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A Review of the Presence of Antibiotic Resistance Problems on *Klebsiella Pneumoniae* Acquired from Pigs: Public Health Importance

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ABSTRACT

Antibiotic resistance is a global public health problem. Antibiotic resistant bacteria such as *Klebsiella pneumoniae* is bacteria that is common in the digestive tract and upper respiratory tract of animals and humans. Several studies have shown that this bacterium is not only found in humans but also in animals, one of which is pigs which are known to be a reservoir for the spread of this bacteria. There are several strains, resistant antibiotics, antibiotic resistance genes and virulence genes of the *Klebsiella pneumoniae* bacteria in pigs which were summarized in this article. Not only in pigs, but this antibiotic resistant bacterium is also known to be found in other food-producing animals, such as cows, chickens and sheep. Many cases of *Klebsiella pneumoniae* in humans have been reported, but cases of *Klebsiella pneumoniae* in humans related to animals or strains related to animals and humans were also summarized in this article. Control and prevention are needed to prevent the spread of antibiotic resistant bacteria from animal to animal, animal to human and vice versa as well as to the surrounding environment.

Keywords: Antibiotic Resistance, *Klebsiella pneumoniae*, Pigs, Public Health

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INTRODUCTION

One of the most important issues for healthcare societies in the world to date is the issue of antibiotic resistance (1). Antimicrobials are commonly used for the treatment and prevention of animal diseases in veterinary medication. In addition, they are also applied as an antimicrobe growth promoter (AGP) to feed ingredients in many countries to improve productivity (2). Over time, there has been much evidence that the use of antimicrobials in animals is helping to establish antimicrobial resistance (AMR) (3,4). The antibiotic resistance is a problem of the use of antibiotics in medicine and its diffusion in environments that encourage the development and propagation of antibiotic resistant bacteria (5). Nine important bacteria are involved in antibiotic resistance and *Klebsiella pneumoniae* is one of the main bacteria (1). In hog farming, pig farmers use antibiotics, metaphylaxis, prophylaxis, and growth promotion in their livestock (7). Antibiotics primarily are used in hog farming. Various studies were documented with the discovery of antibiotic resistant *Klebsiella pneumoniae* bacteria in pigs (8,9). Antibiotics used in pigs are classified into all major antibiotic classes used in clinical practise. Pigs are also known to transmit pneumoniae bacteria of *Klebsiella* to the environment and humans. The disposal of antibiotics with agricultural waste affects the spread, primarily from agricultural fertiliser application and/or irrigation of polluted water supplies to nearby communities, of the antibiotic resistance generation and of resistant bacteria by contaminated soil, land and surface water, atmosphere and plants (10); Horizontal genes may be transmitted to other bacteria of the *Klebsiella pneumoniae* and other

bacteria within an Enterobacteriaceae family through horizontal gene transmission (11). *Klebsiella pneumoniae* is a gram-negative bacterium commonly found in the animals' atmosphere and digestive tract within the enterobacteriaceae family. The *Klebsiella pneumoniae* General causes carnivorous and ungulate pneumonia and urogenital infections, ruminant and pig mastitis, rabbit enterocolitis, and sporadic septicemia for many species (12). The discovery of several *Klebsiella pneumoniae* which are antibiotic resistant to animals has a detrimental effect on public health and an influence on a country's economy, and thus monitoring or prevention needs to take place, in order to address this problem (13). The research was thus conducted to establish *Klebsiella pneumoniae* antibiotic resistance profile, in particular in pigs, focusing on the resistance of *Klebsiella pneumoniae* in pigs, virulence genes, genes mediating resistance to antibiotics, cases in other animals and the relationship between *Klebsiella pneumoniae* in humans and pigs, and monitoring and preventive strategies to resolve these issues, both.

Strain of *Klebsiella pneumoniae* on pigs

Pigs are livestock that are consumed by some people in the world. These food-producing animals may play an important role as transfer of antibacterial resistance among farmers, livestock and the agricultural environment, in fact some studies have focused on the possibility of this transmission (14). As in the research conducted by Kieffer, the strains of *Klebsiella pneumoniae* in pigs that were found were STs, ST45 and ST1563 (15). In the study conducted by Founou, the *Klebsiella pneumoniae* strains were ST14, ST39, ST2958 and ST2959

(16). The bacteria developed by the ESBL-enzyme have been reported to different levels in a clinical sample in Ivory Coast (11). Even the community-acquired urinary tract infections in the city of Cameroon have an incidence of 16.4 percent). (18). The ESBL-producing strains of KI have been reported by Founou. (18)

Research conducted by Mobasser (19) in Malaysia also stated that there was a link between *Klebsiella pneumoniae* strains in pigs and in humans, *Klebsiella pneumoniae* strains in their research, namely: KP2013Z05, KP2013Z12, KP2013Z13, KP2013Z14, KP2013Z15, KP2013Z17, KP2013Z18, KP2013Z22, KP2013Z24, KP2013Z26, KP2013Z27, KP2013Z28, KP2013Z30, KP2013Z31, KP2013Z33, KP2013Z38, KP2013Z39, KP2013Z44, KP2013Z48, KP2015Z01, KP2015Z02, KP2015Z03, PIG201504, KP2015Z05, KP2015Z06, KP2015Z07, KP2015Z08, KP2015Z09, KP2015Z10, KP2015Z11, KP2015Z12, KP2015Z13, KP2015Z14, KP2015Z15, KP2015Z16, KP2015Z17. Transmission of antibiotic-resistant strains from animals to humans can occur through direct such as direct contact with farmers and veterinarians or indirectly such as through consumption of contaminated animal feed, contaminated ground or surface water and animal waste

handling routes (20). *Klebsiella pneumoniae* is an important opportunistic bacterial pathogen that causes infectious diseases in animals, including pigs (8,9,21). This occurs due to the widespread use of antibiotics and the misuse of antibiotics as growth enhancers and treatment of diseases in animals. In research conducted by Yang in Henan Province, China. It has been reported that 42 isolates from the pigs studied were almost all of the isolates resistant to several classes of antibiotics tested. *Klebsiella pneumoniae* strains in studies conducted using multilocus sequence type (MLST) have been reported, namely ST11, ST106, ST235, ST258, ST263, ST270, ST1102, ST1863. ST *Klebsiella pneumoniae* which is most often found is ST11 in pig isolates. ST235 and ST258 are also common ST strains of *Klebsiella pneumoniae* isolated in pigs (13).

The finding of *Klebsiella pneumoniae* strains in food-producing animals, namely pigs, is of course very important and needs to be known as an indication of whether these strains are related to one another. The following is a summary of the strains of *Klebsiella pneumoniae* bacteria in pigs from several studies (41) have been carried out from various countries which are summarized in Table 1.

