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Research article

RESISTANCE TO ANTIBIOTICS BY ENTERIC BACTERIA ASSOCIATED WITH THE SWINE INDUSTRY: *IN SILICO* EXPLORATION OF THE DISTRIBUTION OF RESISTANCE GENES

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Multidrug-resistant (MDR) bacteria are a significant contributor to the global antibiotic resistance crisis, which is predicted to kill more people than cancer by 2050. Livestock production is a contributing factor as it has been one of the fastest-growing industries in the previous century but has the most harmful effects on the environment and human health. The pig is the most widely raised and consumed food-producing animal globally, with an upward trend. The derived residues and the meat products constitute an important reservoir of antibiotic resistance genes (ARGs) that can be transmitted to humans through consumption, direct contact, the environment, or poor handling, leading to relevant zoonotic diseases, especially enteric ones. It is essential to know the diversity, abundance, and distribution of ARGs to have better control and monitoring of their dispersion. In the present study, the ARGs and Mobile Genetic Elements (MGEs) of five enteric and pathogenic species commonly present in the microbiota of both pigs and humans were examined by bioinformatic analysis. This analysis showed that 157 ARGs were distributed across 1869 genomes of five bacterial species, ranked from highest to lowest diversity of ARGs: *Klebsiella pneumoniae*, *Escherichia coli*, *Enterococcus faecium*, *Salmonella enterica*, and *Enterococcus faecalis*. This study contributes to better management of antibiotics, which directly impact the health of both humans and animals.

Keywords: bioinformatic analysis, enteric bacteria, pig farming, antimicrobial resistance genes, mobile genetic elements

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INTRODUCTION

Antibiotic resistance is a global problem that is increasing dangerously. It is caused by selection of bacterial strains through the continuous exposure to these drugs [1]. The intensive use of antibiotics in livestock (Figure 1) and fish farming creates conditions for developing and transferring resistance genes between bacteria in animals, humans, and the environment. It is a common practice to administer antibiotics to healthy animals for prophylactic and growth promotion purposes [2]. Livestock production is one of the principal causes of antibiotic resistance worldwide. Among the different types of livestock production, swine (*Sus scrofa domesticus*) becomes relevant since its great global magnitude (110.975 million tons forecast for 2023) [3] and for being the livestock industry that consumes the highest quantity of antibiotics [2-4].

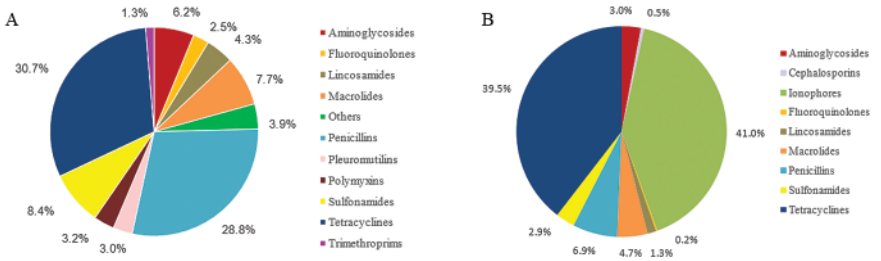


Figure 1. Percentage distribution of antibiotic classes approved for sale in animal production in the US **(A)** and Europe **(B)** (adapted from FDA, 2020 & EMA, 2020).

Also, a reasonably common practice throughout the world is the reuse of livestock biosolids as organic fertilizer in agriculture. However, it is estimated that between 75% and 90% of antibiotics are excreted without being metabolized by animals [5] with the inherent risk of spreading multi-resistant bacteria, resistance genes, and antibiotic residues that can spread across the environment [6,7].

Some studies demonstrate and describe the relationships between the overuse of antibiotics, the presence of antimicrobial resistance genes (ARG), and the range to which they can spread between different hosts and environments when carried by Mobile Genetic Elements (MGE) via horizontal transfer [8-10]. In 2020, Yang et al. [11] highlighted the potential role of pig manure as an essential reservoir of ARGs and MGEs. They analyzed manure from pig farms in China by qPCR and revealed that, in both feces and treated manure, class 1 and 2 integrons as well as conjugative plasmids, were present.

Furthermore, in the United States, Muurinen et al. [12] investigated the influence of antibiotics and alternative growth promoters on the pig fecal resistome, the mobility of ARGs, and their relationship with MGEs. Given the fact that horizontal gene transfer is induced by subtherapeutic concentrations of antibiotics and the activation of bacterial stress response mechanisms. In addition, antibiotics and alternative growth

promoters were also found to strengthen the relationships between ARGs and MGEs directly and proportionally.

It is essential to know that, despite some anatomical and physiological differences, the brain development, immunology, microbiota, and gastrointestinal tract of pigs and humans are similar although the pig is considered a gnotobiotic model for studying gastrointestinal diseases or the response of the normal intestinal microbiota to various factors [13,14]. For instance, Wang et al. [15] performed a comparative metagenomic analysis to characterize the gut microbiota and resistome of pigs and humans. They found 27 shared ARGs, among which the most abundant (between 59 and 60%) were resistant to tetracycline, macrolides, and streptogramin B. Furthermore, it was revealed that MGEs promoted their dispersal. Most of the ARGs came from the Gamma proteobacteria class, which harbors many of the most widely described multidrug-resistant bacteria.

To better understand the prevalence, diversity, and distribution of resistance genes, this study performed a descriptive and comparative bioinformatic analysis of five enteric and pathogenic bacteria commonly found in porcine isolates of *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Salmonella enterica*, based in the information available in public databases of genomes, assemblies, or genomic readings.

MATERIALS AND METHODS

395 genomes of bacteria isolated from pigs were downloaded from the NCBI database. The main criterium for selecting the genomes was that they had gene/protein annotations. 32 genomes correspond to *Enterococcus faecalis*, 201 to *Enterococcus faecium*, 41 to *Escherichia coli*, 31 to *Klebsiella pneumoniae*, and 90 to *Salmonella enterica.*

As a first step, a randomly selected subset of 11 genomes per species were scanned with ResFinder 4.1 [16] and MGEfinder 1.0.3 [17] in order to obtain a representative group of sequences of ARGs and MGEs. The final quantity of genomes to be scanned with Resfinder and MGEfinder was determined, adding one by one until no newer ARGs or MGEs were found. A total of 18 genomes *per species* were sufficient to get the representative group of ARGs and MGEs. We used the following parameters in ResFinder: Threshold for %ID, 85%; Minimum length, 60%; Type of reads, Assembled genomes or contigs.

All sequences, a total of 365, were merged in a single file, and a multiple sequence alignment was performed to establish the similarity between the antibiotic resistance genes of the different bacterial strains and discard the redundant ones to diminish the number of sequences used in the BLAST search.

The remaining 106 unique sequences were used for a broad BLAST search in all the 395 downloaded genomes. We used a standalone BLAST version for Linux installed locally on a desktop computer, a Perl script to organize data, and a spreadsheet to

analyze the results. The cut-off values were for E-value maximum accepted value of 1e-18; coverture minimum accepted value of 40%; and identity minimum accepted value of 65%.

RESULTS

From the local BLAST search, it was found a significant amount of beta-lactamases (~50%) followed by enzymes related to target modification (~35%) and efflux pumps (~15%). The total richness of gene families among the five species of bacteria was 36, with *Klebsiella pneumoniae* being the one with the highest relative abundance per gene family (28 different families), followed by *Escherichia coli* (18), *Enterococcus faecalis* (9), *Enterococcus faecium* (7) and finally *Salmonella enterica* with seven. The information regarding each of the bacterial strains that were examined is shown in the Supplementary Material. Figure 2 details the gene richness of families of ARGs among the five species of bacteria and shows the presence or absence of a gene.

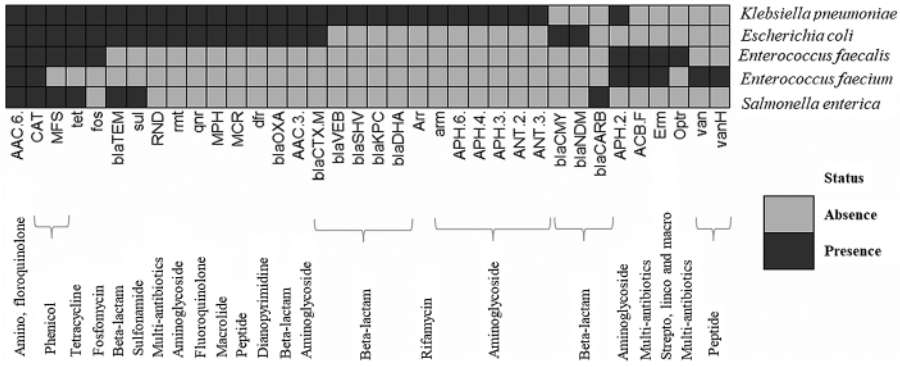


Figure 2. Total richness of antibiotic resistance gene families in the five species of bacteria analyzed. AAC = Aminoglycoside Acetyltransferase Cassette. ANT = Aminoglycoside Nucleotidyltransferase. APH = Aminoglycoside Phosphotransferase. CAT = Chloramphenicol Acetyltransferase. MFS = Major Family Facilitator. MPH = Macrolide Phosphotransferase. RND = Resistance Nodulation Division.

