

Molecular characterization of some virulence genes of *Staphylococcus aureus* isolated from different sources and human.

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Abstract: This study aims to provide information about the genetic structure of *Staphylococcus aureus* strains isolated from (40) samples from humans (mouth, pharynx and hand), (70) samples from poultry and poultry byproducts, (70) samples of milk and milk byproducts. (20) samples of human food. From the collected 200 samples 23 *S. aureus* isolates were identified by morphological, biochemical and molecular methods. Additionally, the strains were screened for virulent genes as (*nuc*, *spa*, *coa*, *icaA*, *Sea*, *Seb*, *Sec*) enterotoxin production. When testing PCR for these group of genes that were identified and searched in 11 isolates showed a positive result for the genes (*nuc*, *spa*, *coa*) in a rate of 100%, except the gene (*Sea*) which had a negative result in all isolates, Where the (*Seb*) gene with a high rate of 100%, while the gene (*Sec*) gave a positive result in (1) isolate with a percentage of (0.09 %). The genes (*icaA*) was positive in all isolates with a rate of (90%) except in the two isolates. the severity of enterotoxin virulence gene in *S. aureus* strains leading to complications to human and animal life, including intestinal poisoning accompanied by diarrhea, nausea, vomition, dehydration and hypotension. Some of these virulent genes resulting in pneumonia, meningitis and septicemia and death

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Keywords: *Staphylococcus aureus*; virulence genes; *nuc*, *spa*, *coa*, *icaA*, *Sea*, *Seb*, *Sec* gene; human, poultry, food and milk.

1. Introduction

Staphylococcus is widely distributed in water, soil and air, in addition to its harmful infection of various animal species and poultry (Goetz et al., 2006). *S. aureus* an important food borne pathogen, a major cause of food poisoning cases and out breaks worldwide (Wang et al., 2012). *Staphylococcus* was firstly detected by a Scottish surgeon Sir Alexander Ogston in 1881. Then, *S. aureus* was also firstly determined by a German scientist Friedrich Julius Rosenbach in 1884 (Khan, et al; 2017). The coagulase-positive *S. aureus* genus inducing infections in humans and animals, specially food intoxication. This genus including the most important species of *S. aureus*, (Betley and Mekalanos, 1988); (Bystroń et al 2005) and (Cremonesi et al; 2007). The genus *Staphylococcus* including 62 species and 30 subspecies based on 16S rRNA sequences (LPSN Bacterio; 2020). Contamination of poultry meat by *Staphylococcus aureus* can be occurred from different retail sites and appliances such as cages, bleeding knife, drum, wooden log, cutting knife, polyethylene

bag, hand swab of butcher, weighing balance, retail outlet wall and retail outlet floor (Vaidye, et al., 2009). El-Nagar et al. (2017) on samples collected from the poultry production chain, the enterotoxin genes (*Seb* and *Sec*) were illustrated in five strains (23.8%) of *S. aureus*, with a percentage of 9.5% for *Seb* and *Sec* while *Sec* was found in six (20.6%) isolates.

Cell proliferation and biofilm formation are known virulence factors mediated by the presence of the *ica* locus, this gene *icaA*, was organized in an operon (*icaA*DBBC) with the regulatory gene *icaR*. This operon is responsible for expression of PIA, present in the cell wall (Cucarella et al., 2004). Biofilm production of *S. aureus* isolated from cases of clinical mastitis and with the presence of *icaA*, in these species was screened by polymerase chain reaction (SalinaF et al., 2020). The Amplification of the mononuclease (*nuc*) gene was carried out by Polymerase Chain Reaction that used for the genotypic characterization of isolated *S. aureus* strains. All tested strains yielded amplification of the

(*nuc*) gene of 270 bp for all examined *S. aureus* isolates (**Abo-Shama, 2014**). The prevalence of *S. aureus* virulence factors such as enterotoxin E (*Sea*) or leukocidin E (*lukE*) was detected that *lukE* may be less common (**Peterson et al., 2019 and Klos et al., 2019**). 12 individual *spa* types identified. t012 (n = 3, 18%) and t021 (n = 3, 18%) were the most commonly identified among this group. Overall, *spa* typing revealed greater diversity among ocular *S. aureus* strains (**William et al., 2021**).

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2-Materials and Methods

Sample collection: -

A total of 200 samples of human samples (40), poultry and poultry byproducts (70), milk and milk byproducts (70) and ready to eat food (20) samples,

were collected aseptically using sterile scissor and forceps in separate sterile plastic bag for each sample. each sample was subjected to bacteriological examination for *S. aureus* isolation (**Sneath et al., 1986**) and (**Monecke et al., 2012**).

