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Data Article

16S rRNA gene sequencing data of plant growth-promoting jute-associated endophytic and rhizobacteria from coastal-environment of Ondo State, Nigeria

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ABSTRACT

This study provides sequence datasets of endophytic and rhizobacteria of jute using 16S rRNA gene sequencing. The plant samples were first surface sterilized and DNA of the bacteria from soil and jute roots and stem was extracted using Quick-DNA™ Fungal/Bacterial Miniprep Kit. The purified DNA was amplified and subjected to polymerase chain reaction using forward and reverse primers. The PCR products were sequenced on Applied Biosystems ABI 3500XL Genetic Analyser (Applied Biosystems, ThermoFisher Scientific). The sequences were analyzed using BioEdit version 7.2.5 and then BLAST on NCBI. The identifiable bacteria include the rhizobacteria, *Citrobacter fruendii* RZS23 (accession number: CP024673.1), endophytic bacteria, *Bacillus cereus* EDR23 (accession number: LN890242.1), and *Morganella morganii* EDS23 (accession number: KR094121.1). The plant growth-promoting traits exhibited by these bacteria suggest their future exploration as bioinoculants.

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Specifications Table

Subject	Microbiology
Specific subject area	Exploration of agriculturally important bacteria as bioinoculants in enhancing coastal environment food productivity
Data format	Raw and analyzed
Type of data	Table
Data collection	The identifiable endophytic and rhizobacteria were isolated from the roots, stem, and soil environments of jute plants. The microbial isolation was achieved through surface sterilization for endophytes and; also, rhizobacteria by serial dilution, pour plating, and streaking plating on nutrient agar. The cultured plates were incubated at 37°C for 18 - 48 hours. After obtaining the pure culture, the bacterial DNA was extracted and sequenced.
Data source location	The soil, roots, and stem of jute plants were collected from a mixed cropping agricultural farmlands at Ilesanmi Street in Okitipupa, Ondo State, Nigeria (Latitude N6°30'46" and Longitude E4° 46'46" and 174°S).
Data accessibility	Repository name: NCBI Data identification number: Not applicable Direct URL to data: The NCBI links to the sequenced data can be accessed at: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA994047 https://www.ncbi.nlm.nih.gov/bioproject/PRJNA994049 https://www.ncbi.nlm.nih.gov/bioproject/PRJNA994048

1. Value of the Data

- The concept of exploring coastal environment resources can profoundly help in ensuring Sustainable Development Goals (SDGs) and boost world blue economy enterprise.
- Screening of plant growth-promoting endophytic and rhizobacteria with promises in the management of diverse agricultural problems.
- This research aims to provide sequence data information on endophytic and rhizobacteria isolated from jute plants in Okitipupa, Nigeria, with further recommendations for exploration to boost agricultural productivity in the region.
- *Citrobacter fruendii* RZS23 from the jute rhizosphere, *Bacillus cereus* EDR23, and *Morganella morganii* EDS23 from the jute endosphere act as copious plant growth enhancers.

2. Background

Agricultural intensification can help ensure food security for sustainable healthy living of individuals worldwide. Exploration of agriculturally important microorganisms has received a boost recently as alternatives to chemical fertilizers usage in enhancing crop productivity [1]. The understanding of plant-soil microbe synergisms and mechanisms promises to maximize their present and future exploration in managing agricultural problems. Endophytic microbes are endosphere inhabitants that cause no harm to the host plants. Similarly, rhizobacteria are dominant bacteria found the plant-soil environments [2]. The rhizosphere harbors more microbiomes than the endosphere due to the release of exudates, which provide nutrients and energy for microbial metabolism [3]. Diverse microbes associated with some food crops like jute and their studies can strategically help in maximizing their exploration as bioinoculants.

Jute (*Corchorus olitorus*) is a medicinal-cash crop constituting human diet in Nigeria [4]. Despite their nutritional and medicinal values, information on their associated bacteria in the coastal line region of Ondo State, Nigeria is less explored, which necessitates this research. Therefore, this study provides the first report on the identifiable endo-rhizobacteria from the jute plants in the study area.

