Int.J.Curr.Microbiol.App.Sci (2026) *15*(4): 1-7

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 15 Number 4 (2026)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2026.1504.001

Klebsiella pneumoniae Associated with a Gastroenteritis Outbreak Linked to the Consumption of Cooked Chicken in the Province of Corrientes, Argentina

Mariano Sebastián Pino[1*], Gladys Roxana Elizabeth Obregón[1], Gladis Isabel Rebak[1], María Bárbara De Biasio[1] and María Carla Zimmermann[2]

[1]*Facultad de Ciencias Veterinarias, Universidad Nacional del Nordeste (FCV-UNNE), Sargento Cabral 2139, Corrientes, Argentina*
[2]*Laboratorio de Genómica. Facultad de Medicina, Universidad Nacional del Nordeste (FM-UNNE), Mariano Moreno 1240, Corrientes, Argentina*

**Corresponding author*

Keywords

Klebsiella pneumoniae; foodborne diseases; PCR; Enterobacteriaceae; Sequencing.

Article Info

Received: 05 February 2026
Accepted: 28 March 2026
Available Online: 10 April 2026

ABSTRACT

Foodborne diseases (FBDs) represent a growing global health challenge, especially in the face of the growing circulation of bacteria that carry antimicrobial resistance mechanisms. Continuous monitoring of indicator microorganisms is a key factor in avoiding risks. *Klebsiella pneumoniae* is a Gram-negative bacterium of the *Enterobacteriaceae* family, considered opportunistic and responsible for serious infections in susceptible individuals. Its presence in food can represent a risk of FBDs. A sample of cooked chicken linked to an outbreak of gastroenteritis affecting 35 people in Itá Ibaté, Corrientes, Argentina, was analyzed. Coliform counts were performed using most probable number (MPN), isolation on Xylose Lysine Deoxycholate (XLD) agar, and molecular detection by endpoint PCR of *K. pneumoniae*, *Salmonella spp.* and *Escherichia coli* O157. The coliform count was > 2 400/g and amplicons of 908 bp specific to *K. pneumoniae* were obtained, confirming its presence as the only identified agent. Molecular characterization of the blaKPC2 gene was also performed by PCR and was not detected. A fragment of DNA from the isolate was sequenced to confirm the identity of the isolate found and compare it with previously reported reference sequences. The findings underscore the need to strengthen Good Manufacturing Practices (GMP) and epidemiological surveillance to prevent future outbreaks.

Introduction

Foodborne diseases (FBDs) are one of the main public health problems worldwide. They are defined as "any disease of an infectious or toxic nature caused by the consumption of contaminated food or water"(WHO, 2024). Each year, it is estimated that 600 million people, almost one in ten globally, fall ill after consuming contaminated food, resulting in approximately 420,000 deaths annually (WHO, 2020). This global burden disproportionately affects children under five years of age, who account for nearly 30% of deaths due to FBDs, as well as immunocompromised individuals and those in vulnerable health settings.

FBDs have a direct impact on public health and the economy, generating significant losses in healthcare systems and the food industry due to product recalls, temporary closures, and loss of consumer confidence (CDC, 2025). The microorganisms most frequently involved include bacteria such as *Salmonella spp.*, *Escherichia coli* (particularly Shiga toxin-producing strains), *Listeria monocytogenes*, *Campylobacter spp.,* and *Staphylococcus aureus*, as well as viruses such as norovirus and hepatitis A, and parasites such as *Toxoplasma gondii* and *Giardia lamblia* (CDC, 2025).

Control of FBDs is based on an integrated "farm to plate" approach, promoted by international organizations such as FAO (Food and Agriculture Organization of the United Nations) and WHO (World Health Organization). This approach aims to ensure food safety at all stages of production through the application of Good Agricultural Practices (GAP), Good Manufacturing Practices (GMP), Hazard Analysis and Critical Control Points (HACCP), and the continuous training of food handlers (FAO and WHO, 2021).

