SUPPLEMENTARY RESULTS

Tables 1a and b provide a complete study of the isolates' Gram stain and biochemical tests such as Catalase, Citrease, Indole, Oxidase, Hydrogen sulphide, coagulase, Motility, Glucose Lactose and citrate test. The probable organisms were *Micrococcus spp*, *Staphylococcus spp*, *Myroides spp*, *Proteus spp* and *Staphylococcus spp*.

Table 1a: Cultural, morphological and biochemical characteristics of isolates

Colony color	Colony shape	Morphology	Gram reaction	Catalase	Citrease	Urease	Indole	Oxidase	Hydrogen sulphide	Possible Organism
Yellow	Circular	Cocci	+	+	+	-	-	-	-	*Micrococcus spp*
Light Cream	Circular	Cocci	+	+	-	-	-	-	-	*Staphylococcus spp*
Light yellow	Round	Rod	-	+	+	+	-	-	-	*Myroides spp*
Creamy	Round	Rod	-	+	+	+	-	-	-	*Proteus spp*
Orange	Circular	Cocci	+	+	-	-	-	-	-	*Staphylococcus spp*

KEY: + = Positive - = Negative

Table 1b: Cultural, morphological and biochemical characteristics of isolates (Cont.)

Coagulase	Motility	Glucose	Lactose	Citrate	Possible Organism
-	-	Ng/A	Ng/A	+	*Micrococcus spp*
-	+	Ng/A	Ng/A	+	*Staphylococcus spp*
+	+	G/A	N/A	-	*Myroides spp.*
+	_	G/A	N/A	-	*Protease spp.*
-	+	Ng/A	Ng/A	+	*Staphylococcus spp*

Key: AK= Alkaline; A= Acid; + = Positive; - = Negative; Ng= no gas production; Na= no acid production; A= Acid production; G= Gas production.

The dressing water samples have a higher bacterial load than the swabbed table and butchering knives on Nutrient agar, MacConkey and Thiosulphate citrate bile salt agar, as shown in Figure 1, which depicts the frequency distribution of three distinct abattoir samples collected at different locations.

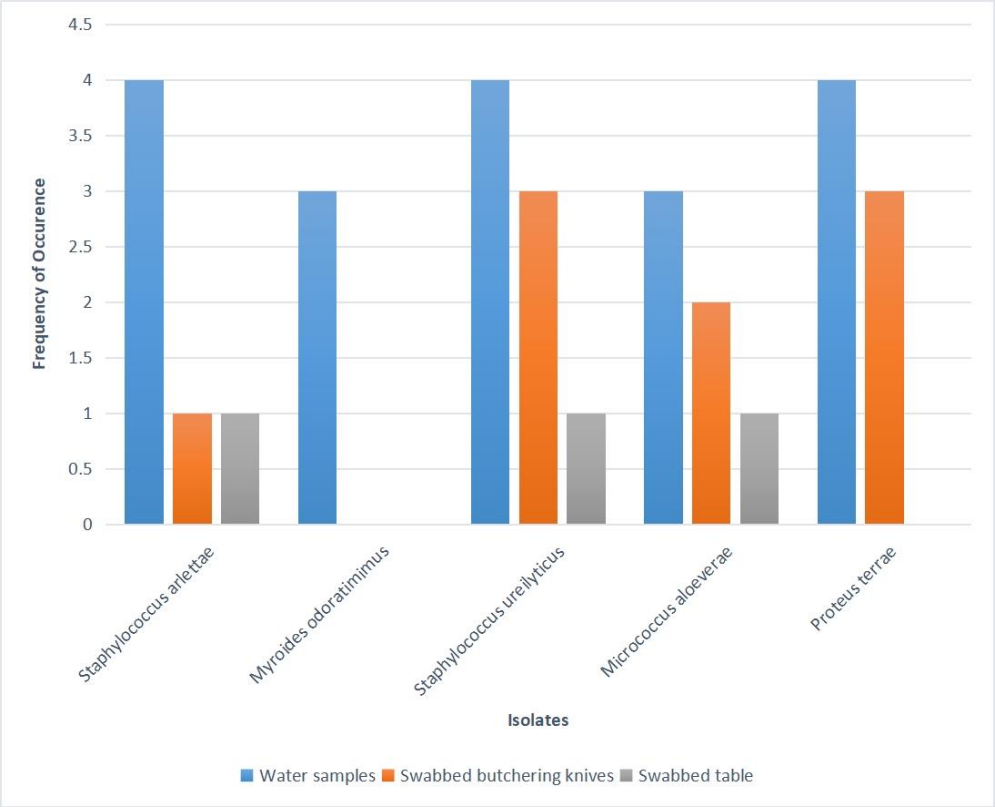


Figure 1: Distribution of frequency of different bacteria isolated from the three different samples

Table 2 provides a detailed analysis of the phytochemical profile of *Allium sativum* extracts obtained using both distilled water and ethanolic extraction. The results demonstrate that all secondary metabolites tested were present in both distilled water and ethanolic extracts, with the exception of saponins, which were lacking in ethanolic extracts, indicating a high degree of phytochemical similarity.

