

**PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF ENTEROTOXIGENIC *E. COLI* ISOLATED FROM DIARRHOIC SAMPLES OF UNDER FIVE CHILDREN IN REMO, OGUN STATE, NIGERIA**Abosede Abolanle Akeredolu\* and Mope Deji- Agboola<sup>1</sup>

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**ABSTRACT**

A total of 195 diarrhoeic samples were collected from the children whose parents gave their consent to participate in selected hospitals in Remo, Ogun State. *Escherichia coli* was isolated from the samples using standard Microbiological and Molecular techniques. Characterization of enterotoxigenic *Escherichia coli* was determined using Molecular methods. Out of 195 diarrhoeic samples analyzed in this study, 84(43.1%) were positive for *Escherichia coli*. Out of the 84 *Escherichia coli* isolated, 82 (97.6%) were confirmed to be positive by the molecular method. Only 15 (17.9%) were enterotoxigenic (ETEC) while others 69 (82.1%) were non-pathogenic.

**KEYWORDS:** Enterotoxigenic *E.coli*, Diarrhoea, Remo.**INTRODUCTION**

Diarrhoea accounts for 11 percent of all under-five deaths worldwide (Black et al., 2010) and claims the lives of 1.8 million children per year worldwide annually (WHO, 2012). In developing countries diarrhoea has the highest mortality rate in young children (Liu et al., 2015). According to UNICEF, (2011) the recent mortality estimates among children under five years old show that just five countries account for 50 percent of global mortalities. Of those five, Nigeria accounts for 11 percent of all deaths. Report from Liu et al., (2015) states that diarrhoea can be prevented, yet responsible for nine percent of all deaths among under age five children worldwide. The causes of diarrhoea include a wide range of viruses, bacteria and parasites, among the bacteria pathogens, *Escherichia coli* play an important role (Peleg et al., 2005).

**MATERIALS AND METHODS**

The study was carried out in Remo Land comprising of Sagamu, Ikenne and Remo North Local Government Areas of Ogun State, Nigeria, between July 2016 and June 2017. The study was approved by Olabisi Onabanjo University Teaching Hospital Health Research Ethics Committee under the authorization number: NHREC/08/10/2012. The sample size calculation was determined as described by Daniel, (2009). A total of 195 diarrhoeic samples were collected from the children that meet the criteria and whose parents gave their

consent to participate in selected hospitals in Remo, Ogun State.

**Collection and processing of specimens**

The stool samples were collected in a sterile sample bottles directly from the children with the assistance of the laboratory staff and health workers in the study site who were educated on how to collect the samples aseptically, the samples were transported to the laboratory for analysis within 30 minutes after collection. Samples were collected for a period of twelve months from children under the age of five (5) years with incidents of diarrhoea as presented by the parents and confirmed by the clinician. The samples were processed in Microbiology Laboratory, Babcock University, Ilesan Remo, Ogun State, Nigeria.

**Isolation and identification of *E.coli***

Using a sterile standard wire loop, a loop full of stool sample was streaked on sterile Mac Conkey agar plates and incubated for 24 hour at 37 °C. All Lactose fermenting colonies were sub cultured on Eosin Methylene Blue (EMB) agar and incubated overnight at 37°C. Colonies that exhibited green metallic sheen colour, characteristic of *E. coli* were sub cultured on Nutrient agar plates and incubated at 37 °C for 24 hour, Biochemical tests such as Indole, Methyl red -Voges-Proskauer (MR-VP), Citrate tests and sugar fermentation test were performed on the colonies. The pure colonies

identified as *E. coli* were inoculated on Nutrient agar slant and were stored in the refrigerator at 4°C.

### Molecular Identification of *E. coli*

#### DNA extraction

The stock cultures of *E. coli* were cultured on Nutrient agar to reactivate them, incubated at 37°C for 18-24 hours. The resuscitated isolates were inoculated in Tryptone soy broth (TSB) and incubated at 37°C overnight, centrifuged at 5000xg for 10 minutes. The supernatant was discarded and the pellet was re-suspended in 150uL of sterilized distilled water. The suspension was subjected to boiling at 100°C in water bath (Uniscop, Surgifriend, England) for 10 minutes, and centrifuged at 5000xg for 30 seconds. The supernatant was then transferred into fresh Eppendorf tubes before it was stored at 4 °C. Aliquots of 5uL of template DNA for Polymerase Chain Reaction (Martins et al., 2015).

