

The Phylogenetic Investigation of Candidate Genes Related to Type II Diabetes in Man and Other Species

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Abstract : Sequences of some of the candidate genes (e.g., CPE, CDKAL1, GCKR, HSD11B1, IGF2BP2, IRS1, LPIN1, PKLR, TNF, PPARG) implicated in some of the complex disease, e.g. 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.*, *Bos taurus*, 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/rate model is the best laboratory choice for experimentation.

Keywords : phylogeny, candidate gene of type-2 diabetes, CPE, CDKAL1, GCKR, HSD11B1, IGF2BP2, IRS1, LPIN1, PKLR, TNF, PPARG

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