Table 2: Phytochemical screening of *Allium sativum* plant extract

Phytochemicals	**Distilled Water Extract**	**Ethanolic Extract**
Alkaloids	+	+
Glycosides	+	+
Flavonoids	+	+
Saponins	+	-
Tannin	+	+
Steroids	+	+

KEY: + indicates the presence of the phytochemical compound

– indicates the absence of the phytochemical compound

Table 3 offers a comprehensive analysis of the phytochemical composition of *Syzygium aromaticum* extracts obtained through various extraction methods. Specifically, the table reveals that tannins and steroids are present in both distilled water and ethanolic extractions, while alkaloids, glycosides and flavonoids are not detected in the distilled water extraction. In contrast, all four of these phytochemical classes are present in the ethanolic extraction, with the exception of saponins and glycosides, which are absent.

Table 3: Phytochemical screening *Syzygium aromaticum* plant extract

Phytochemicals	**Distilled Water Extract**	**Ethanolic Extract**
Alkaloids	-	+
Glycosides	-	-
Flavonoids	-	+
Saponins	+	-
Tannin	+	+
Steroids	+	+

KEY: + indicates the presence of the phytochemical compound

– indicates the absence of the phytochemical compound

Table 4 shows the ethanolic extracts of *Zingiber officinale* contained a diverse array of phytochemicals, including phenolics, glycosides, saponins, tannins and flavonoids. However, surprisingly, only glycosides was detected in the distilled water extracts. In contrast, the aqueous extract of ginger revealed the presence of other phytochemicals except glycoside, which was absent.

Table 4: Phytochemical screening *Zingiber officinale* plant extract

Phytochemicals	**Distilled Water Extract**	**Ethanolic Extract**
Alkaloids	-	+
Glycosides	+	-
Flavonoids	-	+
Saponins	-	+
Tannin	-	+
Steroids	-	+

KEY: + indicates the presence of the phytochemical compound

– indicates the absence of the phytochemical compound

Figure 1: Phylogenetic tree indicating the phylogenetic relationship of the 16S rRNA gene sequences from Gram positive bacteria isolated in this study to those in the genBank database.

The accession numbers of the bacteria are in parentheses while the **bold accession number** were those of the bacteria isolated in this study.

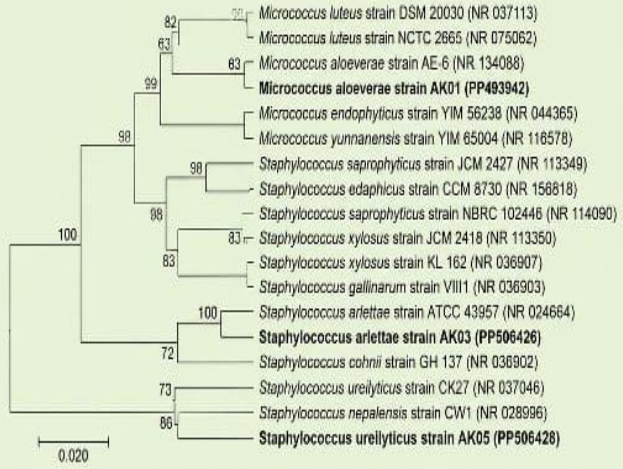
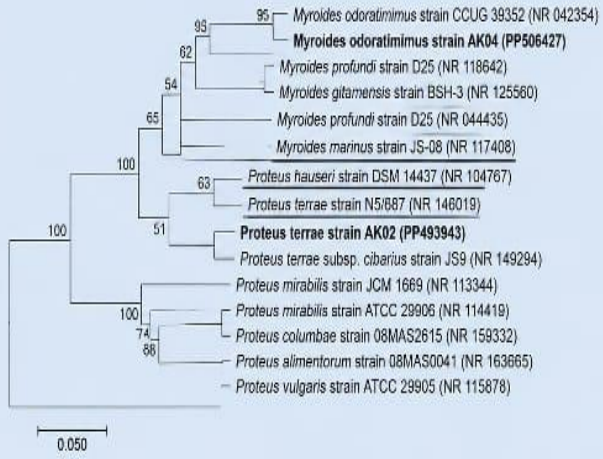


Figure 2: Phylogenetic tree indicating the phylogenetic relationship of the 16S rRNA gene sequences from Gram negative bacteria isolated in this study to those in the genBank database.

