

#### ORIGINAL RESEARCH



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# Characterization of biosurfactant-producing bacterial strains isolated from agroindustrial wastes in southwestern, Nigeria

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#### Abstract

Introduction. The difficulty of managing trash and cleaning up the environment prompted interest in biosurfactants and surface-active proteins made by microbes. The study aims to augment bacterial isolates from agro-industrial wastes targeted for possible mass production of biosurfactants. Methods. Six agro-industrial wastes from Cassava, Palm kernel, and Sawdust from six agro-industrial sites within ljebu area in Ogun State were collected for standard laboratory analyses in the Biotechnology Unit of the Federal Industrial Institute for Research, Oshodi (FIIRO). Five screening methods; blood hemolysis, lipase activity, blue agar hydrolysis, oil spreading, and emulsification index (E124) were carried out to confirm biosurfactant production. Isolates with the highest hyper-production were subjected to 16rRNA molecular identification. Results. The study justified efficient biosurfactant production from 4 bacterial isolates out of 26 screened bacterial isolates from hydrocarbon degraders and 29 heterotrophic screened bacterial isolates, making a total of 55 screened bacterial isolates. Screening results reveal the emulsification capacities of identified Pseudomonas putida strain SG1, Acinetobacter baumanii strain MS14413, Bacillus zhangzhouensis strain cdsV18, and Burkholderia cepacia strain 717. Conclusion. Biosurfactant bacteria produced in all agricultural and industrial wastes considered in this study are capable of mass production.

**Key word:** agro-industrial wastes, biosurfactants, bacteria, optimization, screening.

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#### Introduction

Wastes management has continued to be a serious concern as a substantial amount of wastes, pollutants, and contaminants are released into our environment daily from domestic and industrial sources(1-3). Thus, exploring safer, cheaper, less toxic, and eco-friendly means to reduce, reuse and recycle unwanted materials becomes imperative(4,5). Biosurfactants (BS) are amphipathic biomolecules with hydrophobic and hydrophilic activities obtained from microorganisms (bacteria, yeasts, and filamentous fungi) that have the ability to form micelles (active surface molecules) and break the surface tension of liquid surfaces extracellularly(5,6).

Their hydrophobic and hydrophilic nature enables these characteristics and has been vastly reported for several applications in many fields, including food processing, pharmaceutics, bioremediation, biodegradation, and

enhanced oil recovery(7). Considering the characteristics above and the fact that they can be recovered from cheaper substrates, which include agro-industrial wastes, which are readily available, they are better than chemical surfactants(8). Due to their high production costs and ongoing struggles with optimization, these biosurfactant-producing microorganisms face a significant economic hurdle compared to their chemical counterparts(2,9).

On these bases, the present study focused on the identification of biosurfactant production potential in bacterial strains from agricultural and industrial wastes from southwestern Nigeria, with the following specific objectives(10,11) isolation and characterization of bacterial strains isolated from agro-industrial wastes, screening of isolated bacterial strains for biosurfactant production by blood hemolysis, hydrolysis on blue agar, oil spreading, lipolytic capacity and emulsification index and molecular

characterization of successfully isolated bacterial strains to the strain level by adopting molecular characterization techniques(12). The study aims to augment bacterial isolates from agro-industrial wastes targeted for possible mass production of biosurfactants and biosorption of heavy metals.

#### Materials and methods

#### Study area

The microbiological analysis of the study was carried out at the Federal Institute of Industrial Research Oshodi (FIIRO) in the biotechnology department. Agro-industrial waste samples were collected from the following sites, Agricultural Farm Settlement of the Olabisi Onabanjo University, Ago-Iwoye, Apoje Farms Ijebu-Igbo, Mini campus Sawmill Ago-Iwoye, Oke-Oru Sawmill Oru, Abusi Edumare Sawmill Ijebu-Igbo and Oke-Eri Sawmill, Odogbolu all within South-Western Nigeria.

