IN BRIEF

Gene Expression in Angiosperm Organ Evolution

In 1975, King and Wilson proposed that the phenotypic differences between humans and chimpanzees were predominantly caused by changes in gene expression, rather than changes in protein sequence (King and Wilson, 1975). Over subsequent decades, data supported the importance of expression changes in phenotypic evolution in both animals (Carroll, 2000) and plants (Doebley and Lukens, 1998). The advent of transcriptomics has opened the door to comparisons of expression patterns among species. A recent analysis in mammals revealed that the rates of evolution of gene expression are different in different tissues, lineages, and chromosomes (Brawand et al., 2011). Now, Yang and Wang (pages 71–82, January 2013 issue) have undertaken a similar analysis, finding a correlation across genes in the rates of sequence and gene expression evolution and evidence that genes that are expressed broadly across organs tend to evolve their expression patterns more slowly.

Yang and Wang used available transcriptome data from Arabidopsis thaliana, rice (Oryza sativa), and maize (Zea mays) in combination with alignments of orthologous proteins from the three species to generate a set of interspecific tissue expression data, which were then grouped into seven organs that are believed to be homologous across the three species. They built a neighbor-joining tree based on expression profiles in those organs of the three species (see figure). In this type of tree, the branch length is indicative of the degree of expression divergence; shorter branches were found for vegetative tissues, whereas reproductive tissues had longer branches, pointing to a higher rate of expression evolution in the latter.

This work provides evidence that correlated changes in both sequence and expression divergence are important in organ evolution, similar to what has been previously found for animals. In animals, male reproductive tissue (i.e., testis) was reported to be rapidly evolving due to positive selection (Brawand et al., 2011). By contrast, Yang and Wang found that whereas stamen tissue was evolving rapidly in angiosperms, it was likely due to relaxed functional constraint rather than positive selection.

Functional constraint refers to selective pressure against changes in a sequence due to the importance of the function of that molecule in various tissues. Yang and Wang developed a measure they called expression-based functional constraint based on information from coregulated genes in their data set. This expression-based functional constraint value incorporates ideas that have been proposed in models for gene expression evolution (Khaitovich et al., 2005; Gu and Su, 2007) and is potentially useful for examining a gene’s evolution with regard to its function.

Overall, this work from Yang and Wang serves as a demonstration of what types of information can be gleaned from comparative expression analysis.

Nancy R. Hofmann
Science Editor
nhofmann@aspb.org

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Gene Expression in Angiosperm Organ Evolution
Nancy R. Hofmann
Plant Cell 2013;25;357; originally published online February 12, 2013;
DOI 10.1105/tpc.113.250210

This information is current as of September 20, 2017

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