

Rapid Detection of *Escherichia coli* O157: H7 by Fluorescent Amplification-Based Specific Hybridization (FLASH) PCR

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Abstract

Background: *Escherichia coli* O157:H7 is an enteric pathogen which can be frequently found asymptotically in ruminant mammals, but can cause diseases from mild diarrhea to hemolytic uremic syndrome in humans.

Methods: We developed fluorescent amplification-based specific hybridization (FLASH-PCR) assay to detect the Stx-encoding gene Stx-1 of *E. coli* O157:H7.

Result: PCR product of 336 bp was successfully amplified in a FLASH-PCR.

Conclusion: As rapid detection and confirmation of the presence of *E. coli* O157:H7 are of importance for the medical, food, and water industries, FLASH-PCR is one of selective methods for detection of *E. coli* O157:H7.

Keywords: *E. coli* O157:H7; Stx-1 gene; Detection; FLASH-PCR.

Introduction

Escherichia coli O157: H7 is an enteric pathogen which can be frequently found asymptotically in ruminant mammals, but can cause diseases from mild diarrhea to hemolytic uremic syndrome in humans. A small percentage of healthy cattle may normally harbor the organism and are considered to be the primary reservoir of *E. coli* O157: H7 associated with human disease,

as a result of carcasses and hides becoming contaminated by feces during processing.¹⁻³ Food products from other ruminants such as sheep and deer have also been found to be contaminated after processing.⁴ Potential food sources other than ground meat include unpasteurized juices, milk, dressings and foods such as vegetables that could be contaminated by manure, contaminated water or an infected food handler.^{2,5} In addition, another major reservoir of disease-causing *E. coli* O157:H7 can be water contaminated with feces, such as surface water runoff, irrigation water, insufficiently chlorinated municipal water, and swimming water (pools, lakes, beaches).⁵

Molecular approaches for bacterial detection avoid the need for culture and can be designed

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to be specific. Many molecular-based *E. coli* assays have been developed. Several polymerase chain reaction (PCR),⁶⁻⁸ reverse transcriptase PCR (RT-PCR),^{9,10} and real-time PCR,^{11,12} tests have been developed to detect *E. coli* O157:H7. However, no test used currently detects the *eae* gene and make it possible to obtain confirmation of negative or positive test results in less than 12 h from the receipt of a sample.

One of the simplest approaches to rapid and sensitive diagnosis and identification of pathogens using DNA technologies is a modification of PCR with the detection of fluorescence during the amplification (real-time PCR) or after its termination (PCR-FLASH).¹³ The technique of fluorescent amplification-based specific hybridization (FLASH-PCR), based on determining PCR results by fluorescence intensity, was developed to improve the cost-efficiency of diagnostic laboratories by employing original economical high quality equipment and to eliminate the risk of working zone contamination.^{13,14}

The aim of the present study was to identification of *E. coli* O157:H7 via the detection of *Stx*-encoding gene *Stx-1* using FLASH-PCR.

Materials and Methods

Bacterial strains

Escherichia coli O157:H7 (ATCC 10798TM), *Escherichia coli* C str. (ATCC 8739), *Escherichia coli* (Migula) (ATCC 4351) and *Escherichia coli* (ATCC 25922TM) were originally obtained from American Type Culture Collection (ATCC), USA.

Oligonucleotide primers and Probe design

Primers specific for a conserved region situated within the *E. coli Stx-1* gene were selected (Accession no. AB083044.1). Sequence alignment was performed using Mega 4 (alignment was done using Clustal W, and phylogenetic trees were constructed by

neighbor joining),^{15,16} and BLAST software (NCBI). Primers and fluorescently labeled probes were designed by primer design software (Primer Premier 5.0; Premier Biosoft Inc., Canada), and their secondary structure was examined with Gene Runner version 3.05 (Hastings Software Inc. Hastings, NY, USA, <http://www.generunner.com>). All oligonucleotides were synthesized by BIORON Company (Germany).

