

ISOLATION AND IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) FROM POULTRY MEAT AND POULTRY PRODUCTS.

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ABSTRACT

*A total of 500 different samples were collected from poultry meat, poultry products and their human contacts in abattoirs from different Egyptian Governorates (Damietta, Dakahlia, Giza and Cairo) in 2012 and 2013. The samples were tested for presence of *S. aureus* by isolation and biochemical identification, the results revealed that coagulase positive *S. aureus* was present in 83 samples (61.03%). The isolated strains of coagulase positive *S. aureus* were tested for antimicrobial sensitivity. Most strains were resistant to penicillin and ampicillin, less resistance was appeared to amoxicillin, oxacillin, Methicillin, and ceftriaxone, while all strains were sensitive to, amoxicillin clavulanic acid and vancomycin. Using PCR technique, amplification of 310 bp fragment of *mecA* gene from the extracted DNA of all isolated coagulase positive *S. aureus* strains isolated from different chicken samples and human contacts resulted in 5 samples from muscles and skin were positive, Using sequencing technique to *mecA* gene in three positive strains, the Phylogenetic analysis of *mecA* gene of these isolates were clustered together and little away from other published isolates of MRSA, Amino acid identities were 99.5% among the analyzed isolates, The three isolates shared 87.2%-*

89.2% identity with other *Staphylococcus aureus* isolates.

INTRODUCTION

Poultry meat is a common vehicle of food borne illness, *S.aureus* usually being one of the causes of outbreaks involving large number of peoples (*Geornaras and Von Holy, 2001*).Methicillin-resistant *S. aureus* (MRSA) included those strains that had acquired a gene giving them resistance to methicillin and essentially all other beta-lactam antibiotics. Soon after methicillin was introduced into human medicine to treat penicillin resistant staphylococci, this group of organisms had since emerged as a serious concern in human medicine. MRSA was first reported as a nosocomial pathogen in human hospitals. Although these organisms caused the same types of infections as other *S. aureus*, hospital-associated strains have become resistant to most common antibiotics, and treatment can be challenged (*Fitzgerald et al .,2001*).The *mecA*gene which conferred resistance to methicillin encoded a variant penicillin-binding protein, PBP2a . Native PBP2 catalysed a key step in the synthesis of the bacterial peptidoglycan cell wall, and was bound and inactivated by penicillin-type antibiotics including methicillin. PBP2a was not inhibited by penicillins and could function instead of PBP2 (*Pinhoet al.,2001*). *S.aureus* had developed resistance to most classes of antimicrobial agents. Penicillin was the first choice of antibiotics to treat staphylococcal infection. In 1944, by destroying the penicillin by penicillinase, *S.aureus* becomes resistant. More than 90% *S.aureus* strains were resistant to penicillin. However, methicillin, semi synthetic penicillin, was used to treat Penicillin Resistant *S. aureus* but resistance finally emerged. MRSA is mediated by the presence of PBP-2a which is expressed by an exogenous gene, *mecA* (*Livermore, 2001*). In Japan

however, an MRSA strain of human origin isolated from raw chicken samples appeared capable of producing enterotoxin C (*Kitaiet al., 2005*).

MATERIAL AND METHODS

1. Material:

1.1. Samples:

A total of 500 different samples were collected from poultry meat, poultry products and its human contacts of poultry in abattoirs from different Egyptian Governorates (Damietta, Dakahlia, Giza and Cairo) in 2012 and 2013. All samples used were collected under aseptic condition and safety precautions. (*Rodgerset al., 1999*)

1.2. Preparation of samples:

Muscle and skin samples were collected from chicken's carcasses using sterile scissor and forceps and under aseptic condition. Each sample was collected then marked and placed in an ice box and transferred to the laboratory as soon as possible. And Cloacal swabs were collected from cloacae of living poultry by using sterile cotton swabs contain 2 ml saline.

2. Methods:

Isolation and identification of *Staphylococcus aureus* was done according to (*Sneath et al., 1986*).

Disk diffusion method applied according to (*Koneman et al., 1979*)
Amplification of *mecA* gene from DNA of *Staphylococcus aureus* isolates was done according to (*Spanuet al., 2003*).

