

# **Animal Health Research Journal**

P-ISSN : 2356-7767 On Line-ISSN : 2535-1524 Journal Homepage: https://animalhealth.ahri.gov.eg/ Review Article

Using of some plant extracts against multidrug resistant klebsiella species isolated from different sources

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Received in 15/4/2025 Received in revised from 14/4/2025 Accepted in 19/6/2025

Keywords:

Klebsiella, pneumoniae, antimicrobial resistance, plant extract

Abstract lebsiella species specially klebsiella pneumoniae considered an important pathogenic bacteria affecting human causing (pneumonia, gastrointestinal problems), animal causing (mastitis, respiratory disorders and neonatal septicemia) and has a significant public health concern due to its presence in various food sources (raw, cooked, and processed meats, vegetables, fruits, milk and milk products) and its multiple resistance to different antimicrobial agents, these resistance cause a great threat world wide, because using of these different antibiotics become of no value and the side effect of these different drugs affect human and animal health. These bacteria become more virulent and resistant due to the biofilm formation which is the ability of microbe to protect itself from the surroundings and immune system of the host. therefore, searching for anew approach to overcome this problem become in concern, like medicinal plants and their extracts which used as antimicrobial agents against many animal and human pathogens like klebsiella species, the derived compounds from these plants has antimicrobial action evaluated through laboratory trials after isolation and identification of bacteria (klebsiella species), so that this review aimed to increased awareness and gather information about this micobe and its prevalence from different sources, resistance profiles, virulence factors and different plant extract used against K. pneumoniae to assess the risks to public health and made effective strategies to control its impact on consumers.

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#### Introduction

Klebsiella spp is an important pathogen and Avery common member of the Enterobacteriaceae found in Intestinal tract of animals and man, soil, water, sewage, plants, other places in the environment as sawdust cause severe bacterial infections of the cardiovascular, respiratory, gastrointestinal, renal systems in humans and animals, also normally found in human stool (feces) that can cause healthcareassociated infections (HAIs). (Kowalczyk et al., 2022; Wareth and Neubauer, 2021) and also are a common contaminant in many fresh foods such as meat, milk, fish, vegetables and products such as street food. Therefore, they were considered a significant foodborne pathogen (Davis and Price, 2016; Kakatkar et al., 2017). Klebsiella are non motile, rod-shaped, gram-negative bacteria with a prominent polysaccharide capsule. This capsule encases the entire cell surface, accounts for the large appearance of the organism on gram stain, and provides resistance against many host defense mechanisms. Klebsiella species are serogrouped by 2 types of antigens on their cell surface. The first is a lipopolysaccharide (O antigen); the other is a capsular polysaccharide (K antigen). Both of these antigens contribute to pathogenicity. About 77 K antigens and 9 O antigens exist. The structural variability of these antigens forms the basis for classification into various serotypes. The virulence of all serotypes appears to be similar. Klebsiella have been described.K1,K2 and K5 are venereal transmitted and are the predominant types in the isolates from metritis in mares. (Markey et al. 2013). The genus Klebsiella has many species are associated with illness in humans and animals as K. aerogenes, previously known as Enterobacter aerogenes and Bacterium aerogenes K. granulomatis, K. oxytoca, K. michiganensis, K. pneumoniae (type-species) (K.p. subsp. Ozaenae K. p. subsp. Pneumonia, K.p. subsp. Rhinoscleromatis) K. quasi pneumoniae(K.q. subsp. Quasipneumoniae, K. q. subsp. Similipneumoniae), K. grimontii and K. variecola. (NCBI2019).