A general comparison analysis of the total ARGs in all analyzed strains was also conducted to determine the ten most abundant ones (Table 1). It is evident that tetracycline resistance is the antibiotic group more represented (by *Tet* genes) with three multi-resistant genes (*oqxA*, *oqxB,* and *msrC*).

Regarding the MGEs, Table 2 shows their presence and distribution by class within the five bacterial species. These data are comparable with those of Wang et al. [15], whose results on MGEs were mainly the presence of conjugative elements (integrative and mobilizable) and insertion sequences. The fact that in the present investigation all the bacteria had the insertion sequences as predominant could be explained because they are short chains of genetic material (less than 2.5 Kb of DNA) that can be more easily inserted into the DNA than into other larger elements [18].

Table 1. ARGs most frequently detected in all bacterial strains, from highest to lowest.

ARG	Family of ARG	Resistance to	Frequency
tet(M)	*Tet*	Tetracycline	27
blaTEM-1B	*blaTEM*	Beta-lactam	21
erm(B)	*Erm*	Streptogramin, lincosamide and macrolide	21
sul2	*Sul*	Sulfonamide	19
aac(6')-Ii	*AAC(6')*	Aminoglycoside	18
oqxA	*RND*	Dianopyrimidine, fluoroquinolone, glycylcycline, nitrofuran, and tetracycline	18
oqxB	*RND*	Dianopyrimidine, fluoroquinolone, glycylcycline, nitrofuran, and tetracycline	17
msr(C)	*ACB-F*	Streptogramin, phenicol, lincosamide, macrolide, oxazolidinone, pleuromutilin, and tetracycline	16
sul1	*Sul*	Sulfonamide	16
tet(L)	*Tet*	Tetracycline	16

Table 2. Comparison between the types of MGEs present in the bacterial strains analyzed in this study.

MGE Class	***Enterococcus faecalis***	***Enterococcus faecium***	***Escherichia coli***	***Klebsiella pneumoniae***	***Salmonella enterica***
Integrative and Conjugative Element (ICE)	2	-	1	-	-
Integrative and Mobilizable Element (IME)	1	-	-	-	-
Miniature Inverted-repeat Transposable Element (MITE)	-	-	1	-	1
Insertion Sequence (IS)	11	11	47	24	2
Transposon Unit	3	-	5	1	-

When the diversity (the connection between richness and abundance) of ARGs harbored in the examined bacteria are compared, a pattern coincides with the number of various resistance genes each bacterial species contains. *K. pneumoniae* leads the list of gene richness as it has evolved resistance to 12 different groups of antibiotics and many associated genes (Figure 3). Although *E. faecalis* has a higher ARG richness, *E. faecium* has more abundance, which results in greater diversity. Therefore, the specific order of these two species differs slightly when abundance or richness is considered independently of their diversity.

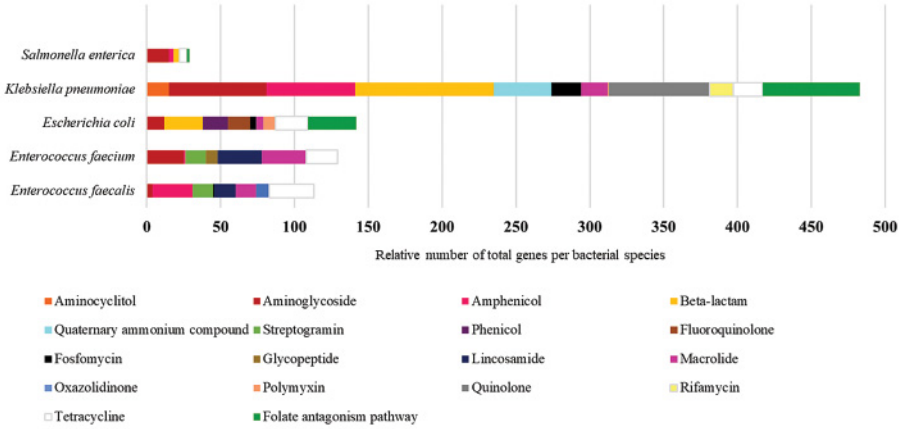


Figure 3. Diversity of ARGs in five bacterial species. The richness and crossed abundance of ARGs in the five bacterial species analyzed. Several genes provide multi-resistance, so the number of genes shown is relative to the antimicrobial class for which it generates resistance.

DISCUSSION

The bacterial species with the highest abundance of resistance genes was *Klebsiella pneumoniae*, followed by *Escherichia coli*, *Enterococcus faecium*, *Enterococcus faecalis*, and *Salmonella enterica* (Figure 2). Consistently, except for *Enterococcus* spp., the gene richness of ARGs among the bacterial species analyzed corresponded equally to their number of genes per genome, resulting in a very similar order of richness by species from highest to lowest. Although analyzed separately, these two variables constitute the local genetic diversity of studied species.

The findings on the richness and abundance of ARGs among the five bacterial species in this study are comparable to the work of Yang et al. [11]. They detected and determined that the genes *tetO*, *tetW*, *tetQ*, *sul1*, *sul2*, *oqxB*, *qnrS*, and *ermC* are prevalent in liquid pig manure. In addition, Jarat et al. [19] reported genes belonging to the *tet*, *qnr*, and *erm* classes. However, the abundance of an ARG is not necessarily proportional to the frequency of the group to which it belongs (Table 1). This may be explained because there are numerous gene families that, however, can transfer the same or similar resistance. Moreover, the potential for spreading ARGs into the environment is mainly through water, air, or land routes. Interestingly, by interconnected processes involving agricultural and fish farming activities, the environment, humans, and wildlife as host and propagation vectors [2] are also spreading potentials. For example, Xiong et al. [20] revealed by HPLC-MS/MS and qPCR the result of the selective pressure of antibiotics on the ARGs of bacterial communities in freshwater sediments polluted with pig manure. They found that selective pressure favoured bacterial genera such as *Escherichia* and *Salmonella*. In descending order, tetracyclines, fluoroquinolones, and sulfonamides were found in water sediment samples. Due to the chemical stability and partitioning capabilities of antibiotics, the sequence was likely reversed in water.

When comparing the gene diversity (Figure 3), it is appreciated that *Klebsiella pneumoniae* is the leading species, with a higher abundance of each gene class. It is known that *K. pneumoniae* is one of the bacteria with the highest frequency and diversity of resistance genes. Even in this species, many ARGs were discovered before being identified in other pathogens, and current scientific evidence suggests that spreading ARGs by horizontal transfer to other bacterial groups and environments is essential; consequently, this bacterium represents a significant and constantly growing threat to public health [21,22]. Similarly, together with *K. pneumoniae*, the bacterium *E. faecalis*, *E. faecium*, and *E. coli* belongs to the group of pathogens known as ESKAPE, which contains some of the known pathogens with the greatest multi-resistance to antibiotics. So, at this point, it is appropriate to notice the similarities between the two *Enterococcus* species, mainly at the richness level, presumably due to shared genes within the same taxonomic genus.

Concerning *E. coli*, the second most ARG-diverse bacteria observed (Figure 3), shows fluoroquinolone resistance through the *qnr* genes, like *K. pneumoniae*. It also highlights the role these genes could play given their plasmid-mediated nature, which can be conjugative or integrative and, therefore, spread via horizontal transfer to other bacterial species, even with different ARGs [23]. Likewise, gene mobility between groups of *Enterobacterales* and *Salmonella*, among others, has been described [24]. This can be explained as the combined result of the selective pressure action exerted by the most frequently used antibiotics (such as tetracyclines, penicillins, macrolides, sulfonamides, and aminoglycosides) and the individual contribution made by each bacterial species. According to Li et al. [25], who tracked the most common ARGs in the air in samples around the world and found the *blaTEM* genes (to be the most frequent, *Klebsiella pneumoniae*), was the one with the most remarkable diversity of resistance genes and, in whose resistome, the *bla* genes stood out.

