Short communication

Shigatoxigenic and atypical enteropathogenic Escherichia coli in fish for human consumption

Marita Vedovelli Cardozo a, *, Clarissa Araújo Borges a, Lívia Gerbasi Beraldo a, Renato Pariz Maluta b, Andressa Souza Pollo a, Mariana Monezi Borzi a, Luis Fernando dos Santos c, Subhashinie Kariyawasam d, Fernando Antônio de Ávila a

a Universidade Estadual Paulista (UNESP), Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, SP, Brazil
b Universidade Estadual de Campinas (UNICAMP), Instituto de Biologia, Campinas, SP, Brazil
c Instituto Adolfo Lutz, Centro de Bacteriologia, São Paulo, SP, Brazil
d Pennsylvania State University, College of Agricultural, State College, PA, United States

Article history:
Received 29 September 2017
Accepted 28 February 2018
Available online 21 May 2018
Associate Editor: Beatriz Cabilio Guth

Keywords:
EPEC
Fish
MLST
STEC
Virulence genes

ABSTRACT

Shigatoxigenic and enteropathogenic Escherichia coli with virulence and multidrug resistance profile were isolated from Nile tilapia. This study finding is of great importance to public health because they help understand this pathogen epidemiology in fish and demonstrate how these animals can transmit E. coli related diseases to humans.

© 2018 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Escherichia coli (E. coli) is not a natural inhabitant of the fish microbiota, nevertheless, it can be isolated from these animals gut due to its presence in contaminated aquatic environments.1 It is worth noticing that this microorganism have pathogenic strains standing out as emerging zoonotic potential, as well as shigatoxigenic (STEC) and enteropathogenic (EPEC) E. coli. STEC strains produce the shiga toxin (Stx), which is its main virulence factor. There are two classes of shiga toxin, Stx1 and Stx2, with the last one presenting seven subtypes.7 The EPEC may be either typical or atypical, with the atypical strains do not carrying virulence factor that encodes the bundle-forming pilus (bfp), but it carries the eae gene, that is located at the locus of enterocyte effacement (LEE), which is a pathogenicity island, that promote attaching and effacing lesions (A/E). The ability to induce A/E lesions is mediated by genes located on the LEE, as well as additional ones that are outside of it.3

Several studies have analyzed STEC and EPEC, and their virulence in humans,4 cattle,5 sheep,6 pigs,7 and buffaloes.8 However, only a few studies have analyzed the presence of STEC and EPEC in fish9,10 and, of these, none has detected presence of adhesion and ESBL genes. In addition, none has performed the stx2 subtyping in STEC strains from fish. In this regard, this pioneer study aimed to compare the prevalence...
of STEC and EPEC strains in intensively farmed fish and free-living fish; as well as to detect their virulence and antibiotic resistant profile and analyze their genetic similarity looking for how these fishes contribute to humans infections.

The Ethics Committee on Animal Use (CEUA) approved this study under the protocol number 04076/14. Primers used are described in Table 1. The samples were collected from the fish species Oreochromis niloticus, from six different fish farms and three ranches located at northeast region of Sao Paulo state. A total of 472 samples were collected. Three hundred and seventy three (373) samples were obtained from fish farm animals and of these, 275 were from stools, 80 from muscles and 18 from the nursery waters. The other 99 samples were obtained from free-living fish, these been 90 from stools and nine from the river water. Samples were transferred to tubes containing BHI broth (Brain Heart Infusion) and after an incubation period, the DNA were extracted by thermal lysis according to Borges.7

Screening for the detection of STEC and EPEC strain were based on, stx1, stx2 and ee genes detection by multiplex PCR.7 When one of these genes were detected, individual colonies from each sample were tested by PCR to isolate STEC and EPEC strains according to the protocol available at www.apzec.ca/en/APZEC/Protocols/pdfs/ECL_PCR_Protocol.pdf. This methodology is in accordance to the OIE Reference Laboratory for Escherichia coli (Ecl – Faculté de Médecine Vétérinaire, Université de Montréal). Isolates were further submitted to another PCR to detect others virulence genes as follow: bfpA, ehxA, saa, iha, toxB, efa1, lpfA0113, lpfA0157/O1-141, lpfA0157/O1-154, astA and paa genes. The Stx2 variants analysis was performed by stx2 subtyping according to Schuetz.2

