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Original Article

Comparison of ERIC-PCR and RAPD-PCR Discrimination Power for Molecular Typing of *Salmonella* Typhimurium Isolates

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Abstract

Introduction: Determination of the molecular relationship among *Salmonella* isolates is important for epidemiological surveillance and control of infections caused by this bacterium. This study aimed to evaluate the discriminatory power of random amplification of enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR) and random amplified polymorphic deoxyribonucleic acid-PCR (RAPD-PCR) methods for molecular typing of *Salmonella* Typhimurium.

Methods: Twenty-two *S.* Typhimurium strains isolated from bovine fecal samples were assessed using ERIC-1 and ERIC -2 primers in ERIC-PCR and 23L, P1254, and OPL12 primers in RAPD-PCR methods.

Results: Overall, 9 electrophoretic patterns were observed in the ERIC-PCR of 22 *S.* Typhimurium, whereas 4, 8, and 13 patterns were obtained for 23L, P1254, and OPL12 primers in RAPD-PCR, respectively. For ERIC-PCR, the dendrogram drawn based on these patterns clustered the isolates in 3 main clusters A, B, and C at 80% similarity with the discrimination index (DI) of 0.982, while the representative values for 3 RAPD-PCR primers were 0.925, 0.936, and 0.955, respectively.

Conclusion: Our findings indicated that ERIC-PCR and RAPD-PCR are reliable, rapid, and powerful techniques for the epidemiological investigations of *S.* Typhimurium genotypes. However, ERIC-PCR DI was higher than all of the separately performed RAPD-PCR assays as well as DI calculated for cumulative RAPD-PCR results. Hence, ERIC-PCR can be used for the genotyping of *S.* Typhimurium isolates instead of RAPD-PCR. Nonetheless, composite analysis revealed that by simultaneous applying of both PCR methods, the DI can reach to 0.998, which was the highest DI among the evaluated approaches.

Keywords: *Salmonella* Typhimurium, RAPD-PCR, ERIC-PCR, Discrimination power

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Introduction

Salmonella is among well-known foodborne pathogens that, in addition to its adverse effects on livestock production, can seriously endanger human health. Hence, these infections are considered major illnesses worldwide (1). In the last decades, over 2,500 different *Salmonella* serotypes have been identified, most of which belong to *Salmonella enterica* subspecies. Notably, Typhimurium and Enteritidis serotypes account for more than half of the isolates in most regions among various serotypes of this subspecies (2, 3).

Salmonella enterica serovar Typhimurium, which is known as the most common *Salmonella* serotype in the world, causes enteritis in a wide range of species (1) One of the important features of this serovar is its ability to survive in a prolonged manner in the environment and food products and to transmit to humans (4). *Salmonellae* is usually transmitted through fecal-oral route but infections may also transfer via the mucous membranes of the conjunctiva or the upper respiratory tract (5).

Consequently, typing of *Salmonella* isolates can be valuable to determine the probable source(s) of infections in human populations and/or animal herds. This, in turn, will be useful to prevent and control *S. enterica* infections. Several molecular methods, including restriction fragment length polymorphism, pulsed-field gel electrophoresis, random amplified polymorphic deoxyribonucleic acid (RAPD), and enterobacterial repetitive intergenic consensus (ERIC), have been introduced in this case to type *Salmonella* strains (6-8).

Polymerase chain reaction (PCR)-based methods are easy, fast, and economically affordable for the epidemiological investigations of genus *Salmonella*, and random whole genome analysis by RAPD-PCR and ERIC-PCR has been reported with extremely good discriminatory indices (9, 10). Accordingly, the present study aims to compare the discrimination powers of ERIC-PCR and RAPD-PCR methods and investigate the clonal relatedness of *S.* Typhimurium isolates.

Materials and Methods

Bacterial Strains

Totally, 22 *S.* Typhimurium strains previously isolated from calves' fecal samples (from 3 industrial dairy farms in Hamedan province, west of Iran) were included in this study. The identity of these strains had been confirmed using common biochemical tests and a serotype specific PCR assay (11).

Extraction of Deoxyribonucleic Acid Samples

Bacterial DNA was extracted from an overnight culture of each isolate in tryptic soy broth. Briefly, 5 mL of the cultured medium was centrifuged at 8,000 rpm for 3 minutes, and the pellet was resuspended in tuberculosis buffer (10 mM Tris and 1 mM ethylenediaminetetraacetic acid). Then, the bacterial DNA was extracted by the boiling method (12), and DNA samples were stored at -20˚C until use.

Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction

DNA samples were replicated with the previously described ERIC primers: ERIC-1 and ERIC-2 (Table 1) to perform ERIC-PCR (13). The ERIC-PCR (20 µL) contained 10 µL of a commercial PCR Master Mix, 3 µL of template DNA, 0.5 µL of each of the primers, and 6 µL distilled water. The amplification was performed in a thermal cycler (Astec, Japan) using the following protocol: Pre-denaturation at 95˚C for 5 minutes, denaturation at 95˚C for 30 seconds, annealing at 49˚C for 1 minute and extension at 72˚C for 5 minutes. Steps 2–4 were repeated for 34 cycles, followed by a final extension at 72˚C for 10 minutes. Eventually, 10 µL of the PCR products were electrophoresed on a 1% agarose gel and photographed under UV light in a gel documentation system.

Random Amplified Polymorphic Deoxyribonucleic Acid-Polymerase Chain Reaction

In brief, 3 single primers, including 23L, P1254 and OPL12, with the sequences given in Table 1, were used to conduct RAPD-PCR (14, 15). Each RAPD-PCR (20 µL) contained the same materials as the previous ERIC-PCR, except that only one primer was utilized in every run of PCR. The reactions were performed under thermal conditions (pre-denaturation at 94˚C for 5 minutes, 32 cycles of denaturation at 94˚C for 1 minute, annealing at 35˚C for 1 minute, and extension at 72˚C for 80 seconds with a final extension at 72˚C for 8 minutes).

Table 1. Primer sequences Used in ERIC-PCR and RAPD-PCR

Primer	Sequence 5′-3′	PCR	Reference
ERIC-1	ATGTAAGCTCCTGGGGATTCAC	ERIC	13
ERIC-2	AAGTAAGTGACTGGGGTGAGCG	ERIC	13
23L	CCGAAGCTGC	RAPD	14
P1254	CCGCAGCCAA	RAPD	14
OPL12	GGGCGGTACT	RAPD	15

Note. ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; RAPD: Random amplified polymorphic deoxyribonucleic acid.

Reproducibility of Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction and Random Amplified Polymorphic Deoxyribonucleic Acid-Polymerase Chain Reaction Assays

The reproducibility of both PCR methods was confirmed by comparing the fingerprint patterns obtained from duplicate reactions. Meanwhile, a negative control containing no DNA sample was included in each PCR run.

Analysis of Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction and Random Amplified Polymorphic Deoxyribonucleic Acid-Polymerase Chain Reaction Data

The DNA fingerprints obtained from both ERIC-PCR and RAPD-PCR were visually analyzed, and the presence or absence of each DNA band was scored as 1 and 0, respectively. Next, the scores were merged to make electrophoretic profiles, which were then analyzed by NTSYSpc software (version 2.1, USA). Moreover, cluster analysis and construction of dendrograms were performed using the unweighted pair group method with arithmetic averages to determine the relatedness of *Salmonella* isolates collected from various dairy herds (16).

Power of Discrimination

The numerical index of the discriminatory capability of ERIC-PCR and RAPD-PCR typing methods was calculated by applying Simpson's index of diversity equation, which is expressed as follows:

$$D = \frac{1}{N(N-1)} \sum_{j=1}^{s} nj(nj-1)$$

N = Total number of isolates
S = Total number of types
Nj = Number of strains belonging to the j^{th} type (17).

Results

Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction

In general, 9 electrophoretic patterns were observed of all 22 *S.* Typhimurium isolates subjected to ERIC-PCR (Figure 1). In total, 5–10 DNA bands were generated by ERIC primers with a molecular size ranging from 100 < to > 1500 bp. The discriminatory index (DI) of this method considering 22 isolates was 0.982.

At 80% similarity, the dendrogram drawn based on

the electrophoretic patterns indicated 3 main clusters (designated as clusters A, B, and C). The results of ERIC-PCR demonstrated that 64% of the isolates were placed in cluster A (Figure 2).

Random Amplified Polymorphic Deoxyribonucleic Acid-Polymerase Chain Reaction

RAPD-PCR was used to assess the relative genetic relationship of *S.* Typhimurium strains isolated from 3 dairy farms. Various DNA fragments were produced from all of the 22 isolates in RAPD-PCR using 3 primers. RAPD-PCRs conducted with 3 primers yielded 3–8 DNA bands per isolate, revealing DNA bands ranging from 100 < to > 1500 bp (Figure 3).