3. Data Description

The raw dataset provided the 16S rRNA sequences of bacteria isolated from the roots, stem, and soil of jute plants. The isolated and identified bacteria were screened for plant growth-promoting properties as presented in Tables 1 and 2.

Table 1
The colony counts (cfu/g), and morphological observations of identifiable bacteria.

Sample source	Colony counts/ Dilutions		Bacterial shape	Bacterial arrangement	Accession Numbers	Bacterial isolates
Stem	10^{-1}	13.00 ± 00^{b}	Rod	Chains	LN890242.1	*Bacillus cereus* EDS23
	10^{-3}	15.00 ± 00^{b}				
Root	10^{-1}	4.00 ± 00^{a}	Rod	Chains	KR094121.1	*Morganella morganii* EDR23
	10^{-3}	12.00 ± 00^{b}				
Soil	10^{-4}	30.00 ± 00^{b}	Rod	Chains	CP024673.1	*Citrobacter fruendii* RZS23
	10^{-5}	25.00 ± 00^{b}				

Key: The same alphabet in superscript across columns indicates no significant differences

Table 2
Plant growth-promoting screening of the bacterial isolates.

Plant growth promoting screening					Extracellular enzyme screening				
Isolate	PS	NF	AMP	EXP	IAA	HCN	Amylase	Cellulase	Protease
C. fruendii RZS23	+	+	+	_	+	+	+	+	+
B. cereus EDS23	+	+	_	+	_	+	+	_	+
M. morganii EDR23	+	+	+	+	+	+	+	+	+

Key: positive +, Negative –, PS- Phosphate solubilization, NF - Nitrogen fixation, AMP - Ammonia production, EXP - Exopolysaccharide, IAA - Indole acetic acid, HCN - Hydrogen cyanide test.

4. Experimental Design, Materials and Methods

4.1. Sampling design, bacterial isolation, screening, and identification

The soil, roots, and stem of Jute were collected aseptically from a mixed cropping agricultural farmland at Ilesanmi Street, Okitipupa, Nigeria. The healthy jute samples were gently uprooted with attached soil and placed in sterile ziplock bags, labeled, and transported to the laboratory for microbial analysis. Before isolation, the stem and root samples were surface sterilized by rinsing in sterile distilled water to remove the debris, specks of dirt, or surface-contaminating materials. 1 g each of the stem and root samples were surface sterilized using 70% ethanol for 3 minutes, followed by immersion in 3% sodium hypochlorite for 3 minutes, 70% ethanol for 30 seconds, and lastly rinsed 5 times with sterile distilled water. Bacterial isolation was achieved by serial dilution, and pipetting 0.1 ml diluents into Petri dishes and pour-plated with sterilized nutrient agar. The plates were incubated at 37°C for 18-24 hours. Pure cultures were obtained by streaking on freshly prepared medium. The biochemical tests and plant growth-promoting screening of the pure bacterial isolates were performed [5]. The bacteria were identified using 16S rRNA Sanger sequencing.

4.2. DNA extraction, polymerase chain reaction (PCR) amplification and gel electrophoresis

The genomic DNA was extracted from the bacterial cultures using Quick-DNA™ Fungal/Bacterial Miniprep Kit (Zymo Research, Catalogue No. D6005) following the manufacturer's protocol. The quality and quantity of the extracted DNA was measured using a nanodrop (Thermo Scientific™ NanoDrop™ One Microvolume UV-Vis Spectrophotometer). The system was blanked using 1µl of DNA Elution Buffer. Afterwards, 1 µl of the DNA was placed on the

pedestal and measured. The concentration (ng/µl), A260/280 ratio, and A260/230 ratio of the sample were subsequently recorded [6].