The antimicrobial susceptibility test was performed using the disc diffusion method.30 The antimicrobials chosen were the ones most used in fish farming and which are important for the detection of resistance genes dissemination. In this regard, drugs tested were ampicillin (10 µg), cephalothin (30 µg), streptomycin (10 µg), gentamicin (10 µg), ciprofloxacin (5 µg), chloramphenicol (30 µg), tetracycline (30 µg), nitrofurantoin (300 µg), nalidixic acid (30 µg), sulfamethoxazole and trimethoprim (25 µg), ceftriaxone (30 µg), cefoxitin (30 µg), kanamycin (30 µg), norfloxacin (10 µg), enrofloxacin (5 µg) (Oxoid). In addition, E. coli isolates were screened for extended-spectrum beta-lactamase (ESBL) genes for the blaCTX-M genotype groups 1, 2, 8, 9 and 25, the blatTEM, and the blashV.11

Phylogenetic E. coli groups’ classification was performed according to the methodology proposed by Clermont.12 Serotyping was performed at the E. coli Reference Center (ECRC) at Pennsylvania State University. The O somatic antigen were determined by agglutination plates, also the PCR-RFLP of flaIC gene, which encodes flagella, were performed to determine the H flagella antigen. Somatic antigens used were O1 to O187, with the exception of O31, O47, O67, O72, O94, O122 and the flagellar antigens used were H1 to H49, except H17, since these serogroups still not have been designated.

The isolates were also characterized by PFGE pattern of the PulseNet protocol as described by Ribot.13 Briefly, the chromosomal DNA was digested with XbaI and the electrophoresis conditions were an initial time of 2.2 s and an end time of 54.2 s in a gradient of 6V and the gels were electrophoresed for 21 h. The fragment similarities were compared using the Dice coefficient and the dendrogram was constructed by neighbor-joining grouping using BioNumerics software (Applied Maths, Sint-Martens-Latem, Belgium). MLST was performed following the Achtmans’s scheme (http://mlst.unice.fr/mlst/dbs/Ecoli), through the sequencing of the PCR amplification products of the adk, fumC, gyrB, icd, mdh, purA, and recA genes. The generated sequences were trimmed and analyzed by the Phred/Phrap/Consed software package.

All the results are shown in Fig. 1. Of the 373 analyzed samples from the fish farm, one (0.2%), from stools, tested positive for a STEC related gene (isolate 125F5). Of the 99 live-fishing fish analyzed samples, six (6%), also from stools, were positive for at least one of the STEC or EPEC related genes (isolates 6F8, 9F8, 10F8, 12F8, 24F8 and 30F8). In addition, all six isolates were collected from the same location, and the stx1, stx2 and ee genes were detected. None of the muscle or water samples tested were positive for the STEC or EPEC markers investigated. Isolates from the fish farms were positive for ehxA, lpfA0113 and saa virulence genes. Also, strains from the free-living fish presented astA, ehxA, lpfA0113, saa, efa1 and paa genes. Regarding Stx2 toxin variants, the subtypes stx2a, stx2c and stx2d were observed at the same isolate.

