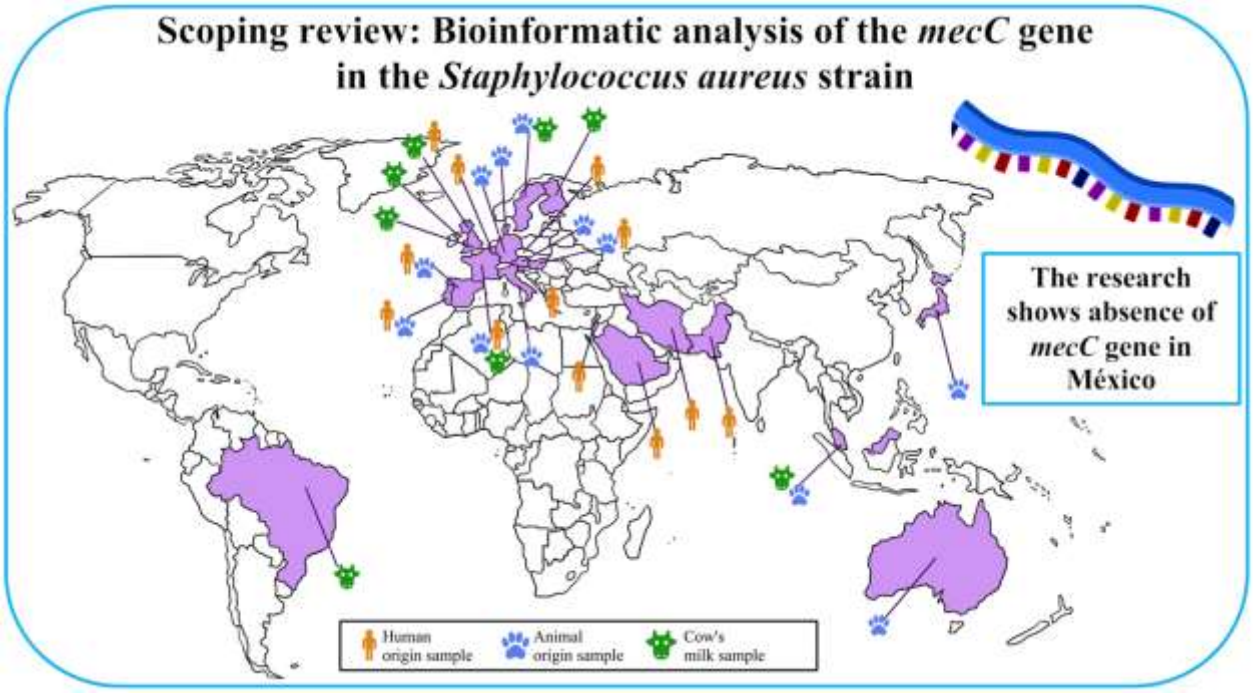
Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

Graphical Abstract

SCOPING REVIEW: BIOINFORMATIC ANALYSIS OF THE *MECC* GENE IN THE *STAPHYLOCOCCUS AUREUS* STRAIN

Juan F. Villa-Díaz de León[1], Paloma S. Ramírez-Almaraz[2], Alberto Ramírez-Mata[3], Mónica A. Olea-Amezcua[4], Arnulfo Villanueva-Castillo[5] y Claudia Mancilla-Simbro[2].



Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

Original article

SCOPING REVIEW: BIOINFORMATIC ANALYSIS OF THE *MECC* GENE IN THE *STAPHYLOCOCCUS AUREUS* STRAIN

Juan F. Villa-Díaz de León[1*], Paloma S. Ramírez-Almaraz[2], Alberto Ramírez-Mata[3], Mónica A. Olea-Amezcua[4], Arnulfo Villanueva-Castillo[5] and Claudia Mancilla-Simbro[2*].

