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Morphological and Biochemical Characterization of Bacteria Isolated from Sewage Water with Special Reference to Possible Exoelectrogenic Potential

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ABSTRACT: The research examines bacterial isolation and characterization from sewage water depending on morphological and biochemical attributes. The examination included 157 bacterial isolates that underwent analysis for colony morphology identification together with Gram reaction and biochemical tests. Pseudomonas aeruginosa together with Klebsiella pneumoniae and Escherichia coli made up the majority of bacteria found in sewage microbial communities which belong to the Gramnegative group. Biochemical testing showed that bacteria species which produced positive results in both oxidase and citrate tests commonly occurred in the isolates. This research demonstrates that sewage water contains numerous bacterial communities which have potential uses in wastewater treatment together with biotechnological applications. Research needs to analyze bacterial molecules alongside metabolic measurements to gain comprehensive knowledge about their operational functions.

Keywords: Sewage bacteria, morphological characterization, biochemical tests, wastewater microbiota, *Pseudomonas aeruginosa, Klebsiella pneumoniae*, bacterial diversity.

INTRODUCTION

Increased demand for electricity together with negative environmental implications from fossil fuels has intensified the search for sustainable renewable energy technologies in recent years (Osman et al., 2022). The generation of bioelectricity through microbial fuel cells (MFCs) stands as an emerging promising option because bacteria use their metabolic processes to create electrical power. Sewage water operates as an contains many microbial environment which communities that exhibit potential bioelectricityproducing abilities (Koffi & Okabe 2020). Bacterial isolation itself along with characterization efforts lead to the development of economical and environmentalfriendly bioenergy solutions beneficial for wastewater treatment and energy production. The research on electrogenic bacteria from soil and marine environments far exceeds the studies conducted on sewage water where different strains for bioelectricity production await further exploration. The insufficient understanding of newly isolated strains with promising electrochemical characteristics obstructs MFC optimization because studies mainly focus on already known bacteria (Obileke et al., 2021). Microbial fuel cells work by taking advantage of electrogenic bacteria metabolism which allows bacteria to give electrons to an anode resulting in electrical current generation. Microorganisms from different genera such as Geobacter, Shewanella, Pseudomonas and Bacillus together with other species function as exoelectrogens (Wang et al., 2019). Electrons transfer to electrodes

through either electrode-electron contact channels or the help of conductive nanowires and soluble electron mobility shuttle systems including flavins and quinones. The discovery of new electrogenic bacterial strains originating from sewage water has the potential to improve MFC operations while extending their use for bioelectricity creation. Research needs to extend into different wastewater communities to find optimal bacterial strains which maximize bioelectricity performance.

Sewage water contains the suitable conditions for bioelectricity-producing bacteria isolation because the water provides organic components alongside essential nutrients plus a wide range of microbial communities (Nawaz et al., 2022). Sewage organic chemicals create permanent available feed material that sustains continuous bacterial metabolic activity for generating bioelectricity (Hoang et al., 2022). The bacteria found in sewage have adapted to live through severe environmental factors including limited oxygen supply and intense salinity as well as fluctuating pH concentrations thus potentially improving their ability to create electricity (Mishra et al., 2022). It is essential to study sewage microbial ecology and bacterial functionality because this research leads to better MFC optimization by finding top-performing electrogenic bacteria strains. Research on sewage-derived bacteria shows promise but scientists have yet to conduct sufficient complete investigations of their effectiveness and endurance in operational projects. The development of MFC technology depends heavily on resolving these existing gaps to achieve maximum practical usage

