Int.J.Curr.Microbiol.App.Sci (2024) *13*(08): 208-215

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 13 Number 8 (2024)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2024.1309.023

Detection of the *tet A* Resistance Gene in Broad Spectrum Beta-lactamase (ESBL)-Producing *Escherichia coli* Strains Isolated from Faecal Waste of Pigs on a Farm in Abidjan, Côte d'Ivoire

Kouadio Kouamé Innocent[1, 5]*, Kouamé Amenan Margueritte[2, 5], Tra Bi Youan Charles[1, 5], Ouattara Mohamed Baguy[3], Kpoda Stéphane[4], Guessennd-Kouadio Nathalie[3] and Aka Boko[5]

[1]Laboratory of Molecular biology and Microbiology, Department of Technology and Foods Sciences, Nangui Abrogoua University, Abidjan, 02 BP 801 Abidjan 02, Côte d'Ivoire
[2]Laboratory of Biochemistry and Tropical Products Processing, Department of Technology and Foods Sciences, Nangui Abrogoua University, Abidjan, 02 BP 801 Abidjan 02, Côte d'Ivoire
[3]National Reference Center for Antibiotics, Department of Bacteriology and Virology, Pasteur Institute, Abidjan, 01 BP 490 Abidjan 01, Côte d'Ivoire
[4]Laboratory of Applied and Nutritional Sciences, Ouaga I Professor Joseph KI-ZERBO University, Ouagadougou, Burkina Faso
[5]Laboratory of Biomass-Energy, Institute for Research on New Energies (IREN), Nangui Abrogoua University, Abidjan, Côte d'Ivoire

**Corresponding author*

Keywords

tet A resistance gene, Tetracycline, Faecal waste, Manure, *E. coli*

Article Info

Received:
05 July 2024
Accepted:
24 August 2024
Available Online:
10 September 2024

A B S T R A C T

The aim of the study was to detect the *tet A* gene coding for tetracycline resistance in ESBL-producing strains of Escherichia coli isolated from faecal waste from pigs used as manure. Thirty-five *E. coli* strains containing genes coding for ESBL resistance were used in the study. These strains were isolated from faecal waste from pigs used to produce manure. They were identified using biochemical tests. An antibiotic susceptibility test was carried out using the agar diffusion antibiogram technique to determine antibiotic resistance profiles and confirmed the presence of ESBL production. PCR was carried out to search for the *tet A* gene coding for tetracycline resistance in strains likely to produce ESBL. Antibiogram results of the 35 *E. coli* strains confirmed the ESBL phenotype. These strains were resistant to several antibiotics. The rate of resistance to tetracycline was 100%. All these strains harboured the *tet A* resistance gene. They also presented five genetic combinations, the most predominant of which was *bla* $_{TEM}$, *tet A* with a frequency of 38%. The detection of tet A resistance genes in *E. coli* represents a risk to public health. Resistance genes circulating in the digestive flora of farm animals therefore need to be monitored to prevent their spread.

Introduction

The agricultural sector, particularly livestock farming, is most often called upon by public policies to meet these needs. Indeed, whether formal or informal, livestock farming is a genuine means of improving people's living conditions (Gomgnimbou *et al.,* 2014). The importance of this activity in Côte d'Ivoire, particularly in the peri-urban areas of Abidjan, remains considerable. This is because of its contribution to improving food security, the adoption of animal traction and the increase in soil fertility through the use of manure produced from faeces as a biofertiliser (Blanchard, 2010). Although livestock farming has development implications, it also raises many concerns about the environment and its impact on health (FAO, 2006). Manure management and livestock rearing close to homes is one of the main issues (Manyi-Loh *et al.,* 2016). Through husbandry, storage and spreading practices, manure tends to concentrate numerous components likely to cause disease in both humans and animals. Whether microbes, bad odours, water and soil pollution factors, greenhouse gases, poor manure management poses a real threat to public health (Bagalwa *et al.,* 2013). This is reflected in an increase in the incidence of certain digestive diseases (Mali.MEADR, 2015).

