Qin Ma, J Comput Sci Syst Biol 2013, 6:4
http://dx.doi.org/10.4172/0974-7230.S1.002

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference on
Integrative Biology Summit
August 05-07, 2013 Embassy Suites Las Vegas, NV, USA

Computational analyses of transcriptomic data reveal the dynamic organization of the *E. coli* chromosome under different conditions

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The circular chromosome of *E. coli* has been suggested to fold into a collection of sequentially consecutive domains, genes in each of which tend to be co-expressed. It has also been suggested that such domains, forming a partition of the genome, are dynamic with respect to the physiological conditions. However, very little is known about which DNA segments of the *E. coli* genome form these domains and what determines the boundaries of these domain segments. We present a computational model here to partition the circular genome into consecutive segments, theoretically suggestive of the physically folded supercoiled domains, along with a method for predicting such domains under specified conditions. Our model is based on a hypothesis that the genome of *E. coli* is partitioned into a set of folding domains so that the total number of unfoldings of these domains in the folded chromosome is minimized, where a domain is unfolded when a biological pathway, consisting of genes encoded in this DNA segment, is being activated transcriptionally. We have predicted seven distinct sets of such domains along the *E. coli* genome for seven physiological conditions. They are highly stable statistically and generally consistent with the experimental data of DNA binding sites of the nucleoid associated proteins that assist the folding of these domains, as well as genome-scale protein occupancy profiles, hence supporting our proposed model. Our study established for the first time a strong link between a folded *E. coli* chromosomal structure and the encoded biological pathways and their activation frequencies.

Biography

Qin Ma earned his Ph.D. in operational research from Shandong University in 2010 and has been a postdoctoral researcher in bioinformatics since 2011 in Department of Biochemistry and Molecular Biology and Institute of Bioinformatics, University of Georgia. He has published 13 papers in reputed journals, e.g. Nucleic Acids Research, Bioinformatics, Discrete Mathematics, etc. His research interests include dynamic organization of bacterial chromosomes, transcriptional regulation mechanism and motif finding for prokaryotic and biclustering analyses of gene expression data. He is particularly interested in the construction of phylogeny model for cancer evolution.

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