In 2020, Capita et al. [26] analyzed preparations of beef, pork, and poultry samples and found that, of 126 total strains, 63% were multi-resistant, 23% resistant, and only 14% were sensitive. Among the bacteria found to be resistant were *E. coli*, *K. pneumoniae*, and *S. enterica*. Torres et al. [27] determined that *E. faecium* and *E. faecalis* resist beta-lactams, streptogramins, glycopeptides, lincosamides, phenicols, macrolides and oxazolidinones carried by farm animals destined for human consumption. Nevertheless, many countries still use antibiotics such as tetracyclines, sulfonamides, streptogramins, and aminoglycosides as growth promoters in animal husbandry; better regulation or absolute restriction, as in developed countries, would try to minimize ARGs.

Hu et al. [28] previously conducted a comparative bioinformatic study using the Resfinder platform between the ARGs harbored in the microbiota of humans, cattle, pigs, and chickens and found that 41 genes were transferred between animals and humans. Besides that, 11 genes corresponded to the tetracycline class, ten to aminoglycosides, nine to macrolide-lincosamide-streptogramin B, five to chloramphenicol, three to beta-lactams, and three to sulfonamides. They also observed that ARGs spread more readily among closely related bacteria in their phylogeny. They suggested that

antibiotic exposure is the cause of selection, the environment is the physical barrier, and phylogeny determines the ability for horizontal transfer to occur through cross-fertilization. This is similar to the results obtained in the present study regarding the classes of antibiotics for which the most significant number of resistance genes were found and the similarity in the composition of ARGs between different species with a high phylogenetic relationship, as in the case of *E. faecalis* and *E. faecium*. The presence of the tet(*M*) and *erm*(*B*) genes, as well as the *bla*, *aac*, *dfr*, and *van* gene families were found to be consistent in addition to the results presented by Wang et al. [29] and the outcomes of our study. Despite the limitations of our findings, this fact suggests the relevance of the horizontal transfer of ARGs, the overuse of the various antibiotic classes, and the interspecific scope that it can have, which is essential for humans and the ecological stability of the environment. Nevertheless, it is recommended to analyze the plasmids detected in these strains that interfere with carrying resistance genes to understand better.

Regarding the individual analysis of ARGs by class of antibiotics (Figure 2), these seem to be proportional to their greater or lesser use in the livestock industry (Figure 1). Tetracyclines (*Tet* genes) are the most widely used class of antibiotics in the world, and one of those with the oldest industrial and clinical development (1950); penicillins (*blaTEM* genes) are the second most used class in the European Union [30]. Consequently, it is inferred and verified [31] that the greater the overuse of antibiotics, the more selective pressure is established to enhance antimicrobial resistance.

Currently, antibiotics in animal husbandry are used mainly to promote growth and not for therapeutic purposes, which generates continuous and biologically unnecessary overexposure to them [32]. Therefore, one of the measures with the most significant impact in preventing the spread of multi-resistance to antibiotics should be adequate control, legislation, and practical limitations regarding their sale and administration in humans and for small and large-scale veterinary use. Despite the existence of various and recent restrictions on its use as growth promotion in cattle raising (European Union, 2006; the United States, 2017; Brazil and China, 2020), its use in this sector in some countries is around 80% of the total antibiotics consumed [12,33,34]. Through the European Medicines Agency (EMA) and the Food and Drugs Administration (FDA), Europe and the United States are the political regions with the most stringent administration and regulation of the use of antibiotics [3,35].

The metagenomic study of six different habitats by Zhang et al. [36] reported the presence of 2561 ARGs, which confer resistance to 24 classes of antibiotics from 4572 samples. This work verified that 23.78% of the ARGs found are risky to health, particularly those that confer multi-resistance. Likewise, this comprehensive analysis exposed the distribution patterns of ARGs in the world. In contrast, First World regions such as Europe and the United States of America stood out for being the ones that concentrated them the most, a fact that concurs with being the countries with the highest livestock production.

In Mexico, there is evidence about the clinical importance and resistance to antibiotics associated with the bacteria discussed in the current article such that *K. pneumoniae* is reported as a producer of extended-spectrum beta-lactamases, which confers resistance to beta-lactams third-generation cephalosporins. Moreover, *E. faecalis* and *E. faecium*, have disclosed resistance to ampicillin (beta-lactam), imipenem (beta-lactam), and vancomycin (glycopeptide), as well as *E. coli* to quinolones [37]. In addition, no law governs the presence of antibiotics in meat products since the one that existed was dissolved in 2014; however, it does not currently encompass a prohibition on the use of antibiotics as growth promoters [38]. As a result, it is recommended to raise awareness among the relevant authorities, encouraging them to become involved in the situation and to take part in decision-making processes that influence the efficient and comprehensive containment of multidrug-resistant bacteria.

Ipso facto, despite the existence of bioinformatic research about ARGs with similar proceedings, this study constitutes an innovative investigation when comparing the resistance genes present in different bacterial species and by linking them up to the use of antibiotics for which they generate resistance; thus, it probably contributes to evidencing the relevance of these bacteria regarding antimicrobial resistance in the world.

CONCLUSION

Antibiotics continue to be widely used as growth enhancers in the livestock industry. This study provides a bioinformatic analysis examining the genetic diversity of strains of five major enteric and pathogenic bacteria isolated from porcine origins. In addition, evidence was provided that suggests an apparent correlation between the more outstanding livestock administration of the classes of antibiotics and the higher resistance reported against them by bacteria that contain ARGs against them. Despite the need for further confirmatory studies, it is strongly recommended that nations evaluate and promote their legislation on the veterinary use of antibiotics to limit the spread of antibiotic resistance.

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Authors' contributions

JRMV participated in the study design, analyzed the data, and drafted the manuscript. JRMV, YPP and VMC carried out the experimental part of the study and contributed substantially to the conception, design and analysis, acquisition, and interpretation of data. VMC, YPP, RCL, LEFR, RCRG, LEGD and LMCG were involved in the final drafting of the manuscript and revised it critically for important intellectual content. All authors read and approved the final manuscript.

Declaration of conflicting interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

REFERENCES

1. World Health Organization (2020). Antibiotic resistance. [https://www.who.int/news-room/fact-sheets/detail/antibiotic-resistance]
2. FAO (Food and Agriculture Organization of the United Nations) 2016. Drivers, dynamics, and epidemiology of antimicrobial resistance in animal production.
3. FDA (Federal and Drug Administration) 2021. Antimicrobials Sold or Distributed for Use in Food-Producing Animals.
4. FDA (Food and Agriculture Organization of the United Nations) 2022. Animal production. [https://www.fao.org/antimicrobial-resistance/key-sectors/animal-production/en/]
5. USDA (United States Department of Agriculture) 2022. Livestock and poultry: world markets and trade.
6. He Y, Yuan Q, Mathieu J, Stadler L, Senehi N, Sun R, Álvarez PJJ. Antibiotic resistance genes from livestock waste: occurrence, dissemination, and treatment. Npj Clean Water 2020, 3:4.
7. Law A, Solano O, Brown CJ, Hunter SS, Fagnan M, Top EM, Stalder T. Biosolids as a source of antibiotic resistance plasmids for commensal and pathogenic bacteria. Front Microbiol 2021, 12.
8. Guo MT, Yuan QB, Yang J. Distinguishing effects of ultraviolet exposure and chlorination on the horizontal transfer of antibiotic resistance genes in municipal wastewater. Environ Sci Technol 2015, 49: 5771-5778.
9. Han XM, Hu HW, Chen QL, Yang LY, Li HL, Zhu YG, Li XZ, Ma YB. Antibiotic resistance genes and associated bacterial communities in agricultural soils amended with different sources of animal manure. Soil Biol Biochem 2018, 126: 91-102.
10. Yuan QB, Zhai YF, Mao BY, Schwarz C, Hu N. Fates of antibiotic resistance genes in a distributed swine wastewater treatment plant. Water Environ Res 2019 [https://doi.org/10.1002/wer.1125]
11. Yang F, Han B, Gu Y, Zhang K. Swine liquid manure: A hotspot of mobile genetic elements and antibiotic resistance genes. Sci Rep 2020,10:15037.
12. Muurinen J, Richert J, Wickware CL, Richert B, Johnson TA. Swine growth promotion with antibiotics or alternatives can increase antibiotic resistance gene mobility potential. Sci Rep 2021, 11:5485.