[1] Lab. Simulaciones Moleculares. Departamento de ciencias básicas. Computacionales Tecnológico Nacional de México, campus Guaymas. Carretera al Varadero Nacional, Las Playitas, 85480 Guaymas, Sonora. México. https://orcid.org/0000-0002-1118-5579

[2 HybridLab.] Fisiología y Biología Molecular de Células Excitables - Instituto de Fisiología. Benemérita Universidad Autónoma de Puebla. Puebla México C.P. 72570. https://orcid.org/0000-0003-3976-3550 , Autor de correspondencia: claudia.mancilla@correo.buap.mx

[3] Lab. Interacción patógeno-planta de Investigaciones - Centro de Ciencias Microbiológicas (ICUAP) Instituto de Ciencias- Benemérita Universidad Autónoma de Puebla. Puebla México C.P. 72570. https://orcid.org/0000-0002-2119-2254

[4] Facultad de Artes Plásticas y Audiovisuales, Benemérita Universidad Autónoma de Puebla, Vía Atlixcáyotl No. 2499, Puebla, Puebla, México, C.P. 72810. https://orcid.org/0000-0001-8649-7748

[5] Facultad de Medicina Veterinaria y Zootecnia. Benemérita Universidad Autónoma de Puebla. Tecamachalco - Cañada Morelos Km. 7.5, El Salado, C.P. 75460 Tecamachalco, Pue. México. Pue. México. https://orcid.org/0000-0002-9430-1503

*Corresponding author: claudia.mancilla@viep.com.mx

Received March 24, 2025; Form revised March 25, 2025; Accepted March 31, 2025

Abstract

Antibiotic resistance is a natural phenomenon that has been accelerated due to its excessive use, resulting in longer hospital stays, increased patient mortality, and higher costs for treating infectious diseases. The *Staphylococcus aureus* strain is an opportunistic pathogen associated with nosocomial infections and often produces suppurative lesions; minor trauma and immunosuppression predispose to an infection development. The *MRSA* (methicillin-resistant *Staphylococcus aureus*) strain has a *SCCmec* segment, it is constituted by a structural *mec* gene that codes the *PBP2a* protein. In 2011, García-Álvarez *et al*. made the first report of the *mecC* gene in *MRSA* strains, obtained from both bovines and humans; this gene shares 69% homology with the *mecA* gene, in addition to having zoonotic potential. A systematic review allows to analyze the geographical distribution of the gene and to understand the genomic characteristics of the studied strains. We employed the PRISMA extension for Scoping-Reviews; the information was collected from 2012 to 2023 in PubMed. The inclusion criteria were: 1) type of sample used in the

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

study, 2) animal or human origin of the sample and 3) geographic region where the samples were taken. The presence of the *mecC* gene was observed in 25 countries around the world, with European countries accounting for the largest number of reports. The *mecC* gene was detected in *MRSA* strains in the *SCCmec XI* segment and most frequently with *CC130* clonal complexes. During the development of the present investigation, no publications were found regarding the presence of this gene in México.

Keywords: *mecC gene, Staphylococcus aureus strain, MRSA*, PRISMA, Scoping-Reviews, geographic distribution.

Introduction

The antibiotic resistance could be defined as the natural phenomenon by which bacteria employ different mechanisms to evade antibiotic drugs. This behavior has been accelerated due to the excessive use of antibiotics, resulting in increased treatment costs, prolonged hospital stays, and an increment in patient mortality [1, 2, 3, 4]. The World Health Organization (WHO) mentions that about 700,000 deaths per year happen because of infections caused by bacteria resistant to some antibiotic. This problem could cause millions of deaths in the future and generate economic losses [4, 5, 6]. Globally, for every 5 human diseases that arise each year, at least 3 are of animal origin [7]. Particularly, it is estimated that the death of human patients because of nosocomial infections is 32 per 100,000 inhabitants [8]. The *Staphylococcus aureus* strain is an opportunistic pathogen associated with nosocomial infections and often produces suppurative lesions; minor trauma and immunosuppression predispose to an infection development [9, 10]. About the specific case of México, at national level, there is no data regarding the percentage of incidence of nosocomial infections in veterinary medicine in the bibliographic review carried out to the date of this article.