# Antimicrobial resistance (AMR) of Klebsiella organisms

Klebsiella organisms are resistant to multiple antibiotics. This is thought to be a plasmid-

mediated property. They secrete β lactamases enzymes responsible for antibiotic resistance, with genes blaTEM, blaSHV, blaCTX-M, and blaOXA detected globally, facilitating the transfer between different environments, humans, and animals (**Khameneh** *et al.*, 2019 and **Wu** *et al.*, 2022). Many factors lead to multidrug resistance and transfer of Klebsiella organisms as:

**1-** Length of hospital stay and performance of invasive procedures are risk factors for acquisition as it an opportunistic pathogen that has rapidly spread worldwide causing nosocomial and community-acquired infections (Sarowska et al., 2022; Tian et al., 2023), Due to their colonization to the medical instruments and equipment in hospitals and transmitted through the hands of medical staff and their contact with patients (Pruss et al., 2023). Those Hospital-acquired infections lead to pneumonia, UTI, wound and gastrointestinal infections and primary or secondary bacteremia, The mortality rate of hospital-acquired pneumonia caused by K. pneumoniae reach more than 50% (Li et al., 2023). Klebsiella pneumoniae causes of nearly 10% of nosocomial infections in Western countries that exhibit multidrug resistance and virulence:. Which known for high phenotypic and genetic diversity, in particular regarding antimicrobial-resistance genes (ARGs) a (Chiaverini et al., 2022).

2- Food as a vehicle for transmitting antimicrobial-resistant bacteria to humans. MDR K. pneumoniae isolates have also been widely detected in milk samples and meat so they transfer from food handlers and consuming unpasteurized milk and raw meat, lead to severe infections such as septicemia and liver abscesses, occurrence of antimicrobial-resistant strains which cause significant public health risks (ALzubaidi and Alkhafaji 2022), The World Health Organization (WHO) represent AMR of *K. pneumoniae* in food vary according to location, food type, and antibiotic use in veterinary medicine. The WHO has classified carbapenem-resistant and third-generation cephalosporin-resistant Enterobacteriaceae, including K. pneumoniae, as critical pathogens needing new treatments, The Centers for Disease Control and Prevention (CDC) have identified K. pneumoniae as one of the ESKAPEE pathogens (Enterococcus faecium, Staphylococcus

aureus, K. pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp and Escherichia coli), highly concerning drug-resistant organisms with significant public health importance (World Health Organization (WHO). 2017).

3– Many virulence genes of Klebsiella organisms like Uge (responsible for smooth lipopolysaccharide and capsule synthesis) and Kfu (iron uptake system), These virulence factors, combined with antibiotic resistance, make klebsiella a significant threat and frequently produces ESBLs, leading to multidrug resistance (El Fertas et al., 2013). Antibiotic resistance was considered a problem to human health, caused by excessive and inappropriate use of antibiotics in human medicine and many sectors (agriculture, animal management and aquaculture) has been increasingly recognized as an important driver of antibiotic resistance. (Sivaraman et al., 2021).

The emergence of antimicrobial resistance in, such as the extended-spectrum  $\beta$ -lactamases (ESBL) and AmpC  $\beta$ -lactamases, is threatening the future of the application of  $\beta$ -lactam drugs in both humans and animals. Antimicrobial resistance increases the risk of antimicrobial treatment failure in humans and animals also are transmitted to humans. Therefore, identification of antibiotic susceptibilities and genetic characteristics of ESBL and AmpC  $\beta$ -lactamases-producing Klebsiella spp. has an important role in the treatment of pathogenic infections. (**Davis** *et al.*, 2015).

The results of antibiotic sensitivity test showed that the highest resistance was to ampicillin (100%), followed by chloramohinicol (76.7%) and the highest sensitivity was to gentamycin (100%), followed by ciprofluxacin and erythromycin (76.7%), nalidexic (73.33%), and streptomycin (53.4%). (Ramadan et al., 2023) which come in agree with (Chiaverini et al., **2022)** who detect 17 isolates (100%) were resistant at least to one antimicrobial. Regarding β-lactams, all K. pneumoniae isolates were resistant to ampicillin, cloxacillin, and cefazolin. All the 16 K. pneumoniae isolates were susceptible to aminoglycosides (amikacin, gentamicin, netilmicin, and kanamycin), and Gomaa (2021) who found that all K. pneumonia isolates were resistant to ampicillin and amoxacil-(100%)lin-clavulinic acid followed

cefepime (72.72%), tetracycline, trimethoprime and trimethoprime/sulphamethaxole (54.54% each), while they were sensitive to imipenem (82%) followed by aztreonam (55%) then amikacin and azithromycin (45%).