Table 1. *Klebsiella pneumoniae* strains in pigs

Year	Strain <i>Klebsiella pneumoniae</i>	References
2015	KP2013Z05, KP2013Z12, KP2013Z13, KP2013Z14, KP2013Z15, KP2013Z17, KP2013Z18, KP2013Z20, KP2013Z21, KP2013Z22, KP2013Z24, KP2013Z26, KP2013Z27, KP2013Z28, KP2013Z30, KP2013Z31, KP2013Z33, KP2013Z38, KP2013Z39, KP2013Z44, KP2015Z01, KP2015Z02, KP2015Z03, PIG201504, KP2015Z05, KP2015Z06, KP2015Z07, KP2015Z08, KP2015Z09, KP2015Z10, KP2015Z11, KP2015Z12, KP2015Z13, KP2015Z14, KP2015Z15, KP2015Z16, KP2015Z17	19
2016	STs, ST45, ST1563	15
2016	ST14, ST39, ST2958, ST2959	16
2017	ST11, ST106, ST235, ST258, ST263, ST270, ST1102, ST1863	13

Antibiotic Resistant of *Klebsiella pneumoniae* on pigs

Many antibiotics are typically overused and unreasonable for multi-infection (22) care clinics, raising the antibiotic resistance and multi-pharmaceutical resistance selectives. Antimicrobial drugs are widely used to treat diseases and to promote animal growth in modern livestock systems, which has led to a climate that increases antibiotic resistance. In large pig farms in China, widespread use and use of antimicrobials, which explains the greater prevalence of antibiotic resistance in the strain of *pneumoniae* isolated from pigs, are popular. Some newly synthesised costly antibiotics in animal husbandry are seldom used and therefore bacteria are less drug resistant than conventional antibiotics. The treatment of animal infections is rarely used, for instance, with GAT, IMP or MEM (23).

Study conducted by Yang, the highest multi-drug resistance (MDR) rates were found among the *Klebsiella pneumoniae* strains from swine (47 isolates), reaching a value of 93.6%, *Klebsiella pneumoniae* in pigs was resistant to the AK antibiotic class 76.6%, AMP 85.1%, AMC 63.8%, AZM 44.7%, CAZ 53.2%, CTX 55.3%, CLI 74.5%, CIP 87.2%, ERY 66.0%, GAT 23.4%, IMP 4.3%, KAN 78.7%, MEM 2.1%, TCY 74.5%, VAN 10.6%, and MDR 93.6%, Yang found that most of the *Klebsiella pneumoniae*

isolates from animals were susceptible to GAT, IMP and MEM, and similar findings revealed that all *Klebsiella pneumoniae* isolates from food animals were susceptible to IMP and MEM (13, 24). In addition, multiresistant strains increase the risk of infection caused by treatment failure in humans and animals. Multiresistant *Klebsiella pneumoniae* isolates have emerged in many countries, including Northwestern Iran, Turkey, Australia and China (25-27). In Founou's study, ESBL-producing *Klebsiella pneumoniae* taken from pig isolates in Cameroon were resistant to AMP, CXM, CTX, CAZ, GE8 TMP / SXT antibiotics. *Klebsiella pneumoniae* isolate was found to be resistant to ampicillin, cefuroxime, cefuroxime-axetil, cefotaxime, ceftazidime and trimethoprim-sulfamethoxazole and not resistant to the antibiotic omeycin. This Cameroonian study also reported that all *Klebsiella pneumoniae* isolated from pigs and humans showed reduced susceptibility to amino penicillin, cephalosporins and trimethoprim (16).

Founou studies of the *fosA* chromosome gene have been reported to have shown several gram-negative dies that are widely used in Europe and Africa for the uncomplicated treatment of the urinary tract infection (28). This provides new knowledge globally as a therapeutic option for treating infection caused by

carbapenem-resistant enterobacteriaceae. The Kieffers analysis showed 17 isolates of the 100 Swab rectal isolates on Portuguese farms were positive and were immune to various antibiotics, including colistin and penicillin, for the use of *Klebsiella pneumoniae*. Amoxicillin (AMX) and tetracycline (TET) were resistant to sulfamethoxazole / trimethoprim (SXT), tobramycin (TMN), chloramphenicol (CHL) and sulfonamide (SUL) (15).

The results of research in Malaysia on *Klebsiella pneumoniae* in pigs were found to be resistant to several antibiotics including: ciprofloxacin, aztreonam, ampicillin, tazobactam, amikacin, nalidixic acid, imipenem, ceftazidime, colistin, tetracycline, cefotaxime, amoxicillin-clavulanate, cefixime. In that study, the highest level of antimicrobial resistance to tetracycline antibiotics. *Klebsiella pneumoniae* species are intrinsically resistant to penicillin and can acquire resistance to third and fourth generation cephalosporins by producing ESBLs. Most strains of *Klebsiella pneumoniae* isolates from swine and humans were resistant to at least one non-β-lactam antibiotic (tetracycline and gentamicin), which is used for the treatment of prophylactic disease and therapy in food-producing animals. There were found 22 MDR strains which showed resistance to more than three categories of antibiotics (19). All strains from the agricultural environment and pigs show resistance to tetracyclines, which are widely used in feed supplements (30).

***Klebsiella pneumoniae* virulence genes on pigs**

Klebsiella pneumoniae has a pathogenicity due to a variety of virulence factors (including the development of capsule, hypermucoviscosity, lipopolysaccharide, iron acquisition system) all of which contribute to the overcoming of the mammalian hosts' innate immunity and the maintenance of infection in this host (31). The hypermucoviscous strain of *Klebsiella pneumoniae* is considered to be a hypervirulent strain. This strain's molecular identity is correlated with the existence of RmpA and MagA genes. RmpA is a mucoid phenotype A gene plasmid controlling gene, a regulator of polysaccharide extracapsular synthesis (32). MagA is a gene encoded in chromosomal hypermucoviscosity, encoded with the K1 serotype. While most of the *Klebsiella pneumoniae* strains have magA, some MagA negative strains that carry the RmpA gene also have this phenotype. HMV (31.9%) were *Klebsiella pneumoniae* (33). In Yang's research, 47 pig isolates, namely magA (6.4%), rmpA (12.8%), mrkD, fimH-1, were taken from the virulence gene ownership of *Klebsiella pneumoniae* (89.0%) (95%), in B (100%) (13).

Genes mediated the antibiotic resistance of *Klebsiella pneumoniae* in pigs

Klebsiella pneumoniae is a bacterium that produces ESBL (34). This enzyme can hydrolyze the β-lactam ring from antibiotics so that antibiotic resistance can occur (35). *Klebsiella pneumoniae* has been confirmed to be able to fight many antibiotics, especially the third generation cephalosporins such as Cefotaxim, Ceftriaxone and Ceftazidime (36). Commonly used treatments for *Klebsiella pneumoniae* infection include β-lactam antibiotics such as cephalosporins and carbapenems, aminoglycosides such as Gentamicin and Quinolones. However, this therapy was not effective against *Klebsiella pneumoniae*, which has a resistance gene to this antibiotic (37). *Klebsiella pneumoniae* is highly resistant to many antibiotics and has many determinants of resistance such as β-lactamase or ESBL, including TEM, SHV, CTX-M and type GES (19).

