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# Genetic and Phylogenetic Diversity of *Escherichia coli* Strains Collected From Fecal Specimens of Patients Admitted to Zabol Hospitals

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## Abstract

**Introduction:** *Escherichia coli* is one of the most prevalent bacterial species which cause gastrointestinal and digestive tract infections in humans and livestock. This study examined genotypic diversity of the *E. coli* isolates taken from fecal specimens in Zabol using random amplification of polymorphic DNA (RAPD) method and phylogenetic background.

**Materials and Methods:** In this study, 100 isolates were collected from human samples and identified by the common biochemical tests. The isolates were categorized into four main phylogenetic groups including group A (28 isolates), group B<sub>1</sub> (7 isolates), group B<sub>2</sub> (48 isolates), and group D (17 isolates). Two primers (H1 & H2) were used to study the genetic variation of *E. coli* and the electrophoresis band pattern was analyzed by the NTSYS.

**Results:** The analysis of the difference in isolates using the RAPD technique showed a genetic similarity between 14% and 100%.

**Conclusion:** The phylogenetic groups B<sub>2</sub> and A were more frequent in fecal isolates. In addition, the number of isolates related to phylogenetic groups B<sub>1</sub> and D was significantly lower than that of the other groups.

**Keywords:** *Escherichia coli*, Genetic diversity, Phylogeny, RAPD-PCR

## Introduction

*Escherichia coli* is a type of bacteria which can colonize and survive in numerous environmental habitats and animal hosts. This bacterium and other intestinal flora bacteria often interact with their hosts in a way that the hosts provide them food, and they, in return, contribute to the regulation of immune system and host protection against the pathogens.<sup>1</sup> Some of the *E. coli* strains have extra-intestinal pathogenic features and are found in various organs such as blood, central nervous system, and the urinary system.<sup>2</sup>

Phylogenetic studies conducted with the polymerase chain reaction (PCR), multilocus enzyme electrophoresis, and ribotyping methods are of paramount importance in evaluating the genetic evolution of the *E. coli*. Identifying the

phylogenetic groups of *E. coli* strains by PCR method is facilitated through determining the presence of *yjaA* and *chuA* genes and the TSPE4.C fragment. Phylogenetic association of *E. coli* standard collection of reference (ECOR) strains indicates that the *E. coli* strains belong mainly to four phylogenetic groups of A, B<sub>1</sub>, B<sub>2</sub>, D<sup>3</sup> which are among the most important groups of *E. coli* bacteria. Previous studies demonstrated that these groups are quite different in many of their characteristics such as resistance to antibiotics, growth rate, and pathogenicity. A proper understanding of these characteristics can be effective in identifying the diversity of bacteria in the environment. The phylogenetic technique has several uses. It has a biotechnological role, and it communicates between the phylogenetic and pathogenic groups. In

addition, this technique functions as a biotechnological screening tool for detecting the pathogenic species. Further, it is a screening means used to identify the *E. coli* K-12 species by PCR and *E. coli* strains from unknown bacterial pathogens.<sup>4</sup>

Furthermore, phylogenetic strains are different in terms of their genome size. The genomes of the strains in groups A and B<sub>1</sub> are smaller than those of the phylogenetic groups B<sub>2</sub> and D. Phylogenetic studies on *E. coli* strains which are responsible for digestive diseases in humans indicate that these strains mainly belong to the B<sub>2</sub> group, but few of them belong to group D. *E. coli* strains show vast genetic diversity depending on the severity of their underlying human diseases.<sup>3</sup> Moreover, random amplification of polymorphic DNA (RAPD) is one of the rapidly developing and fast PCR-based methods requires no specific DNA sequence. Additionally, its primers are designed completely randomly. However, low repeatability and inability to recognize the allelic forms are the major disadvantages of this method. Recognizing the genetic profiles of the *E. coli* isolates which are taken from diverse clinical samples can be beneficial in designing therapeutic strategies. Therefore, the present study aimed to screen the phylogenetic diversity of *E. coli* isolates from fecal specimens of the patients referring to 2 main hospitals in Zabol using the RAPD technique.