**Figure 1**Map of the study area



Source: www.viamichellin.com

#### Isolation of Bacteria

Each sample collected was serially diluted, total bacterial count present in the samples was determined by the pour plate method on nutrient agar. Sample suspensions were prepared by 10-fold serial dilutions with 1 gram of sample, using 10ml peptone water as diluents. Aliquots of the fourth and sixth dilutions were spread with an Eppendorf pipette on triplicates of sterile 12 ml of nutrient agar. The plates were incubated in the incubator for 24 hours in an inverted orientation at 37  $^{\circ}\text{C}(13)$ . Colonies that formed during this incubation period were counted using this formula:

No of Colonies 
$$\times \frac{\text{dilution factor}}{\text{volume of inoculum}}$$

The enumeration of bacteria was carried out using the method reported by Chikere et al.(14) and Nwachukwu et al.(15). After incubation, morphologically and different

colonial colonies were observed and sub-cultured on a nutrient agar by streak method to obtain pure cultures. They were subsequently seeded into 6 ml nutrient agar slants. The slants were kept in the bio-freezer at 4 °C as stock cultures.

#### **Total Heterotrophic Bacterial Count**

The total heterotrophic bacterial counts (THBC) were carried out by measuring one gram of each of the samples and serial diluting them nine-fold in sterile distilled water. One(1) ml of the diluents was aseptically poured into sterile Petri dishes. The dilutions were dispensed aseptically on sterile Petri dishes. The Petri dishes were incubated at 37°C for 24 h, after which the colonies were counted. These were done in triplicates. The colonies were further sub-cultured to obtain pure colonies(13,15).

#### **Total Hydrocarbon Degrading Bacterial Count**

Hydrocarbon using bacterial count was finished utilizing Mineral Salt Medium (MSM) agar on which 1% Double Reason Lamp oil (DPK) was added as the significant carbon source; before this, the DPK was sifted utilizing a Whatman channel paper No 1. Two percent (2%) agar was added to empower the hardening of the medium, as indicated by Venty et al.(16).

### Colonial and morphological characterization of Bacterial isolates

Colonial and morphological characterization of the isolates was done using a standard microbiological method. Shape, pigmentation, elevation, size, appearance, and motility were used for morphological characteristics according to Onajobi et al.(5) and Venty et al.(16).

#### Screening of Bacterial isolates for Biosurfactant production

#### **Blood hemolysis**

Blood hemolytic activity was considered for the screening as a complimentary and qualitative test to confirm biosurfactant-producing bacteria. Bacteria cultures were streaked on nutrient agar supplemented with 5% fresh human blood and incubated at 370C for 48-72 hours. Visual inspections for hemolysis were by indication of red blood lysis by Gizele et al.(17).

#### Blue agar hydrolysis

Mineral Salts Agar (MSA) was supplemented with cetyltrimethylammonium bromide (CTAB: 0.5 mg/ml-methylene blue (MB: 0.2 mg/ml) and was prepared as reported by Nordiyana et al.(17,28). Carbon sources that were tested are glucose, sodium acetate, mannitol, glycerol, sodium acetate, and peptone. The dark blue halo coloration on the plate was considered positive for biosurfactant production.

#### Emulsification index (EI<sub>24</sub>)

The emulsification record for biosurfactantdelivering microscopic organisms was completed utilizing the technique of Raza et al.(18). Mannitol Salt Media was enhanced with 1% Lamp fuel for seven days in an orbital hatchery at 180 cycles each moment (rpm) at 28°C. Without cells, the supernatant was acquired by centrifuging the stock culture at 15,000 rpm for 15 min. Two milliliters of the supernatant of the organic entity inside the response cylinder and 2 ml of lamp fuel were added as hydrocarbon substrate test. The combination was vortexed at high velocity for 2 minutes and noticed for rate emulsification at stretches four h through 24 h. The emulsification record (El24) was determined by estimation of the level of the emulsion layer (a) partitioned by the complete level (b), duplicated by 100 ( [EI] 24=a/b×100). This measure was acted in the same size glass test tubes as per Meenakshisundaram et al.(19).

#### Oil spreading test

The oil impregnation test was completed in polystyrene Petri dishes (100 mm  $\times$  15 mm) containing 20  $\mu L$  of unrefined oil that was thoroughly stratified over 20 mL of refined water. A drop (~10  $\mu L$ ) of separated supernatant was cautiously pipette onto the focal point of the oil layer. The distance across the unmistakable zone on the outer layer of the oil layer was estimated and contrasted with the negative controls, as indicated by Ibrahim et al.(20).