#### PCR amplification for TEcol gene

PCR reaction was carried out using the Solis Biodyne 5X FIREPol Blend Master mix, the concentrated 5X FIREPol Blend Master mix was diluted with sterile

distilled water to 1X. The Blend Master mix contains: 2 unit of FIREPol DNA polymerase (Solis Biodyne), Proofreading Enzyme, 2.0 mM MgCl<sub>2</sub>, 200µM of each deoxynucleoside triphosphates (dNTP) (Solis Biodyne). PCR was performed in 20 µL of a reaction mixture. Therefore, 4 µL master mix, 0.5 µL each of forward and reverse primers (10pMol) (BIOMERS, Germany) as in Table 3.1, 5µL of the extracted DNA and sterile distilled water was used to make up the reaction mixture (Åsa et al., 2015 & Christopher et al., 2019).

Amplification was conducted in a Peltier thermal cycler PTC 100 (MJ Research Series) for an initial activation at 95°C for 15 minutes followed by 35 amplification cycles of 30 seconds for denaturation at 95°C; 1 minute of Annealing at 56°C and 1 minute 30 Seconds of elongation at 72°C. This was followed by a final elongation step of 10 minutes at 72°C. The amplification product was separated on a 1.5% agarose gel and electrophoresis was carried out at 80V for 1 hour 30 minutes. After electrophoresis, DNA bands were visualized by ethidium bromide staining. 100bp DNA ladder was used as DNA molecular weight standard.

**Table 1: Primers used for confirmation of *Escherichia coli*.**

S/N	Primers	Sequence(5 <sup>1</sup> 3 <sup>1</sup> )	Annealing Temperature(°C)	BASE PAIR(b <sub>p</sub> )
1.	TEcol-F	TGGGAAGCGAAAATCCTC	58	1258
	TEcol-R	CAGTTACAGGTAGACTTCTG		

Nolonwabo, et al., (2014).

### Identification of enterotoxigenic *E. coli* by multiplex PCR

#### PCR amplification for enterotoxigenic genes.

A multiplex PCR reaction was carried out using the Solis Biodyne 5X FIREPol Blend Master mix, the concentrated 5X FIREPol Blend Master mix was diluted with sterile distilled water to 1X. The Blend Master mix contains: 2 unit of FIREPol DNA polymerase (Solis Biodyne), Proofreading Enzyme, 2.0 mM MgCl<sub>2</sub>, 200µM of each deoxynucleoside triphosphates (dNTP) (Solis Biodyne). PCR was performed in 20 µL of a reaction mixture. Therefore, 4 µL master mix, 0.5 µL each of forward and reverse primers (10pMol) (BIOMERS, Germany), 5µL of the extracted DNA and sterile distilled

water was used to make up the reaction mixture (Åsa et al., 2015 & Christopher et al., 2019).

Amplification was conducted in a Peltier thermal cycler PTC 100 (MJ Research Series) for an initial activation at 95°C for 5 minutes followed by 35 amplification cycles of 30 seconds for denaturation at 95°C; 1 minute of Annealing at 55°C and 1 minute 30 Seconds of elongation at 72°C. This was followed by a final elongation step of 10 minutes at 72°C. The amplification product was separated on a 2.0% agarose gel and electrophoresis was carried out at 80V for 1 hour 30 minutes. After electrophoresis, DNA bands were visualized by ethidium bromide staining. 100bp DNA ladder was used as DNA molecular weight standard.

**Table 3.2: Primers used in the detection of virulence genes of *Escherichia coli*.**

Pathotype	Target	Name	Primer (5 <sup>1</sup> -3 <sup>1</sup> )	Sequence PCR product size
ETEC	LT St 11	LT-F	GCA CAC GGA GCT CCT CAG TC	218
		LT-R	TCC TTC ATC CTT TCA ATG GCT TT	
		St11-F	AAA GGA GAG CTT CGT CAC ATT TT	129
		St11-R	AAT GTC CGT CTT GCG TTA GGA C	

Nolonwabo, et al., (2014).