![Fig. 1 – A dendrogram representing the genetic similarity relationship and virulence indicators in STEC and aEPEC isolates from fish.](image)
<table>
<thead>
<tr>
<th>Primers</th>
<th>Sequences</th>
<th>Size</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>stx1-F</td>
<td>AGAGCGATGTTACCGGTGTTTG</td>
<td>388</td>
<td>32</td>
</tr>
<tr>
<td>stx1-R</td>
<td>TTGCCCAAGATGCTAGG</td>
<td>32</td>
<td></td>
</tr>
<tr>
<td>stx2-F</td>
<td>TGGGTCTTCTCTGCTGATC</td>
<td>807</td>
<td>32</td>
</tr>
<tr>
<td>stx2-R</td>
<td>GACATCTCTTGGTACACTCTCTT</td>
<td>570</td>
<td>32</td>
</tr>
<tr>
<td>eae-F</td>
<td>AGGCTTCTGACAGCTTG</td>
<td>33</td>
<td></td>
</tr>
<tr>
<td>eae-R</td>
<td>CCACTGCTACAGCAGGAGGA</td>
<td>300</td>
<td>33</td>
</tr>
<tr>
<td>hpaA-F</td>
<td>GGAAGTCATAATCTCAGGGGTAT</td>
<td>340</td>
<td>34</td>
</tr>
<tr>
<td>hpaA-R</td>
<td>GGATTACAGGGACAGCTGAGTAGT</td>
<td>119</td>
<td>17</td>
</tr>
<tr>
<td>ehxA-F</td>
<td>GGTGCAACAGAAAATATTGTA G</td>
<td>1305</td>
<td>35</td>
</tr>
<tr>
<td>ehxA-R</td>
<td>TCTCGGCATAGTTTGGGT A</td>
<td>602</td>
<td>36</td>
</tr>
<tr>
<td>saa-F</td>
<td>CGTGATGAAACAGGCTATTGC</td>
<td>37</td>
<td></td>
</tr>
<tr>
<td>saa-R</td>
<td>ATGCCACATGCTTGAGCAAC</td>
<td>525</td>
<td>34</td>
</tr>
<tr>
<td>toxB-F</td>
<td>TCTACTGACATGCGTGAGCAGC</td>
<td>479</td>
<td>37</td>
</tr>
<tr>
<td>toxB-R</td>
<td>GAGACTCGCCAGAGAAGAG</td>
<td>125</td>
<td>24</td>
</tr>
<tr>
<td>efa1-F</td>
<td>GTGACGTCGAGAAGAG</td>
<td>360</td>
<td>23</td>
</tr>
<tr>
<td>efa1-R</td>
<td>TGGTTCTGATGCTTGAGTAC</td>
<td>300</td>
<td>36</td>
</tr>
<tr>
<td>astA-F</td>
<td>TGGGATGCAATGATATTAG</td>
<td>668</td>
<td>11</td>
</tr>
<tr>
<td>astA-R</td>
<td>GATAGACATGCAATGCTGAC</td>
<td>404</td>
<td>11</td>
</tr>
<tr>
<td>paa-F</td>
<td>ATGGAGAAGGTAATGCTGAG</td>
<td>360</td>
<td>23</td>
</tr>
<tr>
<td>paa-R</td>
<td>TCTGGATGCGTTCTGATAC</td>
<td>525</td>
<td>34</td>
</tr>
<tr>
<td>CTX-M group 1 - F</td>
<td>TTAGGAARTGTGTCGGCTGGTA</td>
<td>800</td>
<td>11</td>
</tr>
<tr>
<td>CTX-M group 1 - R</td>
<td>CATTTCCTGTGCTGACATC</td>
<td>404</td>
<td>11</td>
</tr>
<tr>
<td>CTX-M group 2 - F</td>
<td>GGTAAACGCGGATGATCG</td>
<td>37</td>
<td></td>
</tr>
<tr>
<td>CTX-M group 2 - R</td>
<td>ATCCCGGAGTGTTATGATAAG</td>
<td>360</td>
<td>23</td>
</tr>
<tr>
<td>CTX-M group 2/25 F</td>
<td>TCGAGACCGGAAATGATGCTGA</td>
<td>525</td>
<td>34</td>
</tr>
<tr>
<td>CTX-M group 8/25R</td>
<td>TCAAGGCCGGAACGTTGATAT</td>
<td>561</td>
<td>11</td>
</tr>
<tr>
<td>TEM - F</td>
<td>CATTTCCTGTGCTGACATC</td>
<td>800</td>
<td>11</td>
</tr>
<tr>
<td>TEM - R</td>
<td>CATTTCCTGTGCTGACATC</td>
<td>404</td>
<td>11</td>
</tr>
<tr>
<td>SHV - F</td>
<td>GGTAAACGCGGATGATCG</td>
<td>37</td>
<td></td>
</tr>
<tr>
<td>SHV - R</td>