#### Lipolytic test

The assay medium was composed of (g/l); Tributyrin, 2 ml; Gum Arabic, 4; Agar, 15; Phosphate buffer at pH 4.6, up to 1L. The lipase assay medium was prepared, and the cell-free filtrate of the biosurfactant producer was used as a source of lipase enzyme, as elucidated by Sidkey *et al.*(21). Lipolytic activity was detected by clearing zones around the hole in comparison to the turbid background of the assay plates.

#### Molecular characterization of Bacterial isolates

Bacterial isolates with very high potentials as hyper-producers of biosurfactant were identified further using Molecular Biology tools such as polymerase chain reactions, sequencing, and blast programs through the extraction of the genomic DNA of bacterial isolates, amplification by Polymerase Chain Reaction (PCR) using 16s-rRNA primer, sequencing of the isolate DNA and blast programs were used to reveal the name of the isolate according to the method of Joshi and Deshpande(22).

#### Statistical analyses

Data obtained were subjected to statistical analyses using the Statistical Package for Social Sciences (SPSS) version 20.0. Mean values were compared using Analysis of Variance (ANOVA) according to Zhang and Liang(23). Screening results were presented as Mean±Standard deviation. Post hoc test was adopted using the Student-Newman-Keuls (SNK). A

probability value (p – value) less than 0.05 was considered statistically significant.

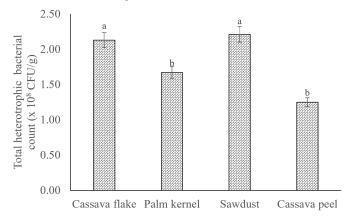
#### Results

#### **Total Heterotrophic Bacterial counts**

The results of the Total Heterotrophic bacterial counts on Cassava flake, Palm kernel, Sawdust, and Cassava peel showed no significant difference in the heterotrophic bacterial counts recorded with Cassava flakes and Sawdust. However, the highest heterotrophic bacterial count was recorded with Sawdust. On the other hand, the lowest heterotrophic bacterial count was recorded with Cassava peel, as presented in Figure 2.

#### Figure 2

Total Heterotrophic Bacterial counts; Bars with similar superscripts are not significantly different at p < 0.05

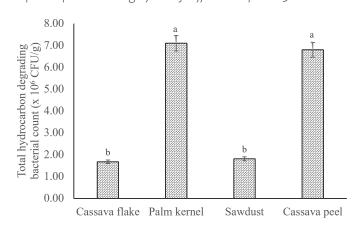


#### Total Hydrocarbon Degrading Bacteria count

The results of the hydrocarbon-degrading bacteria count are shown in Figure 3. Palm kernel had the highest hydrocarbon-degrading bacteria count (7.10 x  $10^6$  CFU/g). This was not significantly different from the Cassava peel (6.80 x  $10^6$  CFU/g). However, the hydrocarbon-degrading bacteria count recorded with the Palm kernel and Cassava peel were significantly higher than those of Sawdust and Cassava flake, respectively.

#### Figure 3

Total Hydrocarbon Degrading Bacteria count; Bars with similar superscripts are not significantly different at p < 0.05



#### Colonial and morphological characterization

The gram reaction and morphological appearance of the heterotrophic samples are presented in Table 1. Most of the samples are gram-positive rods though some have short rods, some appear to have single colonies, some are clustered, and some occur in chains. Likewise, most are mucoidal in colonial appearance, while some are milkfish in color.

