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Abstract

Children with atopic dermatitis (AD) have a higher prevalence of Staphylococcus aureus colonization. Gentamicin is an important topical antibiotic that is used in the treatment of AD lesions. This study aimed to evaluate the prevalence of gentamicin resistance, Panton-Valentine Leukocidin (PVL), and Staphylococcal cassette chromosome mec (SCCmec) type in community-acquired methicillin-resistant Staphylococcus aureus (CA-MRSA), which colonizes the skin of the AD children. Gentamicin resistance in CA-MRSA isolates was detected using the E-test. Polymerase Chain Reaction (PCR) was used to test the genes for aminoglycoside modifying enzymes (AMEs), PVL, and SCCmec types of CA-MRSA isolates. A total of 29 isolates of CA-MRSA were obtained from the skin lesions of 100 patients, and a high prevalence of gentamicin resistance (79.3 %) was detected among these isolates. The most predominant AME gene among the gentamicin resistant isolates was aac(6')-Ie-aph(2')-Ia. However, the PVL gene was detected in 14 (48.3 %) of the isolates. Both gentamicin resistance and PVL were significantly associated with a high SCORAD score. SCCmec type V (31 %) was most common among the CA-MRSA isolates. This study revealed a high prevalence of gentamicin resistance among MRSA that colonises the skin of AD, with the *aac(6')-Ie-aph(2')-Ia* aminoglycoside-resistant determinant predominating. The most frequently observed cassette was SCCmec type V with the emergence of SCCmec type III among the MRSA colonizer strains.

Keywords: Atopic dermatitis, Gentamicin resistance, Methicillin-resistant Staphylococcus aureus, Panton Valentine Leukocidin, Staphylococcal cassette chromosome mec

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Staphylococcal cassette chromosome *mec* (SCC*mec*) typing and Gentamicin resistance in methicillin-resistant Staphylococcus aureus among children with atopic dermatitis in Egypt

Amira H. El-Ashry^{1*}: Rasha H. El-Mahdy¹: Mohammad A. Gaballah²: Rania Talaat³

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¹Department of Medical Microbiology and Immunology, Faculty of Medicine, Mansoura University, Mansoura, 35516, Egypt; ²Department of Dermatology, Andrology and STDs, Faculty of Medicine, Mansoura University, Mansoura, 35516, Egypt; ³Medical Microbiology and Immunology, Faculty of Medicine, Helwan University, Egypt

^{*}Corresponding author E-mail: <u>dr_amirah@mans.edu.eg</u>



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1. Introduction

Atopic dermatitis (AD) is the most common inflammatory skin disorder that is recorded in children (Das *et al.*, 2022). Staphylococcus aureus colonization: especially methicillin-resistant Staphylococcus aureus (MRSA) strains is more common among the children with AD than in the healthy children (Lo et al., 2010). In the skin, Staphylococcus aureus colonization may play a major role in the exacerbation of eczema through the secretion of toxins, mainly Panton-Valentine Leukocidin (PVL), and super antigens (Cavalcante et al., 2015; Chen et al., 2022). According to the previous study conducted by Hiramatsu et al., (2001), the mecA gene is recorded in the staphylococcal chromosome тес (SCCmec). cassette Binary combinations of the *mec* complex and the *ccr* allotype can identify several SCCmec "types" (Chen et al., 2009). MRSA that is relevant to healthcare settings frequently include Types I, II, and III, whereas type IV is predominantly identified in the community-acquired methicillin-resistant Staphylococcus aureus (CA-MRSA) (Kong et al., 2016). Secondary infections in AD patients are very common and are challenging to treat. Gentamicin, fusidic acid, and mupirocin are the most commonly used topical antibiotics to treat secondary bacterial infections (Williamson et al., 2017). Inactivation of aminoglycoside antibiotics by the aminoglycoside-modifying enzymes (AMEs) is the main mechanism of resistance to these drugs (Ramirez and Tolmasky, 2010). Fears that the skin of AD patients acts as a reservoir for this Staphylococcus aureus bacterium are intensified by the increased prevalence of CA-MRSA in skin and in the soft tissue infections (Chung et al., 2008). The objective of this study were to identify the SCCmec types, AMEs, PVL genes among isolates of CA-MRSA that colonises the AD pediatric skin lesions, and to interrelate these variables to the disease extent.