The PCR was used to amplify the 16S rRNA gene to enable DNA sequencing. Briefly, the target region of the PCR product was amplified using the universal primers; forward, 27F – (5'AGAGTTTGATCMTGGCTCAG 3') and reverse, 1492R – (5'CGGTTACCTTGTTACGACTT 3'). The primers were purchased from Inqaba Biotechnological Industrial (Pty) Ltd, Ibadan, Nigeria. A total of 25µL reaction mixture composed of 1µL in template DNA, 0.5 µL (10nM) for 10µM Forward primer was used for the PCR, 0.5µL (10nM) for 10µM Reversed primer, 12.5 µL for One Taq Quick Load 2X Master Mix with standard buffer, 10.5 µL Nuclease free water. The samples were then subjected to the following thermal cycling conditions using the Eppendorf Mastercycler nexus gradient 230. The PCR conditions were set at initial denaturation at 94°C for 5 minutes, denatured1 at 94°C for 30 seconds, annealing1 at 50°C for 30 seconds, extension1 at 68°C for 1 minute 30 seconds, denaturation2 at 94°C for 1 minute 30 seconds, annealing2 at 53°C for 30 seconds, extension2 at 68°C for 1 minute 30 seconds, denaturation3 at 94°C for 30 seconds, annealing3 at 55°C for 30 seconds, extension3 at 68°C for 1 minute 30 seconds, final extension at 68°C for 10 minutes, and hold at 4°C till infinity. A total of 35 cycles of PCR amplification were run after initial denaturation [6]. After PCR amplification, 2µl of each PCR product was run on 1% agarose gel, stained with Safe View Red (5µl), and photographed using a gel documentation system (E-BOX, Vilber Lourmat, Italy).

4.3. Post-PCR purification and sequencing

Firstly, the PCR products were cleaned using an enzymatic method (ExoSAP) as follows: the ExoSAP master mix was prepared by adding the following to a 0.6ml micro-centrifuge tube: **a.** 50µl of 20U/µl Exonuclease I (Catalogue No. NEB M0293L) and **b.** 200µ l of 1U/µl of Shrimp Alkaline Phosphatase (Catalogue No. NEB M0371). Secondly, the reaction mixture was prepared by mixing the following and incubating the resulting mix at 37°C for 15 minutes and at 80°C for 15 minutes. **a.** Amplified PCR Product10 µl and **b.** ExoSAP Mix (step 1) 2.5 µl [6].

The fragments/PCR products were sequenced using the Nimagen, Brilliant Dye™ Terminator Cycle Sequencing Kit V3.1, BRD3-100/1000 and purified (Zymo Research, ZR-96 DNA Sequencing Clean-up Kit™, Catalogue No. D4050) following manufacturer's instructions. The sequencing reaction was done using internal sequencing primers: 785F: (5'GGATTAGATACCCTGGTA 3') forward, and 907R: (5'CCGTCAATTCMTTTRAGTTT 3') reverse. The labeled products were then cleaned with the ZR-96 DNA Sequencing Clean-up Kit (Catalogue No. D4053). The cleaned DNA products of each sample were injected and analyzed on the Applied Biosystems ABI 3500XL Genetic Analyser (Applied Biosystems, ThermoFisher Scientific) with a 50 cm array, using POP7 and sequence data collected [6].

5. Sequence Analysis

The sequences generated by the ABI 3500XL Genetic Analyzer were analyzed using BioEdit Sequence Alignment Editor version 7.2.5 and the consensus sequencing results were obtained by a Basic Local Alignment Search Tool (BLAST) search on the National Center For Biotechnology Information (NCBI).

Data Analysis

The triplicate data obtained were analyzed using Statistical Package for the Social Sciences (SPSS) version 21.

Data Availability

Plant growth-promoting bacteria (Original data) (NCBI).
Plant growth-promoting bacteria (Original data) (NCBI).
Plant growth-promoting bacteria (Original data) (NCBI).

CRediT Author Statement

Bartholomew Saanu Adeleke: Conceptualization, Data curation, Formal analysis, Investigation, Project administration, Resources, Supervision, Methodology, Writing – original draft, Writing – review & editing.

Limitations

None.

Ethics Statement

The authors have read and followed the ethical requirements for publication in Data in Brief and confirmed that the current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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