**Table 1**Morphological appearances and Gram reactions of Heterotrophic bacteria

| S/N | N Isolate codeGram reactions and Microscopy |  |  |  |  |  |
|-----|---|--|--|--|--|--|
| 1   | CF 124 Gram-positive rods in singles.       |  |  |  |  |  |
| 2   | CF 125                                      | Gram-positive rods in singles.               |  |  |  |  |
| 3   | CF 126                                      | Gram-positive rods in clusters.              |  |  |  |  |
| 4   | CF 121                                      | Gram-positive rods in chains and clusters.   |  |  |  |  |
| 5   | CF 122                                      | Gram-positive rods in clusters.              |  |  |  |  |
| 6   | CF 123                                      | Gram-positive rods in chains.                |  |  |  |  |
| 7   | PKB 104                                     | Gram-positive rods in clusters.              |  |  |  |  |
| 8   | PKB 105                                     | Gram-positive ellipsoidal cells in clusters. |  |  |  |  |
| 9   | PKB106                                      | Gram-positive rods in singles.               |  |  |  |  |
| 10  | PKB 107                                     | Gram-positive slender rods in clusters.      |  |  |  |  |
| 11  | PKB108                                      | Gram-positive rods in chains and clusters.   |  |  |  |  |
| 12  | SD 101                                      | Gram-positive rods in long chains.           |  |  |  |  |
| 13  | SD 102                                      | Gram-positive short rods in chains.          |  |  |  |  |
| 14  | SD 103                                      | Gram-positive short rods in clusters         |  |  |  |  |
| 15  | S <sub>2</sub> 33                           | Gram-positive fat rods in singles.           |  |  |  |  |
| 16  | $S_3Q$                                      | Gram-positive long rods in singles.          |  |  |  |  |
| 17  | CS 113                                      | Gram-positive rods in chains and clusters.   |  |  |  |  |
| 18  | PKB 114                                     | Gram-positive rods in chains.                |  |  |  |  |
| 19  | CS 111                                      | Gram-positive rods in chains and clusters.   |  |  |  |  |
| 20  | CS 112                                      | Gram-negative rods in singles and clusters.  |  |  |  |  |
| 21  | CP 101                                      | Gram-positive cocci in singles.              |  |  |  |  |
| 22  | CP102                                       | Gram-positive rods in clusters.              |  |  |  |  |
| 23  | CP 103                                      | Gram-positive rods in singles.               |  |  |  |  |
| 24  | CP 104                                      | Gram-negative rods in singles                |  |  |  |  |
| 25  | CF 131                                      | Gram-negative rods in singles.               |  |  |  |  |
| 26  | CF 132                                      | Gram-positive rods in clusters.              |  |  |  |  |
| 27  | CF 133                                      | Gram-negative rods in clusters.              |  |  |  |  |
| 28  | CSP3MFR                                     | Gram-positive rods in singles.               |  |  |  |  |
| 29  | S33   | Gram-positive rods in singles.               |  |  |  |  |

PK, Palm kernel bargasse; CF, Cassava flake; SD, Sawdust; CP, Cassava peel; CS, Cassava Shaft

The gram reaction and morphological appearance of the hydrocarbon samples are presented in Table 2. Most of the samples are gram-positive rods though some have short rods, some appear to have single colonies, while some are clustered, and some occur in chains. Also, most have a mucoidal colonial appearance, while some are milky.

