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Eukaryotic transcription factors

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Abstract

A comparative study based on four fully sequenced eukaryotic genomes has revealed profound differences in the sets of transcription factors used by plants, fungi and animals.

Significance and context

The recent completion of the *Arabidopsis thaliana* genome sequence allowed the first prediction of a full plant proteome. With the completed genome sequences of *Saccharomyces cerevisiae* (budding yeast), *Caenorhabditis elegans* and *Drosophila melanogaster*, complete proteomes from representatives of three eukaryotic kingdoms (plants, fungi and animals) are now available for comprehensive comparative studies. Using a list of protein sequences, domains and motifs from known transcription factors, Riechmann *et al.* determined the entire complement of these regulators encoded by all four genomes. Both similarities and profound differences were revealed between the sets of transcription factors utilized by representatives of each eukaryotic kingdom. Given that transcription factors act as central regulators of a diversity of developmental and physiological processes, such differences may partly account for the evolutionary distance between these entirely different life forms.

Key results

Within the *Arabidopsis* genome, 1,533 genes were found to encode members of known transcription factor families, 45% of which are from families specific for plants. The fraction of transcription factor genes among all genes is slightly higher in *Arabidopsis* (5.9%) compared with *Drosophila*, *C. elegans* and yeast (4.5, 3.5 and 3.5%, respectively). A variety of prominent transcription factor families are present in all four species, including Myb, basic helix-loop-helix, basic leucine zipper, C2H2 zinc finger and homeodomain transcription factors. Except for the conserved DNA-binding domains, however, there are no significant similarities between members of the same transcription factor family from different kingdoms.

Three types of evolutionary process appear to be mainly responsible for the observed differences in transcription factor complements: the generation of completely novel families; the specific amplification of families common to all three eukaryotic kingdoms; and domain shuffling, leading to new combinations of common transcription factor domains. As well as several small families, the large

families of AP2/EREBP, NAC and WRKY transcription factors, consisting of 144, 109 and 72 members, respectively, are found exclusively in plants. In contrast, nuclear hormone receptors and GAL4-like C6 zinc finger proteins, which are strongly represented in animals and yeast, respectively, appear to be absent from plants. In plants, the Myb superfamily is strongly amplified, comprising 190 members. These regulators, which constitute the largest class of plant transcription factors, are only weakly represented in the other eukaryotic kingdoms. Exon shuffling has led to transcription factors unique to plants that contain both homeodomains and leucine zippers. In addition to these HD-ZIP proteins, leucine zippers can be found in the plant-specific WRKY factors as well as in basic leucine zippers, which are present in all three eukaryotic kingdoms.

Links

[Supplementary data to *Science* 2000, 290:2105-2110](#) are freely available.

Reporter's comments

As the authors point out, the function of approximately 40-50% of the proteins encoded by each genome cannot be determined on the basis of similarities to proteins of known function. The number of proteins that constitute functional transcription factors may therefore be higher than that reported in this paper. Nonetheless, this study reveals striking differences in the regulatory machineries utilized by three different eukaryotic kingdoms. In particular, the existence of a great variety of transcription factors that are unique to distinct kingdoms, such as the large plant-specific AP2/EREBP and WRKY families and the animal-specific nuclear hormone receptors, reflects the need for specific solutions that meet the regulatory challenges connected with entirely different developmental programs and life styles.

Table of links

[Science](#)

[Supplementary data to *Science* 2000, 290:2105-2110](#)

References

1. Riechmann , Heard J, Martin G, Reuber L, Jiang CZ, Keddie J, Adam L, Pineda O, Ratcliffe OJ, Samaha RR, et al: *Arabidopsis* transcription factors: genome-wide comparative analysis among eukaryotes. Science. 2000, 290: 2105-2110. 0036-8075