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Bioinformatics analysis of patatin-like phospholipase domain containing protein (PNPLA) family members from diverse organisms

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The patatin-like phospholipase domain containing protein (PNPLA) family is a novel family of lipid-metabolizing enzymes with homology to plant lipases. Several members of this family have been shown to play critical roles in human metabolism and disease, particularly PNPLA2 (also known as adipose triglyceride lipase, ATGL) and PNPLA3 (or adiponutrin). PNPLA2 catalyzes the rate-limiting step in triacylyglycerol (TAG) hydrolysis. PNPLA3 is a nutritionally-regulated gene that is strongly associated with hepatic steatosis/injury in humans. At least 9 related PNPLA proteins have been identified in humans and numerous other evolutionarily related proteins have been identified in non-human species. Although several of these proteins have been shown to play critical roles in normal physiology and disease, the regulation, function and physiological relevance of many of these proteins remain largely unknown. A bioinformatics analysis of both protein and DNA sequences belonging to a diverse set of animal and plant species was performed. The aim of the study was to evaluate the similarities and differences in lipid metabolism in plant and animal systems with an emphasis on patatin-domain containing proteins. The comparative biology of patatin-like proteins in plants and animals will provide novel insights in the role of intracellular lipid metabolism and its impact on basic cellular processes that impact normal metabolism and disease in both the kingdoms.

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Identification of candidate lipoxygenase genes using expression data in different disease condition

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Lipoxygenases (LOXs) are a group of iron containing oxidative enzyme which catalyze the insertion of oxygen into polyunsaturated fatty acids such as arachidonic acid and linoleic acid to a variety of eicosanoids and have a major impact on human homeostasis as a secondary signal transducers. These enzymes are classified as 5, 8, 12 and 15-lipoxygenases on the basis of their selectivity to oxygenate fatty acids in a specific position. In this work, an attempt has been made to investigate expression pattern of reported arachidonic lipoxygenase genes at different levels (cell, tissue and disease). Cell line datasets for specific genes were retrieved from Human Expression Atlas and Human Protein Atlas Databases. Further data were analyzed using Cluster tool with centroid clustering method and visualized using Treeview. The *in silico* investigation resulted that ALOX5 and ALOX5AP genes were found highly expressed and up-regulated in different sets of data of tissues (example: Brain, breast, colon, heart, kidney, liver etc.), diseases (viz., brain glioma, skin cuteneous melanoma and thyroid carcinoma). All these *in silico* experiment suggests that out of known LOX members only ALOX5 and ALOX5AP having high expression pattern in different glands (salivary, adrenal, pituitary and prostate gland etc), tissues and tumorogenic disease (glioma, melanoma, carcinoma etc). Based on above it can be concluded that lipoxygenases (ALOX5, ALOX5AP, LOXHD1, ALOX3, ALOX15B, ALOX12 and ALOX12B) are mainly involved in some important diseases like neurodegenerative disorder, inflammation, cancers, cardiovascular, metabolic syndrome and kidney diseases. These identified genes can be used as potential drug target for development of suitable inhibitors for identified diseases.

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