Untreated manure used as fertiliser by market gardeners to improve their crop yields contains high numbers of potentially pathogenic bacteria (Hutchison *et al.,* 2004). These pathogenic bacteria include *E. coli* that are multi-resistant to antibiotics, commensal bacteria in the digestive tract of farm animals that can transfer resistance genes to bacteria in the intestinal flora of humans via food and in the environment via hospital effluents and waste water, posing a real risk to public health (Phillips and Casewell, 2004; Sanders *et al.,* 2011). Tetracycline, an antibiotic widely used in animal husbandry in general and in pigs in particular, can prevent and cure infectious diseases and promote daily weight gain (Mc Ewen, 2002). However, the overuse of these antibiotics in livestock farming has led to the emergence of bacteria resistant to tetracycline (Agerso and Sandvang, 2005; Stine *et al.,* 2007). The tetracycline resistance genes expressed by efflux proteins most often detected in faecal isolates from pigs are the *tet A* resistance genes (EFSA, 2011; Agersø and Aarestrup, 2013). In Côte d'Ivoire, the impact of manure management using animal faecal waste and the possible risks to public health are poorly known and documented. In this respect, farming practices and the management of manure from animal faeces in general, and pig faeces in particular, represent a real public health risk. To facilitate microbiological control of manure due to the health impact of antibiotic resistance in bacteria isolated from this waste, the aim of this study was to detect the *tet A* resistance gene in *E. coli* isolated from pig faecal waste used as manure.

Materials and Methods

Identification of bacterial strains

In order to confirm the identification of ESBL-producing *E. coli* isolates carrying the *bla* $_{CTX-M}$, *bla* $_{TEM}$ and *bla* $_{SHV}$ genes previously detected in a previous study, specific biochemical characteristics were investigated. The strains were taken from deep agar plates and subcultured on Mac-Conkey medium and ordinary medium in order to obtain pure cultures after 24 h of incubation at 37°C. Presumptive *E. coli* isolates were identified using a biochemical test. Biochemical identification was carried out by testing for catalase, citochrome oxidase C, urease and indole, Simmons citrate utilisation, glucose and lactose, gas production, hydrogen sulphide, lysine deaminase (LDA) and lysine decarboxylase (LDC) (Farmer, 1999).

Antibiotic susceptibility test

Antibiotic susceptibility testing of these identified *E. coli* strains was carried out using the Muller-Hinton agar diffusion method (Bio-rad, Marne-la-coquette, France). Fourteen (14) antibiotic discs (Bio-rad, Marne-la-coquette, France) were used in the study: Amoxicillin (25 µg), Amoxicillin + clavulanic acid (20/10 µg), Ceftriaxone (30 µg), Cefoxitin (30 µg), Ciprofloxacin (5 µg), Nalidixic acid (30 µg), Tetracycline (30 µg), Trimethoprim / Sulfamethoxazole (1.25/23.75 µg), Chloramphenicol (30 µg), Gentamicin (10 µg), Kanamycin (30 µg), Streptomycin (10 µg), Colistin (50 µg).

Detection of the *tet A* gene encoding tetracycline resistance

E. coli strains that exhibited extended-spectrum Betalactamase phenotypes following antibiotic susceptibility testing were used to screen for the *tet A* gene encoding tetracycline resistance. Conventional PCR was used to detect *tet A* genes encoding tetracycline resistance. Bacterial DNA was extracted using the heat shock technique. The final volume of the reaction

mixture was 50 µL and comprised 5µL of coloured buffer (5X Green GoTaq®), 5µL of uncoloured buffer (5X Colorless GoTaq®), 30.3 µL of ultrapure water (Nuclease- Free Water, Promega, USA), 3µL of MgCl2 (25 mM), 0.5 µL of DNTP (10 mM), 0.5 µL of Forward primer (10 mM), 0.5 µL of Reverse primer (10 mM), 0.2 µL of Taq polymerase (GoTaq®, Promega) and 5 µL of DNA to be amplified. The gene tet A primer used was Forward *tet A* F-5'TTGTTCCTGAAGTGCCAGTAA-3'and Reverse *tet A* R-5'GACGTCGTTCGAGTGAACC AGA-3' with an amplicon size of 370 base pairs (Sunde and Sorum, 2001). The amplification conditions carried out in the thermal cycler (GeneAmp PCR System 9700, Applied Biosystems) are summarised in Table 1. PCR products were analysed by 1.5% agarose electrophoresis (Invitrogen). The reference strain *E. coli* CIP/ RP4 (Institut Pasteur de Paris) carrying the *tet A* gene was used as a positive control in the PCR test.

