

## GENETIC DIVERSITY AMONG *YERSINIA ENTEROCOLITICA* ISOLATED FROM SEWAGE, RAW MILK AND PACKED FOODS

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### ABSTRACT

A total of 90 isolates (40 from sewage, 30 from raw milk and 20 from packed foods) collected to study the incidence of *Yersinia enterocolitica*. It was observed that 61 isolates (32 from sewage, 19 from raw milk and 10 from packed foods) were found contaminated with the bacterium. All the isolated strains were confirmed to *Yersinia enterocolitica*, by using 16S rRNA PCR. Of 61 strains, only five strains (two from sewage and two from packed foods and one from raw milk) were found to be the producers of haemolysin at 37 °C, while among the five strains only two strains from packed foods produced haemolysin at 28 °C. All the isolates showed resistance to amoxicillin and found sensitive to chloramphenicol. Seven strains were producer of High molecular weight proteins (HMWP). 53 strains have produced rough LPS, while the smooth LPS has been observed for 8 isolates. Eleven and six different profiles observed in outer membrane proteins and lipopolysaccharide respectively. Combined primer 1 and 2 RAPD-PCR dendrogram shows eight different genotypic patterns.

**Keywords:** *Y. enterocolitica*, haemolysin, multiple antibiotic resistances Outer membrane protein, Lipopolysaccharide, RAPD-PCR

### INTRODUCTION

*Yersinia enterocolitica* is a Gram-negative bacterium, belonging to the family *Enterobacteriaceae* that causes food-transmitted infections (Keet, 1974; Eden *et al.*, 1977). The Common clinical syndromes include gastroenteritis, various forms of abscesses, septicemia, arthritis, mesenteric lymphadenitis and erythema nodosum (Bottone, 1977). This microorganism has been isolated from water, dairy products, foods, animals and humans in various country where isolation has been attempted (Bottone, 1983, Shayegani *et al.*, 1983). *Y. enterocolitica* is rapidly emerging worldwide as an enteric pathogen and has become a major cause of diarrhea in most of the industrialized world. *Y. enterocolitica* may present in various raw animal foods and causes illness when consumed by human beings. As bacterium can survive at 4°C, so it can grow well in refrigerated foods and survive in frozen foods for long periods. To control and treat the infectious diseases, antimicrobial susceptibility test were used (Phillips *et al.*, 2004). The outer membrane protein (OMP) of the *Y. enterocolitica* is probably involved in the host - bacterial interactions; Because OMP is dependent on the presence of plasmid for expression (Zink *et al.*, 1980). Protein level typing mostly determines the pathogenic species diversity. RAPD – PCR (Random Amplification of Polymorphic DNA) directs a random DNA sequence by using a single primer (Bottone, 1997). Considering the significance of water or food-borne illness and genetic diversity of this bacterium this study has been taken to analyze the antimicrobial resistance, haemolysin activity, LPS, OMP and RAPD-PCR among the contaminated water, raw milk and packed foods.

### MATERIAL AND METHODS

#### Sample collection and isolation

A total of 90 isolates, (comprises 40, 30 and 20 from sewage, raw milk and packed foods respectively) were collected from different locations during winter seasons, mainly in and around Coimbatore, Tamil Nadu. One ml of sewage water, milk samples and 0.1 g of packed food samples were inoculated into 10 ml of yersinia enrichment broth (Hi Media, India) and incubated at 30 °C for 24 h. Then a loopful of culture was transferred and streaked on to Yersinia selective agar (CIN agar) (Hi Media, India), followed by incubated at 28 °C for 18 – 24 h. After incubation, the plates were analyzed for red bull's eye shaped pinpoint colonies.

#### Confirmation of *Y. enterocolitica*

All the isolates were subjected to ten biochemical methods (Voges–Proskauer, urease, sorbitol, ornithine decarboxylation, citrate, DNase, raffinose, esculin hydrolysis, salicin fermentation and lysine iron agar (LIA)), according to Bergey's Manual of Systematic Bacteriology. (Table.2). Further the isolates were identified as *Y. enterocolitica* by PCR based on 16S rRNA gene amplification as described by (Neubauer *et al.*, 2000).