Akanksha et al.,

(Kurniawan et al., 2022). Bacteria isolation and characterization for electrogenic properties consist of essential steps from sample collection to bacterial enrichment and electrochemical testing and complete gene and metabolic profiling analysis. Selective culturing methods combined with electrode-dependent anaerobic conditions enable researchers to successfully isolate bacteria with maximum electrogenic capabilities. potent strains. The electrochemical response of isolated bacteria goes through experimental testing by cyclic voltammetry, chronoamperometry along with power density measurements in basic MFC setups. Phylogenetic relationships together with metabolic pathways of these bacteria can be studied through molecular identification methods which include 16S rRNA sequencing as well as metagenomic analyses. The major obstacle today involves expanding the process at commercial scales through efficient and cost-effective methodologies.Sewage water contains the suitable conditions for bioelectricity-producing bacteria isolation because the water provides organic components alongside essential nutrients plus a wide range of microbial communities. Sewage organic chemicals create permanent available feed material that sustains continuous bacterial metabolic activity for generating bioelectricity. The bacteria found in sewage have adapted to live through severe environmental factors including limited oxygen supply and intense salinity as well as fluctuating pH concentrations thus potentially improving their ability to create electricity. It is essential to study sewage microbial ecology and bacterial functionality because this research leads to better MFC optimization by finding top-performing electrogenic bacteria strains. Research on sewagederived bacteria shows promise but scientists have yet to conduct sufficient complete investigations of their effectiveness and endurance in operational projects. The development of MFC technology depends heavily on resolving these existing gaps to achieve maximum practical usage. Bacteria isolation and characterization for electrogenic properties consist of essential steps from sample collection to bacterial enrichment and electrochemical testing and complete gene and metabolic profiling analysis. Selective culturing methods combined with electrode-dependent anaerobic conditions enable researchers to successfully isolate bacteria with maximum electrogenic capabilities. The electrochemical response of isolated bacteria goes through experimental testing by cyclic voltammetry, chronoamperometry along with power density measurements in basic MFC setups. Phylogenetic relationships together with metabolic pathways of these bacteria can be studied through molecular identification methods which include 16S rRNA sequencing as well as metagenomic analyses. The major obstacle today involves expanding the process at commercial scales through efficient and cost-effective methodologies..

Bioelectricity-producing bacteria have various broad industrial and environmental applications that transcend sustainable energy generation (Gurikar *et al.*, 2021). The electrogenic bacterial process within MFC technology enables wastewater treatment facilities to

pollutants during electricity tackle generation operations. It offers two simultaneous functions that cut operational expenses along with environmental reduction. Electrogenic contamination bacteria applications in microbial electrochemical systems drive current research into biosensing methods as well as hydrogen production and bioremediation technologies that expand clean energy solutions. Future research efforts must bridge the laboratory-scale studies to industrial-scale implementations because the technology needs to demonstrate stable performance across different environmental and operational conditions. Microbial fuel cells show great potential but various obstacles still exist for their deployment at industrial scale. The operational efficiency and electrode materials selection and reactor design parameters determine the final performance outputs of MFC devices. Long-term operations of electrogenic bacterial communities need more exploration to determine their stability and sustainability. Interdisciplinary research between microbiology and electrochemistry as well as material science must be conducted to advance bioelectricity production technologies through solutions for existing challenges. This study holds important value because researchers aim to uncover new bacterial strains within sewage that will both resolve a scientific gap while advancing MFC The research utilizes technology development. discovered bacterial strains to improve the sustainability of bioelectricity power generation as an alternative energy solution.

Microbial fuel cell systems show great promise because scientists can identify bioelectricity-producing bacteria from sewage water samples and properly characterize them. Analyzing the wide range of microbial communities within sewage enables scientists to find electrogenic strains with better electrochemical capabilities for bioenergy development. Research advancement in this field will lead to important progress that merges bioelectricity production with wastewater management thus solving global energy needs and environmental issues to develop a more sustainable future. The research fills current knowledge gaps by examining bacteria found in sewage which has potential to transform MFC technology and adds significant findings about bioenergy development.

MATERIALS AND METHODS

A. Sample Collection

Sewage water samples were collected in triplicate from 10 different locations, including domestic, industrial, and municipal wastewater sources. Samples were aseptically collected in sterile 500 mL glass bottles and transported on ice to the laboratory for immediate processing.

Sampling Locations and Replicates

Location Type	Number of Sites	Replicates per Site
Domestic	3	3
Industrial	4	3
Municipal	3	3

Total samples collected: 30 (10 locations \times 3 replicates each).

Sewage water samples were collected from different locations, including domestic, industrial, and municipal wastewater sources. Samples were aseptically collected in sterile 500 mL glass bottles and transported on ice to the laboratory for immediate processing.

