Application of Bioinformatic Integrated Approach in the Identification of Differentially Expressed Genes in Chronic Lymphatic Leukemia

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Background: Chronic Lymphotic Leukemia (CLL) is a form of blood cancer that has a very high prevalence rate amongst grown-up and it is marked with a phenotypic aggregation of CD5+ B lymphocytes. Objective/Methods: In this study, we used bioinformatic approaches in the analysis of microarray gene expression data to investigate biological process responsible for Chronic Lymphatic Leukemia (CLL). Microarray gene expression dataset was retrieved from Gene Expression Omnibus (GEO) database. We carried out Protein-Protein Interaction networks employing STRING. We employed Gene Ontology (GO) and Protein ANalysis THrough Evolutionary Relationships (PANTHER) to explore Molecular functions, biological process and enrichment analysis of pathway. Results: 250 Differentially Expressed Genes (DEGs) were identified, 128 were up regulated while 122 were down regulated. DEGs upregulated were basically involved in chemokine and cytokine signaling pathway, PI3 Kinase pathway, PDGF signaling pathway and CCKR signaling pathway, while down regulated genes were enhanced in pathways such as TGF-beta signaling pathway, Gonadotropin-releasing hormone receptor pathway and the Notch signaling pathway. PPI analysis revealed that there was more interaction among the proteins suggesting it is not a random interaction, indicative of connection as a group. Conclusion: Moreover, we have been able to predict some proteins expressed from these DEGs that can be specifically targeted in the drug design and delivery pipeline of CLL. This study has been able to establish an interaction responsible for the carcinogenesis of CLL which can be explored in gene therapy and as possible drug targets for CLL initiation and progression.