The MRSA (methicillin-resistant *Staphylococcus aureus*) strain has a *SCCmec* segment, it is constituted by a structural *mec* gene; whether of type: *mecA, mecB* or *mecC*. The *mec* gene belongs to the *SCCmec XI* type and codes the *PBP2a* protein [11, 12], which retains the transglycosylase activity, restoring the peptidoglycan of the bacterial wall interrupted by beta-lactams [13]. In 2011, García-Álvarez et al. [14] made the first report of the *mecC* gene in *MRSA* strains, obtained from both bovines and humans; this gene shares 69% homology with the *mecA*

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

gene, in addition to having zoonotic potential. While Armand-Lefevre et al. conducted a study where they determined the presence of *MRSA* strains in farm caretakers and pigs, both without presenting clinical alterations [15]. Lozano et al. [16] mention that the *mecC* gene is found in clonal complexes (*CC*): *CC49, CC425, CC599, CC1943, CC2361* and mainly in *CC130*. This is in the case of samples taken from humans, although it has also been observed in farm and wild animals.

This is the way; we propose a systematic review of the current literature to analyze the geographic distribution of the gene and the genomic characteristics of the reported strains; with the aim to understand the causes of *mecC* gene epidemiology in *Staphylococcus aureus* strains and its impact on nosocomial diseases.

Methodology

We employed the the PRISMA extension for Scoping-Reviews [17], the data was collected from February to March 2024 from the PubMed database, which contains articles mainly related to the medical field [18]. The search was developed by the keywords: "*Staphylococcus aureus*" and "*mecC*" in a date range from 2012 to 2023. Data extraction was carried out using the methodology proposed by Arksey & O'Malley in 2005 [19]. The inclusion criterion was that the publications had to describe or indicate at least one of the following points: 1) the type of sample used in the study: blood sample, pus sample, sample from an anatomical area, milk, or other, 2) whether the origin of the sample was animal or human, and 3) the geographic region where the samples were taken.

Results

Of the total articles analyzed, 43 met the characteristics described in the methodology. The reports belonged to 25 countries around the world, represented in Figure 1, where it is observed the origin of the sample and the respective country. For samples of animal origin, the countries with presence of *mecC* gene were Spain with 23%, Germany, France, Hungary and Sweden with

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

9% and the rest of the countries with 4%. Human samples have been reported in Pakistan at 16%, Spain, France, and the United Kingdom at 11%, while other countries only 5%. Finally, for the food samples, France and Great Britain indicate 20% and the other countries about 10%.

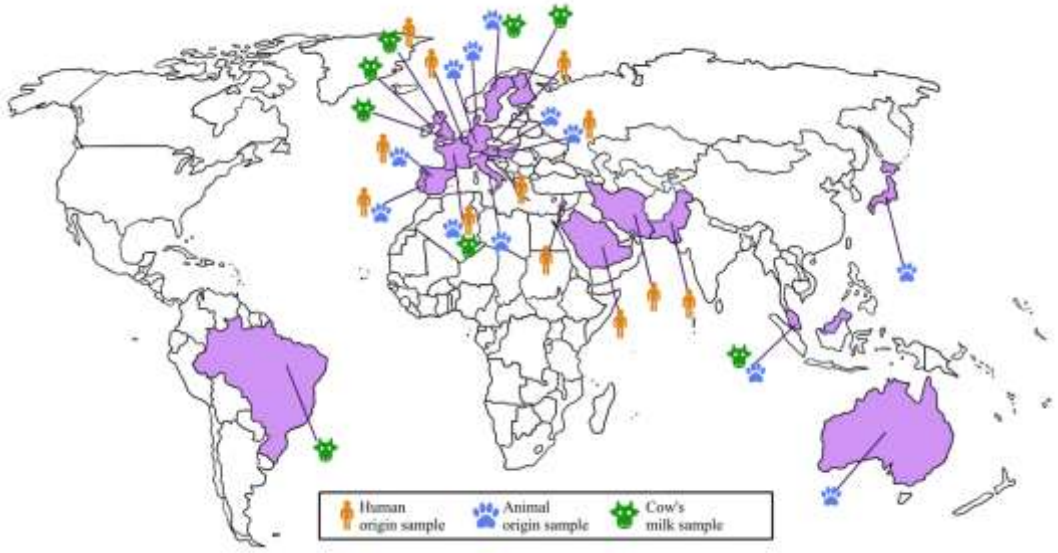


Figure 1: Geographical distribution of the *mecC* gene and the origin of the samples.

