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Discussion

The purpose of this research was to determine the relationship between protein interaction and evolution rates; more specifically it sought to show proteins that are not well conserved and highly connected actually work together by substitution and evolve together. There is data from other research that has shown that well conserved proteins evolve slowly when compared to the evolution rates of other proteins. The researchers hypothesized that evolution rate could be slower because of two distinct reasons. The first is that proteins that are required to have many interactions will have a slower evolution rate because a greater proportion of them are required to function. The second proposed reason is that if a protein is highly involved in an organisms cell cycle, then it is regularly checked for mutations, which means that its sequence has a high probability of being error free, thus reducing the rate of evolution. The hypotheses were tested by a series of throughput tests. The data concluded that the first hypothesis was true; proteins with more interactions evolve slower because large concentrations of the proteins are required for the cell to function properly. This makes a great deal of sense because if the majority of the protein that is being produced is being constantly conserved in interactions, then there is not much time to check for errors and make changes. This is because as soon as it is synthesized, it has to be utilized. Figure 1.exemplifies the results by showing the relationship between the number of protein-protein interactions and the evolutionary distance. Proteins that have a lot of interactions have a shorter distance from the evolutionary to the original ortholog; the graph has a negative slope. Figure 2.shows the two different hypotheses, and disproves the second hypothesis. The second hypothesis can be rejected because a protein’s evolutionary rate is not linked to the fitness of the protein. This shows that even error prone proteins still enable the organism to undergo the multiple series of protein interactions. Figure 3 shows three graphs, A, B, and C. Graph A shows the distribution mean in a protein’s evolutionary rate, and the mean was about 1.3K, which is very low and shows that there has not been much of a change in the evolution of the protein. Graph B shows the fitness effect, the mean was 0.41, which showed the effect of growth rate. Graph C showed the casual model path analysis to compare the fitness effect and the protein interaction with evolutionary rates. The Pathway showed that the evolutionary rate was mediated by the proteins interactions.