolyticus</i>	99.59%

Table 2: Molecular identification of bacteria isolated from water sample of salt licks area

The presence of the Enterobacteriaceae family indicates the potential presence of pathogenic bacteria in the salt lick water, hence, the salt lick water could be the reservoir for the transmission of bacterial diseases to animal and human. Although fecal coliform bacteria are not necessarily disease agents, their presence may indicate the existence of disease-carrying organisms that live in the same surroundings as the fecal coliform bacteria. The presence of coliform does not necessarily suggest wastewater pollution or the existence of another sanitation-related health problems, but it does signal the necessity for an examination of all water system infrastructure and activities to determine the path of organisms entering the water system. This study is significant in term of public health.

Keywords

Salt lick, water, microbial reservoir

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