Results and Discussion

All 35 isolates selected exhibited biochemical characteristics specific to *E. coli* (Table 2). Resistance rates to the different antibiotics determined during antibiotic susceptibility testing are presented in Table 3**.** The ESBL phenotype of the 35 strains was confirmed by the assay and the resistance rates were as follows. Resistance to tetracycline and ceftriaxone was 100%, 90% to streptomycin and amoxicillin, 80% to cotrimoxazole, 70% to gentamicin, kanamycin and amoxicillin + clavulanic acid, 20% to ciprofloxacin and nalidixic acid, 10% to chloramphenicol and 0% to colistin. The 35 strains analysed by PCR showed the presence of the *tet A* resistance gene (100%) with bands 370 base pairs in size (Figure 1). The strains harboured a specific combination of genes: *bla* $_{TEM}$, *bla* $_{CTX-M}$, *bla* $_{SHV}$, *tet A*. Five combinations were detected for the same resistance phenotype. The gene combination *bla* $_{TEM}$, *tet A* was the most predominant with a frequency of 38% (Table 4).

During the study, the 35 ESBL-producing *E. coli* strains isolated from the faecal waste of pigs were all resistant to tetracycline and ceftriaxone, with resistance rates of 100%, 90% to amoxicillin and streptomycin, 80% to cotrimoxazole and 70% to gentamicin. This high rate of resistance to tetracycline during the present study could be justified by the abundant use of this antibiotic in our pig farms. The very high rate of resistance to tetracycline and more than five other antibiotics has also been reported by several authors in studies conducted on *E. coli* strains *E. coli* of animal origin throughout the world (Blanco *et al.,* 1997; Muhammad *et al.,* 2009; Karczmarczyk *et al.,* 2011). In France, a study carried out on the effect of antibiotic use on the resistance of *E. coli* of porcine origin on a farm in Nantes also reported very high rates of resistance to tetracycline, which was 99%, similar to that in the present study (Belloc *et al.,* 2005). Other studies have reported a high rate of tetracycline resistance in *E. coli* strains of animal origin, but lower than that determined in the present study. In India, high resistance to tetracycline and cotrimoxazole (88% and 83% respectively) has been reported in commensal isolated from chicken faeces (Balasubramaniam *et al.,* 2014). These results are also in line with other studies carried out in Toulouse, another French city, where resistance to tetracycline was 90%, streptomycin (82%), chloramphenicol (32%), trimethoprim (58%) and sulphonamide (63%) in *E. coli* from piglets treated with ampicillin (Bibbal *et al.,* 2009). Enne *et al.,* (2007) in Great Britain also detected a tetracycline resistance rate of 78%, 30.8% to cotrimoxazole, 37.5% to streptomycin and 25.4% to ampicillin in *E. coli* strains isolated from a cattle and sheep farm. Daini and Adesemowo (2008) in a study in Nigeria reported tetracycline resistance of 88% and gentamicin resistance of 54% in *E. coli* strains of clinical origin. The majority of studies revealing the high prevalence of tetracycline resistance in *E. coli* isolated from faecal waste from pigs and in the present study showed that tetracycline is one of the most widely used antibiotics in the animal world (McEwen, 2002). This is also reported in an epidemiological study on trends in the use of antibiotics in the pig industry, which revealed that tetracycline was the leading antibiotic (Anses-ANMV, 2014). During the study, all 35 ESBL-producing *E. coli* strains showed the presence of the *tet A* gene (100%). This prevalence of the *tet A* gene is sometimes at odds with other results reported by several authors.

In England, a study carried out on a farm reported a 17.5% prevalence of the *tet A* gene in *E. coli* isolated from pigs and sheep (Enne *et al.,* 2007). In India, another study conducted on commensal *E. coli* strains of avian origin reported a 29% prevalence of the *tet A* gene.

Strains that did not show the presence of the *tet A* resistance gene could contain other genes encoding resistance to tetracycline, such as the *tet B, tet C* and *tet D* genes, or genes encoded by ribosomal protection, such as the *tet M, tet O*, *tet Q* and *tet S* genes.

