

Comparison of TATA-variant in higher plant genomes

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Background

The TATA-box is a regulatory element involved in the Transcription Initiation Complex (TIC) formation and is conserved through the evolution at a strict location in promoters [1]. Some TATA-variants are also TIC binding sequences [2]. Nevertheless, few studies have been dedicated to their sequences and functions. We assume that the more TATA-variants share features with the TATA-box, the more they may be recently diverged motifs. We propose to identify, characterize and compare TATA-variants, in order to investigate their putative evolutionary links with the canonical TATA-box.

Materials and Methods

In plants, a description at the genomic level of the promoter architecture is possible for both *A. thaliana* and *O. sativa* due to the large availability of transcripts. We developed an *ab-initio* approach using the preferential location of motifs to identify biologically relevant regulatory elements[3].

Results

We identified TATA-variants conserved between *A.thaliana* and *O.sativa* and exhibiting the TATA-box topological constraints. Only some of the possible TATA-box substitutions are observed in the variants and thus have been conserved. A third of the plant genes contain a TATA-box or a TATA-variant. Feature analysis of gene sub-sets containing one of these motifs led to a functional TATA-variant classification. While some containing-variant gene sets are highly divergent in expression, function, gene and promoter structures from the TATA-box containing genes, other are close.

Conclusions

Our results might be indicative of the TATA-box expected region adaptation. With few mutations the region could promote rapid changes in expression of functionally diversified duplicate genes. We plan to combine this analysis to a global proximal promoter analysis in order to investigate the question of a functional link between regulatory elements specifically organized in promoters.

References

1. Patikoglou GA, Kim JL, Sun L, Yang SH, Kodadek T, Burley SK: **TATA element recognition by the TATA box-binding protein has been conserved throughout evolution.** *Genes Dev* 1999, **13**(24):3217-3230.
2. Singer VL, Wobbe CR, Struhl K: **A wide variety of DNA sequences can functionally replace a yeast TATA element for transcriptional activation.** *Genes Dev* 1990, **4**(4):636-645.
3. Bernard V, Brunaud V, Serizet C, Martin-Magniette ML, Caboche M, Aubourg S, Lechardy A: **Sélection de motifs candidats pour la régulation des gènes chez *Arabidopsis thaliana* sur des critères topologiques.** In: *Journée Ouvertes de la Bioinformatique et des Mathématiques: July 2006; Bordeaux*; 2006: 17-28.