Network modeling of gene expression microarray in patients with obesity and relationship with lactobacillus probiotic intake

L. A. Torres-González[1], O. Rodríguez-León[1], V. Alvarado-Carrillo[1] and L. Reyes Escogido[2]

[1]*Universidad Iberoamericana León, Blvd. Jorge Vértiz Campero 1640, Col. Cañada de Alfaro, CP 37238, León, Gto., México,* [2]*Universidad de Guanajuato, 20 de Enero 929, Col.Obregón, CP 37000, León, Gto., México,* *adolfo.torres@leon.uia.mx*

The gene expression through microarray technique is a current topic in the field of nutrigenomics for researching the complex gene networks and relationship with nutrition. DNA Microarrays has been used to quantify and compare gene expression on a large scale and to explore a major subset or all genes of an organism. As a consequence, formal methods and computer tools for the modeling and simulation of gene networks are indispensable. We identified the genes associated to the obesity susceptible to modify their expression level in a profile of microarray data and the possible relationship with some bioactive components present in lactobacillus gasseri probiotic. Using international microarray databases, we analyzed responsible obesity genes and the role of probiotic intake in the gene expression for some specific genes (LEP, LEPR, FTO y PPARγ2) to study the interaction patterns networks between them. In addition, we reviewed the clustering of gene networks by applying the mathematical procedure principal component analysis (PCA) to the gene expression data point by introducing an interaction between neighboring points. The identification and comparison of gene expression levels associated with obesity will help to guide future research work focus on effective treatments for patients with this disease. As well, these networks may help to analyze dietary variables associated with probiotics intake, to prevent health problems like obesity and type 2 diabetes and to obtain evidence of their interaction with certain human genome modules based on their analysis of the expression microarray data. This integrative analysis offers a new conceptual framework that could expand our knowledge of nutrigenomics and some human pathologies.