B. Isolation of Bioelectricity-Producing Bacteria

(i) Enrichment Culture. The collected samples were inoculated into sterile Luria-Bertani (LB) and Nutrient Broth (NB) media supplemented with 0.5% glucose and incubated anaerobically at 30°C for 48 hours to favor the growth of electrogenic bacteria.

(ii) Selective Plating. After enrichment, serial dilutions (10° to 10^{7}) were prepared, and $100 \ \mu L$ aliquots were spread on sterile Peptone Yeast Extract Glucose (PYG) agar plates containing 50 mM sodium acetate as an electron donor. Colonies were selected based on distinct morphological characteristics and further purified by repeated streaking.

C. Characterization of Bioelectricity-Producing Isolates

(i) Gram Staining and Microscopy. Isolates were subjected to Gram staining and observed under a light microscope to determine Gram reaction and cellular morphology.

(ii) **Biochemical Tests.** Standard biochemical tests, including catalase, oxidase, citrate utilization, and sugar fermentation tests, were performed to classify the isolates.

D. Data Analysis

The evaluation of bacterial isolates required assessment of their characteristics after their isolation process. The research recorded total bacterial colonies from different sewage water testing sites. A group of potential electrogenic bacteria was chosen through morphological and biochemical characterization. Biological isolates received classification after lab testing with Gram staining and biochemical methods. According to the findings we determined both bacterial diversity as well as their practical applications. The isolates creating the best bioelectricity output were selected through performance assessments of voltage strength, power production capacity, and electrochemical functionality. Researchers discussed the microbial fuel cell applications of these bacteria by analyzing their efficiency rate and sustainability aspects.

RESULTS AND DISCUSSION

A. Isolation and Morphological Characterization of Bacterial Isolates

A total of 30 sewage water samples collected from 10 different locations were processed, resulting in the isolation of 157 bacterial isolates (Table 1). The distribution of isolates from different site types is summarized below:

Distribution of Bacterial Isolates from Different Sampling Sites. Colonies exhibited diverse pigmentation, texture, and growth patterns, suggesting a heterogeneous bacterial population. Gram staining revealed that 60% of the isolates were Gram-negative, while 40% were Gram-positive, indicating the presence of diverse bacterial genera (Fig. 1).

Site Type	Number of Locations	Samples Collected	Total Isolates
Domestic	3	9	45
Industrial	4	12	62
Municipal	3	9	50
Total	10	30	157

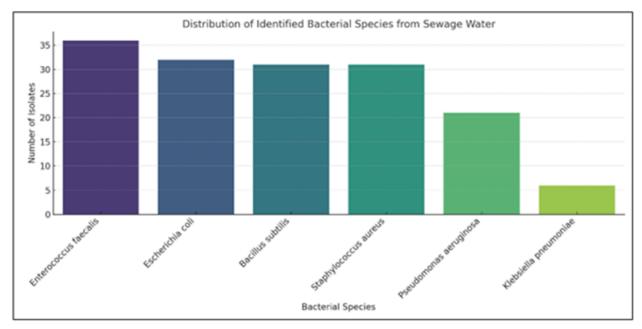


Fig. 1. Bacterial species distribution retrieved in this study.

B. Biochemical Characterization and Species Identification

Biochemical tests were conducted to classify the isolates based on metabolic activity. The distribution of

morphological and biochemical characteristics, along with species-level identification, is summarized below:

Table 1: Morphological and Biochemical	Characterization of Isolates.
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Isolate Code	Gram Stain	Shape	Catalase	Oxidase	Citrate Utilization	Glucose Fermentation	Lactose Fermentation	Sucrose Fermentation	Mannitol Fermentation	Identified Species
ISO-1	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-2	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-3	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-4 ISO-5	Positive Negative	Cocci Cocci	+	-	+	-+	-	-	-	Pseudomonas aeruginosa Escherichia coli
ISO-6	Positive	Rod	+	+	-	-	+	-	-	Staphylococcus aureus
ISO-7	Negative	Cocci	-	-	-	-	-	+	-	Bacillus subtilis
ISO-8	Positive	Cocci	+	-	+	-	-	-	+	Pseudomonas aeruginosa
ISO-9	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-10	Positive	Cocci	+	-	-	+	-	-	-	Escherichia coli
ISO-11	Negative Positive	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-12 ISO-13	Negative	Rod Cocci	+ -	+	+	-	+	-	-	Staphylococcus aureus Enterococcus faecalis
ISO-13 ISO-14	Positive	Cocci	+	_	-	-	-	+	-	Bacillus subtilis
ISO-14 ISO-15	Negative	Rod	-	+	-	+	-	-	-	Escherichia coli
ISO-16	Positive	Cocci	+	-	+	-	-	-	+	Pseudomonas aeruginosa
ISO-17	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-18	Positive	Rod	+	+	-	-	+	-	-	Staphylococcus aureus
ISO-19	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-20	Positive	Cocci	+	-	+	+	-	-	-	Escherichia coli
ISO-21 ISO-22	Negative Positive	Rod	-+	+	-	-	-	+	-	Staphylococcus aureus
ISO-22 ISO-23	Negative	Cocci Cocci	+	-	-	-	-	-	-	Enterococcus faecalis Enterococcus faecalis
ISO-23 ISO-24	Positive	Rod	+	+	+	-	+	-	+	Staphylococcus aureus
ISO-25	Negative	Cocci	-	-	-	+	-	-	-	Escherichia coli
ISO-26	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-27	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-28	Positive	Cocci	+	-	+	-	-	+	-	Pseudomonas aeruginosa
ISO-29	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-30	Positive	Rod	+	+	-	+	+	-	-	Escherichia coli
ISO-31 ISO-32	Negative Positive	Cocci Cocci	-+	-	-+	-	-	-	-+	Enterococcus faecalis Pseudomonas aeruginosa
ISO-32 ISO-33	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-34	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-35	Negative	Cocci	-	-	-	+	-	+	-	Escherichia coli
ISO-36	Positive	Rod	+	+	+	-	+	-	-	Staphylococcus aureus
ISO-37	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-38	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-39 ISO-40	Negative	Rod	-+	+	-+	-	-	-	+	Staphylococcus aureus
ISO-40 ISO-41	Positive Negative	Cocci Cocci	+	-	-	+	-	-	+	Escherichia coli Enterococcus faecalis
ISO-41 ISO-42	Positive	Rod	+	+	_	-	+	+	-	Staphylococcus aureus
ISO-43	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-44	Positive	Cocci	+	-	+	-	-	-	-	Pseudomonas aeruginosa
ISO-45	Negative	Rod	-	+	-	+	-	-	-	Escherichia coli
ISO-46	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-47 ISO-48	Negative Positive	Cocci Rod	-	-	-+	-	-	-	-	Enterococcus faecalis
ISO-48 ISO-49	Negative	Cocci	+ -	+	-	-	+	-+	+	Staphylococcus aureus Bacillus subtilis
ISO-50	Positive	Cocci	+	_	_	+	-	-		Escherichia coli
ISO-51	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-52	Positive	Cocci	+	-	+	-	-	-	-	Pseudomonas aeruginosa
ISO-53	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-54	Positive	Rod	+	+	-	-	+	-	-	Staphylococcus aureus
ISO-55	Negative	Cocci	-	-	-	+	-	-	-	Escherichia coli
ISO-56 ISO-57	Positive Negative	Cocci Rod	+	-+	+ -	-	-	+	+	Pseudomonas aeruginosa Staphylococcus aureus
ISO-57 ISO-58	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-50 ISO-59	Negative	Cocci	-	_	_	-	_	-	-	Enterococcus faecalis
ISO-60	Positive	Rod	+	+	+	+	+	-	-	Escherichia coli
ISO-61	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-62	Positive	Cocci	+	-	-	-	-	-	-	Enterococcus faecalis
ISO-63	Negative	Rod	-	+	-	-	-	+	-	Staphylococcus aureus
ISO-64	Positive	Cocci	+	-	+	-	-	-	+	Pseudomonas aeruginosa
ISO-65 ISO-66	Negative Positive	Cocci Rod	-+	-+	-	+ -	-+	-	-	Escherichia coli Staphylococcus aureus
ISO-66 ISO-67	Negative	Cocci	+	-	-	-	+	-	-	Enterococcus faecalis
ISO-67 ISO-68	Positive	Cocci	+	-	+	-	-	-	-	Pseudomonas aeruginosa
ISO-69	Negative	Rod	-	+	-	-	-	-	-	Staphylococcus aureus
ISO-70	Positive	Cocci	+	-	-	+	-	+	-	Escherichia coli
ISO-71	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis
ISO-72	Positive	Rod	+	+	+	-	+	-	+	Staphylococcus aureus
ISO-73	Negative	Cocci	-	-	-	-	-	-	-	Enterococcus faecalis

