Data Article

Prevalence data of diarrheagenic *E. coli* in the fecal pellets of wild rodents using culture methods and PCR assay

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\textbf{A B S T R A C T}

Wild animals, such as rodents seem to be competent reservoir of bacteria-borne zoonotic diseases which disseminate in human. We investigated the presence of *E. coli*, Shiga toxin-producing *E. coli* (STEC), and *Salmonella* in the feces of six category wild rodent species (*Apodemus agrarius*, *A. peninsulae*, *A. sylvaticus*, *Micromys minutus*, *Myodes regulus*, and *R. norvegicus*) captured from different agricultural regions in South Korea. Among them, *A. agrarius*, which account for 65\% of total (*N* = 52) individuals, are most widely distributed and abundant in various agroecosystems in South Korea. The bacterial identification was performed by cultural and molecular methods. In cultural method, the fecal cultures from 26 individuals formed colonies on *E. coli*-selective EMB agar media. Of them, the fecal cultures from 18 individuals also produced colonies on the Shiga toxin-producing *E. coli*-selective CT-SMAC agar media as well as the EMB agar media. In molecular method, polymerase chain reaction (PCR) was carried out to detect two virulence genes (*stx1* and *stx2*) of isolated *E. coli*. The amplified dataset of *stx1* and *stx2* genes of *E. coli*.

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were sequenced. In this manuscript, *E. coli* and STEC were detected but there were no *Salmonella* species. The wild rodents’ data would provide important information on reservoirs of those pathogenic bacteria.

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### Specifications Table

| Subject area       | Microbiology       |
|--------------------|--------------------|
| Specific subject area | Molecular Microbiology, Diarrheagenic *E. coli* |
| Type of data        | Table, Word, and Figure |
| How data were acquired      | Culture methods, PCR assay, and Sequencing |
| Data format         | Raw and Analyzed   |
| Parameters for data collection | Morphological identification, gene specific PCR amplification and screening, sequencing the target isolates, and the sequences were compared with other homologous sequences deposited in GenBank using BLASTN2.31+ [3]. |
| Description of data collection | We captured wild rodents using Sherman trap in various agricultural and mountainous area in South Korea. The *E. coli* and Shiga toxin-producing *E. coli* (STEC) bacteria in the fecal samples were detected by culturing them using a method described in a previous study [2]. The universal marker of bacterial 16S rRNA genes was amplified with HVR (V1SF and V3AR) primer set for molecular identification. Only a single pure colony of all 26 positive *E. coli* samples was used for PCR amplification. Shiga toxin genes with Stx1 and Stx2 primer sets were used for detection of STEC isolates. One or more pure colonies were randomly selected from all of positive individuals. |
| Data source location | Sobaeksan national park (36°56′45.2″ N, 128°27′43.9″E) in Yeongju, Gyeongsangbuk-do; Gayasan national park (35°48′00.4″ N, 128°08′30.5″E) in Geochang, Gyeongsangnam-do; Odesun national park (37°47′31.7″ N, 128°32′20.9″E) in Pyeongchang, Gangwon-do, South Korea. |
| Data accessibility  | Data are with this article only. Repository Name: NCBI The hypervariable region (HVR) of 16S rRNA gene (V1SF and V3AR) sequences were deposited to under the accession number: KY885178 to KY885185 (direct link from https://www.ncbi.nlm.nih.gov/nuccore/KY885178 to https://www.ncbi.nlm.nih.gov/nuccore/KY885185) and the accession number: KY048442 to KY048446 (direct link from https://www.ncbi.nlm.nih.gov/nuccore/KY048442 to https://www.ncbi.nlm.nih.gov/nuccore/KY048446). The Shiga toxin-producing genes (stx1) were deposited to under the accession number: KY964457 to KY964469 (direct link from https://www.ncbi.nlm.nih.gov/nuccore/KY964457 to https://www.ncbi.nlm.nih.gov/nuccore/KY964469) The Shiga toxin-producing genes (stx2) sequences were deposited to under the accession number: MN266867 to MN266871 (direct link from https://www.ncbi.nlm.nih.gov/nuccore/MN266867 to https://www.ncbi.nlm.nih.gov/nuccore/MN266871) Anyone can see the supplementary data and sequence fasta file to direct URL: Repository Name: [Mendeley Data] Data identification number: DOI: 10.17632/9dkfknynz2.2 Direct URL to data: http://dx.doi.org/10.17632/9dkfknynz2.2 |
| Related research article | M.M. Rahman, K.B. Yoon, S.J. Lim, M.G. Jeon, H.J. Kim, H.Y. Kim, Y.C. Park, Molecular detection by analysis of the 16S rRNA gene of fecal coliform bacteria from the two Korean Apodemus species (*Apodemus agrarius* and *A. peninsulae*), Genet. Mol. Res. 16 (2) (2017), gmr16029510. https://doi.org/10.4238/gmr16029510. |
Value of the Data