13. Wang M, Donovan SM. Human microbiota-associated swine: current progress and future opportunities. ILAR J. 2015, 56(1):63-73.
14. Rose EC, Blikslager AT, Ziegler AL. Porcine models of the intestinal microbiota: the translational key to understanding how gut commensals contribute to gastrointestinal disease. Front Vet Sci 2022, 83:4598.
15. Wang C, Song Y, Tang N, Zhang G, Leclercq SO, Feng J. The shared resistome of human and pig microbiota is mobilized by distinct genetic elements. App Environ Microbiol 2020, 87(5): 01910-20.
16. Bortolaia V, Kaas RS, Ruppe E, Roberts MC, Schwarz S, Cattoir V, Philippon A, Allesoe RL, Rebelo AR, Florensa AF, Fagelhauer L, Chakraborty T, Neumann B, Werner G, Bender JK, Stingl K, Nguyen M, Coppens J, Xavier BB, Malhotra-Kumar S, … Aarestrup FM. ResFinder 4.0 for predictions of phenotypes from genotypes. J Antimicrob Chemother. 2020;75(12):3491-3500.
17. Johansson MHK, Bortolaia V, Tansirichaiya S, Aarestrup FM, Roberts AP, Petersen TN. 2021. Detection of mobile genetic elements associated with antibiotic resistance in *Salmonella enterica* using a newly developed web tool: MobileElementFinder. J Antimicrob Chemother 76:101–109.
18. Golubov A: Genome instability in bacteria: Causes and consequences. In: *Translational Epigenetics, Genome instability*. Academic Press; 2021, 73-90. ISBN 9780323856799. [DOI: 10.1016/b978-0-323-85679-9.00005-2].
19. Jarat C, Tokeeree, Y, Wattanakornsiri A. Antibiotic resistance genes (ARGs) in soil receiving swine wastes in Surin Province, Thailand. Environment Asia 2021, 14:2, 31–39.
20. Xiong W, Sun Y, Ding X, Wang M, Zeng Z. Selective pressure of antibiotics on ARGs and bacterial communities in manure-polluted freshwater-sediment microcosms. Front Microbiol 2015, 6:194.
21. Wyres KL, Holt KE. *Klebsiella pneumoniae* as a key trafficker of drug resistance genes from environmental to clinically important bacteria. Curr Opin Microbiol 2018, 45:131-139.
22. Effah CY, Sun T, Liu S, Wu Y. *Klebsiella pneumoniae*: an increasing threat to public health. Ann Clin Microbiol Antimicrob 2020, 19:1.
23. Jacoby GA, Strahilevitz J, Hooper DC. Plasmid-mediated quinolone resistance. Microbiol Spectr 2014, 2(2).
24. Davin-Regli A, Lavigne JP, Pagès JM. *Enterobacter* spp.: Update on taxonomy, clinical aspects, and emerging antimicrobial resistance. Clin Microbiol Rev 2019, 32:4.
25. Li J, Cao J, Zhu YG, Chen QL, Shen F, Wu Y, Xu S, Fan H, Da G, Huang RJ, Wang, J, Lorelei de Jesús A, Morawska L, Chan CK, Peccia J, Yao M. Global survey of antibiotic resistance genes in air. Environ Sci Technol 2018, 52: 10975-10984.
26. Capita R, Castaño-Arriba A, Rodríguez-Melcón C, Igrejas G, Poeta P, Alonso-Calleja C: Diversity, antibiotic resistance, and biofilm-forming ability of Enterobacteria isolated from red meat and poultry preparations. Microorganisms 2020, 8(8): 1226.
27. Torres C, Alonso CA, Ruiz-Ripa L, León-Sampedro R, Del Campo R, Coque TM. Antimicrobial resistance in *Enterococcus* spp. of animal origin. Microbiol Spectr 2018, 6(4): 6-24.
28. Hu Y, Yang X, Lv N, Liu F, Wu J, Lin IYC, Wu N, Weimer BC, Gao GF Liu Y, Zhu B. The bacterial mobile resistome transfer network connecting the animal and human microbiomes. Appl Environ Microbiol 2016, 82(22): 6672-6681.

29. Wang X, Xe Y, Cai H, Duan S, Song X, Wu Y, Fang T, Dong Q, Liu H. Growth and survival characteristics of *Salmonella enterica* regarding antibiotic resistance phenotypes. LWT 2021, 149: 111872

30. Ventola, C.L. (2015). The antibiotic resistance crisis. *P.T.*, 40(4): 277-283.

31. NHS (National Health Service). 2022. Antibiotic resistance. [https://www.nhs.uk/conditions/antibiotics/antibiotic-antimicrobial-resistance/#:~:text=The%20overuse%20of%20antibiotics%20in,Clostridium%20difficile%20(C]

32. He Y, Yuan Q, Mathieu J, Stadler L, Senehi N, Sun R, Álvarez PJJ. Antibiotic resistance genes from livestock waste: occurrence, dissemination, and treatment. Npj Clean Water 2020, 3:4.

33. World Health Organization. (2017). Stop using antibiotics in healthy animals to prevent the spread of antibiotic resistance. [https://www.who.int/news/item/07-11-2017-stop-using-antibiotics-in-healthy-animals-to-prevent-the-spread-of-antibiotic-resistance]

34. Ministério da Agricultura, Pecuária e Abastecimiento. 2020. Diário oficial da união - Seção 1. *Governo do Brasil*. [https://pesquisa.in.gov.br/imprensa/jsp/visualiza/index.jsp?jornal=515&pagina=6&data=23/01/2020]

35. European Medicines Agency. 2021. Sales of veterinary antimicrobial agents in 31 european countries in 2019 and 2020. [https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2019-2020-trends-2010-2020-eleventh_en.pdf]

36. Zhang Z, Zhang Q, Wang T, Xu N, Lu T, Hong W, Penuelas J, Gillings M, Wang M, Gao W, Qian H. Assessment of global health risk of antibiotics resistance genes. Nature 2022, 13:1553.

37. Rodríguez-Noriega E, León-Garnica G, Petersen-Morfín S, Pérez-Gómez HR, González-Díaz E, Morfín-Otero R. La evolución de la resistencia bacteriana en México, 1973-2013. Biomédica 2014, 34: 181-190.

38. Secretaría de Gobernación. (2014). Diario oficial de la federación. *Gobierno de México*. https://dof.gob.mx/nota_detalle.php?codigo=5363349&fecha=09/10/2014#gsc.tab=0

OTPORNOST ENTERIČNIH BAKTERIJA NA ANTIBIOTIKE U SVINJARSTVU: ISTRAŽIVANJE DISTRIBUCIJE GENA REZISTENTNOSTI

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Bakterije otporne na više lekova (MDR) značajno doprinose globalnoj krizi rezistencije na antibiotike, za koju se predviđa da će do 2050. godine usmrtiti više ljudi nego maligna oboljenja. Stočarska proizvodnja je faktor koji tome značajno doprinosi obzirom da je jedna od najbrže rastućih industrija, ali istovremeno ima štetan uticaj na životnu sredinu i zdravlje ljudi. Svinja je najšire uzgajana i konzumirana životinja za ishranu

ljudi na globalnom nivou, sa daljim trendom rasta. Dobijeni ostaci i proizvodi od mesa predstavljaju važan rezervoar gena otpornosti na antibiotike (ARG) koji se mogu preneti na ljude kroz konzumaciju, direktan kontakt, životnu sredinu ili loše rukovanje, što dovodi do relevantnih zoonotskih bolesti, posebno enteričnih. Neophodno je poznavati raznolikost, obilje i distribuciju ARG-a da biste imali bolju kontrolu i praćenje njihove disperzije. U ovoj studiji, bioinformatičkom analizom ispitani su ARG i mobilni genetski elementi (MGE) pet enteričnih i patogenih vrsta koje su obično prisutne u mikrobioti i svinja i ljudi. Ova analiza je pokazala da je 157 ARG raspoređeno u 1869 genoma pet bakterijskih vrsta, rangiranih od najveće do najniže raznolikosti ARG-a: *Klebsiella pneumoniae*, *Escherichia coli*, *Enterococcus faecium*, *Salmonella enterica* i *Enterococcus faecalis*. Ova studija doprinosi boljem upravljanju u primeni antibiotika, koji direktno utiču na zdravlje ljudi i životinja.