2. Materials and methods

2.1. Samples collection and isolation of *Staphylococcus aureus*

About 100 AD-diagnosed children who attended to the dermatology outpatient clinic at Mansoura University Hospital (M.U.H.) between March 2020 and December 2021, were the subjects of this crosssectional study. The CA-MRSA infected children had median age of 6 (2-11) with a 1.9:1 male to female ratio. The SCORing Atopic Dermatitis (SCORAD) index was implemented to figure out the extent of AD (Park et al., 2016). Exclusion criteria, isolation and identification of the CA-MRSA were carried out as previously described by Ali et al., (2019). Briefly, eczematous plaques were sampled using sterile cotton swabs. Staphylococcus aureus isolation was conducted on nutrient, blood, and mannitol salt agar media, followed by its identification through colony morphology, Gram-stained smears, release of catalase, free coagulase and DNAse (Forbes et al., 2007).

2.2. Antibiotic susceptibility testing

Antibiotic susceptibility of the MRSA isolates was assessed using the disk diffusion panel, according to the CLSI guidelines (Wayne, 2018). The inhibition zone diameter was measured using a calibrated ruler after placing several antibiotics individually on the surface of Mueller-Hinton agar plates followed by incubation at 37°C for 24 h, including erythromycin $(15 \mu g)$, chloramphenicol $(30 \mu g)$, ciprofloxacin $(5 \mu g)$, tetracycline $(30 \, \mu g)$, vancomycin (30 µg), trimethoprim/sulfamethoxazole (1.25/23.75)μg), linezolid (30 µg), fusidic acid (10 µg), rifampicin (5 μ g), tobramycin (10 μ g), and amikacin (30 μ g). Cefoxitin disc (30 g) was used to screen the Staphylococcus aureus isolates for methicillin resistance. The gentamicin sensitivity of MRSA isolates was tested using the minimum inhibitory concentration (MIC) Test Strip (Liofilchem, Roseto degli Abruzzi, Italy), according to the CLSI guidelines (Wayne, 2018).

2.3. DNA isolation

The MRSA isolates were sub-cultured overnight at 37 °C on blood agar plates. About 3-5 colonies were picked for genomic DNA extraction utilizing the protocol of i-genomic BYF DNA extraction mini-Kit (Abdulghany and Khairy, 2014).

2.4. Amplification of *mecA*, *PVL* genes and SCC*mec* typing using PCR

All the cefoxitin resistant isolates of Staphylococcus aureus were subjected to conventional PCR for amplification of mecA and PVL genes (Lina et al., 1999; Mehrotra et al., 2000). Two separate multiplex PCR reactions were performed to screen all the MRSA isolates for AMEs genes, and to characterize them according to SCCmec types using specific primers for SCCmec types III, IV, V (Table 1), in reference to Vakulenko et al., (2003); Lu et al., (2008). MRSA reference strain (ATCC 25923) obtained from The Naval Medical Research Unit No. 3 (NAMRU-3) was employed as a control. Table (1) lists the primers introduced in this study, the product sizes, and PCR programs of the genes examined.

2.5. Statistical analysis

The PVL and gentamicin resistance of the CA-MRSA isolates were linked to AD severity using the Mann-Whitney U test. A *p*-value of 0.05 or less was considered statistically significant.

3. Results

3.1. Identification of MRSA and their resistance to antibiotics

Twenty-nine isolates of CA-MRSA were recovered from the skin lesions of 100 AD children. The MRSA isolates were characterized phenotypically and genotypically. All the CA *Staphylococcus aureus* cefoxitin resistant isolates were found to possess the *mecA* gene. All the CA-MRSA isolates were susceptible to vancomycin and linezolid (100 %), while resistance to erythromycin displayed the highest rate (93.1 %), followed by tetracycline resistance (89.7 %) among the colonizers. Fusidic acid resistance was detected in 72.4 % of the isolates. Fig. (1) demonstrates the antibiotic resistance pattern of CA-MRSA to all the tested antibiotics. The recorded resistance patterns of CA-MRSA isolates' against gentamicin, tobramycin, and amikacin were: 23 (79.3 %); 22 (75.8 %); 17 (58.6 %), respectively. The MIC results for gentamicin ranged between 0.5 and 256 μ g/ml (Fig. 2). The MIC50 and MIC90 values of the gentamicin resistant isolates were 48 μ g/ml and 128 μ g/ml, respectively.