Preparation of samples (pre-enrichment):-

The collected samples from (poultry and poultry byproducts, milk and milk byproducts and ready to eat food). Ten grams of each sample were transferred into a flask containing 90 ml of 0.1% sterile peptone water to get a dilution of 10^{-1} , incubate at 37 °C for 24 hrs under aerobic condition.

Bacterial Isolates and culture media:

The samples were collected aseptically for detection of *S. aureus* strains that differentiated into coagulase positive and coagulase negative *Staphylococcus* isolates.

The coagulase positive *Staphylococcus* isolates were identified by conventional methods, including morphological characters as Gram staining, blood haemolysis, catalase, coagulase and anaerobic fermentation of mannitol tests (**Swayne et al., 1998**) and (**Koneman et al., 2001**). All isolated strains were stored on suitable maintenance media in the National Laboratory for Biochemical tests.

Laboratory center for PCR (**Sambrook et al., 2001**) and (**WHO, 2002**):

The stored isolated strains were re-cultivated on brain heart infusion agar plates and broth for an extraction of DNA to be used in PCR technique.

Molecular biology technique (PCR): (**Riffon et al., 2001**)

PCR amplification was performed with PTC-100 programmable thermal cycler (Peltier Effect cycling, MJ, Research, INC, UK) in a volume of 50 ml consisting of: 12.5µl of Emerald Amp GT PCR master mix (2x premix), 1 µl of 20 pmol of each primer for one sample, 6 µl of the DNA template and water, nuclease-free up to 25 µl in uniplex PCR. While, 25µl of Emerald Amp GT PCR master mix (2x premix), 1 µl of 20 pmol of each primer for one sample, 10µl of the DNA template and water, nuclease-free up to 50 µl in PCR. Primer sequence and PCR amplification cycles of oligonucleotide primers among the selected isolates are illustrated.

3-Result:

S.aureus were detected 11.5% as follow 23 from 200 total sam ples were staphylococcus aureus positive samples of poultry products 10 % (7/70) had been examined ,human samples 17.5%(7/40), milk

and milk byproducts 8%(6/70) and ready to eat food 15 %(3/ 20) samples).

Isolation of *S. aureus* from the examined samples:

S. aureus isolates were Gram positive cocci arranged in clusters. They had yellow colonies

surrounded by yellow medium due to mannitol utilization on mannitol salt agar medium (**Figure 1**). The isolates had black shiny convex colonies surrounded by a clear zone extended onto the opaque medium on baired parker agar medium (**Figure 2**).

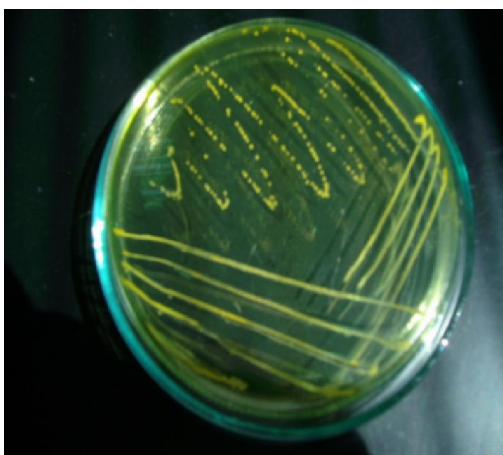


Figure 1: mannitol salt agar showed yellow colonies shiny convex surrounded by yellow medium



Figure 2: Baired parker agar showed black colonies surrounded by a clear zone

Table (4): The prevalence of *S.aureus* strains in the collected samples:-

Sample:	Number of Examined Samples	<i>S. aureus</i> isolation:	
		+ve	%
Poultry and poultry by product	70	7	0.1%
Human	40	7	17.5%
milk and milk by products	70	6	8%
Ready to eat food	20	3	15%
Total:	200	23	11.5%

Table (5): The incidence rates of some virulent genes for the isolated *S. aureus* stains in the collected samples by the using of PCR technique:-

Sample	<i>Nuc</i>	<i>Spa</i>	<i>Coa</i>	<i>icaA</i>	<i>Sea</i>	<i>Seb</i>	<i>Sea</i>
1	+	+	+	+	-	+	-
2	+	+	+	-	-	+	-
3	+	+	+	+	-	+	-
4	+	+	+	+	-	+	-
5	+	+	+	+	-	+	-
6	+	+	+	+	-	+	-
7	+	+	+	+	-	+	-
8	+	+	+	+	-	+	-
9	+	+	+	+	-	+	-
10	+	+	+	+	-	+	+
11	+	+	+	+	-	+	-

Eleven isolates showed a positive result in the following virulent genes (*nuc*, *Spa*, *coa* and *Seb*) with a percentage of 100%. While the gene (*Sea*), had a negative result in all.