In the study by (Wu et al. 2022), the MDR rate was 44%, and the prevalence of blaTEM, blaSHV (b-lactam resistance genes), strA, strB, aadA1 (aminoglycoside resistance genes), aac (60)-Ib-cr (resistance gene on quinolones gene) was over 50%. (Cao et al. 2023) showed strong resistance to β-lactam drugs related to the presence of blaSHV (100%) and blaTEM (65%) genes. It was also found that K. pneumoniae isolates carried genes encoding carbapenem resistance (blaNDM-1 - 37%, bla-VIM - 18%, blaOXA-10 - 19%). Yang et al. (2021) found that 71% of K. pneumoniae isolates in eastern provinces of China harboured at least one of the antimicrobial resistance genes. Among them, blaSHV(68%), blaCTX-M (17%), aac(60)-Ib (15%), aac(60)-II (3%), aph(30)-I (24%), ant(300)-I (20%) and tetA (30%) were found.

The following antimicrobial resistance genes were identified by (Massé et al., 2019): tetA, tetB, sul1, strA/strB, and aadA. Random amplified polymorphic DNA revealed the majority of our isolates as unrelated and having different patterns, indicating environmental contamination as the primary source of infection. All isolates were shown to be biofilm producers Klebsiella isolates showed more than 40% resistance to penicillin, cephalosporin, fluoro-

sistance to penicillin, cephalosporin, fluoro-quinolone, and aminoglycoside. ESCresistance genes, CTX-M groups (CTX-M-3, CTX-M-15, and CTX-M-65), and AmpC (CMY-2 and DHA-1) were most common in the *K. pneumoniae* strains. Some *K. pneumoniae* carrying CTX-M or AmpC were transferred via IncFII plasmids. Two sequence types, ST709 and ST307, from *K. pneumoniae* were most common (Lee *et al.*, 2021).

The prevalence rate of *K. pneumoniae* in milk samples from mastitic cows was 4% (2/50). The antimicrobial susceptibility results showed that *K. pneumoniae* isolates had high resistance rates to ampicillin and ampicillin/clavulanate (100% each) followed by azithromycin, cefepime, and trimethoprim/sulphamethoxazole (91.7% each). Meanwhile, these isolates show high sensitivity levels to chloram-

phenicol (83.3%), Furthermore, 91.7% of *K. pneumoniae* isolates were able to produce the biofilm, where 8.3% was a non-biofilm producer. Out of 11 *K. pneumoniae* isolates, 6 (54.5%), 3 (27.3%) and 2 (18.2%) were moderate, strong and weak biofilm producers, respectively that can be determined by (**Ammar etal 2021**).

# Prevalence of Klebsiella species from different sources:-

#### From human

Klebsiella species can lead to a wide range of disease states, notably pneumonia, urinary tract infections, sepsis, meningitis, diarrhea, peritonitis and soft tissue infections. The majority of human Klebsiella infections are caused by K. pneumoniae, cause serious diseases, including bloodstream infections, pneumonia, sis, meningitis, pyogenic liver abscesses, infections of the urinary tract and wounds (Paczosa and Mecsas, 2016; Kot et al., 2023). lowed by K. oxytoca. Which associated with antibiotic-associated hemorrhagic colitis. antibiotic-associated diarrhea, It is postulated that the overgrowth of cytotoxin-producing strains of K. oxytoca in the colon during antibiotic therapy can cause direct mucosal damage and hemorrhagic changes The right colon is preferentially affected, but disease may extend to the transverse and descending segments. Mucosal edema, erosion, and longitudinal ulcers are also typical Infections are more common in the very young, very old, and those with other underlying diseases, such as cancer and most infections involve contamination of an invasive medical device (Nicole and Panarelli 2024)