Among CA-MRSA gentamicin resistant isolates, the aac(6')-Ie-aph(2'')-Ia, ant(4')-Ia, and aph(3')-IIIagenes were identified in 19, 17 and 11 isolates; respectively, with the predominance of ant(4')-Ia gene in all the CA-MRSA colonizers; moreover, it was additionally detected in 2 tobramycin resistant and 1 amikacin resistant isolates. The three AME genes (ant(4')-Ia, aac(6')-Ie-aph(2'')-Ia, and aph(3')-IIIa) coexisted in 8 of the isolates, while two of these genes coexisted in 10 isolates (ant(4')-Ia and aac(6')-Ieaph(2'')-Ia, while aac(6')-Ie-aph(2'')-Ia and aph(3')-IIIa existed in 2 isolates, and ant(4')-Ia, and aph(3')-IIIa was recorded in a single isolate. Distribution of the AMEs genes among the MRSA isolates is summarized in Table (2).

3.2. Screening for *PVL* gene and SCCmec typing

The *PVL* gene was detected in 14 isolates (48.3 %) of the CA-MRSA (Fig. 3). About 9 (31 %) isolates harbored SCC*mec* type V, 8 (27.6 %) harbored SCC*mec* type III, 6 (20.7 %) harbored SCC*mec* type IV, and 6 (20.7 %) isolates were non typeable, which means that they did not express any of the screened SCC*mec* types.

3.3. Correlation between *PVL* gene and gentamicin resistance to AD severity

Regarding SCORAD index, the CA-MRSA colonized patients that carry the *PVL* gene had significant high SCORAD index of 27.8 %, compared to the CA-MRSA patients that had no PVL gene (17.7 %) (p = 0.016), as demonstrated in Fig. (4).

Table 1. List of primers used in this study to screen the MRSA isolates for *AMEs* genes, and to characterize them according to SCC*mec* types

Gene	Primer sequence (5'-3')	Product size (bp)	PCR program	References	
mecA	ACTGCTATCCACCCTCAAAC	163	5 min. at 94°C, 35 cycles (2 min.	(Mehrotra et al.,	
	CTGGTGAAGTTGTAATCTGG		at 94°C, 2 min. at 57°C, 1 min. at 72°C); 7 min. at 72°C.	<u>2000)</u>	
aac(6')-Ie-	CAGAGCCTTGGGAAGATGAAG	348			
aph(2)-Ia	CCTCGTGTAATTCATGTTCTGGC				
aph(2")-Ib	CTTGGACGCTGAGATATATGAGCAC	867	_		
	GTTTGTAGCAATTCAGAAACACCCTT				
aph(2')-Ic	CCACAATGATAATGACTCAGTTCCC	444	-		
	CCACAGCTTCCGATAGCAAGAG		3 min. at 94°C; 35 cycles (40 sec at 94° C, 40 sec at 55°C, and 40 sec	<u>(Vakulenko <i>et al.</i>,</u> 2003)	
aph(2')-Id	GTGGTTTTTACAGGAATGCCATC	641	$at 72^{\circ}C$; 2 min. at 72°C	<u></u>	
- · ·	CCCTCTTCATACCAATCCATATAACC				
aph(3')-IIIa	GGCTAAAATGAGAATATCACCGG	523	_		
I ()	CTTTAAAAAATCATACAGCTCGCG				
ant(4')-Ia	CAAACTGCTAAATCGGTAGAAGCC	294	_		
	GGAAAGTTGACCAGACATTACGAACT				
luk-PV	ATCATTAGGTAAAATGTCTGGACATGATCCA	433	30 cycles (30 sec at 94°C, 30 sec at 55° C and 1 min at 72° C)	<u>(Lina et al., 1999)</u>	
	GCATCAASTGTATTGGATAGCAAAAGC		55 C, and I min. at 72 C)		
Typing for					
Mec complex		1164 (Type			
-Universal	TATACCAAACCCGACAAC	II Or 998 (Type III			
(mA6)		(Type III	$2 \min_{x \to 0} at 05^{\circ}C$ 20 avalas (20 as a st	$(I_{\rm H}, a_{\rm eff}, a_{\rm eff}, 2008)$	
-Class A	GIGCAGATAGIAACGOIGCIIG	1592	25° C, 30 sec at 58°C, 1.5 min. at	<u>(Lu ei al., 2008)</u>	
		804	72°C); 4 min. at 72°C.		
-Class D	GGTTTCACTCGGATGTCTGT				
-Class C (IS2)	TGAGGTTATTCAGATATTTCGATGT				
Ccr complex			-		
Ccr Type 2	ATCATTACGTCAACAACCGC	315			
~ 1					
	ACTATAACCITCIOIOCITIOC				

