

MOLECULAR EPIDEMIOLOGY AND PRESENCE OF VIRULENCE- ASSOCIATED GENES AMONG *STAPHYLOCOCCUS AUREUS* AND *STAPHYLOCOCCUS EPIDERMIDIS* STRAINS FROM PATIENTS WITH DIABETIC FOOT ULCER: FOCUS ON MRSA AND MRSE STRAINS FROM NEUROPATHIC VS. ISCHEMIC FOOT ULCERS

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The purpose of present study was: (1) to evaluate frequency of virulence genes among *Staphylococcus aureus* (*eta*, *fnbA*, *cna*, *etd*, *edin*) and *Staphylococcus epidermidis* (*atlA*, *icaAB* and IS256 insertion element) strains yielded from diabetic foot ulcer (DFU) patients; (2) to compare gene frequency among strains originating from patients with neuropathic (NFU) vs. ischemic (IFU) foot ulcers and among MRSA vs. MSSA strains; (3) to assess distribution of multi- virulence gene presenting isolates among *S. aureus* strains. Gene analysis showed that *eta* was more often associated with MRSA than MSSA isolates from NFU and with MSSA than MRSA strains from IFU patients ($p < 0.05$). The presence of *eta*, *fnbA* and *edin* genes was more often seen in *S. aureus* strains yielded from ulcer tissue compared to toe web swabs of DFU patients and in strains yielded from ulcer curettage of NFU vs. IFU patients ($p < 0.05$). *S. aureus* isolates originating from NFU were frequently characterized by simultaneous presence of 4 to 5 studied virulence genes. *S. epidermidis*. IS256 insertion factor was significantly more often associated with MRSE than MSSE isolates and its frequency was higher in isolates yielded from ulcer tissue than toe web of DFU patients. It suggest that detection of *eta*, *fnbA* and *edin* genes can be useful to discriminate between invasive and skin colonizing *S. aureus* strains and that IS256 insertion element might be a molecular marker of *S. epidermidis* invasiveness in DFU patients.