Abstract

Information Technology is moving ahead in the discipline of medicine and empowering the researchers with superior tools and techniques that would yield results of immense utility by identifying the Biomarker. Biomarker plays very major role in disease detection at early stages of its stages and also helpful in knowing the state of treatment and how body is acting or responding to the medication. The integrated and synergistic effect of these two disciplines helps in an improved diagnosis of Diabetic Macro Vascular Complications. In this thesis, the proteins/genes that are responsible for Diabetic Macro Vascular Complications are computationally analyzed using Multiple Sequence Alignment (MSA) to understand the reason of the disorder. The in silico methodology employed in the present study has extracted huge amounts of data from various biological databases available online. Diabetic Macro Vascular Complications like Coronary Artery disease, Diabetic Cardiomyopathy, Perpherial Vascular Disease and Stroke were identified by the thorough analysis of huge data and identifying the proteins that cause these complications. After thorough research and analysis of the data, different proteins surfaced as primarily responsible for Diabetic Macro Vascular Complications. The present study utilizes the online tool ClustalW for analysis and representation of the data. This tool produces a phylogenetic tree and a number of other outputs. The health professionals can effectively apply the results of the present study in understanding the status and severity of the disease at gene level. This study has identified 9 genes/proteins in Coronary Artery disease, 8 genes/proteins in Diabetic Cardiomyopathy and 4 genes/proteins in perpherial Vascular disease and 11 for Stroke. Further research studies in this direction may pave way in discovering preventive and curative aspects of Diabetic Macro Vascular Complications in a holistic way. Identifying the Biomarker helps researchers and doctors in many ways.