RESULTS

Table (1): Isolation rate of *Staphylococcus aureus* from different samples of poultry and its products

	No. of tested samples	positive		negative		
		No.	%	No.	%	
Muscles & skin	100	46	46	54	54	
Cloacal swabs	100	32	32	68	68	
products	Burger	23	1	4.35	22	95.65
	Pane	20	0	0	20	100
	parts	57	3	5.26	54	94.74
Human samples	200	54	27	146	73	
total	500	136	27.20	364	72.80	

Table (2): percentages of coagulase positive *Staphylococcus aureus* obtained from different samples of poultry and its products

	No. of tested samples	positive		negative	
		No.	%	No.	%
Muscles & skin	46	29	63.04	17	36.96
Cloacal swabs	32	14	43.75	18	56.25
products	Burger	1	100	0	0
	Pane	0	0	0	0
	parts	3	2	66.67	1
Human samples	54	37	68.52	17	31.48
total	136	83	61.03	53	38.97

Table (3): Interpretation of antimicrobial sensitivity testing for all coagulase positive *S. aureus* isolates.

Antimicrobial disk	Antibiotic sensitivity of Coagulase positive <i>S. aureus</i>					
	Resistant		Intermediate		Sensitive	
	No.	%	No.	%	No.	%
P	64	77.11	-	-	19	22.89
MET	16	19.28	8	9.64	59	71.08
OX	25	30.12	4	4.82	54	65.06
AMP	61	73.49	-	-	22	26.51
AMOXY	23	27.71	2	24.09	58	69.88

AM+CL	-	-	3	3.61	80	96.39
VA	-	-	-	-	83	100
KF	7	8.43	13	15.66	63	75.90
CRO	6	7.2	34	40.96	43	51.81

{P (penicillin), MET (methicillin), OX (oxacillin), AMP (ampicillin), AMOXY (amoxicillin), AM+CL (amoxicillin + clavulanic acid), VA (vancomycin), KF (cephalothin), and CRO (ceftriaxone),}

Amplification of 310 bp fragment of *mecA* gene from the extracted DNA of all isolated coagulase positive *S.aureus* strains

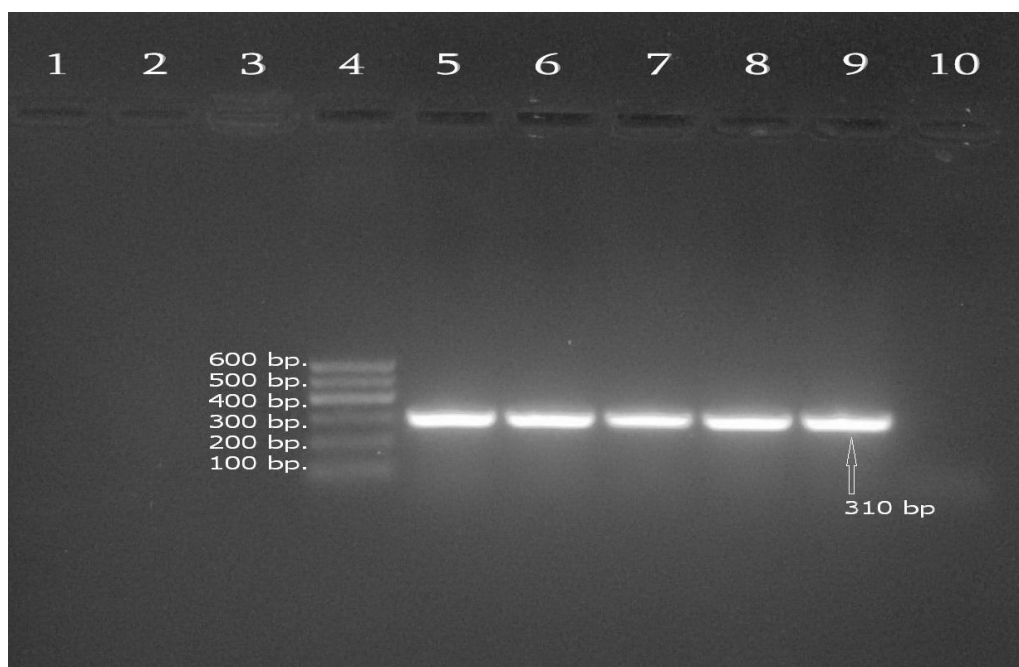


Photo (1): showed the agarose gel electrophoresis with positive PCR amplification of 310 bp fragment of *mecA* gene from DNA of coagulase positive *S. aureus* isolates from different samples. Lanes (5, 6, 7, 8).

Lanes (1, 2, 3): Negative samples

Lane 4: the DNA molecular weight marker (Gel-pilot 100bp ladder).

Lane 9: positive control

Lane 10: negative control

Purified and sequenced *mecA* gene of three isolates were revealed 87.2%-89.2% identity with other *Staphylococcus aureus* isolates.

