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Dynamic gene network selection through stress modulation: An *E. coli* model

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The shifting trend of functional physiology is decided through cross-talks between regulators and regulated genes; and this delicate balance of gene expression gets further modulated through stresses such as change in redox or availability of nutrients. Any stress and its after effects are carried to next phase in life cycle and tracing back the gene expression signature could suggest the possible mechanism by which cell still manages and compromises physiology to get the optimum performance.

We have created an *E. coli* model, wherein cells were subjected to a short term hydrogen peroxide stress and the cellular performance was studied in optimal recovery media. The gene network which brings the optimum performance was predicted based on the dynamic gene expression data using a priori selected genes and their expression through GFP reporter system. In the second scenario the cells were trained at different nutritional level and then subjected hydrogen peroxide stress. The affected genes were selected through the microarray expression data. The dynamic expression data of selected genes using GFP reporter system have been modeled to understand stress mediated emerging network which helps in decision making.

The study proposes that the cellular performance could be substantially modulated by different regulators and their interactions. The relationship between different regulators dynamically shifts and with that the new interactions emerge with re-defined network rules. Using different qualitative stresses, the study shows how stress specific new regulatory partners and their correlation appears. What emerges out of the above two scenarios is, as and when needed, a genetic functionally active module/clusters that dictates the cell fate.

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