- The data will provide important information on competent reservoir of several bacteria-borne zoonotic diseases in wild rodent species and their fecal might play an important role in the transmission of pathogens, such as diarrheagenic E. coli bacteria.
- The dataset provides information about prevalence of diarrheagenic E. coli and could be used for better management of microbial contamination control.
- The data will contribute to understanding the potential factors that lead to increase in food-borne illness of farmers during agricultural production and processing.

1. Data Description

Wild rodents are competent reservoirs of zoonotic diseases that are responsible for significant economic losses and public health problems [3]. The rodents, such as Apodemus agrarius and A. peninsulae, are very common in South Korea and are widely distributed across agricultural farm areas and mountainous forests [4]. They can disseminate zoonotic microorganisms that are a considerable threat to the health of farmers [3,4]. Therefore, they could be important potential factors that lead to increases in food-borne illness during agricultural production and processing. However, wild rodents of A. agrarius, which account for 34 (65%) of the 52 captured individuals, were most commonly captured in the fields (Table 1 and 5). The E. coli and Shiga toxin-producing E. coli, bacteria in the rodent fecal samples were detected by culture and molecular method. For cultural identification, the E. coli or Shiga toxin-producing E. coli colonies were confirmed based on their colony morphology. The E. coli colonies produced metallic sheen color produced on EMB agar media. Sorbitol negative colonies (colorless) were detected onto CT-SMAC agar media (Supplement Fig. S1). We select colorless colony as E. coli O157:H7 positive colonies seem to be STEC-positive on culture media. Moreover, the bacterial colonies on the selective media that had been identified by their morphology were re-identified by PCR using molecular markers. So, a PCR amplification of the bacterial 16S rRNA gene was performed to confirm whether the colonies on the EMB media belonged to E. coli. We randomly selected a single colony from each of the 26 positive EMB agar plates (Table 1) and after PCR amplification with the hypervariable region (HVR) of 16S primer set, the target bands for the 16S rRNA gene were found in all 26 single colonies (Supplement Fig. S2). Thirteen PCR bands were then sequenced (Table 2). A PCR amplification of the Shiga toxin genes (stx1 and stx2) was performed to confirm whether the colonies on the CT-SMAC media belonged to Shiga toxin-producing E. coli. The target PCR bands of 21 E. coli with stx1 gene and 5 E. coli with stx2 gene were amplified and sequenced (Supplement Fig. S3 and S4). Of them, 13 Stx1 PCR bands and 5 Stx2 PCR bands were sequenced (Table 3 and 4). The E. coli and Shiga toxin-producing E. coli sequences were compared for similarity with bacteria deposited in GenBank using NCBI BLAST, which is available at http://www.ncbi.nlm.nih.gov/.