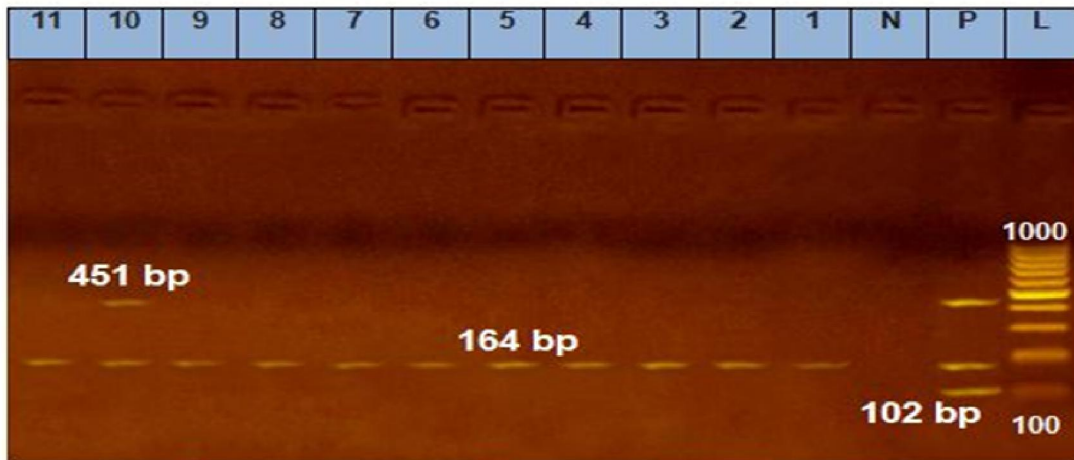


Fig.3. Agarose gel photo documentation for detection of thermo-nuclease toxin Virulence factor encoding genes (*Sea*, *Seb* and *Sec*) of *S. aureus* a genotyping identification of the isolates.

Lane: 100-1000 bp DNA ladder. Pos: **negative** control (at 102 bp).

Lanes 1,2,3,4,5,6,7,8,9,10 and11 *S.aureus* (*Sea*)**gene negative**.

Lane: 100-1000 bp DNA ladder. Pos: **positive** control (at 164 bp).

Lanes 1,2,3,4,5,6,7,8,9,10 and11 *S.aureus* (*Seb*)**gene positive**.

Lane: 100-1000 bp DNA ladder. Pos: **positive** control (at 164 bp).

Lanes 10 *S.aureus* (*Sec*)**gene positive**.