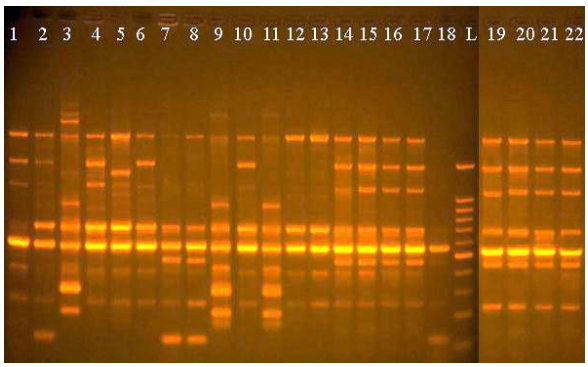

Figure 1. DNA Fragments Obtained From ERIC-PCR for *Salmonella* Isolates
Note. DNA: Deoxyribonucleic acid; ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; *S.* Typhimurium: *Salmonella* Typhimurium. Lanes 1–22: *S.* Typhimurium isolates. Lane L: a 100 bp DNA ladder

Most RAPD profiles (13 electrophoretic patterns) were characterized using the OPL12 primer. However, 8 and 4 RAPD patterns were observed for P1254 and 23L primers, respectively. Dendrograms drawn for each of these RAPD-PCR primers revealed that at 80% similarity, only primer OPL12 had relatively sufficient discriminatory power to genetically differentiate the *S.* Typhimurium isolates among 3 RAPD-PCR primers. Three main clusters were found for this primer, while the other two primers (P1254 and 23L primers) displayed only 1 cluster at 80% similarity in their dendrograms (separate dendrograms for each RAPD-PCR primer are not shown). Consequently, another dendrogram was drawn based on the combined results of all 3 RAPD-PCR primers which, in turn, indicated two main clusters designated as clusters A and B (Figure 4). The calculated DI for 23L, P1254 and OPL12 primers were 0.925, 0.936, and 0.955, respectively. Conversely, the combination of electrophoretic patterns