<td>ATCCCGGAGTGTTATGATAAG</td>
<td>360</td>
<td>23</td>
</tr>
<tr>
<td>stx2a-F</td>
<td>GCCATACTGRBACGTGAGCC</td>
<td>347</td>
<td>2</td>
</tr>
<tr>
<td>stx2a-R</td>
<td>GCCACCTCTCTGCTGATAC</td>
<td>347</td>
<td>2</td>
</tr>
<tr>
<td>stx2b-F</td>
<td>AAATATGGAAGAGAGATATTGTGAGGCG</td>
<td>251</td>
<td>2</td>
</tr>
<tr>
<td>stx2b-R</td>
<td>CAGCAAATGCGAACCCTCGAG</td>
<td>251</td>
<td>2</td>
</tr>
<tr>
<td>stx2c-F</td>
<td>GAAAGTCACTTGTTTATATCACAACGCGGTA</td>
<td>177</td>
<td>2</td>
</tr>
<tr>
<td>stx2c-R</td>
<td>CCGGCCGACTTTGATTGCATAATGTA</td>
<td>179</td>
<td>2</td>
</tr>
<tr>
<td>stx2d-F</td>
<td>AAARTCACTCTTTTATCACAACGCGGTA</td>
<td>177</td>
<td>2</td>
</tr>
<tr>
<td>stx2d-R</td>
<td>TTYCCGGAGCACTTTTATGACTGTA</td>
<td>179</td>
<td>2</td>
</tr>
<tr>
<td>stx2e-F</td>
<td>CGGAGTCAGGAAAGAG GC</td>
<td>411</td>
<td>2</td>
</tr>
<tr>
<td>stx2e-R</td>
<td>CCTCCTGACACCGTCACTGTAAGGTA</td>
<td>411</td>
<td>2</td>
</tr>
<tr>
<td>stx2f-F</td>
<td>TGGGCGTCACTTCTCGGTTG</td>
<td>424</td>
<td>2</td>
</tr>
<tr>
<td>stx2f-R</td>
<td>TAATGCGCCGCTCTGCTCOC</td>
<td>424</td>
<td>2</td>
</tr>
<tr>
<td>stx2g-F</td>
<td>CAAGGGAGTATGTTTATATCTCTGACATGCTGA</td>
<td>573</td>
<td>2</td>
</tr>
<tr>
<td>stx2g-R</td>
<td>GATGCGAACATCAGAAGAACCCTGGCT</td>
<td>573</td>
<td>2</td>
</tr>
<tr>
<td>adk-F</td>
<td>ATTTCTGCTGGCCTGCTGCTGCTG</td>
<td>583</td>
<td>a</td>
</tr>
<tr>
<td>adk-R</td>
<td>CCGCAACATCTGGCTGCTGCTGCTG</td>
<td>583</td>
<td>a</td>
</tr>
<tr>
<td>fumC-F</td>
<td>TCACAGGTCGCGCGGCTCTC</td>
<td>806</td>
<td>a</td>
</tr>
<tr>
<td>fumC-R</td>
<td>GTCGCGAGAGAGAAGATGCTGA</td>
<td>806</td>
<td>a</td>
</tr>
<tr>
<td>gyrB-F</td>
<td>GCGGCCGCAACGCAATGCGGAGC</td>
<td>911</td>
<td>a</td>
</tr>
<tr>
<td>gyrB-R</td>
<td>ATAGCGCGGCTCTAGCGCGGAGC</td>
<td>911</td>
<td>a</td>
</tr>
<tr>
<td>icd-F</td>
<td>ATGGAGAATGAAAGATAGGTGTTTCTCGGCACA</td>
<td>878</td>
<td>a</td>
</tr>
<tr>
<td>icd-R</td>
<td>GAGCCGAGGAGATGCTGTT</td>
<td>878</td>
<td>a</td>
</tr>
</tbody>
</table>
From the 15 antimicrobial drugs tested, the isolates originated from the fish farm animals were resistant to 14 of them, while the isolates from the free-living fish were resistant to three antimicrobials and no ESBL genes were found. All of the STEC strains belong to group B1 and the aEPEC strain to group A as in accord with the classification of Clermont. From seven isolates analyzed by serotyping, three were nontypeable for the O antigen, and three isolates were nontypeable for the H antigen. Thus, the groups detected were O55, O39, O116, H14, H18 and H36; and their serotype is shown in Fig. 1. Seven isolates possessed a heterogeneous profile, by PFGE analysis, and seven distinct sequence types (STs) with four clonal groups (CCs) detected by the MLST technique.