The assessment and monitoring of bacterial groups such as coliforms and the Enterobacteriaceae family have become key tools for assessing hygiene, processing conditions, and microbiological safety within the food chain. Coliforms are traditionally used as indicators of fecal contamination or inadequate handling in food and water (Martin *et al.,* 2016). Enterobacteriaceae, a broader group that includes coliforms, are used as indicators of industrial hygiene and post-processing contamination, as their presence in cooked or ready-to-eat foods suggests failures in cooking or handling. According to Mladenović *et al.,* (2021), the *Enterobacteriaceae* family is considered an indicator of the microbiological quality of food and the hygienic status of production processes, particularly in traditional dairy and meat products. Foodborne infections are not limited to those associated with gastrointestinal symptoms; some, such as *Klebsiella pneumoniae* may cause extraintestinal infections and may not be reported by surveillance systems (Riley, 2020).

K. pneumoniae is an opportunistic pathogen widely recognized in clinical settings, responsible for pneumonia, urinary tract infections, severe enteritis, septicemia, and other serious conditions, particularly in hospitalized or immunocompromised patients (Lopardo, Predari & Vay, 2016; Davis & Price, 2016). Its relevance has also increased as an emerging agent of antimicrobial resistance, particularly in Latin America, where the production of carbapenemases such as KPC (*Klebsiella pneumoniae carbapenemase*), NDM (New Delhi metallo-beta-lactamase) and other mechanisms has been reported in clinically important strains in Argentina (Nicola *et al.,* 2022). Furthermore, recent studies have reported a diversification of KPC-producing clones, including ST307, ST25, ST258, ST11, among others, reinforcing the importance of genetically characterizing clinical and industrial isolates (Cejas *et al.,* 2019; Echegorry *et al.,* 2024).

Although most studies on *K. pneumoniae* have focused on nosocomial infections, its presence in food, animal production, environmental settings and along the food chain has been increasingly documented worldwide in recent years (Riwu *et al.,* 2022), raising concerns for public health due to the risk of zoonotic or foodborne transmission and its potential role as a reservoir of resistance and virulence genes (Nicola *et al.,* 2022; Wyres & Holt, 2022; de Paula *et al.,* 2025). Hartantyo *et al.,* (2020), in samples of ready-to-eat foods, detected the presence of *K. pneumoniae* in 27% of dishes prepared with chicken meat. Guo *et al.,* (2016) in studies on fresh raw chicken indicated that it is an important reservoir of antimicrobial-resistant *K. pneumoniae* and that the potential health risks should not be underestimated.

The objective of the present study was to perform a microbiological and molecular characterization of an agent isolated from a food sample presumably involved in a gastroenteritis outbreak.

Materials and Methods

Sample

A roasted chicken sample associated with 35 individuals presenting symptoms of gastroenteritis in Itá Ibaté, Corrientes, was received. The sample was collected in a sterile container and kept under refrigeration until its arrival at the Food Technology Laboratory, Faculty of Veterinary Sciences-UNNE.

Microbiological analysis

At the Food Technology Laboratory, 10 g of sample were homogenized in 90 mL of buffered peptone water (Britania®) to obtain the initial suspension. From this suspension, three serial dilutions (10^{-1}, 10^{-2}, 10^{-3}) were prepared, and 1 mL of each dilution was inoculated into three sets of three tubes containing 10 mL of 2% Brilliant Green Bile broth (Britania®) with Durham tubes. The tubes were incubated at 35 °C for 48 h. A tube containing culture medium and sterile water as inoculum was used as a negative control. The most probable number (MPN) was calculated using the McGrady table, and results were expressed as MPN/g of sample.

Simultaneously, the initial suspension was incubated at 35 °C for 18±2 h for non-selective enrichment. Subsequently, 1 mL of this suspension was transferred into a tube containing 10 mL of Rappaport Vassiliadis broth (Britania®) and incubated at 41.5 °C for 24 hours for selective enrichment.

Thereafter, the culture was streaked in duplicate using a loop onto Xylose Lysine Deoxycholate agar (XLD) (Oxoid®) and incubated at 37 °C for 24 h.

Molecular analysis

DNA extraction

Genomic DNA was extracted from colonies obtained on XLD agar using CTAB (Cetyl Trimethyl Ammonium Bromide, Sigma Aldrich®) digestion, followed by purification with chloroform: isoamyl alcohol (Cicarelli®) and precipitation with isopropanol (Cicarelli®). The extracted DNA was resuspended in nuclease-free water and stored at -20 °C until use.