#### Hemolytic activity

All the isolates *Y. enterocolitica* were individually enriched in 5 ml of brain heart infusion broth (BHI, Hi Media, India) and incubated at 37 °C for 16-18 h. Supernatant fluids were carefully removed after centrifugation at 10,000 *xg* for 30 min at 4 °C. About 100 µl of supernatant fluids were mixed with an equal volume of 2 % (v/v) suspension of rabbit erythrocytes in a 96-well 'V'-bottom microtitre plate. The mixture was incubated for 30 min at 37 °C and then for 30 min at 4 °C. An erythrocyte suspension in phosphate-buffered saline (PBS) was included in each assay as a negative control. Haemolysin production was recorded by visual inspection (Table 3).

#### Antimicrobial susceptibility test

All the isolates were tested for their multiple antibiotic resistances against 21 different antibiotics (Table 4), using Mueller-Hinton agar (Hi Media, India) by adopting standard disc diffusion method (Bauer *et al.*, 1966). Following disc diffusion all the plates were incubated at 28 °C for 24 h. After the incubation period, the diameter of the inhibition were measured and compared with the Performance Standards for Antimicrobial Disk Susceptibility Test CLSI (2012).

#### Extraction of outer membrane protein (OMP)

The *Y. enterocolitica* strains were grown in 20 ml of Nutrient broth (Hi Media, India) overnight at 37 °C. Preparation of OMP was done according to Winder *et al.* (2000). The pellet containing the OMP was resuspended in deionised water (1 ml) and stored at - 20 °C until required. The samples were subjected to 12 % polyacrylamide gels containing SDS (SDS-PAGE) and the gel was stained with Coomassie brilliant blue R-250 (Laemmli UK, 1970)

**Extraction of lipopolysaccharide (LPS)**

Cells were grown in nutrient broth for 48 h at 37 °C. LPS from cells was obtained by the hot phenol - water method (Rezania et al., 2011). Twenty µl of LPS suspension was applied in each slot of 12.5 % SDS - PAGE gel. The separated LPSs were visualized by silver staining (Tsai and Frasch, 1982).

**Random Amplification of Polymorphic DNA (RAPD) PCR**

The primer used in this study was primer 1 (5'-CCGCAGCCAA-3') and primer 2(5'-GAGACGACA-3'). Each 25 µl reaction mix contains 30 ng genomic DNA, 1 U Taq DNA polymerase, 1 X Taq DNA polymerase buffer (Chromous Biotech, Bangalore), 2.5 mM MgCl<sub>2</sub>, 400 µM dNTPs (Helini Biomolecules, India) and 20 pmol / µl primer. RAPD used for the study of diversity among *Y. enterocolitica* isolates was performed as described by Leal et al. (1999). RAPD data were coded, analysed, all molecular markers were combined in a final analysis. Each amplified product revealed by electrophoresis was recorded as binary data, presence (1) and absence (0): an initial matrix of 0 and 1 was constructed. The genetic similarities amongst isolates were calculated from the matrix data using the simple matching (SM) index (Duart et al., 1999). The cluster analysis was performed by mean of the unweighted paired group method using arithmetic average (UPGMA) (Saitou and Nai, 1987). The statistical robustness of the inferred tree was estimated by means of the cophenetic correlation coefficient (CCr) (Duart et al., 1999), bootstrap, and best-cut test. Dendrogram branches with bootstrap values higher than 50% and relationships on the right side of best-cut-test vertical line were considered significantly supported. All of these analyses were made with the NTSYS-PC software, version 2.02j (Duart et al., 1999) and PHYLIP ver. 3.6 software (Saitou and Nai, 1987).

**RESULTS AND DISCUSSION**

Environment is the most common source for *Y. enterocolitica* bacterium, than any other. Among the environmental sources, water is the most significant one. Incidence of the bacterium has been reported from freshwater such as rivers, lakes and drinking water (Langeland, 1983; Massa et al., 1988; Kuznetsov and Timchenko, 1998). They have also been isolated from sewage (Ruhle et al., 1990; Ziegert and Diesterweg, 1990). Falcao et al. (2004) reported that 26 % of the total isolates of sewage origin were found to be *Y. enterocolitica*. In our study, of the 90 samples collected, 61 were found contaminated with *Y. enterocolitica* (Table 1), which confirmed by using biochemical tests (Table 2) and 16S rRNA PCR. Maximum incidence of contamination was recorded for sewage samples was 80 %. This is most significant value with respect to the incidence of this bacterium. In another study, 36.6 % of raw milk samples were positive for this organism (Hamama et al., 1992). Similarly, the incidence of *Y. enterocolitica* has been reported from raw milk samples as 20 %, 81.4 % and 10.6 % by Franzin et al. (1984), Vidon and Delmas, (1981) and Subha et al. (2009) respectively. In our study, 64 % of the raw milk samples were recorded as positive for this bacterium. Seventy six cheese curd samples tested, 9.2 % were positive for *Y. enterocolitica* (Schiemann, 1978). It report 50 % of packed foods samples were contaminated with *Y. enterocolitica*.

