

POSTER PRESENTATION

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Transcriptional and translational analysis of subsequent infection with *Staphylococcus aureus* and *Proteus mirabilis* in *Caenorhabditis elegans*

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Background

Caenorhabditis elegans can be effectively used to study the dynamics of polymicrobial infections. *Proteus mirabilis* as an opportunistic pathogen does not cause death in *C. elegans*. Hence, in the present study, the *C. elegans* was pre infected with the pathogen *Staphylococcus aureus* to make the *C. elegans* immuno compromised to study the effect of *P. mirabilis* in the host.

Methods

This study involved in investigation of impact of subsequent infections at physiological, transcriptional and translational levels using *C. elegans*.

Results

Physiological status of *C. elegans* was analyzed using killing assay, CFU count and CLSM analysis. The mRNA expression analysis indicated the regulation of host specific immune regulatory genes, CUB like proteins (*F08G5.6*), neuropeptide like factors (*nlp-29*) and C type lectin genes (*clec-60* and *clec-87*) during subsequent infections. To study which protein is regulated against subsequent infections, SDS-PAGE analysis was performed using the proteins extracted from *C. elegans* exposed with subsequently infected samples for different time intervals. Results of 1D electrophoresis clearly suggested that subsequently infected samples showed significantly more differentially regulated proteins compared to their respective controls.

Conclusion

The physiological assays and molecular studies demonstrated the vulnerability of a host as an integral event

during *S. aureus* infections that enables the bacteria to suppress the host immune system, which subsequently lead to the opportunistic pathogen *P. mirabilis* to exert its pathogenicity in a host system. Further studies are needed to check the translational status of the host during subsequent infections.

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