#### Klebsiella From animal

Klebsiella spp cause economic problems in farm animals as causing mastitis in dairy cows and affect animal welfare due to pain from infection, Also cause respiratory disorders in ruminants and neonatal septicemia in calves (Cheng et al., 2020). Klebsiella species could be isolated from different sources most of them were from pig, cattle, pork and milk and the rest of isolates were isolated from vegetables, pets, livestock and farm animals (Klaper et al., 2021). Infections with Klebsiella spp. cause a variety of syndromes in livestock, the most important being endometritis, infertility and abor-

tion in mares, mastitis in cows and sows, and neonatal septicaemia, particularly in foals.. K. pneumoniae could be isolated by (Ramadan et al., 2023) from clinically diseased cattle and buffaloes in percent of 10.5% and 8.33% from cattle and buffaloes respectively (nasal swabs, milk samples, anal swabs) Klebsiella species can be isolated from clinical mastitis cases in Canada, were identified to Klebsiella pneumoniae (n = 40), Klebsiella oxytoca (n = 9), Raoultella ornithinolytica (n = 2), and Raoultella planticola (n = 2). Raoultella, a genus closely related to Klebsiella (Massé et al., **2020).** It is isolated in 2 to 9% of milk samples from clinical mastitis cases by (Levison et al., **2016)**, it Can cause mammary gland infection characterized by severe clinical signs a major decrease in milk production and leads to economic losses. Affected animals are frequently removed from the herd (Sugiyama et al., 2022; Fuenzalida and Ruegg, 2019). The prevalence of Klebsiella from clinically mastitic cows was 36% of milk samples positive detected by (Fu et al., 2022), also Klebsiella spp. in clinical bovine mastitis showed 7% higher than in subclinical cases (4%) detected by (Liu et al. 2022), The prevalence of K. pneumoniae in the northern areas of China was 3% in 2018 and 2019 (Song et al., 2022), 10% (Yang et al., 2021) or 15% (Cao et al., 2023) in the eastern provinces (Jiangsu and Shandong) the prevalence was 27% (Wu et al., **2022).** The prevalence of *K. pneumoniae* in China indicates that these bacteria pose an increasing hazard to the dairy industry.

Bovine mastitis caused by Klebsiella spp is difficult to be controlled, decrease milk production, increase mortality rate and this microorganism has a zoonotic importance, overall, *K. pneumoniae* strains were detected in 90 (81.8%) samples, 23 (25.6%) were from chicken, 32 (35.6%) from bovine samples and 35 (38.9%) from pork. Moreover, 23 of 35 (65.7%) chicken samples, 32 of 35 (91.4%) bovine samples, and 35 of 40 (87.5%) pork samples were positive for *K. pneumonia* (Langoni *et al.*, 2015).

K. pneumoniae become a source of human infection due to its presence in livestock, retail meats, and vegetables, Contaminated food including vegetables, raw meat, and dairy products (Riwu et al., 2022). on dairy farms organ-

samples from West Bengal and Himachal Pradesh, respectively, were positive for ESBL-producing *K. pneumonia* (Bandyopadhyay et al., 2018). A multi-state study in India found that 4.4%, 13%, and 6% of bovine milk samples from West Bengal, Jharkhand, and Mizoram, respectively, contained ESBL-producing *K. pneumoniae* (Koovapra et al., 2016). In Lebanon, 23.4% of milk samples from healthy cattle tested positive for *K. pneumoniae* using MALDI-TOF-MS, and all were ESBL producers.

K. pneumoniae has been found in milk and milk products including camel's milk, raw cow's milk, raw fermented milk, Ricotta cheese, soft cheese, full cream milk powder, milk powder infant formula, cereal baby food, and growing-up formula., Out of 234 samples, 16 (6.8%) exhibited mucoid colonies indicative of K. pneumoniae. This identification was confirmed using 16S rRNA molecular techniques. Antibiotic susceptibility tests on 12 of the isolates showed resistance to more than eight antibiotics, with two isolates producing metallobeta-lactamase (MBL). (Azwai et al., 2024).

K. pneumoniae from Fruits and Vegetables:-A South Korean study found that 8.5% of ready-to-eat (RTE) vegetables K.pneumoniae, with 69% of the isolates carrying blaTEM-1, 94% carrying blaSHV, 50% carrying blaCTX-M-14, and 19% carrying blaCTX-M-15 (He et al., 2016) In Oman, 13 K. pneumoniae isolates were recovered from 105 fresh raw vegetable and fruit samples (Al-Kharousi et al., 2016). In Algeria, 13 thirdgeneration cephalosporin-resistant K. pneumoniae isolates from fresh fruits and vegetables were found to harbor sulfonamide, quinolone, β-lactam, and aminoglycoside resistance genes (Mesbah Zekar et al., 2020) K. pneumoniae has also been detected in sugarcane juice, showing resistance to antimicrobials like gentamicin, kanamycin, and neomycin.