In Figure 2, we present the incidence according to the sample type, with swabs from an anatomical area of animal origin having the highest number of reports. The incidences of human origin were found in those classified as other types of samples, while those of food origin only came from milk samples. Being located more frequently in swabs from anatomical areas of animals could indicate that the gene does not require a clinical or hospital environment for its dissemination. Which is important to understand, since the *Staphylococcus aureus* strain is an opportunistic pathogen associated with nosocomial infection.

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

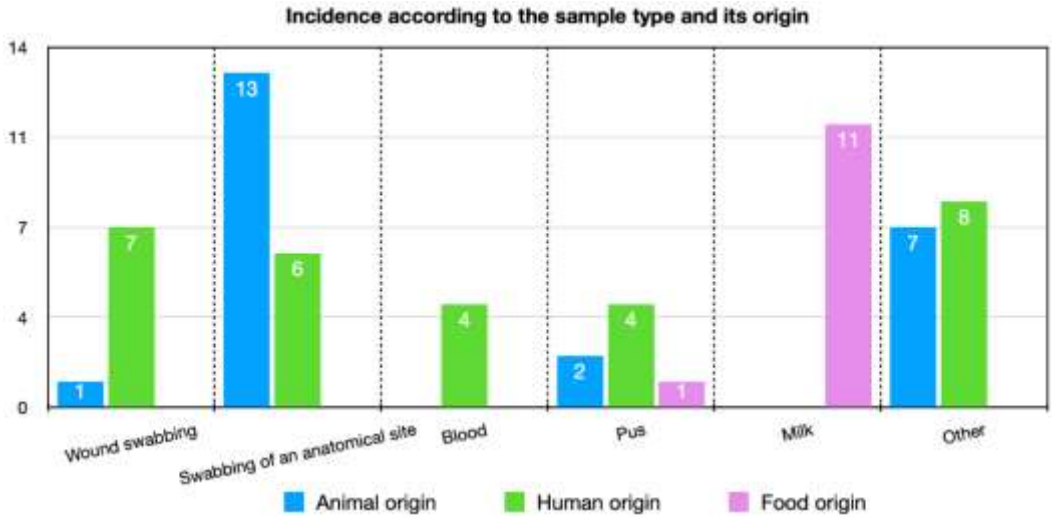


Figure 2: Incidence graph of sample types and where the *mecC* gene was found.

Regarding the genomic characteristics in Figure 3, we noticed that 30% of the countries reported the *SCCmec XI* type. From the works that mentioned the *CC*, in Figure 4 we show how 77% registered the presence of *CC130*, 8% the *CC425* and 7% the *CC49* type.

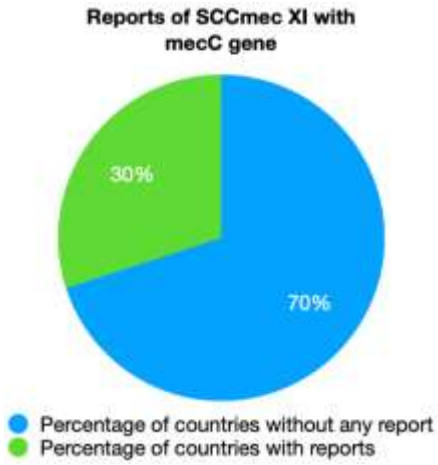


Figure 3: Percentage incidence of *SSCmec X*I type with the *mecC* gene.

