Elucidating Host-Pathogen Interactions Based on Post-Translational Modifications Using Proteomics Approaches

Microbes with the capability to survive in the host tissue and efficiently subvert its innate immune responses can cause various health hazards. There is an inherent need to understand microbial infection patterns and mechanisms in order to develop efficient therapeutics. Microbial pathogens display host specificity through a complex network of molecular interactions that aid their survival and propagation. Co-infection states further lead to complications by increasing the microbial burden and risk factors. Quantitative proteomics based approaches and post-translational modification analysis can be efficiently applied to gain an insight into the molecular mechanisms involved. The measurement of the proteome and post-translationally modified proteome dynamics using mass spectrometry, results in a wide array of information, such as significant changes in protein expression, protein abundance, the modification status, the site occupancy level, interactors, functional significance of key players, potential drug targets, etc. This mini review discusses the potential of proteomics to investigate the involvement of post-translational modifications in bacterial pathogenesis and host pathogen interactions.

General information
State: Published
Organisations: Department of Systems Biology, Infection Microbiology, Center for BioProcess Engineering, Novo Nordisk Foundation Center for Biosustainability, Quantitative Phosphor Proteome Analysis of E-Coli, Research Groups, Chalmers University of Technology
Contributors: Ravikumar, V., Jers, C., Mijakovic, I.
Number of pages: 7
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Frontiers in Microbiology
Volume: 6
Article number: 1312
ISSN (Print): 1664-302X
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Web of Science (2017): Impact factor 4.019
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
Web of Science (2016): Impact factor 4.076
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.15 SJR 1.869 SNIP 1.193
Web of Science (2015): Impact factor 4.165
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.76 SJR 1.879 SNIP 1.148
Web of Science (2014): Impact factor 3.989
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.56 SJR 1.776 SNIP 0.949
Web of Science (2013): Impact factor 3.941
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.78 SJR 1.46 SNIP 0.722