RegulonDB. THE MOST IMPORTANT DATABASE IN TRANSCRIPTIONAL REGULATORY NETWORK, OPERON ORGANIZATION, AND GROWTH CONDITIONS OF *ESCHERICHIA COLI* K12

Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México (Center of Genomic Sciences, UNAM). Cuernavaca, Morelos; México
* Corresponding author: e-mail: heladia@ccg.unam.mx

RegulonDB is the most important specialized database in transcriptional regulation, operon organization and regulatory network in *Escherichia coli* K12. Currently, it is the largest electronically-encoded database of the regulatory network of any free-living organism. Continuous curation of original scientific literature provides the evidence behind every single object and feature, and it is complemented with computational predictions of promoters, transcription units and DNA binding sites for regulatory proteins across the complete genome. The complex biology of regulation is simplified in a navigation scheme based on three major streams: genes, operons and regulons. Regulatory knowledge is directly available in every navigation step. Displays combine graphic and textual information and are organized allowing different levels of detail and biological context.

Based on the compiled data, we have development some tools which facilitate the use and analysis of its content. These have been associated to RegulonDB such as: GetTools (http://www.ccg.unam.mx/Computational_Genomics/GETools/) to facilitate the comparison with microarray experiments and links to the Regulatory Sequence Analysis (http://embnet.cifn.unam.mx/rsa-tools/), the Genome Browser, a new network graphic display or Network Tool, as well as links to Nebulon, a tool to predict groups of functionally related genes.

We have started expanding the curation beyond transcriptional regulation. In addition, we have been curating different physiological systems, information which will be soon available in RegulonDB. Our main objective is to achieve a complete view of the cell regulatory networks knowledge.