										Total			
	AMEs genes			Type of	SCCmec	CCmec		Resistance					
aut(A') La	aao(6!) Io	anh(2!) III a		V	11/	N/T [*]	CN	TOD	AV	1100			
ani(4)-1a	aac(0)-1e-	apn(5)-111a	111	v	IV	IN I	CN	IUB	AK				
	aph(2")-Ia		No.	No.	No.	No.							
+	+	+	5	2		1	8	7	6	8			
+	+	-	2		2	3	7	7	4	7			
-	+	-		1		1	2	2	2	2			
+	-	-			3	1	1	3	2	4			
+	-	+		1			1	1	1	1			
-	+	+	1	1			2	2	2	2			
-	-	-		4	1		2	0	0	5			
20	19	11	8	9	6	6	23	22	17	29			

Table 2. Distribution of the AMEs genes and SCCmec type among the CA-MRSA isolates

Where; *NT: non-typeable, CN: Gentamicin, TOB: Tobramycin, AK: Amikacin



Fig. 1: Antibacterial resistance patterns of the CA-MRSA isolates among the AD children, where sensitivity is represented by blue columns and resistance by orange columns

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Fig. 2: Gentamicin susceptibility testing using the MIC Test Strip according to CLSI guidelines. Gentamicin resistant CA-MRSA isolate ($MIC_{50} = 48 \ \mu g/ \ ml$, $MIC_{90} = 128 \ \mu g/ \ ml$)

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Fig. 3: Gel electrophoresis of PCR amplified *PVL* gene (433 bp) among CA-MRSA isolated from AD children. Where; Lane (M): DNA ladder (100 bp). Lanes 4, 5, 6: positive results for *PVL* (433 bp). Lane 2: MRSA ATCC 25923 positive control for PVL (433 bp). Lane 1: negative control. Lanes 3, 7: negative results for *PVL*



Fig. 4: The SCORAD score of children with AD colonized with 14 *PVL* positive CA-MRSA (median 27.8) versus AD patients colonized with 15 *PVL* negative CA-MRSA (median 17.7). The error bars represent SCORAD Score values in both *PVL* Positive and negative MRSA. The *p*-value was 0.016

Moreover, the SCORAD index in patients colonized with gentamicin resistant MRSA (26.5 %) was significantly

higher than that in the gentamicin susceptible MRSA isolates (15.2 %), recording p = 0.009 (Fig. 5).



Fig. 5: The SCORAD score of children with AD colonized with 23 gentamicin resistant CA-MRSA (median 26.5), versus AD children colonized with 6 gentamicin sensitive CA-MRSA (median 15.2). The error bars represent SCORAD Score values in both gentamicin sensitive and resistant MRSA. The *p*-value was 0.009

4. Discussion

Atopic dermatitis patients are at growing threat of emerging microbiological resistance, and will become subsequently colonized with MRSA, due to of the repeated usage of topical and systemic antibiotics (Lipnharski et al., 213; Ogonowska et al., 2021). In several previous studies, the rate of MRSA colonization of the skin of AD pediatric patients varied between 0.5 % to 41.8 % (Balma-Mena et al., 2011; Jagadeesan et al., 2014; Park et al., 2016; Cavalcante et al., 2021). In this study, colonization of skin lesions with CA-MRSA was detected in 29 % of the cases. This high-level rate may be attributed to the low socioeconomic conditions, hot humid weather, status. overcrowding, nutritional prevalence of parasitic infections, and to the difference in geographical area, in accordance with the results of Jagadeesan et al., (2014).