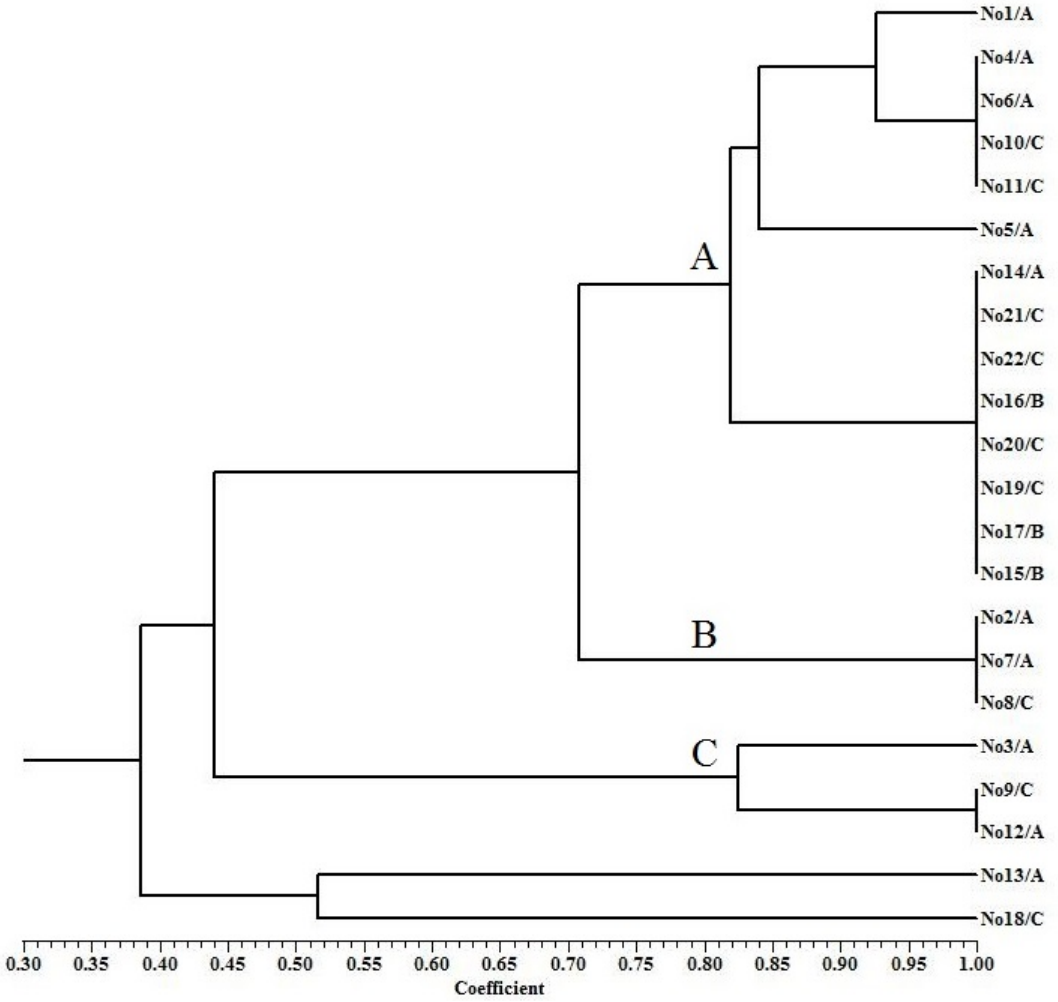

Figure 2. Dendrogram of Genetic Relationship Among 22 *S.* Typhimurium Strains Based on the Results of ERIC-PCR
Note. ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; *S.* Typhimurium: *Salmonella* Typhimurium. Isolates numbers: 1–22; dairy farms: A, B, and C

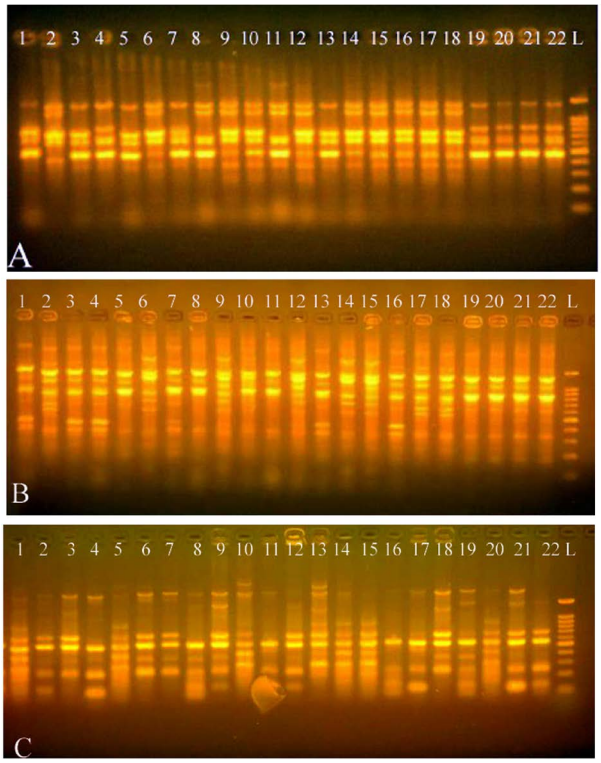

Figure 3. Electrophoretic Patterns of RAPD-PCR Obtained for *Salmonella* Typhimurium Isolates
Note. ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; *S.* Typhimurium: *Salmonella* Typhimurium. A: Primer 23L, B: Primer P1254, C: Primer OPL12. Lanes 1–22: *S.* Typhimurium isolates. Lane L: a 100 bp DNA ladder

obtained by these primers could increase DI to 0.972.

Composite Analysis of Enterobacterial Repetitive Intergenic Consensus-Polymerase Chain Reaction and Random Amplified Polymorphic Deoxyribonucleic Acid-Polymerase Chain Reaction Results

The RAPD-PCR method produced 3–7 DNA bands, whereas ERIC-PCR could produce 3–10 DNA bands. When composite analysis was performed by considering the DNA fragments obtained from ERIC-PCR and RAPD-PCR methods using NTSYSpc software, 21 patterns were totally obtained for 22 strains. Figure 5 depicts the dendrogram drawn based on the results of both ERIC-PCR and RAPD-PCR assays. By composite analysis, the DI increased to 0.998. At a dissimilarity coefficient of 80%, 4 major clusters (A, B, C, and D) were observed, each of which was further divided into more subclusters.

Discussion

In the present study, ERIC-PCR and RAPD-PCR were evaluated as molecular techniques to determine *Salmonella* genotypes isolated from bovine fecal samples since both assays are efficient, simple, and relatively inexpensive methods and have been employed in many epidemiological studies for this purpose (14). Complex DNA fingerprint patterns were recognized by applying these PCR assays, resulting in good discrimination of *Salmonella* isolates. Based on the generated ERIC-PCR

