

Application of Proteomics in the study of Microbial Physiology: Taking advantage of changes in the microbe's normal functions under stress conditions

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Abstract

Stress conditions cause microorganisms to adjust their normal functions to counter the deleterious effects of the stress. This includes modulating relevant proteins in response to the stress. In our studies, we seek to decipher the message inherent in the picture painted by the network of the modulated proteins, with the aim of understanding the physiology of the bacteria and viruses. For example, under exposure to sub-lethal concentrations of the herbicide, glyphosate, and its breakdown product, amino methyl phosphonic acid (AMPA), *E. coli* upregulated 18 and downregulated 14 proteins under glyphosate stress. Under AMPA stress, the bacterium upregulated 32 and downregulated 8 proteins. *E. faecalis* upregulated 67 and downregulated 16 proteins under glyphosate stress, but upregulated 172 and down-regulated 104 proteins under AMPA stress. For *E. coli*, majority of the regulated proteins under glyphosate and AMPA stress were transport, stress response and nitrate metabolic proteins. Exposure of *Helicobacter hepaticus* under the stress of bile –an antimicrobial agent which is produced in the liver, concentrated in the gallbladder and released into the gut during digestion of fatty foods, resulted in the modulation of different proteins. In bovine, porcine or human bile, the bacterium modulated differently the expression of several virulence determinants including the cytolethal distending toxin (CDT), urease, superoxide dismutase, flagellin and ferritin.

For example, superoxide dismutase was downregulated in the three types of bile; CDT was downregulated in bovine and human bile, but was unaffected by porcine bile; urease was downregulated in bovine bile, upregulated in porcine bile and unaffected in human bile. The data suggested that bile serves as an environmental cue for protein expression by *H. hepaticus*, and may modulate its virulence factors. Genetic modification of organisms, e.g. insertion of unrelated foreign gene into the genome of an organism (transgenesis) also can be considered a type of stress given that the organisms are forced to adapt to the effects of the genetic manipulation. The introduction of the haemagglutinin and nucleoprotein genes of the H1N1 influenza virus into the genome of Modified Vaccinia virus Ankara resulted in the modulation of 32 virus encoded proteins that are involved in various pathways of the virus replication. Overall, application of proteomics in conjunction with other complimentary molecular biology tools, has enabled us to contribute towards understanding the physiology of these organism.

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