Currently, 82.8 % of the CA-MRSA isolates carried the AMEs genes. Moreover, a high rate of gentamicin resistance was reported in this study (79.3 %). Aminoglycoside resistance is intimately linked to methicillin-resistance, due to proximity of the mecA and AME genes (Choi et al., 2003; Fathi et al., 2022). Similarly, a high frequency of gentamicin resistance (58.8 %) was recorded in the previous study conducted in Korea by Chung et al., (2008). On the contrary, lower rate was reported in Brazil (Cavalcante et al., 2015). Distribution of the aminoglycoside resistance determinants varied among the different regions; even in those isolates recovered from the same city, and is also linked to type of the used aminoglycoside (Ida et al., 2001; Ardic et al., 2006). In this study, although ant(4')-Ia was the most common detected gene in the isolates of CA-MRSA; however, aac(6')-aph(2'') was the most common gene detected in the gentamicin resistant isolates, which was also reported recently by Al-Mayahi and Srhan (2021). Similarly, several studies conducted in Kuwait and Japan reported that ant(4')-Ia was the most common aminoglycosideresistant determinant (Udo and Dashti, 2000; Ida et al., 2001). aac(6')-aph(2'')Meanwhile, the was predominant gene in other previous reports (Choi et al., 2003; Ardic et al., 2006; Fathi et al., 2022). In this study, about 2-3 AMEs genes coexisted in the gentamicin resistant isolates. We observed that combination of the aac(6')-aph(2'') and ant(4')-Ia, in addition to aac(6')-aph(2''), ant(4')-Ia and aph(3')-IIIa genes, were the most common genotypes. Combination of AMEs genes was also reported in another previous study conducted by Udo and Dashti, (2000).

In accordance with results of the preceding studies conducted by Chung et al., (2008); Tang et al., (2011) on CA-MRSA in the AD children; all the current MRSA isolates were susceptible to vancomycin, while resistance to erythromycin displayed the highest rates followed by tetracycline resistance among the colonizer isolates. Fusidic acid resistance was detected in 72.4 % of the isolates, which was the matter of Danish AD patients that previously exhibited 41 % resistance to fusidic acid (Edslev et al., 2018). On the contrary, lower rate of fusidic acid resistance (11.8 %) was documented among the MRSA, which were isolated from Children with Eczematous AD Lesions (Chung et al., 2008). High prevalence of fusidic acid resistance may be attributed to the frequent use of fusidic acid treatment, which likely results in the emergence of more resistant strains.

Panton-Valentine leukocidin (PVL) is a cytotoxin that is responsible for destruction of the leukocytes, and causes tissue necrosis by destruction of the cell membranes. PVL is frequently associated with community-acquired necrotic lesions of the skin and subcutaneous tissues (Lina *et al.*, 1999). PVL was detected in about half of the current CA-MRSA isolates, and was significantly associated with high SCORAD score. In accordance, similar rate of PVL prevalence among the MRSA isolates was documented in the pediatric AD patients (Lo *et al.*, 2010). However, contribution of PVL in recrudescence of severity of AD in the children is controversial (Edslev et al., 2018; Cavalcante et al., 2021).

Among the MRSA isolates, SCCmec V was the most common type. Also, SCCmec V was the most common cassette previously reported by Lo et al., (2010) in pediatric AD. Meanwhile, other studies in the same group of patients reported SCCmec IV as the predominant cassette (Chung et al., 2008; Cavalcante et al., 2015; Abad et al., 2020). Although, type IV SCCmec is the most common element in CA-MRSA; however, SCCmec I-III elements were common in the nosocomial MRSA (Sadeghi Moghaddam et al., 2022). In this study, type III was detected in 27.6 % of the CA-MRSA isolates. A study conducted in Iran by Fasihi et al., (2017) reported that the most common cassette types in the community were SCCmec types I and III. This establishes the idea of transmission of CA-MRSA from population to the hospital settings, and transmission of hospital-acquired MRSA from hospital settings to the community (Yeung et al., 2011). Another study conducted in Brazil revealed the association of SCCmec type III with the multidrugresistant isolates, which supports the hypotheses that hospital is the origin of these MRSA strains, and that these strains are currently increasing as colonizing pathogens in the pediatric community (Lamaro-Cardoso et al., 2009).

Conclusion

Current data revealed a high frequency of gentamicin resistance among the CA-MRSA that colonise the skin of the atopic dermatitis children; with the predominance of aac(6')-*Ie-aph(2')-Ia* aminoglycoside-resistant determinant, followed by ant(4')-*Ia*. Moreover, SCCmec type V was the most common cassette with the possible emergence of SCCmec type III among the CA-MRSA colonizers.

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None to declare.

Conflict of interest

All authors declare non-existence of conflict of interests.

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Ethical approval

This work was ethically approved by the Faculty of Medicine's Institutional Research Board (IRB) (Code number: R/22.11.1932), Mansoura University. An informed consents were provided by the participants and parents that shared in this study.

