Abstract

Proteins are evolving at different rates in same species depending on their intrinsic property. It is a great challenge to explore the actual underlying reason behind the variation of rates of protein evolution. A recent study revealed the importance of the features of the interacting partners, viz., coefficient of functionality and clustering coefficient in controlling the protein evolutionary rates in a protein-protein interaction (PPI) network in yeast. Taking into account the complex forming ability, we found that all the complex forming proteins evolve slower than the non-complex forming proteins irrespective of their localization in the network or the affiliation of their partners. To analyze the role of protein complexes, we divided the subunits of whole yeast protein complex data into core and attachment classes. We observed core protein subunits are the main functional elements, whereas attachment proteins act as modifiers or activators in protein complexes. However, we found that core proteins are evolving at a faster rate than attachment proteins despite their functional importance. Interestingly, our investigation revealed that attachment proteins are present in a higher number of macromolecular complexes than core proteins in yeast. Finally, our results suggest that the observed differences in the rates of protein evolution between core and attachment proteins are due to the differences in protein complex number and expression level. Since, protein complex number plays a crucial role in controlling the rates of protein evolution in the unicellular organism like yeast, we chose the human as a multicellular organism to analyze the role of protein complexes. We observed human disease and non-disease genes were found to evolve with similar rates in the group of housekeeping genes due to their equal expression breadth and similar protein complex number. However, tissue-specific disease genes are evolutionarily conserved due to their higher protein complex number and elevated gene expression level than tissue-specific non-disease genes. Thus, our study reveals that the protein complex forming property is one of the major parameters in controlling the protein evolution in the unicellular as well as the multicellular organism.

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