**Table 1** Incidence of *Y. enterocolitica* in various samples

Sample	No. of samples	% positive
Sewage	40	80 % (n = 32)
Raw milk	30	64 % (n = 19)
Packed foods	20	50 % (n = 10)

**Table 2** Biochemical results of various tests against the isolates

Biochemical test <sup>a</sup>	No. positive	% positive
Voges -proskauer	75	83
Urease	73	81
Sorbitol	70	78
Ornithine decarboxylation	45	50
Citrate	65	72
DNase	46	51
Raffinose	61	68
Esculin hydrolysis	5	6
Salicin fermentation	5	6
Lysine Iron Agar (LIA)	61	68

<sup>a</sup>All biochemical tests completed at 36 °C unless otherwise noted

Haemolysin activity was carried out for all *Y. enterocolitica* strains. It showed that only 8 % were found to produce haemolysis. Production of haemolysin is said to be one of the virulence factors among pathogenic microorganisms. However, based on the haemolysin production alone, one should not confirm the pathogenicity. Non-haemolytic isolates of *Y. enterocolitica* have also been

confirmed as pathogens to human and animals (Subha et al., 2009). Influence of temperature on activity of haemolysin was also studied. This bacterium shows haemolytic activity at 37 °C and 28 °C as well (Franzin et al., 1984). Similarly in the present study for haemolytic activity, all five were found to carry out haemolysis at 37 °C, while two isolates among them were able to produce haemolysin at 28 °C (Table 3). In a study conducted in Italy, of 131 *Yersinia* sp., 74 were positive for haemolysin production and also, they could lyse both RBCs of chicken and rabbit with 0.5 % lecithin at 28 °C (Franzin et al., 1984). Phillips et al., (2000) reported that *Y. enterocolitica* could produce haemolysin at both the temperature 28 °C and 37 °C. In contrast, Singh and Virdi (2004) reported that clinical isolates of *Y. enterocolitica* shows haemolytic activity at 37 °C at pH 7.5, incubated for 144 h. However, in our study, haemolytic activity was observed within 24 h. This study clearly reveals the genetic diversity among the isolates.

**Table 3** Haemolytic activity of *Y. enterocolitica* isolated from different sources

No. of strains	Haemolysin assay % positive
61 (at 28 °C)	3.27 % (n=2)
61 (at 37 °C)	8.19 % (n=5)

The increased resistance to various antibiotics poses a serious challenge to physicians in order treat microbial infections. Now-a-days, most of the organisms exhibit multi-drug resistance which may have been triggered due to the mechanism of horizontal gene transfer (HGT) which happens in natural environment. Antimicrobial resistance among food-borne pathogens and therapeutical intervention has always been an important issue in public health. It can be another reason for antibiotic resistance transfer to humans via the food chain (Ezekiel et al., 2011). In the present study, the 21 different antibiotics tested, it was observed that all the *Y. enterocolitica* were sensitive to chloramphenicol, while all the organisms showed resistance towards amoxicillin. It was also observed that 98 %, 80 %, 55 %, 80 %, 79 % and 82 % of the strains were found resistant to ampicillin, erythromycin, gentamycin, kanamycin, piperacillin and tetracycline respectively (Table 4), which was very close to the findings of Yazdi et al. (2011).

Stock and Wiedemann, 1999; Okwari et al., 2007 reported 99% *Y. enterocolitica* were resistant to amoxicillin from humans, animal and environment which was similar to our finding. *Y. enterocolitica* of milk origin were found reported to towards ampicillin and sensitive to chloramphenicol (Subha et al., 2009). In contrast, chloromphenicol resistant strains have been also been reported (Yazdi et al., 2011), while for other antibiotics, controversy results have been recorded. This clearly indicates the impacts geographical locations and environment. This bacterium is well known for the horizontal gene transfer, through that, it may acquire these resistance genes and exhibited such kinds of character.