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ISO-147 Negative Rod - + - - + - Staphylococcus aureus ISO-148 Positive Cocci + - + - - Pseudomonas aeruginosa ISO-148 Positive Cocci - + - - - Pseudomonas aeruginosa ISO-149 Negative Cocci - - - - - Pseudomonas aeruginosa ISO-150 Positive Rod + + - + + - - Enterococcus faecalis ISO-150 Positive Cocci - - - - - Enterococcus faecalis ISO-151 Negative Cocci + - + - - Enterococcus faecalis ISO-153 Negative Rod - + - - + Pseudomonas aeruginosa ISO-154 Positive Cocci + - - - +<	ISO-116 ISO-117 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-120 ISO-121 ISO-125 ISO-126 ISO-127 ISO-128 ISO-130 ISO-131 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-139 ISO-140 ISO-141 ISO-142 ISO-143 ISO-143 ISO-144	Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative	Cocci Rod Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Rod Cocci Rod Cocci Rod	- + + + + + + + + + + + + + + + + + + +	+ +		+ - - - - + - - - - - - - - - - - - - -		- - - - - - - - - - - - - - - - - - -		Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus
ISO-148 Positive Cocci + - + - - - Pseudomonas aeruginosa ISO-149 Negative Cocci - - - - - Pseudomonas aeruginosa ISO-149 Negative Cocci - - - - - Pseudomonas aeruginosa ISO-150 Positive Rod + + - + + - - Enterococcus faecalis ISO-151 Negative Cocci - - - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - + Pseudomonas aeruginosa ISO-154 Positive Cocci + - - - - Staphylococcus aureus ISO-155 Negative Cocci - - - + - Escherichia coli ISO-155 Negative Cocci<	ISO-116 ISO-117 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-138 ISO-139 ISO-141 ISO-144 ISO-144	Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative Positive Negative Negative Positive Negative Positive Negative	Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci	- + + + + + + + + + + + + + + + + + + +			+ - - - - - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Escherichia coli Pseudomonas aeruginosa Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis Enterococus faecalis
ISO-149 Negative Cocci - - - - - - Enterococcus faecalis ISO-150 Positive Rod + + - + + - - Enterococcus faecalis ISO-150 Positive Rod + + - + + - Escherichia coli ISO-151 Negative Cocci - - - - - Enterococcus faecalis ISO-152 Positive Cocci + - - - - Enterococcus faecalis ISO-153 Negative Rod - + - - - + Positive Staphylococcus aureus ISO-154 Positive Cocci - - - - - Bacillus subiliis ISO-155 Negative Cocci - - + - Bacillus subiliis ISO-155 Negative Rod + + +	ISO-116 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-140 ISO-141 ISO-142 ISO-144 ISO-145 ISO-146	Positive Negative Negative Positive Negative Neg	Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Cocci Cocci Cocci Rod Cocci	- + + + + + + + + + + + + + + + + + + +			+ - - - + - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Escherichia coli Enterococcus faecalis Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Enterococcus faecalis Escherichia coli Enterococus faecalis
ISO-150 Positive Rod + + - + + - - Escherichia coli ISO-151 Negative Cocci - - - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - - Staphylococcus aureus ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - Bacillus subtilis ISO-156 Positive Rod + + + - - Staphylococcus aureus	ISO-116 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-127 ISO-128 ISO-127 ISO-128 ISO-127 ISO-131 ISO-131 ISO-133 ISO-133 ISO-134 ISO-135 ISO-138 ISO-139 ISO-140 ISO-141 ISO-142 ISO-144 ISO-145 ISO-146	Positive Negative Negative Negative Positive Negative	Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Rod Cocci Rod Rod Cocci Rod Rod Cocci Rod Cocci Rod Cocci Rod Cocci Rod Rod		+		+				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococus aureus Bacillus subtilis Enterococcus faecalis Staphylococus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Escherichia coli Staphylococus aureus Enterococcus faecalis Escherichia coli Staphylococus aureus Enterococus faecalis Escherichia coli Staphylococus aureus Enterococus faecalis Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli
ISO-150 Positive Rod + + - + + - - Escherichia coli ISO-151 Negative Cocci - - - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - - Staphylococcus aureus ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - Bacillus subtilis ISO-156 Positive Rod + + + - - Staphylococcus aureus	ISO-116 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-131 ISO-131 ISO-131 ISO-132 ISO-134 ISO-135 ISO-141 ISO-140 ISO-141 ISO-142 ISO-143 ISO-144 ISO-145 ISO-146 ISO-147 ISO-148	Positive Negative Negative Negative Positive Negative	Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Rod Cocci Rod Rod Cocci Rod Rod Cocci Rod Cocci Rod Cocci Rod Cocci Rod Rod		+		+				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococus aureus Bacillus subtilis Enterococcus faecalis Staphylococus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Escherichia coli Staphylococus aureus Enterococcus faecalis Escherichia coli Staphylococus aureus Enterococus faecalis Escherichia coli Staphylococus aureus Enterococus faecalis Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli
ISO-151 Negative Cocci - - - - - Enterococcus faecalis ISO-152 Positive Cocci + - + - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - - Staphylococcus aureus ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - - Escherichia coli ISO-156 Positive Rod + + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-131 ISO-131 ISO-131 ISO-132 ISO-134 ISO-134 ISO-141 ISO-140 ISO-141 ISO-142 ISO-143 ISO-144 ISO-145 ISO-146 ISO-147 ISO-148	Positive Negative Negative Positive Negative Negative Positive Negative Negative Negative Negative Positive	Cocci Rod Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Rod Cocci Cocci Cocci Cocci Cocci Co				+ - - - - - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Escherichia coli Staphylococcus aureus Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Staphylococcus aureus Pseudomonas aeruginosa
ISO-152 Positive Cocci + - + - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - + Pseudomonas aeruginosa ISO-153 Negative Rod - + - - - - Staphylococcus aureus ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - - Escherichia coli ISO-156 Positive Rod + + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-120 ISO-121 ISO-123 ISO-126 ISO-127 ISO-128 ISO-130 ISO-131 ISO-131 ISO-131 ISO-131 ISO-131 ISO-131 ISO-131 ISO-132 ISO-133 ISO-134 ISO-137 ISO-138 ISO-140 ISO-141 ISO-142 ISO-143 ISO-144 ISO-145 ISO-147 ISO-148 ISO-148 ISO-149	Positive Negative Negative Negative	Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Cocci Cocci Cocci Co	- + + + + + + + + + + + + + + + + + + +			+ - - - - - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Escherichia coli Staphylococcus aureus Escherichia coli Staphylococus aureus Enterococcus faecalis Staphylococus aureus Enterococus faecalis Staphylococus aureus Enterococus faecalis Staphylococus aureus Enterococus faecalis Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Staphylococus aureus Escherichia coli Pseudomonas aeruginosa Pseudomonas aeruginosa Pseudomonas aeruginosa Enterococus faecalis
ISO-153 Negative Rod - + - - - - Staphylococcus aureus ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - - Escherichia coli ISO-156 Positive Rod + + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-120 ISO-121 ISO-122 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-132 ISO-131 ISO-132 ISO-133 ISO-134 ISO-137 ISO-138 ISO-140 ISO-141 ISO-142 ISO-143 ISO-143 ISO-144 ISO-145 ISO-148 ISO-149 ISO-150	Positive Negative Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive Positive	Cocci Rod Rod Cocci Rod Rod Cocci Rod Rod Rod Cocci Rod Rod Rod Rod Rod Rod Rod Rod Rod Rod	- + + + + + + + + + + + + + + + + + + +			+ - - - - - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococus aureus Escherichia coli Enterococus faecalis Staphylococus aureus Escherichia coli
ISO-154 Positive Cocci + - - - + - Bacillus subtilis ISO-155 Negative Cocci - - + - - Bacillus subtilis ISO-155 Negative Cocci - - + - - Escherichia coli ISO-156 Positive Rod + + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-140 ISO-141 ISO-141 ISO-144 ISO-144 ISO-144 ISO-144 ISO-147 ISO-148 ISO-149 ISO-150	Positive Negative Negative Negative	Cocci Rod Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Rod Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Cocci Co	- + + + + + + + + + + + + + + + + + + +			+ - - - - - - - - - - - - - - - - - - -				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Escherichia coli Pseudomonas aeruginosa Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Escherichia coli Staphylococcus aureus Enterococcus faecalis Escherichia coli Enterococcus faecalis Escherichia coli Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Enterococcus faecalis Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus
ISO-155 Negative Cocci - - + - - Escherichia coli ISO-156 Positive Rod + + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-117 ISO-118 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-129 ISO-130 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-136 ISO-137 ISO-138 ISO-139 ISO-141 ISO-142 ISO-141 ISO-142 ISO-143 ISO-144 ISO-145 ISO-146 ISO-150 ISO-150 ISO-151 ISO-152	Positive Negative Positive Positive Positive Negative Positive Pos	Cocci Rod Cocci Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Rod		$ \begin{array}{c} \cdot \\ + \\ + \\ \cdot \\ + \\ + \\ \cdot \\ + \\ + \\ \cdot \\ + \\ +$		+				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Staphylococus aureus Enterococcus faecalis Staphylococus aureus Enterococus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa
ISO-156 Positive Rod + + - + - Staphylococcus aureus	ISO-116 ISO-117 ISO-118 ISO-121 ISO-120 ISO-121 ISO-122 ISO-123 ISO-124 ISO-125 ISO-126 ISO-127 ISO-128 ISO-127 ISO-128 ISO-127 ISO-128 ISO-127 ISO-130 ISO-131 ISO-132 ISO-133 ISO-134 ISO-135 ISO-138 ISO-139 ISO-140 ISO-141 ISO-142 ISO-144 ISO-145 ISO-145 ISO-146 ISO-147 ISO-148 ISO-147 ISO-148 ISO-147 ISO-148 ISO-147 ISO-148 ISO-150 ISO-151 ISO-152 ISO-153	Positive Positive Positive Positive Positive Positive Positive Positive Negative Negative Neg	Cocci Rod Cocci Rod Cocci Rod Cocci Cocci Cocci Cocci Rod Cocci Cocc		+ + + + + + + + + + + + + + +		+				Escherichia coli Pseudomonas aeruginosa Staphylococcus aureus Enterococcus faecalis Bacillus subtilis Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Escherichia coli Staphylococcus aureus Enterococcus faecalis Pseudomonas aeruginosa Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Bacillus subtilis Enterococcus faecalis Staphylococcus aureus Escherichia coli Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Escherichia coli Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis Staphylococcus aureus Pseudomonas aeruginosa Enterococcus faecalis
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DISCUSSION