PCR amplification

Five endpoint PCR assays were performed to identify *K. pneumoniae*, *Salmonella spp.*, *E. coli* O157, *blaKPC2, and 16S rRNA.* Reactions were carried out in 25 µL final volume with: 1× PCR buffer, MgCl2; 0.2 µM of each primer (See Table 1); 0.2 mM of an equimolecular mixture of dNTPs and 2 U of Taq DNA polymerase. Thermal cycling conditions for each amplification consisted of an initial denaturation at 94 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 60 s; primer annealing (see temperatures in Table 1); extension: 72 °C 60 s; and a final extension at 72 °C for 7 min, followed by incubation at 4 °C until use. Negative and positive controls were included in each amplification reaction, consisting of sterile water and DNA from each of the analyzed bacteria, respectively.

Agarose gel electrophoresis

Amplification products were separated by electrophoresis in 2% agarose gels in 1× TBE buffer, stained with ethidium bromide and visualized under ultraviolet (UV) transillumination.

DNA sequencing

From the 908 bp amplicon specific for *K. pneumoniae*, purification was performed with AMPure XP magnetic beads (Beckman Coulter, Inc.) to a final volume of 30 µl. Two Sanger sequencing reactions were carried out using the commercial BigDye Terminator v3.1 Cycle Sequencing Kit (Thermo Fisher Scientific Inc.) in a standard 10 µL reaction: 4 µL of BigDye Terminator 3.1 Ready Reaction Mix, 2 µL of forward or reverse primer, 2 µL of purified amplicon, and 2 µL of sterile nuclease-free water. Cycling conditions consisted of an initial denaturation at 96 °C for 1 minute, followed by 25 cycles of denaturation at 96 °C for 10 seconds, annealing at 50 °C for 5 seconds and extension at 60 °C for 4 minutes with a final incubation at 4 °C for 10 minutes. Amplicons were purified by precipitation with EDTA 125 mM and Ethanol 100 %, followed by washes with Ethanol 70 %. Purified products were eluted in Hi-Di Formamide (Thermo Fisher Scientific Inc.) and subjected to capillary electrophoresis using an ABI 3500 Genetic Analyzer under the standard 125-minute sequencing protocol, with a 50 cm capillary array and POP-7 polymer (Thermo Fisher Scientific Inc.). The final sequence was obtained using SeqScape Software v4.0 (Thermo Fisher Scientific Inc.) and identified using the SkyBLAST "blastn" tool (NCBI).

Results and Discussion

In the total coliform count, all tubes tested positive (presence of turbidity and gas in the Durham tubes), yielding an MPN table value > 2 400/g. On XLD agar, multiple yellow mucoid colonies compatible with *Klebsiella spp.* and/or *Enterobacter spp.* were observed (Figure 1).

Following DNA extraction from the obtained culture and subsequent amplification assay targeting *K. pneumoniae*, *Salmonella spp.*, *E. coli* O157, *blaKPC2,* a 908 bp amplification product specific for *K. pneumoniae* was obtained, whereas no amplification was detected for *Salmonella spp.*, *E. coli* O157 and *blaKPC2* (Figure 2).

From the processed sample, a 754 bp sequence was obtained, showing 99% identity with the genome of *Klebsiella pneumoniae* subsp. *pneumoniae* (NC_016845.1). The following variants were identified: 1492000A, 1492146T, 1492299A, 1492527T.

The detection of *K. pneumoniae* in a portion of roasted chicken associated with a gastroenteritis outbreak represents an atypical finding, as this microorganism is more commonly associated with infections in hospital settings (Nicola *et al.,* 2022; Hartantyo *et al.,* 2020; Galvis & Moreno, 2019; Crippa *et al.,* 2023). However, according to several authors (Riley, 2020; Davis & Price, 2016; de Paula *et al.,* 2025) it may act as a foodborne transmission agent and also serve as a reservoir of resistance and virulence genes.