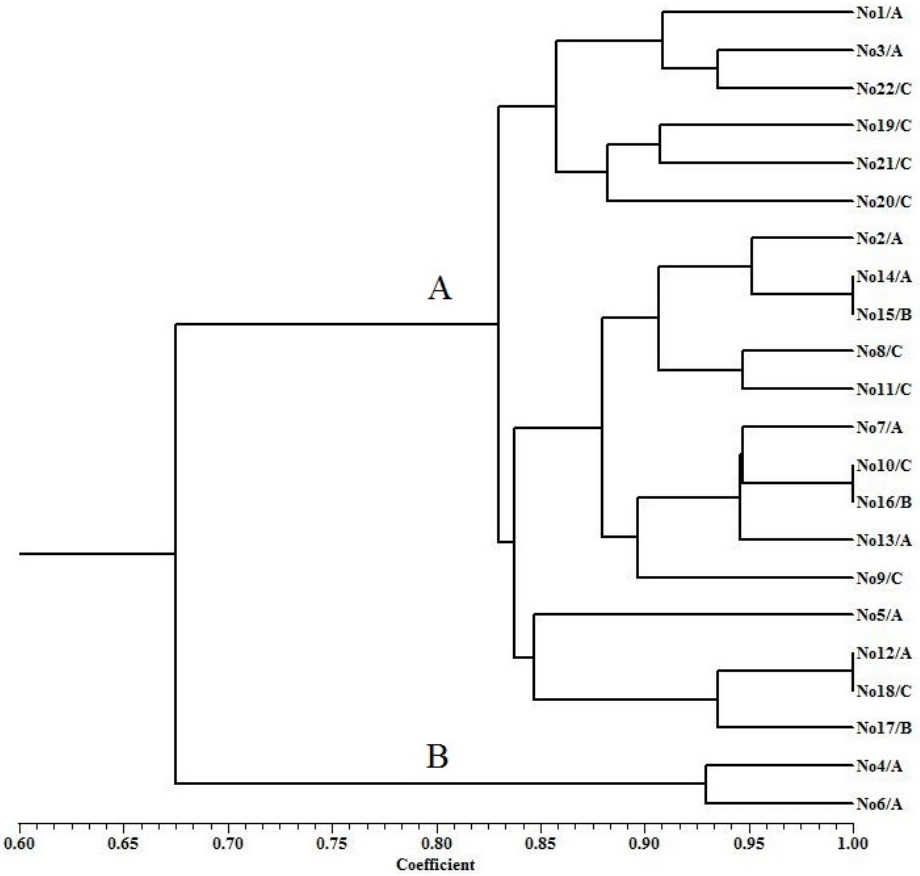

Figure 4. Dendrogram of Genetic Relationship Among 22 *S.* Typhimurium Strains Based on the Results of RAPD-PCR
Note. ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; *S.* Typhimurium: *Salmonella* Typhimurium. Isolates numbers: 1–22; dairy farms: A-C

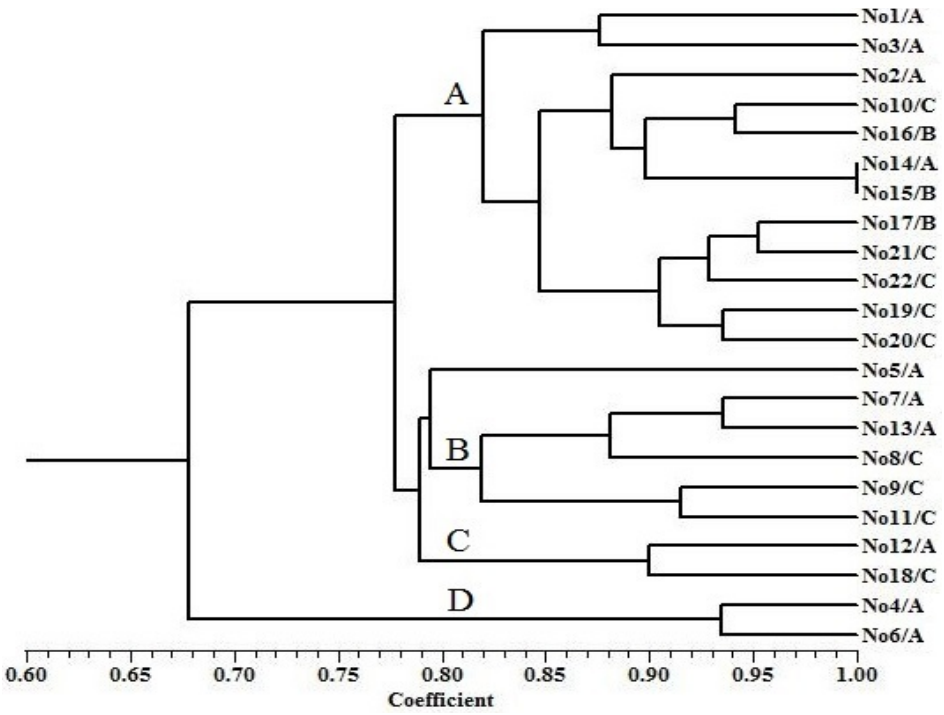

Figure 5. Dendrogram for 22 *S.* Typhimurium Isolates Based on the ERIC-PCR and RAPD-PCR
Note. ERIC-PCR: Enterobacterial repetitive intergenic consensus-polymerase chain reaction; *S.* Typhimurium: *Salmonella* Typhimurium. Isolates numbers: 1–22; dairy farms: A-C