Although STEC and aEPEC strains isolated from fish are not natural inhabitants of its microbiota, these strains can colonize the fish through a contaminated environment of which they live. In both establishments that these positive strains were isolated, presence of cattle were observed around the nurseries and rivers. It is important to notice that bovine is considered the main reservoir of pathogenic E. coli.

Moreover, in this study, all muscle and water samples were negative for the presence of STEC or EPEC. This result should not be taken lightly, because the samples were collected by dissecting the animal using aseptic conditions so that muscles samples were carefully separated from the intestinal content, which it does not occur at the fishermen or slaughterhouses daily practice. Commonly, a cut is made between the anus and the fish’ head, releasing all of its intestinal contents and, in the process, contaminating the muscle. In this regard, according to Kim, pathogenic E. coli can enter the human food chain mainly through food contamination. Moreover, none of the water samples tested positive for STEC or EPEC and this was associated with the large water flow at the nurseries and rivers.

These pathogens have already detected in Brazil, and in other countries such as United States, Argentina, Netherlands, Iran, Tunisia, and Australia. These studies, as well as the present one, are fundamental to understand these pathogens epidemiology, since they have great importance in animal and public health.

In this study, one STEC strain with eae gene also contained several other genes, efa1, ehxA, lpfA, and paa, which have been associated with cases of diarrhea. The presence of saa gene was shown to be closely related to the presence of the ehxA gene in STEC strains devoid of eae gene, regardless of their serotype. In an STEC isolated, the presence of astA gene, which is important for pathogenesis of diarrhea and plays a key role in this strain’ virulence, was observed. Also, the lpfA gene was shown in previous reports to have a high prevalence in STEC isolated from different animals. Regarding Stx2 toxin variants, the stx2a, stx2c and stx2d subtypes were observed in the same isolate; this combination is very unusual and makes this strain fairly unique and with aggravated virulence. The presence of stx2a, stx2c and stx2d subtype are often associated with the hemorrhagic colitis and with hemolytic uremic syndrome.

The quinolones, tetracyclines, aminoglycosides and amphenicols are the most commonly used antimicrobials in fish farming; and thus, it may explain the multiresistance observed in the fish farm isolates. All of the tested quinolones, tetracyclines, aminoglycosides and amphenicols were ineffective. Although it was observed multiresistance, no ESBL genes were found. The ESBL would confer an even greater risk for the raw fish consuming population, because these bacteria’s can produce an enzyme that are able to hydrolyze the beta lactam ring of penicillins, cephalosporins and aztreonam, thus conferring resistance to these antimicrobials. However, this multiresistance profile shows a phenotypic response from the isolates, and due to the selective pressure originated from the abusive use of broad-spectrum cephalosporins, according to data obtained in the present study, ESBL strains can emerge rapidly, as it is already observed in other animal productions.

According to the phylogenetic results of this study, it is confirmed that tropical populations can harbor strains of group A and B1 preferentially, which may be one of the factors that could explain tropical countries higher diarrhea frequency. Although much is reported about the O157 strains, non-O157 STEC strains are the most prevalent in animals and food. For this reason, chances of humans becoming infected by these strains are large, indicating the importance of this serogroups to public health. Therefore, the O116 serogroup observed in the present study is relevant due to the fact that it is often associated with severe human disease. Furthermore, the strain with the flagellar antigen H18 which contains the stx2 but not the eae gene, has also shown frequent association with infections in animals. Moreover, the ONT: H18 serotype in eae negative and saa positive strains, similarly to the ones in this study, has previously been detected in pathogenic E. coli in cattle, thus emphasizing the fact that these animals were, likely, the source of this pathogen infection in fish.

