

INVITED LECTURE H3

Proteomic analysis of daumone signaling pathway in *Caenorhabditis elegans*

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With the availability of its complete genome sequence and unique biological features relevant to human disease, *C. elegans* has become an invaluable model organism for the studies of proteomics, leading to the elucidation of nematode gene function (Paik et al., 2006, *Expert Rev Proteomics*, 3, 439-453). In an attempt to understand a biology of daumone, which signals worms to enter dauer stage (Jeong et al., 2005, *Nature*, 433, 541-545), we analyzed proteomic profiles of *C. elegans* upon treatment of daumone using various proteomic tools including 2D-LC-MS/MS and DIGE. Our preliminary data showed that there are multi-level changes in protein expression in the area of energy metabolism and oxidative defense system, suggesting that differential changes in various metabolic pathways appear to accommodate this non-aged state. This study was also paralleled by DNA microarray work, resulting in a direct comparison of proteomic and genomic profiles in dauer state. To construct a comprehensive map of proteins involved in daumone and cholesterol signaling pathways, *C. elegans* proteome project (CEPP) has been launched recently. Some progress obtained from the pilot phase of CEPP and a few lessons with respect to data management and functional annotation will also be presented (Supported by BioGreen21 Project).