In Yang's study, 21 isolates from pigs (44.7%) strains of *Klebsiella pneumoniae* produced ESBL and resistance genes *Klebsiella pneumoniae* blaKPC (51.1%), blaNDM (2.1%), blaSHV (14.9%), blaTEM (29.8%), qnrA (61.7%), qnrB (40.4%), tolC (74.5%) (13). Study conducted by Fonou et al., in Cameroon with porcine isolates, it was obtained ESBL-producing *Klebsiella pneumoniae* with resistance genes: strA, strB, blaTEM-116, blaSHV-28, blaCTX-M-15, oqxA, oqxB, QnrB1, fosA, sul1, sul2, tet (A), dfrA15, aac 3-IIa, aadA1, blaTEM-1B, blaSHV-27, blaSCO-1, fosA, mph (A), catA113 (16). All isolates contained genes that were resistant to sulfonamides (sul1), fosfomycin (fosA) and quinolones (oqxA and oqxB). Various determinants of β-lactamase coding were detected with blaCTX-M-15, blaTEM-1B and blaSCO-1 being the most common. Likewise, the dfrA15 gene which is responsible for trimethoprim resistance, encodes strA and strB for aminoglycoside resistance, as does the tet (A) gene which is responsible for tetracycline resistance. None of the *Klebsiella pneumoniae* isolates contained the virulence gene (16).

This resistant phenotype was confirmed by the identification of the CTX-M-15, SHV-28, and TEM-116 genes by WGS which was also explained by various determinants of resistance to non-β-lactam antibiotics, especially aminoglycoside resistant genes (strA, strB), genes plasmid-mediated quinolone resistance (QnrB1, oqxA, oqxB), phosphomycin (fosA) resistance genes and sulfonamide resistance genes (sul1 and sul2) which were not phenotypically proven. Detection of CTX-M-15 is consistent with multicentre studies conducted in five African and two Vietnamese cities where it was detected in 74% of isolates and was the dominant ESBL among African isolates. This study further reports the predominance of determinant QnrB among African strains (17). The CTX-M-15 gene is currently the most widely distributed CTX-M enzyme worldwide (16).

Furthermore, the wide-ranging distributions of the fosA gene in Fonou's analysis indicate that the gene can be used as a reservoir for this gene and can easily be transmitted to phospho-depleted organisms such as *E. Coli* (16). Although it is difficult to bring these results into perspective because of molecular epidemiological studies scarce in Africa, these findings are consistent in several studies from Asia (38-40) and European countries showing several ESBL-*E. coli*-production fosA lines (41). The interest in the reuse of old antibiotics must therefore be carefully taken into consideration and given current genes of ambient resistance (16).

Research conducted by Kieffer was stated that out of 100 swab rectal isolates in Portuguese farms, 17 isolates tested positive for *Klebsiella pneumoniae* which had the mcr-1 gene. Among these positive isolates, 10 exhibited the ESBL phenotype. Sequencing revealed that all mcr-positive isolates had genes that were 100% identical to mcr-1. All MCR-1 producing isolates had the blaTEM-1 gene and all ESBL producers had the blaCTX-M-2 gene. Among the chloramphenicol resistant isolates, positive for the floR resistance gene (15).

In Malaysia, research on the *Klebsiella pneumoniae* bacteria was also carried out in pigs that have antibiotic-resistant genes including: SHV-61, SHV-12, SHV-11, TEM-1, CTXM-15, CTX-M-2 and CTX-M-1. In this study, TEM was the most common β-lactamase enzyme detected on 15/18 ESBL producing strains of *Klebsiella pneumoniae*, all of which were identified as TEM-119. TEM-1 hydrolyzes penicillin and initial cephalosporins and is known as class

2b b-lactamase but is unable to significantly hydrolyze broad-spectrum cephalosporins or 10 ceftazidime (42). Members of the betalactamase family of TEM, SHV and CTX-M are found in Enterobacteriaceae; MDR Klebsiella pneumoniae, which produces ESBL, contains mostly TEM, SHV and types CTX-M (43). beta-lactamase type CTX-M has been reported as the dominant gene coding for ESBL, and other ESBLs such as SHV and TEM have also been reported in many countries (44). Study done by Mobasser found that SHV was a common ESBL enzyme among *Klebsiella pneumoniae* strains, detected in 15/18 ESBL-producing *K. pneumoniae* strains and identified as SHV-11, SHV-12, and SHV-61. SHV-11 and SHV-61 are known as class 2b beta-lactamase enzymes (19, 42).

The CTX-M-1 group was detected in 7/16 of the ESBL-producing strains, which were identified as CTX-M-1 and CTX-M-15. The CTX-M-2 group was found in two strains of *Klebsiella pneumoniae* isolated from pigs and the environment. CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-24 and CTX-M-32 are the most common CTX-M type ESBLs in pigs (19). CTX-M appears to be the dominant ESBL enzyme worldwide (42). The CTX-M-15 gene is one of the most common ESBL CTX-M types among the Enterobacteriaceae family. Nosocomial infections caused by *Klebsiella pneumoniae* producing CTX-M-15 have dramatically increased in recent years (45). In Asian countries, CTX-M-15 is the main ESBL enzyme reported (46). Carbapenemase-producing *Klebsiella pneumoniae* strains are reported in pig farms in Germany and elsewhere around the world (47-49).

Case of antibiotic resistant *Klebsiella pneumoniae* in another animal

Yang's studies find that resistant isolates of pigs and chickens have a greater prevalence of than resistant isolates of cattle and sheep among animal isolates. Ciprofloxacin (13) has been found to be of highest resistance among chicken and pig isolates (82.2 and 87.2 per cent). Quinolones are commonly available antimicrobial agents which have been commonly used in food processing in China, including chicken and pork (50). There are some data showing that 80.0 percent of chicken isolates are ciprofloxacin resistant (51). In *Klebsiella pneumoniae*, the most frequent ST was ST11, which was commonly found in isolates from five hosts, one of which was pigs in people (34.6%), pigs (36.2%), chickens (15.6%), bovine (28.0%) and sheep (30.0%). Also common STs of *K. pneumoniae* are ST235 and ST258. *Klebsiella pneumoniae* isolated from humans (46.2%), pigs (42.6%) and chicken (57.8%) (13). Effendi has researched to find 10 positive isolates of *Klebsiella pneumoniae* from rectal swabs of milk cows, beef cattle, broiler chickens and tilapia for *Klebsiella pneumoniae*, and has found positive *Bacteria* from *Klebsiella pneumoniae* in 45 animals. The rectal swab samples showed 20% (4/20) of *Klebsiella pneumoniae* bacterial animal beef, 40% (2/5), 10% (1/10) of broiler chicken and 30% (3/10) of tilapia in the rectal swab. The resistance to LMA was present in 90 percent (9/10) and sensibility to other antibiotics was shown for all *Klebsiella pneumoniae* isolates. The results of the examination of DNA extraction of samples using an electrophoresis of agarose gel have revealed that the blaTEM-F and blaTEM-R primers have been successfully amplified. Nine (90 per cent) samples from the 10 PCR samples tested for the blaTEM gene (52).