Supplementary file

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Klebsiella pneumoniae	19110124	Anal swab	swine	taxon:573	China:henan	2019-06
Klebsiella pneumoniae	606B	fecal swab	pig	taxon:573	Brazil: Minas Gerais State	2012
Klebsiella pneumoniae	1101433	feces	swine	taxon:573	Belgium	07-Feb-2018
Klebsiella pneumoniae	RGF4-1	feces	swine	taxon:573	China: Nantong, Jiangsu province	2019-05
Klebsiella pneumoniae	RGF15-2-1	feces	swine	taxon:573	China: Nantong, Jiangsu province	2019-05
Klebsiella pneumoniae	RGF105-1	feces	swine	taxon:573	China: Nantong, Jiangsu province	2019-05
Klebsiella pneumoniae	RGF140-1	feces	swine	taxon:573	China: Nantong, Jiangsu province	2019-05
Klebsiella pneumoniae	YTF18-2	feces	swine	taxon:573	China: Yangzhou, Jiangsu province	2020-07
Klebsiella pneumoniae	YTF53-1	feces	swine	taxon:573	China: Yangzhou, Jiangsu province	2020-07
Klebsiella pneumoniae	JP20	feces	Swine	taxon:573	China:Changchun	2018
Klebsiella pneumoniae	930	feces	pig	taxon:573	China: Hunan province	2019-10
Klebsiella pneumoniae	CVUAS 1701	feces	pig	taxon:573	Germany	2006
Klebsiella pneumoniae	CVUAS 11252	feces	Pork	taxon:573	Germany	2016
Klebsiella pneumoniae	CVUAS 11213	feces	Pork	taxon:573	Germany	2016
Klebsiella pneumoniae	CVUAS 10863.3	feces	pig	taxon:573	Germany	2017
Klebsiella pneumoniae	CVUAS 11744.2	feces	pig	taxon:573	Germany	2017
Klebsiella pneumoniae	CVUAS 30301	feces	pig	taxon:573	Germany	2017
Klebsiella pneumoniae	K-1L	feces	swine	taxon:573	China:Guangxi	2019-05-12
Klebsiella pneumoniae	ECCTRSRTH01	Rectal swab	Homo sapiens	taxon:573	Thailand: Nakhon Pathom	2016-06-15
Klebsiella pneumoniae	KPCTRSRTH08	Rectal swab	Homo sapiens	taxon:573	Thailand: Nakhon Pathom	2016-11-18
Klebsiella pneumoniae	PN030E4	nares	pig	taxon:573	Cameroon: Yaounde	Mar-2016
Klebsiella pneumoniae	PN089E1	nares	pig	taxon:573	Cameroon: Yaounde	Mar-2016
Klebsiella pneumoniae	PN085E1IA	nares	pig	taxon:573	Cameroon: Yaounde	Mar-2016

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Klebsiella pneumoniae	ZYST1	nares	pig	taxon:573	China	Sep-2017
Klebsiella pneumoniae subsp. pneumoniae	KPSW+01	Rectal swab	Homo sapiens	taxon:72407	Thailand: Lamphun	2015-03-08
Klebsiella pneumoniae subsp. pneumoniae	KPSW+02	Rectal swab	Homo sapiens	taxon:72407	Thailand: Lamphun	2015-03-08
Klebsiella pneumoniae subsp. pneumoniae	KPSW+03	Rectal swab	Homo sapiens	taxon:72407	Thailand: Lamphun	2015-03-08
Klebsiella pneumoniae subsp. pneumoniae	KPCTRSRTH02	Rectal swab	Swine	taxon:72407	Thailand: Chachoengsao	2016-08-11
Klebsiella pneumoniae subsp. pneumoniae	KPCTRSRTH06	Rectal swab	Swine	taxon:72407	Thailand: Nakhon Pathom	2016-10-04
Klebsiella pneumoniae subsp. pneumoniae	KPCTRSRTH07	Rectal swab	Swine	taxon:72407	Thailand: Nakhon Pathom	2016-11-04
Klebsiella pneumoniae subsp. pneumoniae	KPCTRSRTH09	Rectal swab	Swine	taxon:72407	Thailand: Nakhon Pathom	2016-12-18
Klebsiella pneumoniae subsp. pneumoniae	KPCTRSRTH01	Rectal swab	Swine	taxon:72407	Thailand: Nakhon Pathom	2016-08-01
Escherichia coli 2.3916	2.3916	Rectal swab	pig	taxon:869688	Thailand: Nakhon Pathom	2016-08-01
Escherichia coli 9.1649	9.1649	Rectal swab	pig	taxon:869685	Thailand: Nakhon Pathom	2016-08-01
Escherichia coli AI27	AI27	feces	pig	taxon:1089445	South Korea	2016-08-01
Escherichia coli B41	B41	feces	pig	taxon:869694	USA	1980
Escherichia coli	NCTC10674	feces	pig	taxon:562	USA	1980
Escherichia coli	pV01-15-R02-025-053	feces	pig	taxon:562	South Korea: Gyeongsangbuk-do	2015-12-31
Escherichia coli	STB20-1	feces	pig	taxon:562	China: Jiangsu	2017-08
Escherichia coli	SFE8	feces from pig	swine	taxon:562	China:Sichuan	2019-06-25
Escherichia coli	SCZE5	feces from pig	swine	taxon:562	China:Sichuan	2019-06-27

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	CP131_Sichuan	slaughterhouse	pig	taxon:562	China: Sichuan	Jul-2016
Escherichia coli	CP66-6_Sichuan	slaughterhouse	pig	taxon:562	China: Sichuan	Jul-2016
Escherichia coli	CP61_Sichuan	slaughterhouse	pig	taxon:562	China: Sichuan	Jul-2016
Escherichia coli	CP8-3_Sichuan	slaughterhouse	pig	taxon:562	China: Sichuan	Jul-2016
Escherichia coli	CP55_Sichuan	slaughterhouse	pig	taxon:562	China: Sichuan	Jul-2016
Escherichia coli	16EC	fecal swab	pig	taxon:562	China: Shenzhen	20-Jan-2018
Escherichia coli	SLPE	lung	swine	taxon:562	China: Changchun	2014
Escherichia coli	EC4	lung	swine	taxon:562	China	2016
Escherichia coli	EC6	lung	swine	taxon:562	China	2016
Escherichia coli	EC9	lung	swine	taxon:562	China	2017
Escherichia coli	EC10	lung	swine	taxon:562	China	2018
Escherichia coli	EC13	lung	swine	taxon:562	China	2016
Escherichia coli	K_EC180	feces	swine	taxon:562	South Korea	2019-07-17
Escherichia coli	PPECC42	lung	pig	taxon:562	China: Hunan	2006
Escherichia coli	ZWW-1	feces	pig	taxon:562	China: Yunnan	2018-04-12
Escherichia coli	ZB-1	feces	pig (Saba)	taxon:562	China: Yunnan	2018-03-16
Escherichia coli	GDB8P65M	feces	pig	taxon:562	China: Qinyuan City, Guangdong Province	02-Nov-2018
Escherichia coli	GDB8P70M	feces	pig	taxon:562	China: Qinyuan City, Guangdong Province	02-Nov-2018
Escherichia coli	GDB8P77M	feces	pig	taxon:562	China: Qinyuan City, Guangdong Province	02-Nov-2018
Escherichia coli	GDB8P75M	feces	pig	taxon:562	China: Qinyuan City, Guangdong Province	02-Nov-2018

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	GDB8P64M	feces	pig	taxon:562	China: Qinyuan City, Guangdong Province	02-Nov-2018
Escherichia coli	ZLWT	feces	pig	taxon:562	China:Beijing	2020-08-25T12:30:01Z
Escherichia coli	U90	intestinal tract	swine	taxon:562	China: Nanjing	2018
Escherichia coli	ZWW-1	feces	pig	taxon:562	China: Yunnan	2018-04-12
Escherichia coli	ZB-1	feces	pig	taxon:562	China: Yunnan	2018-03-16
Escherichia coli	ZB-1	feces	pig	taxon:562	China: Yunnan	2018-03-16
Escherichia coli	ZWW-1	feces	pig	taxon:562	China: Yunnan	2018-04-12
Escherichia coli	E41	liver	pig	taxon:562	China:Henan	2018-10
Escherichia coli	EA7	liver	pig	taxon:562	China:Henan	2016-10
Escherichia coli	EA2	liver	pig	taxon:562	China:Henan	2017-10
Escherichia coli	EA13	liver	pig	taxon:562	China:Henan	2017-10
Escherichia coli	ZTA15/00702EC	stool	porcine	taxon:562	Spain	2015
Escherichia coli	LZYWN_4	liver	swine	taxon:562	China:Yangling	2017-05-21
Escherichia coli	210221272	cecum	swine	taxon:562	USA:Illinois	17-May-2016
Escherichia coli	U74	intestinal tract	swine	taxon:562	China: Nanjing	2018
Escherichia coli	19-5	heart	swine	taxon:562	China:Yangling	2019-05-14
Escherichia coli	tcmA_3	liver	swine	taxon:562	China:Yangling	2016-10-11
Escherichia coli	TCM_B_2	intestinal and liver	swine	taxon:562	China:Yangling	2014-06-17
Escherichia coli	EC_J_9	intestine	swine	taxon:562	China:Yangling	2016-10-11
Escherichia coli	INpi59	intestine	pig	taxon:562	India: Karnataka	2019
Escherichia coli	PF1	intestine	pig	taxon:562	India: Mizoram	2016
Escherichia coli	NEP15	intestine	pig	taxon:562	India: Meghalaya	2015
Escherichia coli	PF10 32	intestine	pig	taxon:562	India: Mizoram	2016

