

ISOLATION AND IDENTIFICATION OF *BACILLUS CEREUS* AND *ESCHERICHIA COLI* FROM FOOD SAMPLE SOLD WITHIN, KADUNA TOWN

Abstract

This study was carried out to isolate and identify *Bacillus cereus* and *Escherichia coli*. *Bacillus cereus* and *Escherichia coli* were isolated and identified from food samples sold from local food vendors within Kaduna town, Nigeria. This was done using conventional standard method. The molecular characteristics were confirmed by the Polymerase Chain Reaction (PCR) technique. The results of the microscopic characteristics of the isolates revealed that *B. cereus* is a Gram positive, rod shaped bacterium. The colony of the bacteria appeared rough with dried pink background surrounded by egg yolk precipitate on MYP medium while *E. coli* appeared Gram negative rod shaped under the microscope. And its colony on plate appeared flat with green metallic sheen on Eosin Methylene Blue (EMB) agar. The biochemical identification showed that *B. cereus* is positive to haemolysis, catalase, citrate, Voges Proskauer, motility and spore tests. While *E. coli* is positive to catalase, indole, methyl red and motility tests and showed a green sheen characteristics on Eosin Methylene blue agar. The PCR showed band at 204bp amplicons of 16S rDNA primer targeting bacterial DNA templates V3 hyper-variable region for *B. cereus* and *E. coli* respectively. The amplified DNA was sequenced and BLAST and accession number of KY962911.1 and KY009556.1 were obtained for *B. cereus* and *E. coli* respectively

Key word: *Bacillus cereus*, *Escherichia coli* Isolation and Identification.

INTRODUCTION

Bacillus cereus has been implicated in food intoxication; it is an opportunistic human pathogen that has been reported to cause local and systematic infections. Food poisoning caused by *Bacillus cereus* occurs all year round without any ecological distribution (Rasko *et al.*, 2005). Literatures have associated *B. cereus* with diarrhea, emetic syndrome and fatal meningitis in humans. *Bacillus cereus* is a Gram positive, facultative anaerobic, rod shaped, motile, spore formers, catalase positive, beta-hemolytic and does not ferment mannitol (Rosenquist *et al.*, 2005). The Spore of *Bacillus cereus* are widely disseminated and can survive extreme environmental conditions for a long time, it has been recovered from samples of soils, dust, cereal, crops, dirt, and water (Rahimi *et al.*, 2013). *Bacillus cereus* has a growth temperature

range from 10°C to 48°C, with optimal growth between 28°C and 35°C, PH values of 4.9 to 9.3 and water activities of 0.92 to 1.0 (Sibanda *et al.*, 2010)

Escherichia coli is a Gram-negative, facultative anaerobic, rod-shaped, coliform bacterium of the genus *Escherichia*. It is commonly found as a commensal organism in the lower intestine of warm-blooded animals including humans (Tenaillon *et al.*, 2010). Although most strains of *E. coli* have not been associated with disease condition, some serotypes have been implicated in serious food poisoning, following ingestion of contaminated food substances. The harmless strains are part of the normal flora of the gut, and can benefit their hosts by producing vitamin K₂, and preventing colonization of the intestine by pathogenic bacteria (Yu *et al.*, 2014). *E. coli* is expelled into the environment with fecal matter and grows massively in the fecal matter under aerobic conditions for 3 days, but its numbers decline slowly afterwards. *E. coli* and other facultative anaerobes constitute about 0.1% of gut flora, and faeco–oral transmission is the major route through which pathogenic strains of the bacterium cause disease. This makes them potential indicator organisms to test environmental samples for fecal contamination (Tenaillon *et al.*, 2010).

The increase rate of food borne diseases is posing a major challenge in the public health sector therefore, this study was carried out to isolate and identify the major bacteria associated with food borne diseases.

MATERIALS AND METHOD

Samples Collection

Food samples were randomly purchased from local food vendors within Kaduna metropolis; samples bought were collected into sterile wide mouth universal bottles with tight-fitting caps. The samples were transported in ice pack thermo-flask to the Medical Laboratory of the Department of Microbiology, Faculty of Science, Kaduna State University for isolation. Food samples purchased were raw meat, roasted meat (Suya), smoked fish, Jollof rice, awara (Soya Cheese).

Isolation of *Bacillus cereus* and *E. coli*

Ten (10) grams of the different food samples were homogenized respectively with 90ml of 0.1% peptone water in a screw capped flasks by means of horizontal and vertical agitation for few minutes and incubated for 24 hours at 37^oc. After 24 hours, clear supernatants of homogenized samples were each sub-cultured on freshly prepared plates of MacConkey, and Mannitol Egg Yolk Polymyxin B (MYP) agar plates (Broth, 2014, Cheesbrough, 2009). All cultures were incubated for 24 hours at 37^oc (Rasko *et al.*, 2005)). The plates were observed and each positive plate (one to three discrete colonies of presumptive *Bacillus cereus* and *E. coli* *were* sub-cultured on nutrient agar and kept in the refrigerator for further confirmation of the identity of the organism (Cheesbrough, 2009).

