Proteins are organic molecules that express the biological information of the genes. C-Jun NH$_2$-terminal kinases (JNKs) are proteins involved in signal transmission within the living cell. JNK activation occurs typically after stress-related stimuli, such as the cell’s exposure to UV radiation and growth factor deprivation. Once activated, the JNKs phosphorylate their substrates mediating a complex biochemical response in the cell. The response consists of changes in DNA transcription as well as in cellular functions including cell migration and apoptosis.

An evolutionary analysis of human JNKs and their substrates was performed to study how the complexity of the JNK pathway has evolved during the evolution and to find possible functional redundancies. For this purpose ten organisms from difference branches of evolution were selected and protein databases were searched to identify and compare proteins homologous to human JNKs and their substrates. An additional effort was made to determine the conservation of the phosphorylation sites of the substrates.

The experimental results of this study suggest that there is a lack of sequence data in the protein databases that affects the analysis of JNKs. Nonetheless, the following observations were concluded: (i) the alpha–beta variance observed in human JNKs becomes increasingly difficult to detect as the evolutionary distance increases, (ii) JNK substrate homologs were found despite the lack of JNK homologs even over long evolutionary distances and (iii) possible phosphorylation sites in JNK substrates can be identified in organisms that are evolutionary close to human.

Keywords: MAPK, JNK, JNK substrate, BLAST, ClustalW, sequence analysis