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	NEP10Fa	intestine	pig	taxon:562	India: Meghalaya	2015
Escherichia coli	SEC470	intestine	pig	taxon:562	China	Oct-2016
Escherichia coli	B41M	intestine	pig	taxon:562	USA: South Dakota	Oct-2016
Escherichia coli	2012FS133	intestine	pig	taxon:562	China: Guangdong	2012
Escherichia coli	2012FS032	intestine	pig	taxon:562	China: Guangdong	2012
Escherichia coli	2016FS061	intestine	pig	taxon:562	China: Guangdong	2016
Escherichia coli	2010FS024	intestine	pig	taxon:562	China: Guangdong	2010
Escherichia coli	2013FS003	intestine	pig	taxon:562	China: Guangdong	2013
Escherichia coli	2010FS332	intestine	pig	taxon:562	China: Guangdong	2010
Escherichia coli	2010FS021	intestine	pig	taxon:562	China: Guangdong	2010
Escherichia coli	2012FS138	intestine	pig	taxon:562	China: Guangdong	2012
Escherichia coli	2005FS026	intestine	pig	taxon:562	China: Guangdong	2005
Escherichia coli	2010FS061	intestine	pig	taxon:562	China: Guangdong	2010
Escherichia coli	PJXMCRB120	porcine heart	pig	taxon:562	China: Jiaxing, Zhejiang	2020-07
Escherichia coli	PJXMCRO420	pork	pig	taxon:562	China: Jiaxing, Zhejiang	2020-07
Escherichia coli	PJXMCRW720	pork	pig	taxon:562	China: Jiaxing, Zhejiang	2020-07
Escherichia coli	YSP4-1	stool	swine	taxon:562	China: Jiangmen City, Guangdong Province	2017-07
Escherichia coli	XDXN3-3-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	YSB7-2	stool	swine	taxon:562	China: Jiangmen City, Guangdong Province	2017-07
Escherichia coli	G3P11-1	stool	swine	taxon:562	China: Guigang City, Guangxi Province	2017-08
Escherichia coli	GDXB17-2	stool	swine	taxon:562	China: Guigang City, Guangxi Province	2017-08
Escherichia coli	G3X12-2	stool	swine	taxon:562	China: Guigang City, Guangxi Province	2017-08

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	G3P8-2	stool	swine	taxon:562	China: Guigang City, Guangxi Province	2017-08
Escherichia coli	THX2-1	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07
Escherichia coli	XDP6-1-2	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	XDXN5-2-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	THP14-1	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07
Escherichia coli	XDP9-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	THX3-2	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07
Escherichia coli	XDP15-1-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	XDBN7-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	YSB3-1	stool	swine	taxon:562	China: Jiangmen City, Guangdong Province	2017-07
Escherichia coli	XFYP7-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	XDXN8-1-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	XFYP18-1	stool	swine	taxon:562	China: Heyuan City, Guangdong Province	2017-07
Escherichia coli	GQ65-1	stool	swine	taxon:562	China:NanningCity, Guangxi Province	2017-11
Escherichia coli	LHZ4-1	stool	swine	taxon:562	China: Zhangshu City, Jiangxi Province	2017-07
Escherichia coli	LHP6-1	stool	swine	taxon:562	China: Zhangshu City, Jiangxi Province	2017-07
Escherichia coli	THX8-2	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	HCP21-2	stool	swine	taxon:562	China: Jiangmen City, Guangdong Province	2017-07
Escherichia coli	LHZ2-1	stool	swine	taxon:562	China: Zhangshu City, Jiangxi Province	2017-07
Escherichia coli	DDX6-3	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07
Escherichia coli	DDX16-1	stool	swine	taxon:562	China: Nanping City, Fujian Province	2017-07
Escherichia coli	WQMCR	stool	pig	taxon:562	China: Shandong Province	Jul-2016
Escherichia coli	ECOR17	stool	pig	taxon:562	Indonesia	Jul-2016
Escherichia coli	ECOR45	stool	pig	taxon:562	Indonesia	Jul-2016
Escherichia coli	ECCTRSRTH02	Rectal swab	Homo sapiens	taxon:562	Thailand: Chachoengsao	2016-08-11
Escherichia coli	ECCTRSRTH04	Rectal swab	Swine	taxon:562	Thailand: Nakhon Pathom	2016-09-06
Escherichia coli	ECCTRSRTH03	Rectal swab	Swine	taxon:562	Thailand: Nakhon Pathom	2016-08-01
Escherichia coli	ECSW+04	Rectal swab	Homo sapiens	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECSW+06	Rectal swab	Homo sapiens	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECSW+05	Rectal swab	Homo sapiens	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECSW+08	Rectal swab	Swine	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECSW+07	Rectal swab	Swine	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECSW+09	Rectal swab	Homo sapiens	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECCTRSRTH05	Rectal swab	Swine	taxon:562	Thailand: Nakhon Pathom	2016-09-09
Escherichia coli	ECCTRSRTH06	Rectal swab	Swine	taxon:562	Thailand: Nakhon Pathom	2016-09-06
Escherichia coli	ECCTRSRTH07	Rectal swab	Swine	taxon:562	Thailand: Chachoengsao	2016-09-23
Escherichia coli	ECCTRSRTH09	Rectal swab	Swine	taxon:562	Thailand: Chachoengsao	2016-10-25

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	ECCTRSRTH10	Rectal swab	Homo sapiens	taxon:562	Thailand: Nakhon Pathom	2017-02-04
Escherichia coli	ECSW+12	Rectal swab	Homo sapiens	taxon:562	Thailand: Lamphun	2015-03-08
Escherichia coli	ECCTRSRTH11	Rectal swab	Homo sapiens	taxon:562	Thailand: Nakhon Pathom	2016-08-01
Escherichia coli	IBUN9016YEC	drag swab from a swine farm	pig	taxon:562	Colombia	20-Nov-2014
Escherichia coli	IBUN9096YEC	rectal swab	pig	taxon:562	Colombia	20-Nov-2014
Escherichia coli	ECCTRSRTH08	Rectal swab	Swine	taxon:562	Thailand: Nakhon Pathom	2016-10-04
Escherichia coli	13P477T	stool	pig	taxon:562	Hong Kong	Apr-2013
Escherichia coli	13P484A	stool	pig	taxon:562	Hong Kong	May-2013
Escherichia coli	13P460A	stool	pig	taxon:562	Hong Kong	Mar-2013
Escherichia coli	cq9	feces	pig	taxon:562	China:Chongqing	2012-07-01
Escherichia coli	13-220M	fecal sample	pig	taxon:562	France	2013
Escherichia coli	12-246M	fecal sample	pig	taxon:562	France	2012
Escherichia coli	12-269M	fecal sample	pig	taxon:562	France	2012
Escherichia coli	PN256E8	nares	pig	taxon:562	South Africa: Stanger	2016-10
Escherichia coli	D72	nares	pig	taxon:562	China: Henan	2017-10-01
Escherichia coli	PigCaeca_2	feces	pig	taxon:562	United Kingdom: Yorkshire and the Humber	2015
Escherichia coli	PigCaeca_1	feces	pig	taxon:562	United Kingdom: Yorkshire and the Humber	2015
Escherichia coli	FWSEC0629	manure from farm	porcine	taxon:562	United Kingdom: Yorkshire and the Humber	2015
Escherichia coli	E455	feces	pig	taxon:562	Hong Kong	2009