## RESULTS AND DISCUSSION

### Age and gender distribution of diarrhoea cases in study population

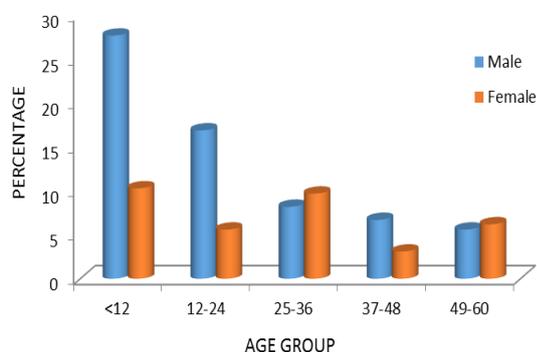
The age distribution of the children with highest cases of diarrhoea in this study showed that they were mainly

infants (less than or equal to 12 months) in which 54 (27.6%) were boys and 20 (10.2%) were girls as presented in Figure 4.1. This corresponds to the result of Thielman and Guerrant (2004); Avisek et al., (2015); Ayuk et al., (2015); Magbagbeola et al., (2017);

Mohammed et al., (2018) and Thiagarajah et al., (2018) reported that the rates of diarrhea were highest for infants 6-11 months of age, remained at a high level among 1-year-old children and decreased when children got older. A decrease in number of cases among older children is due to the acquisition of immunity over the time which resist against infection agent. The results of this study is also in accordance with reports from Bahrain (Krishnamurthy, 1990), Saudi Arabia (Qadri et al., 1990 and Albert et al., 1995) which showed that 50%, 43.4% and 53.6% respectively of the children hospitalized with diarrhoea were below 1 year of age also support the results. The age-specific differences suggest that infants apart from having immature immune systems may be exposed to contaminated formula of milk, foods or environment or may have not been protected completely by maternal antibodies in breast feeding (Akbar, 2008). Furthermore, results of this study revealed that number of males 127 (65.1%) with diarrhoea were higher than in females 68 (34.8%) (Figure 1). This agrees with report of (Ogunlesi et al., 2006; Ogbu et al., 2008; Ohaeri & Odukaesime, 2011) and is consistent with results of other researchers Ishiyama et al., (2001); Abdullahi et al. (2010), Anasari (2012), Ifeoma et al., (2017); Angela et al., (2018) which reported that male children were more infected than female children but in contrast to Gupta et al., (2015); John et al., (2016) and Bui et al., (2018).

### 1: Bacteria isolated from children diarrhoeic stool samples

Bacteria	Frequency (n=195)	Percentage
<i>Escherichia coli</i>	84	43.1
Non <i>Escherichia coli</i>	85	43.6
Without growth	26	13.3
Total	195	100.0



**Figure1: Age and gender distribution of diarrhoea cases in study population.**

### Isolation, Phenotypic and Genotypic characteristics of *Escherichia coli* isolates from children diarrhoeic stool samples

Out of the 195 diarrhoeic samples analyzed in this study, 84 (43.1%) of the samples were positive for *Escherichia coli* as presented in Table 1 and 82 (97.6%) were

confirmed positive by Molecular characterization (Figure 2). The prevalence of *Escherichia coli* from this study is lower than 89.4% reported from similar study in Benin Teaching Hospital, Benin, Nigeria; 83.1% reported in Abakaliki, South eastern Nigeria (Ogbu et al., 2008); 62.8% obtained in a study carried out in the Federal Capital Territory Abuja, Nigeria by Ifeanyi et al (2010) among children presented with diarrhea. Furthermore the prevalence is also lower than 61.76% recorded by Babu et al (2009) in Rajah Hospital, Annamalainagar, Tamil Nadu, in India and also lower compared with other studies carried out in Iran (Alikhani et al, 2006; Jafari et al, 2009; Al-Zogibi and Onizan Godian, 2015;). In contrast, it is higher than 34% recorded by Sule et al (2011) in Kaduna, another Northern State in Nigeria. Clarence et al (2007) had 41.3% prevalence of *Escherichia coli* in a study conducted among children with diarrhoea, attending Madonna University Teaching Hospital (MUTH) Elele, in Rivers State, in South South, Nigeria while Olanipekun, (1996) documented 26% prevalence among children with diarrhoea attending Jos University Teaching Hospital, Jos in Plateau State, in North east, Nigeria. It is reasonable to attribute the differences in prevalence of *Escherichia coli* to region, countries and geographical area.

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