A view of protein evolution from the perspective of yeast protein-complexes

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Proteins evolve at different rates. The evolutionary rate differences are primarily governed by the protein expression level. However, proteins do not work alone, they form macromolecular-complex(es) or interact with other protein(s) to execute biological function(s). Considering the yeast protein-complexes, we found that the subunits of the protein-complexes are conserved irrespective of the features of their interacting partners. On the basis of the iterative clustering procedure and frequency of occurrence in the macromolecular-complexes, the protein subunits have been categorized as core and attachment. The core protein subunits are the main functional elements, whereas the attachment proteins act as modifiers or activators in protein complexes. Using the yeast protein-complex dataset, we found that core proteins are evolving at a faster rate than attachment proteins despite their functional importance. Interestingly, our investigation revealed that the attachment proteins are present in more protein-complexes than the core proteins. The proteins, which are present in different protein-complexes, have enhanced their expression levels. We also observed that the protein-complex number (defined as the number of protein-complexes in which a protein subunit belongs) and expression level have a stronger negative influence on evolutionary rates. Similarly, in human, the tissue-specific disease genes evolve slower than the non-disease genes due to their higher protein-complex number and elevated expression level. However, in housekeeping disease and non-disease genes were found to evolve with similar rates due to similar protein-complex number. Thus, our study reveals that the protein complex forming property is one of the major parameters in controlling the protein evolution with the expression level.