5. References

Abad, E.D.; Ferreira, D.C.; Cavalcante, F.S.; Saintive, S.; Goudouris, E.; Prado, E.A. et al. (2020). High incidence of acquiring methicillinresistant *Staphylococcus aureus* in Brazilian children with Atopic Dermatitis and associated risk factors. Journal of Microbiology, Immunology and Infection. 53(5): 724-730.

https://doi.org/10.1016/j.jmii.2018.12.014

Abdulghany, H.M. and Khairy, R.M. (2014). The Frequency of Methicillin-Resistant *Staphylococcus aureus* and Coagulase Gene Polymorphism in Egypt. International Journal of Bacteriology. 2014: 680983. <u>https://doi.org/10.1155/2014/680983</u>

Ali, H.A.; El-Mahdy, R.H. and Gaballah, M.A. (2019). Community-acquired methicillin-resistant *Staphylococcus aureus* colonization in atopic dermatitis patients in Mansoura, Egypt. Biomedical Dermatology. 3(2): 1–5. https://doi.org/10.1186/s41702-019-0040-412

Al-Mayahi, A. and Srhan, F. (2021). A preliminary study of Aminoglycoside Modifying Enzymes (AMEs) of Multiple Antibiotic Resistance of Methicillinresistant *Staphylococcus aureus* (MRSA) isolated from clinical specimens in Al-Diwaniya/Iraq. Jordan Journal of Biological Sciences. 14(4): 733-741. https://doi.org/10.54319/jjbs/140414.

Ardic, N.;Sareyyupoglu, B.;Ozyurt, M.;Haznedaroglu, T. and Ilga, U. (2006). Investigationof aminoglycoside modifying enzyme genes inmethicillin-resistant staphylococci.MicrobiologicalResearch.161(1):49-54.https://doi.org/10.1016/j.micres.2005.05.002

Balma-Mena, A.; Lara-Corrales, I.; Zeller, J.; Richardson, S.; McGavin, M.J.; Weinstein, M. et al. (2011). Colonization with community-acquired methicillin-resistant *Staphylococcus aureus* in children with atopic dermatitis: a cross-sectional study. International Journal of Dermatology. 50(6): 682-688. https://doi.org/10.1111/j.1365-4632.2010.04751.x19

Cavalcante, F.S.; Saintive, S.; Carvalho Ferreira, D.; Rocha Silva, A.B.; Guimarães, L.C.; Braga, B.S. et al. (2021). Methicillin-resistant *Staphylococcus aureus* from infected skin lesions present several virulence genes and are associated with the CC30 in Brazilian children with atopic dermatitis. Virulence. 12(1): 260-269. https://doi.org/10.1080/21505594.2020.1869484

Cavalcante, F.S.; Abad, E.D.; Lyra, Y.C.; Saintive, S.B.; Ribeiro, M.; Ferreira, D.C. et al. (2015). High prevalence of methicillin resistance and PVL genes among *Staphylococcus aureus* isolates from the nares and skin lesions of pediatric patients with atopic dermatitis. Brazilian Journal of Medical and Biological Research. 48(7): 588-594. https://doi.org/10.1590/1414-431X20154221

Chen, H.; Zhang, J.; He, Y.; Lv, Z.; Liang, Z.; Chen, J. et al. (2022). Exploring the Role of *Staphylococcus aureus* in Inflammatory Diseases. Toxins. 14(7): 464. https://doi.org/10.3390/toxins14070464

Chen, L.; Mediavilla, J.R.; Oliveira, D.C.; Willey, B.M.; de Lencastre, H. and Kreiswirth, B.N. (2009). Multiplex real-time PCR for rapid Staphylococcal cassette chromosome *mec* typing. Journal of Clinical Microbiology. 47(11): 3692-3706. https://doi.org/10.1128/JCM.00766-09.

Choi, S.M.; Kim, S.H.; Kim, H.J.; Lee, D.G.; Choi, J.H.; Yoo, J.H. et al. (2003). Multiplex PCR for the detection of genes encoding aminoglycoside modifying enzymes and methicillin resistance among *Staphylococcus* species. Journal of Korean Medical Science. 18(5): 631-636. https://doi.org/10.3346/jkms.2003.18.5.63123

Chung, H.J.; Jeon, H.S.; Sung, H.; Kim, M.N. and Hong, S.J. (2008). Epidemiological characteristics of methicillin-resistant *Staphylococcus aureus* isolates from children with eczematous atopic dermatitis lesions. Journal of Clinical Microbiology. 46(3): 991-995. <u>https://doi.org/10.1128/JCM.00698-0711</u>