**Table 2**Colonial appearances and microscopy of hydrocarbon utilizing pure bacterial isolates

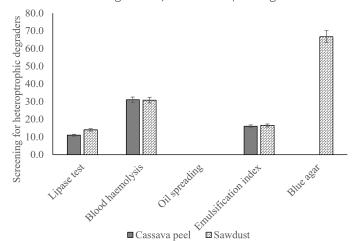
| 5/N | Isolate<br>code     | Colonial appearance  | Microscopy and<br>Morphology                   |
|-----|---------------------|--|--|
| 1   | CSP <sub>1</sub>    | Mucoidal and convex shape<br>and entire with 10mm size in<br>diameter    | Gram-positive rods in single                   |
| 2   | S <sub>2</sub> 3    | Milkish and translucent column<br>shape is oval and about 4mm<br>in size | Gram-positive rods in single                   |
| 3   | PKBJ                | Mucoidal and convex with an entire shape of about 10mm size in diameter  | Gram-positive rods in clusters                 |
| 4   | S <sub>3</sub> (2)  | Mucoidal and convex, with a wavy edge and about 12mm size                | Gram-positive long rods in clusters            |
| 5   | $S_2Q$              | Milkish and raised colonies,<br>with an entire shape 5mm in<br>size      | Gram-negative rods in clusters                 |
| 6   | S <sub>2</sub> 31   | Milkish and raised colonies, with an entire shape 5mm in size            | Gram-positive long rod in singles              |
| 7   | S3                  | Mucoidal and convex with an entire shape size equal to 12mm              | Gram-positive long rods in singles             |
| 8   | S <sub>3</sub> Q1   | Convex shape with light yellow pigment shape equal to 2-4mm              | Gram-negative long rods in clusters and single |
| 9   | PKBMY2              | Translucent colonies   | Gram-negative rods in singles                  |
| 10  | PKBMYQ              | Pinkish colony with a convex structure size is 4mm                       | Gram-positive rods in clusters                 |
| 11  | PKBMR(2)            | Mucoidal with wavy edge and size is 12mm                                 | Gram-positive rods in clusters                 |
| 12  | PKBJ2               | Mucoidal with wavy edge and size is 12mm                                 | Gram-negative rods in single                   |
| 13  | CSP3MT(1)           | Mucoidal with entire edge and size is 6mm                                | Gram-negative rods in singles                  |
| 14  | CJP2                | Mucoidal and convex shape 6-8mm  | Gram-positive rods in clusters                 |
| 15  | CSPMAR3             | Translucent and convex structure size equal to 8-10mm                    | Gram-negative rods in singles                  |
| 16  | PKBMY(2)            | Milky and translucent colonies in size 10mm                              | Gram-positive cocci in singles                 |
| 17  | PKBJ22              | Mucoidal and oval in shape, translucent size equal to 10mm               | Gram-positive rods in singles and cluster      |
| 18  | S2                  | Mucoidal and with wavy edge size 12mm                                    | Gram-positive long and slender rods in singles |
| 19  | $S_1Q$              | Mucoidal and milky in color  | Gram-negative rods in singles                  |
| 20  | CSF2                | Mucoidal and milky in color  | Gram-negative rods in singles                  |
| 21  | CSP <sub>3</sub>    | Mucoidal and milky in color  | Gram-positive rods in single                   |
| 22  | S <sub>2</sub> 4    | Mucoidal and milky in color  | Gram-negative short and fat rods in single     |
| 23  | PKBJ3               | Mucoidal, translucent, 10mm in size                                      | Gram-positive rod in singles and long chain    |
| 24  | S <sub>3</sub> (2)1 | Mucoidal, translucent, 10mm in size                                      | singles  |
| 25  | S <sub>2</sub> Q1   | Mucoidal, light yellow pigment size equal to 6m                          | Gram-positive rod in singles                   |
| 26  | S <sub>2</sub> 32   | Wavy edge, Milkish and 8-<br>10mm size in diameter                       | Gram-positive rod in short chain               |

 ${\sf PK}, {\sf Palm\,kernel\,bargasse}; {\sf CF}, {\sf Cassava\,flake}; {\sf S}, {\sf Sawdust}; {\sf CP}, {\sf Cassava\,peel}; {\sf CS}, {\sf Cassava\,Shaft}$ 

#### Substrate Screening results for Heterotrophic degraders

The sample screening results for heterotrophic degraders. Results showed no significant difference (p > 0.05) in the reactions of both the Cassava peel and Sawdust to Lipase test and Blood hemolysis. Also, Cassava peel and Sawdust showed no reaction to the oil spreading test. The emulsification index was highest with the Sawdust. This was, however, not significantly different from that of the Cassava peel. Similarly, Sawdust showed a positive response (66.7%) to the Blue agartest, as presented in Figure 4.

**Figure 4**Substrates screening results for heterotrophic degraders



The substrate screening results for hydrocarbon degraders are presented in Table 3. Cassava flake showed no reaction to the Lipase test. However, this reaction to the Lipase test was significantly higher with the Palm kernel than with the Sawdust and Cassava peel, respectively. Similarly, Cassava peel showed no reaction to the Blood hemolysis test. Reaction to Blood hemolysis test was also highest with the Palm kernel and lowest with Sawdust. On the other hand, the Palm kernel showed no reaction to the oil spreading test.

Reactions to the oil spreading test were significantly higher with Cassava peel. This was followed by Sawdust and Cassava flake, respectively. Results, however, showed a significantly higher Emulsification index with the Palm kernel. However, the Emulsification index recorded with Sawdust, Cassava flake, and Cassava peel were not significantly different. This was lowest with cassava peel. Meanwhile, Cassava peel and Cassava flake showed a negative response (100%) to the Blue agar test. However, Sawdust (50.0%) and Palm kernel (14.3%) showed some positive responses to the Blue agartest.

## Bacterial isolates screening results for heterotrophic degraders

The results for screening for the heterotrophic degraders are presented in Table 4.4, with isolate S233 with 18.3 having the highest average.

