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### The phylogenetic investigation of candidate genes related to type-II diabetes in human and other species

Srijoni Banerjee<sup>1</sup> and T S Vasulu<sup>2</sup>

<sup>1</sup>Indian Institute of Technology, India

<sup>2</sup>Indian Statistical Institute, India

Sequences of some of the candidate genes (e.g., CPE, CDKAL1, GCKR, HSD11B1, IGF2BP2, IRS1, LPIN1, PKLR, TNF, SPPARG) implicated in some of the complex disease such as type II diabetes in man has been compared with other species to investigate phylogenetic affinity. Based on mRNA sequence of these genes of 7 to 8 species, using bioinformatics tools Mega 5, Bioedit, Clustal W, distance matrix was obtained. Phylogenetic trees were obtained by NJ and UPGMA clustering methods. The results of the phylogenetic analyses show that of the species compared: *Xenopus l.*, *Danio r.*, *Macaca m.*, *Homo sapiens s.*, *Rattus n.*, *Mus m.* and *Gallus g.*, *Bostaurus*, both NJ and UPGMA clustering show close affinity between clustering of *Homo sapiens s.* (Man) with *Rattus n.* (Rat), *Mus m.* species for the candidate genes, except in case of Lipin1 gene. The results support the functional similarity of these genes in physiological and biochemical process involving man and mouse/rat. Therefore, in understanding the complex etiology and treatment of the complex disease mouse/rat model is the best laboratory choice for experimentation.

#### Biography

Srijoni Banerjee is working as a Senior Research Fellow in Department of Chemical Engineering, Indian Institute of Technology, Kharagpur, India in the field of Computational Biology. She completed her Master of Technology in Environmental Biotechnology from Jadavpur University. She did Post-graduation diploma in Bioinformatics from National Institute of Electronics and Information Technology, Department of Electronics & Information Technology, Ministry of Communications and Information Technology, Government of India. She also has one international, one national and three conference publication.

[srijoni.ju@gmail.com](mailto:srijoni.ju@gmail.com)