Table.1 PCR amplification conditions for the *tet A* gene

Amplification steps	Conditions temperature/duration *tet A* Gene
Initial denaturation	95°C / 1 min
Cyclic denaturation	95°C / 30 s
Hybridization	50°C / 30 s
Cyclic elongation	72°C / 20 s
Final elongation	72°C / 7 min
Number of cycles	25

Source: Sunde and Sorum, 2001

Table.2 Biochemical characteristics determined to confirm the identification of *E. coli* strains

GRAM negative **Mobile peritrich**
Pink colonies surrounded by precipitated bile salt halo on MacConkey agar
Positive in indole test
Positive for urea hydrolysis
Negative in citrate test
Negative in oxidase test
Positive for glucose fermentation
Positive for lactose femenation
Negative hydrogen sulphide
Positive gas production **Positive decarboxylase lysine** **Negative desaminase lysine**

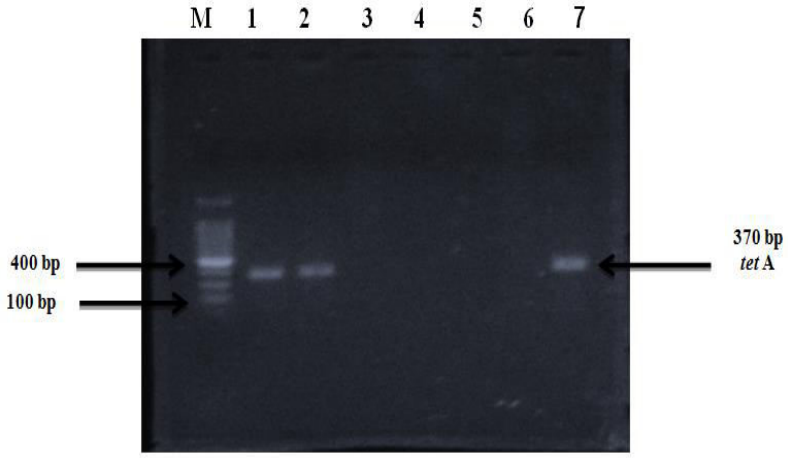
Table.3 Antibiotic resistance rate of ESBL-producing *E. coli* strains isolated from pig faecal Waste

Antibiotics (concentration µg)	Number of ESBL-producing *E. coli* isolates (N=35)	Resistance rate (%)
Tetracycline (30)	35	100
Cotrimoxazole (1.25/23.75)	28	80
Gentamicin (10)	25	70
Kanamycin (30)	25	70
Streptomycin (10)	32	90
Ceftriaxone (30)	35	100
Amoxicillin (25)	32	90
Ciprofloxacin (5)	7	20
Nalidixic acid (30)	7	20
Chloramphenicole (30)	3	10
Amoxicillin + clavulanic acid (20/10)	25	70
Colistin (50)	0	0

Table.4 Distribution of resistance genes detected in ESBL-producing *E. coli* strains

Number of ESBL-producing *E. coli* (n = 35)	Profile of resistance genes detected
13 (38%)	*tet A*, *bla* $_{TEM}$,
7 (20 %)	*tet A*, *bla* $_{TEM}$, *bla* $_{CTX-M}$
7 (20%)	*tet A*, *bla* $_{TEM}$, *bla* $_{CTX-M,}$ *bla* $_{SHV}$
4 (11%)	*tet A*, *bla* $_{TEM}$, *bla* $_{SHV}$
4 (11%)	*tet A*, *bla* $_{CTX-M,}$

Figure.1 Electrophoretic profile of *tet* A gene amplification product



Line M: Molecular weight marker (Benchtop, 100 bp DNA Ladder, USA);
Line 2 and 7: strains analysed harboring *tet A* gene
Line 1: Positive control strain

On the other hand, a high prevalence of 97.6% of the *tet A* resistance gene compared with the present study was reported by Hu *et al.,* (2013) in a study carried out in China on *E. coli* isolated from ducks. This high prevalence of the *tet A* resistance gene, amounting to 97.7% in *E. coli* of animal origin, has been reported elsewhere in several countries (Lanz *et al.,* 2003; Shwaiger *et al.,* 2010; Zhang *et al.,* 2010).