### Materials and Methods

A number of 100 *E. coli* isolates were gathered from the stool specimens of patients with diarrhea who referred to 2 major hospitals, namely Imam Khomeini and Amir-Al-Momenin in Zabol from December to March 2013. Then, biochemical tests (i.e., oxidase, fermentation, movement, urease, citrate hydrolysis, nitrate reduction, the Methyl Red and Voges-Proskauer, hydrogen sulfide, and indole production) were performed to characterize the *E. coli* species. The genomic DNA of the *E. coli* isolates was extracted based on the study by Rashki et al.<sup>5</sup> In addition, the phylogenetic distribution of the *E. coli* isolates was determined by the Triplex-PCR, as described by Clermont et al, using primers provided in Table 1.<sup>4</sup> Then, 5 µL of the PCR product was loaded in 2% agarose gel, stained with ethidium bromide, and visualized using a Gel-Doc (LOURMAT, France) device (Figure 1).

Further, the RAPD-PCR reaction was performed employing H2 and H3 primers (Table 1).

The reaction condition was conducted as described by Heydari and Rashki.<sup>6</sup> The PCR amplicons were electrophoresed in agarose 2% and speculated under UV illumination after staining by ethidium bromide (Figure 2).

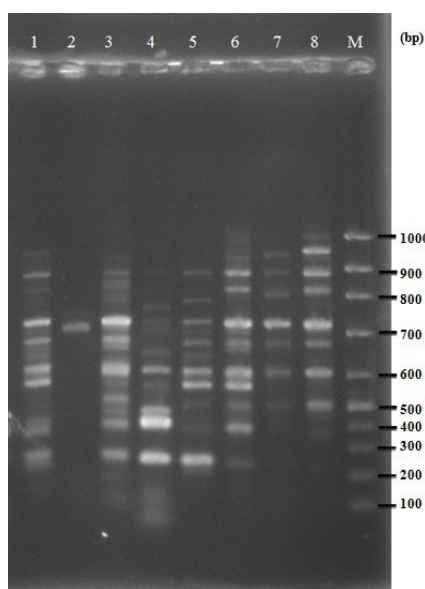
In the data matrix created in the NTSYS-pc software, version 2.02, numbers 1 and 0 denoted the presence or absence of a particular band and the phylogenetic tree was prepared for each case. The Jaccard pairwise correspondence was applied for similarities between



**Figure 1.** An Image of the Gel Electrophoresis Produced by PCR of *chuA*, *yjaA* genes and TSPE4.C2 Fragment.

**Table 1.** Primers Used in Phylogenetic Analysis Study

Gene	Sequence of the Primer (3-5)	(bp) Size
<i>chuA</i>	F- GAC GAA CCA ACG GTC AGG AT R- TGC CGC CAG TAC CAA AGA CA	279
<i>yjaA</i>	F- TGA AGT GTC AGG AGA CGC TG R- ATG GAG AAT GCG TTC CTCAAC	211
TspE4.C2	F- GAG TAA TGT CCG GGC ATT CA R- CGC GCCAAG AAA GTA TTACG	152
H2	AAGCTTCGACTGT	Variable
H3	AAGCTTGATTGCCC	Variable



**Figure 2.** The RAPD-PCR Gel Electrophoresis Image.

the strains using the means of matrix correspondence and unweighted pair-group method (UPGMA).<sup>7</sup> The closest neighbor-joining clustering method was used to demonstrate the relationships between the similar groups.