and RAPD-PCR dendrograms, at 80% similarity, the isolates were grouped into 3 and 2 clusters, respectively, implying that the genetic differences of *S.* Typhimurium isolates were enough to be clustered separately. However, most isolates belonged to cluster A for both PCR assays. Meanwhile, the genotypes were distributed among various dairy farms. Nevertheless, there were also some isolates from different dairy farms that shared the same genetic profiles, which may indicate the circulation of those isolates among the dairy farms.

Totally, the RAPD-PCR results obtained from 3 primers revealed that the OPL12 primer had the highest DI (0.955), suggesting the application of this primer in the case of *S.* Typhimurium typing using the RAPD-PCR method. Nevertheless, none of the RAPD-PCR assays had advantage over ERIC-PCR since the DI calculated for ERIC-PCR (0.982) was higher than the DIs obtained for RAPD-PCRs. The ERIC-PCR DI was even higher than DI calculated for the cumulative results of all 3 RAPD-PCR primers (0.982 > 0.972), indicating that considering the studied primers, ERIC-PCR is a more appropriate technique for the genotyping of *S.* Typhimurium isolates compared to RAPD-PCR. Furthermore, if the researchers look for more discrimination power, it is recommended that they apply both methods and combine the results, because the highest discriminatory power (0.998) was achieved by the composite analysis of ERIC-PCR and RAPD-PCR results.

In fact, each of these two methods has its own advantages and drawbacks. While RAPD-PCR has high discriminatory power and usually covers whole-genome length, it is also considered a cheap and fast technique that benefits from a simple setup and does not require prior knowledge about template sequence. Therefore, many comparative studies have reported higher polymorphism indices for RAPD than for ERIC (18, 19). However, RAPD-PCR results are sensitive to PCR conditions, polymerase, and DNA concentration, causing poor reproducibility across runs and inter-lab variability. Multiple studies flag this as the main drawback for this method (20). On the other hand, ERIC-PCR targets conserved repetitive elements that may lead to better standardization potential. In addition, ERIC primers amplify specific repetitive intergenic consensus sequences, producing electrophoretic patterns that are often easier to reproduce than RAPD under certain conditions (21). Additionally, ERIC-PCR is an appropriate method to group related isolates since it frequently shows clearer grouping for closely related isolates (22). However, this method occasionally indicates lower discriminatory power. In some cases, ERIC produces fewer DNA fragments than RAPD, and, therefore, it may fail to discriminate closely related strains that RAPD can separate (23).

Several studies have evaluated such molecular methods in the genotyping of bacterial isolates. Chmielewski et al examined 31 *S. enteritidis* isolates from poultry samples in Poland by ERIC-PCR and reported a DI of 0.985 (24). In another study, 70 *Salmonella* strains isolated from poultry samples were analyzed by RAPD-PCR to determine their genetic relationship. The similarity coefficient among the isolates varied from 0.60 to 0.86, and all *Salmonella* isolates were classified into 7 groups based on dendrogram analysis (16). Likewise, Madadgar et al showed the application of primers 23L and P1254 in the RAPD-PCR of 30 *S.* Typhimurium isolates. They further found that the discriminatory power of RAPD-PCR for

S. Typhimurium was low but the combination of this method with other methods could be useful for the typing of *S.* Typhimurium isolates (3). In a study performed by Albufera et al, in Mauritius, the ERIC-PCR and RAPD-PCR typing of *Salmonella* isolates from human and food sources yielded acceptable discriminatory power. Moreover, these researchers discriminated the *Salmonella* isolates of the same serogroups by generating different profiles (25). Similarly, Nath et al analyzed 113 *S. enterica* serotype Typhi isolated from typhoid patients' samples by ERIC-PCR and RAPD-PCR methods. They concluded that ERIC-PCR is a highly efficient method with a DI of 0.982 (10). Despite its satisfactory discrimination, RAPD-PCR showed a DI of 0.897, which is in agreement with our results. Nevertheless, in other studies performed by Pourshafie et al and Millemann et al, poor discriminatory indices were reported for the ERIC-PCR-based analysis of 56 *S.* Typhimurium and 14 *S. enteritidis* strains isolated from poultry samples (26, 27).

