

Involvement of evolutionary age in transcription factor mediated gene regulatory network

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ABSTRACT

In the era of ever increasing number of genome-available organisms, direct estimation of functionally related genes from genome is a fundamental challenge in bioinformatics. Despite the great efforts to search for genomic features associated with the functional relationships of genes, they are still poorly understood. We have tried to clarify such genomic features in model plant *Arabidopsis thaliana* by using gene coexpression data in ATTED-II (<http://atted.jp>). Gene coexpression, a similarity of gene expression profiles, provides a genome-wide approximation of functional gene relationships at transcriptional regulation level. In comparative analysis between the similarity of genomic features and the strength of gene coexpression, we found that genes having similar CDS length tend to be coexpressed strongly. We also demonstrated that the evolutionary age of structural genes is a key factor in dictating the CDS length variation: the older genes tend to have a longer CDS length. These observations suggest that the basic structure of gene coexpression network is strongly dominated by gene age, namely, it is a multilayered structure consisting of several gene modules created at each evolutionary step. Gene ontology enrichment analysis actually confirmed the evidence for functional compartmentalization of genes along the evolution, that is, the evolutionary older genes possess a central role in cellular activities, whereas the younger genes are likely to participate in lineage- or species-specific phenotypic evolution. We further analyzed the relationship between the evolutionary age of transcription factors and one of their target genes. As a result, it was revealed that each transcription factor preferentially regulate genes of the same evolutionary age. We anticipate our results to be a starting point for understanding the mechanisms underlying cellular systems evolution, and for developing a genome-based gene function prediction method.