**Results**

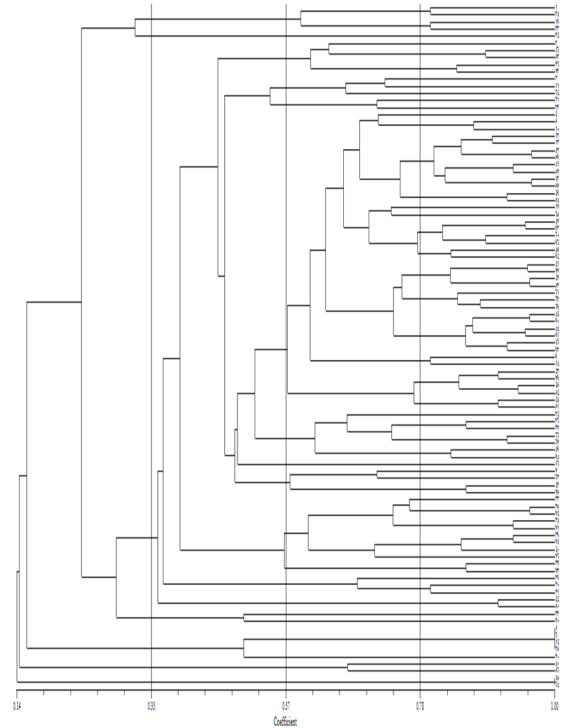
Totally, 100 *E. coli* isolates collected from the stool samples were assigned into 4 groups of B<sub>2</sub> (48 %), B<sub>1</sub> (7 %), A (28 %), and D (17 %) (Table 2).

The results of the dendrogram indicated that all the isolates were in separate clusters. Furthermore, the results obtained from the RAPD-PCR demonstrated that all the isolates had a different pattern indicating a high differentiating capability of the used primers and high polymorphisms in the collected isolates (Figure 3). The genetic distance of the studied genotypes varied from 14% to 100 % using the Jaccard's coefficient in the dendrogram.

**Discussion**

*Escherichia coli*, as a common resident of the human lower intestine, is typically a part of the normal flora of the intestine. However, some strains might cause poisoning, tissue damage, and invasion. In this study, 100 isolates of *E. coli* collected from the feces were divided into four groups of B<sub>2</sub>, B<sub>1</sub>, A, and D with respective frequencies of 48%, 7%, 28%, and 17%, respectively. Using a Triplex-PCR method for phylogenetic analysis of the *E. coli* isolates, Derakhshandeh et al demonstrated that the isolates were related to groups A (n = 69), B<sub>2</sub> (n = 18), and D (n = 15), but no isolate belonged to group B<sub>1</sub>.<sup>8</sup> Moreover, Lee et al indicated that phylogenetic distribution of *E. coli* strains was similar between blood and urine isolates.<sup>9</sup> These results regarding the phylogenetic diversity of fecal isolates in the B<sub>2</sub> group are quite consistent with those of the present study. Another research was conducted on 138 isolates collected from the human stool in order to assess the phylogenetic distribution of *E. coli* strains using the Triplex-PCR. Based on the results, no isolates belonged to group B<sub>2</sub> while the highest number of isolates belonged to group B<sub>1</sub>.<sup>10</sup> In another research, the phylogenetic grouping of 168 *E. coli* isolates collected from the human stool samples was assessed in three different geographic populations including France, Croatia, and Mali. Most of the isolates were relevant to group B<sub>2</sub>. Additionally, the remaining isolates belonged to groups A, B<sub>1</sub>, and D with respective frequencies of 40, 34 and 15%, respectively.<sup>11</sup>

In their study on the phylogenetic groups of the *E. coli* strains using the Triplex-PCR, Clermont et al found that the isolates belonged to groups A (n = 43), B<sub>1</sub> (n = 23),