**Table 3**Substrate screening results for Hydrocarbon degraders

| Screening test         | Lipase test             |                          | Oil                      | Emulsification          | Pluo agar        |  |
|------------------------|-------------------------|--------------------------|--------------------------|-------------------------|------------------|--|
| Agro-industrial wastes | Lipase test             | hemolysis                | spreading                | index                   | Dide agai        |  |
| Cassava peel           | 15.13±3.12 <sup>b</sup> | 0.00±0.00 <sup>c</sup>   | 44.50±12.02 <sup>a</sup> | 9.67±5.51 <sup>b</sup>  | Negative (100%)  |  |
| Cassava flake          | 0.00±0.00 <sup>c</sup>  | 32.00±2.00 <sup>a</sup>  | 11.00±1.00 <sup>c</sup>  | 13.00±3.00 <sup>b</sup> | Negative (100%)  |  |
| Palm kernel            | 25.50±5.66 <sup>a</sup> | 33.75±14.05 <sup>a</sup> | 0.00±0.00 <sup>d</sup>   | 31.43±8.12 <sup>a</sup> | Positive (14.3%) |  |
| Sawdust                | 18.48±8.19 <sup>b</sup> | 22.13±6.74 <sup>b</sup>  | 20.57±8.08 <sup>b</sup>  | 18.43±2.62 <sup>b</sup> | Positive (50.0%) |  |

 $abcd Means (\pm Standard\ deviation) in the same\ column\ having\ similar\ superscript\ are\ not\ significantly\ different\ at\ p<0.05.$ 

The results for screening for the hydrocarbon degraders are presented in Table 5, with isolate S2Q from Sawdust, with 35.7 having the highest average, and isolate CSP3MT(1) from cassava shaft having the lowest average of 3.7.

**Table 4**Screening result for heterotrophic degraders

| S/IN | Isolate           | Lipase B |      | $\cap$ c | Blue | Average |
|------|-------------------|----------|------|----------|------|---------|
|      | code              | Test     | Н    | 03       | Agar | Average |
| 01   | S33               | 13       | 31   | 0        |      | 14.9    |
| 02   | CSP3MFR           | 11       | 31   | 0        | -    | 14      |
| 03   | S <sub>2</sub> 33 | 20       | 35   | 0        | -    | 18.3    |
| 04   | S <sub>3</sub> Q  | 9        | 26.5 | 0        | +    | 11.8    |

### Molecular identification of the four most successful biosurfactants hyper-producing strains of Bacteria

The molecular identities of the four most successfully screened isolates are represented in Table 6 with their different ascension numbers. The isolates are completely from Sawdust and Palm kernel.

The gel electrophoresis result is represented in Plate 1, revealing positions of DNA molecular markers, DNA bands of four isolates *Pseudomonas putida* strain SG1, Acinetobacter baumanii strain MS14413, Bacillus zhangzhouensis strain cdsV18 and Burkholderia cepacia strain 717 respectively.

**Table 5**Screening results for hydrocarbon degraders

| S/N   | Isolate            | Lipase | Blood     | Oil       | Dluggar   | Average |
|-------|--------------------|--------|-----------|-----------|-----------|---------|
| -5/IN | code               | test   | hemolysis | spreading | Blue agar |         |
| 1     | CSP <sub>1</sub>   | 16     | -         | 36        | -         | 17.3    |
| 2     | S <sub>2</sub> 3   | 31.5   | 17.5      | 14        | +`        | 21      |
| 3     | PKBJ               | 12.5   | 25.5      | 0         | +         | 12.7    |
| 4     | S <sub>3</sub> (2) | 26     | 27        | 14        | +         | 22.3    |
| 5     | $S_2Q$             | 25     | 21        | 61        | -         | 35.7    |
| 6     | S <sub>2</sub> 3   | 18.3   | 35        | 17        | -         | 23.5    |
| 7     | S3                 | 12.5   | 19.5      | 13        | -         | 15      |
| 8     | $S_3Q$             | 8      | 17.5      | 17        | +         | 14.2    |
| 9     | PKBMY2             | Ο      | 13.5      | Ο         | -         | 4.5     |
| 10    | PKBMYQ             | 17.5   | 26        | Ο         | -         | 14.5    |
| 11    | PKBMR(2)           | 30     | 44.5      | Ο         | -         | 24.2    |
| 12    | PKBJ21             | 31     | -         | Ο         | -         | 10.3    |
| 13    | CSP3MT(1)          | 11     | -         | 0         | -         | 3.7     |
| 14    | CJP2               | 18.5   | -         | 53        | -         | 23.8    |
| 15    | CSPMAR3            | 15     | -         | 0         | -         | 5       |
| 16    | PKBMY(2)           | 10     | 44.5      | Ο         | -         | 18.2    |
| 17    | PKBJ2              | 52     | 48.5      | 0         | -         | 33.5    |
| 18    | S2                 | 14     | 25.5      | 0         | -         | 13.2    |
| 19    | $S_1Q$             | 12.5   | 14        | 8         | +         | 11.5    |
| 20    | CSF1               | -      | 32        | 11        | -         | 14.3    |