		Percent Identity																								
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23		
Divergence	1	■	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	99.6	98.4	99.6	99.6	99.6	89.2	88.7	88.7	1	Staphaureus-R99-SCCmecIVa-and4CM-geneti
	2	0.4	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	2	Staphaureus-CA-347.
	3	0.4	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	3	Staphaureus-typeIX-staphylococcusasset
	4	0.4	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	4	Staphaureus M1 COMPLETE
	5	0.4	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	5	Staphaureus-SCC4610-andtypeI-Staphyloco
	6	0.4	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	6	Staphaureus-stMERSA P126
	7	0.4	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	7	Staphaureus-Z172
	8	0.4	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	8	Staphaureus-stUSA300-R114
	9	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	9	Staphaureus SA40
	10	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	10	StaphAUREUS SA957
	11	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	11	Staphaureus-stATCC 4300
	12	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	12	Staphaureus-Bmb9393
	13	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	13	Staphaureus-SCCmec-isolate-CMFT535
	14	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	14	Staphaureus-SCCmec-isolate-CMFT352
	15	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	100.0	98.8	100.0	100.0	100.0	89.2	88.7	88.7	15	Staphaureus-SCCmec-isolate-CMFT33
	16	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	■	98.8	100.0	100.0	100.0	89.2	88.7	88.7	16	Staphaureus-SCCmec-isolate-CMFT3119
	17	1.6	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	■	98.8	98.8	98.8	87.7	87.2	87.2	17	Staphylococcus sp. X7602B
	18	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	■	100.0	100.0	89.2	88.7	88.7	18	Staphylococcus aureus strain X196 MERSA
	19	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	0.0	■	100.0	89.2	88.7	88.7	19	Staphylococcus aureus strain ATCC 43300
	20	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	0.0	0.0	■	89.2	88.7	88.7	20	Staphylococcus SP CNS 45C
	21	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	■	99.5	99.5	21	mersa42-f
	22	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	2.3	0.6	0.6	0.6	0.6	■	99.5	22	MERSA-43
	23	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	2.4	0.6	0.6	0.6	0.6	0.6	■	23	AHNEDEGAZY-F
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23			

Mersa42-f: sample (1)

mersa43: sample (2)

Mersa-F: sample (3)

DISCUSSION

Today, poultry meat industry has become the predominant source of protein from meat in the diet of the population of most developing countries (*Robert, 1990*). But during conventional slaughter procedures and further processing, microorganisms are introduced into and onto carcasses (*Holder et al., 1997*).

During processing, contamination of carcasses with *S. aureus* increased to $> 10^3$ CFU /g of skin. , Plucking and evisceration appeared to be the main stages at which contamination of carcasses with *S. aureus* occurred (*Notermans et al., 1982*).

In the present work, all *S.aureus* isolates showed yellow colonies surrounded by yellow halo on mannitol salt agar that agree with *Howard and Kloss, 1993* who mentioned that the selectivity of MSA is based on its high concentrations of salt. Also after 18 to 24 hrs incubation, Staphylococci appear as opaque, smooth, circular colonies with a butyrous consistency in blood agar.

In this study, Table (1) showed that the total prevalence of coagulase positive *S.aureus* from chickens and human contacts samples were 61.03 % of the samples (83/136), while, 38.97 % were coagulase negative Staphylococci (53/136).

out of 46 muscles and skin samples, 29 samples were coagulase positive with the percentage of 63.04%, that nearly agree with the results of *Kawano et al. (1996)* who isolated *S.aureus* strains from the skin of 103 chickens with percentage of 79.2% of the 130 chickens.

Regarding to the current study 32 cloacal swabs subjected for isolation of *S.aureus*, The overall isolated coagulase positive *S.aureus* was 14 with the percentage of 43.75 %,On the other hands *Kinsman et al. (1981)* concluded that the natural populations of *S.aureus* found on the skin and respiratory tract of healthy birds were probably contributing to the source of infection when the clinical disease develops.

Studying of 83 strains of coagulase positive *S.aureus* against 9antimicrobial discs revealed different dgree of sensitivity. those results Kafrelsheikh Vet. Med. J. Vol. 13 No. 1 (2015)

coincide with many authors as *Gardiniet al. (2003)* who found that *Staphylococci* were generally susceptible to beta -lactams, but 12 strains were resistant to methicillin, 8 were resistant to oxacillin, and 9 were resistant to penicillin G.