**Figure 3.** Dendrogram Schemed With NTSYS.

D (n = 51), and B<sub>2</sub> (n = 113).<sup>4</sup> Similarly, Etebarzadeh et al used Triplex-PCR to investigate phylogenetic status of the *E. coli* isolates and indicated that 65% of the strains were related to group B<sub>2</sub> while the other strains belonged to group D (19%) and phylogenetic group A (16%).<sup>12</sup> Overall, a large number of pathogenic extra-intestinal *E. coli* strains were relevant to group B<sub>2</sub> whereas a smaller number belonged to group D. However, the majority of the commensal strains were related to group A.<sup>13</sup> Lee et al in their research found that the phylogenetic group B<sub>2</sub> was more frequent.<sup>9</sup> As regards the present study, the highest frequency was related to the isolates A and B<sub>2</sub>. Although a number of isolates were distributed into groups B<sub>1</sub> and D, group B<sub>2</sub> strains were the most common (48%) while the strains of group B<sub>1</sub> were the least common (7%) among the fecal specimens. This is further in conformity with the results of Escobar-Páramo et al.<sup>3</sup>

In the current study, molecular typing was performed on 100 *E. coli* isolates employing the RAPD method designed

**Table 2.** Phylogenetic Classification of the Pattern Designed Based on the Presence or Absence of the Duplication Bands

Phylogenetic Group	The Number of Isolates	Percent	<i>chuA</i>	<i>yjaA</i>	TSPE4.C2
B2	48	35	+	+	+
		13	+	+	-
D	17	6	+	-	+
		11	+	-	-
A	28	25	-	+	-
		3	-	-	-
B1	7	7	-	-	+
Total	100	100	-	-	-



for detecting genetic polymorphisms in different strains of the studied isolates. In addition, it is useful for describing the distribution of the strains in the field ecology of the pathogen. Further, the RAPD, the results of which are comparable to the results of the expensive pulsed-field gel electrophoresis (PFGE) method, is a reliable technique for screening the genetic diversity of various bacterial species.<sup>14</sup> Based on the findings of Suardana et al, genetic maps of the *E. coli* isolates had several superiorities over the other methods using the RAPD technique. Furthermore, it is considered as time and cost-saving method with high sensitivity and easy applicability compared to methods such as amplified fragment length polymorphism (AFLP), and analysis of chromosomal DNA restriction patterns by PFGE. Therefore, such procedures can provide researchers with a wealth of information regarding the genetic diversity of various bacterial isolates.<sup>15</sup> Moreover, Kanungo represented that a significant genetic link was established between the *E. coli* strains, isolated from identical locations, using 2 different primer sets by exploiting the RAPD method.<sup>16</sup> In an analyzing the *E. coli* strains using the RAPD, Kilic et al asserted that this technique had the highest separation capacity for determining the genetic diversity of *E. coli* isolates despite a large genetic dissonance between the *E. coli* strains.<sup>17</sup> Additionally, Salehi et al concluded that the RAPD can be a useful method for determining the genetic differences between the *E. coli* isolates.<sup>18</sup> Similar to other studies, the analysis of dendrogram represented high genetic diversity in *E. coli* isolates, indicating the participation of different pollution centers in spreading the bacteria.<sup>19,20</sup>

Similarly, the results of the current study demonstrated that different isolates of the same *E. coli* species yielded no similar phylogenetic relationship. In addition, very negligible genetic variations may exist between the fecal *E. coli* isolates. Further studies are needed to determine the prevalence, distribution, ecology, and epidemiology of the fecal *E. coli* isolates.

### Conclusion

This study was conducted to provide an efficient classification for phylogenetic isolates collected from the fecal samples of patients residing in 2 different hospitals of Zabol. Generally, the results revealed that the highest number of isolates belonged to phylogenetic group B<sub>2</sub>, indicating a probable extra-intestinal origin.

Further, the RAPD method was employed to study the genetic difference of *E. coli* strains, which is a highly reliable and accurate technique in classifying and determining the phylogenetic diversity of bacterial strains. Analyzing the collected *E. coli* isolates from the fecal specimens across different geographic regions can provide useful information on phylogenetic epidemiology and distribution of drug-resistant strains.

### Ethical Approval

The informed consent was obtained from the patients before using their samples and the data were kept confidential.

### Competing Interest

There are no competing interests to declare.

### Acknowledgments

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