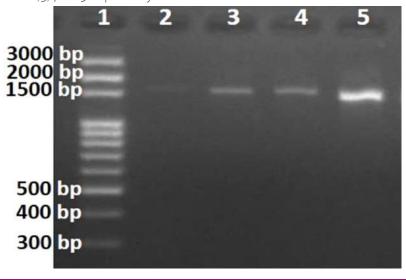
 $PK, Palm\,kernel\,bargasse; CF, Cassava\,flake; S, Sawdust; CP, Cassava\,peel; CS, Cassava\,Shaft$ 

 $\textbf{Table 6}\\ Molecular identities of the four most successful biosurfactants hyper-producing strains of Bacteria$ 

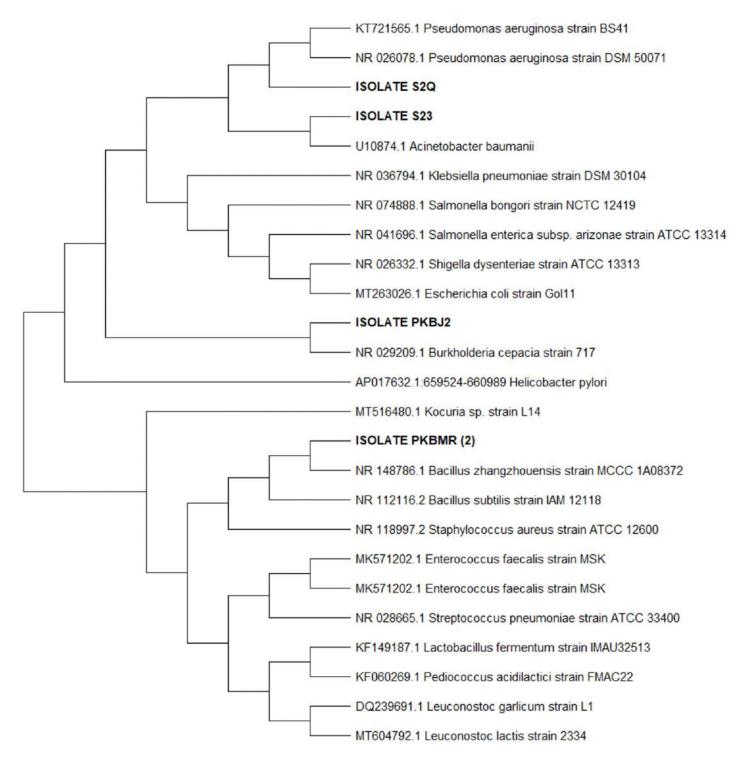
| S/N | Isolate codes | Identity                       | % Similarity | Accession Number |
|-----|---------------|--------------------------------|--------------|------------------|
| 1   | $S_2Q$        | Pseudomonas putida SG 1        | 100          | MN318320.1       |
| 2   | $S_23$        | Acinetobacter baumanii MS14413 | 100          | CP054302.1       |
| 3   | PKBMR (2)     | Bacillus zhangzhouensis cdsV18 | 100          | MN826587.1       |
| 4   | PKBJ2         | Burkholderia cepacia 717       | 100          | NR_029209.1      |

#### Plate<sub>1</sub>

Gel electrophoresis showing DNA molecular markers, DNA bands of Pseudomonas putida strain SG1, Acinetobacter baumanii strain MS14413, Bacillus zhangzhouensis strain cdsV18 and Burkholderia cepacia strain 717 on lanes 2, 3, 4 and 5 respectively



**Figure 4** Phylogenetic tree of bacterial strains



#### Discussion

The outcomes got in the current study showed that cassava squanders recorded the biggest number of province counts, as heterotrophic microscopic organisms have more state counts over the hydrocarbon utilizers since they are critical, as recently detailed by Banat *et al.*(24). In the meantime, Bacillus species were disengaged from every one of the squanders, despite the fact that more are from cassava piece like Gharaei-Fathabad(25) that chipped away at bacterial biosurfactants in the drug industry.