2. Experimental Design, Materials, and Methods

2.1. Sample collection

We captured wild rodents using Sherman traps in various agroecosystems across South Korea (Table 1). Each captured wild rodent was placed into a disposable vinyl zipper bag and then released after collecting its feces. The fecal samples were brought to the laboratory in ice boxes and processed within three hours. The sample collections were conducted under the permission and guideline of local governments.
### Table 1

Culture and molecular detection *E. coli*, and Shiga toxin-producing *E. coli* in the rodent fecal samples collected from different environments.

| Individual No. | Species           | Fecal sample ID | Sex     | Agricultural environment | Collection locality | E. coli | Shiga toxin E. coli | E. coli | M. M. | Apodemus agrarius | MuApAg-1 | Male | Dry area | Odaesun ×× – – – | – | – | – | – | – | – | – | – |
|----------------|-------------------|-----------------|---------|--------------------------|---------------------|---------|--------------------|---------|------|-----------------|----------|-----|---------|----------------|---|---|---|---|---|---|---|---|
| 1              | Apodemus agrarius | MuApAg-1        | Male    | Dry area                 | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 2              | Apodemus agrarius | MuApAg-2        | Male    | Nearby forest            | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 3              | Apodemus agrarius | MuApAg-3        | Male    | Nearby forest            | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 4              | Apodemus agrarius | MuApAg-4        | Female  | Dry area                 | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 5              | Apodemus agrarius | MuApAg-5        | Male    | Dry area                 | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 6              | Apodemus agrarius | MuApAg-6        | Female  | Watery area              | Odaesun             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 7              | Apodemus agrarius | MuApAg-7        | Male    | Nearby forest            | Gayasan             | 0       | 0                  | 0       | ×    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 8              | Apodemus agrarius | MuApAg-8        | Male    | Nearby forest            | Gayasan             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |
| 9              | Apodemus agrarius | MuApAg-9        | Male    | Nearby forest            | Gayasan             | ×       | ×                  | –       | –    | –               | Apodemus |    | –       |                       |   |   |   |   |   |   |   |   |

(continued on next page)
Table 1 (continued)

| Individual No. | Species          | Fecal sample ID | Sex   | Agricultural environment | Collection locality | Culture detection | Molecular detection |
|----------------|------------------|-----------------|-------|--------------------------|---------------------|------------------|---------------------|
|                |                  |                 |       |                          |                      | E. coli         | Shiga toxin producing E. coli |
|                |                  |                 |       |                          |                      | 16S rRNA gene   | Shiga toxin gene (stx1) | Shiga toxin gene (stx2) |
| 37             | A. peninsulae     | MuApPe-3        | Male  | Nearby forest            | Sobaeksan           | ×                | –                  | –                  |
| 38             | A. peninsulae     | MuApPe-4        | Male  | Dry area                 | Sobaeksan           | ×                | –                  | –                  |
| 39             | A. peninsulae     | MuApPe-5        | Male  | Nearby forest            | Sobaeksan           | × ×              | –                  | –                  |
| 40             | A. peninsulae     | MuApPe-6        | Female| Watery area              | Sobaeksan           | × ×              | –                  | –                  |
| 41             | A. sylvaticus     | MuApSy-1        | Male  | Nearby forest            | Gayasan             | o ×              | o                  | ×                  |
| 42             | A. sylvaticus     | MuApSy-2        | Male  | Dry area                 | Gayasan             | o o              | o                  | ×                  |
| 43             | A. sylvaticus     | MuApSy-3        | Female| Watery area              | Gayasan             | o o              | o                  | ×                  |
| 44             | Micromys minutus  | MuMiMi-1        | Male  | Dry area                 | Gayasan             | × ×              | –                  | –                  |
| 45             | M. minutus        | MuMiMi-2        | Male  | Nearby forest            | Gayasan             | × ×              | –                  | –                  |
| 46             | M. minutus        | MuMiMi-3        | Male  | Watery area              | Gayasan             | × ×              | –                  | –                  |
| 47             | Myodes regulus    | CrMyRe-1        | Male  | Nearby forest            | Bukhansan           | × ×              | –                  | –                  |
| 48             | M. regulus        | CrMyRe-2        | Male  | Nearby forest            | Bukhansan           | × ×              | –                  | –                  |
| 49             | M. regulus        | CrMyRe-3        | Female| Watery area              | Bukhansan           | o o              | –                  | –                  |
| 50             | Rattus norvegicus | MuRaNo-1        | Male  | Watery area              | Gayasan             | o o              | o                  | ×                  |
| 51             | R. norvegicus     | MuRaNo-2        | Female| Nearby forest            | Gayasan             | × ×              | –                  | –                  |
| 52             | R. norvegicus     | MuRaNo-3        | Male  | Dry area                 | Gayasan             | o o              | o                  | ×                  |