The genetic diversity analysis showed that, although the isolates belonged to the same bacterial species, they had genetic diversities that were highlighted though the PFGE technique. The same was observed with the MSLT data, indicating that although they had a common ancestral origin, the transference of genetic information, though time, made this
isolates very diverse, thus explaining their distinct phylogene-
tic classification.
Ours results shows that fish can harbor an important com-

bination of Stx2 subtypes and putative adhesions genes. Also,

it draws attention to the fact that the indiscriminate use of
antibiotics in fish farming has the potential to endanger
consumer health through the dissemination of antibiotic
resistance genes. And finally, it highlights the role of STEC and
ePEC as foodborne pathogens in fish for human consump-

**Acknowledgments**

The authors would like to thank FAPESP for all research sup-
port granted (2011/07358-2 and 2011/15050-8).

**References**


Escherichia coli in fresh water fish, Jenynsia.multidens tata and


sequence-based protocol for subtyping shiga toxins and


enteropathogenic Escherichia coli infection and prolonged


Distribution of virulence profiles related to new toxins and

putative adhesins in shiga toxin – producing Escherichia coli

isolated from diverse sources in Brazil. FEMS Microbiol Lett.


5. Brusa V, Restovich V, Galli L, et al. Isolation and

characterization of non-0157 Shiga toxin-producing

Escherichia coli from beef carcasses, cuts and trimmings of


pathogenic Escherichia coli in healthy, pasture-raised sheep


and atypical enteropathogenic Escherichia coli in the feces

and carcasses of slaughtered pigs. Foodborne Pathog Dis.


toxigenic (STEC) and enteropathogenic (EPEC) Escherichia coli


9. Manna SK, Das R, Manna C. Microbiological quality of

finfish and shellfish with special reference to shiga toxin-producing


10. Ribeiro LF, Barbosa MMC, Rezende Pinto F, et al. Shiga

toxigenic and enteropathogenic Escherichia coli in water and


of multiplex PCR assays for the detection of genes encoding

important β-lactamases in Enterobacteriaceae. J Antimicrob


Escherichia coli phylo-typing method revisited: improvement of


of pulsed-field gel electrophoresis protocols for the subtyping of

Escherichia coli O157:H7, Salmonella, and Shigella for


toxin-producing Escherichia coli in drinking water supplies of


15. Herman KM, Hall AJ, Gould LH. Outbreaks attributed to fresh


2015;143:3011–3021.


characterization of Escherichia coli virulence genes isolated

from diseased pigs in the central region of Argentina. Vet


17. Paton AW, Paton JC. Multiplex PCR for direct detection of

Shiga toxigenic Escherichia coli strains producing the novel


Escherichia coli pathotypes in north and north-west provinces of


resistance and molecular characterization of virulence

genes, phylogenetic groups of Escherichia coli isolated from

diarhetic and healthy camel-calves in Tunisia. Comp Immunol


Shiga toxin-producing Escherichia coli infection in Australia.


virulence genes linked with diarrhea due to atypical

Enteropathogenic Escherichia coli by DNA microarray analysis


non-locus of enterocyte effacement pathogenic

island-related genes in Escherichia coli carrying eae from

patients with diarrhea and healthy indi-viduals in Japan. J


Escherichia coli heat-stable enterotoxin 1 represents another

subfamily of E. coli heat-stable toxin. Proc Natl Acad Sci U S A.

1993;90:3093–3097.


association of Escherichia coli AIDA-USTb, rather than EAST1

pathotype, with diarrhea in piglets and antibiotic sensitivity of


25. Rigos G, Troisi GM. Antibacterial agents in Mediterranean

finfish farming: a sinopsis of drug pharmacokinetics in

important euryhaline fish species and possible

environmental implications. Rev Fish Biol Fish. 2005;15:

53–55.


of Human Infections with Shiga Toxin-Producing Escherichia coli

(STEC) to Livestock Sources and Identification of Source-Specific


Health; 2017.

27. Escobar-Páramo F, Grenet K, Menac’h AL, et al. Large-scale

population structure of human commensal Escherichia coli


28. Eklund M, Scheutz F, Siitonen A. Clinical isolates of

non-O157 shiga toxin-producing Escherichia coli: serotypes,

virulence characteristics, and molecular profiles of strains of


virulence genes, and intimin types of Shiga toxin-producing

Escherichia coli (STEC) and enteropathogenic E. coli (EPEC)

isolated from calves in São Paulo, Brazil. Int J Food Microbiol.