The fluorescent reporter dye at the 5' termini of the probe was 6-carboxyfluorescein (FAM), and a quencher of fluorescent was BHQ1 at the 3' termini. A BLAST search of the GenBank database demonstrates a high predicted specificity, with the cross-reacting bacteria *Escherichia coli* C str. and *Escherichia coli* (Migula). To determine the analytical sensitivity of this assay, bacterial DNA for testing was prepared by using the Genomic DNA isolation Kit (GeNetBio, Korea) according to the manufacturer's instructions. The DNA concentration was determined by measuring the optical density at 260 nm with the GeneQuant spectrophotometer (Pharmacia, Piscataway, N.J.). The DNA concentration was 3 (0.3) mg/ml. Serial dilutions of the extract were tested, and the described assay was able to detect 10 fg of DNA.

DNA Extraction and FLASH-PCR

DNA extracts were prepared from cultured organisms by using the Genomic DNA isolation Kit (GeNetBio) according to the manufacturer's instructions.

PCR was performed as suggested by standard manuals.^{17,18} A 25 µl volumes containing 2.5 µl of 10× PCR buffer (750 mM Tris-HCl, pH 8.8, 200 mM ammonium sulfate, 0.1% Tween-20), 1 mM each of the four deoxynucleoside triphosphates, 3 mM MgCl₂, 1 µl of template DNA, 12.5 pM of each primer, 25 pM probe and 2.5 U of Taq DNA polymerase (BIORON, Germany).

The PCR amplifications were performed in a thermal cycler (DNA Technology, Russia) using the following cycling conditions: an initial

denaturation at 94°C for 5 min and 30 cycles, with 1 cycle consisting of 30 s at 94°C, 50 s at 58°C for detection of Stx-1, 40 s at 70°C, followed by a final step 2 min at 70 °C, 1 min at 93°C, 1 min at 40°C, and 10 min at 20°C.

FLASH analysis of PCR results was performed using a PCR-detector (DNA technology).

Electrophoresis

PCR products were separated by electrophoresis in 1% agarose gels in TAE (40 mM Tris–HCl,

20 mM acetic acid, 1 mM EDTA) containing 0.5 µg/ml ethidium bromide and visualized using an Uvitec transilluminator (Gel Imager 2, Russia). The molecular weights were estimated using a Gene Ruler marker (DIALAT Ltd., Russia).

Results

Species-specific forward (EC-F) and reverse (EC-R) primers generated a PCR product of 336 bp (Table 1).

Table 1: Primers and probe for detection of E. coli O157:H7.

Target gene	PCR Product Length	Primer & Probe Seq.	ATCC	Cross-reaction
Stx-1	336 bp	F: 5'-GCGATGTTACGGTTTGTTACT-3'	10798™	1- Escherichia coli C str. ATCC 8739
		R: 5'-ACGGACTCTTCCATCTGCC-3'		2- Escherichia coli (Migula) ATCC 4351
		Probe: 5'-FAM - ccctcgcttgccagaatggcatctgatggcaggg-BHQ1-3'		3- Escherichia coli ATCC 25922™

The results of testing the samples using the FLASH format are expressed in (Fig. 1).

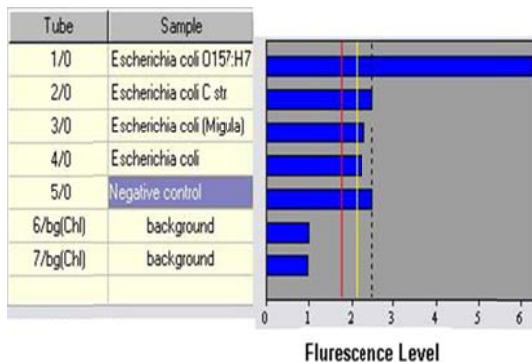


Fig.1: The results of samples by FLASH analysis.