In China, a mcr-1 carrying *K. pneumoniae*was isolated from fresh fruit samples, also containing resistant genes blaSHV-110, tetA, and qnrS1 (Yang *et al.*, 2019) A Singapore study found *K. pneumonia* in 15% of RTE foods and 45% of raw food samples like vegetables and meat, although only 7% of RTE foods carried a virulence gene (Hartantyo *et al.*, 2020). In

Ethiopia, 12.3% of food handlers had a fecal carriage of *K. pneumonia* (Eibach et al., 2018). European studies reported *K. pneumoniae* in ready-to-eat raw vegetables like carrots, tomatoes, and pumpkins, with resistance genes identified through whole genome sequencing (Centorotola et al., 2021). Additionally, *K. pneumoniae* was isolated from cheese manufacturing plants and raw materials like milk powder and cheese cans (Giri et al., 2021). A 2022 multicentric study in Europe found high levels of *K. pneumoniae* in chicken meat (60%) and salads (30%) (Rodrigues etal., 2022).

### 1) Microbiology of klebsiella:-

# a) Morphology and Culture characters:-

Klebsiella were gram negative bacilli arranged single or in short chain, can grow in many media as Tryptic soya agar appeared as large, smooth, raised, and cream yellow colonies. While on MacConkey agar appears as large, pink, round, smooth, and muciod colony. On XLD yellow muciod colony, on Brilliant green agar yellow—green colonies, on EMB violet metallic muciod colonies and on blood agar non hemolytic colonies were observed. (Markey et al. 2013, He et al. 2022; Ramadan et al., 2023).

# b) Virulence factors:-

K. pneumoniae pathogenicity is associated with several virulence factors including capsules, siderophores, LPSs, and pili that help it to invade the host's immune system these virulence factors include capsules, exo- polysaccharides ,lipo-polysaccharides (LPSs), adhesins, and iron uptake systems. these factors cause multiple antibiotic resistance and nosocomial infections in humans, The capsule is a significant virulence factor, involved in two pathogenic mechanisms, that is, the protection of bacteria from phagocytosis and direct inhibition of the vulnerable host response. Several capsule types (K), especially, K1, K2, K54, K57, K20, and K5, are associated with pyogenic liver abscess, septicemia, and pneumonia. (Wei et al., 2016, Cheng et al., 2020, Parrott et al., 2021).

Capsular antigen can prevent *K. pneumoniae* from being recognized by the host immune system through some immune escape mechanisms such as antiphagocytosis, inhibition of

ic bedding materials and cattle feces are sources of Klebsiella species, which lead to contamination of dairy products (Cheng et al., 2021).

#### K. pneumoniae from Meat

K. pneumoniae has been detected in various meat sources worldwide, particularly in beef, pork, chicken, mutton, and chevon. Studies have shown a prevalence of K. pneumoniae in chicken ranging from 3.6% to 60%. In one study, 31 out of 70 samples of beef, turkey, and chicken from grocery stores tested positive for K. pneumoniae and all isolates were resistant to antibiotics like ampicillin, tetracycline, streptomycin, gentamicin, and kanamycin. The most commonly detected resistance genes were aadA1, tetA, blaSHV-1, and blaTEM-1 (Kim et al., 2005). In Turkey, 21 K. pneumoniae isolates were recovered from 60 raw meat and chicken samples, with 28.3% being ESBL-producers, exhibiting resistance to extended-spectrum β-lactam antibiotics. Additionally, 55%, 53%, and 47% of isolates exhibited siderophore production, serum resistance, haemolytic activity, respectively and (Gundogan et al., 2007).