Total individual (N) 26 18 26 0 2

'o' = detected, '×' = not detected and '-' = not tested.
Table 2
Molecular identification of *E. coli* in the rodent fecal samples using 16s rRNA gene sequences.

| Species                  | No. of host individuals used for fecal culture | No. of host individuals with *E. coli*-positive colonies on EMB | No. of host individuals with *E. coli*-positive PCR band | No. of the sequences obtained from PCR bands | No. & Host individual ID | No. Sequenced colony ID | Size (bp) | GenBank accession No. | Coverage (%) | Identity (%) | Similarity analysis in GenBank | Identification of bacteria by the similarity analysis of 16s rRNA gene sequences in GenBank | Remarks |
|-------------------------|-----------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------|-----------------------------------------------|----------------------------|------------------------|-----------|----------------------|---------------|--------------|---------------------------------|-------------------------------------------------|---------|
| *Apodemus agrarius*     | 34                                            | 19                                                            | 19                                                     | 7                                             | MuApAg-7                   | M1–6                   | 539       | KY048445             | 100           | 100          | *E. coli* MRY15–131 (AP017620.1) | General *E. coli*                                |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-18                  | M_1_Sobeksan-edit          | 584       | KY885178             | 100           | 100          | *E. coli* AR_0104 (CP020116.1) | A. peninsularis                                   |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-19                  | M_2_S                    | 569       | KY885179             | 100           | 100          | *Escherichia* sp. BAB-6436 (KY672923.1) |                                           |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-20                  | M_3_Sobeksan_edit          | 604       | KY885180             | 100           | 100          | *E. coli* AR_0104 (CP020116.1) | A. sylvaticus                                    |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-22                  | M_4_S                    | 611       | KY885181             | 100           | 100          | *E. coli* NCF1 (CP0160071) |                                          |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-23                  | M_6_S                    | 539       | KY048444             | 100           | 100          | *E. coli* MRY15–131 (AP017620.1) | A. peninsulae                                    |         |
|                         |                                               |                                                               |                                                        |                                               | MuApAg-27                  | M_10_s                   | 585       | KY885182             | 100           | 100          | *E. coli* 20Ec-P-124 (AP017630.1) |                                           |         |
| *A. peninsularis*       | 6                                             | 1                                                             | 1                                                      | 1                                             | MuApPe-1                   | M2M-3                   | 579       | KY048443             | 100           | 99           | *E. coli* NCF1 (CP0160071) | A. sylvaticus                                    |         |
| *A. sylvaticus*         | 3                                             | 3                                                             | 3                                                      | 2                                             | MuApSy-1                   | MWM-1                   | 454       | KY048442             | 100           | 100          | *E. coli* BLR (DE3) (NZ_CP020368.1) |                                           |         |
| *Micromys minutus*      | 3                                             | ×                                                             | –                                                      | –                                             | MuApSy-2                   | MWM2-iii                 | 600       | KY885185             | 100           | 100          | *E. coli* MDR 56 (CP019903.1) | Micromys nissus                                   |         |
| *Myodes regulus*        | 3                                             | 1                                                             | 1                                                      | 1                                             | CrMyRe-3                   | SFM                      | 565       | KY048446             | 100           | 99           | *E. coli* BLR (DE3) (NZ_CP020368.1) | R. norvegicus                                    |         |
| *R. norvegicus*         | 3                                             | 2                                                             | 2                                                      | 2                                             | NuRaNo-1                   | SFM 3_BKNP               | 571       | KY885183             | 100           | 100          | *E. coli* 20Ec-P-124 (AP017630.1) |                                           |         |
| Total (N)               | 52                                            | 26                                                            | 26                                                     | 13                                            | NuRaNo-3                   | SFM 4_BKNP               | 498       | KY885184             | 100           | 99           | *E. coli* sch21 (JC294878.1) |                                          |         |