Biochemical Tests for Identification of *Bacillus cereus* and *Escherichia coli*

Biochemical tests used to identify the isolates include catalase, haemolysis, indole production, methyl red, Voges-proskauer test, citrate utilization, oxidase test, spore test and motility test respectively (Holt *et al.*, 1993).

Molecular Identification

Molecular identification was by the 16s RNA polymerase chain reaction.

Molecular confirmation of isolates was determined according to the 16S rRNA gene region. The PCR amplifiability was checked using 16S ribosomal RNA primers V3F-CCAGACTCCTACGGGAGGCAG and backward V3R-CGTATTACCGCGGCTGTCTGG. Extraction was carried out using Extraction buffer (Liferiver Biotech), using manufacturer's protocol. 50µl of the buffer was added to 50µl of isolate solution in molecular biology grade water, and incubated at 100°C for 10minutes using a thermocycler (ABI, Proflex, Life Technologies) and centrifuge at 1300rpm. 5µl of the supernatant was used as template for Polymerase Chain Reaction (PCR). 5µl bacterial Deoxyribo Nucleic Acid (DNA) extract and controls were amplified with 0.5mM primers using 5X Firepol Mastermix ready to load PCR kit (Solis Biodyne). Amplification conditions for PCR were as follows: 5minute at 94°C to denature the DNA, followed by 30 cycles of denaturation at 94°C for 30seconds, primer annealing at 55°C for 40seconds and extension at 72°C for 5minutes on a kyratech Supercycler Trinity thermal cycler. Polymerase Chain Reaction (PCR) fragments were separated on a 1% agarose gel and DNA bands were visualized with ethidium bromide product and were quantified by comparing the intensity of the band to bands of known intensity in a 100Bp DNA Ladder (Promega). The gel was viewed under UV light after fluorescent dye staining. The ladder on the agarose gel indicated the base pair fragment of the DNA of the bacterial. Amplified Polymerase Chain Reaction (PCR) fragments were purified and sequenced with universal primers using Dye Terminator Cycle sequencing kit. Gene sequence chromatograms of the isolates were observed. The similarity search was conducted in-silico using the Nucleotide Basic Local Alignment Search Tool at the National Centre for Biotechnology Institute (NCBI) server. The phylogenetic and molecular evolutionary analyses were conducted using MEGA version 7 (Kumar, Stecher, and Tamura 2016) using the neighbor-joining method.

Result and Discussion

Bacillus cereus is a common soil saprophyte and is easily spread to many types of foods such as dairy products, rice, cereals and cereals derivatives, dried foods, spices, eggs, vegetables and meats (Granum, 2005). It is also the causative agents of two forms of food

poisoning; the diarrhoeal and emetic forms (Mahler *et al.*, 1997), the wide spread of the organism and the ability of its spores to survive dried storage means that most raw and ready to eat foods may contain *B. cereus*. *Bacillus cereus* was determined based on the colonial morphology, precipitation of hydrolyzed lecithin around colonies and its failure to utilize mannitol sugar as reported by Mossel *et al.* (1967). Generally, the colonies of *Bacillus cereus* on Mannitol Yolk Polymyxin B (MYP) appeared rough and dried with a bright pink background surrounded by an egg yolk precipitate (Broth, 2014). According to Abraha *et al.*, (2017), *B. cereus* is a Gram positive (purple coloured), rod shaped cells. Biochemical characteristics of this organism included catalase positive, β -hemolysis on blood agar plate, does not ferment mannitol, it is motile, and spore-forming.

Escherichia coli are bacteria commonly found in the lower intestine of warm blooded organism. Most pathogenic *E. coli* are transmitted by faeco-oral routes from food materials, water, animals and environment. Food surfaces such as meat, eggs, or fish can be used to isolate *E. coli*. Phenotypic characterization revealed *Escherichia coli* ferment lactose on macConkey and produce pink, round medium sized colonies. *E. coli* appears green metallic sheen color colonies growth on Eosin Methylene Blue (EMB) agar plates. Its cellular morphology was revealed to be Gram negative short-rods due to the presence of thin layer of peptidoglycan that made it unable to retain the primary dye. The biochemical characteristic of *E. coli* was due to its cell wall components and enzyme activity. It was found to be methyl red, indole, citrate positive, and oxidase, and Voges-Proskauer (Whitman *et al.*, 2012). Holt *et al.*, (1993) have reported similar phenotypic characteristics. The bacterial species were identified as *Bacillus cereus* and *Escherichia coli* using both conventional and molecular methods. The amplified DNA was sequenced

and BLAST and the organisms found were similar to those with accession numbers KY962911.1 and KY009556.1 for *E. coli* and *B. cereus* respectively.

The molecular characteristics were confirmed by Polymerase Chain Reaction (figure 1.). Bands showed 204bp amplicons of 16S rDNA primer targeting bacterial DNA templates V3 hyper-variable region. The bacterial species were identified as *Bacillus cereus* and *Escherichia coli* using both conventional and molecular methods.