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

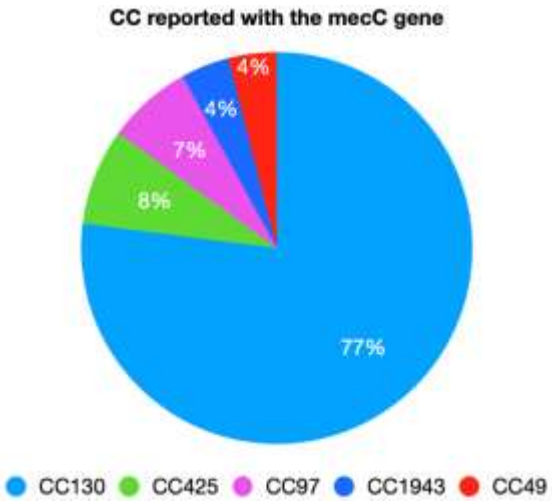


Figure 4: Clonal complexes (*CC*) in which the *mecC* gene has been reported.

Finally, in Table 1, the clonal complexes and the countries in which they were reported are listed.

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

Table 1: Countries and *CCs* that have been reported with the *mecC* gene.

Country with reports	***CCmec***				
Belgium	*CC97*				
Hungary		*CC130*			
Portugal		*CC130*			
Iran		*CC130*			
Brazil	*CC97*				
Spain		*CC130*			
Czech Republic		*CC130*	*CC425*		
France		*CC130*			
United Kingdom		*CC130*			
Italy		*CC130*			
Slovenia		*CC130*			
Belgium		*CC130*			
England		*CC130*			
Great Britain		*CC130*		*CC49*	*CC1943*
Sweden		*CC130*	*CC425*		

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

Conclusions

Along this Scoping Review, we observed that the geographic distribution of the *mecC* gene is not homogeneous throughout the world, as European countries generate the largest number of reports. While the development of this research, no reports were found about the presence of the *mecC* gene in México. The population at greatest risk of acquiring the MRSA strain with the *mecC* gene, is that which is in constant contact with animals, whether domestic or wild. Regarding the genomic characteristics, we confirmed that the *mecC* gene in present in the *SCCmec XI* type, with a variability on the *CC* composition. Understanding the epigenetics of antibiotic resistance genes promotes the search for solutions that mitigate the clinical consequences of pathogens [20, 21]. Based on the analysis of the results obtained, the prospects that we propose in this work are: 1) to develop a meta-analysis that includes more databases to provide a broader picture of the *mecC* epidemiology, 2) continue in-depth research on the presence of the *mecC* gene in México or other countries in the Americas. To comprise the epidemiology of infectious diseases to help in their prevention, as well as in public global health care.

Acknowledgments

This paper was supported by VIEP # 24016 BIOINFORMÁTICA INCLUSIVA: DISCAPACIDAD VISUAL. The authors declare that they have no competing interest.

Privacy Statement

The personal data provided by the authors to Revista Ciencia Veterinaria y Biotecnología will be used exclusively for the purposes stated by the company and will not be made available for any other purpose or provided to third parties.

Declaration of no conflict of interest

The authors declare that there is no conflict of interest.

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

References

[1] Centers for Disease Control, Prevention, et al. Antimicrobial resistance questions and answers. *Centers for Disease Control and Prevention. US Department of Health & Human Services*, 2022.

[2] Fernanda C. Lessa and Dawn M. Sievert. Antibiotic resistance: A global problem and the need to do more. *Clinical Infectious Diseases*, 77(Supplement_1):S1–S3, 2023.

[3] Jill E. Maddison, Stephen W. Page, and David B. Church. *Small animal clinical pharmacology*, volume 5. Elsevier Health Sciences, 2008.

[4] Kenia Barrantes J., Luz Chacón J., and María Arias A. El impacto de la resistencia a los antibióticos en el desarrollo sostenible. *Población y Salud en Mesoamérica*, 19(2):305–329, 2022.

[5] Haiyang Yu, Xu Han, and Dianelys Quiñones P. La humanidad enfrenta un desastre: la resistencia antimicrobiana. *Revista Habanera de Ciencias Médicas*, 20(3), 2021.

[6] WHO. *La resistencia a los antimicrobianos y el Marco de Cooperación de las Naciones Unidas para el Desarrollo Sostenible: orientaciones para los equipos de las Naciones Unidas en los países*. World Health Organization, WHO, 2021.

[7] OMS. Día mundial de las zoonosis: proteger la salud animal ayuda a preservar la salud humana, 2023.