These results showed that during the elongation process in E.coli O157:H7 tube, DNA polymerase destroys the probe due to its 5'-exonuclease activity. This leads to the separation of the fluorophor and quencher and the enhanced fluorescence level.

A gel electrophoretic analysis of the test system for E.coli (Fig. 2) showed that, with the use of primers strictly specific for this pathogen, only the E.coli O157:H7 is clearly identified (lane 2), whereas the amplification with the DNAs of Escherichia coli C str. and Escherichia coli (Migula) give no amplicons (lanes 1 & 4).

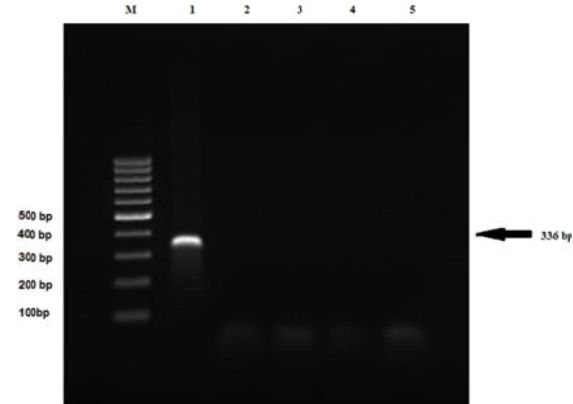


Fig.2: The results of samples by gel electrophoresis. M. Marker, lane 1. E. coli O157:H7, 2. E.coli C. str, 3. E.coli (Migula), 4. E.coli, 5. Negative Control.

Discussion

FLASH-PCR provides a useful approach for the detection of pathogens in environmental and other samples. Numerous researchers have studied and diagnosed *E. coli* O157:H7 using PCR on various samples, such as fecal samples from infected persons or contaminated food samples (raw milk or meat) suspected as causative of outbreak.^{19, 20} The use of a single pair of primers specific to target genes that are characteristics of *E. coli* O157:H7, eg, *vt eaeA*, *EHEC_{hlyA}* or *uidA*, is unable to give an unambiguous positive result as there are a variety of other gram-negative organisms possessing the same target genes of *E. coli* O157:H7.^{21,22}

The visualization of the *E. coli* O157:H7 PCR product by electrophoresis is a laborious and time-consuming process, which inevitably leads upon large-scale screenings to the

contamination by amplification products. In order to simplify and accelerate the procedure and avoid the problems associated with possible contamination, we modified the analysis of the results of PCR amplification and transferred it into the FLASH format.

The fluorescence signal for FLASH-PCR of *E. coli* O157:H7 is 6.40 and the maximum fluorescence signal for FLASH-PCR of other related species is 2.50 (Fig 1). These results indicate that these primers and probe is specific for *E. coli* O157:H7. This modified FLASH-PCR protocol has a potential to be used for rapid, sensitive and specific method in the specific detection of *E. coli* O157:H7.

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Conflict of interest: None declared.

References

1. Barkocy-Gallagher GA, Arthur TM, Rivera-Betancourt M, Nou X, Shackelford SD, Wheeler TL, et al. Characterization of O157:H7 and other *Escherichia coli* isolates recovered from cattle hides, feces, and carcasses. *J Food Prot* 2004;67(5):993-8.
2. Besser RE, Griffin PM, Slutsker L. *Escherichia coli* O157: H7 gastroenteritis and the hemolytic uremic syndrome: an emerging infectious disease. *Annu Rev Med* 1999;50:355-67.
3. Sheng H, Davis MA, Knecht HJ, Hovde CJ. Rectal administration of *Escherichia coli* O157:H7: novel model for colonization of ruminants. *Appl Environ Microbiol* 2004;70(8):4588-95.
4. Keene WE, Sazie E, Kok J, Rice DH, Hancock DD, Balan VK, et al. An outbreak of *Escherichia coli* O157:H7 infections traced to jerky made from deer meat. *Jama* 1997;277(15):1229-31.
5. Islam M, Doyle MP, Phatak SC, Millner P, Jiang X. Persistence of enterohemorrhagic *Escherichia coli* O157:H7 in soil and on leaf lettuce and parsley grown in fields treated with contaminated manure composts or irrigation water. *J Food Prot* 2004; 67(7):1365-70.
6. Bayardelle P, Zafarullah M. Development of oligonucleotide primers for the specific PCR-based detection of the most frequent Enterobacteriaceae species DNA using *wec* gene templates. *Can J Microbiol* 2002;48(2):113-22.
7. Osek J. Rapid and specific identification of *Shiga toxin-producing Escherichia coli* in faeces by multiplex PCR. *Lett Appl Microbiol* 2002; 34(4):304-10.
8. Campbell GR, Prosser J, Glover A, Killham K. Detection of *Escherichia coli* O157:H7 in soil and water using multiplex PCR. *J Appl Microbiol* 2001; 91(6):1004-10.
9. Yaron S, Matthews KR. A reverse transcriptase-