In the USA, a study on K. pneumoniae from food and clinical samples found that 32% of meat isolates were resistant to multiple drugs like ampicillin, gentamicin, and tetracycline, a higher percentage than in clinical samples (Diab 2017). In Ghana, a study found 81 ESBL-producing isolates out of 200 poultry meat samples, with 35 being K. pneumoniae, and blaCTX-M-15 detected in 86% of the isolates. The common sequence types were ST2570, ST147, and ST15 (Gaffer 2019). In Europe, a multi-centric study reported that 60% of chicken samples harbored K. pneumonia (Rodrigues, 2022), while in Turkey, 3.6% of raw chicken meat samples tested positive for ESBL-producing K. pneumonia (Tekiner and Özpınar, 2016).

Studies from Greece, South Africa, Iraq, and Assam reported high prevalence rates of *K. pneumoniae* in meat samples, with Greece showing 82% in pork, chicken, and beef (Theocharidi *et al.*, 2022), South Africa 32% in retail beef (Montso *et al.*, 2019), Iraq 76%

in retail beef (Klaif et al., 2019), and Assam 21.43% in beef (Chauhan et al., 2013). In Anand, Gujarat, 57% of chevon samples tested positive for K. pneumoniae (Prajapati et al., 2022), while in Pakistan, the prevalence was 36.4% in beef samples (Junaid et al., 2022). Another study from Iraq found a 56% prevalence in retail beef samples (Al-Dabbagh 2022), In Indonesia, 7.8% of chicken cloacal swabs were positive for K. pneumoniae, compared to 28% in a similar study from China (Hartantyo et al., 2020). In Gujarat, India, 6% of chicken meat samples tested positive for K. pneumoniae (Modh et al., 2021).

# K. pneumoniae from Street foods

A study in China tested various retail food samples, including meatballs and raw meat from different livestock species, for the presence of K. pneumoniae. They found a high percentage of virulence genes such as fimH, ureA, wabG, and uge. The isolates exhibited high resistance to ampicillin, streptomycin, piperacillin, and tetracycline, with nearly 18% being multidrug resistant (Zhang et al., 2018), Similarly, a study in India revealed that 28.12% of paani puris and chaats were positive for K. which was more common pneumoniae, (27.12%) than Escherichia coli (22.88%) in retail foods. The isolates showed high resistance to ampicillin, cefepime, cefuroxime, and cefotaxime. Additionally, eight isolates were metallo-beta-lactamase producers, and two isolates were positive for all three ESBL genes: blaCTX-M, blaSHV, and blaTEM (Giri *et al.*, 2021).

In Shijiazhuang city, China, 9.9% of 998 food samples tested were positive for *K. pneumoniae*. In Benin, nearly 20% of 216 street food samples were positive for *K. pneumoniae*, with 27% of isolates resistant to imipenem and 20% carrying ESBL genes (**Moussé** *et al.*, 2016).

K. pneumonia from Milk and Milk product

ESBL-producing *K. pneumoniae* has been found in raw milk and various milk products such as khoa, ice cream, kareish, and domiati cheese in studies from India (**Bobbadi** *et al.*, **2020**), Indonesia (**Budiarso** *et al.*, **2021**), and Egypt (**Gelbíčová** *et al.*, **2021**). In India, a study reported that 3% and 27% of bovine milk

early inflammatory response, neutralization of antimicrobial peptides to reduce the body's immune response (Paczosa and Mecsas, 2016), also these bacteria can absorb the iron of the host via four siderophores such as aerobactin, salmochelin, enterobactin and yersiniabactin for metabolism and enhance the virulence to cause infection (Wang et al., 2020).

K. pneumoniae has fimbriae : type 1 (fim) and type 3 (mrk) fimbriae. Type 1 fimbriae can enhance virulence by adhering to mucosal or epithelial surfaces and type 3 fimbriae adhere to the cell surface and promote biofilm formation (Schroll et al., 2010). Lipid A, a component of lipopolysaccharide, reduces the inflammatory response during K. pneumoniae infection and prevents the bactericidal effect of cationic antimicrobial peptides. O antigen is the outermost subunit of LPS, which eliminates the lysis of bacteria by the complement membrane attack complex (Paczosa and Mecsas, 2016). In a study by (Schonborn et al. 2017), 84% of Klebsiella spp. isolates were shown to produce visible biofilm formation in a tube method, biofilm formation for this pathogen in isolates recovered from bovine mastitis cases (Massé et al., 2019), This results is coordinated with that reported by (Massé et al. 2020). While, (Gomaa 2021) stated that 81.81% of K. pneumonia isolates could produce biofilms, those categorized as strong (33.33%), moderate (22.22%) or weak (44.44%) biofilm producers, whereas 18.18% of the isolates were nonbiofilm producers.