Study conducted by Ahmed and Shimamoto, the blaTEM gene as the coding for antimicrobial resistance was found

as many as 23 isolates (20.5%) from 34 isolates of gram-negative bacteria, including mastitis cases in cattle in Egypt and *Klebsiella pneumoniae* bacteria found as many as 7 blaTEM genes. isolates or 6.3% of the total sample obtained. Most of the ESBL originates from the TEM type enzyme encoded by the blaTEM gene. The blaTEM gene is the most frequently detected gene for antibiotic resistance in plasmids in the clinical population of gram-negative microorganisms (53).

Relation to strains of *Klebsiella pneumoniae* in humans and animals

Klebsiella pneumoniae, provided by ESBL, goes beyond health to a broad range of ecological niches, including poultry, food products, soils and wastewater. ESBL-produced *Klebsiella pneumoniae* can in reality be colonised or infected by human beings when in contact with ESBL-carrying ELD blood, saliva, faeces and urine or if contaminated water or food products are consumed (54). In *Klebsiella pneumoniae*, the most frequent ST was ST11, which was commonly found in isolates from five hosts, one of which was pigs in people (34.6%), pigs (36.2%), chickens (15.6%), bovine (28.0%) and sheep (30.0%). ST235, ST258 and *Klebsiella pneumoniae* were typical human isolated ST strains (46.2%), pigs (42.6%) and chicken strains (57.8%) (16). (16).

The numbers of studies have isolated MDR *Klebsiella pneumoniae* from a range of animals and people (24,55) but few studies have assessed the molecular relationship of livestock infected *Klebsiella pneumoniae* isolates (49). Research carried out by Yang raises the likelihood of this multiresistant strain being transmitted between humans and animals. The survey also documented the molecular characterization and antimicrobially resistant *Klebsiella pneumoniae* strain in Henan, China. Resulted from his study, many strains of *Klebsiella pneumoniae* of different origin had the same molecule type and similar phenotypes, with high incidences of multiresistant pneumonia between humans and various animals. These strains may possibly have been transmitted between humans and animals (13).

A common ST MDR mainly found in Asia and South American 56, the *Klebsiella pneumoniae* strain ST11, is the primary ST in hospitals and veterinarian clinics in China (57). 56 These findings are consistent with Yang's survey showing that ST11 is a human and cattle isolate for *Klebsiella pneumoniae* that indicates that Str11 can spread between humans and livestock. ST11 *Klebsiella pneumoniae* in addition, ST235 and ST258 were identified in human isolates, pigs and chickens, suggesting that these STs can be associated with transmission from humans to animals. Correlation study of the STs, genes for pharmaceutical resistance, virulence genes and phenotypic features showed a large correlation between different types of molecules with multiple resistance or virulence genes (13).

In a study in Cameroon with pig and human isolates, it was shown that the *Klebsiella pneumoniae* strains were overlapping and interrelated between pig and human sources in and across the abattoir (Figure 1). Specifically, the *Klebsiella pneumoniae* ST14 strain colonized human and swine nares located at two different slaughterhouses (SH001 and SH003) whereas *Klebsiella pneumoniae* ST39 was detected in the nose of the pigs and hands of workers present in the same abattoir, SH002 (Figure 1). This can be related to neglected hygiene and sanitation practices that apply during the production, transportation, storage and/or retail stages. Fonou also reported that *Klebsiella*

pneumoniae isolated from humans has also shown reduced susceptibility to amino penicillin, cephalosporins and trimethoprim (16).

The ST14 and ST39 clonal lineages are the leading causes of nosocomial infection and outbreak situations worldwide, although their evolutionary emergence is somewhat less documented in developing countries. In fact, *Klebsiella pneumoniae* ST14 producing OXA-181 was detected in South Africa where it was responsible for outbreaks among tertiary hospital-treated patients (58), whereas *Klebsiella pneumoniae* was multi-drug resistance biofilm that was resistant to multiple drugs and biofilms. The *Klebsiella pneumoniae* strain belonging to ST14 was detected in India also in tertiary care (59). Likewise,

Klebsiella pneumoniae ST39 was responsible for the outbreak in a children's hospital in Algeria (60).

The emergence of this ESBL-producing *Klebsiella pneumoniae* in exposed pigs and workers in and between slaughterhouses in Cameroon is particularly important as it confirms the spread of their active clones by direct contact, and indicates their indirect spread across the food chain in the country. These findings further demonstrate that pigs, pig and slaughterhouse workers represent a potential reservoir and source of ESBL-producing *Klebsiella pneumoniae* infection in Cameroon and reinforce the importance of implementing appropriate food safety measures and promoting rational antibiotic use (16).

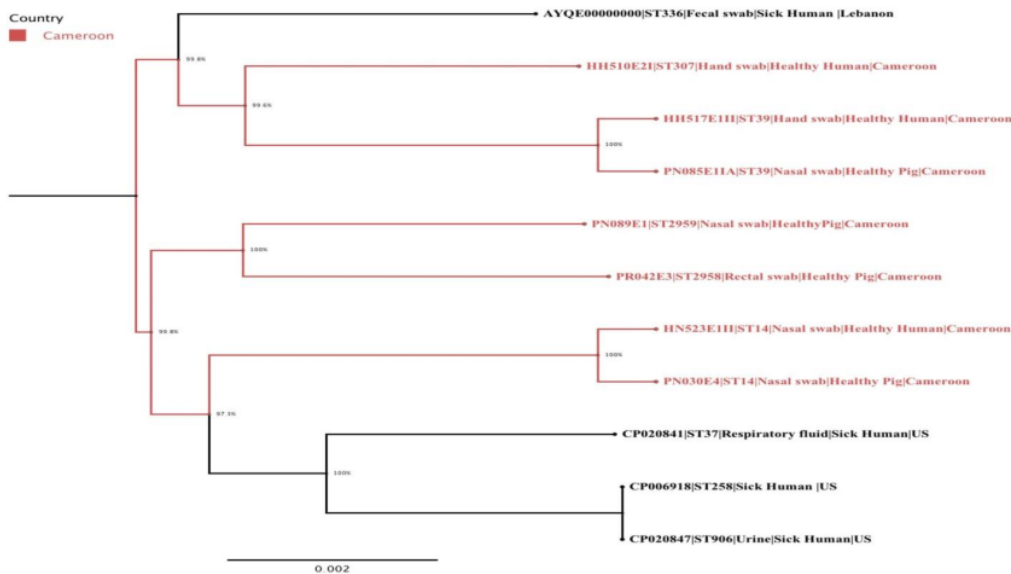


Figure 1. Overlapping and interrelated *Klebsiella pneumoniae* between pig and human sources in and across slaughterhouses in Cameroon (16).