**Table 4** Antibiotic susceptibility of *Y. enterocolitica* isolated from different samples

Antibiotics	Disc potency (µg)	Resistance	% Resistance
Amoxicillin	25	61	100
Ampicillin	10	60	98
Amikacin	30	24	39.3
Chloramphenicol	10	0	0
Ciprofloxacin	5	60	98
Erythromycin	15	49	80.3
Gentamicin	10	34	55.7
Imipenam	10	23	37.7
Kanamycin	30	49	80.3
Methicillin	10	4	6.55
Nalidixic acid	30	3	4.91
Novobiocin	30	15	24.5
Oxytetracyclin	30	2	3.27
Penicillin G	10units	57	93.4
Polymyxin-B	50units	5	8.16
Piperacillin	75	48	78.6
Rifampicin	5	13	21.3
Streptomycin	10	57	93.4
Tetracycline	30	50	81.9
Tobramycin	10	3	4.91
Trimethoprim-sulfamethoxazole	10	8	13.11

The full expression of virulence due to 70 Kb pYV plasmid, which correlates with the massive release of a set of proteins (Yops) (Gemski et al., 1980). It became clear that pYV and Yops are essential for the pathogenicity of yersinia species including *Y. enterocolitica* (Bliska et al., 1991). In our study, five strains (S34, S46, S54, S55 and S58) are 1B biotype, which shows high pathogenicity among others. In general, the banding pattern of total and membrane proteins not very useful in distinguishing between strains because of the numerous bands

displayed (Kwaga and Iversen, 1992). High molecular weight protein (HMWP) with a molecular weight of 150 – 220 kDa determines pathogenic isolates. From 61 strains tested, we observed that three isolates (S34, S46 and S54) have produced similar kind of protein, which confirms the presence of high pathogenic strains among other isolates and eleven different banding patterns (Fig. 1). In another study the presence of both HMWP1 and HMWP2 are present in pathogenic strains of *Y. enterocolitica* (Schubert et al., 1998).