Das, P.; Mounika, P.; Yellurkar, M.L.; Prasanna, V.S.; Sarkar, S.; Velayutham, R. et al. (2022). Keratinocytes: An Enigmatic Factor in Atopic Dermatitis. Cells. 11(10): 1683. https://doi.org/10.3390/cells11101683

Edslev, S.M.; Clausen, M.L.; Agner, T.; Stegger, M. and Andersen, P.S. (2018). Genomic analysis reveals different mechanisms of fusidic acid resistance in *Staphylococcus aureus* from Danish atopic dermatitis patients. The Journal of Antimicrobial Chemotherapy. 73(4): 856-861. https://doi.org/10.1093/jac/dkx481

Fasihi, Y.; Kiaei, S. and Kalantar-Neyestanaki, D.(2017). Characterization of SCCmec and spa types of
methicillin-resistant Staphylococcus aureus isolates
from health-care and community-acquired infections
in Kerman, Iran. Journal of Epidemiology and Global
Health, 7(4): 263-267.
https://doi.org/10.1016/j.jegh.2017.08.004

Fathi, J.; Hashemizadeh, Z.; Dehkordi, R.S.; Bazargani, A.; Javadi, K.; Hosseini-Nave, H. et al. (2022). Evaluation of aminoglycoside modifying enzymes, SCC*mec*, coagulase gene and PCR-RFLP coagulase gene typing of *Staphylococcus aureus* isolates from hospitals in Shiraz, southwest of Iran. Heliyon. 8(8): e10230. https://doi.org/10.1016/j.heliyon.2022.e10230

Forbes, B.A.; Sahm, D.F. and Weissfeld, A.S. (2007). Bailey and Scott's Diagnostic Microbiology. 12th Edition, Mosby Elsevier, China. pp. 842-855.

Hiramatsu, K.; Cui, L.; Kuroda, M. and Ito, T. (2001). The emergence and evolution of methicillinresistant *Staphylococcus aureus*. Trends in Microbiology. 9(10): 486-493. https://doi.org/10.1016/s0966-842x(01)02175-86

Ida, T.; Okamoto, R.; Shimauchi, C.; Okubo, T.; Kuga, A. and Inoue, M. (2001). Identification of aminoglycoside-modifying enzymes by susceptibility testing: epidemiology of methicillin-resistant *Staphylococcus aureus* in Japan. Journal of Clinical Microbiology. 39(9): 3115-3121. https://doi.org/10.1128/JCM.39.9.3115-3121.2001

Jagadeesan, S.; Kurien, G.; Divakaran, M.V.; Sadanandan, S.M.; Sobhanakumari, K. and Sarin, A. (2014). Methicillin-resistant *Staphylococcus aureus* colonization and disease severity in atopic dermatitis: a cross-sectional study from South India. Indian Journal of Dermatology, Venereology and Leprology. 80(3): 229-234. <u>https://doi.org/10.4103/0378-6323.132250</u>

Kong, E.F.; Johnson, J.K. and Jabra-Rizk, M.A. (2016). Community-Associated Methicillin-Resistant *Staphylococcus aureus*: An Enemy amidst Us. PLoS Pathogens. 12(10): e1005837. https://doi.org/10.1371/journal.ppat.1005837

Lamaro-Cardoso, J.; de Lencastre, H.; Kipnis, A.; Pimenta, F.C.; Oliveira, L.S.; Oliveira, R.M.; Nouer, S.S. et al. (2009). Molecular epidemiology and risk factors for nasal carriage of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* in infants attending day care centers in Brazil. Journal of Clinical Microbiology. 47(12): 3991-3997. https://doi.org/10.1128/JCM.01322-09 Lina, G.; Piémont, Y.; Godail-Gamot, F.; Bes, M.; Peter, M.O.; Gauduchon, V. et al. (1999). Involvement of Panton-Valentine leukocidinproducing *Staphylococcus aureus* in primary skin infections and pneumonia. Clinical Infectious Diseases. 29(5): 1128-1132. https://doi.org/10.1086/313461

Lipnharski, C.; d'Azevedo, P.A.; Quinto, V.P.; Bessa, G. and Bonamigo, R.R. (2013). Colonization by *Staphylococcus aureus* increases the EASI and the number of appointments by patients with atopic dermatitis: cohort with 93 patients. Anais Brasileiros de Dermatologia. 88(4): 518-521. https://doi.org/10.1590/abd1806-4841.20132046

