

Comparative proteomic analysis of extracellular proteins expressed by various clonal types of *Staphylococcus aureus* and during planktonic growth and biofilm development

ABSTRACT

Staphylococcus aureus is well known for its biofilm formation with rapid emergence of new clones circulating worldwide. The main objectives of the study were (1) to identify possible differences in protein expression among various and closely related clonal types of *S. aureus*, (2) to establish the differences in protein expression in terms of size of protein spots and its intensities between bacteria which are grown statically (biofilm formation) with that of under aeration and agitation, and (3) to compare the differences in protein expression as a function of time (in hours). In this study, we selected six clinical isolates comprising two similar (MRSA-527 and MRSA-524) and four different (MRSA-139, MSSA-12E, MSSA-22d, and MSSA-10E) types identified by *spa* typing, MLST and SCCmec typing. We performed 2D gel migration comparison. Also, two MRSA isolates (527 and 139) were selected to determine quantitative changes in the level of extracellular proteins at different biofilm growth time points of 12, 24, and 48 h. The study was done using a strategy that combines 2-DGE and LC-MS/MS analysis for absolute quantification and identification of the extracellular proteins. The 2DGE revealed that the proteomic profiles for the isolates belonging to the similar *spa*, MLST, and SCCmec types were still quite different. Among the extracellular proteins secreted at different time points of biofilm formation, significant changes in protein expression were observed at 48 h incubation as compared to the exponential growth at 12 h incubation. The main conclusion of the work is that the authors do observe differences among isolates, and growth conditions do influence the protein content at different time points of biofilm formation.

Keyword: Biofilm; Clone types; *S. aureus*; 2DGE; LC-MS/MS