The high coliform count observed suggests post-cooking contamination or deficiencies in hygienic-sanitary conditions during food handling, storage, transport or processing. This finding is consistent with studies linking elevated coliform levels to failures in cooking, handling or preservation of ready-to-eat meat products (Martin *et al.,* 2016; Mladenović *et al.,* 2021). The recovery of yellow mucoid colonies on XLD agar, compatible with *Klebsiella* spp., was consistent with PCR and sequencing results, which identified *K. pneumoniae subsp. pneumoniae* with high identity (99%). Molecular identification, together with the absence of *Salmonella spp.* and *E. coli O157*, supports that the isolated microorganism was *K. pneumoniae* rather than another classical foodborne pathogen. Recent studies have documented the presence of *K. pneumoniae* in raw meats, prepared foods, and commercial kitchen environments, reinforcing its relevance in the food chain (Riwu *et al.,* 2022; Hartantyo *et al.,* 2020; Guo *et al.,* 2016). Riwu *et al.,* (2022) demonstrated that *K. pneumoniae* can persist on food-contact surfaces and utensils, facilitating cross-contamination. Although the literature indicates that the microorganisms most frequently involved in foodborne diseases include bacteria such as *Salmonella* spp., *Escherichia coli*, *Listeria monocytogenes*, *Campylobacter* spp. and *Staphylococcus aureus*, as well as viruses such as hepatitis A virus (CDC, 2025). Our results do not align with these reports. In our study, specifically aimed at detecting DNA from *E. coli* and *Salmonella* spp., no genetic material from either pathogen was identified, despite their common association with foodborne diseases.

The absence of *Salmonella* and *E. coli O157* growth may be due to their absence in the sample, low bacterial load and/or competition with other organisms such as *K. pneumoniae,* or the presence of nonviable bacteria in the analyzed chicken sample that could not be recovered by culture. Our findings highlight that enterobacteria such as *K. pneumoniae* may play a role in the etiology or at least contribute to risk, and therefore should be considered in surveillance protocols and outbreak investigations of foodborne diseases.

The detection of point variants in the sequenced genome may be associated with the wide genetic diversity described for *K. pneumoniae*, a species characterized by a high degree of recombination and genomic plasticity (Wang *et al.,* 2025). Although these variants were not functionally analyzed, their presence underscores the importance of further molecular characterization in outbreak studies, particularly in the context of emerging hypervirulent and highly resistant lineages in Latin America (Nicola *et al.,* 2022; Cejas *et al.,* 2019).

The significant global increase in the prevalence of multidrug-resistant (MDR) K. pneumoniae represents a serious public health concern (Wang, 2025), although the blaKPC2 resistance gene was not detected in the isolate analyzed in this study. In Argentina, the epidemiology of K. pneumoniae has shown the expansion of high-risk KPC-producing clones such as ST307, ST258, ST11 and ST25 (Cejas *et al.,* 2019), making it relevant to assess whether foodborne isolates are related to these lineages.

The absence of blaKPC2 detection provides evidence that reduces the likelihood of its community dissemination, although other antimicrobial resistance genes that may be present should be investigated.

Bloodstream isolates of *K. pneumoniae* in hospital settings have been reported to increase significantly during periods of high temperature and humidity (Anderson *et al.,* 2008), possibly due to higher rates of fecal carriage and, consequently, increased environmental dissemination. This finding is particularly relevant to the present study, as the province of Corrientes present several factors that may promote the spread of foodborne diseases, including high temperatures and humidity, frequent power outages, especially during the summer period, and the widespread sale of street-prepared foods, among others. These factors may have contributed to the development of the gastroenteritis outbreak that prompted this investigation.

Figure.1 Yellow mucoid colonies on XLD agar.