'×' = not detected and '-' = not tested.
### Table 3
Molecular identification of Shiga toxin-producing *E. coli* in the rodent fecal samples using Shiga toxin gene (stx1) sequences.

| Species            | No. of the host individuals used for fecal culture | No. of host individuals with fecal *Shiga* toxin *E. coli*-positive colonies on CT-SMAC PCR bands | No. of host individuals with the colonies with *Shiga* toxin gene (stx1)-amplified PCR bands | No. of the sequences obtained from the colonies with *Shiga* toxin gene (stx1)-amplified PCR bands | Host individual ID | Sequenced colony ID | GenBank accession No. | Size (bp) | Coverage (%) | Identity (%) | Identified genes and their products were found in GenBank | Identification of bacteria by the similarity analysis of *Shiga* toxin gene (stx1) sequence in GenBank | Remarks |
|--------------------|---------------------------------------------------|------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|---------------------------------------------------------------------------------------------|-------------------|-------------------|----------------------------|-----------|---------------|--------------|-------------------------------------------------|-------------------------------------------------|---------|
| *Apodemus agrarius* | 34                                                | 12                                                                                           | 12                                                              | 5                                                                                           | MuApAg-7          | SFM1_2            | KY964461                  | 570       | 100           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain AH01 (CP055251.10)               | Pathogenic |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApAg-11         | SFM2d-1          | KY964458                  | 302       | 100           | 100          | alef (S)-ureidoglycine aminohydrolase             | *E. coli* strain MS6192 (CP054940.1)               | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApAg-12         | SFMd3–24        | KY964459                  | 342       | 100           | 100          | pBpc (penicillin-binding protein 1C)            | *E. coli* strain MS6192 (CP054940.1)               | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApAg-13         | SFMW-16          | KY964460                  | 364       | 100           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain AH01 (CP055251.10)               | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApAg-18         | M1_5              | KY964457                  | 267       | 100           | 99           | pphc gene (proline-serine/threonine phosphatase PphC) | *E. coli* strain 04–00,955 (CP035498.1)           | *E. coli* |
| *A. peninsulae*     | 6                                                 | 0                                                                                           | –                                                               | –                                                                                           | MuApSy-1          | MWM1_10           | KY964462                  | 504       | 100           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain 88–3510 (CP026765.1)              | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApSy-2          | MWM2_4            | KY964463                  | 223       | 100           | 98           | pphc gene (proline-serine/threonine phosphatase PphC) | *E. coli* strain SCU-484(CP051744.1)             | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApSy-3          | MWM2_5            | KY964464                  | 311       | 100           | 99           | Regulator gene                                  | *E. coli* strain EcP7(CP054232.1)                 | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MWM3_7            | KY964465          | 581                        | 100       | 99           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain SCU-316 (CP054371.1)             | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MWM3_9            | KY964466          | 584                        | 100       | 99           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain SCU-316 (CP054371.1)             | *E. coli* |
| *A. sylvaticus*     | 3                                                 | 3                                                                                           | 3                                                               | 5                                                                                           | MuApSy-1          | MWM1_10           | KY964462                  | 504       | 100           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain 88–3510 (CP026765.1)              | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApSy-2          | MWM2_4            | KY964463                  | 223       | 100           | 98           | pphc gene (proline-serine/threonine phosphatase PphC) | *E. coli* strain SCU-484(CP051744.1)             | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuApSy-3          | MWM2_5            | KY964464                  | 311       | 100           | 99           | Regulator gene                                  | *E. coli* strain EcP7(CP054232.1)                 | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MWM3_7            | KY964465          | 581                        | 100       | 99           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain SCU-316 (CP054371.1)             | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MWM3_9            | KY964466          | 584                        | 100       | 99           | 99           | pBpc (penicillin-binding protein 1C)            | *E. coli* strain SCU-316 (CP054371.1)             | *E. coli* |
| *Micromys minutus*  | 3                                                 | 0                                                                                           | –                                                               | –                                                                                           | CrMyBe-3          | x                 | –                          | –         | –            | –            | –                                                | –                                                | –        |
| *Myodes regulus*    | 3                                                 | 1                                                                                           | 1                                                               | 0                                                                                           | CrMyBe-3          | x                 | –                          | –         | –            | –            | –                                                | –                                                | –        |
| *R. norvegicus*     | 3                                                 | 2                                                                                           | 2                                                               | 3                                                                                           | MuRaNo-1          | NRW1–14           | KY964467                  | 420       | 100           | 99           | alef (S)-ureidoglycine aminohydrolase             | *E. coli* strain MS6192(CP054940.10)              | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuRaNo-1          | NRW1_1B           | KY964468                  | 248       | 100           | 100          | pphc gene (proline-serine/threonine phosphatase PphC) | *E. coli* strain MS6192 (CP054940.10)             | *E. coli* |
|                    |                                                   |                                                |                                                                 |                                                                                             | MuRaNo-3          | NRW3–15           | KY964469                  | 274       | 99            | 99           | pphc gene (proline-serine/threonine phosphatase PphC) | *E. coli* strain SCU-316 (CP054371.1)             | *E. coli* |
| Total (N)          | 52                                                | 18                                                                                          | 18                                                              | 13                                                                                          | –                 | –                 | –                          | –         | –            | –            | –                                                | –                                                | –        |