Acinetobacter baumanii MS14413 was isolated from Sawdust which is similar to Lee et al. (26), who reported systems biotechnology for strain improvement using mollases. Pseudomonas putida strain SG1 was isolated from Sawdust, similar to Meenakshisundaram et al.(19), which studied future microbial surfactants. Burkholderia cepacia strain 717 was isolated from palm kernel baggasse, another likely novel biosurfactant producer.

Bustamante et al.(27) screened 68 bacterial disconnects from soil and saw just 6% of secludes with great

emulsification action of up to 61%, which is in line with the high emulsification of *Pseudomonas putida* SG1 and *Burkholderia cepacia* strain 717 in the current review. Estimating emulsification units helps pick the carbon and energy hotspots for evaluating biosurfactant creation. Adeyemi et al. (2) utilized a cassava flour handling emanating as a substrate surfactant delivered by *B. subtilis*, which concurred with the current concentrate where *Bacillus zhangzhouensis* was separated been a comparative strain.

The ability of the bacterial isolates from these wastes to produce biosurfactants is important, considering the level of pollution and contamination in the said areas and the need to use indigenous and ecologically friendly products in the remediation process. Moreover, since interest in biosurfactants as a novel research area continue to gain the attention of intending scientist, this demand the development of many methods for the screening of biosurfactant-producing strains. Emulsification capacities of Pseudomonas putida strain SG1, Acinetobacter baumanii strain MS14413, Bacillus zhangzhouensis strain cdsV18 and Burkholderia cepacia strain 717 make them a new potential candidate for biosurfactant production. It is noted to state that more of the most outstanding biosurfactant-producing bacteria came from Palm kernel bargasse and Sawdust. Although the most producing isolate Pseudomonas putida strain SG1 was isolated from Sawdust. This investigation supports Kalvandi et al. (3) theory that surfactants generated by all three isolates are responsible for the release of TPH from the soil. The SHA302 isolate was chosen as an effective isolate for molecular identification owing to its increased efficiency in TPH release. The findings of the 16S rRNA gene sequencing showed the highest degree of affinity (93.98%) between our strain and Bacillus pumilus strain ATCC 7061 (T), accession number NR 043242. The strain has the entry number OK285074 and was listed in the gene bank as Bacillus sp. strain SHA302(T).

It was referred to from Sidkey et al. (21) that it is critical to take note that a large portion of the scientists has involved most extreme few evaluating techniques for the choice of biosurfactants makers; they proposed that a solitary strategy isn't reasonable to distinguish all sort of biosurfactants. Thusly, a mix of different techniques is expected for powerful screening. This examination concurred with the crafted by Nordiyana et al. (28) that likewise detached Bacillus subtilis. They involved Potato substrate as a carbon hotspot for biosurfactant creation.

The screening results of the present study are also in alignment with the work of Femi-Ola et al.(29), which screened and characterized biosurfactant-producing bacteria from soil samples in Ogun State, Nigeria. Silva et al.(30) and Makkar et al.(31) reported the application of a modified drop-collapse technique for surfactant quantization and screening of biosurfactant-producing microorganisms, which is another complimentary screening method but was not considered in the current study.

#### Conclusion

Cassava peel from the study reveals to have a potential production level than Sawdust and Cassava flake to the oil spreading test, while Palm kernel has a very high emulsification index. All the Agro-industrial wastes considered in this work harbor biosurfactant strains producers with the capacity of mass production. More work should be carried out on these novel biosurfactant production strains.

#### **Author Contribution Statement**

The authors confirm their contribution to the paper as follows:

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Data collection: Ismail B. Onajobi, Jamiu O. Adeyemi, Frank A. Orji, Oyindamola J. Samson.

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All authors reviewed the results and approved the final version of the manuscript. All authors agreed to be responsible for all aspects of the work to ensure the accuracy and integrity of the published manuscript.

#### Conflict of interest

The authors declare no conflict of interest.

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#### Ethics statement

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#### Availability of data

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