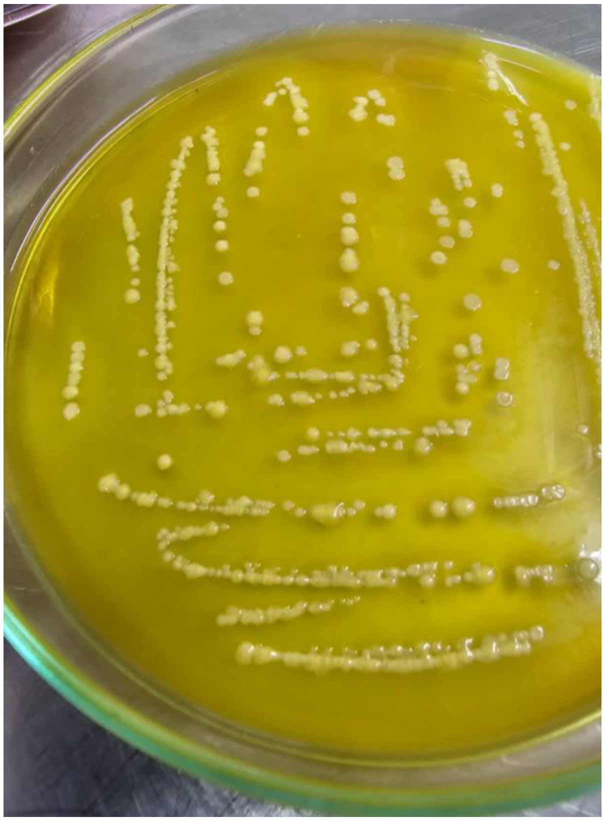

Figure.2 *2% agarose gel electrophoresis.* Panel a: *Salmonella spp*. PCR. Lane 1: molecular weight marker (Cienmarker, Biodynamics), Lane 2: bacterial colony DNA, Lane 3: PCR positive control, Lane 4: PCR negative control. Panel b: O157 PCR. Lane 1: molecular weight marker (Cienmarker, Biodynamics), Lane 2 and 3: bacterial colony DNA, Lane 4: PCR positive control, Lane 5: PCR negative control. Panel c: *Klebsiella pneumoniae* PCR. Lanes 1 and 2: bacterial colony DNA, Lane 3: PCR positive control, Lane 4: PCR negative control, Lane 5: molecular weight marker (Cienmarker, Biodynamics)

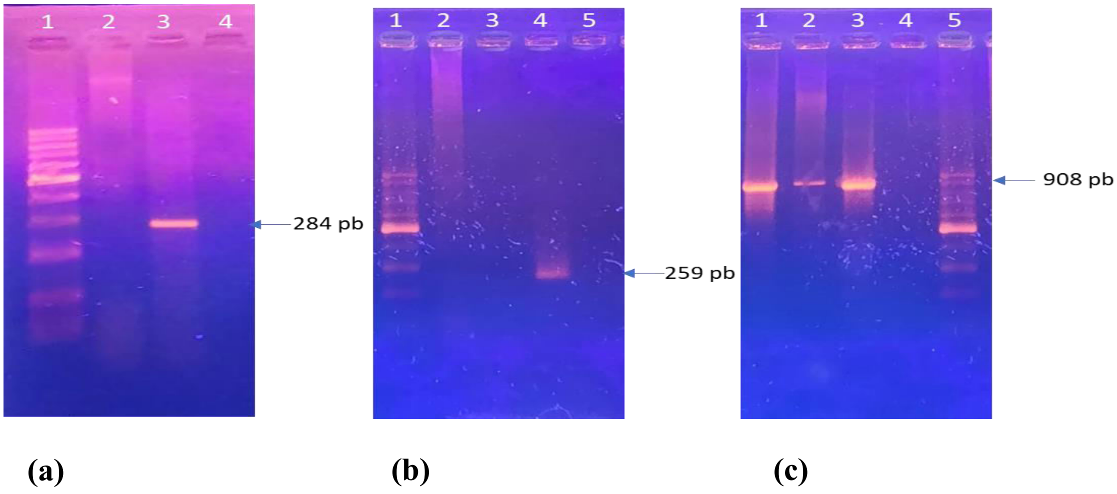

Table.1 Targets analyzed by PCR, annealing temperatures, $MgCl_2$ condition, size of specific amplification products and bibliographic references

Target of interest	Ta	$MgCl_2$ (mM)	Amplicon Size (bp)	Reference
Klebsiella pneumoniae	60	1.5	908	(Galvis & Moreno, 2019)
Salmonella spp.	60	1.5	284	(Wibisono *et al.,* 2021)
E. coli O157	58	1.5	259	(Villalobos *et al.,* 2008)
blaKPC	50	1.5	916	(Pasteran *et al.,* 2008)
16S rRNA	52	2.0	1532	(Romanov *et al.,* 2004)

Currently, *K. pneumoniae* is not a regulated indicator microorganism for any food according to the Argentine Food Code (CAA).

However, considering our results, the need to evaluate its inclusion or complementary monitoring within the food sector should be considered.

Author Contributions

MV. Mariano Sebastián Pino: Conceptualization, Methodology, Investigation, Writing - Original Draft Preparation. MV. Gladys Roxana Elizabeth Obregón: Methodology, Investigation, Writing - Review & Editing. Dra. Gladis Isabel Rebak: Conceptualization, Investigation, Writing - Review & Editing. MSc María Bárbara De Biasio: Methodology, Investigation, Writing - Original Draft Preparation Writing - Review & Editing. Dra. María Carla Zimmermann: Methodology, Investigation, Writing - Original Draft Preparation Writing - Review & Editing.