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	2ZN37-2	feces	pig	taxon:562	China: Guangdong	19-Mar-2018
Escherichia coli	2FT38-2	feces	pig	taxon:562	China: Guangdong	20-Jan-2018
Escherichia coli	2FT39	feces	pig	taxon:562	China: Guangdong	20-Jan-2018
Escherichia coli	PU-1	blood from piglet with acute sepsis	Swine	taxon:562	China: Jiangxi province	30-Nov-2013
Escherichia coli	912	feces	pig	taxon:562	Denmark	2003
Escherichia coli	RF14A	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF11	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF8A	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF8B	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF2C	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF6B	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF5A	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF6A2	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF2B	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF6A1	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF7A	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF12A	feces	pig	taxon:562	Ireland	2017
Escherichia coli	RF9	feces	pig	taxon:562	Ireland	2017
Escherichia coli	GDX7P323P	nasal swabs	pig	taxon:562	China: Gungdong	2017
Escherichia coli	I003p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G031p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	L020p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	L057p	fecal sample	pig	taxon:562	China: Shandong	2015-07

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	J041p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	H001p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	J034p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	H058p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G041p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G049p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G047p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G029p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G009p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G017p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G009p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G008p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G007p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G006p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G005p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	L001p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G003p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	F060p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	F056p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	F037p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	E036p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	F037p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	E024p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	D010p	fecal sample	pig	taxon:562	China: Shandong	2015-07

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli	C023p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	D008p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	B013p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	C017p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	C013p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	B010p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	A062p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	A053p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	A043p2	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	A043p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	H022p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	G006p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	E040p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	E024p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	D026p	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	B013p1	fecal sample	pig	taxon:562	China: Shandong	2015-07
Escherichia coli	1916D18	feces	swine	taxon:562	China:Henan	2019-07-01
Escherichia coli	1916D6	feces	swine	taxon:562	China:Henan	2019-07-01
Escherichia coli	1919D3	feces	swine	taxon:562	China:Henan	2019-07-01
Escherichia coli	1919D62	feces	swine	taxon:562	China:Henan	2019-07-01
Escherichia coli	A/10	feces	pig	taxon:562	China: Lufeng County, Chuxiong City, Yunnan	2017-11-05
Escherichia coli	PE15	feces	pig	taxon:562	China: Henan	2018-04-01
Escherichia coli UMNF18	UMNF18	lesion swab of diarrheal isolate	porcine	taxon:1050617	USA	2007

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	UMNK88	porcine neonatal diarrhea	porcine	taxon:696406	USA	2007
Escherichia coli UMNK88	51892776	not known	porcine	taxon:58097	United Kingdom	1970/1980
Escherichia coli UMNK88	653308	not known	porcine	taxon:58097	United Kingdom	1970/1980
Escherichia coli UMNK88	276608	not known	porcine	taxon:58097	United Kingdom	1970/1980
Escherichia coli UMNK88	V22	not known	porcine	taxon:85569	United Kingdom:Scotland	1994
Escherichia coli UMNK88	V35	not known	porcine	taxon:85569	United Kingdom:Scotland	1994
Escherichia coli UMNK88	V02	not known	porcine	taxon:85569	United Kingdom:Scotland	1990
Escherichia coli UMNK88	V39	not known	porcine	taxon:85569	United Kingdom:Scotland	1994
Escherichia coli UMNK88	V40	not known	porcine	taxon:85569	United Kingdom:Scotland	1996
Escherichia coli UMNK88	V120	not known	porcine	taxon:85569	United Kingdom:Scotland	2007
Escherichia coli UMNK88	V125	not known	porcine	taxon:85569	United Kingdom:Scotland	2009
Escherichia coli UMNK88	V76	not known	porcine	taxon:85569	United Kingdom:Scotland	1993
Escherichia coli UMNK88	V85	not known	porcine	taxon:85569	United Kingdom:Scotland	1994
Escherichia coli UMNK88	V111	not known	porcine	taxon:85569	United Kingdom:Scotland	2001

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	V113	not known	porcine	taxon:85569	United Kingdom:Scotland	2003
Escherichia coli UMNK88	EWV9	not known	porcine	taxon:85569	United Kingdom:England	2002
Escherichia coli UMNK88	EWV5	not known	porcine	taxon:85569	United Kingdom:England	2003
Escherichia coli UMNK88	D15-043619	lung	porcine	taxon:90371	USA: Minnesota	2015
Escherichia coli UMNK88	s09	Mesenteric Lymph Node	swine	taxon:90371	Brazil	2015-08-04
Escherichia coli UMNK88	s07	Mesenteric Lymph Node	swine	taxon:90371	Brazil	2015-08-04
Escherichia coli UMNK88	s08	Mesenteric Lymph Node	swine	taxon:595	Brazil	2015-08-04
Escherichia coli UMNK88	07CR553	Mesenteric Lymph Node	pig	taxon:28144	France: Brittany	2007
Escherichia coli UMNK88	ISU-SAL240-15	intestinal contents	swine	taxon:440524	USA	2015
Escherichia coli UMNK88	ISU-SAL244-16	intestinal contents	swine	taxon:90371	USA	2016
Escherichia coli UMNK88	ISU-SAL245-16	intestinal contents	swine	taxon:440524	USA	2016
Escherichia coli UMNK88	ISU-SAL243-14	intestinal contents	swine	taxon:90371	USA	2014
Escherichia coli UMNK88	ISU-SAL242-16	intestinal contents	swine	taxon:28144	USA	2016
Escherichia coli UMNK88	s06	Mesenteric Lymph Node	Swine	taxon:29472	Brazil	2015-03-19

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	s04	Mesenteric Lymph Node	Swine	taxon:29472	Brazil	2015-03-19
Escherichia coli UMNK88	s05	Mesenteric Lymph Node	Swine	taxon:29472	Brazil	2015-03-19
Escherichia coli UMNK88	s03	Mesenteric Lymph Node	swine	taxon:353569	Brazil	2015-03-17
Escherichia coli UMNK88	s02	Mesenteric Lymph Node	swine	taxon:353569	Brazil	2014-09-12
Escherichia coli UMNK88	42	Mesenteric Lymph Node	swine	taxon:90371	Brazil: Rio Grande do Sul	2000
Escherichia coli UMNK88	CVCC 3383	liver	pig	taxon:119912	China: Harbin	2019-05-12
Escherichia coli UMNK88	CVCC 503	intestine	pig	taxon:119912	China: Beijing	2019-05-12
Escherichia coli UMNK88	CICC 21501	intestine	pig	taxon:119912	Bulgaria	2019-04-15
Escherichia coli UMNK88	CVCC 79102	intestine	pig	taxon:119912	China: Jiangsu	2019-05-12
Escherichia coli UMNK88	STy015	slaughterhouse	swine	taxon:90371	Brazil	2015
Escherichia coli UMNK88	SE142	swine	swine	taxon:611	USA: Indiana	2002
Escherichia coli UMNK88	SE143	swine	swine	taxon:611	USA: Minnesota	2002
Escherichia coli UMNK88	SE146	swine	swine	taxon:611	USA: Minnesota	2002
Escherichia coli UMNK88	SE144	swine	swine	taxon:611	USA: Minnesota	2009

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	798	swine	porcine	taxon:1008297	USA: Minnesota	2009
Escherichia coli UMNK88	SA_078	intestinal content	Swine	taxon:611	Brazil: Lajeado	2015
Escherichia coli UMNK88	SA_074	intestinal content	Swine	taxon:611	Brazil: Lajeado	2015
Escherichia coli UMNK88	SA_041	intestinal content	Swine	taxon:611	Brazil: Lajeado	2015
Escherichia coli UMNK88	SCMYP1	liver	swine	taxon:211968	China: Mianyang	2017-09-23
Escherichia coli UMNK88	SE471	liver	swine	taxon:90371	USA	1999
Escherichia coli UMNK88	SE89	liver	swine	taxon:108619	USA: UT	2001
Escherichia coli UMNK88	SE93	liver	swine	taxon:108619	USA: KS	2002
Escherichia coli UMNK88	SA20082869	liver	porcine	taxon:2583588	Canada: Quebec	2008-06-17
Escherichia coli UMNK88	SE470	liver	swine	taxon:90371	USA	1999
Escherichia coli UMNK88	D97C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	D67H1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	A46HEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B10CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	E76H1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	A50CEB2	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	D79C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	D55C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C72CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C72CEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C72CEB22	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	F93CEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	E94H1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B53HEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B3CEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C73CEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C73CEB22	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C66CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	D51HEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C93C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	E77C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C93CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B15CEB12	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C73CEB23	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B24HEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C73CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	C44C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	E90C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	SH16SP46	pork	pig	taxon:90371	China: Wuhan	2016-10
Escherichia coli UMNK88	F28H2	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	F32H1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	E6C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Escherichia coli UMNK88	F28C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	B70CEB11	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	D51C1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	A22HEB21	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	A97HEB1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	A20HEB1	pork	swine	taxon:90371	USA: TX	25-Mar-2015
Escherichia coli UMNK88	SHSN006	heart	pig	taxon:1324340	China: Shanghai	2008
Enterococcus faecalis D32	D32	feces	pig	taxon:1206105	Denmark	2001
Enterococcus faecalis EnGen0060	7330257-1	feces	pig	taxon:1151201	Denmark	2001
Enterococcus faecalis EnGen0071	7430416-3	feces	pig	taxon:1151207	Denmark	2001
Enterococcus faecalis EnGen0072	7430821-4	feces	pig	taxon:1151208	Denmark	2001
Enterococcus faecalis EnGen0078	7330082-2	feces	pig	taxon:1151198	Denmark	2001
Enterococcus faecalis EnGen0079	7330245-2	feces	pig	taxon:1151200	Denmark	2001
Enterococcus faecalis EnGen0080	7330112-3	feces	pig	taxon:1151199	Denmark	2001