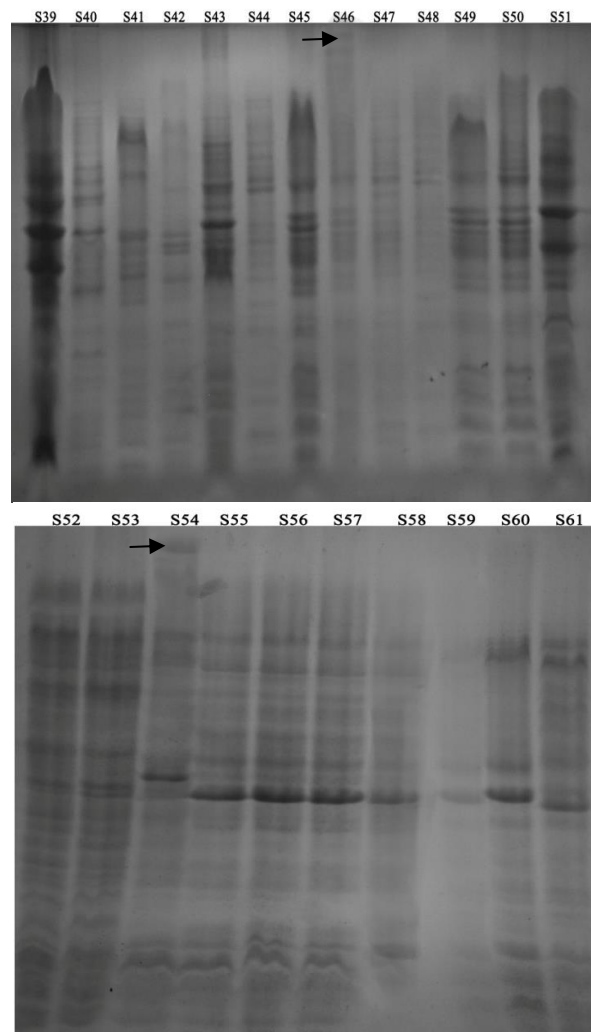
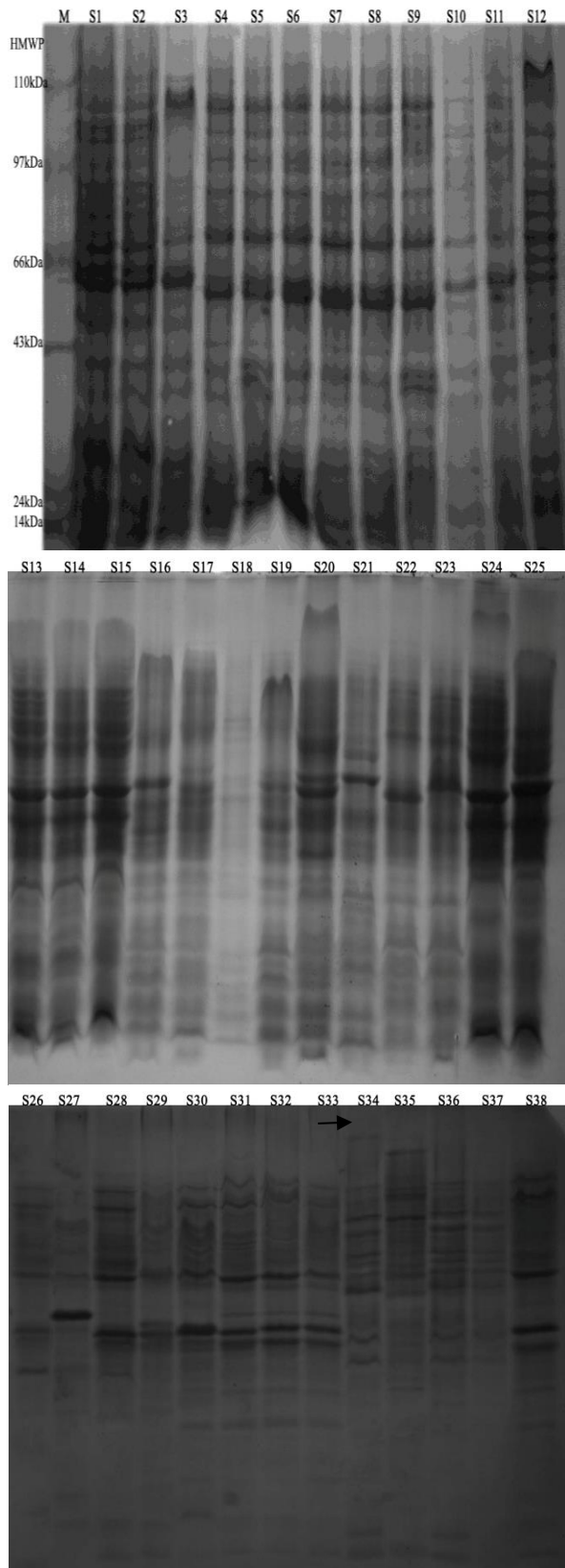
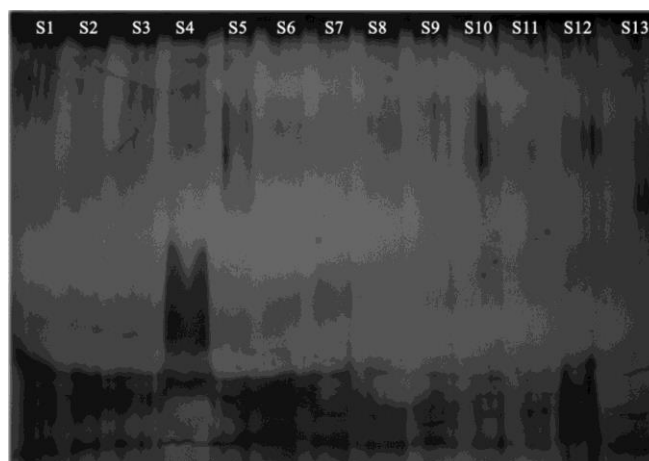


Figure 1 Outer membrane protein of isolated *Y. enterocolitica*

LPS is the major immunogenic component of the Gram-negative enterobacterium *Y. enterocolitica*. LPS has branched repeating pentasaccharide units, therefore, we observed the distinct repeating bands. *Y. enterocolitica* cultures incubated at 25 and 37 °C differ in several characteristics. Pathogenic strains can be identified under the temperature of 37 °C, so we undergone the protein isolation in the same temperature. *Y. enterocolitica* bio-serotype 1B/O: 8 show pathogenicity when incubated at 37 °C in the absence of Ca<sup>2+</sup> (Michiels et al., 1990). Several investigators worked on the characterization of LPSs produced by *Y. enterocolitica* (Pai and Mors, 1978, Boyce et al., 1979, Francis et al., 1980, Zhang et al., 1997). In our study, 53 strains have produced rough LPS, while the smooth LPS has been observed for 8 isolates only (Fig. 2). The isolates could be rough mutants that arose from an originally smooth isolate during *in vivo* passage (Kawaoka et al., 1986).