Conclusion

In this study, two molecular epidemiological methods were used to type *S.* Typhimurium isolated from bovine fecal samples based on their whole genome. The results confirmed that the ERIC-PCR had higher discriminatory power in comparison to cumulative RAPD-PCR results. Consequently, it is recommended that epidemiological studies use ERIC-PCR for the genotyping of *S.* Typhimurium isolates instead of RAPD-PCR. However, composite analysis revealed that by the simultaneous applying of both PCR methods, the DI could reach 0.998, which was the highest achieved DI.

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Authors' Contribution

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Resources: Maryam Najafi Asl, Aliasghar Bahari, Ali Goudarztalejerdi
Software: Reza Hakimi Alni
Supervision: Pezhman Mahmoodi, Aliasghar Bahari, Ali Goudarztalejerdi
Validation: Pezhman Mahmoodi, Aliasghar Bahari, Ali Goudarztalejerdi
Visualization: Maryam Najafi Asl, Reza Hakimi Alni
Writing-original draft: Maryam Najafi Asl, Pezhman Mahmoodi
Writing-review & editing: Pezhman Mahmoodi, Aliasghar Bahari, Ali Goudarztalejerdi

Competing Interests

The authors declare that there are no competing financial interests.

Ethical Approval

Not Applicable.

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References

1. Hughes LA, Shopland S, Wigley P, Bradon H, Leatherbarrow AH, Williams NJ, et al. Characterisation of *Salmonella enterica* serotype Typhimurium isolates from wild birds in northern England from 2005 - 2006. BMC Vet Res 2008;4:4. doi:10.1186/1746-6148-4-4
2. Popoff MY, Bockemühl J, Gheesling LL. Supplement 2002 (no. 46) to the Kauffmann-White scheme. Res Microbiol 2004;155(7):568-70. doi:10.1016/j.resmic.2004.04.005
3. Madadgar O, Tadjbakhsh H, Zahraei Salehi T, Mahzounieh M, Feizabadi MM. Evaluation of random amplified polymorphic DNA analysis and antibiotic susceptibility application in discrimination of *Salmonella* Typhimurium isolates in Iran. New Microbiol 2008;31(2):211-6.
4. Ranjbar R, Sarshar M, Morovvati S. A Study of ribotype patterns of *Salmonella enterica* serovar enteritidis strains isolated in Tehran, Iran. J Isfahan Med Sch 2012;30(180):238-47.
5. Zhang J, Wei L, Kelly P, Freeman M, Jaegerson K, Gong J, et al. Detection of *Salmonella* spp. using a generic and differential FRET-PCR. PLoS One 2013;8(10):e76053. doi:10.1371/journal.pone.0076053
6. Foley SL, Zhao S, Walker RD. Comparison of molecular typing methods for the differentiation of *Salmonella* foodborne pathogens. Foodborne Pathog Dis 2007;4(3):253-76. doi:10.1089/fpd.2007.0085
7. Zahraei Salehi T, Madadga O, Ghafari MM, Ashrafi Tamai I, Madani SA. Molecular epidemiology of systemic Salmonella enterica serovar Typhimurium outbreak in canaries. Iran J Microbiol 2009;1(3):7-11.
8. Kjeldsen MK, Torpdahl M, Pedersen K, Nielsen EM. Development and comparison of a generic multiple-locus variable-number tandem repeat analysis with pulsed-field gel electrophoresis for typing of *Salmonella enterica* subsp. *enterica*. J Appl Microbiol 2015;119(6):1707-17. doi:10.1111/jam.12965
9. Kim S, Frye JG, Hu J, Fedorka-Cray PJ, Gautom R, Boyle DS. Multiplex PCR-based method for identification of common clinical serotypes of *Salmonella enterica* subsp. *enterica*. J Clin Microbiol 2006;44(10):3608-15. doi:10.1128/jcm.00701-06
10. Nath G, Maurya P, Gulati AK. ERIC PCR and RAPD based fingerprinting of *Salmonella typhi* strains isolated over a period of two decades. Infect Genet Evol 2010;10(4):530-6. doi:10.1016/j.meegid.2010.02.004
11. Najafi Asl M, Mahmoodi P, Bahari A, Goudarztalejerdi A. Isolation, molecular identification, and antibiotic resistance profile of *Salmonella* Typhimurium isolated from calves fecal samples of dairy farms in Hamedan. J Med Microbiol Infect Dis 2022;10(1):42-7. doi:10.52547/JoMMID.10.1.42
12. Holmes DS, Quigley M. A rapid boiling method for the preparation of bacterial plasmids. Anal Biochem 1981;114(1):193-7. doi:10.1016/0003-2697(81)90473-5
13. Versalovic J, Koeuth T, Lupski JR. Distribution of repetitive DNA sequences in eubacteria and application to fingerprinting of bacterial genomes. Nucleic Acids Res 1991;19(24):6823-31. doi:10.1093/nar/19.24.6823
14. Lin AW, Usera MA, Barrett TJ, Goldsby RA. Application of random amplified polymorphic DNA analysis to differentiate strains of *Salmonella enteritidis*. J Clin Microbiol 1996;34(4):870-6. doi:10.1128/jcm.34.4.870-876.1996
15. Yin Y, Liu X, Shi Z, Ma Z. A multiplex allele-specific PCR method for the detection of carbendazim-resistant *Sclerotinia sclerotiorum*. Pestic Biochem Physiol 2010;97(1):36-42. doi:10.1016/j.pestbp.2009.12.002
16. Thakur YR, Bajaj BK. Antibiotic resistance and molecular characterization of poultry isolates of *Salmonella* by RAPD-PCR. World J Microbiol Biotechnol 2006;22(11):1177-83. doi:10.1007/s11274-006-9159-8
17. Hunter PR, Gaston MA. Numerical index of the discriminatory ability of typing systems: an application of Simpson's index of diversity. J Clin Microbiol 1988;26(11):2465-6. doi:10.1128/jcm.26.11.2465-2466.1988