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Table 1: Cultural, Cellular and Biochemical Characteristic of the Isolates

Cultural Morphology	Cellular Morphology	Biochemical Characteristic										Most Probable Organism
		He	Ca	Ci	In	Mr	Vp	Ox	Mt	S	EMB	
Rough, dried with pink background surrounded by egg yolk precipitate on MYP	Gram Positive rod	+	+	+	-	-	+	-	+	+	-	<i>Bacillus cereus</i>
Flat colonies with Green metallic sheen, mucoid Colonies	Gram negative rods	-	+	-	+	+	-	-	+	-	+	<i>Escherichia coli</i>

Key: +=Positive, -=Negative, **He**=Haemolysis, **Ca**=Catalase, Citrate utilization test, **In**=Indole, **Mr**=Methyl Red, **Vp**=Voges Proskauer, **Ox**=Oxidase, **Mt**=Motility, **S**=Spore, **EMB**= Eosin Methylene Blue

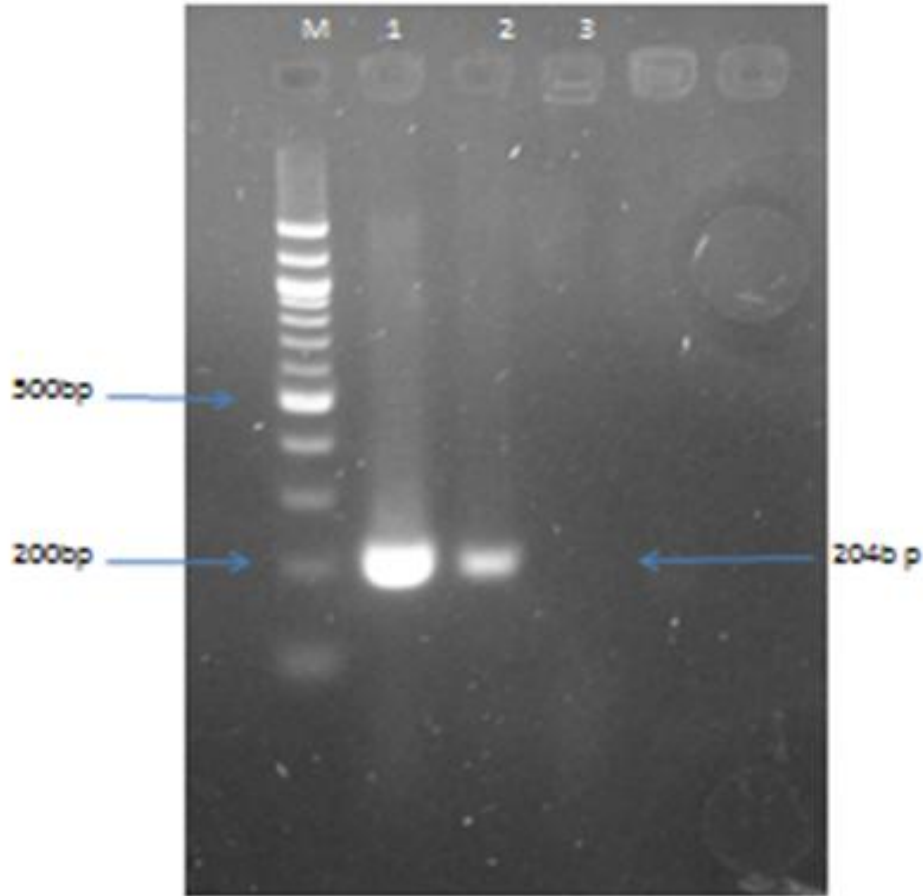


Figure 1: Agarose gel electrophoresis showing positive bands for *B. cereus* and *E. coli*

Sequence of *E. coli* and *B. cereus*

TCAATGGGCGCAGCCTGATGCAGCCATGCCGCGTGWATGAWGAAGGCCTTCGGGT
 GTAAAGYWCTTCAKCGGGARGAAGGGAGTAAAGWTAATMCSTTTGCTCATTGAC
 GKTACCCRCASAARAAGCMCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGA

CCATGCACGAAGTCTGACKCSAGCMCTGCCGCGTGAGTGATGAAGGCYTTCGGRTY
 GTAAACTCTGTTGTTAGGGAAGAACAAGTGCTARTTGAWTAWSYTGGCWCCTGA
 CGGWMCCTAACCAKAARGCCMCGGYTAAYTASKTGCCASCRGCCSGGWAWTMG
 GA

Table 2: Molecular Characterization of *Escherichia coli* and *Bacillus cereus*

Organism	Maximum Score	Total Score	Query Cover	E-value	Accession Number
<i>Escherichia coli</i>	307	307	99%	8e-80	KY962911.1
<i>Bacillus cereus</i>	1284	1284	100%	00-00	MG557810.1

Conclusion

Escherichia coli and *Bacillus cereus* were isolated from the food samples sold from food samples within Kaduna, Kaduna state in Nigeria.

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