بسم الله الرحمن الرحيم

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شبكة المعلومات الجامعية

التوثيق الالكتروني والميكروفيلم

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MONA MAGHRABY

شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكروفيلم

جامعة عين شمس

التوثيق الإلكتروني والميكروفيلم

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Studies on Antimicrobial Resistance and Virulence Profiling of *Staphylococcus aureus* Recovered from Milk and its Public Health Impact

A Thesis presented by

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(M.V.Sc., Cairo University, 2015)

For the attainment of the Degree of Doctor of Philosophy
in Veterinary Medical Sciences, Microbiology

Under the Supervision of

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Abstract

Among common listed etiological agents causing contagious bovine mastitis, *Staphylococcus aureus* is topping the list. In addition, they are known to precipitately acquire resistance to accessible antimicrobial agents which in turn upsurge its public health risk and associated consequences. This study investigated *S. aureus* existence in raw milk samples gathered from 103 cows in dairy farms in Egypt, and disclosed its antimicrobial resistance profile, and related virulence/resistance-encoding genes. Conventional laboratory tests as well as the vitek2 compact system were used to determine and screen the isolates. *S. aureus* was isolated from (188) mastitis and (224) sub-clinically mastitis milk samples with an incidence of 50% (n=94) and 17.5% (n=39) respectively. Out of 133 positive *S. aureus* isolates, 69 were randomly selected and subjected to antimicrobial susceptibility testing using a vitek2 compact system whereas they were challenged with a set of 15 antibacterial agents commonly used in the medical and veterinary fields. In addition, 39 isolates were selected randomly and screened for *sea*, *seb*, *sec*, *sed*, and *see* enterotoxin-encoding genes by polymerase chain reaction (PCR). The tested isolates exhibited high resistance to Streptomycin, Penicillin-G, and Oxytetracycline while presented high sensitivity to Gentamycin, Amoxycillin +Clavulinic acid and fluoroquinolone antimicrobials (Enrofloxacin and Ciprofloxacin). According to the antimicrobial sensitivity test results, 8 isolates were selected and experienced further molecular typing techniques (PCR and hybridization) for detection of *S. aureus* virulence genes namely *spa, hlg, coa, tst, nuc, clfA*, as well as resistance genes *blaZ* and *mecA*. *Spa* gene was the most dominant virulence gene identified in the isolates (n=5), followed by coa and hlg (n=4), *nuc* and *clfA* (n=3) and the least detected gene was *tst* (n=2). The *blaZ* gene, that is considered the commonest beta-lactam resistance mechanism for *S. aureus*, was observed in all isolates (n=8/8), while methicillin resistance mediated by *mecA* gene was noticed in 75% of the screened isolates (n=6/8). None of the isolates possessed *sea*, *sec* or *sed*, while *seb* and *see* detected in 13% and 56.5% of the isolates. These results have shown that milk could be a source for transmission of antibiotic resistant *S. aureus* to humans, hence it is representing an escalating potential public health risk and might adversely affect the treatment options offered to human infected with such strains.

Key words: Antimicrobial resistance, Mastitis, Public health, *Staphylococcus aureus*

Dedication

♥ To my mother, my father's soul,

My brothers Ihab and Abdo

My husband, El Sayed

My daughters, Reham & Aya,

And My son, Mohamed ♥

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