ABSTRACT

Recently available large-scale genomic data enables us to examine complex interactions among functional components at the system level. For this purpose, protein-protein interaction networks provide a major platform. First, I will present some different architectural rules between yeast and human protein interaction networks, which suggests different driving forces in the evolution of the interaction networks. Second, in the context of the human protein interaction network, I will discuss the regulatory role of microRNAs, a major class of post-transcriptionally regulatory genes in higher eukaryotes. I found a global correlation between protein connectivity and microRNA regulation complexity in the corresponding genes, and that microRNA regulation likely coordinates the behavior of interacting partners.