The accession numbers of the bacteria are in parentheses while the **bold accession numbers** were those of the bacteria isolated in this study.



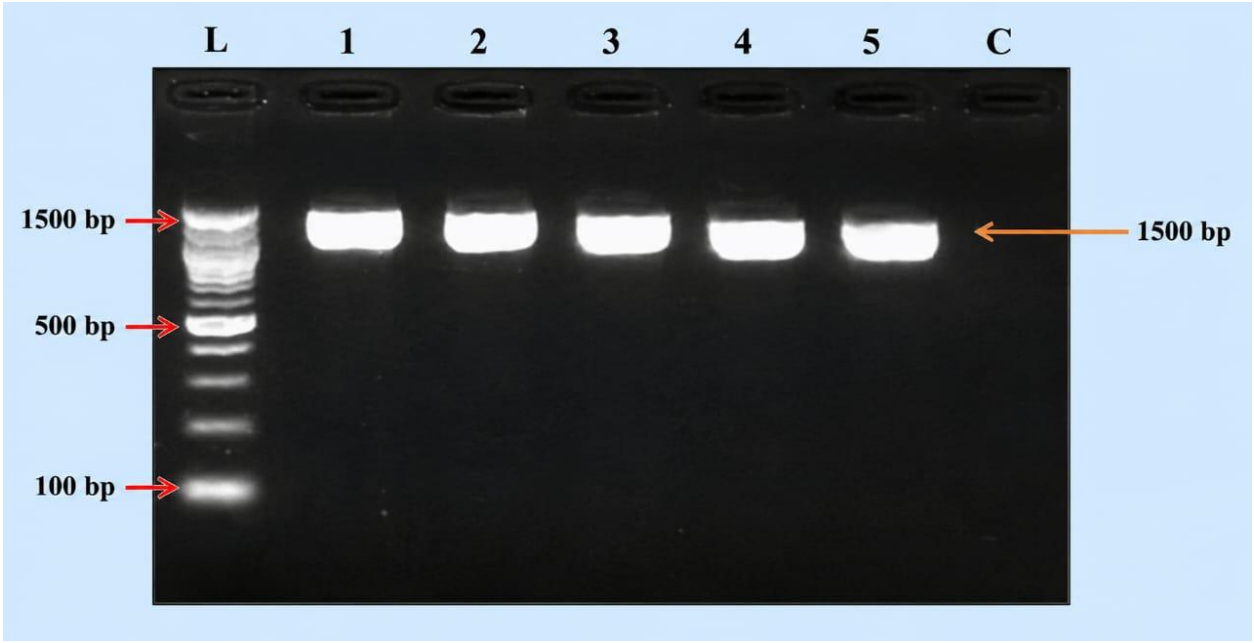


Figure 2: Ethidium bromide-stained agarose gel (2.0 %) electrophoresis of 16S rRNA genesamplified from genomic DNA of the bacterial isolates

Key:

L: ladder, 1: $MB10^{-5}$, 2: $NA10^{-5}$, 3: $NE10^{-5}$, 4: $NH10^{-5}$, 5: $TF10^{-1}$, C: Control

We are grateful to the reviewer for this valuable remark. The authors recognize that in the current study a statistical analysis was not conducted. This was due mainly to the aim of the study being a preliminary exploratory study to identify bacteria contaminants, their antibiotic resistance profile and potential antibacterial activity of selected plant extracts. Thus, descriptive presentation with numerical values and percentages of the observed results was used. The authors acknowledge that the statistical assessments (variance and significance testing) would have further enhanced the interpretation and robustness of results. In the revised manuscript this limitation has been recognized and future studies will use adequate statistical analysis in larger sample sizes and repeated experimental designs.

APPENDIX

NUCLEOTIDE SEQUENCES

Micrococcus aloeverae strain AK01 **(PP493942)**

GCTTACACATGCAGTCGAACGATGAAGCCCAGCTTGCTGGGTGGATTAGTGGCGAAC
GGGTGAGTAACACGTGAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGG
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AAGCGAAAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACGTGCCAGCAGCC
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GGGCCCGCCAAGCGGCGGAGCATGCGGATATCGATGCAACGCGAGACTACAGGCTG
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Proteus terrae strain AK02 **(PP493943)**

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ACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCGGTGGCGAAGGCGGCC
CCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGA
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Staphylococcus arlettae strain AK03 **(PP506426)**

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Myroides odoratimimus strain AK04 **(PP506427)**

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Staphylococcus ureilyticus strain AK05 **(PP506428)**

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