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Bio 320: Molecular Genomics & Proteomics

Fraser Reading Assignment

Evolutionary Rate in the Protein Interaction Network

*Saccharomyces cerevisiae* is used as a simple cellular model to understand more complex cellular functions as well as their protein interaction networks. Protein interaction networks are organizational structures within cells that affect evolution. The connectivity of well-conserved proteins in protein networks negatively correlate with their rate of evolution. Fraser hypothesizes that the greater the protein network interactions, the slower the evolution of the cell. He also hypothesized that the interaction sites of cellular proteins may change by co evolution because interacting proteins evolve at similar rates. This theory was analyzed using genome sequencing based on the belief that orthologs occur as a result of co evolution. Orthologs are different species which share a gene that originated by vertical descent from a single gene of the last common ancestor. The theory of co-evolution as a result of protein network interactions was organized using nematode *C. elegans*. **Figure 1**. shows the relationship between number of protein interactions and the evolutionary rate, as estimated by the evolutionary distance, are compared. The graph shows a negative correlation with the number of protein interactions increasing as the evolutionary rate, estimated by the evolutionary distance, decreases. Co evolution proves to provide species with organism fitness as wells as stronger selection against mutations when a genetic parallel analysis was conducted. **Figure 2**. Incorporates a flow chart of how protein interactions, protein fitness, and other random effects all work to collectively influence the evolutionary rate (K) in species. **Figure 3** further supports the previous figures’ findings, but also suggests that other factors influence the way different cells experience protein evolution. Results of the study convey that co evolution of interacting proteins may be largely responsible for the observed

Wynter 2

similarity in rates of evolution. Correlations between protein interaction, fitness effect, and evolutionary rate may provide a means by which multiple bioinformatics data sets can be quickly cross referenced.