

Summary

The current study aims for identifying the genetic patterns of some toxins produced by *Staphylococcus aureus* by isolating the *Staphylococcus aureus* resistant to methicillin and vancomycin antibiotic , Where five hundred and seventy-six (576) nasal swabs are isolated from restaurants workers in Thi-Qar province from February to June, 2018. All samples are subjected to culture on the mannitol salt agar and were subjected to biochemical tests and confirmation diagnosis by Api Staph. Only 50 (8.7 %) isolates of *S. aureus*. All of the isolates show an appearance the phenotypic resistance to methicillin and 13 isolates resistant to vancomycin according to by disk diffusion method .

At the same time, about 5 ml of blood from carriers restaurants workers and 30 blood samples from healthy restaurant workers are also taken for comparison , to measure the flow of the immune cells by Abbott Diagnostic and to measure the level of immunoglobulin A by ELISA .

The results of our study show that the level of immune cells in carriers restaurant workers is within normal levels when compared with healthy restaurant workers. The level of immunoglobulins A, the study shows that there is a significant increase in immunoglobulins A for carriers restaurants workers when compared with healthy restaurants workers (0.295 ± 0.039 vs 0.250 ± 0.014) respectively .

All (50) isolates are subject to molecular detection of the resistance genes of antibiotics , methicillin resistance gene (*mecA*) and vancomycin resistance gene (*vanA*) and also toxin genes , exfoliative toxin gene (*eta*) which responsible of Staphylococcal Scalded Skin Syndrome and enterotoxin gene (*sea*) which responsible of food poisoning . under study using PCR technique. The results show that 38 (76%) isolates are

carrying the *mecA* gene and 3 (26%) isolates carrying gene *vanA*. These three isolates included in 13 isolates which appearance the phenotypic resistance to vancomycin

The number of isolates carrying the *sea* gene is 38 (76%), While the gene (*eta*) is negative a result for this gene.

Using sequencing technique, the sequence of nucleotide bases is defined for one isolate is carries both resistance genes (*mecA*, *vanA*) where the *mecA* gene shows a 100% match while *vanA* shows a 99% match ratio . When compared with standard isolates obtained from NCBI Gen Bank (<http://www.ncbi.nlm.nih.gov>). .

In the end, Multilocus Sequence Typing is tested using the PCR technique for isolates carrying the (*mecA*, *vanA*, *sea*) genes to detect the housekeeping genes (*yqil*, *aroe*, *glpf*, *gmk*, *pta*, *tpi* & *arcc*), and then sequencing method by Sanger dideoxy sequencing for these isolates, where these isolates are discovered , novel strains when compared with MLST- Database.

Twenty-three genes were recorded at the NCBI site with the codes following (MK214488 , MK214489 , MK214467 , MK214468 , MK214469 , MK214470 , MK214471 , MK214472 , MK214473 , MK214474 , MK214475 , MK214476 , MK214477 , MK214478 , MK214479 , MK214480 , MK214481 , MK214482 , MK214483 , MK214484 , MK214485 , MK214486 , MK214487) .