In 2017, it was also reported that *Klebsiella pneumoniae* was found in pigs that have strains similar to *Klebsiella pneumoniae* in humans, namely in a study conducted by Kieffer, *Klebsiella pneumoniae* strains in pigs were found, namely STs, ST45 and ST1563 where the strain is the same as the *Klebsiella pneumoniae* strain in humans (15). In the Mobaseri study also stated that there was an association between *Klebsiella pneumoniae* isolates in pigs and *Klebsiella pneumoniae* isolates in humans, most of the strains of both isolates from pigs and humans were resistant to at least one non-b-lactam antibiotic such as tetracycline and gentamicin, which were used for treatment, prophylactic disease and therapy in food-producing animals. There were 22 MDR strains in this study, which showed resistance to more than three categories of antibiotics (19).

Control and Prevention

Basic indications for the use of antibiotics can be classified into antibiotics for definitive therapy, empirical therapy and prophylactic therapy. Therapy is definitively only used to treat bacterial infections. To find out whether the infection is caused by bacteria, you can do a bacterial culture, sensitivity test, serological test, or other test.

Based on available reports, an antibiotic with a narrow spectrum, low toxicity, affordable price and highest effectiveness should be prescribed in definitive therapy. In empirical therapy, antibiotics are given in cases of infection with unknown germs such as in emergency cases due to sepsis, immunocompromised patients and so on. Antibiotic therapy in this case was given based on existing germ epidemiological data. While prophylactic therapy is antibiotic therapy that is given for prevention in patients who are prone to infection. The antibiotics given are narrow spectrum and specific (61). Antibiotic resistance occurs when microorganisms undergo changes causing the drugs given with the aim of curing infections by microorganisms to become ineffective. This is a serious concern because it can cause death, spread, and impose high costs on individuals and society (62).

The use of antibiotics wisely is closely related to the use of narrow spectrum antibiotics with the right indication, adequate doses, and not longer than needed. Many studies have reported the occurrence of antibiotic resistance problems due to inaccurate use of antibiotics in the veterinary field, such as in livestock (63-68), pets (69-73), poultry (74-76), and fisheries (77-79), as well as those

isolated from animal products (80, 81). Therefore, to prevent further transmission of *Klebsiella pneumoniae* between humans and animals, strict infection control measures, such as the rational application of antibiotics in clinical and livestock settings, routine disinfection of the livestock environment, reduction of human-animal contact and screening of drugs are necessary. More effective, must be implemented. Prudent use of antimicrobials in human and livestock clinical therapy as well as control measures for transmission of *Klebsiella pneumoniae* between humans and animals is also needed (13), as well as increasing public awareness of the dangers of AMR transmission (82).

The isolation of this *Klebsiella pneumoniae* strain always urges the adoption of strict infection and control measures and constant surveillance of antibiotic resistance in the hospital. Similar rigorous interventions must be made in the food production industry if we are to successfully contain the spread of their clones in the food chain (16).

CONCLUSION

ESBL-producing *Klebsiella pneumoniae* can actively spread to pigs, other animals at humans worldwide and may be underestimated given the absence of molecular epidemiological studies. This underscores the potential negligible food safety and public health threats associated with resistant strains in various countries especially if they spread to susceptible persons such as immunocompromised. In general, *Klebsiella pneumoniae* producing MDR and ESBL is becoming a serious problem in humans and animals, increasing resistance to most of the available antibiotics. *Klebsiella pneumoniae* is a bacterium that is commonly found as multidrug resistant and several strains of *Klebsiella pneumoniae* are BL producers. All ESBL producers carry ESBL coding genes such as blaSHV, blaCTX-M, blaTEM as well as other antibiotic coding genes that have been summarized in this journal. This BL-producing *Klebsiella pneumoniae* strain causes resistance to several antibiotics such as aminoglycosides and trimethoprim and various other antibiotics that have been described in this journal. Control and prevention are needed to prevent further transmission of *Klebsiella pneumoniae* between humans and animals, strict infection control measures, such as the rational application of antibiotics in clinical and livestock settings, routine disinfection of the farm environment, reduced human-animal contact and drug screening which more effective, must be implemented. Therefore, the prudent use of antimicrobials in human clinical therapy and animal production as well as control measures for transmission of *Klebsiella pneumoniae* between humans and animals is also needed.

REFERENCES

1. World Health Organization. 2014. Antimicrobial Resistance: Global Report on Surveillance.
2. Pagel SW, Gautier P. Use of antimicrobial agents in livestock. *Rev Sci Tech*. 2012;31(1):145-188.
3. Marshall BM, Levy SB. Food animals and antimicrobials: impacts on human health. *Clin Microbiol Rev*. 2011;24(4):718-733.
4. Landers TF, Cohen B, Wittum TE, Larson EL. A review of antibiotic use in food animals: perspective, policy, and potential. *Public Health Rep*. 2012;127(1):4-22.