*×* = not detected and *-* = not tested.
Table 4
Molecular identification of Shiga toxin-producing E. coli in the rodent fecal samples using Shiga toxin gene (stx2) sequences.

| Species                          | No. of the host individuals used for fecal culture | No. of host individuals with Shiga toxin-producing E. coli-positive colonies on CT-SMAC | No. of host individuals with the Shiga toxin gene (stx2)-amplified PCR bands | No. of the sequences obtained from the Shiga toxin gene (stx2)-amplified PCR bands | Host individual ID | Sequenced colony ID | GenBank accession No. | Size (bp) | Coverage (%) | Identity (%) | Identified genes and their products were found in GenBank | Identification of bacteria by the similarity analysis of Shiga toxin gene (stx2) sequence in GenBank |
|---------------------------------|---------------------------------------------------|------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|---------------------------------------------------------------------------------|-------------------|-------------------|---------------------|----------|--------------|--------------|----------------------------------------------------------|----------------------------------------------------------------------------------|
| Apodemus agrarius               | 34                                                | 12                                                                                       | 2                                                                            | 2                                                                               | MuApAg-11         | SFM21-1          | MN266871             | 219      | 100          | 96           | helix-turn-helix transcriptional regulator                | E. coli O145:NM strain FWSEC0002 (CP031919.1)                                   |
|                                 |                                                   |                                                                                          |                                                                              |                                                                                 | MuApAg-13         | SFMW-16          | MN266867             | 456      | 100          | 100         | stxA2 gene (Shiga toxin Stx2 subunit A)                  | E. coli O157:H7 strain ECP17-1298 (CP040570.1)                                   |
| A. peninsulae                    | 6                                                 | 0                                                                                       | –                                                                            | –                                                                               | –                 | –                 | –                   | –        | –            | –            | –                                                        | –                                                                               |
| A. sylvaticus                    | 3                                                 | 3                                                                                       | 1                                                                            | 1                                                                               | MuApSy-3          | MWM3-9            | MN266868             | 461      | 100          | 100         | stx2gA (shiga toxin 2g subunit A)                         | E. coli O157:H7 strain COPRO21317 (CP035706.1)                                   |
| Micromys minutus                 | 3                                                 | 0                                                                                       | –                                                                            | –                                                                               | –                 | –                 | –                   | –        | –            | –            | –                                                        | –                                                                               |
| Myodes regulus                  | 3                                                 | 1                                                                                       | 0                                                                            | 0                                                                               | CrMyRe-3          | x                 | –                   | –        | –            | –            | –                                                        | –                                                                               |
| R. norvegicus                    | 3                                                 | 2                                                                                       | 2                                                                            | 2                                                                               | MuRaNo-1          | NRW1-14           | MN266869             | 321      | 100          | 95           | helix-turn-helix transcriptional regulator               | E. coli strain 89–3156 (CP027366.1)                                              |
|                                 |                                                   |                                                                                          |                                                                              |                                                                                 | MuRaNo-3          | NRW3-15           | MN266870             | 327      | 99           | 95           | helix-turn-helix transcriptional regulator               | E. coli O145:NM strain FWSEC0002 (CP031919.1)                                   |
| Total (N)                       | 52                                                | 18                                                                                      | 5                                                                            | 5                                                                               | –                 | –                 | –                   | –        | –            | –            | –                                                        | –                                                                               |

