



KINEXUS

Phosphoproteomics Mass Spectrometry Study Provides Insights into Early Mechanisms of Infection by Salmonella

Over 9500 phosphorylation sites tracked in human cells for regulation by a major bacterial pathogen for human disease

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VANCOUVER, British Columbia – Kinexus Bioinformatics Corporation, a world-leader in molecular intelligence research, announced the publication this week in the journal *Science Signaling* (<http://stke.sciencemag.org/cgi/content/abstract/sigtrans;4/191/rs9>) the results of a major study to investigate the host signalling pathways that are impacted by *Salmonella enterica*, a food-borne bacteria that is a leading cause of food poisoning in North America and around the world. The study was undertaken in collaboration with researchers at the Centre for High Throughput Biology at the University of British Columbia (UBC). Mass spectrometric analyses revealed that more than 24% of 9500 phosphorylation sites tracked in human cells were significantly altered with 20 minutes of *Salmonella* infection. Phosphosites often function as on/off switches to regulate intracellular communication systems and their phosphorylation is catalyzed by protein kinases. Application of Kinexus' Kinase Predictor algorithm for 493 human protein kinases against each of the top *Salmonella* affected phosphosites permitted identification of specific protein kinases that are affected by *Salmonella*, including the proto-oncogene-encoded protein kinase Pim1. Specific inhibition of Pim1 in follow up studies was found to mitigate some of the pathogen effects of this bacteria, and implicated this kinase as a possible target for therapeutic drug intervention.

Over 100,000 human phosphosites in over 14,000 of the 23,000 proteins encoded by the human genome have now been experimentally confirmed. This study has led to the identification of over 6000 previously unknown phosphosites, and these have been posted for open access on the Kinexus PhosphoNET website (<http://www.phosphonet.ca>). Kinexus' bioinformatics programs have led to the prediction and characterization of over 650,000 human phosphosites.

“The mass spectrometry analyses were performed at the Centre for High Throughput Biology at UBC, and the work represents one of the major studies of this kind undertaken to date” commented Dr. Steven Pelech, President and Chief Scientific Officer of Kinexus and a professor in the Department of Medicine at the University of British Columbia. “In combination with the predictive algorithms developed at Kinexus, it is becoming possible to map out the complex architecture of cell signalling networks and identify the sites of action of toxins that are produced by pathogenic viruses and bacteria.”

For 12 years, Kinexus has been a unique provider of proteomics services to academic and industrial laboratories to track protein kinases and their phosphoprotein targets in experimental tissue and cell specimens. The company has developed a diverse panel of microarrays and complementary technologies that can monitor the presence and activity levels of hundreds of kinases and their targets, their interactions, and the effects of promising drug candidates. The application of this knowledge positions Kinexus and its clients for improved disease diagnosis and personalized drug therapies to improve human health.

**For further information, please contact Kinexus Bioinformatics Corporation
toll free at 1-866-KINEXUS or email csutter@kinexus.ca or visit our
website at www.kinexus.ca**