5. Pruden A, Larsson DG, Amézquita A, Collignon P, Brandt KK, Graham DW, et al. Management options for reducing the release of antibiotics and antibiotic resistance genes to the environment. *Environ Health Perspect*. 2013;121(8):878-885.
6. Effah CY, Sun T, Liu S, Wu Y. *Klebsiella pneumoniae*: an increasing threat to public health. *Ann Clin Microbiol Antimicrob*. 2020;19(1):1.
7. Sekyere JO. Antibiotic Types and Handling Practices in Disease Management among Pig Farms in Ashanti Region, Ghana. *Journal of Veterinary Medicine*. 2014(1):1-8.
8. Hiroi M, Yamazaki F, Harada T, Takahashi N, Iida N, Noda Y. Prevalence of extended-spectrum β -lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* in food-producing animals. *J Vet Med Sci*. 2012;74(2):189-195.
9. He T, Wang Y, Sun L, Pang M, Zhang L, Wang R. Occurrence and characterization of blaNDM-5-positive *Klebsiella pneumoniae* isolates from dairy cows in Jiangsu, China. *J Antimicrob Chemother*. 2017;72(1):90-94.
10. Darwish WS, Eldaly EA, El-Abbasy MT, Ikenaka Y, Nakayama S, Ishizuka M. Antibiotic residues in food: the African scenario. *Jpn J Vet Res*. 2013;61 Suppl: S13-S22.
11. Wyrres KL, Holt KE. *Klebsiella pneumoniae* as a key trafficker of drug resistance genes from environmental to clinically important bacteria. *Curr Opin Microbiol*. 2018; 45:131-39.
12. Prescott JF. Veterinary Microbiology and Microbial Disease. *Can Vet J*. 2003;44(12):986.
13. Yang F, Deng B, Liao W, Wang P, Chen P, Wei J. High rate of multiresistant *Klebsiella pneumoniae* from human and animal origin. *Infect Drug Resist*. 2019; 12:2729-2737.
14. Finley RL, Collignon P, Larsson DG, McEwen SA, Li XZ, Gaze WH, et al. The scourge of antibiotic resistance: the important role of the environment. *Clin. Infect. Dis*. 2013;57(5):704-710.
15. Kieffer N, Aires-de-Sousa M, Nordmann P, Poirel L. High Rate of MCR-1-Producing *Escherichia coli* and *Klebsiella pneumoniae* among Pigs, Portugal. *Emerg Infect Dis*. 2017;23(12):2023-2029.
16. Founou LL, Founou RC, Allam M, Ismail A, Djoko CF, Essack SY. Genome Sequencing of Extended-Spectrum β -Lactamase (ESBL)-Producing *Klebsiella pneumoniae* Isolated from Pigs and Abattoir Workers in Cameroon. *Front Microbiol*. 2018; 9:188.
17. Breurec S, Guessennd N, Timinouni M, Le TA, Cao V, Ngandjio A, et al. *Klebsiella pneumoniae* resistant to third-generation cephalosporins in five African and two Vietnamese major towns: multiclonal population structure with two major international clonal groups, CG15 and CG258. *Clin. Microbiol. Infect*. 2013; 19:349-355.
18. Nzalio RNT, Gonsu HK, Koulla-Shiro S. Bacterial etiology and antibiotic resistance profile of community-acquired urinary tract infections in a Cameroonian city. *Int. J. Microbiol*. 2016:3240268.
19. Mobasser G, The SJ, Ooi PT, Shiang CT, Thong KL. Molecular Characterization of Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Producing *Klebsiella pneumoniae* Isolated from Swine Farms in Malaysia. *Microbial Drug Resistance*. 2019;25 (7).

20. Daniel DS, Lee SM, Dykes GA, Rahman S. Public Health Risks of Multiple-Drug-Resistant Enterococcus spp. in Southeast Asia. *Appl Environ Microbiol.* 2015;81(18):6090-6097.
21. Bidewell CA, Williamson SM, Rogers J, Tang Y, Ellis RJ, Petrovska L, et al. Emergence of *Klebsiella pneumoniae* subspecies *pneumoniae* as a cause of septicaemia in pigs in England. *PLoS One.* 2018;13(2): e0191958.
22. Van Cuong N, Nhung NT, Nghia NH, et al. Antimicrobial consumption in medicated feeds in vietnamese pig and poultry production. *Ecohealth.* 2016;13(3):490-498.
23. Moran D. Antimicrobial resistance in animal agriculture: understanding user attitudes and behaviours. *Vet Rec.* 2017;181(19):508-509.
24. Davis GS, Price LB. Recent research examining links among *Klebsiella pneumoniae* from food, food animals, and human extraintestinal infections. *Curr Environ Health Rep.* 2016;3(2):128-135.
25. Ahangarzadeh RM, Langarizadeh N, Aghazadeh M. First report of class 1 and class 2 integrons in multidrug-resistant *Klebsiella pneumoniae* isolates from northwest Iran. *Jpn J Infect Dis.* 2012;65(3):256-259.
26. Chowdhury PR, Ingold A, Vanegas N, Martínez E, Merlino J, Merlier AK, et al. Dissemination of multiple drug resistance genes by class 1 integrons in *Klebsiella pneumoniae* isolates from four countries: a comparative study. *Antimicrob Agents Chemother.* 2011; 55:3140-49.
27. Xu H, Huo C, Sun Y, Zhou Y, Xiong Y, Zhao Z, et al. Emergence and molecular characterization of multidrug-resistant *Klebsiella pneumoniae* isolates harboring bla CTX-M-15 extended-spectrum β -lactamases causing ventilator-associated pneumonia in China. *Infect Drug Resist.* 2018; 12:33-43.
28. Xu H, Miao V, Kwong W, Xia R, Davies J. Identification of a novel fosfomycin resistance gene (fosA2) in *Enterobacter cloacae* from the Salmon River, Canada. *Letts. Appl. Microbiol.* 2011; 52:427-429.
29. Ito R, Mustapha MM, Tomich AD, Callaghan JD, McElheny CL, Mettus RT, et al. Widespread fosfomycin resistance in gram-negative bacteria attributable to the chromosomal fosA gene. *mBio.* 2017;8(4): e00749-17.
30. Health Action International Asia Pacific (HAIAP) Third World Network (TWN) Penang in association with Consumers' Association of Penang. 2013. Antibiotic Use and Antibiotic Resistance in Food Animals in Malaysia: A Threat to Human and Animal Health.
31. Li B, Zhao Y, Liu C, Chen Z, Zhou D. Molecular pathogenesis of *Klebsiella pneumoniae*. *Future Microbiol.* 2014;9(9):1071-1081.
32. Fang CT, Chuang YP, Shun CT, Chang SC, Wang JT. A novel virulence gene in *Klebsiella pneumoniae* strains causing primary liver abscess and septic metastatic complications. *J Exp Med.* 2004; 199:697-705
33. El Fertat-Aissani R, Messai Y, Alouache S, Bakour R. Virulence profiles and antibiotic susceptibility patterns of *Klebsiella pneumoniae* strains isolated from different clinical specimens. *Pathol Biol.* 2013; 61:209-216. doi: 10.1016/j.patbio.2012.10.004.
34. Grady C, Dickert N, Jawetz T, Gensler G, Emanuel E. An analysis of U.S. practices of paying research participants. *Contemporary Clinical Trials.* 2005;26(3):365-375.
35. Paterson DL, Bonomo RA. Extended-Spectrum beta-Lactamases: a Clinical Update. *Clinical Microbiology Reviews.* 2005;18(4):657-86
36. Yeh KM, Kurup A, Siu LK, Koh YL, Fung CP, Lin JC, et al. Capsular serotype K1 or K2, rather than magA and rmpA, is a major virulence determinant for *Klebsiella pneumoniae* liver abscess in Singapore and Taiwan. *J Clin Microbiol.* 2007;45(2):466-471.
37. Qureshi, S. *Klebsiella Infections Treatment & Management.* M. Bronze, Ed. 2015; <http://emedicine.medscape.com/article/219907-treatment>.
38. Wachino J, Yamane K, Suzuki S, Kimura K, Arakawa Y. Prevalence of fosfomycin resistance among CTX-M-producing *Escherichia coli* clinical isolates in Japan and identification of novel plasmid-mediated fosfomycin-modifying enzymes. *Antimicrob Agents Chemother.* 2010;54(7):3061-64.
39. Hou J, Yang X, Zeng Z, Lv L, Yang T, Lin D, et al. Detection of the plasmid-encoded fosfomycin resistance gene fosA3 in *Escherichia coli* of food-animal origin. *J. Antimicrob. Chemother.* 2013;68(4):766-770.
40. Chan J, Lo WU, Chow KH, Lai EL, Law PY, Ho PL. Clonal diversity of *Escherichia coli* isolates carrying plasmid-mediated fosfomycin resistance gene fosA3 from livestock and other animals. *Antimicrob. Agents Chemother.* 2015;60(1):537-543
41. Benzerara Y, Gallah S, Hommeril B, Genel N, Decré D, Rottman M, et al. Emergence of plasmid-mediated fosfomycin-resistance genes among *Escherichia coli* isolates, France. *Emerg Infect Dis.* 2017;23(9):1564-1567
42. Ur Rahman S, Ali T, Ali I, Khan NA, Han B, Gao J. The Growing Genetic and Functional Diversity of Extended Spectrum Beta-Lactamases. *Biomed Res Int.* 2018; 2018:9519718.
43. Magiorakos AP, Srinivasan A, Carey RB, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012;18(3):268-81.
44. Nematzadeh S, Shahcheraghi F, Iversen A, Giske CG. Successful international clones of blaCTX-M-15-producing *Klebsiella pneumoniae* with coexpression of plasmid-mediated quinolone resistance (PMQR) determinants in Tehran hospitals. *Diagnostic Microbiology and Infectious Disease.* 2015;83(4):371-374.
45. Zhou K, Lokate M, Deurenberg RH, et al. Characterization of a CTX-M-15 Producing *Klebsiella pneumoniae* Outbreak Strain Assigned to a Novel Sequence Type (1427). *Front Microbiol.* 2015; 6:1250.
46. Al-Marzooq F, Mohd Yusof MY, Tay ST. Molecular Analysis of Antibiotic Resistance Determinants and Plasmids in Malaysian Isolates of Multidrug Resistant *Klebsiella pneumoniae*. *PLoS One.* 2015;10(7): e0133654.
47. García-Cobos S, Köck R, Mellmann A, Frenzel J, Friedrich AW, Rossen JW. Molecular Typing of Enterobacteriaceae from Pig Holdings in North-Western Germany Reveals Extended- Spectrum and AmpC β -Lactamases Producing but no Carbapenem Resistant Ones. *PLoS One.* 2015;10(7): e0134533