- polymerase chain reaction assay for detection of viable *Escherichia coli* O157: H7: investigation of specific target genes. *J Appl Microbiol* 2002; 92 (4): 633-40.
10. McIngvale SC, Elhanafi D, Drake MA. Optimization of reverse transcriptase PCR to detect viable Shiga-toxin-producing *Escherichia coli*. *Appl Environ Microbiol* 2002; 68(2):799-806.
 11. Jothikumar N, Griffiths MW. Rapid detection of *Escherichia coli* O157:H7 with multiplex real-time PCR assays. *Appl Environ Microbiol* 2002; 68(6): 3169-71.
 12. Belanger SD, Boissinot M, Menard C, Picard FJ, Bergeron MG. Rapid detection of Shiga toxin-producing bacteria in feces by multiplex PCR with molecular beacons on the smart cycler. *J Clin Microbiol* 2002; 40(4): 1436-40.
 13. Abramova SL, Riazantsev D, Voinova TM, Zavriev SK. [Diagnostics of phyto-pathogen fungi *Septoria tritici* and *Stagonospora nodorum* by fluorescent amplification-based specific hybridization (FLASH) PCR]. *Bioorg Khim* 2008;34(1):107-13.
 14. Laptinov IA. PCR diagnosis without electrophoresis.: Moscow: Chelovek, 2005.
 15. Thompson JD, Higgins DG, Gibson TJ. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* 1994; 22(22): 4673-80.
 16. Tamura K, Dudley J, Nei M, Kumar S. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol Biol Evol* 2007; 24(8): 1596-9.
 17. Rumsby G. An introduction to PCR techniques. *Methods Mol Biol* 2006; 324:75-89.
 18. Sambrook J, Russell DW. The condensed protocols from *Molecular cloning* : a laboratory manual. Cold Spring Harbor, N.Y.: Laboratory Press, 2006.
 19. Arthur TM, Bosilevac JM, Nou X, Koohmaraie M. Evaluation of culture- and PCR-based detection methods for *Escherichia coli* O157:H7 in inoculated ground beef. *J Food Prot* 2005;68(8):1566-74.
 20. Holland JL, Louie L, Simor AE, Louie M. PCR detection of *Escherichia coli* O157:H7 directly from stools: evaluation of commercial extraction methods for purifying fecal DNA. *J Clin Microbiol* 2000; 38(11): 4108-13.
 21. Paton AW, Paton JC. Detection and characterization of Shiga toxigenic *Escherichia coli* by using multiplex PCR assays for *stx1*, *stx2*, *eaeA*, enterohemorrhagic *E. coli* *hlyA*, *rfbO111*, and *rfbO157*. *J Clin Microbiol* 1998; 36(2): 598-602.
 22. Fratamico PM, Sackitey SK, Wiedmann M, Deng MY. Detection of *Escherichia coli* O157:H7 by multiplex PCR. *J Clin Microbiol* 1995; 33(8): 2188-91.