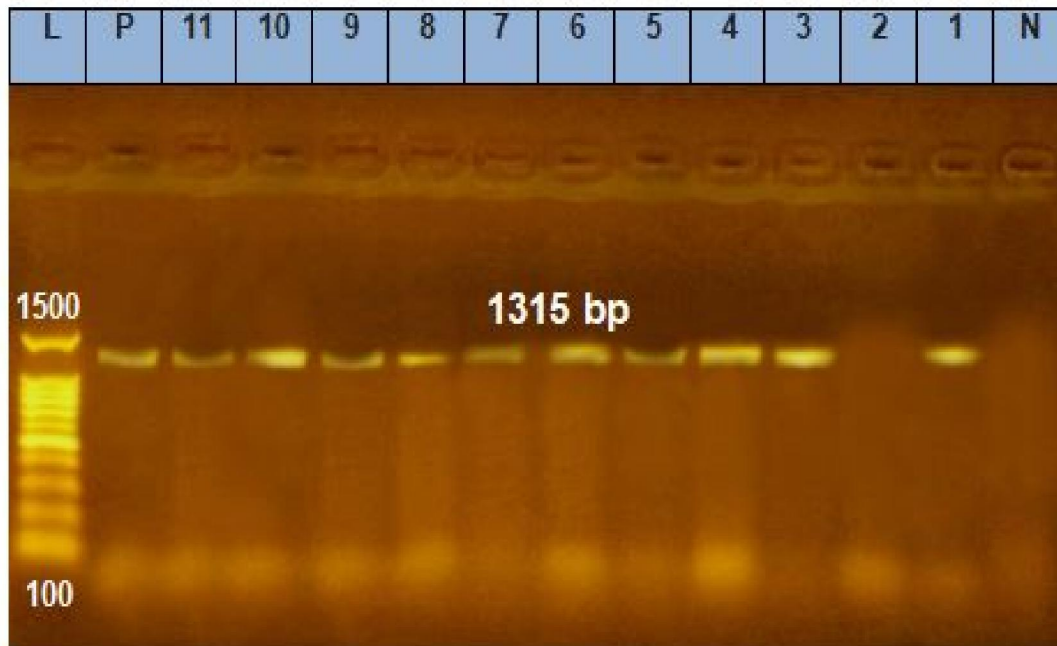


Fig.4. Agarose gel photo documentation for detection virulence factor encoding gene (*icaA*) of *S.aureus* as a genotyping identification of the isolates.

Lane: 100-1500 bp DNA ladder. Pos: **positive** control (at 1315 bp).

Lanes 1,2,3,4,5,6,7,8,9,10 and11 *S.aureus* (*icaA*)**gene positive**.

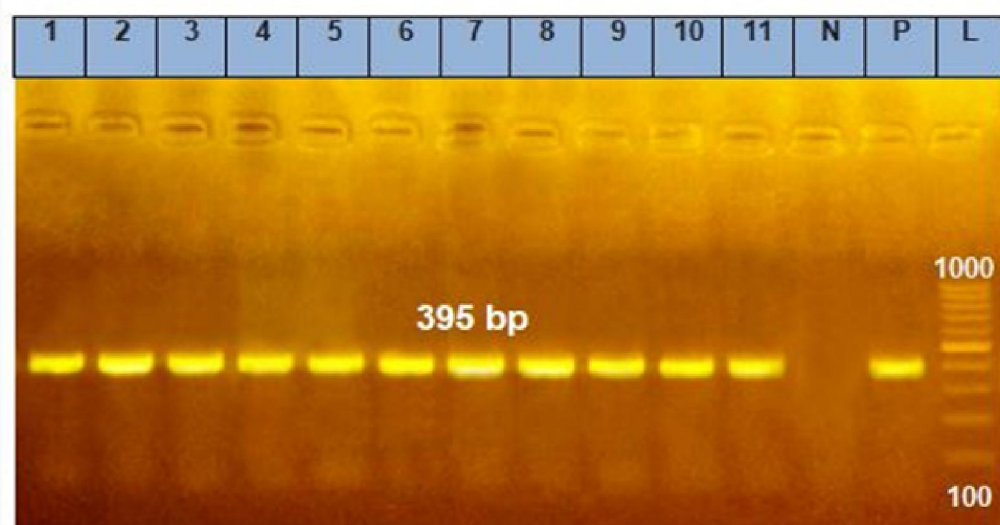


Fig.5. Agarose gel photo documentation for detection of thermo- nuclease toxin Virulence factor encoding gene (*nuc*) of *S.aureus* a genotyping identification of the isolates.

--Lane: 100-1000 bp DNA ladder. -Pos: positive control (at 395 bp).

-Lanes 1,2,3,4,5,6,7,8,9,10 and11 *S.aureus (nuc)gene* positive.

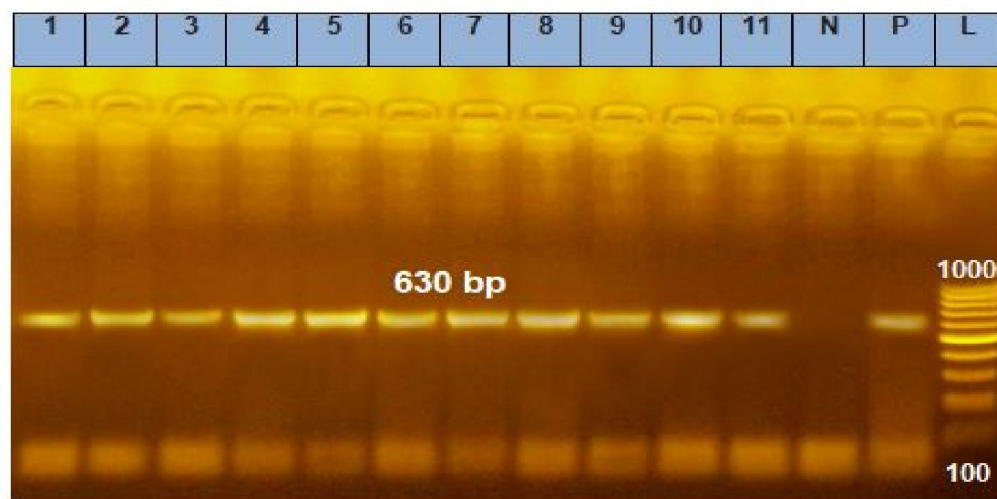


Fig.6. Agarose gel photo documentation for detection of thermo- nuclease toxin Virulence factor encoding gene (*Coa*) of *S.aureus* a genotyping identification of the isolates.