Lo, W.T.; Wang, S.R.; Tseng, M.H.; Huang, C.F.; Chen, S.J. and Wang, C.C. (2010). Comparative molecular analysis of meticillin-resistant *Staphylococcus aureus* isolates from children with atopic dermatitis and healthy subjects in Taiwan. The British Journal of Dermatology. 162(5): 1110-1116. https://doi.org/10.1111/j.1365-2133.2010.09679.x

Lu, P.L.; Chang, J.C.; Hsu, H.T.; Chen, J.H.; Chen, F.J.; Lin, S.F. al. (2008). One tube multiplex PCR for simple screening of SCC*mec* I-V types of methicillin-resistant Staphylococcus aureus. Journal of Chemotherapy. 20(6): 690-696. https://doi.org/10.1179/joc.2008.20.6.690

Mehrotra, M.; Wang, G. and Johnson, W.M. (2000). Multiplex PCR for detection of genes for *Staphylococcus aureus* enterotoxins, exfoliative toxins, toxic shock syndrome toxin 1, and methicillin resistance. Journal of Clinical Microbiology. 38(3): 1032-1035. <u>https://doi.org/10.1128/JCM.38.3.1032-1035.2000</u>

Ogonowska, P.; Gilaberte, Y.; Barańska-Rybak, W.andNakonieczna, J. (2021). ColonizationWith Staphylococcus aureus in Atopic DermatitisPatients: Attempts to Reveal the Unknown. FrontiersinMicrobiology. 11: 567090.https://doi.org/10.3389/fmicb.2020.567090

Park, J.M.; Jo, J.H.; Jin, H.; Ko, H.C.; Kim, M.B.; Kim, J.M. et al. (2016). Change in Antimicrobial Susceptibility of Skin-Colonizing *Staphylococcus aureus* in Korean Patients with Atopic Dermatitis during Ten-Year Period. Annals of Dermatology. 28(4): 470-478.

https://doi.org/10.5021/ad.2016.28.4.470

Ramirez,M.S. andTolmasky,M.E.(2010).Aminoglycoside modifying enzymes.Drug ResistanceUpdates.13(6):151-171.https://doi.org/10.1016/j.drup.2010.08.003

Sadeghi Moghaddam, T.; Namaei, M.H.; Afshar, D. and Yousefi, M. (2022). High frequency of SCCmec type IV and multidrug-resistant SCCmec type I among hospital acquired methicillinresistant *Staphylococcus aureus* isolates in Birjand Imam Reza Hospital, Iran. Iranian Journal of Microbiology. 14(1): 67-75. https://doi.org/10.18502/ijm.v14i1.8803.

Tang, C.S.; Wang, C.C.; Huang, C.F.; Chen, S.J.;Tseng, M.H. and Lo, W.T. (2011). Antimicrobialsusceptibility of *Staphylococcus aureus* in childrenwith atopic dermatitis. Pediatrics International. 53(3):363-367.<u>https://doi.org/10.1111/j.1442-</u>200X.2010.03227.x

Udo, E.E. and Dashti, A.A. (2000). Detection of genes encoding aminoglycoside-modifying enzymes in staphylococci by polymerase chain reaction and dot blot hybridization. International Journal of Antimicrobial Agents. 13(4): 273-279. https://doi.org/10.1016/s0924-8579(99)00124-7

Vakulenko,S.B.;Donabedian,S.M.;Voskresenskiy,A.M.;Zervos,M.J.;Lerner,S.A.andChow,J.W. (2003).MultiplexPCR for detectionofaminoglycosideresistancegenesinEnterococci.AntimicrobialAgentsandChemotherapy.47(4):1423-1426.https://doi.org/10.1128/AAC.47.4.1423-

Wayne, P. (2018). Performance Standards for Antimicrobial Susceptibility Testing. Supplement

M100. Clinical and Laboratory Standards Institute (CLSI). 28th Edition: 30-102.13.

Williamson, D.A.; Carter, G.P. and Howden, B.P. (2017). Current and Emerging Topical Antibacterials and Antiseptics: Agents, Action, and Resistance Patterns. Clinical Microbiology Reviews. 30(3): 827-860. <u>https://doi.org/10.1128/CMR.00112-16</u>

Yeung, M.; Balma-Mena, A.; Shear, N.; Simor, A.; Pope, E.; Walsh, S. et al. (2011). Identification of major clonal complexes and toxin producing strains among *Staphylococcus aureus* associated with atopic dermatitis. Microbes and Infection. 13(2): 189-197. https://doi.org/10.1016/j.micinf.2010.10.023