[8] diputados.gob.mx. Por infecciones en hospitales, en México mueren al año 32 pacientes por cada 100 mil habitantes, 2017.

[9] Vincent A. Fischetti, Richard P. Novick, Joseph J. Ferretti, Daniel A. Portnoy, Mirian Braunstein, and Julian I. Rood. *Gram-positive pathogens*. John Wiley & Sons, 2019.

[10] D.S. McVey, M. Kennedy, M.M. Chengappa, and R. Wilkes. *Veterinary Microbiology.* Wiley, 2022.

[11] Jhih-Hang Jiang, David R. Cameron, Cara Nethercott, Marta Aires-de Sousa, and Anton Y. Peleg. Virulence attributes of successful methicillin-resistant staphylococcus aureus lineages. *Clinical microbiology reviews*, 36(4):e00148–22, 2023.

[12] Karsten Becker, Britta Ballhausen, Robin Köck, and André Kriegeskorte. Methicillin resistance in Staphylococcus isolates: the mec alphabet with specific consideration of mecc, a mec homolog associated with zoonotic S. aureus lineages. *International Journal of Medical Microbiology*, 304(7):794–804, 2014.

[13] Tomasz A Łeski and Alexander Tomasz. Role of penicillin-binding protein 2 (PBP2) in the antibiotic susceptibility and cell wall cross-linking of staphylococcus aureus: evidence for the cooperative functioning of PBP2, PBP4, and PBP2A. *Journal of bacteriology*, 187(5):1815–1824, 2005.

[14] Laura García-Álvarez, Matthew T.G. Holden, Heather Lindsay, Cerian R. Webb, Derek F.J. Brown, Martin D. Curran, Enid Walpole, Karen Brooks, Derek J. Pickard, Christopher Teale, et al. Meticillin-resistant Staphylococcus aureus with a novel mecA homologue in human and bovine populations in the UK and Denmark: a descriptive study. *The Lancet infectious diseases*, 11(8):595–603, 2011.

Available online at
https//revcienvetbio.buap.mx
https://doie.org/10.10122/RevCienVeB.2025597880

[15] Laurence Armand-Lefevre, Raymond Ruimy, and Antoine Andremont. Clonal comparison of staphylococcus aureus isolates from healthy pig farmers, human controls, and pigs. *Emerging infectious diseases*, 11(5):711, 2005.
[16] Carmen Lozano, Rosa Fernández-Fernández, Laura Ruiz-Ripa, Paula Gómez, Myriam Zarazaga, and Carmen Torres. Human mecc carrying MRSA: Clinical implications and risk factors. *Microorganisms,* 8(10):1615, 2020.
[17] Andrea C. Tricco, Erin Lillie, Wasifa Zarin, Kelly K. O'Brien, Heather Colquhoun, Danielle Levac, David Moher, Micah DJ Peters, Tanya Horsley, Laura Weeks, et al. Prisma extension for scoping reviews (prisma-scr): checklist and explanation. *Annals of internal medicine*, 169(7):467–473, 2018.
[18] Jacob White. Pubmed 2.0. *Medical reference services quarterly*, 39(4):382–387, 2020.
[19] Hilary Arksey and Lisa O'malley. Scoping studies: towards a methodological framework. *International journal of social research methodology,* 8(1):19–32, 2005.
[20] R.O. Pérez, R.A. Mata, G.A. Domínguez, et al. Retrospective brucellosis study in México. *Int. J. Vet. Med.*, 3(1):1–6, 2024.
[21] M.S. Claudia, R.P. Olaf, R.M. Alberto, et al. Brucella infection mechanisms responsible for abortion in pregnant women. *Int. Jr. Infect. Dis. & Epidemlgy*, 24(5):1.

 Available Online First: 28 marzo 2025.Please cite this article as: Juan F. Villa-Díaz de León, Paloma S. Ramírez-Almaraz, Alberto Ramírez-Mata, Mónica A. Olea-Amezcua, Arnulfo Villanueva-Castillo y Claudia Mancilla-Simbro. Rev Cien Vet Bio 2025; Vol. 2 (1):1-11. https://doie.org/10.10122/RevCienVeB.2025597880