-Lane: 100-1000 bp DNA ladder. -Pos: positive control (at 630 bp). ---

-Lanes 1,2,3,4,5,6,7,8,9,10 and11 *S.aureus (Coa)gene* positive.

4. Discussion:-

To accomplish this study, 200 samples were taken from different sources, where we obtained 23 isolates (10.1%) of *S. aureus*, and this corresponds to some extent with each of reported that only 3 (7.5%) *S. aureus* strains by (Pereira et al; 2018). These results were aggregated. While this result was disaggregated with (Emine Kayili and Pinar Sanlibaba, 2020), as the positive samples of *S. aureus*

was 25.93% in Korea,(Jang et al., 2018) 87.32% in Serbia, (Bulajic et al., 2017) 73.6% in Brazil, (Pereira et al., 2018) 50% in Italy, (Spanu et a., 2012) 45% in Norway, (Mehli et al., 2017) 27.7% in China, (Liu et al; 2017) 50% in Poland, (Rola et al; 2016) and 25% in Iranian, (Arefi et al., 2014).

Eleven isolates showed a positive result in the following virulent genes (*nuc*, *spa*, *coa* and *Seb*) with a percentage of 100%, these results may be due the

collected samples from endemic area with *S.aureus* enterotoxigenic strains and bade hygienic measures. The tabulated results were disagreed with the results of **El-Nagar et al. (2017)** and **(Salina et al., 2021)**. While the virulent gene (*Sea*), had a negative result in all isolates, this is may be due to the competition between the different virulent genes and the low excretion from the *S.aureus* strains. But this corresponds somewhat to **both (Afsaneh Mozafarianari et al., 2019)** who found the gene (*Sea*) at 6%. It does not agree with **El-Nagar et al. (2017)**, **Peterson et al. (2019)** and **Klos et al. (2019)**. Moreover, **(Pourmand et al., 2009)** studied the prevalence of the *Sea* gene of *S. aureus* was 46.9%. Other investigators defined the rate of enterotoxin gene-positive *S. aureus* isolates among the food handler in central Iran and explained that the rate of *Sea* was at food **(Fooladvand et al., 2019)**.

The gene (*icaA*,) were positive in most of the isolates by (90%), and this corresponds to some extent with, **(Aguilar et al., 2001; Azara et al., 2017a)** Percentage (100%). and different with **(Salina et al., 2021)**. Percentage (68%), and The *icaAD* gene was detected in 16(32%) *staphylococcal* isolates **(Rasha et al; 2012)**.

While the gene (*Sec*) gave a positive result in one isolate with a percentage of (0.09%), and this is identical with **(El-Nagar et al. (2017)**

It does not match with **(Argudín et al., 2012)** Where the results showed that the gene (*Sec*) by (%16.1).

The results of these studies are inconsistent with our results. Another researcher screened the *S. aureus* nasal strains to detect toxin genes and showed that 15% and 13% of the genes were *TST* and *Sec*, respectively **(Piechowiec et al., 2011)**. This bacterium might induce allergic inflammatory responses via secreting enterotoxin (*Se*) and could lead to toxic shock syndrome toxin 1 (TSST-1). Humans are the main storage for *S. aureus* in nature. Approximately 30% of healthy people are involved in a bacterium **(Klotz at al., 2003; Ludwig et al., 2019) and Cucarella et al., 2004)**.

Conclusion

PCR assumed to be rapid, sensitive and accurate with the ability to deal with large number of samples for studying of Genotyping characters of virulence factors encoding genes of *S. aureus* that isolated from humans and animals samples. Finally results of antibiotics and sensitivity tests improved the treatment of mastitis and decrease the time and costs of mastitis treatment. Also by the using of PCR technique we determined the rate of virulence genes (*nuc*, *spa*, *coa* and *Seb*) with a percentage of 100%. While the

virulent gene (*Sea*), had a negative result in all isolates.

It is possible to prospectively define potential *S. aureus* virulence factors or other genetic determinants that may inducing infection in specific disease settings, thereby deepening our understanding of this important animal and human pathogen.

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