48. Webb HE, Bugarel M, den Bakker HC, et al. Carbapenem-Resistant Bacteria Recovered from Faeces of Dairy Cattle in the High Plains Region of the USA. *PLoS One*. 2016;11(11): e0147363.
49. Köck R, Daniels-Haardt I, Becker K, et al. Carbapenem-resistant Enterobacteriaceae in wildlife, food-producing, and companion animals: a systematic review. *Clin Microbiol Infect*. 2018;24(12):1241-1250
50. Zhang S, Yang G, Ye Q, Wu Q, Zhang J, Huang Y. Phenotypic and Genotypic Characterization of *Klebsiella pneumoniae* Isolated from Retail Foods in China. *Front Microbiol*. 2018; 9:289.
51. Wu H, Wang M, Liu Y, et al. Characterization of antimicrobial resistance in *Klebsiella* species isolated from chicken broilers. *Int J Food Microbiol*. 2016; 232:95-102.
52. Effendi MH, Bintari IG, Aksono EB, Hermawan IP. Detection of *bla*TEM Gene of *Klebsiella pneumoniae* Isolated from Swab of Food Producing Animals in East Java. *Tropical Animal Science Journal*. 2018;41(3):174-178.
53. Ahmed AM, Shimamoto T. Molecular characterization of antimicrobial resistance in gram-negative bacteria isolated from bovine mastitis in Egypt. *Microbiol. Immunol*. 2011;55: 318-27.
54. Founou LL, Founou RC, Essack SY. Antibiotic Resistance in the Food Chain: A Developing Country-Perspective. *Front Microbiol*. 2016; 7:1881.
55. Yang Y, Zhang A, Lei C, Wang H, Guan Z, Xu C, et al. Characteristics of plasmids coharboring 16S rRNA methylases, CTX-M, and virulence factors in *Escherichia coli* and *Klebsiella pneumoniae* isolates from chickens in China. *Foodborne Pathog Dis*. 2015;12(11):873-880.
56. Ovejero CM, Escudero JA, Thomas-Lopez D, Hoefer A, Moyano G, Montero N, et al. Highly tigecycline-resistant *Klebsiella pneumoniae* sequence type 11 (ST11) and ST147 isolates from companion animals. *Antimicrob Agents Chemother*. 2017;61(6): e02640-16.
57. Gu D, Dong N, Zheng Z, Lin D, Huang M, Wang L, et al. A fatal outbreak of ST11 carbapenem-resistant hypervirulent *Klebsiella pneumoniae* in a Chinese hospital: a molecular epidemiological study. *Lancet Infect Dis*. 2018;18(1):37-46.
58. Jacobson RK, Manesen MR, Moodley C, Smith M, Williams SG, Nicol MP, et al. Molecular characterisation and epidemiological investigation of an outbreak of *bla*OXA-181 carbapenemase-producing isolates of *Klebsiella pneumoniae* in South Africa. *S Afr Med J*. 2015; 105:1030-1035.
59. Rafiq Z, Sam N, Vaidyanathan R. Whole genome sequence of *Klebsiella pneumoniae* U25, a hypermucoviscous, multidrug resistant, biofilm producing isolate from India. *Mem Inst Oswaldo Cruz*. 2016;111(2):144-146.
60. Belbel, Z., Chettibi, H., Dekhil, M., Ladjama, A., Nedjai, S., and Rolain, J.-M. Outbreak of an *armA* methyltransferase-producing ST39 *Klebsiella pneumoniae* clone in a pediatric Algerian Hospital. *Microb. Drug Resist*. 2014; 20:310-315.
61. Carlet J, Jarlier V, Harbarth S, et al. Ready for a world without antibiotics? The Pensières Antibiotic Resistance Call to Action. *Antimicrob Resist Infect Control*. 2012;1(1):11.
62. Sadikin, ZD. Rational Use of Drugs. *J Indonesia Med Assoc*. 2011; 61(4).
63. Effendi, M.H., Oktavianto, A and Hastutiek, P. Tetracycline Resistance Gene in *Streptococcus Agalactiae* Isolated from Bovine Subclinical Mastitis in Surabaya, Indonesia. *Philipp. Journal of Veterinary Medicine*. 2018; 55 (SI): 115-120.
64. Tyasningsih, W., Effendi, M. H., Budiarto, B., & Syahputra, I. R. Antibiotic Resistance to *Staphylococcus aureus* and Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolated from Dairy Farms in Surabaya, Indonesia. *Indian Vet J*, 2019; 96(11), 27-31.
65. Putra, A.R. Effendi, M.H. Koesdarto, S. Suwarno, S. Tyasningsih, W. and Estoepangestie, A.T. Detection of the extended spectrum β -lactamase produced by *Escherichia coli* from dairy cows by using the Vitek-2 method in Tulungagung regency, Indonesia. *Iraqi Journal of Veterinary Sciences*, 2020; 34 (1): 203-207.
66. Putra ARS, Effendi MH, Koesdarto S, and Tyasningsih W. Molecular Identification of Extended Spectrum Beta-Lactamase (ESBL) Producing *Escherichia coli* Isolated from Dairy Cows in East Java Province, Indonesia. *Indian Vet. J*. 2019; 96 (10): 26 - 30.
67. Widodo, A., Effendi, M.H., Khairullah, A.R. Extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* from livestock. *Sys Rev Pharm*, 2020;11(7): 382-392.
68. Effendi M.H, Harijani N, Budiarto, Triningtya N.P, Tyasningsih W. and Plumeriastuti H. Prevalence of Pathogenic *Escherichia Coli* Isolated from Subclinical Mastitis in East Java Province, Indonesia. *Indian Vet. J*. 2019; 96 (03): 22 - 25.
69. Riwu KHP, Effendi MH, Rantam FA. A review of extended-spectrum β -Lactamase (ESBL) producing *Klebsiella pneumoniae* and Multidrug-Resistant (MDR) on companion animals. *Sys Rev Pharm*, 2020; 11 (7): 270-277.
70. Rahmaniar, R. P., Yunita, M. N., Effendi, M. H., Yanestria, S. M. Encoding Gene for Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolated from Nasal Swab of Dogs. *Indian Vet. J*, 2020; 97(02), 37-40.
71. Kristianingtyas L, Effendi, MH, Tyasningsih W, Kurniawan F. Genetic Identification of *bla*CTX-M Gene and *bla*TEM Gene on Extended Spectrum Beta Lactamase (ESBL) Producing *Escherichia Coli* from Dogs. *Indian Vet. J*. 2020; 97 (01): 17 - 21
72. Decline, V., Effendi, M. H., Rahmaniar, R. P., Yanestria, S. M., Harijani, N. Profile of antibiotic-resistant and presence of methicillin-resistant *Staphylococcus aureus* from nasal swab of dogs from several animal clinics in Surabaya, Indonesia. *Intl J One Health*, 2020; 6(1), 90-94.
73. Yunita, M. N., Effendi, M. H., Rahmaniar, R. P., Arifah, S., Yanestria, S. M. Identification Of Spa Gene For Strain Typing Of Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolated From Nasal Swab Of Dogs. *Biochem. Cell. Arch*. 2020; 20 (1), 2999-3004.
74. Wibisono FJ, Sumiarto B, Untari T, Effendi MH, Permatasari DA, Witaningrum AM. The Presence of Extended Spectrum Beta-Lactamase (ESBL) Producing *Escherichia coli* On Layer Chicken Farms In Blitar Area, Indonesia. *Biodiversitas*. 2020; 21 (6): 2667-2671.