The ecpA gene was detected in *K. pneumoniae* strains from 14 (46.7%) chicken and 16 (53.3%) bovine specimens. Moreover, the fimH-1 and mrkA genes, encoding type 1 and type 3 fimbrial adhesins, were present in 15 (16.7%) and 65 (72.2%) strains of *K. pneumoniae* isolates, respectively. Among the 15 samples, the fimH-1 gene was present in 33.3% of the three categories of meat Products. Among the 65 isolates, the mrkA gene was present in 50 of the chicken and bovine meat products and 15 of the pork meat products (**Theocharidi** *et al.*, 2022).

K. pneumoniae can form biofilm which is one of the crucial conditions for maintaining its activity. and it accumulates in such cells em-

bedded in the self-generated matrix of the extracellular polymeric substance Extracellular polymeric substances are complex structures containing polysaccharides, proteins, and DNA. Many genes responsible for formation biofilm as blaNDM, fabZ; lpxC Biofilm homeostasis,, YfgL (BamB) biofilm formation; transcriptional expression of type 1 pili and KpOmpA Cell-cell recognition, adhesion, and immune response; pathogenicity (Guoying Wang et al. 2020).

Most clinically apparent *K. pneumoniae* biofilm is formed on the catheter and the inner surface of internal devices *K. pneumoniae* biofilm can lead to colonization in the respiratory, gastrointestinal, and urinary tracts, as well as the development of invasive infections (especially in immune-deficient patients). The development of *K. pneumoniae* biofilm on the surface of hard objects undergoes the adhesion of cells, the formation of small colonies, maturation, and the propagation as ultimately free-living cells.

The most important surface structures of K. pneumoniae involved in the formation process are type 3 pili and capsular polysaccharides (CPs) Pili mediate steady adhesion, while CPs ultimately affect biofilm structure and intercellular communication. Given the dynamics of biofilm formation and the variability of environmental stimuli, embedded bacterium must have the ability to rapidly and extensively change gene expression. Transcriptional regulation is regulated by quorum sensing, a system coordinating the signals and responses that control gene expression in a microbial population. The putative quorum-sensing-related regulators and autoinducers in K. pneumoniae have been identified, but the relevant available data is still incomplete (Clegg et al., **2016)**. *K. pneumoniae* with biofilm is protected from the host immune response, in part. This matrix inhibits the proximity of antibodies and antimicrobial peptides, and reduces the effects of complement and phagocytosis. Mutations in some specific genes of K. pneumoniae can also affect the function of biofilm. Found that fabZ and lpxC mutations lead to lpxC inhibitor-dependent growth of K. pneumoniae, which leads to the loss of biofilm homeostasis (Mostafavi et al., 2018). In recent years, the research on the outer membrane protein of K. pneumoniae has attracted the attention of researchers. Hsieh et al. (2016) reported that YfgL (BamB) lipoprotein is involved in the biofilm formation of K. pneumoniae and the transcriptional expression of type 1 pili, which is critical for the anti-phagocytosis of K. pneumoniae in vivo (Hsieh et al., 2016). Besides this, K. pneumoniae's outer membrane protein A (KpOmpA) is reported to be involved in cell adhesion and cell-cell recognition, as well as immune response of host. Meanwhile, the L3 site on the KpOmpA surface may be related to pathogenicity of K. pneumoniae (Saurel et al. 2017). Oxidative stress may oxidize and destroy the biofilm of K. pneumoniae, resulting in the loss of major membrane proteins and activity of K. pneumoniae

#### **Plant extracts**

Plant-derived chemicals are a large group of chemical compounds that have been found naturally in plants. The wide uses of these compounds are in the form of antioxidant, antibacterial, and antifungal activities. They enable the application of older antibiotics by increasing their efficacy and avoid the development of resistance. they will be classified into many major groups that include alkaloids, sulfurcontaining compounds, terpenoids, and polyphenols (Khameneh et al., 2019).

