

Ministry of Higher Education and Scientific Research
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Bacteriological and Molecular Study of *Staphylococcus aureus* Bacteria Isolated From Women Breast Abscess in Al- Qadisiyah Governorate

A Thesis

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Summary

The study aimed at isolating and diagnosing *Staphylococcus aureus* from breast abscesses in women using some morphological and molecular methods as well as detect some of the virulence factors of the same bacteria. The clinical samples were collected from women with abscesses in the breast and different age groups under the supervision of a specialized medical staff in Al-Diwaniyah Education and maternity hospital and children in the province of Diwaniyah for the period from September 2017 to April 2018, the number of samples was taken from 85 samples ,

Results of biochemical tests, microscopy, Api Staph and MASSTSTAP showed 23 isolates of *S.aureus* bacteria with 27% .

The results of the present study showed that the highest age group with *S.aureus* infection was(21 -30) years (39.3%). The most affected women were Breastfeeding women (29.31%). While the incidence of these bacteria in non- Breastfeeding women is (22.22%), especially non-breast-feeding women with Mastitis and breast cancer (33.3%), It was also the most common infection among women in rural areas (29.1%).

All isolates of *S.aureus* isolates were tested for 18 antibiotics in the manner of proliferation of the tablets. All isolates were resistant to the antibiotics Penicillin, Amoxicillin / Clavulanic acid, 100%, 78.2% Resistant to Cefapodoxime, 43.3% Resistant to azithromycin, 39.1% Resistant to trimethoprim, clindamycin, 34.7% Resistant to Cefepime, 30.4% Resistant to Gentamycin, 13% Resistant to Chloramphenicol, Tobramycin, 8.6% Resistant to Doxycycline, Norfloxacin, 4.3% Antibacterials, Ciprofloxacin, Vancomycin Amikacin, Impenim, while all isolates were sensitive to nitrofurantoin and sulphamethaxazole / trimethoprim and by 100%

All isolates were diagnosed with a *16srRNA* gene (100%), as well as some genes were detected using PCR technique. The results showed that 21 isolates of the *Luks* gene (91.3%) And 20 isolates possessed of the *blaz* gene (86.9%), and isolated one possessing a *eta* gene (4,3%).

DNA sequence sequencing and phylogenetic tree analysis were used for nine samples of *S.aureus* isolates based on the sequence of *16srRNA* gene, which is the diagnostic gene for *S.aureus* bacteria (3 isolates), *blaz* gene (3 isolates) and *Luks* gene (3 isolates) Using the program (MEGA 6). The results of the genetic analysis showed a clear genetic affinity between the local isolates and isolates recorded in the gene bank. The results of the genetic analysis showed the probability of occurrence of Transition substitution mutation in the sequence of gene sequences between the local isolates and the global registered isolates Genes .