18. Abdel-Rhman SH, Rizk DE. Comparative assessment of different PCR-based typing methods of *Pseudomonas aeruginosa* isolates. Infect Drug Resist 2021;14:1019-35. doi:10.2147/idr.S298838
19. Stefańska I, Kwiecień E, Górzyńska M, Sałamaszyńska-Guz A, Rzewuska M. RAPD-PCR-based fingerprinting method as a tool for epidemiological analysis of *Trueperella pyogenes* infections. Pathogens 2022;11(5):562. doi:10.3390/pathogens11050562
20. Pakbin B, Akhondzadeh Basti A, Khanjari A, Azimi L, Brück WM, Karimi A. RAPD and ERIC-PCR coupled with HRM for species identification of non-dysenteriae *Shigella* species; as a potential alternative method. BMC Res Notes 2021;14(1):345. doi:10.1186/s13104-021-05759-6
21. Ranjbar R, Tabatabaee A, Behzadi P, Kheiri R. Enterobacterial repetitive intergenic consensus polymerase chain reaction (ERIC-PCR) genotyping of *Escherichia coli* strains isolated from different animal stool specimens. Iran J Pathol 2017;12(1):25-34.
22. Finger SA, Velapatiño B, Kosek M, Santivañez L, Dailidiene D, Quino W, et al. Effectiveness of enterobacterial repetitive intergenic consensus PCR and random amplified polymorphic DNA fingerprinting for *Helicobacter pylori* strain differentiation. Appl Environ Microbiol 2006;72(7):4713-6. doi:10.1128/aem.00894-06
23. Millemann Y, Lesage-Descauses MC, Lafont JP, Chaslus-Dancla E. Comparison of random amplified polymorphic DNA analysis and enterobacterial repetitive intergenic consensus-PCR for epidemiological studies of *Salmonella*. FEMS Immunol Med Microbiol 1996;14(2-3):129-34. doi:10.1111/j.1574-695X.1996.tb00279.x
24. Chmielewski R, Wieliczko A, Kuczkowski M, Mazurkiewicz M, Ugorski M. Comparison of ITS profiling, REP- and ERIC-PCR of *Salmonella enteritidis* isolates from Poland. J Vet Med B Infect Dis Vet Public Health 2002;49(4):163-8. doi:10.1046/j.1439-0450.2002.00544.x
25. Albufera U, Bhugaloo-Vial P, Issack MI, Jaufeerally-Fakim Y. Molecular characterization of *Salmonella* isolates by REP-PCR and RAPD analysis. Infect Genet Evol 2009;9(3):322-7. doi:10.1016/j.meegid.2007.12.003
26. Pourshafie MR, Saifi M, Mousavi SF, Sedaghat M, Nikbakht GH, Rubino S. Clonal diversity of *Salmonella enterica* serotype typhi isolated from patients with typhoid fever in Tehran. Scand J Infect Dis 2008;40(1):18-23. doi:10.1080/00365540701481529
27. Millemann Y, Gaubert S, Remy D, Colmin C. Evaluation of IS200-PCR and comparison with other molecular markers to trace *Salmonella enterica* subsp. *enterica* serotype Typhimurium bovine isolates from farm to meat. J Clin Microbiol 2000;38(6):2204-9. doi:10.1128/jcm.38.6.2204-2209.2000