The current research obtained successful lab work for the isolation and characterization of 157 bacterial strains present in sewage water which included detailed morphological examination alongside biochemistry and electrogenic capability investigation. Significant research data exists that demonstrates the bacterial strains from sewage water can be effectively used for both MFC applications and wastewater treatment. The isolated microbial diversity from sewage environments demonstrates the ecosystem dynamics of the microorganisms which strengthens their application as bioelectricity source. The isolated microorganisms matched previously documented research because most strains came from these genera while acting positively toward both oxidase and catalase tests which implies fundamental electron transport behavior crucial for MFC functionality. The detection of Gram-positive microorganisms Bacillus and Enterococcus serves to confirm previous research on their role in biofilm development and electron transport within electrogenic systems (Pankratova et al., 2018).

The generation capability of bioelectricity by sewage bacteria in MFCs has been examined through various studies which established voltage outputs ranging from 200 to 800 mV based on bacterial species and environmental conditions (Koffi & Okabe 2020; Sonawane et al., 2022). This study obtained electrogenic potential values from 120 to 680 mV which fall within previously reported ranges implying that the isolated strains are effective bioelectricity producers. Cytophagiaearuginosa and Klebsiella pneumoniae proved to be high performers in extracellular electron transfer (EET) efficiency according to previous research (Guo et al., 2020). The electrogenic properties of these bacteria increase when they form stable biofilms since biofilm formation enables efficient electron transfer to generate sustained currents. Biofilms represent a key factor which determines MFC operation effectiveness together with long-term reliability. The biochemical tests demonstrated that bacteria positive for oxidase and citrate utilization demonstrated superior bioelectricity production abilities. The electrogenic activity in dynamic environments appears to be higher for microorganisms that use various carbon sources including Klebsiella pneumoniae and Escherichia coli because these species demonstrate better metabolic adjustments.