75. Rahmahani J, Salamah, Mufasirin, Tyasningsih W, and Effendi MH. Antimicrobial Resistance Profile of *Escherichia coli* From Cloacal Swab of Domestic Chicken in Surabaya Traditional Market. *Biochem. Cell. Arch.* 2020; 20 (1): 2993-2997.
76. Wibisono, F.J., Sumiarto, B., Untari, T., Effendi, M.H., Permatasari, D.A., Witaningrum, A.M. CTX Gene of Extended Spectrum Beta-Lactamase (ESBL) Producing *Escherichia coli* on Broilers in Blitar, Indonesia. *Sys Rev Pharm* 2020;11(7): 396-403.
77. Helmi, AM, Mukti, AT, Soegianto, A and Effendi, MH. A Review of Vibriosis in Fisheries: Public Health Importance. *Sys Rev Pharm*, 2020;11(8):51-58
78. Helmi, AM., Mukti, AT., Soegianto, A., Mahardika, K., Mastuti, I., Effendi, MH., Plumeriastuti, H. A Review of Bacterial Zoonoses and Antimicrobial Resistant (AMR) on Grouper fish (*Epinephelus sp.*). *Sys Rev Pharm* 2020;11(9):79-88
79. Yanestria, S.M., Rahmانيar, R.P., Wibisono, F.J., Effendi, M.H. Detection of *invA* gene of *Salmonella* from milkfish (*Chanos chanos*) at Sidoarjo wet fish market, Indonesia, using polymerase chain reaction technique, *Veterinary World*, 2019; 12(1): 170-175.
80. Khairullah, AR, Sudjarwo, SA, Effendi, MH, Harijani, N, Tyasningsih, W, Rahmahani, J, Permatasari, DA, Ramandinianto, SC, Widodo, A, Riwu, KHP.. A Review of Methicillin-Resistant *Staphylococcus aureus* (MRSA) on Milk and Milk Products: Public Health Importance. *Sys Rev Pharm* 2020;11(8): 59-69.
81. Ramandinianto, S.C., Khairullah, A.R., Effendi, M.H., Tyasningsih, W. and Rahmahani, J. Detection of Enterotoxin type B gene on Methicillin Resistant *Staphylococcus aureus* (MRSA) isolated from raw milk in East Java, Indonesia. *Sys Rev Pharm*, 2020;11(7):290-298.
82. Effendi, MH., Cicilia, R., Rahmahani, J., Tyasningsih, W. 2020. Public Awareness for Antimicrobial Resistance from *Escherichia coli* Isolated from Beef Sold on Several Wet Market in Surabaya, Indonesia. *Indian Journal of Public Health Research & Development*, 2020; 11(9): 295-300.

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Yamê Miniero Davies, Marcos Paulo Vieira Cunha, Milena Dropa, Nilton Lincopan et al. "Pandemic Clones of CTX-M-15 Producing *Klebsiella pneumoniae* ST15, ST147, and ST307 in Companion Parrots", *Microorganisms*, 2022

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Luria Leslie Founou, Raspail Carrel Founou, Mushal Allam, Arshad Ismail, Sabiha Yusuf Essack. "Draft genome sequence of an extended-spectrum β -lactamase (CTX-M-15)-producing *Escherichia coli* ST10 isolated from a nasal sample of an abattoir worker in Cameroon", *Journal of Global Antimicrobial Resistance*, 2018

Publication

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Matthew E. Falagas, Evridiki K. Vouloumanou, George Samonis, Konstantinos Z. Vardakas. "Fosfomycin", *Clinical Microbiology Reviews*, 2016

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Yone da Silva, Rafaela Ferrari, Victor Augustus Marin, Carlos Adam Conte Junior. "A Global Overview of β -lactam Resistance Genes in *Klebsiella pneumoniae*", *The Open Infectious Diseases Journal*, 2019

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