'x' = not detected and '-' = not tested.
2.2. Detection of diarrheagenic E. coli bacteria

The E. coli and Shiga toxin-producing E. coli, bacteria in the fecal samples were detected by culturing them using the method described in a previous study [2]. The fecal samples (0.1 g to 1 g) were first cultured in 10 mL non-selective buffered peptone water (BPW) at 37°C overnight and then a 10 μL enrichment broth of containing the samples was streaked with a loop onto the E. coli-selective eosin methylene blue Agar (EMB) media and Shiga toxin-producing E. coli-selective cefixime tellurite sorbitol MacConkey agar (CT-SMAC) media and incubated at 37°C for 24-48 hrs. The plates were examined for colony forming units (CFU) and sub-cultivated was conducted on EMB so that pure colonies could be collected. The E. coli or Shiga toxin-producing E. coli colonies were confirmed based on their colony morphology [5]. E. coli (NCPP: 14,034) and E. coli O157:H7 (ATCC-95,150) were used as a positive control. The E. coli colonies produced metallic sheen color produced on EMB agar media. Sorbitol negative colonies (colorless) were detected onto CT-SMAC agar. From each plate, 2 to 3 colonies were picked from CT-SMAC media. We select colorless colony as E. coli O157:H7 positive colonies seem to be STEC-positive on culture media. The STEC colonies have morphological differences in CT-SMAC compared to the general E. coli. Finally, the STEC E. coli was detected based on morphology, PCR band, and sequence analysis.

2.3. Extraction of total genomic DNA and PCR amplification

The bacterial colonies on the selective media or differential media had been identified by their morphology and re-identified by PCR using molecular markers. The colonies were streaked onto nutrient agar media and then a single colony was collected using sterilized toothpicks. The colonies were incubated at 35°C for 18 hrs in 5 ml lactose broth (LB) solution. Genomic DNA was extracted from 1 ml LB culture fluid using a DNeasy Blood and Tissue Kit™ according to the manufacturer’s instructions (Valencia, CA, USA).

The PCR amplification was performed using a final 25 μL reaction volume containing 10 mMTris–HCl (pH 8.4), 50 mM KCl, 4 mM MgCl₂, 200 mM of each dNTP, 50 pmol of each primer, 2 U ExTaq polymerase, and 1 μL of genomic DNA. The E. coli colonies on the EMB were molecularly identified by PCR amplification of the bacterial 16S rRNA gene which was performed using the HVR primer set [6]. The Shiga toxin-producing E. coli colonies on CT-SMAC were molecularly identified by PCR amplification using the Stx1 and Stx2 primer set [7,8].

The PCR reaction was conducted using the following reaction conditions: an initial denaturation for 5 min at 94°C, followed by 35 cycles of denaturation for 1 min at 94°C, an annealing
temperature of 55 °C (HVR, Stx1, and Stx2 primers) for 60 sec, extension for 1 min at 72 °C, and then a final extension for 10 min at 72 °C. The PCR products were subjected to electrophoresis in 1.0% agarose gel and purified using a DNA gel extraction kit (Qiagen, Valencia, CA, USA). The purified PCR products were sent to Macrogen (South Korea) for sequencing. The obtained sequences were compared with other homologous sequences deposited in GenBank using BLASTN2.2.31+

[1].

**Ethics Statement**

The sample collections were conducted under the permission and guideline of local governments.

**Declaration of Competing Interest**

The authors declare that they have no competing interest or financial relationships which have influenced the work reported in this article.

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**Supplementary Materials**

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.dib.2020.106439.

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