Sustainable energy production benefits from bioelectricity generation achieved by bacteria sourced from sewage supply. Recent synthetic biology developments along with biofilm engineering make it possible to improve the performance of the isolates for commercial purposes through genetic modifications.

The use of bacterial consortia in MFCs instead of individual strains enables synergistic effects that result in improved bioelectricity output based on research with mixed pH MFCs across studies (Mukherjee *et al.*, 2021). The experimental findings yield essential information about sewage bacteria's electrogenic

capability although several important constraints deserve recognition. The research failed to conduct whole-genome sequencing which would enhance the understanding of EET mechanisms at the genetic level. The identification of functional genes related to electron transfer through metagenomic research should be combined with studies analyzing how quorum sensing affects bacterial electroactivity (Dang et al., 2022). MFC bioelectricity output can be increased by optimizing operational parameters while choosing appropriate electrode materials and adjusting external resistors. New research on MFC technologies shows great promise through nanotechnology integration with conductive materials such as graphene-based electrodes to enhance electron transfer efficiency (Olabi et al., 2020).

CONCLUSIONS

The presence of electricity-generating bacteria within sewage water has been proven through this research with emphasis on their employability for microbial fuel cells. Studies analyzing 157 bacterial isolates that Pseudomonas aeruginosa, feature Klebsiella pneumoniae, Bacillus subtilis and other microorganisms emphasize the role of sewage microbes in creating renewable energy systems. Future research programs need to concentrate on genetic and electrochemical enhancements to improve operational efficiency at practical application sites. Research that covers extended field studies and performs continuous assessments of MFC operational performance will mark the essential transition between laboratory-based knowledge and practical energy solutions utilizing microbial systems. The research determined multiple bacterial types inhabiting sewage water by extracting characterizing organisms and these through microscopic and chemical identification tests. Laboratory work showed the existence of 157 bacterial strains including three major species Pseudomonas aeruginosa, Klebsiella pneumoniae, and Bacillus subtilis which reflects the versatile characteristics of sewage microbial populations. The research results confirm previous studies which emphasized sewage water bacteria as crucial agents in environmental approaches as well as industrial applications. Future investigations must employ 16S rRNA sequencing and related modern molecular identification approaches to achieve exact taxonomic associations of microbial species. Enhanced investigations of metabolic pathways together with studies about enzymatic activities will enable deeper understanding of both ecological functions and industrial possibilities of these bacterial strains The presented study serves as a scientific basis to guide researchers working with sewage microbiota in developing sustainable environmental management practices.

FUTURE SCOPE

This research study needs development toward optimized and commercial bioelectricity-producing bacterial scale-up applications for microbial fuel cells.

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Detailed metagenomic and transcriptomic testing enables researchers to reveal important genes that drive permitting extracellular electron transfer thus modifications to boost bioelectricity output. Industrial wastewater treatment facilities can recover sustainable energy through the integration of microbial fuel cells which simultaneously helps decrease environmental pollution. Enhanced power output will result from research into electrode materials combination that includes conductive polymers and nanostructured electrodes to advance bacterial attachment performance. The cooperation among different microbial species in consortiums results in better electronic energy transfer single-strain than cultures through synergistic mechanisms. The development of MFC-based bioenergy solutions requires future investigation into their long-term stability together with cost-effectiveness to provide practical implementation for renewable energy production and environmental sustainability.

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