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Enterococcus faecalis EnGen0081	7330259-5	feces	pig	taxon:1151202	Denmark	2001
Enterococcus faecalis EnGen0082	7330948-5	feces	pig	taxon:1151204	Denmark	2001
Enterococcus faecalis EnGen0083	7430275-3	feces	pig	taxon:1151205	Denmark	2001
Enterococcus faecalis EnGen0084	7430315-3	feces	pig	taxon:1151206	Denmark	2001
Enterococcus faecalis EnGen0086	HEF39	feces	pig	taxon:1157368	Denmark	2001
Enterococcus faecalis	ES-1	feces	pig	taxon:1351	China:Nanjing	2017
Enterococcus faecalis	L11	Rectal swab	Swine	taxon:1351	Brazil: Distrito Federal	2013
Enterococcus faecalis	L10	Rectal swab	Swine	taxon:1351	Brazil: Sao Paulo	2013
Enterococcus faecalis	L13	Rectal swab	Swine	taxon:1351	Brazil: Santa Catarina	2013
Enterococcus faecalis	L16	Rectal swab	Swine	taxon:1351	Brazil: Mato Grosso	2013
Enterococcus faecalis	L18	Rectal swab	Swine	taxon:1351	Brazil: Santa Catarina	2013
Enterococcus faecalis	L21	Rectal swab	Swine	taxon:1351	Brazil: Parana	2013
Enterococcus faecalis	L17	Rectal swab	Swine	taxon:1351	Brazil: Parana	2013
Enterococcus faecalis	L9	Rectal swab	Swine	taxon:1351	Brazil: Distrito Federal	2013
Enterococcus faecalis	L12	Rectal swab	Swine	taxon:1351	Brazil	2013
Enterococcus faecalis	Enfs85	faecal sample	pig	taxon:1351	Malaysia	2012
Enterococcus faecalis	P.En250	faecal sample	pig	taxon:1351	Malaysia	2012
Enterococcus faecalis	P. En090	faecal sample	pig	taxon:1351	Malaysia	2012
Enterococcus faecalis	IBUN9046YE	rectal swab	pig	taxon:1351	Colombia	20-Nov-2014
Enterococcus faecalis	C25	faecal swab	Pig	taxon:1351	China: Sichuan	2017-11

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Enterococcus faecalis	C54	faecal swab	Pig	taxon:1351	China: Sichuan	2017-11
Enterococcus faecalis	L15	Rectal swab	swine	taxon:1351	Brazil: Distrito Federal	2013
Enterococcus faecalis	L8	Rectal swab	Swine	taxon:1351	Brazil: Sao Paulo	2013
Enterococcus faecalis	L14	Rectal swab	Swine	taxon:1351	Brazil: Parana	2013
Enterococcus faecium EnGen0008	E0688	Rectal swab	Swine	taxon:1138887	Brazil: Parana	2013
Enterococcus faecium EnGen0014	E0679	Rectal swab	Swine	taxon:1138885	Brazil: Parana	2013
Enterococcus faecium EnGen0019	E0680	Rectal swab	Swine	taxon:1138886	Brazil: Parana	2013
Enterococcus faecium EnGen0124	7230532-1	Rectal swab	Swine	taxon:1157418	Brazil: Parana	2013
Enterococcus faecium EnGen0125	7330381-1	Rectal swab	Swine	taxon:1157419	Brazil: Parana	2013
Enterococcus faecium EnGen0126	7330519-3	Rectal swab	Swine	taxon:1157421	Brazil: Parana	2013
Enterococcus faecium EnGen0128	9730219-1	Rectal swab	Swine	taxon:1157429	Brazil: Parana	2013
Enterococcus faecium EnGen0129	7330884-2	Rectal swab	Swine	taxon:1157423	Brazil: Parana	2013
Enterococcus faecium EnGen0130	841V03	Rectal swab	Swine	taxon:1157425	Brazil: Parana	2013
Enterococcus faecium EnGen0132	9730357-1	Rectal swab	Swine	taxon:1157430	Brazil: Parana	2013
Enterococcus faecium EnGen0133	7330446-2	Rectal swab	Swine	taxon:1157420	Brazil: Parana	2013

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Enterococcus faecium EnGen0134	7430166-3	Rectal swab	Swine	taxon:1157424	Brazil: Parana	2013
Enterococcus faecium EnGen0135	7330614-1	Rectal swab	Swine	taxon:1157422	Brazil: Parana	2013
Enterococcus faecium EnGen0136	9731349-1	Rectal swab	Swine	taxon:1157431	Brazil: Parana	2013
Enterococcus faecium EnGen0137	9731352-4	Rectal swab	Swine	taxon:1157432	Brazil: Parana	2013
Enterococcus faecium EnGen0138	9830091-5	Rectal swab	Swine	taxon:1157433	Brazil: Parana	2013
Enterococcus faecium EnGen0140	9830512-2	Rectal swab	Swine	taxon:1157435	Brazil: Parana	2013
Enterococcus faecium EnGen0142	9830565-4	Rectal swab	Swine	taxon:1157437	Brazil: Parana	2013
Enterococcus faecium EnGen0145	9930238-2	Rectal swab	Swine	taxon:1157440	Brazil: Parana	2013
Enterococcus faecium EnGen0146	9931110-4	Rectal swab	Swine	taxon:1157441	Brazil: Parana	2013
Enterococcus faecium EnGen0147	A17 Sv1	Rectal swab	Swine	taxon:1157442	Brazil: Parana	2013
Enterococcus faecium EnGen0148	E8sv3	Rectal swab	Swine	taxon:1157443	Brazil: Parana	2013
Enterococcus faecium EnGen0156	S658-3	Rectal swab	Swine	taxon:1157451	Brazil: Parana	2013
Enterococcus faecium EnGen0185	HF50104	Rectal swab	Swine	taxon:1157480	Brazil: Parana	2013
Enterococcus faecium EnGen0186	HF50105	Rectal swab	Swine	taxon:1157481	Brazil: Parana	2013

Organism	Strain	Isolation_source	Host	db_xref	Country	Collection_ date
Enterococcus faecium EnGen0187	HF50106	Rectal swab	Swine	taxon:1157482	Brazil: Parana	2013
Enterococcus faecium EnGen0188	HF50203	Rectal swab	Swine	taxon:1157483	Brazil: Parana	2013
Enterococcus faecium EnGen0189	HF50204	Rectal swab	Swine	taxon:1157484	Brazil: Parana	2013
Enterococcus faecium EnGen0190	HF50215	Rectal swab	Swine	taxon:1157485	Brazil: Parana	2013
Enterococcus faecium	70-61-7	Rectal swab	pig	taxon:1352	Denmark	2011
Enterococcus faecium	70-8-2	Rectal swab	pig	taxon:1352	Denmark	2011
Enterococcus faecium	CICYT-205	Rectal swab	pig	taxon:1352	Spain	2011
Enterococcus faecium	70-7-8	Rectal swab	pig	taxon:1352	Denmark	2011
Enterococcus faecium	70-36-8	Rectal swab	pig	taxon:1352	Denmark	2011
Enterococcus faecium	70-40-11	Rectal swab	pig	taxon:1352	Denmark	2011
Enterococcus faecium	Sw348	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019
Enterococcus faecium	Sw342	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019
Enterococcus faecium	Sw290	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019
Enterococcus faecium	Sw292	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019
Enterococcus faecium	SW245	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019
Enterococcus faecium	Sw253	Rectal swab	pig	taxon:1352	Switzerland: Zurich	2019