The presence of plasmid-borne *tet A* resistance genes detected in these strains of *E. coli* of animal origin could therefore constitute a health risk for consumers as they would be capable of transferring the gene to commensal bacteria that form part of the human intestinal flora via the food chain or the environment (Wegener *et al.,* 1999). Koo and Woo (2011) reported in a study that 98.3% of *E. coli* carrying *tet A* resistance genes from animal meat were able to transfer the gene to recipient bacteria. Another study also reported that multi-resistant bacteria carrying genes encoding resistance to tetracycline, located on plasmids, isolated from wastewater intended for watering plants, transferred their gene horizontally to other bacterial strains (Sczczepanowski *et al.,* 2004).

The results showed that the strains harboured a specific combination of resistance genes *bla* $_{TEM}$, *bla* $_{CTX-M}$, *bla* $_{SHV}$, *tet A*. *The bla* $_{TEM}$, *tet A* gene combination was the most predominant with a frequency of 38%.

These cross-resistances would be justified by the fact that the mobile genetic elements contain several antibiotic resistance genes, since the transfer of a single mobile genetic element would consequently lead to the transfer of several antibiotic resistance genes from one bacterium to another through the use of a single antimicrobial agent (Aarestrup, 2006).

The presence of *tet A* resistance genes in *E. coli* of animal origin such as the pigs in the present study has a negative impact on public health because this gene has the capacity to spread to other commensal bacteria in humans via food or the environment. In addition, the risk of transfer of the *tet A* gene by zoonotic pathogenic bacteria seems very high. Rigorous monitoring of resistance genes circulating in the digestive flora of farmed food-producing animals and good food hygiene practices are therefore necessary to avoid any dissemination of genes from commensal bacteria to pathogenic bacteria.

Acknowledgements

The authors sincerely thank pig farmers in the village of Adiopodoumé and laboratory staff in Molecular biology and Microbiology, in Biomass-Energy of Nanguy Abrogoua University and Pasteur Institute in Abidjan for their contribution to this work.

Author Contributions

Kouadio Kouamé Innocent: Conceived the original idea and designed the model and wrote the manuscript and Methodology (microbiological and genotypic analysis); Kouame Amenan Margueritte: Carry out biochemical identification and contribute to the drafting of the manuscript; TRA Bi Youan Charles: Contribute to genotypic study; Ouattara Mohamed Baguy: Visualization; KPODA Stéphane: Data Curation, Validation; Guessennd-Kouadio Nathalie: Project Administration, and Funding Acquisition; AKA Boko: Supervision

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

Aarestrup, F.M. 2006. Antimicrobial Resistance in Bacteria of Animal Origin, ASM Press, Washington DC, 2006.

Agerso Y. and Sandvang D. 2005. Class 1 integrons and tetracycline resistance genes in *Alcaligenes, Arthrobacter,* and *Pseudomonas* spp. isolated from pigsties and manured soil. *Applied Environnental Microbiology.* 71: 7941-7947. https://doi.org/10.1128/AEM.71.12.7941-7947.2005

Agersø, Y. and Aarestrup, F. M. 2013. Voluntary ban on cephalosporin use in Danish pig production has effectively reduced extended-spectrum cephalosporinase-producing *Escherichia coli* in slaughter pigs. *Journal of Antimicrobial and Chemotherapy.* 68(3):569–572. https://doi.org/10.1093/jac/dks427

Anses-ANMV. 2014. Suivi des ventes de médicaments vétérinaires contenant des antibiotiques en France en 2013. Volumes et estimation de l'exposition des animaux aux antibiotiques. Edit.,A., ed. Maisons-Alfort. (www.anses.fr).

Bagalwa M., Karume K., Mushagalusa N G., Ndegeyi K., Birali M., Zirirane N., Macheka Z et Bayongwa C. 2013. Risques potentiels des déchets domestiques sur la santé des populations en milieu rural: cas d'Irhambi Katana (Sud-Kivu, République Démocratique du Congo). Vertigo 13:2 https://doi.org/10.4000/vertigo.14085

Balasubramaniam A, Arthanari Eswaran M, Suresh P, Sukumar K 2014. Detection of tetracycline resistance determinant *tet* A gene and antimicrobial resistance pattern in *Escherichia coli* isolates recovered from healthy layer chickens, *Veterinary World.* 7(9):635-638. https://doi.org/10.14202/vetworld.2014.635-638

Belloc C., Lam D. C., Pellerin J. L., Beaudeau F., Laval A. 2005. Effect of quinolone treatment on selection and persistence of quinolone-resistant *Escherichia coli* in swine faecal flora. *Journal of Applied Microbiology*. 99:954–959. https://doi.org/10.1111/j.1365-2672.2005.02667.x.