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

Anderson DJ, Hervé R, Chen LF, Spelman DW, Hung YJ, Huang AT, *et al.,* (2008). Seasonal variation in *Klebsiella pneumoniae* bloodstream infection on 4 continents. *The Journal of infectious diseases*, 197(5), 752-756.

Cejas D, Elena A, Nuñez DG, Platero PS, De Paulis A, Magariños F, *et al.,* (2019). Changing epidemiology of KPC-producing *Klebsiella pneumoniae* in Argentina: Emergence of hypermucoviscous ST25 and high-risk clone ST307. *Journal of global antimicrobial resistance*, 18, 238-242. https://doi.org/10.1016/j.jgar.2019.06.005

Centers for Disease Control and Prevention (CDC). (2025). Estimates: burden of foodborne illness in the United States. CDC Food Safety [Internet]. https://www.cdc.gov/food-safety/php/data-research/foodborne-illness-burden/index.html

Crippa C, Pasquali F, Rodrigues C, De Cesare A, Lucchi A, Gambi L, *et al.,* (2023). Genomic features of Klebsiella isolates from artisanal ready-to-eat food production facilities. Scientific reports, 13(1), 1-12. https://doi.org/10.1038/s41598-023-37821-7

Davis GS, Price LB. (2016). Recent research examining links among *Klebsiella pneumoniae* from food, food animals, and human extraintestinal infections. *Current environmental health reports*, 3(2), 128-135. https://doi.org/10.1007/s40572-016-0089-9

de Paula CL, Rissetti RM, Yamada AY, Bertani AM, Sacchi CT, Campos KR, *et al.,* (2025). *Klebsiella pneumoniae* complex isolated from diseased companion animals reveals genomic diversity, multidrug resistance, and extended-spectrum β-lactamase-encoding genes. *Journal of Applied Microbiology*, 136(6), lxaf128. https://doi.org/10.1093/jambio/lxaf128

Echegorry M, Marchetti P, Sánchez C, Olivieri L, Faccone D, Martino F, *et al.,* (2024). National Multicenter Study on the Prevalence of Carbapenemase-Producing Enterobacteriaceae in the Post-COVID-19 Era in Argentina: The RECAPT-AR Study. *Antibiotics*, 13, 1139. https://doi.org/10.3390/antibiotics13121139.

Food and Agriculture Organization & World Health Organization. (2021). FAO, WHO set an example of collaborative action for safe food with a systems approach. https://www.who.int/europe/news/item/08-06-2021-fao-who-set-an-example-of-collaborative-action-for-safe-food-with-a-systems-approach

Galvis SF, Moreno RL. (2019). Molecular characterization and detection of blaCTX-M group 1 and 9 genes in ceftazidime-resistant *Klebsiella pneumoniae* in a hospital in San José de Cúcuta, Colombia. *Chilean Journal of Infectology*, 36(3), 304-311. https://dx.doi.org/10.4067/S0716-10182019000300304

Guo Y, Zhou H, Qin L, Pang Z, Qin T, Ren H, *et al.,* (2016). Frequency, antimicrobial resistance and genetic diversity of *Klebsiella pneumoniae* in food samples. *PloS one*, 11(4), 1-13. https://doi.org/10.1371/journal.pone.0153561

Hartantyo SH, Chau ML, Koh TH, Yap M, Yi T, Cao DY, *et al.,* (2020). Foodborne *Klebsiella pneumoniae*: virulence potential, antibiotic resistance, and risks to food safety. *Journal of food protection*, 83(7), 1096-1103. https://doi.org/10.4315/JFP-19-520

Lopardo HA, Predari SC, Vay C. (2016). Manual of Clinical Microbiology of the Argentine Association of Microbiology. *Argentine Journal of Microbiology*. Volume I. Bacteria of Clinical Importance. Part IIc 1.3. pp 111-124. 1st ed. - Autonomous City of Buenos Aires: Argentine Association of Microbiology. Digital book, PDF Digital File: download ISBN 978-987-26716-8-6

Martin NH, Trmčić A, Hsieh TH, Boor KJ y Wiedmann M. (2016). The evolving role of coliforms as indicators of unhygienic processing conditions in dairy foods. *Frontiers in microbiology*, 7:1-8. https://doi.org/10.3389/fmicb.2016.01549.