Archer and Niemeyer (1994) determined that The *S. aureus* had acquired a gene (*mecA*) coding for the altered penicillin-binding protein 2A, allowing the organism to grow in the presence not only of methicillin but also all new β -lactams. While *Strommengeret al. (2006)* confirmed that all isolated *S.aureus* that carrying the *mecA* gene mediated resistance to β -lactam antibiotics.

Few studies were planned for detection of *mecA* among chickens (*Perez-Roth et al., 2001*). In present study 5 from 83 samples were containing *mecA* gene which are lower than that recorded by *Lee (2003)* who found only three (10%) from chickens (6%).

There are also concerns about MRSA as a possible zoonosis. Both human-to-animal and animal-to-human transmission are known to be possible; however, it has not yet been determined whether animals are an important primary source of MRSA infections for humans, or if most animals are colonized after contact with human carriers (*Baptisteet al.,2005; Duquette and Nuttall, 2004;Weeseet al., 2006*). In contrary, some authors conclude that, currently the risk to human health from zoonotic MRSA seems to be very small (*Duquette and Nuttall, 2004*).

the Phylogenetic analysis of *mecA* gene of three *Staphylococcus aureus* isolates with other *staph* isolates based on amino acid sequence showed that all isolates under study clustered together and little away from other published isolates of MRSA, Amino acid identities is 99.5% among the analyzed isolates, The three isolates shared 87.2%-89.2%

identity with other *Staphylococcus aureus* isolates. Nucleotide similarity report of 195 base and amino acid similarity report of 66 amino acids of three isolates with other reference staph isolates showed that Sequenced part of the *mecA* gene showing partial homology to other *Staphylococcus aureus* strains.

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عزل وتصنيف الميكروب المكور العنقودي الذهبي المقاوم للميزيسلن من لحوم ومنتجات الدواجن

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*قسم البكتريولوجيا والفطريات والمناعة كلية الطب البيطري - جامعة كفرالشيخ ، مصر

**المعمل المرجعي للرقابة البيطرية على الإنتاج الداجني ، معهد بحوث صحة الحيوان ، دقي ، جيزة ، مصر

***قسم البكتريولوجيا والفطريات والمناعة كلية الطب البيطري - جامعة كفرالشيخ ، مصر

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من الفحص البكتيري لعدد 500 عينة لحوم ومنتجات الدواجن وعمال المجازر لها من أجل عزل الميكروب العنقودي الذهبي كانت 83 عينة ايجابية للتخثر للميكروب العنقودي الذهبي بنسبة 61.03 % وهذه النسبة الايجابية كانت ممثلة في 55.4% من الدجاج (59.2% ، 30.4% ، 6.5 % من الجلد والعضلات، مسحات المجمع و منتجات الدواجن بالترتيب) وسلبية بنسبة 44.6 % من العاملين المخالطين للحوم الدواجن في المجازر. وقد تم عمل اختبار الحساسية للعينات المعزولة ايجابية للتخثر للميكروب العنقودي الذهبي. ووجد أن معظم المعزولات كانت مقاومة للبنيسيلين و الامبيسيلين وأقل مقاومة كانت ظاهرة للميزيسلن واللاموكساسيلين، اوكساسيلين، ، بينما كل المعزولات كانت حساسة الى الفانكوميسين. على الوجه الاخر اظهرت المعزولات مقاومة متوسطة لكلا من سيفاتركسون، و سيفالوسينواموكساسيلين + كلافيولينك اسيد وباستخدام تفاعل البلمرة المتسلسل تم زيادة جزء من جين *mecA* وزنه الجزيئي 310 bp بعد استخلاص الحامض النووي من العينات الايجابية التجلط للميكروب العنقودي الذهبي المعزولة من عينات الدجاج المختلفة والعاملين المخالطين لها. نتج عن

تفاعل البلمرة المتسلسل 10.9%. (46/5) عينة ايجابية من عينات الجلد والعضلات من عينات الدجاج. بينما العينات ايجابية التخثر للميكروب العنقودي الذهبي المعزولة من مسحات المجمع ومنتجات الدواجن ومن العاملين المخالطين كانت لا تحتوى على جين *mecA*. ويعمل تحليل جيني لثلاثة من هذه المعزولات وإسناد النتائج لعنترات المكورات العنقودية الذهبية المرجعية الموجودة في بنك الجينات وجد انها تتشابه فيما بينها بنسبه 99.5% ونسبة التماثل علي مستوى الأحماض الامينية بين المعزولات الاخري كانت 87.2%.