Bibbal D., Dupouy V, Prere M. F., Toutain P. L., Bousquet-Melou A. 2009. Relatedness of *Escherichia coli* strains with different susceptibility phenotypes isolated from swine feces during ampicillin treatment. *Applied and Environmental Microbiology.*75 (10):2999-3006

https://doi.org/10.1128/AEM.02143-08

Blanchard M. 2010. Gestion de la fertilité des sols et rôle du troupeau dans les systèmes coton-céréales-élevage au Mali-Sud. Savoirs techniques locaux et pratiques d'intégration agriculture élevage. Thèse Doctorat. Université Paris-Est, Créteil Val de Marne.12p

Blanco, J. E., Blanco, M., Mora, A. and Blanco, J. 1997. Prevalence of bacterial resistance to quinolones and other antimicrobials among avian *Escherichia coli* strains isolated from septicemic and healthy chickens in Spain. *Journal of Clinical Microbiology.* 35(8): 2184-2185. https://doi.org/10.1128/jcm.35.8.2184-2185.1997

Daini, O. A. and Adesemowo, A. 2008. Antimicrobial susceptibility pattern and R plasmid of clinical strains of *Escherichia coli*. *Australian Journal of Basic Applied Sciences*. 2: 397-400.

EFSA. 2011. Scientific opinion on the public health risks of bacterial strains producing extended-spectrum beta-lactamases and/or AmpC beta-lactamases in food and food producing animals. EFSA Journal, 9(2322). https://doi.org/10.2903/j.efsa.2011.2322

Enne V, Cassar C, Sprigings K, Martin J. Woodward, Peter M. Bennett M. 2007. A high prevalence of antimicrobial resistant *Escherichia coli* isolated from pigs and a low prevalence of antimicrobial resistant *E. coli* from cattle and sheep in Great Britain at slaughter. *FEMS Microbiology Letters.* 278:193–199. https://doi.org/10.1111/j.1574-6968.2007.00991.x

FAO, 2006. Livestock's long shadow. Environmental issues and options. Rapport de la FAO. Rome: FAO. 390p

Farmer. (1999). *Enterobacteriaceae:* Introduction and identification In: Manual of clinical Microbiology, P. R. Murray, E. J. Baron, M. A. Pfatter, Tenoven F. C. and R. H. Yolken (eds) *7th ed. American Society for Microbiology*. 442-458

Gomgnimbou A. P. K., Nacro H. B., Sanon O. H., Sieza I., Kiendrebeogo T., Sedogo M. P. et Martinez J. 2014. La gestion des déjections animales dans la zone périurbaine de Bobo-Dioulasso (Burkina Faso): structure des élevages, perception de leur impact environnemental et sanitaire, perspectives. Cahiers Agricultures, vol. 23, n°6. 345-406 p

Hu G Z, Pan Y S, Wu H, Hu H, Xu R, Yuan L, Liu J L, Feng J K. 2013. Prevalence of tetracycline resistance genes and identification of tet(M) in clinical isolates of *Escherichia coli* from sick ducks in China. Journal of Medical Microbiology. 62, 851–858 https://doi.org/10.1099/jmm.0.051896-0

Hutchison, M. L., Walters, L. D., Avery, S. M., Synge, B. A., Moore, A. 2004. Levels of zoonotic agents in British livestock manures. Lett. Appl. Microbiol. 39 (2), 207–214. https://doi.org/10.1111/j.1472-765X.2004.01564.x

Karczmarczyk, M., Walsh, C., Slowey R., Leonard N., and Fanning, S. 2011. Molecular characterization of multidrug- resistant *Escherichia coli* isolates from Irish cattle farms. *Applied of Environmental Microbiology*. 77(20): 7121-7127. https://doi.org/10.1128/AEM.00601-11

Koo H. and Woo G. 2011. Distribution and transferability of tetracycline resistance determinants in *Escherichia coli* isolated from meat and meat products. *International Journal of Food Microbiology.* 145 (2-3): 407-413. https://doi.org/10.1016/j.ijfoodmicro.2011.01.003