Mladenović KG, Grujović MŽ, Kiš M, Furmeg S, Tkalec VJ, Stefanović OD, *et al.,* (2021). Enterobacteriaceae in food safety with an emphasis on raw milk and meat. *Applied microbiology and biotechnology*, 105(23), 8615-8627. https://doi.org/10.1007/s00253-021-11655-7.

Nicola F, Cejas D, González-Espinosa F, Relloso S, Herrera F, Bonvehí P, *et al.,* (2022). Outbreak of *Klebsiella pneumoniae* ST11 resistant to KPC-31-producing ceftazidime-avibactam and the new KPC-115 variant during the COVID-19 pandemic in Argentina. *Microbiology spectrum*, 10 (6), 1-7. https://doi.org/10.1128/spectrum.03733-22

Pasteran FG, Otaegui L, Guerriero L, Radice G, Maggiora R, Rapoport M, *et al.,* (2008). *Klebsiella pneumoniae* Carbapenemase-2, Buenos Aires, Argentina. *Emerging infectious diseases*, 14(7), 1178–1180. https://doi.org/10.3201/eid1407.070826

Riley LW. (2020). Extraintestinal foodborne pathogens. *Annual review of food science and technology*, 11(1) 275-294. https://doi.org/10.1146/annurev-food-032519-051618

Riwu, K. H. P., Effendi, M. H., Rantam, F. A., Khairullah, A. R., & Widodo, A. (2022). A review: Virulence factors of *Klebsiella pneumonia* as emerging infection on the food chain. *Veterinary world*, 15(9), 2172. https://doi.org/10.14202/vetworld.2022.2172-2179

Romanov MN, Bato RV, Yokoyama MT, Rust SR. (2004). PCR detection and 16S rRNA sequence-based phylogeny of a novel *Propionibacterium acidipropionici* applicable for enhanced fermentation of high moisture corn. *Journal of applied microbiology*, 97(1), 38–47. https://doi.org/10.1111/j.1365-2672.2004.02282.x

Villalobos LB, Martínez RE, Blanco AC, Maldonado AJ, Bastardo JW. (2008). Molecular detection of shiga toxin-producing *Escherichia coli* (Stx1) and rotavirus in feces of children with diarrhea. *Clinical Research*, 49(3), 387-395.

Wang J, Li J, Ji X, Zhang L, Wang R, Wang H, *et al.,* (2025). Antimicrobial resistance and molecular epidemiology of *Klebsiella pneumoniae* isolated from bovine mastitis in seven provinces in China. *BMC microbiology*, 25(1), 407. https://doi.org/10.1186/s12866-025-04147-5

Wibisono FM, Faridah HD, Wibisono FJ, Tyasningsih W, Effendi MH, Witaningrum AM, *et al.,* (2021). Detection of *invA* virulence gene of multidrug-resistant *Salmonella* species isolated from the cloacal swab of broiler chickens in Blitar district, East Java, Indonesia. *Veterinary world*, 14(12), 3126–3131. https://doi.org/10.14202/vetworld.2021.3126-3131

World Health Organization (WHO). (2024). Food safety – Key facts. https://www.who.int/news-room/fact-sheets/detail/food-safety

World Health Organization (WHO). (2020). Strengthening efforts on food safety. 73rd World Health Assembly.

Wyres K, Holt, K. (2022). Regional differences in carbapenem-resistant *Klebsiella pneumoniae*. *The Lancet. Infectious diseases*, 22(3), 309–310. https://doi.org/10.1016/S1473-3099(21)00425-4

How to cite this article:

Mariano Sebastián Pino, Gladys Roxana Elizabeth Obregón, Gladis Isabel Rebak, María Bárbara De Biasio and María Carla Zimmermann. 2026. *Klebsiella pneumoniae* Associated with a Gastroenteritis Outbreak Linked to the Consumption of Cooked Chicken in the Province of Corrientes, Argentina. *Int.J.Curr.Microbiol.App.Sci.* 15(4): 1-7. **doi:** https://doi.org/10.20546/ijcmas.2026.1504.001