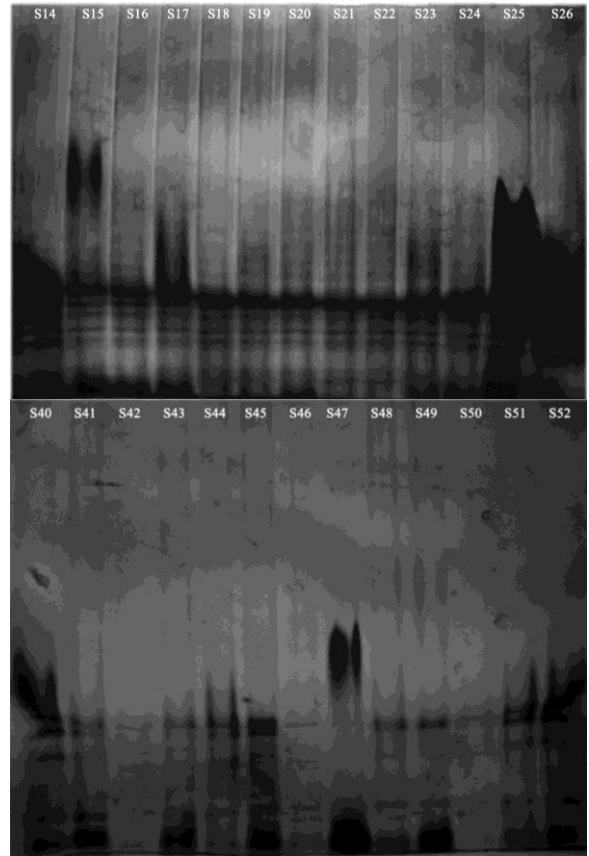
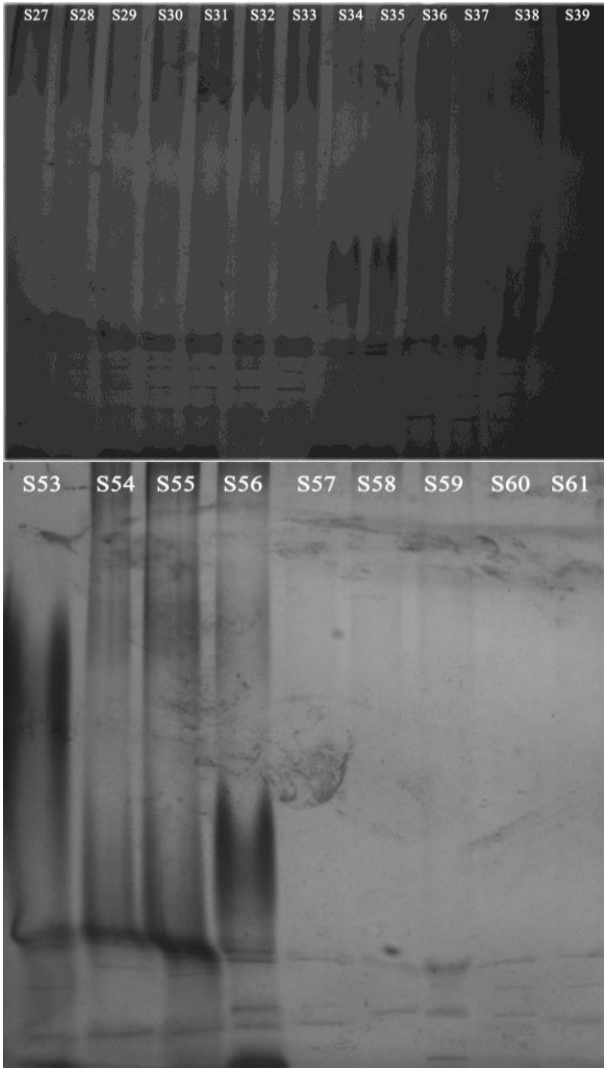


Figure 2 Lipopolysaccharides of 61 isolated *Y. enterocolitica*

In this study, we also generated a dendrogram combining the primer 1 and primer 2 RAPD dendrograms (Fig 4). The diversity of 61 strains in RAPD-PCR was analyzed using two primers (primer 1 and primer 2) (Fig. 3a and 3b), which combined dendrogram shows eight different banding pattern with 0.610 average coefficient (Fig. 4). Similarly in a study conducted with 48 *Y. enterocolitica* isolates of clinical origin, they were able to group them into 13 different groups (Odinot *et al.*, 1995). In another study, it was analyzed with the same primer, the genetic diversity of 20 *Y. enterocolitica* isolated from human and swine sources and found five different genotypic profiles among them (Leal *et al.*, 1999). All the OMP, LPS and RAPD-PCR profiles further confirm the wide genetic diversity among the strains tested.