This approach provide a safe and low-cost medicinal plant having antibacterial activities with a promising future. More than half a million plants worldwide have medical uses essential to treat or prevent many infections with less toxicity and side effects and could be a good substitute for traditional synthetic chemical antibiotics and overcome multidrugresistant bacteria, The most important of these bioactive constituents are alkaloids, tannins, flavonoids, and phenol, all of which are accoutered for new antibacterial agents, It is believed that crude extracts from some medicinal plants are more biologically active than isolated compounds due to their synergistic effects. (Voon et al. 2012).

Plant extracts have shown promising antibacterial effects. This review focuses on the activities of some plant extract like green tea, cinna-

mon and *Rhazya stricta* leaf extracts against *K. pneumoniae*.

# The Rhazya stricta

The *Rhazya stricta* leaf extracts exerted antibacterial and antibiofilm effects against *K. pneumoniae*. Both ethanolic and methanolic extracts, rich in flavonoids and phenolic acids like quercetin and caffeic acid, were effective in inhibiting bacterial growth and biofilm formation. The ethanolic extract showed slightly better antibacterial and antibiofilm activities, with up to 98.7% biofilm inhibition, due to higher concentrations of compounds like quinol and p-coumaric acid. These findings suggest that *R. stricta* extracts could serve as promising way to cotrol *K. pneumoniae* infections (Hassan et al., 2023).

#### Green tea extract

Green tea extract (GTE) has a natural antimicrobial agent against *K. pneumoniae* (Aneja and Gianfagna, 2001). it contains compounds like catechins such as epicatechin gallate (ECg) and epigallocatechin gallate (EGCg), which disrupt bacterial cell membranes and inhibit essential bacterial enzymes (Zhao et al., 2001). Studies found that higher doses of GTE, such as 5 mL lead to significantly decrease in bacterial numbers. GTE can be used as natural solution to controlling contamination of *K. pneumoniae* in raw chicken meat (Kaderi et al., 2023).

#### **Cinnamon extract**

Cinnamon extract, rich in compounds like cinnamaldehyde and eugenol, these compounds target and disrupt the bacterial cell wall and membrane, leading to structural damage and cell death. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) for cinnamon extract were 500  $\mu$ l/ml, demonstrating its effectiveness as a bactericidal agent. (**Ouattara** *et al.*, 1997).

Cinnamon extract was more effective over a short duration within 6–8 hours. Similarly, green tea extract caused rapid cell death due to the hydrophobic nature of its compounds, which disrupt bacterial membranes, rendering them more permeable (El-Farmawi *et al.* 2014, Sikkema *et al.* 1995).

#### Lemon extract

Lemon extract, particularly from its peel, has shown antimicrobial activity against *K. pneumoniae* (Nada et al., 2024). The bioactive compounds in lemon, such as flavonoids, essential oils, and limonoids, disrupt bacterial cell walls and inhibit growth (Harfouch et al. 2019). Studies have demonstrated that ethanolic and methanolic extracts of lemon peel are more effective than aqueous extracts. However, *K. pneumoniae* tends to exhibit higher resistance compared to Gram-positive bacteria (Hindi & Chabuck 2013).

#### Conclusion

Klebsiella spp is a opportunistic bacterium that can survive and difficult to eradicate once present in the food system. To prevent its spread, it is essential to implement good hygiene practices and maintain proper cooking and storage temperatures. The global proplem of drugresistant K. pneumoniae is a major concern due to its ability to infect various human tissues, including critical organs. K. pneumoniae's virulence mechanisms remain unclear, therefore application of plant extracts to avoid bacterial resistant and overcoming this virulence is very important for human and animal health also the antimicrobial resistance and K. pneumoniae infections requires cooperation between medical, veterinary, pharmacological, microbiological, and environmental sectors for inhibiting the growth of pathogenic microorganisms and enhancing food safety.

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