International Journal of Basic and Applied Biology
Print ISSN: 2349 – 5820; Online ISSN: 2349 – 5839; Volume. 2 No. 2, November 2014. pp. 106

http://www.krishisanskriti.org/ijbab.html

Computational Analysis of unc-51 like Kinase 1 (ULK1) gene and its Association with Autophagy

Rohit Randhawa[1], Manika Sehgal[1], Tiratha Raj Singh[1], Ajay Duseja[2], Harish Changotra[1*]

[1]Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan 1732 34, Himachal Pradesh, India
[2]Department of Hepatology, Postgraduate Institute of Medical Education and Research, Chandigarh 160 012, India.

Abstract : Autophagy is a fundamental eukaryotic process of degradation involving lysosomal machinery for the breakdown of damaged organelles like endoplasmic reticulum, mitochondria etc. into their building blocks to maintain homeostasis. ULK1, a serine/threonine kinase, plays a central role in autophagy pathway and is the functional equivalent of Atg1 complex in yeast. The activity of this complex is known to be regulated via protein-protein interactions and post-translational modifications. Applying *in-silico* analysis we identified evolutionary relationship of ULK1 between the species. A total of 23 TFBS were identified which are distributed throughout ULK1 and nuclear factor (erythroid-derived) 2 (NFE2) is of utmost significance which has already been shown to involve in autophagy pathway and we suggest that this information could be utilized to transform this pathway by modifying interactions of these TFs with ULK1. Here, 83 phosphorylation sites were identified out of which 26 are already known and 57 are new that include one at tyrosine residue which could further be studied for its involvement in ULK1 regulation and hence in autophagy mechanism. Furthermore, protein-protein interactions were also studied for gaining better insight in autophagy pathway. This kind of analysis provides valuable insights in understanding the whole process of autophagy in an extensive manner.