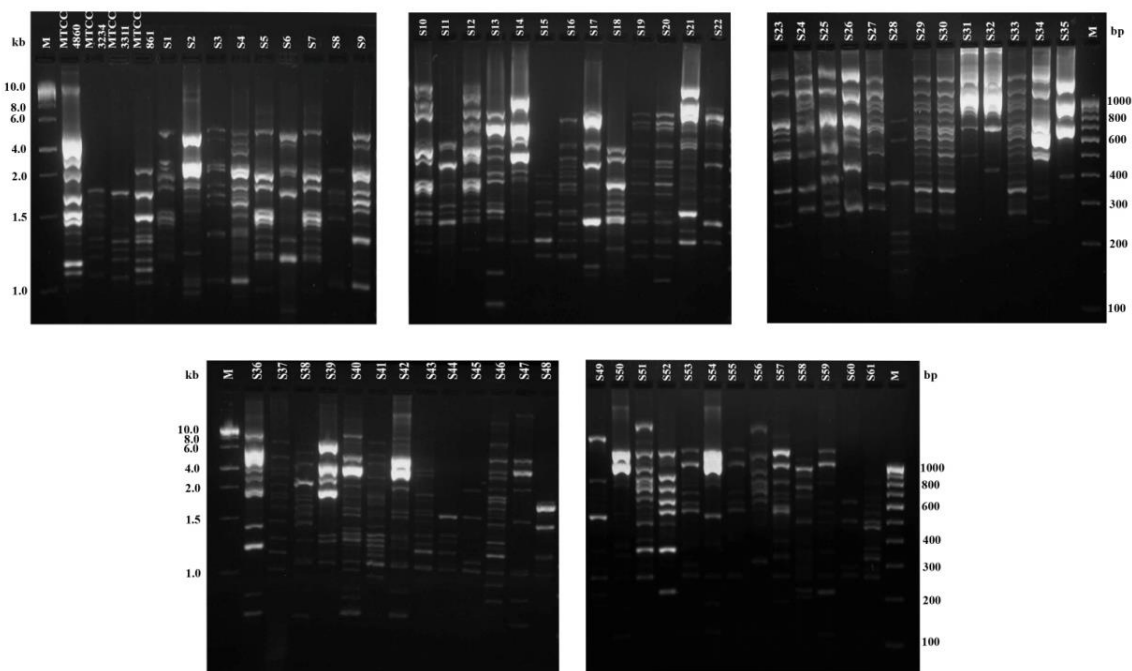


Figure 3a Amplification efficiency of Primer 1 for RAPD-PCR for *Y. enterocolitica* isolates