Lanz R., Kuhnert P., Boerlin P. 2003. Antimicrobial resistance and resistance gene determinants in clinical *Escherichia coli* from different animal species in Switzerland. *Vetenary Microbiology*. 91: 73– 84. https://doi.org/10.1016/s0378-1135(02)00263-8

Mali. Meadr, 2015. Ministère de l'environnement, de l'assainissement et du développement durable. Rapport troisième communication nationale du Mali à la convention cadre des nations unies sur les changements climatiques.15 P

Manyi-Loh C. E., Mamphweli S. N., Meyer E. L., Doré S., Simon M. et Okoh A. I. 2016. Un aperçu du contrôle des bactéries pathogènes dans le fumier de bétail. Int. J. Environ. Rés. Santé publique, 13, no. 9: 843p.

McEwen S. 2002. Uses of antimicrobials in food animals in Canada: impact on resistance and human health. Report of the Advisory Committee on Animal Uses of Antimicrobials and Impact on Resistance and Human HealthVeterinary Drugs Directorate, Health Canada.., ed. 75p.

Muhammad A. A., Hassan, S. M. R., Alam, S. and Shirin, M. 2009. Antibiotic resistance of *Escherichia coli* isolated from poultry and poultry environment of Bangladesh. *American Journal of Environmental Science.* 5(1): 47-52. https://doi.org/10.3844/ajessp.2009.47.52

Phillips I. and Casewell M. 2004. "Does the use of antibiotics in food animals pose a risk to human health? A critical review of published data."*Journal of Antimicrobial Chemotherapy.* 53 (1): 28-52 https://doi.org/10.1093/jac/dkg483

Sanders P., Bousquet-Mélou A., Chauvin C., Toutain, P. L. 2011. Utilisation des antibiotiques en élevage et enjeux de santé publique. INRA *Production Animale*. 24 (2): 199–204. https://doi.org/10.20870/productions-animales.2011.24.2.3254

Schwaiger K., lzel C., Bauer J. 2010. Resistance gene patterns of tetracycline resistant *Escherichia coli* of human and porcine origin. *Vetenary Microbiology.* 142: 329–336. https://doi.org/10.1016/j.vetmic.2009.09.066

Sorum H. and Sunde M. 2001. Resistance to antibiotics in the normal flora of animals. *Vetenary Research.* 32:227-241. https://doi.org/10.1051/vetres:2001121

Stine M. S. and Morris J. G. 2007. Widespread distribution of tetracycline resistance genes in a confined animal feeding facility. *International Journal of Antimicrobial Agents*. 29: 348-352. https://doi.org/10.1016/j.ijantimicag.2006.11.015

Szczepanowski R., Krahn I., Linke B. 2004. Antibiotic multiresistance plasmid pRSB101 isolated from a wastewater treatment plant is related to plasmids residing in phytopathogenic bacteria and carries eight different resistance determinants including a multi-drug transport system. *Microbiology*. *150*: 3613-3630. https://doi.org/10.1099/mic.0.27317-0

Wegener H. G., Aarestrup F. M., Gerner-Smidt P., Bager F. 1999. Transfer of antibiotic resistant bacteria from animals to man. *Acta Veterinaria. Scandinavica Supplementum.* 92: 51-57.

Zhang C. P., Ning Yi-B., Song Li. 2010. Resistance to tetracycline and distribution of tetracycline resistance determinants in commensal *Escherichia coli* isolated from clinically healthy chickens and Pigs. *Sci Agric Sin.* 43:2578-2583. https://doi.org/10.3864/j.issn.0578-1752.2010.12.024

How to cite this article:

Kouadio Kouamé Innocent, Kouamé Amenan Margueritte, Tra Bi Youan Charles, Ouattara Mohamed Baguy, Kpoda Stéphane, Guessennd-Kouadio Nathalie and Aka Boko. 2024. Detection of the *tet A* Resistance Gene in Broad Spectrum Beta-lactamase (ESBL)-Producing *Escherichia coli* Strains Isolated from Faecal Waste of Pigs on a Farm in Abidjan, Côte d'Ivoire. *Int.J.Curr.Microbiol.App.Sci.* 13(9): 208-215.
doi: https://doi.org/10.20546/ijcmas.2024.1309.023