

Comparative phosphoproteomics analysis of synovial fluid proteins in Indian-German osteoarthritis patients

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Osteoarthritis (OA) is a degenerative disease of joints with mechanical abnormalities affecting nearly 151 million individuals worldwide. Recent advancement in the study of post translation modification such as phosphoproteomics is high-throughput and sensitive mass spectroscopy-coupled technique that is providing new opportunities to examine the physiology and pathophysiology of disease state. We used this technique to study the differential phosphoproteomic profiling of synovial fluid samples from Indian and German osteoarthritis (OA) patients. On comparison of differentially expressed protein spots using 2D Delta software, 19 out of 27 spots were found to be significantly different between German and Indian OA patients.

Furthermore, we have identified the associated functions of differentially expressed proteins using Ingenuity Pathway Analysis (IPA), extracellular nature of proteins using Gene ontology (GO) and used STRING 9.0, KEGG and REACTOME pathway databases to study the insight into the links among the identified phosphoproteins. The Kinase specific phosphorylation

sites were predicted using the NetPhosK 1.0 server and biological process study showed metal ion homeostasis and regulation of immune response.

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