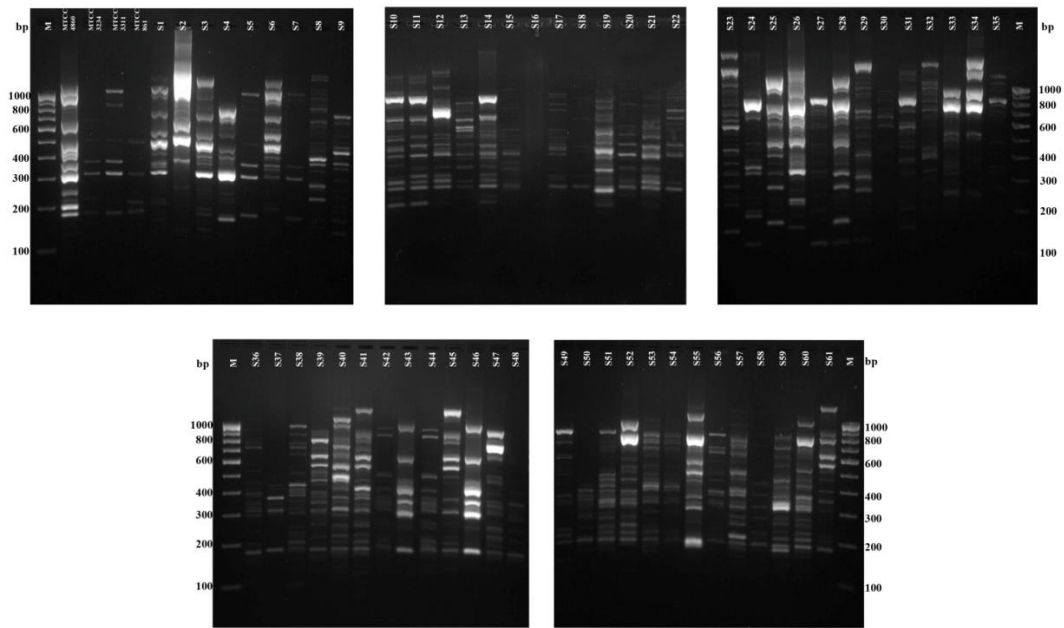


Figure 3b Amplification efficiency of Primer 2 for RAPD-PCR for *Y. enterocolitica* isolates

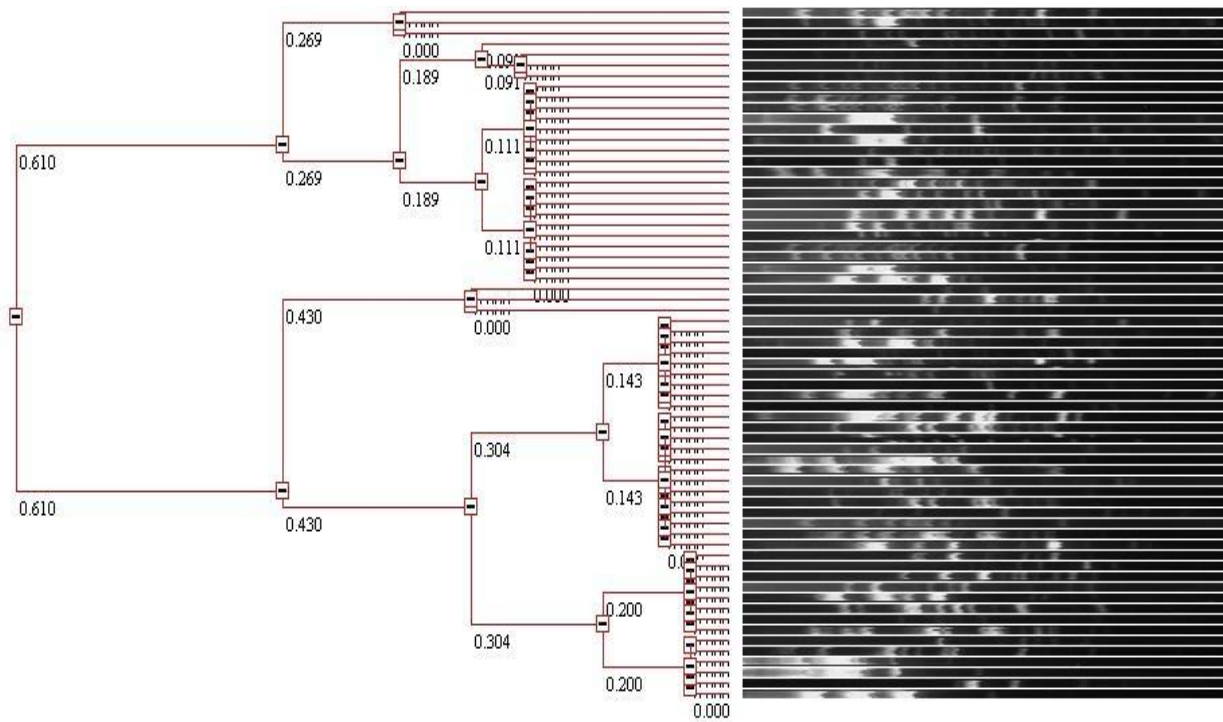


Figure 4 Combined dendrogram for RAPD-PCR (amplified by two different primers) for *Y. enterocolitica* causing simple-match similarity matrix clustered by the unweighted pair-group with arithmetic mean

**CONCLUSION**

Based on the previous and current reports, it is very clear that none of the *Y. enterocolitica* isolate is having identical pattern for antibiotic resistance. It varies from source, time and locations, which is based on the resistant genes present in them. This strongly supports the significant impact of geographical location, local selective pressure and other factors in the determination of antibiotic resistance among the *Y. enterocolitica* isolates. This report is an alarm to the public health authorities. Depends on the type of MAR index valve, we may go for the further treatment. Interestingly, all the three tools have proved their ability in differentiating the isolates of *Y. enterocolitica* in this study. In conclusion, we strongly recommend using these typing techniques in the epidemiological investigations with special reference to *Y. enterocolitica* also.

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